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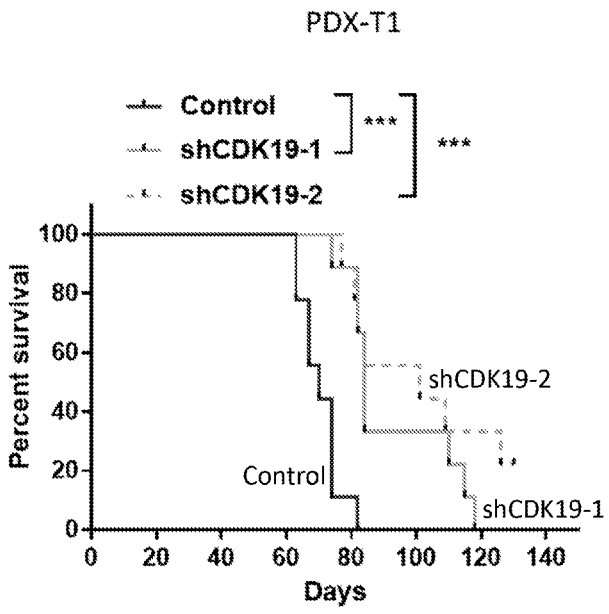
FIG. 4E



(57) Abstract: The invention is directed to methods of treating TNBC in a patient by administering to the patient an agent that inhibits the expression or activity of cyclin-dependent kinase 19 (CDK19). In some embodiments, the agent may be a small molecule inhibitor, a polynucleotide (e.g., shRNA. siRNA), or a protein (e.g., an antibody). In some embodiments, the agent does not inhibit the activity or expression of CDK8.

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[Continued on next page]

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METHODS FOR TREATING TRIPLE-NEGATIVE BREAST CANCER

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present patent application claims benefit of priority to U.S. Provisional Patent Application No.: 62/560,140, filed September 18, 2017, which is incorporated by reference in its entirety for all purposes.

FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

[0002] Work described in this specification was supported by NIH/NCI 5R01 CA100225, Department of Defense grant W81XWH-11-1-0287, Department of Defense/Breast Cancer Research Program (BCRP) Innovator Award W81XWH-13-1-0281 and NIH S10 Share Instrument Grant (1S10RR02933801).

FIELD OF THE INVENTION

[0003] The invention relates to the field of biomedicine, *e.g.*, oncology.

BACKGROUND

[0004] Triple-negative breast cancer (TNBC) is an aggressive breast cancer subtype disproportionately affecting younger women and associated with poor prognoses. See Bauer et al. "Descriptive analysis of estrogen receptor (ER)-negative, progesterone receptor (PR)-negative, and HER2-negative invasive breast cancer, the so-called triple-negative phenotype: a population-based study from the California cancer Registry" *Cancer* 109, 1721-1728, doi:10.1002/cncr.22618 (2007). Despite affecting 20% of all breast cancer patients, there are currently no clinically approved targeted therapies for these patients. There exists a need in the art for effective methods of treating TNBC.

SUMMARY

[0005] The invention is directed to methods of treating TNBC in a patient by administering to the patient an agent that inhibits the expression or activity of cyclin-dependent kinase 19 (CDK19).

[0006] In one aspect, the invention features a method of treating a patient diagnosed with triple-negative breast cancer (TNBC) by administering a therapeutically effective dose of an agent that inhibits expression or activity of cyclin-dependent kinase 19 (CDK19) and achieves at least one of a reduction in cachexia, increase in survival time, elongation in time to tumor progression, reduction in tumor mass, reduction in tumor burden and/or a prolongation in time to tumor metastasis, time to tumor recurrence, tumor response, complete response, partial response, stable disease, progressive disease, or progression free survival.

[0007] In another aspect, the invention features a method of treating a patient diagnosed with triple-negative breast cancer (TNBC), wherein the cancer is characterized by a tumor comprising $EpCAM^{med/high}/CD10^{-/low}$ epithelial cells. The method includes administering a therapeutically effective dose of an agent that inhibits cyclin-dependent kinase 19 (CDK19) expression or activity, wherein the treatment reduces the number of $EpCAM^{med/high}/CD10^{-/low}$ cells in the tumor, reduces to number of $EpCAM^{med/high}/CD10^{-/low}$ cells per unit volume of the tumor, or results in a reduction of the ratio of $EpCAM^{med/high}/CD10^{-/low}$ epithelial cells to normal ($EpCam^{Hi}/CD10^{-}$) epithelial cells in the tumor.

[0008] In yet another aspect, the invention features a method of reducing metastasis of TNBC in a patient by administering a therapeutically effective dose of an agent that inhibits expression or activity of CDK19.

[0009] In some embodiments of all aspects of the invention described herein, the patient is treated with a combination therapy comprising (a) an agent that inhibits expression or activity of CDK19 and (b) radiation therapy and/or chemotherapy.

[0010] In some embodiments, the method comprises detecting $EpCAM^{med/high}/CD10^{-/low}$ cells in a tissue sample from the patient prior to or after initiating therapy.

[0011] In some embodiments, the agent administered to the patient in the methods described herein does not significantly inhibit expression or activity of CDK8. In some embodiments, the agent inhibits expression or activity of CDK19 to a greater extent than it inhibits expression or activity of CDK8.

[0012] In some embodiments of the methods describe herein, the agent is a nucleic acid. In some embodiments, the agent is a protein. In some embodiments, the agent is a CRISPR/Cas9 system.

[0013] In some embodiments of the methods describe herein, the agent is a CDK19 targeting shRNA.

[0014] In some embodiments of the methods describe herein, the agent is a CDK19 targeting siRNA.

[0015] In some embodiments of the methods describe herein, the agent is a CDK19 targeting shRNA or siRNA complementary or substantially complementary to the 3' UTR of CDK19, but not to the 3'UTR CDK8.

[0016] In some embodiments of the methods describe herein, the agent is a CDK19 targeting shRNA or siRNA complementary or substantially complementary to the coding region of CDK19, but not to the coding region of CDK8.

[0017] In some embodiments of the methods describe herein, the agent is a CDK19 targeting shRNA or siRNA selected from: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, or SEQ ID NO: 11.

[0018] In some embodiments, the agent binds CDK19 in the cytoplasm of a breast epithelial cell.

[0019] In another aspect, the invention also features a method of predicting the likely therapeutic responsiveness of a subject with TNBC to a CDK19 targeting agent. The method includes (a) quantitating $EpCAM^{med/high}/CD10^{-/low}$ cells in a tumor sample obtained from the subject; (b) comparing the quantity of $EpCAM^{med/high}/CD10^{-/low}$ cells in (a) to a reference value characteristic of tumors responsive to a CDK19 targeting therapy, and treating the patient with the CDK19 targeting agent if the quantity of $EpCAM^{med/high}/CD10^{-/low}$ cells is equal to or exceeds the reference value. In some embodiments, the CDK19 targeting agent is an inhibitor of CDK19 expression or activity

BRIEF DESCRIPTION OF THE DRAWINGS

[0020] FIG. 1A is a schematic for RNAi dropout viability screens. Two separate screens were performed in a TNBC PDX (PDX-T1). Cells in one experiment were grown *in vitro* as organoid colonies and in the other *in vivo* as PDXs in NSG mice.

[0021] FIGS. 1B-1D are graphs showing that *CDK19* knockdown significantly decreased the viability of TNBC cells (FIG. 1B: MDA-MB231 cells; FIG. 1C: MDA-MB468 cells; and FIG. 1D: HS578T cells) assessed 4 days after transduction with control shRNA or *CDK19* targeting shRNA (shCDK19-1, shCDK19-2).

[0022] FIG. 1E is a graph showing that *CDK19* knockdown significantly decreased the formation of organoid colonies in PDX-T1.

[0023] FIG. 1F is a graph showing that *CDK19* knockdown does not decrease the viability of non-transformed human mammary epithelial cells (HMEC).

[0024] FIGS. 1G-1J are graphs showing that *CDK19* knockdown significantly inhibits the proliferation of PDX tumors (FIG. 1G: PDX-T1; FIG. 1H: PDX-T2; FIG. 1I: PDX-T3; and FIG. 1J: PDX-T4) grown in NSG mice.

[0025] FIGS. 1K and 1L are bar graphs showing that *CDK19* knockdown prevented transduced (RFP positive) TNBC cells (FIG. 1K: PDX-T1 and FIG. 1L PDX-T4) from metastasizing to the lungs in mice.

[0026] FIG. 1M shows that in PDX tumors transduced with *CDK19* shRNA (images in the second and third rows), very little RFP (images in the last column) is visible. These tumors are composed primarily of un-transduced GFP positive tumor cells (images in the middle column). PDX tumor cells were first labeled with green fluorescent protein (GFP) (middle column) and cells subsequently infected with either *CDK19* shRNA or control shRNA were additionally labeled with red fluorescent protein (RFP) (right column).

[0027] FIG. 1N shows representative images of mouse lungs with PDX-T1 metastases. Lungs from mice with PDXs transduced with control shRNA (top row), shCDK19-1 (middle row) or shCDK19-2 (bottom row) are shown. In PDX-T1, which normally metastasizes to the lung, *CDK19* knockdown eliminated the detection of any lung metastases by those cells. Bright field images (left column) show gross lung morphology, FITC images (middle column) identify metastatic tumor cells labeled with GFP, and metastatic tumor cells subsequently infected

with either *CDK19* shRNA or control shRNA were additionally labeled with red fluorescent protein (RFP) (right column).

[0028] FIG. 2A shows data from representative flow cytometry analyses of a TNBC (PDX-T1) using EpCAM and CD49f (left) or EpCAM and CD10 (right) as cell surface markers.

[0029] FIG. 2B is a graph that compares the organoid colony forming capabilities of the $EpCAM^{med/high}/CD10^{-/low}$ and $EPCAM^{low/med}/CD10^{low/+}$ cell sub-populations.

[0030] FIG. 2C is a table showing the number of tumors formed and the number of injections performed for six groups of PDX tumor cells. Populations and injections where tumors formed are bolded. PDX tumor cells were isolated by flow cytometry based on the expression of EpCAM and CD10 (as in FIG. 2A, right)

[0031] FIGS. 2D-2G are bar graphs showing that *CDK19* expression is higher in the $EpCAM^{med/high}/CD10^{-/low}$ cells compared to the $EPCAM^{low/med}/CD10^{low/+}$ cells in PDX-T1, PDX-T2, and PDX-T8.

[0032] FIG. 3A includes Venn diagrams showing the number of genes upregulated (upper diagram) and downregulated (lower diagram) by *CDK19* knockdown, *CDK8* knockdown, or by both *CDK19* and *CDK8* (overlap region).

[0033] FIG. 3B is a Venn diagram of Hallmark gene sets enriched across the genes upregulated (upper diagram) or downregulated (lower diagram) by *CDK19* knockdown, *CDK8* knockdown, or by both *CDK19* and *CDK8* knockdowns (overlap region) as determined by GSEA.

[0034] FIGS. 3C and 3D are graphs showing that CHIP-Seq signals across the CDK19KD-H3K27AcUP and CDK19KD-H3K27AcDOWN regions are significantly different in the *CDK19* knockdown samples compared to control.

[0035] FIGS. 3E and 3F are graphs showing a gene set enrichment analysis (GSEA) of CDK19KD-EnhancerUP and CDK19KD-EnhancerDOWN genes using averaged *CDK19* knockdown versus control expression data.

[0036] FIG. 3G is a graph showing the hallmark gene sets identified as enriched in Metascape analysis of the CDK19KD-EnhancerUP 'core' genes (top and middle bars) and CDK19KD-EnhancerDOWN 'core' (bottom bar) genes. The individual genes contributing to the enrichment of each hallmark gene set are shown to the right of each bar.

[0037] FIGS. 4A and 4B are graphs showing that in inducCDK19KD-PDX-T1 cells, induction of *CDK19* shRNA by addition of doxycycline significantly decreased the number of organoid colonies in the doxycycline treatment group compared to control. Number of organoid colonies at Day 0 (FIG. 4A) and Day 16 (FIG. 4B) after initiating doxycycline treatment is shown.

[0038] FIGS. 4C and 4D are graphs showing that the induction of *CDK19* shRNA in pre-established tumors impaired tumor growth. The growth of pre-established tumors in the doxycycline fed NSG mice and control NSG mice are shown for inducCDK19KD-PDX-T1 (FIG. 4C) and inducCDK19KD-PDX-T3 (FIG. 4D).

[0039] FIG. 4E is a graph showing that *CDK19* knockdown extends the survival of NSG mice with PDX-T1 tumors.

[0040] FIG. 4F shows the chemical structure of CCT251921, an orally bioavailable selective inhibitor of CDK19 and CDK8.

[0041] FIG. 4G is a graph showing that the treatment of mice with CCT251921 by daily oral gavage significantly impaired the growth of pre-established PDX-T1 xenograft tumors.

[0042] FIGS. 5A and 5B are graphs showing the shRNA counts in the *in vivo* growth experimental sample versus the shRNA counts in the baseline sample (FIG. 5A) and the shRNA counts in the *in vitro* growth experimental sample versus the shRNA counts in the baseline sample (FIG. 5B).

[0043] FIG. 5C is a schematic of the criteria used to narrow the initial list of hits from the *in vitro* and the *in vivo* screens down to 46 candidate genes.

[0044] FIG. 5D is a list of 46 candidate genes determined from the *in vitro* and the *in vivo* screens after filtering with the criteria shown in FIG. 5C. *CDK19* is boxed.

[0045] FIG. 6A is a bar graph showing that TCGA breast cancer samples from patients with the TNBC subtype are enriched in *CDK19* copy number amplifications or *CDK19* mRNA upregulation compared to other subtypes.

[0046] FIG. 6B includes confocal immunofluorescent images of PDX-T1 stained with cytokeratin 8 (CK8) antibodies (first image from the left), CDK19 antibodies (second image), and DAPI (third image). The composite image composed from all three aforementioned images is shown on the far right (images are representative of three independent experiments).

[0047] FIGS. 7A and 7B are bar graphs showing that *CDK19* targeting shRNA effectively silences *CDK19* in TNBC cells lines. Expression of *CDK19* in MDA-MB231 (FIG. 7A) or MDA-MB468 (FIG. 7B) determined by RT-qPCR for cells transduced with control shRNA, shCDK19-1, and shCDK19-2.

[0048] FIG. 7C is a bar graph showing that *CDK19* targeting shRNA effectively silences *CDK19* in a TNBC PDX. Expression of *CDK19* in PDX-T1 as determined by RT-qPCR for cells transduced with control shRNA, shCDK19-1, and shCDK19-2.

[0049] FIG. 7D includes images of tissue samples and representative images of mouse lungs bearing PDX-T4 metastases. Lungs from mice with PDXs transduced with control shRNA (top row), shCDK19-1 (middle row), or shCDK19-2 (bottom row) are shown. Bright field images (left column) show gross lung morphology, FITC images (middle column) identify metastatic tumor cells labeled with GFP, and Texas-Red images (right column) identify shRNA-transduced metastatic cells labeled with RFP.

[0050] FIG. 8A is a graph showing the flow cytometry analyses of TNBC (PDX-T1) using EpCAM and CD49f and the overlap of the $EpCAM^{med/high}/CD10^{-/low}$ (1), $EPCAM^{low/med}/CD10^{low/+}$ (3) and $EpCAM^{-}/CD10^{-}$ ((2)) sub-populations.

[0051] FIG. 8B is a bar graph showing that the induction of *CDK19* shRNA with doxycycline effectively silences *CDK19* in inducCDK19KD-PDX-T1 cells. Expression of *CDK19* in control inducCDK19KD-PDX-T1 cells (black bar) and doxycycline treated inducCDK19KD-PDX-T1 cells (gray bar) as determined by RT-qPCR.

[0052] FIG. 8C shows that *CDK19* knockdown effectively prevents the growth of xenograft tumors in a limiting dilution assay.

[0053] FIG. 8D is a graph showing ELDA (Hu et al., *Journal of Immunol. Methods* **347:**70-78, 2009) analysis of the data from FIG. 8C to determine tumor initiating frequencies in the doxycycline (Group +Dox) and control groups (Group NoDox). P-values as determined by the ELDA software.

[0054] FIG. 9 shows the amino acid sequence alignment showing 84% sequence homology between CDK19 and CDK8. Amino acid positions are shown above the sequence. Alignment is performed using Clustal W method with MegAlign (DNAStar).

[0055] FIG. 10 is a table showing hallmark gene sets found enriched by GSEA of the genes upregulated or downregulated by either *CDK19* knockdown or *CDK8* knockdown.

[0056] FIG. 11 is a graph showing that genome-wide H3K27Ac CHIP-Seq signals across all identified H3K27Ac peak regions are not significantly different between the *CDK19* knockdown, *CDK8* knockdown, and control samples. Aggregate plots of normalized H3K27Ac CHIP-Seq signals across all H3K27Ac peak regions in the *CDK19* knockdown (1), *CDK8* knockdown (2) and control (3) samples (ns is $P > 0.05$, all samples n = 3, experiments performed three times).

[0057] FIGS. 12A and 12B show heat map of the expression of CDK19KD-EnhancerUP 'core' genes (FIG. 12A) and CDK19KD-EnhancerDOWN 'core' genes (FIG. 12B). Normalized expression of each gene in each biological replicate of the *CDK19* knockdown and Control samples are shown.

[0058] FIGS. 13A-13D are graphs showing representative genes where *CDK19* knockdown leads to changes in H3K27Ac signals and corresponding changes in gene expression. Representative gene tracks depicting H3K27Ac signals at the loci of select CDK19KD-EnhancerUP 'core' (FIGS. 13A and 13B) and CDK19KD-EnhancerDOWN 'core' genes (FIGS. 13C and 13D).

[0059] FIG. 13E is a heat map of the normalized gene expression of *ELF3*, *ETV7*, *CHI3L2,* and *CRTAM* across each of the three biological replicates in control and *CDK19* knockdown samples.

[0060] FIGS. 14A and 14B are graphs showing that total body weights of mice were not significantly different between the mice fed doxycycline rodent feed (doxycycline group) compared to the mice fed standard rodent feed (control group) in the inducCDK19KD-PDX-T1 (mean ± s.d., n = 5, experiments performed twice) (FIG. 14A) and inducCDK19KD-PDX-T3 (mean ± s.d., n = 5, experiment performed once) (FIG. 14B) tumor experiments.

[0061] FIG. 14C is a graph showing that total body weights of mice were not significantly different between the mice receiving oral gavage with CCT251921 compared to Vehicle (mean ± s.d., n = 5, experiment performed once).

[0062] FIG. 15 is a table showing the pathological features and patient information for the patient derived xenograft tumors used in the experiments.

[0063] FIGS. 16A-16D show a nucleic acid alignment of the 3' UTR of CDK8 and CDK19. The underlined and bolded text indicates the overlapping regions.

[0064] FIG. 17 shows a nucleic acid alignment of the 5' UTR of CDK8 and CDK19. The underlined and bolded text indicates the overlapping regions.

DETAILED DESCRIPTION OF THE INVENTION

1. INTRODUCTION - CDK19 IS REQUIRED FOR TRIPLE-NEGATIVE BREAST CANCER (TNBC) GROWTH

[0065] We have discovered that reducing expression or activity of CDK19 in TNBC cell lines or breast cancer patient derived xenografts in mice inhibits growth and metastases of Triple Negative Breast Cancer (TNBC) tumors. See §4 below (Examples). We have also shown that the biological functions of CDK19 are distinct from those of its paralog, CDK8, and that the CDK19-mediated effect on TNBC tumors is independent of CDK8 activity. These data demonstrate that TNBC can be treated by agents that inhibit CDK19 but do not inhibit CDK8, or agents that preferentially inhibit CDK19 compared to CDK8. The discovery that inhibition of CDK19 is necessary and sufficient for inhibition of TNBC growth and metastases is significant, in part, because of the potential advantages of CDK19 as a therapeutic target. Compared to other ubiquitous transcriptional co-factors, such as CDK8, CDK9, and BRD4, CDK19 has more limited tissue distribution, suggesting reduced toxicity and a broader therapeutic window for CDK19 inhibitors.

[0066] In addition to demonstrating that *CDK19* knockdown had tumor growth inhibitory effects, *CDK19* expression was also shown to be enriched in tumor initiating cells, e.g., tumorigenic cells having $EpCAM^{med/high}/CD10^{-/low}$ expressions, compared to the less tumorigenic cells, e.g., cells having $EPCAM^{low/med}/CD10^{low/+}$ expressions (see, e.g., Example 4). Further studies also showed that *CDK19* knockdown significantly decreased tumor initiating frequencies (FIG. 8D). This discovery indicates that, compared to other agents, targeting CDK19 will result in a more pronounced and significant effect on highly tumorigenic (e.g., tumor initiating) cells. These discoveries also allow development of theranostic methods for identifying certain TNBC patients likely to respond to CDK19 targeted therapy.

2. DEFINITIONS

2.1 Triple-Negative Breast Cancer (TNBC)

[0067] Triple-negative breast cancer (TNBC) is a breast cancer subtype characterized by lack of expression of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (Her2). Receptor expression can be measured by immunohistochemical staining or other methods. TNBC is generally a diagnosed by exclusion. Widely used breast cancer therapies that target these receptors are not effective against TNBC, making TNBC treatment particularly challenging.

2.2 Cyclic-Dependent Kinase 19 (CDK19)

[0068] Cyclic-Dependent Kinase 19 (CDK19) is described in Broude et al., *Curr. Cancer Drug Targets* 15:739, 2015 and Sato et al., *Molecular Cell* 14:685-691, 2004. CDK19 belongs to a subset of the CDK family that is reportedly more associated with regulation of RNA polymerase II (RNAPII) transcription (see, e.g., Galbraith et al., *Transcription* **1:** 4-12, 2010) than cell cycle progression. See UniProt entry NP_055891.1; Genbank entries AY028424 & AL603914. The mRNA sequences for CDK19 are also disclosed herein (e.g., SEQ ID NOs:12 - 15).

2.3 Cyclic-Dependent Kinase 8 (CDK8)

[0069] CDK8 is a paralog of CDK19 with 84% amino acid sequence homology to CDK19. See FIG. 9. CDK8 is described in Broude et al., *Curr. Cancer Drug Targets* 15:739, 2015 and Sato et al., *Molecular Cell* 14:685-691, 2004. See UniProt entry CAA59754.1; Genbank entries X85753 & AL590108. The mRNA sequences for CDK8 are also disclosed herein (e.g., SEQ ID NOs:16-18).

2.4 Agent

[0070] As used here, the term "agent" refers to a biological molecule (e.g., nucleic acids, proteins, peptides, antibodies) or small organic molecule (e.g., having a molecular weight less than 1000, usually less than 500) that can reduce or inhibit the expression or activity of CDK19.

2.5 Inhibitors

[0071] As used herein, the term "inhibitor" as used in the context of CDK19, refers to a compound, composition or system that reduces the expression or activity of CDK19. An agent may also selectively inhibit CDK19 expression or activity over that of CDK8.

2.6 Knockdown

[0072] As used herein, the term "knock down" refers to a reduction in the expression level of the *CDK19* gene. Knocking down *CDK19* gene expression level may be achieved by reducing the amount of mRNA transcript corresponding to the gene, leading to a reduction in the expression level of CDK19 protein. Knocking down *CDK19* gene expression level may also be achieved by reducing the amount of CDK19 protein. An knockdown agent is an example of an inhibitor.

2.7 Knockout

[0073] As used herein, the term "knock out" refers to deleting all or a portion of the *CDK19* gene in a cell, in a way that interferes with the function of the *CDK19* gene. For example, a knock out can be achieved by altering the *CDK19* sequence. Those skilled in the art will readily appreciate how to use various genetic approaches, e.g., CRISPR/Cas systems, to knockout the *CDK19* gene or a portion thereof. An knockout agent is an example of an inhibitor.

2.8 Reduction relative to a reference level

[0074] As used here, the terms "decrease," "reduced," "reduction," and "decreasing" are all used herein to refer to a decrease by at least 10% as compared to a reference level, for example a decrease by at least about 5%, at least about 10%, at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% decrease (i.e. absent level as compared to a reference sample), or any decrease between 10-100% as compared to a reference level.

2.9 Nucleic Acids

[0075] As used herein, the terms "polynucleotide," "nucleic acid," and "oligonucleotide" are used interchangeably and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides or analogs thereof. A polynucleotide can comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, or otherwise be modified by art-known methods to render the polynucleotide resistant to nucleases, improve delivery of the polynucleotide to target cells or tissues, improve stability, reduce degradation, improve tissue distribution or to impart other advantageous properties. For example, the DNA or RNA polynucleotide may include one or more modifications on the oligonucleotide backbone (e.g., a phosphorothioate modification), the sugar (e.g., a locked

sugar), or the nucleobase. If present, modifications to the nucleotide structure can be imparted before or after assembly of the oligonucleotide. The sequence of nucleotides can be interrupted by non-nucleotide components. An oligonucleotide can be further modified after polymerization, such as by conjugation with a label component, a targeting component, or other component. Polynucleotides may be double-stranded or single-stranded molecules. Furthermore, in order to improve the oligonucleotide delivery, the DNA or RNA oligonucleotide may be packaged into a lipid molecule (e.g., lipid nanoparticles) or be conjugated to a cell-penetrating peptide.

2.10 Treatment

[0076] As used herein, the terms "treatment," "treating," and the like, refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease. "Treatment," as used herein, can include treatment resulting in inhibiting the disease, i.e., arresting its development; and relieving the disease, i.e., causing regression of the disease. For example, in the case of cancer, a response to treatment can include a reduction in cachexia, increase in survival time, elongation in time to tumor progression, reduction in tumor mass, reduction in tumor burden and/or a prolongation in time to tumor metastasis, time to tumor recurrence, tumor response, complete response, partial response, stable disease, progressive disease, progression free survival, overall survival, each as measured by standards set by the National Cancer Institute and the U.S. Food and Drug Administration for the approval of new drugs and/or described in Eisenhauer, EA1, et al. "New response evaluation criteria in solid tumours: revised RECIST guideline (version 1.1)." *European journal of cancer* 45.2 (2009): 228-247.

2.11 Administration

[0077] As used herein, the term “administering” or “administration” includes any route of introducing or delivering an agent that inhibits the expression or activity of CDK19 to the subject diagnosed with TNBC. Administration can be carried out by any route suitable for the delivery of the agent. Thus, delivery routes can include, e.g., intravenous, intramuscular, intraperitoneal, or subcutaneous deliver. In some embodiments, the agent is administered directly to the tumor, e.g., by injection into the tumor.

2.12 Therapeutically Effective Dose

[0078] As used here, the term “therapeutically effective amount” refers to an amount, e.g., pharmaceutical dose, effective in inducing a desired biological effect in a subject or patient or in treating a patient having TNBC described herein. The term "therapeutically effective amount" refers to an amount of an active agent being administered that will treat to some extent a disease, disorder, or condition, e.g., TNBC, relieve one or more of the symptoms of the disease being treated, and/or that amount that will prevent, to some extent, one or more of the symptoms of the disease that the subject being treated has or is at risk of developing. For example, for a given parameter (e.g., tumor volume, tumor diameter, metastases, etc.), a therapeutically effective amount will show an increase or decrease of therapeutic effect of at least 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100%, or at least 1-fold, 2-fold, or 3-fold. A therapeutically effective dose is usually delivered over a course of therapy that may extend for a period of days, weeks, or months. A therapeutically effective dose of an agent may be taken alone or in combination with other therapeutic agents. In some cases, a therapeutically effective amount of a CDK19 inhibitor is am amount sufficient to effect a partial response in a patient with TNBC (e.g., a greater than 20% reduction, sometimes a greater than 30% reduction, in the measurable diameter of lesions).

2.13 Patient or subject

[0079] A "patient" or "subject," as used herein, is intended to include either a human or non-human animal, preferably a mammal, e.g., non-human primate. Most preferably, the subject or patient is a human.

2.14 Antisense Strand

[0080] A "antisense strand" refers to the strand of a double stranded RNAi agent (siRNA or shRNA) which includes a region that is complementary or substantially complementary to a target sequence (e.g., a human CDK8 or CDK19 mRNA including a 5' UTR, exons of an open reading frame (ORF), or a 3' UTR). Where the region of “complementarity” or “substantially complementary” need not be fully complementary to the target sequence and may have sequence % identity or % similarity of least 70%, 75%, 80%, 85%, 90%, 95%, or 100%.

2.15 Sense Strand

[0081] A "sense strand," as used herein, refers to the strand of a RNAi agent (siRNA or shRNA) that includes a region that is complementary or substantially complementary to a region of the antisense strand.

3. METHODS OF TREATMENT

[0082] In one approach the invention provides a method of treating a patient diagnosed with triple-negative breast cancer (TNBC), comprising administering a therapeutically effective dose of an agent that inhibits expression or activity of cyclin-dependent kinase 19 (CDK19). In some embodiments, the treatment results in an at least 10% reduction in tumor volume within 6 month of initiating therapy.

[0083] In one approach the invention provides a method of treating a patient diagnosed with triple-negative breast cancer (TNBC), wherein the cancer is characterized by a tumor comprising $EpCAM^{med/high}/CD10^{-/low}$ epithelial cells, the method comprising administering a therapeutically effective dose of an agent that inhibits cyclin-dependent kinase 19 (CDK19) expression or activity, wherein the treatment results in a reduction of the ratio of cells having a medium to high expression level of EpCAM and a low expression level of CD10 to normal cells in the tumor. In some embodiments, the method includes the step of detecting $EpCAM^{med/high}/CD10^{-/low}$ epithelial cells in a tissue sample from the patient prior to or after initiating therapy.

[0084] To determine the phenotype of a tumor or to assess treatment prognosis, a biopsy may be obtained from the patient diagnosed with TNBC. A biopsy may be a needle biopsy, or may be a liquid biopsy be obtained from blood vessels and/or lymph nodes that supply the breast, e.g., internal mammary arteries, lateral thoracic arteries, thoracoacromial arteries, axillary lymph nodes.

[0085] As described in §4, below, CD10 and EpCAM biomarkers identify three distinct sub-populations of Tumor Initiating Cells (TICs) in TNBC. $EpCAM^{med/high}/CD10^{-/low}$, $EPCAM^{low/med}/CD10^{low/+}$, and $EpCAM^{-}/CD10$. The phenotype of cancer cells in a TNBC patient can be determined using art-known methods. In one approach a tissue is obtained from the patient and the cell phenotype determined using immunohistochemistry, mass spectrometry analysis, fluorescence activated cell sorting (FACS) or other methods. The cell phenotype can be assigned relative to standard values characteristic of health or cancerous tissue. In one approach the ratio of $EpCAM^{med/high}/CD10^{-/low}$ cells to normal breast epithelial cells is

determined prior to initiation of treatment to assess the likely response of the patient to CDK19 targeted therapy. In one approach a change in the ratio of $EpCAM^{med/high}/CD10^{-/low}$ cells to normal cells, or a change in the quantity of $EpCAM^{med/high}/CD10^{-/low}$ cells per volume tissue is detected after initiation of treatment.

[0086] In one approach the invention provides a method for reducing metastasis of TNBC in a patient, the method comprising administering a therapeutically effective dose of an agent that inhibits expression or activity of CDK19

[0087] In some embodiments, methods of the invention may be used to treat inflammatory TNBCs or TNBCs that are chemo-resistant. In other embodiments, the methods of the invention may be used to slow down or prevent the metastasis of TNBCs. In further embodiments, the methods described herein that target the *CDK19* gene or its corresponding protein may further modulate clinically relevant TNBC pathways regulated by CDK19, such as P53 signaling, KRAS signaling, androgen response, NOTCH signaling, TGF BETA signaling, and IL6-JAK-STAT3 signaling (FIG. 3B), and make them more therapeutically susceptible to cancer treatments.

3.1 THERAPEUTIC AGENTS (INHIBITORS)

3.1.1. POLYNUCLEOTIDES

[0088] As demonstrated in the examples, the *CDK19* gene is essential for the growth of TNBC. Methods of treating TNBC in a subject as described herein may be accomplished by administering a polynucleotide (e.g., oligonucleotide) to the subject to decrease or inhibit the expression of the *CDK19* gene. In some embodiments, the polynucleotide may be, for example, a DNA oligonucleotide or an RNA oligonucleotide. In other embodiments, the oligonucleotide may be used in a CRISPR/Cas system. An oligonucleotide that inhibits or decreases the expression of the *CDK19* gene may knock out or knock down the *CDK19* gene (e.g., the *CDK19* gene in a TNBC cell) in the subject.

[0089] In some embodiments, the oligonucleotide may be an shRNA or an miRNA. In some embodiments, the oligonucleotide may mediate an RNase H-dependent cleavage of the mRNA transcript of the *CDK19* gene. In other embodiments, the oligonucleotide may be used in a CRISPR/Cas system.

[0090] In some embodiments, the mRNA transcript of the *CDK19* gene may be targeted for cleavage and degradation. Different portions of the mRNA transcript may be targeted to decrease or inhibit the expression of the *CDK19* gene. In some embodiments, a DNA oligonucleotide may be used to target the mRNA transcript and form a DNA:RNA duplex with the mRNA transcript. The duplex may then be recognized and the mRNA cleaved by specific proteins in the cell. In other embodiments, an RNA oligonucleotide may be used to target the mRNA transcript of the *CDK19* gene.

3.1.1.1. shRNA

[0091] A short hairpin RNA or small hairpin RNA (shRNA) is an artificial RNA molecule with a hairpin turn that can be used to silence target gene expression via the small interfering RNA (siRNA) it produced in cells. See, e.g., Fire et. al., *Nature* 391:806-811, 1998; Elbashir et. Al., *Nature* 411:494-498, 2001; Chakraborty et al. *Mol Ther Nucleic Acids* 8:132-143, 2017;, Bouard et al., *Br. J. Pharmacol.* 157:153-165, 2009. Expression of shRNA in cells is typically accomplished by delivery of plasmids or through viral or bacterial vectors. Suitable bacterial vectors include but not limited to adeno-associated viruses (AAVs), adenoviruses, and lentiviruses. Once the vector has integrated into the host genome, the shRNA is then transcribed in the nucleus by polymerase II or polymerase III depending on the promoter choice. The resulting pre-shRNA is exported from the nucleus and then processed by Dicer and loaded into the RNA-induced silencing complex (RISC). The sense strand is degraded by RISC and the antisense strand directs RISC to an mRNA that has a complementary sequence. A protein called Ago2 in the RISC then cleaves the mRNA, or in some cases, represses translation of the mRNA, thus, leading to its destruction and an eventual reduction in the protein encoded by the mRNA. Thus, the shRNA leads to targeted gene silencing. shRNA is an advantageous mediator of siRNA in that it has relatively low rate of degradation and turnover.

[0092] In some embodiments, the methods described herein include treating TNBC in a subject using an shRNA. The methods may include administering to the subject a therapeutically effective amount of a vector, wherein the vector includes a polynucleotide encoding an shRNA capable of hybridizing to a portion of an mRNA transcript of the *CDK19* gene. In some embodiments, the vector may also include appropriate expression control elements known in the art, including, e.g., promoters (e.g., tissue specific promoters),

enhancers, and transcription terminators. Once the vector is delivered to the TNBC cell, the shRNA may be integrated into the cell's genome and undergo downstream processing by Dicer and RISC (described in detail further herein) to eventually hybridize to the mRNA transcript of the *CDK19* gene, leading to mRNA cleavage and degradation. In some embodiments, the shRNA may include a nucleic acid sequence that has at least 85% sequence identity to the sequence of GCGAGAATTGAAGTACCTTAA (SEQ ID NO: 1) or the sequence of ACCAGCAAATATCCTAGTAAT (SEQ ID NO: 2). In particular embodiments, the shRNA may target the amino acids at the N-terminus of an mRNA transcript of the *CDK19* gene. In other embodiments, the shRNA may target the amino acids at an internal region of an mRNA transcript of the *CDK19* gene.

[0093] As demonstrated in the Examples, e.g., FIGS. 1G-1J, both shRNAs (GCGAGAATTGAAGTACCTTAA (SEQ ID NO: 1) and ACCAGCAAATATCCTAGTAAT (SEQ ID NO: 2)) targeted against the *CDK19* gene were able to knockdown the gene, which led to a significant reduction in the percentage of RFP positive cells in tumors from all three TNBC PDXs. Further, *CDK19* knockdown also inhibited the growth of an aggressive PDX obtained from the brain metastasis of a patient with a chemotherapy-resistant inflammatory breast cancer (FIG. 1J), which was known to be aggressive, difficult to treat, and associated with extremely poor prognoses. In addition to inhibiting tumor growth, shRNAs also inhibited the lung metastases of these tumors in mice (FIG. 1L).

[0094] In some embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to GCGAGAATTGAAGTACCTTAA (SEQ ID NO: 1). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to ACCAGCAAATATCCTAGTAAT (SEQ ID NO: 2). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to GCTTGTAGAGAGATTGTACTT (SEQ ID NO: 3). In some embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to GAGGACTGATAGTTCTTCTTT (SEQ ID NO: 4). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to

GATATTAGAAAGATGCCAGAA (SEQ ID NO: 5). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to GCCAACAGTAGCCTCATAAAG (SEQ ID NO: 6). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to CGTTCGTATTTATCTAGTTTC (SEQ ID NO: 7). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to GCATGACTTGTGGCATATTAT (SEQ ID NO: 8). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to GCTTGTAGAGAGATTGCACTT (SEQ ID NO: 9). In other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to AGGACTGATAGCTCTTCTTTA (SEQ ID NO: 10). In yet other embodiments, an shRNA targeted against the *CDK19* gene may have at least 85% sequence identity (e.g., 87%, 89%, 91%, 93%, 95%, 97%, or 99% sequence identity) to GTATGGCTGCTGTTTGATTAT (SEQ ID NO: 11). One of skill in the art has the knowledge and capability to design shRNAs that target different portions of the *CDK19* gene (e.g., the 5' UTR region or the 3' UTR region) to achieve the desired reduction in expression of the gene. For example, available tools for designing shRNAs include, e.g., Project Insilico, Genomics and Bioinformatics Group, LMP, CCR, NIH. In some embodiments, an shRNA may be designed to knockout the *CDK19* gene.

CDK8 and CDK19 shRNA

[0095] There are a number of structural elements that can affect shRNA efficacy. For specific RNAi knockdown of a desired target gene an shRNA can be designed in consideration of its multiple structural elements. Generally, an shRNA should be about 80 nucleotides in length and designed (from 5' to 3') to comprise of the following structural elements to make the hairpin structure of the shRNA: (1) a sense strand (e.g., upper stem); (2) followed by a hairpin loop; (3) an antisense strand (e.g., lower stem or guide strand) that has perfect or near perfect complementary to the target mRNA and is antisense to the target mRNA; (4-5) two cleavage motifs such as, "U" or "UH" at the first position of the guide strand, and "UUC" or "CUUC" at the tail region of the guide strand; and (6) arbitrary spacer nucleotides of about

two nucleotides in length between the first nucleotide of guide strand "U" motif and the hairpin loop, and between the last nucleotide of the sense strand and the hairpin loop. The sense strand and antisense strand, making up the stem, may be designed to consist of a range from about 19 to 29 nucleotides in length, which will form the stem. The loop structure may be designed to consist of a range about 2 to 15 nucleotides in length, and preferably free of any internal secondary structure. Some examples of sequences that may be used for making the hairpin loop, include but are not limited to, a nine nucleotide loop comprising the sequence (TTCAAGAGA), and a seven nucleotide loop comprising the sequence (TCAAGAG). Other design strategies can be found in the relevant disclosure of Ros XB-D, Gu S. Guidelines for the optimal design of miRNA-based shRNAs. *Methods (San Diego, Calif)* 2016;103:157-166, which is herein incorporated by reference in its entirety for all purposes. There are also several design programs available such as, The RNAi Consortium software from The Broad Institute, which is made available through Sigma-Aldrich and Thermo-Fisher Scientific.

[0096] The specificity of the target sequence should also be considered, as many mRNAs can share similar sequences. Care should be taken in selecting target sequence that has low sequence homology to other genes in the genome to allow for gene-specific knockdown. Where a gene has multiple forms, to achieve complete knockdown of gene expression, shRNA should target sequences shared among all isoforms of the target mRNA.

[0097] An alignment of CDK19 and CDK8 mRNA sequences can identify not identical or low percent identity or similarity nucleotide sequence regions which can be used to design shRNAs that have a preference to target to CDK19 mRNA but not CDK8, see for example the 3' UTR and 5' UTR alignments in FIG. 16 and FIG. 17.

[0098] In some embodiments, shRNA that targets a CDK19 mRNA transcript, and not of CDK8 mRNA transcript can be designed. In one approach the mRNA sequences for human CDK19 and CDK8 from National Center for Biotechnology Information (NCBI, found at Pubmed.gov) and an alignmenti is performed (e.g., with pairwise alignment program such as, LALIGN). A region of about 19 to 29 contiguous nucleotides (e.g., 19-20, 19-21, 19-22, 19-23, 19-24, 19-25, 19-26, 19-27, 19-28, or 19-29) in length is selected based on low sequence identity (e.g., less than 75%, identity, sometimes less than 70% identity, sometimes less than 60% identity. In some embodiments the 19 to 29 nt region has very low (e.g., less than 40%,

less than 30% or less than 20% or sequence identity. The contiguous sequence can be in a protein coding region, the 5'-UTR, the 3'-UTR, or span two regions.

[0099] In one embodiment, target-specific knockdown of CDK19 can be accomplished by designing an shRNA with a guide strand that is complementary of the 3' UTR region of CDK19 (SEQ ID NO:42) and has low or no homology to the 3'UTR of CDK8 (SEQ ID NO:44). The guide strand may be 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29 nucleotides in length. Some exemplary sequence regions that may be used to design a CDK19 shRNA, include but are not limited to, CTCCAGCTCCCGTTGGGCCAGGCCAGCCC (SEQ ID NO: 20), AGCCCAGAGCACA
GGCTCCAGCAATATGT (SEQ ID NO: 21), CTGCATTGAAAAGAACCAAAAAAATGCAA (SEQ ID NO: 22), ACTATGATGCCATTTCTATCTAAAACTCA (SEQ ID NO: 23), TACACATGGGAG GAAAACCTTATATACTG (SEQ ID NO: 24), AGCATTGTGCAGGACTGATAGCTCTTCTT (SEQ ID NO: 25), TATTGACTTAAAGAAGATTCTTGTGAAGT (SEQ ID NO: 26), TTCCCCTATCTCAGCA CCCCTTCCCTGCA (SEQ ID NO: 27), TGTGTTCCATTGTGACTTCTCTGATAAAG (SEQ ID NO: 28), CGTCTGATCTAATCCCAGCACTTCTGTAA (SEQ ID NO: 29), or CCTTCAGCATTTCTTT GAAGGATTCTATC (SEQ ID NO: 30). One of ordinary skill guided by this disclosure understands that other low homology sequence regions in the '3 UTR could also be used. See, for example, FIGS. 16A-D the low homology sequence regions from (1-1186) and (2418-4570). In one embodiment, the shRNA may be designed to be targeted to upstream of CDK19, downstream of CDK19, or in the exons of CDK19. In some cases the expression of the CDK19 shRNA results in knockdown of CDK19 at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100%. In another embodiment the expression of the CDK19 shRNA can preferentially knockdown CDK19 compared to CDK8.

[0100] To make shRNAs that preferentially target CDK19 one would identify a unique region of CDK19, a region that does not have significant homology to other CDKs (e.g., CDK8) or other mRNAs in the genome. One would use this sequence to make a guide strand that is antisense to this target and comprises 19 to 29 nucleotides in length. To make the expression cassette one would add an appropriate promoter such as a pol II or pol III promotor at the beginning of the cassette, followed by the complementary sense strand (e.g., complementary to the targeting guide strand), which is them followed by the loop structure of about 2 to 15 nucleotides in length. In addition, the two Ago cleavage motifs,

"U" or "UH" should be included at the first position of the guide strand, and "UUC" or "CUUC" at the tail region of the guide strand along to 1-2 spacer nucleotides at the end of the loop structure. See, for example US Application No. US2008/0293142 and Ros XB-D, Gu S. Guidelines for the optimal design of miRNA-based shRNAs. *Methods (San Diego, Calif)* 2016;103:157-166, which is herein incorporated by reference in its entirety for all purposes.

[0101] In another embodiment, target-specific knockdown of CDK8 can be performed by using an shRNA with a guide strand that comprises a complementary to the 5'UTR of CDK8 (SEQ ID NO: 43) and has low or no homology to the 5' UTR of CDK19 (SEQ ID NO:41). The guide strand may be 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29, nucleotides in length. Some exemplary sequences that may be used to design a CDK8 shRNA include but are not limited to, TGGCCGCCCCGCCGCTCCCGCCGCAGCAG (SEQ ID NO: 31), GAGCAGAACGCGCGGCCGGAGA GAGCGGC (SEQ ID NO: 32), GGAGCCGGCGCCCAGGGAGCCCGCGGGGA (SEQ ID NO: 33), CAAGGGCAGAGACACCGCTCCCCACCCCC (SEQ ID NO: 34),AGCCCTCGTCCCTCGGCTCTCCTTCGCCG (SEQ ID NO: 35), GGGGATCCTCCCCGTTCCTCCACCCCCGG (SEQ ID NO: 36), CCGGCCTCTG CCCCGCCGTCCCCCTGGAT (SEQ ID NO: 37), GTCCCTGGCGCTTTCGCGGGGCCTCCTCC (SEQ ID NO: 38), TGCTCTTGCCGCATCAGTCGGGCTGGTGC (SEQ ID NO: 39), or TGCGGCCGGCGGGCGTAGAGC GGGCGGGT (SEQ ID NO: 40). One of ordinary skill in the art would understand that other low homology sequence regions in the '5 UTR could also be used. See, for example, FIG. 17 the low homology sequence regions from (1-33) or (223 -504). In another embodiment the shRNA may be designed to be targeted to upstream of CDK8, downstream of CDK8, or in the exons of CDK8. In some cases, the expression of the CDK8 shRNA can result in a knockdown of CDK8 at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100%. .

[0102] To make shRNAs that preferentially target CDK8 one would identify a unique region of CDK8, a region that does not have significant homology to other CDKs (e.g., CDK19) or other mRNAs in the genome. One would use this sequence to make a guide strand that is antisense to this target and comprises 19 to 29 nucleotides in length. To make the expression cassette one would add an appropriate promoter such as a pol II or pol III promotor at the beginning of the cassette, followed by the complementary sense strand

(e.g., complementary to the targeting guide strand), which is them followed by the loop structure of about 2 to 15 nucleotides in length. In addition, the two Ago cleavage motifs, "U" or "UH" should be included at the first position of the guide strand, and "UUC" or "CUUC" at the tail region of the guide strand along to 1-2 spacer nucleotides at the end of the loop structure. See, for example US Application No. US2008/0293142 and Ros XB-D, Gu S. Guidelines for the optimal design of miRNA-based shRNAs. *Methods (San Diego, Calif)* 2016;103:157-166, which is herein incorporated by reference in its entirety for all purposes.

[0103] The specificity or knockdown level of an shRNA or siRNA can be confirmed using real-time PCR analysis for mRNA level or ELISA assay for the protein level. Experimental controls may be run in parallel to assess knockdown. Some examples of experimental controls that may be used, include but are not limited to, a mock-infected or mock-transfected sample, an empty vector, an shRNA encoding a scrambled target or seed region, an shRNA targeting another gene entirely such as, housekeeping genes GAPDH or Actin, or a GFP positive control.

[0104] To determine if an siRNA or shRNA (e.g., RNAi agent) preferentially targets CDK19 over CDK8 one can transfect or transduce the shRNA or siRNA tagged to marker such as GFP in a cell line or other expression system, select the GFP positive cells (e.g. transformed cells), and determine the level of CDK19 knockdown relative to CDK19 expression in the cell system without transfection or transduction with the RNAi agent. In some embodiments, the expression of RNA is measured. In other embodiments, the expression of the protein is measured. In one example, mRNA may be measured by any PCR-based assay known in the art (e.g., RT-PCR or qRT-PCR or the like). In one example, the protein level may be measured by an immunoassay (e.g., ELISA assay or any antibody-based method known in the art).

[0105] In some embodiments, a targeting CDK19 shRNA or siRNA results in CDK19 expression less than about 30% and CDK8 greater than about 70% relative to a system without transfection or transduction. In some other embodiments, a targeting CDK19 shRNA or siRNA results in CDK19 expression at less than about 50% and CDK8 greater than about 95%. In some embodiments, a targeting CDK19 shRNA or siRNA results in CDK19 expression less than about 5% and CDK8 greater than about 80%. In some embodiments, a targeting CDK19 shRNA or siRNA results in CDK19 expression less than about 1% and CDK8 greater than about 60%. In some embodiments, a targeting CDK19 shRNA or siRNA results

in CDK19 expression at less than about 0.5% and CDK8 greater than about 90%. In some embodiments, a targeting CDK19 shRNA results in CDK19 expression at about 0% and CDK8 at about 100% relative to a system without transfection or transduction. In some embodiments, the expression of RNA is measured. In other embodiments, the expression of the protein is measured.

CDK8 and CDK19 siRNA

[0106] The present disclosure also provides siRNA-based therapeutics for inhibiting expression of CDK8 and CDK19 in a patient with triple-negative breast cancer. The double stranded RNAi therapeutic includes a sense strand complementary to an antisense strand. The sense or antisense strands of the siRNA may be about 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length. The antisense strand of the siRNA-based therapeutic includes a region complementary to a part of an mRNA encoding CDK8 or CDK19. Additional methods to make therapeutic siRNA can be found in U.S. Pat No. US9399775, which is incorporated by reference in its entirety for all purposes.

[0107] In some cases, the expression of CDK19 siRNA may result in a knockdown of CDK19 at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100%. In another embodiment, the expression of CDK19 siRNA may preferentially knockdown CDK19 compared to CDK8. In some cases, the expression of CDK8 siRNA may result in a knockdown of CDK8 at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100%.

[0108] In a preferred embodiment, CDK19 siRNA may result in a knockdown of CDK19 at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% and CDK8 at least about 10%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, or 30%.

shRNA and siRNA Delivery

[0109] Depending on whether transient or stable expression is desired one can select an appropriate delivery vector. Examples of delivery vectors that may be used with the present disclosure are viral vectors, plasmids, exosomes, liposomes, bacterial vectors, or nanoparticles. The present disclosure also provides for delivery by any means known in the art.

[0110] For targeted delivery to triple-negative breast cancer cells, one skilled in the art would appreciate that delivery vectors may be genetically modified to target a specific cell

type or to tissue type. To make a targeted delivery vector or plasmid one can identify a unique molecule expressed or associated with a triple-negative breast cancer (e.g., receptor, protein, glycoprotein, or combination thereof) and then create a delivery vector or plasmid that harbors or expresses these markers, preferably on the outside of the delivery vector or plasmid (e.g., cytosol facing). In addition, depending on the required therapeutic duration a viral delivery vector can be genetically modified to be continuously replicating, replication-defective, or conditionally replicating as described in, Sliva K, Schnierle BS. Selective gene silencing by viral delivery of short hairpin RNA. *Virology Journal*. 2010.

[0111] In one embodiment, the CDK8 or CDK19 shRNA or siRNA can be delivered by an adenovirus vector. Adenoviruses non-enveloped viruses with a nucleocapsid and a linear dsDNA genome. While they are able to replicate in the nucleus of mammalian cells, they do not efficiently integrate into the host's genome and therefore pose only minimal risks of insertional mutagenesis but are inadequate for long-term therapy.

[0112] In another embodiment, the CDK8 or CDK19 shRNA or siRNA can be delivered by an adeno-associated viral vector (AAV). AAV is one of the smallest viruses and belongs to the genus *Dependovirus*. It has a small, single-stranded DNA genome and can accommodate about eight individual shRNA. AAV permits entry retargeting, allowing delivery of the shRNA to specific cell or tissue types. In a further embodiment, the present disclosure provides for a modified AAV that is targeted for delivery to a triple-negative breast cancer cell or tissue type.

[0113] In another embodiment, the CDK8 or CDK19 shRNA or siRNA can be delivered by a retrovirus vector. A retrovirus is a single-stranded RNA virus that belongs to the family of *Retroviridae* and replicate through a double-stranded DNA intermediate. They can integrate into a host's genome thereby allowing long-term expression of a shRNA. The Env protein plays a central role in targeting retrovirus to a target cell. In a further embodiment, the present disclosure provides for a retrovirus vector with a modified *env* gene or its protein product for delivery to a triple-negative breast cancer cell or tissue type. In a further embodiment, the present disclosure provides for delivery of CDK8 or CDK19 shRNA of siRNA using a retrovirus vector with protease-activated Env proteins.

[0114] In another embodiment, the CDK8 or CDK19 shRNA or siRNA can be delivered by a lentivirus vector. Lentivirus is a subclass of retrovirus in the genus *Lentivirinae* which can

accommodate large amounts of DNA. For some applications, it may be preferable to use a lentivirus vector engineered to be "self-inactivating" known as “SIN” vectors. In a further embodiment, the present disclosure provides for delivery of a CDK8 or CDK19 shRNA by a lentivirus vector with a modified *env* gene or its protein product for delivery to a triple-negative breast cancer cell or tissue type.

[0115] In another embodiment, the shRNA or siRNA can be delivered by a nanoparticle. Examples of nanoparticles that can be use with the present disclosure, include but are not limited to, exosomes, liposomes, organic nanoparticles, or inorganic nanoparticles. Other non-limiting examples of nanoparticles include, but are not limited to, e.g., those provided in Hong, Cheol Am, and Yoon Sung Nam. “Functional Nanostructures for Effective Delivery of Small Interfering RNA Therapeutics.” *Theranostics* 4.12 (2014): 1211–1232. *PMC*. Web. 13 Sept. 2018, which is hereby incorporated by reference in its entirety for all purposes. In some embodiments, the delivery of the shRNA or siRNA is mediated by receptor, protein, glycoprotein or combination thereof present or specific to triple-negative breast cancer cells.

[0116] In some embodiments, the siRNA CDK19 therapeutic is administered in a solution. The siRNA may be administered in an unbuffered solution. In one embodiment, the siRNA is administered in water. In other embodiments, the siRNA is administered with a buffer solution, such as an acetate buffer, a citrate buffer, a prolamine buffer, a carbonate buffer, or a phosphate buffer or any combination thereof. In some embodiments, the buffer solution is phosphate buffered saline.

3.1.1.2. RNASE H-MEDIATED MRNA DEGRADATION/ANTISENSE

[0117] RNase H-dependent antisense oligonucleotides (ASOs) are single-stranded, chemically modified oligonucleotides that bind to complementary sequences in target mRNAs and reduce gene expression both by RNase H-mediated cleavage of the target RNA and by inhibition of translation by steric blockade of ribosomes.

[0118] RNase H is an endonuclease enzyme that catalyzes the cleavage of RNA in an RNA:DNA duplex. The most well studied endogenous function for this enzyme is the removal of Okazaki fragments (small RNAs) used to prime the DNA duplication during cell division. In some embodiments, to target the mRNA transcript of the *CDK19* gene for degradation, a nucleic acid (e.g., DNA oligonucleotide) capable of hybridizing to a portion of the mRNA may

be administered to the subject. Once inside the cell (e.g., a TNBC cell), the DNA oligonucleotide base pairs with its targeted mRNA transcript. RNase H may bind to the resulting duplex and cleave the mRNA transcript at one or more places. The DNA oligonucleotide may further bind to other mRNA transcripts to target them for RNase H degradation. Thus, the expression of the *CDK19* gene may be greatly reduced in a subject with TNBC.

[0119] The DNA oligonucleotide capable of hybridizing to an mRNA transcript of a *CDK19* gene may contain, e.g., between 10 and 30 nucleotides (e.g., 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, or 30 nucleotides). In some embodiments, the DNA oligonucleotide may have 100% complementarity to the portion of the mRNA transcript it binds. In other embodiments, the DNA oligonucleotide may have less than 100% complementarity (e.g., 95%, 90%, 85%, 80%, 75%, or 70% complementarity) to the portion of the mRNA transcript it binds, but can still form a stable RNA:DNA duplex for the RNase H to cleave the mRNA transcript. The DNA oligonucleotide may bind to the 5' UTR or the 3' UTR of the mRNA transcript of the *CDK19* gene.

[0120] Further, the DNA oligonucleotide capable of hybridizing to an mRNA transcript of a *CDK19* gene may contain modified nucleotides at the 5' end and the 3' end. The modified nucleotides at the termini may function to protect the internal portion of the DNA oligonucleotide from nuclease degradation and to increase the binding affinity for the target mRNA transcript. In some embodiments, the modified nucleotides at the termini may include a modified nucleobase (e.g., 5-methylcytosine) and/or a modified sugar (e.g., a locked sugar). In some embodiments, 3-5 nucleotides at each of the 5' and 3' ends of the DNA oligonucleotide may be modified.

3.1.1.3. miRNA

[0121] A microRNA (miRNA) is a small non-coding RNA molecule that functions in RNA silencing and post-transcriptional regulation of gene expression. miRNAs base pair with complementary sequences within the mRNA transcript. As a result, the mRNA transcript may be silenced by one or more of the mechanisms such as cleavage of the mRNA strand, destabilization of the mRNA through shortening of its poly(A) tail, and decrease translation efficiency of the mRNA transcript into proteins by ribosomes. In some embodiments, miRNAs resemble the siRNAs of the shRNA pathway, except that miRNAs derive from regions of RNA

transcripts that fold back on themselves to form short hairpins, which are also called pri-miRNA. Once transcribed as pri-miRNA, the hairpins are cleaved out of the primary transcript in the nucleus by an enzyme called Drosha. The hairpins, or pre-miRNA, are then exported from the nucleus into the cytosol. In the cytosol, the loop of the hairpin is cleaved off by an enzyme called Dicer. The resulting product is now a double strand RNA with overhangs at the 3' end, which is then incorporated into RISC. Once in the RISC, the second strand is discarded and the miRNA that is now in the RISC is a mature miRNA, which binds to mRNAs that have complementary sequences.

[0122] The difference between miRNAs and siRNAs from the shRNA pathway is that base pairing with miRNAs comes from the 5' end of the miRNA, which is also referred to as the seed sequence. Since the seed sequence is short, each miRNA may target many more mRNA transcript. In some embodiments, an miRNA targeting the *CDK19* gene may be used in methods described herein.

3.1.2. CRISPR/CAS SYSTEM

[0123] In some embodiments, the knocking out or knocking down of the *CDK19* gene is performed using a gene editing system such as the CRISPR/Cas system. See Sanders and Joung, *Nature Biotechnol* 32:347-355, 2014, Huang et al., *J Cell Physiol* 10:1-17, 2017 and Mitsunobu et al., *Trends Biotechnol* 17:30132-30134, 2017. The CRISPR/Cas system includes a Cas protein and at least one or two ribonucleic acids that are capable of directing the Cas protein to and hybridizing to a target motif in the *CDK19* sequence. The Cas protein then cleaves the target motif and results in a double-strand break or a single-strand break. Any CRISPR/Cas system that is capable of altering a target polynucleotide sequence in a cell can be used in methods described here. In some embodiments, the CRISPR/Cas system is a CRISPR type I system. In some embodiments, the CRISPR/Cas system is a CRISPR type II system. In some embodiments, the CRISPR/Cas system is a CRISPR type V system.

[0124] The Cas protein used in the methods described herein can be a naturally occurring Cas protein or a functional derivative thereof. A "functional derivative" includes, but are not limited to, fragments of a native sequence and derivatives of a native sequence polypeptide and its fragments, provided that they have a biological activity in common with the corresponding native sequence polypeptide. A biological activity contemplated herein is the ability of the functional derivative to hydrolyze a DNA substrate (e.g., a *CDK19* gene) into

fragments. The term "derivative" encompasses both amino acid sequence variants of polypeptide, covalent modifications, and fusions thereof. Suitable derivatives of a Cas protein or a fragment thereof include but are not limited to mutants, fusions, or covalent modifications of Cas protein.

[0125] In some embodiments, the Cas protein used in methods described herein is Cas9 or a functional derivative thereof. In some embodiments, the Cas9 protein is from Streptococcus pyogenes. Cas9 contains 2 endonuclease domains, including an RuvC-like domain which cleaves target DNA that is noncomplementary to crRNA, and an HNH nuclease domain which cleaves target DNA complementary to crRNA. The double-stranded endonuclease activity of Cas9 also requires that a short conserved sequence (e.g., 2-5 nucleotides), known as a protospacer-associated motif (PAM), follows immediately after the 3′ end of a target motif in the target sequence.

[0126] In some embodiments, the Cas protein is introduced into TNBC cells in polypeptide form. In certain embodiments, the Cas protein may be conjugated to a cell-penetrating polypeptide. Non-limiting examples of cell-penetrating peptides include, but are not limited to, e.g., those provided in Milletti et al., *Drug Discov. Today* 17: 850-860, 2012, the relevant disclosure of which is hereby incorporated by reference in its entirety. In other embodiments, a TNBC cell may be genetically engineered to produce the Cas protein.

[0127] In some embodiments, the target motif in the *CDK19* gene, to which the Cas protein is directed by the guide RNAs, may be between 15 and 25 nucleotides in length (e.g., 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleotides in length). In some embodiments, the target motif is at least 20 nucleotides in length. In some embodiments, the target motif in the *CDK19* gene immediately precedes a short conserved sequence known as a protospacer-associated motif (PAM), recognized by the Cas protein. In some embodiments, the PAM motif is an NGG motif. In some embodiments, the target motif of the *CDK19* gene is within the first exon. In some embodiments, the target motifs can be selected to minimize off-target effects of the CRISPR/Cas systems. Those skilled in the art will appreciate that a variety of techniques can be used to select suitable target motifs for minimizing off-target effects (e.g., bioinformatics analyses).

[0128] The ribonucleic acids that are capable of directing the Cas protein to and hybridizing to a target motif in the *CDK19* gene are referred to as single guide RNA ("sgRNA"). The sgRNAs

can be selected depending on the particular CRISPR/Cas system employed, and the sequence of the target polynucleotide, as will be appreciated by those skilled in the art. In some embodiments, the one or two ribonucleic acids can also be selected to minimize hybridization with nucleic acid sequences other than the target polynucleotide sequence. In some embodiments, the one or two ribonucleic acids are designed to hybridize to a target motif immediately adjacent to a deoxyribonucleic acid motif recognized by the Cas protein. Guide RNAs can also be designed using available software, for example, CRISPR Design Tool (Massachusetts Institute of Technology). In some embodiments, the one or more sgRNAs can be transfected into TNBC cells, according to methods known in the art.

[0129] The use of antibodies for therapeutic purposes has been used to treat cancer. Passive immunotherapy involves the use of monoclonal antibodies (mAbs) in cancer treatments (see for example, Devita, Hellman, And Rosenberg's *Cancer: Principles & Practice Of Oncology*, Eighth Edition (2008), DeVita, V. et al. Eds., Lippincott Williams & Wilkins, Philadelphia, Pa., pp. 537-547, 2979-2990). These antibodies can have inherent therapeutic biological activity both by direct inhibition of tumor cell growth or survival and by their ability to recruit the natural cell killing activity of the body's immune system. The antibodies can be administered alone or in conjunction with radiation or chemotherapeutic agents. Trastuzumab, approved for treatment of breast cancer is an example of such a therapeutic. Alternatively, antibodies can be used to make antibody-drug conjugates in which the antibody is linked to a drug and directs that agent to the tumor by specifically binding to the tumor. Ado-Trastuzumab emtansine (T-DM1) is an example of an approved antibody-drug conjugate used for the treatment of breast cancer (see, Deng *et al., Curr. Med. Chem.*, Vol. 24(23), 2505-2527 (2017). Another type of immunotherapy is active immunotherapy, or vaccination, with an antigen present on a specific cancer (*e.g.,* TNBC cells) or a DNA construct that directs the expression of the antigen, which then evokes the immune response in the subject, *i.e.,* to induce the subject to actively produce antibodies against their own cancer.

[0130] Antibodies have been highly effective in targeting cell surface proteins involved in disease. Though it is generally believed that their large size, complex architecture, and structural reliance on disulfide bonds preclude intracellular application, a number of examples of both *in situ*-expressed (see, e.g, Miersch and Sidhu, F1000Res doi: 10.12688/f1000research.8915.1, 2016) and exogenously supplied whole antibodies shown to

maintain functional intracellular activity exist in the literature (see, e.g., Biocca *et al.,* Expression and targeting of intracellular antibodies in mammalian cells. *EMBO J.* (1990); 9(1): 101–8 and Steinberger *et al.*, Functional deletion of the CCR5 receptor by intracellular immunization produces cells that are refractory to CCR5-dependent HIV-1 infection and cell fusion. *Proc Natl Acad Sci U S A.* (2000); 97(2): 805–10). Attempts to use smaller, less complex binding proteins such as antigen-binding fragments (Fabs) and single-chain variable fragments (scFvs) for intracellular application have similarly shown success in their ability to bind and modulate cytoplasmic protein function (See for example, Marasco *et al.,* Design, intracellular expression, and activity of a human anti-human immunodeficiency virus type 1 gp120 single-chain antibody. *Proc Natl Acad Sci U S A.* (1993); 90(16): 7889–93).

[0131] As used herein, the term "antibody" encompasses, but is not limited to, whole immunoglobulin (*i.e.*, an intact antibody) of any class. Native antibodies are usually heterotetrameric glycoproteins, composed of two identical light (L) chains and two identical heavy (H) chains. Typically, each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (V(H)) followed by a number of constant domains. Each light chain has a variable domain at one end (V(L)) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light and heavy chain variable domains. The light chains of antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, and several of these may be further divided into subclasses (isotypes), *e.g.*, IgG-1, IgG-2, IgG-3, and IgG-4; IgA-1 and IgA-2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called alpha, delta, epsilon, gamma, and mu, respectively.

[0132] As used herein, the term "epitope" is meant to include any determinant capable of specific interaction with the provided antibodies. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. Identification of the epitope that the antibody recognizes is performed as follows. First, various partial structures of the target molecule that the monoclonal antibody recognizes are prepared. The partial structures are prepared by preparing partial peptides of the molecule. Such peptides are prepared by, for example, known oligopeptide synthesis technique or by incorporating DNA encoding the desired partial polypeptide in a suitable expression plasmid. The expression plasmid is delivered to a suitable host, such as *E. coli*, to produce the peptides. For example, a series of polypeptides having appropriately reduced lengths, working from the C- or N-terminus of the target molecule, can be prepared by established genetic engineering techniques. By establishing which fragments react with the antibody, the epitope region is identified. The epitope is more closely identified by synthesizing a variety of smaller peptides or mutants of the peptides using established oligopeptide synthesis techniques. The smaller peptides are used, for example, in a competitive inhibition assay to determine whether a specific peptide interferes with binding of the antibody to the target molecule. If so, the peptide is the epitope to which the antibody binds. Commercially available kits, such as the SPOTs Kit (Genosys Biotechnologies, Inc., The Woodlands, TX) and a series of multipin peptide synthesis kits based on the multipin synthesis method (Chiron Corporation, Emeryvile, CA) may be used to obtain a large variety of oligopeptides.

[0133] The term antibody or fragments thereof can also encompass chimeric antibodies and hybrid antibodies, with dual or multiple antigen or epitope specificities, and fragments, such as F(ab')2, Fab', Fab and the like, including hybrid fragments. Thus, fragments of the antibodies that retain the ability to bind their specific antigens are provided. For example, fragments of antibodies which maintain CDK19 binding activity are included within the meaning of the term antibody or fragment thereof. Such antibodies and fragments can be made by techniques known in the art and can be screened for specificity and activity according to general methods for producing antibodies and screening antibodies for specificity and

activity (See Harlow and Lane. Antibodies, A Laboratory Manual. Cold Spring Harbor Publications, New York (1988)).

Also included within the meaning of antibody or fragments thereof are conjugates of antibody fragments and antigen binding proteins (single chain antibodies) as described, for example, in U.S. Patent No. 4,704,692, the contents of which are hereby incorporated by reference in their entirety.

[0134] In one embodiment, a therapeutic antibody (or antibody fragment) can be prepared using methods known in the art, having specificity for an antigen present in breast cancer, and in particular TNBC cells, that is absent or present only at low levels in any normal (non-cancerous) tissue. The therapeutic antibody would therefore have biological activity against TNBC cells and be able to recruit the immune system's response to treat the disease. The therapeutic antibody can be administered as a therapeutic alone or in combination with current treatments (such as chemotherapy, radiation, or platinum-based therapies) or used to prepare immunoconjugates linked to toxic agents, such as drugs.

[0135] Monoclonal antibodies to CDK19 (*e.g.,* anti-CKD19 antibodies), made by methods known in the art, can be used to identify the presence or absence of cancerous cells in breast tissue, for purposes of diagnosis or treatment. Anti-CKD19 antibodies can also be used to identify the presence or absence of cancerous cells, or the level thereof, which are circulating in the blood after their release from a solid tumor. Such circulating antigen can include an intact CDK19 antigen, or a fragment thereof that retains the ability to be detected according to the methods taught herein. Such detection may be effected for example, by FACS analysis using standard methods commonly used in the art.

[0136] In some embodiments, methods of targeting CDK19 can include administering to a subject in need thereof, a therapeutically effective amount of an antibody (*e.g.,* an anti-CKD19 antibody) that is immunoreactive to CDK19 for the treatment of breast cancer, in particular treatment of TNBC. In one embodiment, the antibody having immunoreactivity to CDK19 targets intracellular signaling molecules, such as kinases, as opposed to cell surface molecules, whereby the specificity of the antibody is provided by neutralizing epitope(s) present on CDK19 that are not present on CDK8. In another embodiment, the anti-CDK19 antibody can target the PI3K/mTOR/AKT pathway or ERK5 (see, Ocana and Pandiella, *Oncotarget*, 8(13), 22218-22234 (2017)). In one embodiment, the anti-CDK19 antibody can target multiple

intracellular signaling molecules, for example, the PI3K/mTOR and JAK/STAT pathway. In yet another embodiment, the anti-CDK19 antibody can comprise an engineered protein that binds to a neutralizing epitope present on CDK19 that is not present on CDK8.

[0137] In one embodiment, methods of targeting CDK19 can include administering to a subject in need thereof, a therapeutically effective amount of a tumor antigen (TA)-specific monoclonal antibody for the treatment of TNBC. In one embodiment, the TA-specific mAB can be directed to an intracellular antigen associated with TNBC (See for example, Wang *et al., Molecular Oncology*, Vol. 9(10), (2015) 1982-1993 and Just, *FEBS letters*, 2:21 (2014), 350-355).

[0138] In one aspect, provided is a method of treating a subject with breast cancer, the method including the step of administering to the subject a pharmaceutically effective amount of a composition comprising a CDK19 targeting agent. The CDK19 targeting agent may be a CDK19 targeted antibody, a CDK19 targeted peptide, a CDK19 targeted small molecule, a CDK19 targeted RNA molecule, or a combination thereof. In some instances, the CDK19 targeted agent may be conjugated to a therapeutic agent. In some instances, the method further includes administering a second form of cancer therapy (e.g., chemotherapy or radiation therapy) to the subject. In one embodiment, the breast cancer is TNBC.

In another aspect, provided is a method of inhibiting expression of the CDK19 gene in a breast cancer cell, the method including the steps of contacting a breast cancer cell expressing the CDK19 gene with a synthetic CDK19 targeted RNA molecule.

[0139] In another aspect, provided is a method of assessing responsiveness of a subject with cancer to a CDK19 targeted agent including the steps of: (a) measuring in a tumor sample from a subject the amount of CDK19; (b) determining if a subject has a cancer characterized as having a high level of CDK19 expression; and (c) indicating that the subject is more likely to respond to the CDK19 targeted agent if the subject's cancer is characterized as having a high level of CDK19 expression or that the subject is less likely to respond to the CDK19 targeted agent if the subject's cancer is characterized as having a low level of CDK19 expression.

[0140] In one aspect, provided is a method of treating a subject with cancer, the method comprising administering to the patient a pharmaceutically effective amount of a composition comprising a CDK19 targeted agent. The CDK19 targeted agent is an agent that specifically binds to CDK19 protein or to CDK19 mRNA. CDK19 targeted agents include antibodies, or

fragments thereof, peptides, small molecules, and polynucleotides (such as RNA molecules) that specifically bind to CDK19 protein or to CDK19 mRNA. The composition may further comprise a pharmaceutically acceptable carrier. In some instances, CDK19 targeted agents that bind to the CDK19 protein may directly inhibit CDK19 activity. In other instances, CDK19 targeted agents that bind to CDK19 mRNA may inhibit CDK19 expression and thereby inhibit CDK19 activity.

[0141] In one instance, the CDK19 targeted agent may comprise a CDK19 targeted antibody. The CDK19 targeted antibody may be a monoclonal antibody. In some instances, the CDK19 targeted antibody may be a humanized antibody. In another instance, the CDK19 targeted agent may be a CDK19 targeted peptide. In yet another instance, the CDK19 targeted agent may be a CDK19 targeted small molecule. The CDK19 targeted peptides and small molecules may be derived in a variety of manners as discussed further below. In some instances, the peptides are derived from the sequence of a CDK19 targeted antibody.

[0142] In some instances, treating a subject with the methods described herein inhibits at least one of: formation of a tumor, the proliferation of tumor cells, the growth of tumor cells, or metastasis of tumor cells in the subject. In another embodiment, treating a subject with the methods described herein may result in reduction of tumor size and, in some instances, elimination of one or more tumors in the subject.

3.1.4. SMALL MOLECULE INHIBITORS

[0143] In one approach, methods for treating TNBC include targeting the CDK19 protein using a small molecule inhibitor of CDK19 activity. Examples of small molecule inhibitors of CDK19 are described in US Patent No. 9,321,737, US Patent Publication No. US 20170071942, Mallinger et al., *J. Med. Chem*. 59:1078, 2016, and Czodrowski et al., *J. Med. Chem*. 59:9337, 2016. In some embodiments, the small molecule inhibitors bind to the ATP binding site of CDK19 to inhibit its activity.

[0144] The small molecule inhibitor of CDK19 may bind to the ATP binding site of CDK19 covalently or non-covalently to inhibit its activity. In other embodiments, the small molecule inhibitor may bind to other parts of CDK19 outside of the ATP binding site. For example, the small molecule inhibitor may form a covalent interaction with an amino acid (e.g.,

methionine, tyrosine, or serine) outside of the ATP binding site to inhibit CDK19 activity. In addition to occupying the ATP binding to inhibit kinase activity, a small molecule inhibitor may also bind to CDK19 to cause a conformational change in CDK19 that prevents CDK19 from functioning. In some embodiments, the small molecule inhibitor may bind to CDK19 with a higher affinity than to CDK8. As shown in FIG. 9, the vast majority of amino acid differences between CDK19 and CDK8 are in the C-terminal domain. In some embodiments, without being bound by any theory, a small molecule inhibitor may bind to an amino acid or a portion in the C-terminal domain of CDK19, that is different from the corresponding amino acid or portion of CDK8, to achieve selective inhibition of CDK19 over CDK8.

[0145] In some embodiments the small molecule inhibitor is other than a compound described in US Patent No. 9,321,737. In some embodiments the small molecule inhibitor is other than a compound described in US Patent Publication No. US 20170071942. In some embodiments the small molecule inhibitor is other than a compound described in, Mallinger et al., *J. Med. Chem.* 59:1078, 2016. In some embodiments the small molecule inhibitor is other than a compound described in Czodrowski et al., *J. Med. Chem.* 59:9337, 2016. In some embodiments the small molecule inhibitor is other than one or more compounds selected from the group consisting of Cortistatin A, Sorafenib, Linifanib, Ponatinib, Senexin B, CCT251545, and CCT251921

3.1.5. CDK19 INHIBITORS THAT DO NOT SIGNIFICANTLY INHIBIT EXPRESSION OR ACTIVITY OF CDK8 OR WHICH INHIBITS EXPRESSION OR ACTIVITY OF CDK19 TO A GREATER EXTENT THAN IT INHIBITS EXPRESSION OR ACTIVITY OF CDK8.

[0146] Agents that inhibitors expression or activity of CDK19 but do not inhibit expression or activity of CDK8, or agents that inhibit expression or activity of CDK19 to a greater extent than expression or activity of CDK8 is inhibited can be designed based on differences in sequence and structure of the CDK19 and CDK8 proteins and their corresponding genes and mRNAs. For example, an alignment of CDK19 and CDK8 mRNA sequences can identify non-identical or low identity nucleotide sequences that can be used to design shRNAs or other nucleic acid agents that associate with CDK19 mRNA but not CDK8 sequences. (see, FIGS 16 and 17). Likewise, aligning CDK19 and CDK8 amino acid sequences can identify divergent regions and antibodies or other binding agents can be produced to specifically bind the CDK19

protein. Likewise, small molecule agents can be identified (by rational drug design or screening) that specifically inhibit CDK19 activity or inhibit CDK19 activity to a greater degree that CDK8 activity.

[0147] The term "an agent that inhibits CDK19 activity but does not significantly inhibit activity of CDK8" as used herein, refers to an agent that is capable of specifically binding and inhibiting the activity of CDK19 such that minimal CDK19 activity is detected *in vivo* or *in vitro*; while the agent causes no significant decrease in CDK8 activity under the same conditions. For example, an agent that inhibits activity of CDK19 can specifically bind to CDK19 and fully or significantly inhibit CDK19 activity *in vivo* or *in vitro*. In some cases, a CDK19 inhibitor can be identified by its ability to preferentially bind to the CDK19 gene or a CDK19 gene product, and fully inhibit expression or activity of CDK19. Inhibition of CDK19 occurs when CDK19 activity, when exposed to an agent, is at least about 70% less, for example, at least about 75%, 80%, 90%, or 95% less than CDK19 activity in the presence of a control or in the absence of the agent. No significant decrease in CDK8 activity occurs when CDK8 activity, upon exposure to the agent, is at least about 90%, for example, at least 95%, 96%, 97%, 98%, 99%, or 100%, in comparison to CDK8 activity in the absence of the agent. As set forth herein, the agent can include small molecules (*i.e.,* a molecule having a formula weight of 1000 Daltons or less), such as small molecule chemical inhibitors or large molecules, such as siRNA, shRNA, antisense oligonucleotides, or proteins.

[0148] Determining the effect of the agent on CDK19 and/or CDK8 activity can be measured using one or more methods known in the art, including but not limited to, half maximal inhibitory concentration (IC_{50}), dissociation constant (K_D), and inhibitor constant (K_I). For example, IC_{50} is a measure of the effectiveness of a substance in inhibiting a specific biological or biochemical function. This value indicates the concentration of the substance needed to inhibit a given biological process (or component of the biological process) by half. The IC_{50} values are typically expressed as molar concentration. According to the Food and Drug Administration (FDA), IC_{50} represents the concentration of a drug required for 50% inhibition *in vitro*. In one embodiment, an agent that inhibits CDK19 activity but does not significantly inhibit activity of CDK8 has an IC_{50} that is at least about 2-fold, 5-fold, 10- fold, 50-fold, 75-fold, or 100-fold, lower than the concentration of the agent required to effect CDK8 activity under the same conditions. In another embodiment, the IC_{50} for the agent to inhibit CDK19

activity is at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99%, lower than the IC_{50} for the agent to inhibit the activity of CDK8.

[0149] In another embodiment, the effect of the agent on CDK19 and CDK8 activity can be determined by calculating the equilibrium dissociation constant (K_D) of the agent to each CDK. For example, an agent that inhibits the activity of CDK19 but does not significantly inhibit activity of CDK8 has a K_D that is at least about 2-fold, 5-fold, 10- fold, 50-fold, or 100-fold lower than the K_D of the agent to CDK8 under the same conditions. In one embodiment, the K_D for the agent (to CDK19) is at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99%, lower than the K_D for the agent (to CDK8). In a preferred embodiment, the K_D is lower for the agent to CDK19 as compared to the K_D of the agent to CDK8. Said differently, the equilibrium dissociation constant of the agent (to CDK8) is greater than the equilibrium dissociation constant of the agent (to CDK19). In one embodiment, the agent can include an antibody having a K_D value in the micromolar (10^{-6}) to nanomolar (10^{-7} to 10^{-9}) range. In another embodiment, the agent can include an antibody having a K_D in the nanomolar range (10^{-9}) to the picomolar (10^{-12}) range. In yet another embodiment, the agent can have a nanomolar (nM) equilibrium dissociation constant to CDK19 and a micromolar (μM) equilibrium dissociation constant to CDK8. US Patent Publication No. US20120071477 describes kinase inhibition assays in which a compound at a single concentration (2,000 nM) to inhibit ATP pocket binding.

[0150] In another embodiment, the effect of the agent on CDK19 and CDK8 activity can be determined by calculating the inhibitor constant (K_I) of the agent to each CDK. The K_I is an indication of how potent an inhibitor is; it is the concentration required to produce half maximum inhibition. The lower the K_I, the greater the binding affinity between the agent and the *CDK* gene. For example, an agent that inhibits the activity of CDK19 but does not significantly inhibit activity of CDK8 has a K_I that is at least about 2-fold, 5-fold, 10- fold, 50-fold, 75-fold, or 100-fold lower than the K_I of the agent (to CDK8) under the same conditions. In one embodiment, the K_I for the agent to CDK19 is at least about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99%, lower than the K_I for the agent to CDK8. In a preferred embodiment, the K_I is lower for the agent to CDK19 as compared to the K_I of the agent to CDK8. Said differently, the inhibitor constant of the agent to CDK8 is greater than the inhibitor constant of the agent to CDK19. For example, an agent that inhibits activity of CDK19 can

bind to CDK19 and significantly inhibit CDK19 activity *in vivo* or *in vitro*. In some cases, a CDK19 inhibitor can be identified by its ability to preferentially bind to CDK19 and fully inhibit activity of CDK19. Inhibition of CDK19 occurs when CDK19 activity, when exposed to an agent of the invention, is at least about 70% less, for example, at least about 75%, 80%, 90%, 95%, 96%, 97%, 98%, 99% less, or totally inhibited, in comparison to CDK19 activity in the presence of a control or in the absence of the agent. No significant decrease in CDK8 activity occurs when, CDK8 activity upon exposure to the agent, is at least about 90%, for example, at least 95%, 96%, 97%, 98%, 99%, or 100%, in comparison to CDK8 activity in the absence of the agent.

[0151] The term "an agent that inhibits activity of CDK19 to a greater extent than it inhibits activity of CDK8" as used herein, refers to an agent that is capable of binding and inhibiting the activity of CDK19 significantly more than the agent's effect on inhibiting the activity of CDK8 under the same conditions. For example, an agent that inhibits activity of CDK19 to a greater extent than inhibiting the activity of CDK8, occurs when CDK19 activity, when exposed to an agent of the invention, is at least about 10% less, for example, at least about 15%, 20%, 30%, 40%, or 50% less, than the activity of CDK8 under the same conditions *in vitro* or *in vivo*. In a preferred embodiment, an agent inhibits the activity of CDK19 to a greater extent than the activity of CDK8, when the activity of CDK19 observed is at least 10% less than the activity of CDK8 under the same conditions. In another embodiment, an agent inhibits the activity of CDK19 to a greater extent than CDK8 activity, when at least 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold less CDK19 activity is observed as compared to CDK8 activity under the same conditions. The extent of inhibition (*i.e.,* comparing CDK19 activity to CDK8 activity) can be determined using one or more methods known in the art, including but not limited to assays described herein in the Examples section of the specification and for example, "Percent Of Control (POC)" or "Normalized Percent Inhibition (NPI)". POC and NPI are methods that normalize data and are often used when comparing multiple agents (*e.g.,* various antibodies or small molecules) against multiple targets (*e.g.,* CDK19 and CDK8). For example, POC is a method that corrects for plate-to-plate variability (for example in high-throughput drug screening) by normalizing an agent's measurement relative to one or more controls present in the plate. Raw measurements for each agent can be divided by the "average" of within-plate controls. NPI is a control-based method in which the difference between the agent

measurement and the mean of the positive controls is divided by the difference between the means of the measurements on the positive and the negative controls (Malo *et al., Nature Biotechnology*, Vol. 24, 167-175 (2006)). By normalizing the extent of inhibition observed, accurate conclusions can be made regarding which agent(s) are effective at inhibiting the activity of each target under investigation.

3.1.6. COMBINATION THERAPY

[0152] In one approach the patient is treated with a combination therapy comprising an agent that inhibits expression or activity of CDK19 and (a) radiation therapy and/or chemotherapy. In one approach radiation or chemotherapy eliminates the bulk of the tumor mass and the CDK19 inhibitor reduces the number of viable cancer stem cells (e.g., $EpCAM^{med/high}/CD10^{-/low}$) cells. In one approach the chemotherapy comprises administration of an anthracycline (e.g., Doxorubicin or Epirubicin), a taxane (e.g., Paclitaxel or Docetaxel), an anti-metabolite (e.g., Capecitabine or Gemcitabine), a platinum agent (e.g., Carboplatin or Cisplatin), Vinorelbine, or Eribulin.

3.2 METHODS OF ASSESSING OR PREDICTING THERAPEUTIC EFFECT

[0153] A course of therapy with the CDK19 inhibitor will have a beneficial outcome for the patient, including, for example, a reduction in tumor volume, a reduction in metastases, and a reduction in tumor cells having the phenotype $EpCAM^{med/high}$ and $CD10^{-/low}$.

[0154] Tumor volume may be measured using art-known methods. See, e.g., Wapnir et al., *Breast Cancer Res Treat* 41:15-19, 1996; Sapi et al., *PLoS One* 10:e0142190, 2015. Tumor volume may be reduced by at least 10%, optionally at least 20% and sometimes by at least 50% after a course of treatment with a CDK19 inhibiting agent as monotherapy or in combination with other agent(s) or treatments. In some embodiments, the reduction in tumor volume (e.g., at least 10%, 20%, or 30% reduction in tumor volume) may be observed as soon as within 1 month of initiating therapy. In other embodiments, the reduction in tumor volume (e.g., at least 10%, 20%, 30%, 40%, 50%, or 60% reduction in tumor volume) may be observed within 2, 3, 4, 5, or 6 months of initiating therapy. In other embodiments, the methods described herein to treat TNBC may also slow down or inhibit the further growth of

a tumor. In some embodiments a patient receives combination therapy and a therapeutic benefit is observed that exceeds that of monotherapy with the second agent.

[0155] A reduction in metastases in an individual may be determined as described in Makela et al., *Sci Rep*. 7:42109, 2017 and may be observed in a population according to standard methodology.

[0156] In some embodiments, the presence or amount of cancer cells having the expression profile $EpCAM^{med/high}$ and $CD10^{-/low}$ in a TNBC tumor tissue obtained from a subject may be used to predict or assess the therapeutic responsiveness of the subject to treatments that target the *CDK19* gene or its corresponding protein. As described and demonstrated herein, cells having the expression profile $EpCAM^{med/high}/CD10^{-/low}$ have a high tumor initiating capacity and are also enriched in CDK19. In some embodiments, subjects having a high percentage of $EpCAM^{med/high}$ and $CD10^{-/low}$ TNBC cells may be especially responsive.

[0101] In one approach the likely therapeutic responsiveness of a subject with TNBC to a CDK19 targeting agent is determined by (a) quantitating $EpCAM^{med/high}/CD10^{-/low}$ cells in a tumor sample obtained from the subject; (b) comparing the quantity of $EpCAM^{med/high}/CD10^{-/low}$ cells in (a) to a reference value characteristic of tumors responsive to a CDK19 targeting therapy, and treating the patient with an inhibitor of CDK19 expression or activity if the quantity of $EpCAM^{med/high}/CD10^{-/low}$ cells is equal to or exceeds the reference value. The reference value can be determined by quantitating $EpCAM^{med/high}/CD10^{-/low}$ cells in healthy and TNBC populations and calculating statistically significant ranges characteristic of healthy and tumor tissues. In another approach tumor tissue and healthy tissue from the same subject can be tested, and subjects with elevated $EpCAM^{med/high}/CD10^{-/low}$ cells in tumor relative to healthy tissues can be identified as likely to respond to CDK19 targeted therapy.

3.3 DELIVERY OF AGENTS

[0157] The pharmaceutical compositions used in methods described herein may include an active ingredient and one or more pharmaceutically acceptable carriers or excipients, which can be formulated by methods known to those skilled in the art. In some embodiments, a pharmaceutical composition of the present invention includes, in a therapeutically effective amount, a DNA or RNA oligonucleotide that decreases the expression level of the *CDK19* gene. In other embodiments, a pharmaceutical composition of the present invention includes, a

pharmaceutical composition of the present invention includes a DNA or RNA oligonucleotide in a therapeutically effective amount, a small molecule that inhibits the activity of CDK19. The therapeutically effective amount of the active ingredient in a pharmaceutical composition is sufficient to prevent, alleviate, or ameliorate symptoms of a disease or to prolong the survival of the subject being treated. Determination of a therapeutically effective amount is within the capability of those skilled in the art.

[0158] In certain embodiments, a pharmaceutical composition of the present invention is formulated as a depot preparation. In general, depot preparations are typically longer acting than non-depot preparations. In some embodiments, such preparations are administered by implantation (for example subcutaneously) or by intramuscular injection. In some embodiments, depot preparations are prepared using suitable polymeric or hydrophobic materials (for example an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

[0159] In some embodiments, a pharmaceutical composition may include a delivery system. Examples of delivery systems include, but are not limited to, exosomes, liposomes, and emulsions. In some embodiments, an active ingredient may be loaded or packaged in exosomes that specifically target a cell type, tissue, or organ to be treated. Exosomes are small membrane-bound vesicles of endocytic origin that are released into the extracellular environment following fusion of mutivesicular bodies with the plasma membrane. Exosome production has been described for many immune cells including B cells, T cells, and dendritic cells. Techniques used to load a therapeutic compound into exosomes are known in the art and described in, e.g., U.S. Patent Publication Nos. US 20130053426 and US 20140348904, and International Patent Publication No. WO 2015002956, which are incorporated herein by reference. In some embodiments, therapeutic compounds may be loaded into exosomes by electroporation or the use of a transfection reagent (i.e., cationic liposomes). In some embodiments, an exosome-producing cell can be engineered to produce the exosome and load it with the therapeutic compound. For example, exosomes may be loaded by transforming or transfecting an exosome-producing host cell with a genetic construct that expresses the active ingredient (i.e., a DNA or RNA oligonucleotide), such that the active ingredient is taken up into the exosomes as the exosomes are produced by the host cell. Various targeting moieties may be introduced into exosomes, so that the exosomes can be

targeted to a selected cell type, tissue, or organ. Targeting moieties may bind to cell-surface receptors or other cell-surface proteins or peptides that are specific to the targeted cell type, tissue, or organ. In some embodiments, exosomes have a targeting moiety expressed on their surface. In some embodiments, the targeting moiety expressed on the surface of exosomes is fused to an exosomal transmembrane protein. Techniques of introducing targeting moieties to exosomes are known in the art and described in, e.g., U.S. Patent Publication Nos. US 20130053426 and US 20140348904, and International Patent Publication No. WO 2015002956, which are incorporated herein by reference.

4. EXAMPLES

4.1 Example 1 - Materials and Experimental Methods

Chemical reagents

[0160] The following are the chemical names for the compounds used in this study. CCT152921 is 4-[(2-Phenylethyl)amino]-6-quinazolinecarbonitrile (NIH NCAT). The compound was re-suspended in vehicle (PBS + 0.5% Methocel (w/v) + 0.25% Tween 20 (v/v)) to a concentration of 3 mg/mL and mice were dosed at 30 mg/kg. CCT251921 or vehicle was administered via daily oral gavage.

shRNA expression lentiviral plasmids

[0161] Pairs of complementary ssDNA oligonucleotides containing the sense target sequence, a 15-mer loop sequence (5'-GTTAATATTCATAGC-3' SEQ ID NO: 19), and the reverse complement of the sense sequence were synthesized (Elim Biopharmaceuticals). The oligonucleotides were annealed in 50 µM annealing buffer (10 mM Tris-HCl pH 8.0, 50 mM NaCl, 1 mM EDTA). The double-stranded DNA oligo templates were subsequently cloned into the pRSI12-U6-(sh)-HTS4-UbiC-TagRFP-2A-Puro shRNA expression vector (Cellecta) digested with *BbsI* for constitutively active shRNA vector constructs and pRSITUR-U6Tet-(sh)-UbiC-TetRep-2A-TagRFP digested with *BbsI* for inducible shRNA vector constructs. The sense strands in the shRNA vectors used in this study were: 5'-GCG AGA ATT GAA GTA CCT TAA-3' (shCDK19-1 (SEQ ID NO: 1)), 5'-ACC AGC AAA TAT CCT AGT AAT-3' (shCDK19-2 (SEQ ID NO:2)), and 5'-GCA GGG TAA TAA CCA CAT TAA-3' (shCDK8-2 (SEQ ID NO: 3)). The unmodified pRSI12-U6-(sh)-HTS4-UbiC-TagRFP-2A-Puro shRNA expression vector above was used as the 'empty' control shRNA. The pHIV-ZsGreen expression vector (Addgene) was used to produce GFP

positive tumor cells. The DECIPHER 27K Pooled shRNA lentivirus library – Human Module 1 (Cellecta) used for the RNAi screen contains 27,500 unique shRNA constructs targeting 5,043 human genes (approximately five or six redundant shRNAs per gene) in the same pRSI12 shRNA expression vector.

Cell lines

[0162] MDA-MB231, MDA-MB468, HS578T, and 293T cells were obtained from ATCC. HMEC cells were obtained from ThermoFisher Scientific. These cells were certified by the vendors to be mycoplasma free. None of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC. All cell lines used were passaged less than 10 times from when the original cells from the vendors were thawed. All MDA-MB231, MDA-MB468, 293T, and HS578T cells were grown in DMEM (Invitrogen) supplemented with PSA (Life Technologies), 10% FBS (Hyclone), Glutamax (ThermoFisher Scientific), and sodium pyruvate (Life Technologies). HMEC cells were grown in HuMEC Ready Medium (ThermoFisher Scientific).

Mice

[0163] Nod *scid* gamma (NSG) mice (NOD.Cg-Prkdc^{scid} IL2Rg^{tm1Wjl}/SzJ) were purchased from the Jackson Laboratory. Mice used for PDX experiments were adult female mice between 8 and 10 weeks old. All the mice used in this study were maintained at the Stanford Animal Facility in accordance with a protocol approved by the Stanford University APLAC committee. Mice were maintained in-house under aseptic sterile conditions. Mice were administered autoclaved food and water. For PDX experiments utilizing doxycycline inducible constructs, mice were provided rodent feed containing 625 mg Doxycycline hyclate/kg diet (Envigo) in place of their normal rodent diet.

PDX Tumors and their pathological and clinical characteristics

[0164] For human samples, informed consent was obtained after the approval of protocols by the Institutional Review Boards of Stanford University and The City of Hope. See FIG. 15 for a full description of all the PDX tumors used in this study.

Single cell suspension of PDX tumor cells

[0165] Xenografts were mechanically chopped with a razor blade to approximately 1 mm pieces and then incubated at 37 ºC for 3 to 4 hours with collagenase and hyaluronidase (Stem Cell Technologies) in Advanced DMEM/F12 (Invitrogen) with 120 µg/mL penicillin, 100 µg/mL

streptomycin, 0.25 µg/mL amphotericin-B (PSA) (Life Technologies). Cells were then treated with ACK lysis buffer (Gibco) to lyse red blood cells, followed by 5 mins of treatment with pre-warmed dispase (Stem Cell Technologies) plus DNAseI (Sigma) and filtered through a 40 µm nylon mesh filter. Cells were finally washed with flow cytometry buffer (HBBS, 2% FCS, PSA).

Enrichment of PDX tumor cells

[0166] After PDX tumors were dissociated into single cells, the number of live cells were determined with Trypan blue staining and manually counted with a hemocytometer. Cells were resuspended with flow cytometry buffer to a concentration of 10^6 live cells/mL and incubated 1:50 (v/v) with Biotin anti-human CD326 (EpCAM) antibody (Biolegend) for 20 mins at 4 ºC. Cells were washed with flow cytometry buffer and then resuspended to 80 µL and incubated with 20 µL anti-biotin microbeads (Miltenyi Biotec) for 20 mins at 4 ºC. Cells were then washed with flow cytometry buffer and resuspended in 500 µL of buffer. Cells were applied to magnetized LS columns (Miltenyi Biotec), washed, and eluted off magnet per manufacturer's protocol.

Lentivirus production

[0167] Lentivirus was produced with Packaging Plasmid Mix (Cellecta) and subcloned pRSI12 shRNA expression plasmids using Lipofectamine 2000 (Thermofisher Scientific) in 293T cells per manufacturer's instructions. Supernatants were collected at 48 h and 72 h, filtered with a 0.45 µm filter and precipitated with Lentivirus Precipitation Solution (Alstem LLC) per manufacturer's instructions. Virus was resuspended in 1/100 original volume. Viral titers were determined by flow cytometry analyses of 293T cells infected with serial dilutions of concentrated virus.

Lentivirus infection

[0168] For *in vitro* cell line experiments, concentrated lentiviral supernatant (to achieve an MOI of 3) was mixed with cells at the time of seeding. Cells were monitored by visualization of RFP under fluorescence microscopy. All flow cytometry analyses were performed after at least 72 hours of infection.

[0169] For *in vivo* PDX tumor growth and organoid colony formation experiments, concentrated lentiviral supernatant (to achieve an MOI of 10) was mixed with single cell suspensions of PDX tumor cells in organoid media with 4 µg/mL of Polybrene (Sigma-Aldrich). Organoid media consisted of: Advanced DMEM/F12 (Invitrogen), 10% FBS (Hyclone), 2.5%

growth factor-reduced Matrigel (BD), 10 ng/mL mouse EGF (R&D), 100 ng/mL Noggin (R&D), 250 ng/mL RSPO-I (R&D), 1X B27 (Invitrogen), 1X N2 (Invitrogen), and PSA (Life Technologies). Cells were then spinoculated by centrifuging at 15 ºC for 2 hours at 1200x*g*. Cells were resuspended by pipetting and left overnight in 48-well ultra-low attachment cell culture plates (Corning).

[0170] For organoid colony formation assays, cells were transferred the next day to matrigel. For *in vivo* PDX assays, approximately 75% of the cells were injected into NSG mice as described in the PDX tumor engraftment section. The remainder 25% of cells were plated on matrigel and grown in organoid media for 72 hours until the cells became RFP positive. At that point media was removed and exchanged for dispase and incubated for 2-3 h until the matrigel dissolved. Dissociated cells were resuspended in flow cytometry buffer and analyzed by flow cytometry to determine the 'baseline' RFP percentage for cells that were injected into the mice.

Organoid colony formation assay

[0171] Irradiated L1-Wnt3a feeder cells (generous gift of Dr. Roel Nusse) were mixed with growth factor reduced matrigel (BD Biosciences) and allowed to solidify at 37 ºC. Single cell suspensions of PDX tumor cells were transferred onto the solidified matrigel/feeder cell mix substrate and grown in organoid media. Cells were grown for approximately 2 weeks in a 37 ºC incubator with 5% CO_2. 50% of media was exchanged with fresh media every 3-4 days. Colonies were counted under fluorescence microscopy. Only RFP positive colonies (which represent transduced cells) were counted. For experiments in which we induced expression of CDK19 shRNA, doxycycline hyclate was added to a final concentration of 100 ng/mL into the media.

Cell viability assay

[0172] For cell lines treated with chemical or infected with lentivirus, WST-1 Cell Proliferation Reagent (Roche) was added at 1:10 (v/v) final dilution to each well per manufacturer's instructions. Cells were subsequently incubated at 37 ºC and 5% CO_2. Between 1 and 4 hours after addition of reagent, plates were analyzed on a SpectraMax M3 Bioanalyzer (Molecular Devices). Absorbance for each well was measured at 450 nm (signal wavelength) and 650 nm (reference wavelength). Thus, the signal for each experimental sample was $Absorbance_{experimental}$ (A_{450nm}-A_{650nm}). To correct for the effect of media,

$Absorbance_{background}$ (A_{450nm}-A_{650nm}) was obtained by measuring absorbance in a blank well. Thus, the background corrected signal for each sample $A_{corrected}$ = $Absorbance_{experimental}$ - $Absorbance_{background}$. All $A_{corrected}$ values for the knockdowns were normalized to the $A_{corrected}$ value for the control sample to obtain a 'Relative Viability'.

Quantitative PCR RNA expression analyses

[0173] Cells were lysed with Trizol (Life Technologies) and RNA was extracted according to the manufacturer's instruction. RNA was then treated with DNAseI to remove contaminating genomic DNA. RNA was reverse transcribed to cDNA using SuperScript III First Strand Synthesis kit (Life Technologies) according to the manufacturer's instructions. TaqMan Gene Expression Master Mix (Applied Biosystems) and the following TaqMan Gene Expression Assays (Applied Biosystems) were used following manufacturer's instructions: *ACTB*, Hs00357333_g1; *CDK19*, Hs01039931_m1; *CDK8*, Hs00993274_m1. Data was collected on a 7900HT Fast Real-Time PCR System (Applied Biosystems) and data analyzed with SDS 2.4 software (Applied Biosystems). Gene expression data in each sample was normalized against the expression of beta-actin.

PDX tumor cell engraftment and limiting dilution assays

[0174] Single cell suspensions of PDX cells were resuspended in 50% (v/v) mixtures of normal matrigel (BD Biosciences) and flow cytometry buffer in a total volume of 50-100 µL. Using an insulin syringe, cells were injected subcutaneously into the nipple of female NSG mice at the fourth abdominal fat pad. For limiting dilution assays, the specific number of cells injected into the mice were determined by flow cytometry and secondarily by manual counting with a hemocytometer.

PDX tumor growth and total body weights

[0175] PDX tumors were detected by palpation. Tumor volumes were determined by measuring the length (l) and width (w) and calculating volumes using the ellipsoid formula $1/6 \times l \times w^2 \times \pi$. Tumors volumes and mice weights were determined twice per week.

Mouse PDX tumor and lung dissection

[0176] Xenograft tumors and mice lungs were surgically resected after the mice were euthanized. A 3 to 4 mm section is cut from each tumor and saved in ice cold PBS for imaging. The mice lungs and tumors were imaged on a M205FA Fluorescence Stereo Microscope (Leica) and images were captured with a DFC310FX camera (Leica).

Flow cytometry to determine RFP percentage

[0177] Flow cytometry was performed with a 100 µm nozzle on a Flow Cytometry Aria II (BD Biosciences) with Diva software (BD Biosciences). Data analysis was performed using Flowjo software (Flowjo). For all experiments, side scatter and forward scatter profiles (area and width) were used to eliminate debris and cell doublets. Dead cells were eliminated by excluding 4',6-diamidino-2-phenylindole (DAPI)-positive cells (Molecular Probes). For PDX tumor cells, they were gated for GFP positivity and then for RFP positivity. RFP percentage is the percentage of GFP positive cells that are also RFP positive. For each sample, we obtain the RFP fraction that is: the RFP % in the tumor divided by the baseline RFP % (see 'Lentivirus infection' section). RFP fraction for each sample is then normalized to the RFP fraction for the shRNA control sample which is set at 100% to obtain the 'Normalized % RFP'.

Flow cytometry using EpCAM, CD10, and CD49f cell surface markers for analysis and cell sorting

[0178] Flow cytometry for analysis and cell sorting was performed as previously described. Human antibodies used included: EpCAM–Alexa Fluor 488 (clone 9C4, Biolegend); 1 µg mL^{-1}, CD49f–APC (clone GoH3, Biolegend); CD10 PeCy7/Apc–Cy7 (clone H110a, Biolegend); 1 µg mL^{-1} and H-2Kd biotin/Pacific Blue (clone SF1-1.1, Biolegend); 1 µg mL^{-1}.

RNAi dropout viability screen

[0179] GFP positive PDX-T1 tumors grown in NSG mice were dissected, processed to single cells, and enriched with EpCAM as described previously. Analysis of cells at this point showed that they were approximately 98%-100% GFP positive.

[0180] For the *in vitro* RNAi dropout viability screen, 60 million dissociated PDX-T1 cells were transduced with the DECIPHER 27K Pooled shRNA lentivirus library–Human Module 1 (Cellecta) at an MOI of 1 in the presence of polybrene and then spinoculated for 2 hours as described previously. The next day, half the cells were spun down and frozen as the *in vitro* baseline reference sample. A small number of cells were plated separately in organoid colony formation conditions to determine lentiviral infection percentage after 72 hours (cells were found to be approximately 80% RFP positive). The remainder of the cells were plated into twelve 150 mm dishes prepared with 12 mL matrigel containing irradiated L1-Wnt3a feeder cells at 250,000 cells/mL of matrigel. The cells were grown for 19 days with an exchange for fresh media every 3-4 days. On the final day, all the media was exchanged with dispase in

order to dissolve the matrigel and to recover the cells. The cells from all the plates were pooled, washed, and frozen as the *in vitro* organoid growth experimental sample.

[0181] For the *in vivo* RNAi dropout viability screen, 30 million dissociated PDX-T1 cells were transduced with the DECIPHER 27K Pooled shRNA lentivirus library–Human Module 1 (Cellecta) at an MOI of 1.25 in the presence of polybrene and then spinoculated for 2 hours as described previously. The next day, half the cells were spun down and frozen as the *in vivo* baseline reference sample. A small number of cells were plated separately in organoid colony formation conditions to determine lentiviral infection percentage after 72 hours (cells were found to be approximately 70% RFP positive). The remainder of the cells were resuspended in 50% (v/v) mixtures of normal matrigel (BD Biosciences) and flow cytometry buffer in a total volume of 1.8 mL. These cells were injected evenly into the right and left mammary fat pads of seventeen NSG mice. When tumors reached approximately 10 mm in diameter, the mice were euthanized and the tumors dissected as previously described. These tumors were then processed into single cells, pooled, washed, and frozen as the *in vivo* growth experimental sample.

[0182] The two pairs of samples, *in vitro* baseline reference sample and *in vitro* organoid growth experimental sample and *in vivo* baseline reference sample and *in vivo* growth experimental sample, were submitted to Cellecta, Inc. for genomic DNA extraction, bar code amplification, high-throughput sequencing and de-convolution. Twenty million barcode reads were performed for each sample.

'Hit' selection algorithm from the *in vivo* and *in vitro* RNAi dropout viability screens

[0183] Please see the schematic in FIG. 5C for an overview. We applied an algorithm to narrow our hits to a more manageable number for validation. 1) for each individual shRNA we determined a 'dropout ratio' that was shRNA barcode counts in the growth experimental sample divided by shRNA barcode counts in the baseline reference sample. In each screen, these were ranked from lowest to highest. 2) We examined the top 5% of the lowest dropout ratios in each experiment and identified genes targeted by ≥ 2 shRNA. 3) We cross-referenced the shRNA gene targets in the *in vivo* screen (208 genes) with those in the *in vitro* screen (150 genes) to identify genes that overlapped between the two experiments. These 46 overlapping 'hit' genes are shown in FIG. 5A.

Immunofluorescence of PDX tumors

[0184] Sections of the PDX tumors were fixed in formalin overnight and then transferred to 70% ethanol. Samples were then embedded in paraffin and sectioned for histology. Formalin fixed paraffin embedded sections were de-parafinized in xylene and rehydrated in an ethanol gradient. Antigen retrieval was performed in a Tris-EDTA buffer by heating in a microwave for 20 min. The primary antibodies, polyclonal Rabbit anti-CDK19 (Sigma) and polyclonal chicken anti-CDK8 (Novus Biologicals), were diluted 1:50 and 1:100, respectively, in TBS + 1% BSA before applying to samples overnight. After overnight incubation, the secondary antibodies, Cy3 Donkey anti-Rabbit (Jackson ImmunoResearch) and Alexa 488 Goat anti-Chicken (Life Technologies) were diluted 1:500 in TBS + 1% BSA and incubated with the samples at room temperature. After DAPI staining, sections were mounted with ProLong® Gold antifade (Cell Signaling). A Zeiss LSM710 Confocal microscope (Carl Zeiss) was used to take the immunofluorescence images. Images for publication were processed with Fiji software.

Microarray Experiment

[0185] EpCAM enriched PDX-T1 cells were infected with shCDK19-2, shCDK8-2 or control shRNA and grown in organoid culture conditions for 72 hours. They were subsequently recovered from matrigel with dispase, resuspended in flow cytometry buffer and sorted by flow cytometry to obtain cells that were both GFP and RFP positive. RNA was extracted from these cells by RNeasy plus micro kit (Qiagen) according to manufacturer's instructions and quantified on an Agilent 2100 Bioanalyzer. 50 ng of total RNA from each sample was used. *In vitro* transcription, fragmentation, labeling, hybridization to the microarray and scanning was performed by the Stanford Protein and Nucleic acid facility (PAN facility). Samples were hybridized on PrimeView Human Gene Expression Arrays (Affymetrix). Gene Level Differential Expression Analysis was performed with the Transcriptome Analysis Console (Affymetrix). Downregulated genes were defined as those for which $\log_2$ (sample/control) < -1.5 and upregulated genes $\log_2$ (sample/control) > 1.5.

H3K27Ac Chromatin Immunoprecipitations

[0186] ChIP assays were performed as described in, e.g., Zarnegar et al., *Nucleic Acids Research*, gkx648, July, 2017. Approximately 250,000 to 500,000 MDA-MB231 cells were used per ChIP. 1µg of anti-H3K27ac (Active Motif #39133) were used per ChIP.

Library construction

[0187] ChIP enriched DNA was quantified using a Qubit 3.0 and dsDNA HS assay. Up to 1 ng of DNA was used for library construction using transposition based NEXTERA XT (followed manufacturer's protocol with ~14 PCR cycles for indexing). Indexed samples were pooled and submitted for sequencing on a NextSeq500 to obtain 75 bp single end reads with read depths of ~60 million reads.

Sequence analysis.

[0188] Raw sequence reads were uploaded to Galaxy (usegalaxy.org) and aligned to the human genome (hg19) using Bowtie2 (-very-fast-local). Only uniquely mapped reads were retained for further analysis. To visualize data, alignment files were used to produce signal tracks with DeepTools (100 bp bins with 200 bp read extensions and RPKM normalization) and BigWig files were loaded into Broad's Integrated Genome Browser. MACS2 was used to call peaks (-nomodel, p=0.01, -broad, cuttoff 0.1, duplicates = auto, extension 200) for each replicate. A consensus peak list containing only those peaks occurring in all replicates, was generated using Bedtools. We performed differential peak analysis across consensus peaks using DiffBind. The DiffBind output peak list was annotated by fetching the nearest non-overlapping feature of the human RefSeq table from UCSC. Data for aggregation plots of ChIP signal across various peaks sets were generated using DeepTools' computeMatrix (scale-regions: 1000; 50 bp bins) and plotProfile. Data was then plotted with GraphPad Prism software.

GSEA Analysis

[0189] Gene set enrichment analysis (GSEA) was performed using the javaGSEA desktop application (GSEA 3.0) with $\log_2$ fold change values for *CDK19* knockdown versus Control as the ranking metric and Hallmarks, CDK19KD-EnhancerUp and CDK19KD-EnhancerDOWN as the gene sets that were tested for enrichment.

Metascape Analysis

[0190] Metascape custom enrichment analysis of Hallmark gene sets using the CDK19KD-EnhancerUP 'core' genes and the CDK19KD-EnhancerDOWN 'core' genes (using the following parameters: *H. Sapiens* as the input species, p-value cutoffs of 0.01 and minimum enrichment 1.5) was performed online (www.metascape.org).

Statistical Analysis

[0191] Results are shown as mean ± s.d. Statistical calculations were performed with GraphPad Prism software (GraphPad Software Inc). Variance was analyzed using the F-test. To determine *P*-values, *t*-test was performed on homoscedastic populations, and *t*-test with Welch correction was applied on samples with different variances. For animal studies, sample size was not predetermined to ensure adequate power to detect a pre-specified effect size, no animals were excluded from analyses, experiments were not randomized and investigators were not blinded to group allocation during experiments.

4.2 Example 2 - Identification of Genes Essential for TNBC Growth

[0192] To identify genes essential for the growth of TNBC, two pooled RNAi dropout viability screens were performed using a 27,500 shRNA library targeting 5000 genes in PDX-T1, a TNBC PDX (FIG. 15). The screens were performed in two different formats, *in vitro* as organoid cultures and *in vivo* as PDXs in *nod scid gamma* (NSG) mice (FIG. 1A). The abundance of individual shRNA in each experimental sample and the baseline reference samples were determined by high throughput sequencing of the shRNA barcodes. The goal was to identify genes whose knockdown by shRNA inhibited the growth of PDX tumor cells across different experimental conditions. Consistent with screens in other tumors, the *in vivo* screen had a more significant shRNA dropout rate (FIG. 5A) compared to the *in vitro* screen (FIG. 5B). FIGS. 5A and 5B are graphs showing the shRNA counts in the *in vivo* growth experimental sample (FIG. 5A) and in the *in vitro* growth experimental sample (FIG. 5B) versus the shRNA counts in the baseline sample. Control shRNA targeting luciferase (light gray dots) and shRNA targeting *CDK19* (dark gray dots) are highlighted. All other shRNA are shown as black dots (each experiment performed once). The final candidate list was restricted to genes with the lowest 5% of shRNA ratios in each screen that were targeted by more than two shRNAs and were also identified both *in vitro* and *in vivo* (FIG. 5C). This resulted in the identification of 46 candidate genes (FIG. 5D).

[0193] CDK19 was chosen because data from the Cancer Genome Atlas (TCGA) showed that *CDK19* copy number amplifications and mRNA upregulation were more prevalent in TNBC patient samples (23%) compared to samples from other breast cancer subtypes (see, e.g., Cancer Genome Atlas Research, N. *et al.* The Cancer Genome Atlas Pan-Cancer analysis

project. *Nat Genet* 45:1113-1120, 2013; FIG. 6A). Additionally, high *CDK19* expression has been reported to correlate with poor relapse free survival in breast cancer patients (see, e.g., Broude et al., *Current cancer drug targets* 15, 739-749, 2015 and Porter et al., *Proc Natl Acad Sci U S A* 109: 13799-13804, 2012). CDK19 belongs to a subset of the CDK family that is reportedly more associated with regulation of RNA polymerase II (RNAPII) transcription than cell cycle progression. CDK19 and its paralog, CDK8, can both form the CDK module (CKM) by binding with three other proteins: MED12, MED13, and Cyclin C. The presence and nuclear localization of CDK19 in our PDX cells were confirmed by immunofluorescence (FIG. 6B). In FIGS. 6A and 6B, the percentage shows the percentage of samples with *CDK19* copy number amplifications or *CDK19* mRNA upregulation in triple-negative, HER2 positive, estrogen receptor positive, and all breast cancers. The fractions show the number of positive samples and total samples in each group. Data obtained from cBioPortal (see, e.g., Gao et al., *Sci Signal* 6, pl1, 2013).

4.3 Example 3 - Growth Inhibitory Effects of *CDK19* Knockdown

[0194] To validate the growth inhibitory effect of *CDK19* knockdown, three commonly used TNBC cell lines: MDA-MB231, MDA-MB468, and HS578T were used. Using two different shRNAs (shCDK19-1 (SEQ ID NO: 1) and shCDK19-2 (SEQ ID NO: 2)) that independently target *CDK19*, the knockdown of *CDK19* (FIGS. 7A and 7B) was confirmed. For both FIGS. 7A and 7B, the relative expression of *CDK19* in *CDK19* knockdown cells is normalized to the mean expression of *CDK19* in cells transduced with control shRNA. Gene expression in each condition is normalized to beta-actin as a housekeeping gene (**$P < 0.01$; ****$P < 0.0001$, mean ± s.d., (FIGS. 7A and 7B) n = 3 (FIG. 7C) n =2, experiments performed twice). The knockdown of *CDK19* also showed that it caused decreased proliferation in all three TNBC cell lines (FIGS. 1B-1D). FIGS. 1B-1D demonstrate that *CDK19* knockdown significantly decreased the viability of TNBC cells (viability of MDA-MB231 cells, ****$P < 0.0001$ (FIG. 1B), MDA-MB468 cells, ***$P < 0.001$; ****$P < 0.0001$ (FIG. 1C), or HS578T cells, *$P < 0.05$; ****$P <$ 0.0001 (FIG. 1D) assessed 4 days after transduction with control shRNA or *CDK19* targeting shRNA (shCDK19-1, shCDK19-2)). All values in FIGS. 1B-1D were normalized to control shRNA sample (mean ± s.d., n = 3, experiment performed twice, *P* values determined by unpaired t-test).

[0195] In the same TNBC PDX used in the initial dropout screen (PDX-T1), *CDK19* knockdown (FIG. 7C) also inhibited the formation of organoid colonies (FIG. 1E). In FIG. 1E, colonies were counted 2 weeks after transduction with either control shRNA or *CDK19* targeting shRNA (shCDK19-1, shCDK19-2), ***$P < 0.001$ (unpaired t-test) (mean ± s.d., n = 6, experiment performed twice). To determine the effects of *CDK19* knockdown in non-transformed mammary cells, human mammary epithelial cells (HMEC) were infected with shRNA targeting *CDK19*. In HMECs, neither of the two *CDK19* knockdowns affected the viability of the cells (FIG. 1F). In FIG. 1F, viability of HMEC cells was assessed 4 days after transduction with control shRNA or *CDK19* targeting shRNA (shCDK19-1, shCDK19-2). All values are normalized to control shRNA sample, ns is $P > 0.05$ (mean ± s.d., n = 6, experiment performed twice, *P* values determined by unpaired t-test). Collectively, the studies show that *in vitro*, *CDK19* knockdown inhibits the proliferation of multiple TNBC cell lines and the formation of PDX organoid colonies but does not adversely affect the growth of non-transformed mammary epithelial cells.

[0196] We extended our studies to more physiologically relevant *in vivo* systems by knocking down *CDK19* in three different TNBC PDXs grown in NSG mice. These PDXs: PDX-T1, PDX-T2, and PDX-T3 were derived from chemotherapy naive patients (FIG. 15). In these studies, all PDX tumor cells were first labeled with green fluorescent protein (GFP) and cells subsequently infected with either *CDK19* shRNA or control shRNA were additionally labeled with red fluorescent protein (RFP). Measuring the percentage of GFP-labeled tumor cells that were also RFP positive allowed us to determine the effect the shRNA had on the PDX tumor cells. With each of the two *CDK19* shRNAs tested, *CDK19* knockdown led to a significant reduction in the percentage of RFP positive cells in tumors from all three TNBC PDXs (FIGS. 1G-1I and FIG. 1M). Tumor growth was monitored and tumors were analyzed when they exceeded 17 mm. The percentage of RFP positive cells in PDX-T1, ***$P < 0.001$; ****$P < 0.0001$ (FIG. 1G), PDX-T2, ****$P < 0.0001$ (FIG. 1H), PDX-T3, **$P < 0.01$ (FIG. 1I), or PDX-T4, **$P < 0.01$ (FIG. 1J) were determined by flow cytometry and normalized to the mean RFP percentage of the control shRNA sample that was set to 100%. Each data point represents one mouse. For FIGS. 1H and 1H, mean ± s.d., n = 9, experiment performed three times. For FIGS. 1I and 1J, mean ± s.d., n = 3, experiment performed once. For all, *P* values determined by unpaired t-test).

[0197] FIG. 1M shows representative images of PDX-T1 tumors transduced with control shRNA (top row), shCDK19-1 (middle row), or shCDK19-2 (bottom row). Bright field images (left column) show gross tumor morphology, FITC images (middle column) identify tumor cells labeled with GFP and Texas-Red images (right column) identify shRNA-transduced cells labeled with RFP.

[0198] These results confirmed that CDK19 is critical for tumor growth *in vivo*. *CDK19* knockdown prevented transduced (RFP positive) TNBC cells from metastasizing to the lungs in mice. Percentage of mice with RFP positive lung metastases from mice bearing PDX-T1 (FIG. 1K) or PDX-T4 (FIG. 1L) tumor xenografts are shown. Number of mice with RFP positive lung metastases and total number of mice in each treatment group is shown as a fraction for each condition. PDX tumor cells were transduced with either control shRNA or *CDK19* targeting shRNA (shCDK19-1, shCDK19-2) (For FIG. 1K, n = 9, experiment performed three times; For FIG. 1I, n = 3, experiment performed once). Furthermore, in PDX-T1, which normally metastasizes to lung, *CDK19* knockdown eliminated the detection of any lung metastases by those cells (FIG. 1K and FIG. 1N). In FIG. 1N, bright field images (left column) show gross lung morphology, FITC images (middle column) identify metastatic tumor cells labeled with GFP, and Texas-Red images (right column) identify shRNA-transduced metastatic cells labeled with RFP. We also tested the effect of *CDK19* knockdown on PDX-T4, an aggressive PDX obtained from the brain metastasis of a patient with a chemotherapy-resistant inflammatory breast cancer. Since inflammatory breast cancers are known to be aggressive, difficult to treat, and associated with extremely poor prognoses, it is notable that *CDK19* knockdown inhibited both the growth of the PDX (FIG. 1J) and the lung metastases in these mice (FIG. 1L and FIG. 7D). These data show that *in vivo*, *CDK19* knockdown not only affected primary tumor growth, but also inhibited tumor metastasis.

4.4 Example 4 - Identification of Tumor Initiating Cells (TICs) within the TNBC PDXs

[0199] Given that *CDK19* knockdown inhibited growth in two independent assays commonly used to assess tumorigenicity (PDX growth *in vivo* and organoid colony formation *in vitro*) and genes critical for tumor initiation are frequently amplified or overexpressed in a subset of cancers, it is hypothesized that the tumor initiating cells (TICs) might be sensitive to CDK19 inhibition. Thus, we sought to identify the TICs within the TNBC PDXs. Previously,

EpCAM and CD49f were utilized to isolate cell sub-populations in normal breast tissue and in breast cancers. However, in many TNBC PDXs, EpCAM and CD49f often cannot clearly separate cells into distinct sub-populations (FIG. 2A, left). Thus, we utilized the basal cell marker, CD10 with EpCAM to FACS-sort breast cancer PDXs. We discovered that CD10 and EpCAM can separate PDX cells into three distinct sub-populations, $EpCAM^{med/high}/CD10^{-/low}$, $EPCAM^{low/med}/CD10^{low/+}$, and $EpCAM^{-}/CD10^{-}$ (FIG. 2A, right). In FIG. 2A, the large inseparable cell population (left) seen using EpCAM and CD49f, becomes three distinct sub-populations using EpCAM and CD10 (right): $EpCAM^{med/high}/CD10^{-/low}$ (gate (1)), $EPCAM^{low/med}/CD10^{low/+}$ (gate (2)) and $EpCAM^{-}/CD10^{-}$ (gate (3)). The overlap of these three sub-populations using EpCAM and CD49f is also shown (FIG. 8A).

[0200] To test the tumor initiating capacity of the three EpCAM/CD10 separated sub-populations, we performed organoid colony formation assays *in vitro* and transplantation limiting dilution assays (LDA) *in vivo*. In organoid colony forming assays, the $EpCAM^{med/high}/CD10^{-/low}$ cells formed significantly more organoid colonies than the $EpCAM^{low/med}CD10^{low/+}$ cells (FIG. 2B). In FIG. 2B, the $EpCAM^{med/high}/CD10^{-/low}$ cells formed significantly more organoid colonies than the $EPCAM^{low/med}/CD10^{low/+}$ cells, $*P < 0.05$ (unpaired t-test) (mean ± s.d., n = 3, experiment performed twice). In transplantation assays performed in NSG mice, injection of $EpCAM^{med/high}/CD10^{-/low}$ cells from all six PDXs consistently formed tumors (FIG. 2C), sometimes with the transplant of as little as 100 cells (PDX-T1 and PDX-T2). In contrast, transplant of $EPCAM^{low/med}/CD10^{low/+}$ cells only formed tumors in two PDXs (PDX-T1 and PDX-T2), and only when transplanting high cell numbers (i.e. 2500 cells) (FIG. 2C). Furthermore, no tumors formed from the transplant of $EpCAM^{-}/CD10^{-}$ cells from *any* PDX. Hence, TIC's are enriched in the $EpCAM^{med/high}/CD10^{-/low}$ sub-population of all PDX breast tumors we examined.

[0201] Having identified these distinct subpopulations, we next investigated whether *CDK19* expression was enriched in the more tumorigenic $EpCAM^{med/high}/CD10^{-/low}$ cells compared to the less tumorigenic $EPCAM^{low/med}/CD10^{low/+}$ cells. In three of the four PDXs examined, *CDK19* expression was higher in the more tumorigenic $EpCAM^{med/high}/CD10^{-/low}$ cells compared to the less tumorigenic $EPCAM^{low/med}/CD10^{low/+}$ cells (FIGS. 2D-2G). To generate the data in FIGS. 2D-2G, relative expression of *CDK19* in the $EPCAM^{low/med}/CD10^{low/+}$ and the $EpCAM^{med/high}/CD10^{-/low}$ cells as determined by RT-qPCR. Gene expression in each

condition is normalized to beta-actin as a housekeeping gene. Relative expression of *CDK19* is normalized to the mean expression of *CDK19* in the $EPCAM^{low/med}/CD10^{low/+}$ cells. $*P < 0.05$ (unpaired t-test) (PDX-T1: mean + s.d., n = 2; PDX-T2: mean + s.d., n = 6 ($EpCAM^{low/med}/CD10^{low/+}$) and n = 3 ($EpCAM^{med/high}/CD10^{-/low}$); PDX-T3: mean + s.d., n = 6 ($EpCAM^{low/med}/CD10^{low/+}$) and n = 3 ($EpCAM^{med/high}/CD10^{-/low}$); PDX-T8: mean + s.d., n = 3. All experiments performed at least twice). Thus, while *CDK19* was expressed in all the PDX tumors we examined, it was expressed at higher levels in the more tumorigenic $EpCAM^{med/high}/CD10^{-/low}$ sub-population in three of the four tumors that we investigated.

[0202] To determine tumor initiating frequencies in the setting of *CDK19* knockdown, we performed LDA using PDX-T1 cells transduced with a doxycycline-inducible *CDK19* knockdown construct to produce inducCDK19KD-PDX-T1 cells where we can control *CDK19* expression (FIG. 8B). In FIG. 8B, the relative expression of *CDK19* in doxycycline treated inducCDK19KD-PDX-T1 cells is normalized to the mean expression of *CDK19* in control inducCDK19KD-PDX-T1 cells. Gene expression in each condition is normalized to beta-actin as a housekeeping gene ($*P < 0.05$, mean ± s.d., n =2, experiments performed twice). By comparing the *in vivo* transplantation of inducCDK19KD-PDX-T1 cells in the presence of doxycycline (+Dox) with inducCDK19KD-PDX-T1 cells without doxycycline (No Dox), we find that *CDK19* knockdown eliminates tumor formation in all the cell transplantation conditions examined (FIG. 8C). inducCDK19KD-PDX-T1 cells were injected into the mammary fat pads of NSG mice at 50, 250 and 1250 cells. Mice in the doxycycline group were fed a doxycycline containing rodent feed to induce *CDK19* shRNA, while mice in the control group were fed a normal rodent diet. Tumors were detected by palpation of tumors. The number of tumors that formed and the number of injections that were performed are indicated for each population. Populations and injections where tumors formed are bolded (n = 5 per group) in FIG. 8C. Using ELDA, we discovered that the tumor initiating frequencies significantly decreased from 1 in 342 cells (95%CI: 1 in 828 to 1 in 142) in the control (No Dox) group to 1 in ∞ cells (95%CI: 1 in ∞ to 1 in 2587) in the *CDK19* knockdown (+Dox) group (FIG. 8D). Both the significant decrease in tumor initiating frequency caused by *CDK19* knockdown and *CDK19*'s higher expression in the TIC sub-population suggests that TIC inhibition is likely responsible for the impaired tumor growth observed with *CDK19* knockdown.

4.5 Example 5 - Identification of Genes and Pathways Regulated by CDK19

[0203] There is an 84% amino acid sequence homology between CDK19 and its well described paralog, CDK8 (FIG. 9). CDK8 has been shown to play a role in a variety of malignancies including colon cancer, acute myeloid leukemia, and melanoma. Higher expression of CDK8 has been associated with worse prognosis in colon cancer (Firestein et al., *Nature* 455:547-551, 2008). CDK8 knockout in embryonic stem cells was shown to prevent embryonic development (Porter et al., *Proc Natl Acad Sci USA*, 109:13799-13804, 2012) due to its essential role in the pluripotent stem cell phenotype. The known cancer-relevant activities of CDK8 may include positive regulation of Wnt/β- catenin pathway, growth factor-induced transcription, and TGFP signaling. Depending on context, CDK8 has also been shown to either negatively or positively regulate transcription. However, recent evidence has suggested that CDK19 may function differently from CDK8. *In vitro* studies showed that CDK19 and CDK8 participate mutually exclusively of each other in binding to other CKM components, while gene knockdown studies in cell lines of cervical cancer and colon cancer showed that CDK19 and CDK8 regulate different genes. Our goal was to investigate in TNBC whether CDK19 and CDK8 have distinct biological functions by examining global gene expression changes resulting from targeted knockdown of *CDK19* or *CDK8*.

[0204] To understand whether the molecular targets of CDK19 in TNBC are unique from CDK8, we knocked down each gene in MDA-MB231 and examined the respective gene expression changes relative to control. Overall, *CDK19* knockdown affected 3909 genes and *CDK8* knockdown affected 4233 genes (FIG. 3A). However, only 12% of upregulated and 5% of downregulated genes in the *CDK19* knockdown experiment were also affected by *CDK8* knockdown. This suggested that CDK19 and CDK8 largely regulate distinct genes (FIG. 3A).

[0205] Gene set enrichment analysis (GSEA) of the *CDK19* and *CDK8* knockdown genes allowed us to identify enriched Hallmark gene sets amongst the most upregulated or downregulated genes (FIG. 3B and FIG. 10). In FIG. 10, the Hallmark gene sets uniquely enriched in the knockdown of *CDK19* or *CDK8* are shown in black, enriched in both the knockdown of *CDK19* and *CDK8* are marked by "*" and enriched by genes expressed in opposite directions between the knockdown of *CDK19* and *CDK8* are marked by "**". Normalized enrichment scores and FDR q-value are determined by the GSEA software. An FDR cutoff of < 0.25 was used to select significant Hallmarks. These Hallmark gene sets consist

of genes that are specifically involved in certain biological states or pathways. Genes associated with known breast cancer-related Hallmarks such as mitosis (E2F targets, G2M Checkpoint, Mitotic Spindle), PI3K-AKT-MTOR signaling, MYC pathways (Myc Targets v1), glycolysis, apoptosis, and oxidative phosphorylation were changed in the same direction by *CDK19* and *CDK8* knockdowns (FIG. 3B, middle overlap region), demonstrating a co-regulatory relationship between CDK19 and CDK8. Further, genes associated with early estrogen response, epithelial to mesenchymal transition (EMT), cholesterol homeostasis, MYC pathways (Myc Targets v2), interferon alpha response, and fatty acid metabolism changed in the opposite direction in response to knockdown by *CDK19* compared to *CDK8* (FIG. 3B, boxes), which suggests a counter-regulatory relationship exists between CDK19 and CDK8. Hallmark gene sets enriched by the expression of genes in opposite directions by *CDK19* knockdown compared to *CDK8* knockdown are boxed. A number of the Hallmark gene sets were only enriched in the genes that uniquely changed due to *CDK19* knockdown (FIG. 3B, left region). Hallmarks reflected by these gene sets included P53 signaling, KRAS signaling, androgen response, NOTCH signaling, TGF BETA signaling, and IL6-JAK-STAT3 signaling, which may be potential biological pathways for targeted therapies for TNBC. All of these biological pathways represent active areas of clinical investigation in the evaluation of targeted therapies for TNBC. Consistent with our findings, a number of the pathways found enriched in our *CDK19* knockdown experiments, such as cholesterol homeostasis, P53 signaling, mitosis, and NFκB pathways have been shown previously in other cell types to also be regulated by CDK19.

[0206] In summary, these analyses showed that CDK19 and CDK8 have the potential to co-regulate certain pathways, while counter-regulating others. Furthermore, CDK19, like CDK8, is capable of positively or negatively regulating biological pathways. The multitude of clinically relevant TNBC pathways regulated by CDK19 suggests that targeting CDK19 can provide the opportunity to modulate multiple pathways simultaneously and at the same time, avoid potential toxicity because of the advantageous limited tissue distribution of CDK19. This approach could overcome the resistance to single agent therapy commonly seen in TNBC and also potentially enable the targeting of 'undruggable' processes such as those involving P53 or MYC.

4.6 Example 6 - Effects of CDK19 and CDK8 on Epigenetic Modifications

[0207] Recent studies have highlighted the role of CDK19 and CDK8, as well as other transcriptional CDKs (CDK7, CDK12/CDK13), in regulating the transcription of critical oncogenic genes by acting at large clusters of enhancers (also called 'super-enhancers') that are marked by histone 3 lysine 27 acetylation (H3K27Ac). The exact mechanism for this gene regulation is unclear, but is believed to occur in part through interactions of the CKM with Mediator to regulate RNAPII-Mediator interactions and in part by phosphorylating serine residues in the C-terminal domain of RNAPII. Given the propensity of transcriptional CDKs to function at enhancers, we wanted to investigate whether CDK19 and CDK8 can also regulate the epigenetic modifications at enhancer sites as a mechanism to control gene expression. While enhancer modification through other signaling pathways have been identified, this mechanism of gene control has not yet been reported for the CDKs.

[0208] To explore the role of CDK19 in epigenetic regulation, chromatin immunoprecipitation and sequencing (CHIP-Seq) for the H3K27Ac modification was performed on MDA-MB231 cells under three different conditions: Control (empty vector transduction), *CDK19* knockdown, and *CDK8* knockdown. Genome-wide analysis of all H3K27Ac modified regions showed that both *CDK19* knockdown and *CDK8* knockdown had similar global H3K27Ac levels compared to control (FIG. 11). In FIG. 11, H3K27Ac CHIP-Seq signals across all identified H3K27Ac peak regions are normalized to 1-Kb and centered on the middle of those regions. Signals of the flanking 2-Kb regions are also shown. To compare relative signal changes, the total signal of each biological replicate was determined by summing the signals of each 50-base window 1-Kb around the center of each region. *P*-values between total CHIP-Seq signals of each sample were determined by unpaired t-test. Through comparative analysis of H3K27Ac levels in the *CDK19* knockdown compared to the control, we identified 3034 peak regions with increased H3K27Ac signal (All-H3K27UP) and 502 peak regions with decreased H3K27Ac signal (All-H3K27DOWN). By excluding peak regions that were also different in *CDK8* knockdown compared to control, we identified 2309 peak regions with increased H3K27Ac signal (CDK19KD-H3K27UP) and 432 regions with decreased H3K27Ac signal (CDK19KD-H3K27DOWN) that were unique to *CDK19* knockdown. The specificity of these regions for CDK19 was investigated by comparing the H3K27Ac levels at these regions in *CDK19* knockdown, *CDK8* knockdown, and control. Compared to control,

enrichment of H3K27Ac levels across the CDK19KD-H3K27UP regions (FIG. 3C) and depletion of H3K27Ac levels across the CDK19KD-H3K27DOWN regions (FIG. 3D) were significant only for *CDK19* knockdown and not for *CDK8* knockdown. In FIGS. 3C and 3D, ***$P < 0.001$; ns is $P > 0.05$ (all samples n = 3, experiments performed three times). H3K27Ac CHIP-Seq signals of the CDK19KD-H3K27AcUP or CDK19KD-H3K27AcDOWN regions are normalized to 1-Kb and centered on the middle of those regions. Signals of the flanking 2-Kb regions are also shown. To compare relative signal changes, the total signal of each biological replicate was determined by summing the signals of each 50-base window 1-Kb around the center of each region. *P*-values between total CHIP-Seq signals of each sample were determined by unpaired t-test. Thus, CDK19KD-H3K27UP and CDK19KD-H3K27DOWN define peak regions where the H3K27Ac signal is more specific for, and most sensitive to, knockdown of *CDK19* compared to knockdown of *CDK8*.

[0209] We next assessed whether increases or decreases in H3K27Ac levels as a result of *CDK19* knockdown corresponded to changes in gene output. For this, the previously defined All-H3K27UP and All-H3K27DOWN peak regions were annotated by proximity to the nearest gene to establish two gene sets: CDK19KD-EnhancerUP (1593 genes) and CDK19KD-EnhancerDOWN (341 genes) for further analysis (Table 1 and Table 2). GSEA of these gene sets with our *CDK19* knockdown gene expression data indicated that genes most upregulated by *CDK19* knockdown were enriched for the CDK19KD-EnhancerUP genes (NES 1.68, FDR q-value = 0.000) (FIG. 3E), while genes most downregulated by *CDK19* knockdown were enriched for the CDK19KD-EnhancerDOWN genes (NES -1.84, FDR q-value = 0.000) (FIG. 3F). Thus, as a result of *CDK19* knockdown, perturbations to the H3K27Ac signal at the putative enhancer elements of genes correlated well and in the expected direction with changes in gene expression.

Table 1

CHIPSEQ_CDK19-KD ENHANCERDOWN							
NDRG3	TTLL11	CYB561	KAZN	PPM1A	SLC25A32	GRAMD4	S100Z
SNRK	YWHAZ	FAM168A	KIAA1524	CDH4	PAQR5	KCNK12	NSMAF
RNF169	SLC35F3	HDAC8	KCNAB1	CDKAL1	ZFYVE9	AK7	DDX31
WDHD1	RNF144B	DGKB	FKTN	C6orf203	EPB41L2	RUNX2	CXCL8
PLXNA4	TOX2	XPO6	PGM2	TRIM60	PKP2	TWSG1	RGCC
AZU1	NORAD	ARFIP1	SSH2	ALKBH8	TMBIM4	IPO5	TTC39C
KITLG	C11orf87	SCN5A	ZCCHC24	FBXO11	RAI14	ABCA8	PRNP
OC90	STX8	LOC341056	MAGT1	FOS	LPA	OPHN1	FGF9
MPP4	IQCJ	RPL7L1	ZFAT	ABCA13	CSGALNACT2	KIAA0586	RNF114
TOX	G6PC2	BACH2	RGMB	C1QTNF3	MOK	MED27	WWC1
SPRED1	C11orf63	C12orf75	HRH1	NTNG1	GGCX	ADCK2	PDE7B
UBASH3B	ZNF281	LOC100506797	SLCO4A1-AS1	WDR27	RBM5	AKR1B15	ENKUR
CACNA1A	WDR89	SLIT2	SHTN1	ALK	TLE1	FAM107B	ELOVL5
FZD8	CSTF2	XRRA1	ARSF	STX18	KIF3C	SLC25A12	HIVEP1
SATB2-AS1	SNX14	IDNK	OXCT1	ZNF133	TAPT1	STK38	STRA8
TMEM18	UTP18	VAPA	CCR1	SPPL3	MBP	ASAP3	SEMA4D
TBL1X	SMYD3	ITGB1BP1	CRTAM	MDM1	TRHR	FAF1	STK4
SMIM19	DNAJA3	PDE8B	TSNARE1	KCNV1	AVEN	FAM20B	CDH13
KIAA1109	KHDC1	DAP	HIPK3	OR10V1	VTI1A	FIP1L1	AKAP1
C20orf85	PPP4R1L	IL10	PIK3CB	ALG10B	ATAD1	ZBTB10	TNRC6A
COMMD2	MLEC	NCK2	FAM171A1	SGPL1	NFATC1	GRB10	NECAB1
AMOTL1	RHOH	HDAC9	PDE4B	RFX8	NR2F1-AS1	RNF34	TMSB10
KYNU	TMEM235	SLC26A8	SIK3	CHI3L2	PPP3CA	HESX1	CORIN
ARHGAP18	SYAP1	OLIG2	THG1L	MAST2	PPA2	BTBD9	GPR68
EPB41L1	OLFML2A	CFAP36	KLHL5	PRDM5	COMMD7	CEP112	SVIL
C1orf21	PUM2	ST3GAL6	MTCL1	RPAP2	ATG5	PLEKHM3	EDEM3
SAP18	PANX1	MAB21L2	PTPN20	DSCR9	SIPA1L1	SUMF1	CDK5RAP2
UBR5	GBF1	UBE3A	INHBC	EPS15L1	CD226	TCF7	TGFBR2
HTR7	BCAP29	PRLR	USP43	ATP6AP1L	RPS6KA5	EXOSC7	RAB10
KCNG1	CPD	KIAA1147	RPS3A	CCDC152	ATF7IP	CCDC88A	CASS4
ADM2	GTF2H5	FER1L6	DDR2	PARD3	PREP	RPL5	C1GALT1C1
GJD4	WWP2	SVIP	FZD4	BPGM	ARMC9	ERICH6B	MAP1B
TCP11	PLS3	NT5DC3	CBLN1	C5orf42	LIN7A	FIBP	TSEN2
CSNK2A1	UBE2V2	CMTM8	ARHGAP25	KAT7	BLCAP	IFI44	TMEM38B

CHIPSEQ_CDK19-KD ENHANCERDOWN							
EDNRA	LOC285696	GOLIM4	NEK1	C3orf67	PRDM8	TBXAS1	SND1
ANAPC10	TSPAN9	ARC	ETV1	CTDSPL	NDRG1	WWTR1	WASF2
ADH7	NNT	SLC46A3	CTNND2	MBD2	HYPM	RNF217	CHST11
CLDN2	STAG2	INTS6	ZMIZ2	CHSY3	MRPS28	CBFA2T2	BTD
CEP290	RIN2	COX7A2L	TMEM30B	WASF3	APCDD1L	PARP12	FAM46C
TCF12	FKBP1A	ARFGAP2	PUDP	LDHD	ADGRL3	TMEM50A	TRDMT1
TSEN15	BAZ2A	TANC1	NANS	TAOK1	MAPK8	PPP4R3B	FAM196A
OAT	AGA	DNAH6	ARHGEF4	PSMC4	ANTXR2	BASP1	TPTE2P1
OR2AT4	MMAB	DENND2D	C7orf73	ST18			

Table 2

CHIPSEQ_CDK19-KD ENHANCERUP							
HLCS	EFCAB13	FBXL20	AGR2	ABCC11	MFSD7	RIC8B	KCNT2
IGF1	SLC12A8	AZIN1	LYSMD4	AVIL	ATP2B4	ASS1	MARCKSL1
CDYL	CRABP2	ERCC8	OSR2	CASQ2	ACTL7B	TNFRSF11A	NAV2
LHFPL2	TEX35	SLC22A16	LUM	PRKCZ	RDH16	ERICH2	STPG2
HGC6.3	PTPRE	GPCPD1	BEGAIN	BEST3	ABCG1	ZFPM2	SOWAHC
MYL4	TCF7L2	HAS2	IGSF22	BDKRB1	MYL12A	DNAJB11	LOC100506797
NNAT	SCAF8	LOC100268168	PPP1R36	CDC42EP5	EDN1	SP4	SOWAHB
NEURL1	TSC1	MIS18A	RALGPS1	SH3BP4	C15orf53	GJA4	FOPNL
RPIA	STOM	VEGFA	AHDC1	DBX1	PHACTR1	ALDH1A3	DACT1
SLC1A2	SRPX2	PLXNA2	TBC1D14	RAD23B	MAP1A	ECHDC3	GLI2
IQSEC1	ANKRD16	CHAT	MAGEF1	NOL6	SUB1	RFK	CHRNE
DENND3	NEK6	S1PR1	C12orf76	DIEXF	DHRS9	ERICH5	SCCPDH
TAF1B	XPR1	RYBP	ANP32C	MCHR1	DLX4	OSBPL11	ARHGAP12
FGD2	SNTG1	PTGER4	AGMO	PTRHD1	FANCA	AES	KRBA2
ZC3HC1	TRIM24	HMHB1	IRF2BP2	INPP5F	CACNG2	HHLA3	CFI
TTLL5	ACBD3	PLB1	EDIL3	IGFN1	TROAP	HAUS8	NOV
HPSE2	YARS	PROC	LEPROTL1	EFHD1	GALNT12	KANK4	JAK3
TMEM170B	DCLK1	PTPRN	SPATA16	CCDC97	ZNF787	TPRG1	DAPK3
KIF25	LMCD1	AADACL4	RFXAP	ALOX5AP	BIRC7	GBA3	C1R
TMPRSS5	TMEM100	OR1M1	ENO2	PTPN3	FAM196B	CLEC14A	TSPAN1
NPC1L1	TBL1X	PTPRR	LOC100130872	FAM136A	HSPH1	STK17B	GSTA3
ACKR3	OPTC	CREB5	PHTF2	SMIM20	SPRED2	SHE	AGAP1
CTAGE1	KIF16B	TRAF4	FAM57A	KIAA1211L	CORO6	SPNS2	MAOB
SOAT1	TRIB1	KCTD4	CELF2	TWIST2	C19orf38	TMEM40	THEM4
GSX2	ADAT2	USF2	NRP2	NSUN7	SEMA3E	ZNF462	SUGCT
BCAT1	CSNK1A1	RAD51AP2	FFAR4	NINJ1	SHH	SPIB	PSAT1
CLDN1	ERGIC1	SLC15A1	KISS1	C11orf49	NAT2	HECW1	EXOC6B
KLHL31	YAE1D1	PIM3	DGKZ	MEF2A	USB1	CAB39L	PCSK1N
MAST2	STON2	HIP1R	ELF3	C4orf26	ZNF429	DISC2	CENPB
MTCH1	PALLD	GLRA3	ZSWIM3	NMBR	C14orf37	GPR108	GSTP1

CHIPSEQ_CDK19-KD ENHANCERUP							
ATP1A2	RBM47	SORBS3	RAB14	RPS29	ACVR2A	C11orf94	DAW1
THADA	CKAP4	SF3B5	ANO6	BTBD16	XRCC2	OTOS	EMX1
EPS8L3	PTK2	ZNF318	RTN2	CAMK2D	MRPL4	VGLL3	LMNTD2
CAB39	PAPSS2	TRIML1	ZSCAN18	HCAR1	RPS3A	FAM81A	FIZ1
NEK2	EHF	NEDD4L	SYT2	LEPROT	MAP7D3	PRTFDC1	SEC14L5
HYI	SLC44A1	BAG1	GFI1	MFSD4B	GCG	PPEF1	LAMB4
NANOS1	YWHAEP7	ATG9B	GCNT3	ATXN1	LIMD1	P2RY1	TMEM120B
SLC37A1	GRHL3	OTUD3	VWA2	IGFL1	P2RX7	TLR10	KIAA1324
MAPK8IP1	SLC2A8	RHOB	CAMSAP2	TMEM95	FAT1	TFAM	APIP
PPM1L	ETS2	KPNA7	HRK	ACOT11	RGS7	TMEM106B	CERS4
NXPH2	SLC30A6	RREB1	EML5	WFIKKN2	PAK1	FJX1	HMGCR
RCAN1	GUCY1A2	LAMC3	RBFOX2	BMP6	DSG3	PITPNM3	ISL1
PACSIN2	TSN	BCOR	HES1	NIPBL	STAT4	CDH3	PSG2
SLC39A10	XIRP1	NAB1	DYNC2H1	TMEM51-AS1	ARRB2	CCL20	MINK1
MRPL15	LY86	PLEKHA1	METTL6	LRRC8D	SPR	SCRT2	RALA
MAPK1IP1L	EGLN3	CRISPLD2	PAPLN	MOAP1	COL24A1	MYO5C	SLC28A3
MAP3K7CL	RB1CC1	SERPINB10	TPD52L1	PPARA	MZT1	ATP8B2	RASSF6
PIGU	ADTRP	CYP1B1	LRRFIP2	NLN	ZC3HAV1L	NECTIN1	CELA2A
SYT14	CDCA4	FBXO3	ASCC3	SH2B2	C3orf58	ENOX2	PLEKHG4
DAAM1	TINAGL1	YIPF6	GPR135	ZNF160	ANXA1	ERCC3	SLC39A11
CDKN3	CBX4	RALGDS	TUBA1A	PMAIP1	MN1	ADAMTS10	FGFR3
EPAS1	ZCCHC10	LRRC4C	DUSP18	CXCR5	CRABP1	MAST3	ABLIM2
INO80C	TLR2	AKAP10	RASAL2	NR4A1	PNOC	SCN3A	NOCT
DDC	TACC2	IFNLR1	COL4A5	FOXQ1	DSG2	PPFIBP2	MAD2L1
FILIP1L	ASH2L	TJP3	NID2	DAOA-AS1	CAPZA2	RMND5A	SLC8A2
STC1	DDX47	RXFP3	COL6A3	PDE8A	RGS1	TMEM119	MXRA5
KCTD16	WDFY3	EMILIN2	PSAP	SETBP1	GPRC5C	MAST4	DNAH1
RPUSD4	KCNJ15	CCDC9	COX6B2	MEDAG	IL6R	NUAK1	ZP4
CD276	EVA1C	DPEP2	ABHD5	MRPS22	GLDN	RPH3AL	AQP7
LRRFIP1	GHSR	NME9	SALL4	F5	MCOLN3	GPATCH1	VSTM2L
PDLIM1	KIAA0753	STK39	TNFRSF11B	HSPBAP1	SLC9B2	PEX26	CNGB1
CDKAL1	SLC34A3	KERA	UBAP1	JADE1	IQCA1	FKBP6	SARM1
DLX1	P3H2	ITPR2	BTBD10	FBLN2	HES2	C1orf100	KRT10
NEDD9	GATA6	PLAC8	FAM198B	FBP2	BSN	SPINK2	PFKP

CHIPSEQ_CDK19-KD ENHANCERUP							
C11orf88	SIN3B	ORMDL3	TBX21	GPR173	KAZN	KIAA0040	HDAC11
FAM96A	DCHS2	UPF2	KCNMA1	PLA2G4E	ARL4C	HCN3	COL14A1
BEST1	ACSBG2	NPFFR1	TMEM178A	CDC123	NDUFA12	CDNF	RBM45
CBLB	PIM1	CTSO	DUSP6	LHFPL5	BCL2L10	DIXDC1	TCF12
TNFAIP8	PPM1H	SMARCD3	RAD54B	C4orf45	CREB3L2	NPVF	OR6B1
HMGCS1	SSR3	CXCL13	TTC8	MAPRE3	SLC2A6	SERPINB7	HTR3A
USP36	VIT	C17orf99	CYP27C1	NFKBIZ	AHCYL2	DHRS7C	KRT32
COL19A1	NOL10	MUC1	SYT17	GRHL1	DENND2C	CLCA1	WNT11
INTS10	CRELD2	LGR6	FHL1	ARRDC5	PARVB	CRK	NECAP2
KRTAP4-5	CLMP	NCF2	GGT7	INSR	PIK3C2B	C11orf65	CLUAP1
MBL2	ASPSCR1	YBX3	SLC35F2	NEMP2	CLDN22	DAB2IP	MAMDC2
IL37	CDCA7	GAREM1	DCN	ATP12A	REPS2	FAM216B	CTTN
KLHDC9	CDKL2	AGRN	ATP9A	OXT	OLIG2	TSEN54	KIRREL2
HECTD1	ME3	INTU	PGRMC2	RFX2	DSPP	LSM8	TEX9
MYEOV	POLR1A	PKIG	NEBL	SOX4	HFM1	OSBPL5	TANK
CALHM3	TLE1	TRIM66	SACS	SLC10A7	MTM1	KLHL38	SHCBP1L
SRP19	TMC1	TOR2A	FNDC3B	XIAP	JARID2	ALG1L	NYX
BMP10	TRAF3IP2	WISP2	SCN1B	C15orf56	ARHGEF3	EPB41L4A	AFG3L2
MON1A	PSMA6	TRIP13	ACTR10	GJD3	EFCAB11	IRF4	SLC22A23
INPP4B	HNF1B	KIAA1522	ALPP	KRT37	MMP24	CMTR2	ARHGAP29
SSUH2	NUBPL	RRAD	CDH2	CREB1	ZNF621	APOBEC1	HIPK3
METAP1D	SPOCK2	PTPN1	INHBE	ACHE	UGP2	PITX2	RPS5
PTAFR	P2RX4	GJB4	PRKCSH	C12orf71	ZNF292	PKP1	MAOA
YPEL5	NKAIN1	KCNG1	EXD1	KRT39	STAU2	AFAP1L2	MIER3
ATG14	HRH1	CYB5B	QPCT	TRAK2	IL12B	AP4S1	ACSL1
LAMA3	GJA1	OR51B6	FOXS1	RPTOR	VAPA	ASIP	SPIN1
ZNF542P	THRB	COX11	RPS23	PIGC	CREBL2	PIN1	UNC13A
GPBP1	ATOH8	PPFIA2	DMKN	ZBTB43	INPP5K	STRA6	ABR
DEF6	DACH1	LILRB3	POLE4	CAPZA3	SNX13	MMP16	MOGAT2
NRCAM	NRARP	GATA2	TMEM65	FBN2	INTS7	INPP4A	TMEM38B
C10orf67	ATXN7L1	GPM6A	GSTZ1	GARNL3	USP38	AKTIP	NR2F1-AS1
KMT5B	LGALS9	ZFP36L2	CD200R1L	GPATCH2	DLL1	CNGA2	GAS7
RIPPLY3	FAM161A	C10orf113	TRPC4	RAB27B	CD109	TNS3	CDHR2
TNFRSF21	FAM50B	CAGE1	RNF220	ARFGEF3	RALB	INTS1	VWA3B
SLC30A1	ITCH	UPP2	LZTS3	YTHDF1	AKR1D1	TAS2R16	DPF3

CHIPSEQ_CDK19-KD ENHANCERUP							
IL15	LGMN	ST8SIA4	PROSER2	SHC3	PLEKHH1	GRIN2D	CCDC184
PLEKHG6	METTL25	CYP26B1	SHC4	GSG1L	BMPER	C3orf38	STEAP4
FA2H	TMEM88B	PPARGC1A	IGFBP3	HSD17B14	RNF112	CXCR4	TESC
AHR	CDK14	CD36	CLTC	TFCP2	PRRX2	FOXD2	ATP6V1H
GALNT15	FSCB	YTHDC2	C10orf35	ZNF92	COMMD10	RPTN	RGS11
C9orf135	IFT81	TTI1	AMTN	LPIN1	IRS2	SLTM	MYO1G
FGFBP1	LRRC25	RPS6KA3	BCR	EEPD1	RSPH1	LAMC1	KLF5
HRASLS2	FOXN3	ANO10	GTF2E2	TRIM9	PAPPA	RABEP2	PCLO
ATF3	PAFAH1B2	PRSS57	FAM3B	CYP24A1	CARTPT	NPEPPS	NTF3
TLR3	CABLES1	SLN	ANGPT1	TUFT1	CLCNKA	ANXA4	NCALD
LTBP1	CPPED1	DYNLT1	MREG	C4orf19	AIG1	THNSL2	RBM3
SMG6	OR2S2	AMER3	NAV3	RNF13	PPP1R2	SLC43A3	WIPI2
PANK1	TAMM41	ST6GALNAC4	TRIM54	NAT1	PTPRC	COX20	CCDC65
NRDE2	SPAG9	DCTN6	GABBR2	UPP1	ARHGEF18	C1orf226	TTC39C
TGFB3	EIF4A2	UNC5A	TPK1	LBH	PRKAR1A	SERBP1	TOPBP1
LARP4B	SERPINB1	C12orf74	GOSR2	OSCP1	PSTK	KNOP1	C1orf228
CD9	ACSL5	CT62	DENND5A	BAIAP3	SLIT2	NFATC1	DNAJC6
ADAMTS6	ADAM29	FRMD3	RAB8B	OR10H1	RAB11FIP4	TMEM45B	FABP3
NNMT	WDFY1	CEP152	ARHGAP42	HIC1	SHQ1	TARBP2	SNX7
C10orf90	RAD51B	LRRC20	GNLY	TIMM22	SMARCA2	DUSP8	SOX8
NCOA6	CCNY	COX7A2	TRAF3IP1	SLC6A3	KBTBD12	ARHGAP39	MDFIC
PPM1B	SEMA3A	PLA2G2E	DNAH11	EGR4	DUSP27	TMPRSS7	NFE2
CACUL1	TMEM86B	TRABD2A	REEP3	NDUFB11	CCDC186	C7orf57	CC2D2A
LEKR1	ATP6V1G1	MPZL2	SLC4A1	MGAT4C	TMPRSS9	COL21A1	LBP
TMEM247	CCDC34	IGF2R	CLDN4	WNT7A	APBB1IP	CPA4	DTWD1
NSMCE4A	GDPD5	ANKRD33	PLEKHG3	CYP11A1	CDCA7L	NID1	MAF
NUP155	CAMK2B	ZEB2	ARID5A	FRMD4B	ATXN7	LSM3	FGGY
ABI3BP	PNPLA5	ATXN3L	ZNF396	SOCS2	MBTPS2	HS1BP3	C9orf3
MUC20	IL7R	FIGN	PPP2R2C	USP2	ENKUR	RALBP1	MRPS18A
CNIH3	ULK1	ADGRF1	FLJ23867	CRIP2	PTHLH	FAM187B	SH2D3C
SH3GL3	ODC1	LGALSL	PRRC1	GC	NEK10	MAMLD1	C4orf32
SH3TC1	LGI1	SLC6A20	CD180	PLCE1	THY1	CTSH	SLCO4A1
SLC26A9	MPL	AACSP1	COL26A1	SSR2	CMAHP	ID4	ALCAM

CHIPSEQ_CDK19-KD ENHANCERUP							
TAGLN2	COBL	SCNN1G	TRAF7	MYOZ1	AKR1C3	CER1	AREG
ABCG2	DCK	CCDC174	PRKCE	CBLC	SYNM	BCAS2	BDKRB2
NABP1	TBC1D1	DHRS3	TES	USHBP1	UBQLN4	ETV7	CCR8
AGPAT2	MLXIPL	SLC13A1	ADAD1	NOSTRIN	QRFPR	RHOBTB1	SCFD2
PPP4R3A	E2F6	CDK4	PABPC1P2	COL5A3	RAB31	PPP1R14D	CASK
ADAMTS15	CRTAC1	HRC	KCNQ4	UBE3D	MIEN1	KIF18A	BPI
KIAA0895	SIM2	LITAF	RNF165	CCDC77	DIO2	ABCA6	ZNF473
FHAD1	BRINP1	GRAMD1C	TAF1L	EMC7	TRIM29	AGXT2	CD300LF
PPP1R12B	GPR37L1	WAPL	AQP3	LZTFL1	YIPF5	ENOX1	ZC2HC1A
GIN1	FHDC1	PBOV1	DERA	FGD4	TYK2	ACP6	NLGN1
ULK4	BANK1	PER1	ITGA2	LLGL2	ALDH8A1	FBRSL1	TPPP3
TNNI2	TMEM167A	RGS4	PDGFB	ZDHHC17	APOBEC2	THBD	HGF
BTN3A1	EXOC3-AS1	NAA20	VAV1	ZNF664	TRMO	TMEM139	PRR15
PHLPP1	GINS2	GMDS	PCDH1	PARD3B	MYH13	C1orf43	ARSB
TMEM217	SLC22A2	IL1RN	FMN1	KCNJ12	RASAL3	HTR1B	PCDH8
BRDT	NEK7	MCM10	NPSR1-AS1	ARID5B	SEMA3C	UBB	TACR2
VSX1	LOC100132215	MMD2	MEF2C	SPON1	FLVCR2	SNX25	GLOD5
STK38L	ZNF555	YKT6	NR5A1	DNAJC10	SYNPO2L	APEH	ALDH3A1
DPYSL2	ETFB	GCM2	FGF19	GRN	GNAS	FCHO1	DBN1
TCEANC	SOCS6	CEP128	RBM24	HEATR5A	ASAH1	CHMP6	RPS26
MRVI1	PLA2R1	CDC14B	SCARB1	SLC7A10	SLC13A2	WDR89	VPS45
INSIG2	GJA3	MCM5	TRPS1	CHMP4B	ZNF366	SRMS	CNTN6
MYO5B	AGTPBP1	TMC8	FAM173A	PITX3	TRAFD1	PNPLA8	CD28
YWHAQ	C9orf116	SLC16A3	VPS37D	ASB5	JSRP1	UGT8	WBP2NL
TSPAN2	EGFR	SRD5A3	CDC16	NDUFA10	SPOPL	NR5A2	ZC3H4
KLF4	C9orf153	GADD45A	C18orf12	EMX2	BMF	PPP2R5A	MKL2
TIMM17A	CMIP	METTL4	FEM1C	ST6GALNAC5	PIWIL3	SRL	CCBE1
CIT	ASB7	C15orf54	TMEM71	TGIF1	ARVCF	MEGF6	TPPP
TNFRSF19	RAB11FIP1	MRPS36	FTH1	ETS1	MAN1A1	PELO	OXER1
DYM	SLC23A3	MMP20	KCMF1	TRY2P	RPS6KA5	NPAS2	SLC25A19
CCDC112	SOX9	RGS9	NUTF2	OXSR1	MAGEB2	AVP	TMEM59
C9orf50	ABHD11-AS1	GPR132	PLCD1	NATD1	OTUD1	PLA2G4D	BHLHE41
AAED1	TMIE	NDUFB6	SPCS3	PRRG4	GCLC	CEACAM22P	LIN28A

CHIPSEQ_CDK19-KD ENHANCERUP							
KIF5C	PHLDB1	E2F8	EPHA5	CITED2	SLC5A1	TBC1D23	PLEKHG4B
BANF2	GLP2R	HSD17B2	PTPRK	SLC7A7	SLC9A7	SNX9	SND1-IT1
OLA1	PEBP1	TAPT1	LOC401052	CLIC5	CPEB4	KDM4C	SLC20A1
RAPGEF2	SGK1	TANGO6	SNCB	SEMA3D	FLRT2	NTRK2	LEPR
C9orf131	IFI6	LVRN	ZNF214	C14orf2	SSFA2	PABPC4L	TMEM244
C1QTNF1	TMC5	WDR18	BRMS1L	CTNNB1	PDE1A	SH3PXD2B	NTN4
LIMCH1	PSD3	SLC38A11	HTRA1	DIRAS1	EPHB6	HTRA3	PTGIR
YY1AP1	TFAP2A	GTPBP4	ARFGAP3	LDHAL6A	ZNF331	EPC1	SNRPC
CREG2	ZBTB7C	CDK20	KIAA0825	RXFP2	GPR182	CASZ1	ZBED2
ASAP2	INPP5A	UBE2O	WNT7B	TNFRSF8	RANBP3L	SORBS1	GUSB
CFAP126	SNHG7	COL18A1	CACNA1A	FKBP8	TEKT3	RPEL1	GNAT2
FAM107B	LCA5	MAP1S	RHOD	ADSSL1	SLC8A1	PKP2	ABHD15
FAM86B3P	SNRNP35	SLC1A4	CLDN23	INHBB	FAM110B	TMEM207	HMCN1
ADAM12	PRF1	CD38	METRNL	OPCML	RAP1GAP2	IQUB	TP63
RECQL5	PIK3R1	KRT20	CYP1A1	DUSP14	FTHL17	EPYC	CCDC134
B4GALNT2	FOXE1	ADAMTSL1	SCIN	POPDC2	NXNL1	RFX7	VTCN1
CPA2	IL21	PPP2R2A	RAPGEF4	ARNT2	GSN	SIGLEC8	LRRC29
ZNF385B	NLRC5	FUZ	CCR3	VLDLR	MELTF	BDNF	ACSL3
ZNF488	FRAT2	BATF3	C11orf96	SULT4A1	ITGAV	ADGRL3	SKIL
SIRT4	MORN3	RIPK2	KLLN	MYO6	MTCL1	UBA7	JPH2
DYSF	TYROBP	CCDC83	RHOU	NFIL3	FKBP11	LRPAP1	CLDN10
ERP44	IPMK	LTBP4	BBS10	RNLS	SPAG17	YOD1	BPTF
FERMT2	SYT12	CCDC150	S1PR2	PRSS41	FAM120B	TPH2	CDKL3
SFXN4	NDRG4	FAM171A1	ANKRD10	SLC29A3	IRAK3	KCNA10	ZBTB16
MICAL3	C5orf51	NAA16	EDNRA	PRMT9	DCST1	PDC	VCL
RAD51C	OSER1	SFRP2	VSTM5	BCLAF1	CXCL16	BFSP1	SHISA2
LGALS3BP	SCG2	TYMP	NENF	TEX36	C17orf107	ST6GALNAC 1	C5orf30
KCNJ6	AGTR2	SHANK2	GPR156	MICALL1	ZNF608	CCDC63	AQP9
MSX2	GPC1	GFPT1	GPRC5B	LACC1	NPFFR2	FBXO7	PARP11
TIGD2	ANKRD9	LRRN3	UBASH3A	CCDC68	TDRD7	ARHGAP24	SH3BGRL2
PNMA2	SLC1A3	ABCA13	CIPC	SPIRE2	H3F3C	EFHC2	VILL
CACNA1H	KCTD12	UBE4B	NYAP2	DUSP23	CCDC124	RHOBTB2	ERBB4
RAB35	ITPK1	PIK3R3	SPTSSA	MMP27	UBASH3B	PYM1	SPAG16
TOMM5	TLE6	MRPL21	JPH1	PKD1L2	TMEM94	LANCL3	IL2RG

CHIPSEQ_CDK19-KD ENHANCERUP							
FUNDC1							

[0210] The aforementioned GSEA also enabled us to identify the leading edge 'core' genes that contribute the most to each enrichment (FIGS. 12A and 12B). At these 'core' genes, differences in H3K27Ac enhancer signals due to *CDK19* knockdown (FIGS. 13A-13D) result in large corresponding changes in gene expression (FIG. 13E). The gene tracks at the *ELF3* (FIG. 13A) and *ETV7* (FIG. 13B) loci show enrichment of H3K27Ac signals in the *CDK19* knockdown samples, whereas the gene tracks at the *CHI3L2* (FIG. 13C) and *CRTAM* (FIG. 13D) loci show enrichment of H3K27Ac signals in the Control samples. Upper tracks denote Control samples, while lower tracks denote *CDK19* knockdown samples. Gray bars denote regions identified by DiffBind to be different between control and *CDK19* knockdown samples (FDR < 0.05). Metascape analysis was then used to evaluate Hallmark gene sets enriched within the CDK19KD-EnhancerUP 'core' and the CDK19KD-EnhancerDOWN 'core' genes. Within the CDK19KD-EnhancerUP 'core' genes, early Estrogen Response (p-value = 8.72e-5) and Epithelial Mesenchymal Transition (p-value = 1.08e-3) were Hallmarks identified as enriched (FIG. 3G, dark gray bars). Similarly, within the CDK19KD-EnhancerDOWN 'core' genes Androgen Response (p-value = 1.89e-3) was the Hallmark found to be enriched (FIG. 3G, light gray bar). Thus, a subset of genes (FIG. 3G) within the early Estrogen Response, Epithelial to Mesenchymal Transition, and Androgen Response gene sets have changes in H3K27Ac enhancer signals and strong corresponding changes in gene expression. These genes constitute a small fraction of the total genes in each Hallmark gene set (5-10%), but highlight key genes within these biological processes where CDK19 can epigenetically regulate gene transcription.

4.7 Example 7 - Effects of *CDK19* Knockdown on the Growth of Pre-established Organoids

[0211] We explored the effect of *CDK19* knockdown on the growth of pre-established organoids *in vitro* and in pre-established PDX tumors *in vivo*. This aimed to model the treatment of patients' pre-existing tumors. *In vitro*, adding doxycycline to the treatment group (to induce *CDK19* shRNA) significantly reduced the number of pre-established organoids compared to the control (no doxycycline) (FIGS. 4A and 4B). In FIGS. 4A and 4B, number of organoid colonies at Day 0 (FIG. 4A) and Day 16 (FIG. 4B) after initiating doxycycline

treatment is shown, ****$P < 0.0001$; ns is $P > 0.05$ (mean ± s.d., n = 6, experiment performed twice, P values determined by unpaired t-test). *In vivo*, feeding doxycycline to mice with pre-established inducCDK19KD-PDX-T1 or inducCDK19KD-PDX-T3 (PDX-T3 cells transduced with a doxycycline-inducible *CDK19* knockdown construct) tumors significantly impacted the growth of these tumors (FIGS. 4C and 4D). In FIGS 4C and 4D, the growth of pre-established tumors in the doxycycline fed NSG mice and control NSG mice are shown for inducCDK19KD-PDX-T1, ****$P < 0.0001$; ***$P < 0.001$ (mean ± s.d., n = 5, experiment performed twice, P values determined by unpaired t-test) (FIG. 4C) and inducCDK19KD-PDX-T3, ****$P < 0.0001$; ***$P < 0.001$ (mean ± s.d., n = 5, experiment performed once, P values determined by unpaired t-test) (FIG. 4D). *CDK19* shRNA induced tumors were ultimately 82% smaller in inducCDK19KD-PDX-T1 tumors and 38% smaller in inducCDK19KD-PDX-T3 tumors when compared to control tumors (FIGS. 4C and 4D). In both inducCDK19KD-PDX-T1 and inducCDK19KD-PDX-T3 experiments, mouse total body weights were not significantly different between the treatment and control groups (FIGS. 14A and 14B). Finally, survival studies showed that overall survival was significantly longer in mice whose PDX-T1 tumors were transduced with *CDK19* shRNA compared to mice transduced with control shRNA (FIG. 4E). Shown in FIG. 4E are Kaplan-Meir survival curves for mice engrafted with PDX-T1 xenografts transduced with control shRNA (black line), shCDK19-1 (solid gray line) or shCDK19-2 (dashed gray line). Mice were followed with weekly measurements of tumor diameters. Mice were sacrificed when the longest diameter of their tumor exceeded 17 mm. Two mice in the shCDK19-2 group did not develop PDX tumors and were sacrificed at the end of the experiment. These mice were censored when constructing the survival curve for the shCDK19-2 group, ***$P < 0.001$ (n = 9, experiment performed three times, log-rank (Mantel-Cox) test used to determine P values). In summary, these experiments showed that even in pre-established tumors, specifically knocking down *CDK19* can significantly decrease tumor growth and that *CDK19* knockdown can prolong survival in mice.

4.8 Example 8 - Effects of CCT251921 on Pre-Established PDX Tumors

[0212] To model the use of a CDK19 targeted therapy clinically, we treated mice with pre-established PDX tumors with CCT251921 (FIG. 4F), an orally bioavailable inhibitor of both CDK19 and the closely related paralog, CDK8. PDX-T1 tumors were pre-established in mice before starting daily oral administration (30 mg/kg) of CCT251921 or vehicle. Treatment with

CCT251921 resulted in a significant reduction in tumor growth by day 14 (FIG. 4G). Final volumes of the tumors in CCT251921 treated mice were over 30% smaller than the tumors of vehicle treated mice (FIG. 4G). NSG mice with pre-established PDX-T1 xenograft tumors were treated with daily oral gavage of CCT251921 or vehicle. Mice were followed with twice weekly determinations of tumor volume, $^{****}P < 0.0001$; $^{***}P < 0.001$ (mean ± s.d., n = 5, experiment performed once, *P* values determined by unpaired t-test). Mice in both the CCT251921 and vehicle cohorts suffered an overall weight loss, but this was not significantly different between the two groups and most likely due to the effect of daily oral gavage on their feeding habits (FIG. 14C). It is well known that different biological outcomes can arise from gene knockdown versus chemical inhibition. We show here in pre-established tumors that chemical inhibition of CDK19 kinase activity can recapitulate the effects of total *CDK19* loss shown in our knockdown studies.

[0213] From our data, we conclude that CDK19 regulates multiple cancer relevant pathways and that it is a potential therapeutic target in TICs. Thus, CDK19 inhibition is useful both to therapeutic strategies targeting transcriptional co-factors such as CDK8, CDK9, and BRD4, and to those targeting TICs and their self-renewal pathways such as Hedgehog, Wnt/β-catenin, and Notch. However, some therapeutic approaches may be limited by toxicity caused to normal cells. This can be attributed to the ubiquitous expression of transcriptional co-factors in normal tissues and the importance of self-renewal pathways in normal stem cells. BRD4 inhibition, for example, resulted in a disruption of tissue homeostasis in multiple organs in mice. Similarly, due to the challenge of narrow therapeutic indices, Hedgehog, Notch, and Wnt pathway inhibitors have had limited clinical success thus far. The biology of CDK19 points towards potential advantages as a therapeutic target. Compared to other ubiquitous transcriptional co-factors such as its paralog CDK8, CDK9, and BRD4, CDK19 has more limited tissue distribution (see, e.g., Tsutsui et al., *Genes to cells : devoted to molecular & cellular mechanisms* 16:1208-1218, 2011), potentially limiting the toxicity from CDK19 inhibition, while *CDK8*, *CDK9*, and *BRD4* knockouts are lethal (see, e.g., Brown et al., *Mamm Genome* 23:632-640, 2012; Westerling, *Molecular and Cellular Biology* 27:6177-6182, 2007; and Houzelstein et al., *Molecular and Cellular Biology* 22, 3794-3802, 2002). In addition, the limited expression of CDK19 in tissues could broaden the therapeutic window to enable the otherwise toxic inhibition of stem cell pathways such as NOTCH, or critical processes, such as

G2/M checkpoint. Our studies showing that small molecule inhibition of CDK19 impaired PDX growth affirms the potential of therapeutically targeting CDK19 in TNBC.

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[0214] While the foregoing invention has been described in some detail for purposes of clarity and understanding, it will be appreciated by those skilled in the relevant arts, once they have been made familiar with this disclosure, that various changes in form and detail can be made without departing from the true scope of the invention in the appended claims. The invention is therefore not to be limited to the exact components or details of methodology or construction set forth above. Except to the extent necessary or inherent in the processes themselves, no particular order to steps or stages of methods or processes described in this disclosure, including the Figures, is intended or implied. In many cases the order of process steps may be varied without changing the purpose, effect, or import of the methods described.

[0215] All publications and patent documents cited herein are incorporated herein by reference as if each such publication or document was specifically and individually indicated

to be incorporated herein by reference. Citation of publications and patent documents (patents, published patent applications, and unpublished patent applications) is not intended as an admission that any such document is pertinent prior art, nor does it constitute any admission as to the contents or date of the same.

[0216] CDK19 Transcript Variant 1 (NM_015076.4) (SEQ ID NO: 12)

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[0217] CDK19 Transcript Variant 2 (NM_001300960.1) (SEQ ID NO: 13)

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481 gagcatgact tgtggcatat tattaagttt caccgtgcat caaaagcaaa taaaaagccc
541 atgcagttgc caagatctat ggttaaatcc ttactttacc agattcttga tggtatccat
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901 agaacaacgt atgccaacag tagcctcata aagtacatgg agaaacacaa ggtcaagcct
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1261 accaacggga ccgcaggtgg ggctggggcc ggggtcgggg gcaccggagc agggttgcag
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2761 caagaatctt tttcattgca ctgaatgatt tcttttgccc ctaggagaaa acttaataat
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2881 tttccattat ctatgaatta gtggctgagt tctttcttag ctgctttaag gagcccctca
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[0218] CDK19 Transcript Variant 3 (NM_001300963.1) (SEQ ID NO: 14)

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[0219] CDK19 Transcript Variant 4 (NM_001300964.1) (SEQ ID NO: 15)

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1201 gggcaccgga gcagggttgc agcacagcca ggactccagc ctgaaccagg tgcctccaaa
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1861 tatagtttta tacttcatga actgatttag caacacaggt aaaaatgcac cttttaaagc
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2281 atggcccaca ccaaaacgct gaagagagta acaactgcac taggatttct gtaaggagta
2341 attttgatca aaagacgtgt tacttccctt tgaaggaaaa gtttttagtg tgtattgtac
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2401 ataaagtcgg cttctctaaa gaaccattgg tttcttcaca tctgggtctg cgtgagtaac
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5941 atgactgtta aaactaaaat aaattacatt gcatttattt tatattcttg gttgaaataa
6001 aatttaattg actttg

[0220] Cyclin dependent kinase 8 (CDK8), transcript variant 1 (NM_001260.2) (SEQ ID NO: 16)

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   1 gagtgccctc cctcctcctc tctttgagga ggtaccggct gttgtgcggc tctgcccttc
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 121 aggcgtgagt gcgcgtgtga gaggacgaga gcccgcctgg ccgccccgcc gctcccgccg
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 301 cgggggatcc tccccgttcc tccacccccg gccggcctct gccccgccgt ccccctggat
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 421 cggccggcgg gcgtagagcg ggcgggttcc cgggggctgc ggctgcccgt gcttccccgg
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1741 gaagaaagtg agagttgttc ctcctaccac tacctcaggt ggacttatca tgacctcaga
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1861 gcagagcagc atgggatact cagctacctc ccagcagcct ccacagtact cacatcagac
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2101 aagttgtacc tattttggag ttagacttga aaagaaagtg ctagcacagt ttgtgttgtg
2161 gatttgctac ttccatagtt tacttgacat ggttcagact gaccaatgca ttttttttcag
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2941 tagaattttt gaggaaaaaa aaacctataa catacaatgt actgtatcaa actattttac
3001 atgaatgaca caagtattct gaataaaaaa taattgaaca ttgttaaaaa caaggtgtta
3061 tgtaataaat ttatttttca taaatcaaaa aaaaaaaaaa a

[0221] Cyclin dependent kinase 8 (CDK8), transcript variant 2 (NM_001318368.1) (SEQ ID NO: 17)

1 gagtgccctc cctcctcctc tctttgagga ggtaccggct gttgtgcggc tctgcccttc
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121 aggcgtgagt gcgcgtgtga gaggacgaga gcccgcctgg ccgccccgcc gctcccgccg
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601 atacgagggc tgcaaagttg gccgaggcac ttatggtcac gtctacaaag ccaagaggaa

661 agatgggaag gatgataaag actatgcttt aaaacaaata gaaggaactg ggatctctat
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[0222] Cyclin dependent kinase 8 (CDK8), transcript variant 3 (NM_001346501.1) (SEQ ID NO: 18)

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121 aggcgtgagt gcgcgtgtga gaggacgaga gcccgcctgg ccgccccgcc gctcccgccg
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2581 tatgttgtca ttgatataaa cctgtttggt tcagcaaaca aactaaaatg attgtcatag
2641 acagtgtttt atttttcctg ttggtgttgc tgatttgtga gcatgcttta agatgaaaaa
2701 agcatgaatg ataacttcct taaaaaggtg cggcatccaa ttcaaatatt ttcgtcctga
2761 ttttaaagct ggttggtgta gtgctattaa aatttcgttc agttaatttt ccttttgaaa
2821 acttgttcgc acgttgttta gggtgccctt acttcagcaa aggagaagga gtaggagagc
2881 cttagaattt ttgaggaaaa aaaaacctat aacatacaat gtactgtatc aaactatttt
2941 acatgaatga cacaagtatt ctgaataaaa aataattgaa cattgttaaa aacaaggtgt
3001 tatgtaataa atttatttt cataaatcaa aaaaaaaaaa aaa

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What is claimed is:

1. A method of treating a patient diagnosed with triple-negative breast cancer (TNBC), comprising administering a therapeutically effective dose of an agent that inhibits expression or activity of cyclin-dependent kinase 19 (CDK19), wherein the agent inhibits CDK19 gene expression to a greater extent than it inhibits cyclin-dependent kinase 8 (CDK8) gene expression, wherein the agent comprises an inhibitory nucleic acid selected from an RNA capable of hybridizing to a portion of a CDK19 RNA transcript and decreasing CDK19 gene expression, an RNAse H dependent antisense oligonucleotide capable of binding to a CDK19 transcript, and a guide RNA that directs a Cas protein to a CDK19 gene sequence, and wherein administration of the agent results in at least one of a reduction in cachexia, increase in survival time, elongation in time to tumor progression, reduction in tumor mass, reduction in tumor burden, prolongation in time to tumor metastasis, prolongation in time to tumor recurrence, and progression free survival.

2. A method of treating a patient diagnosed with triple-negative breast cancer (TNBC) characterized by a tumor comprising $EpCAM^{med/high}$ and $CD10^{-/low}$ epithelial cells, the method comprising administering a therapeutically effective dose of an agent that inhibits cyclin-dependent kinase 19 (CDK19) expression or activity, wherein the agent is an shRNA capable of hybridizing to a portion of a CDK19 RNA transcript and decreasing CDK19 gene expression, an siRNA capable of hybridizing to a portion of a CDK19 RNA transcript and decreasing CDK19 gene expression, an RNAse H dependent antisense oligonucleotide capable of binding to a CKD19 transcript, or a guide RNA that directs a Cas protein to a CDK19 polynucleotide sequence, wherein the treatment reduces the number of $EpCAM^{med/high}$ and $CD10^{-/low}$ cells in the tumor, reduces the number of $EpCAM^{med/high}$ and $CD10^{-/low}$ cells per unit volume of the tumor, or results in a reduction of the ratio of $EpCAM^{med/high}$ and $CD10^{-/low}$ epithelial cells to normal cells in the tumor.

3. A method of reducing metastasis of TNBC in a patient, the method comprising administering a therapeutically effective dose of an agent that inhibits expression or activity of

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CDK19, wherein the agent is a nucleic acid comprising at least one of an RNA capable of hybridizing to a portion of a CDK19 RNA transcript and decreasing CDK19 gene expression, an expression vector encoding such an RNA, an RNAse H dependent antisense oligonucleotide capable of binding to a CKD19 transcript, or a guide RNA that directs a Cas protein to a CDK19 polynucleotide sequence.

4. The method of any one of claims 1-3, wherein the patient is treated with a combination therapy comprising (a) an agent that inhibits expression or activity of CDK19 and (b) radiation therapy and/or chemotherapy.

5. The method of any one of claims 1-4, comprising detecting $EpCAM^{med/high}/CD10^{-/low}$ cells in a tissue sample from the patient prior to or after initiating therapy.

6. The method of any one of claims 1-5, wherein the agent is a CRISPR/Cas9 system.

7. The method of any one of claims 1-5, wherein the agent is a CDK19 targeting shRNA or a CDK19 targeting siRNA.

8. The method of any one of claims 1-5, wherein the agent is a CDK19 targeting shRNA comprising a sequence selected from: SEQ ID NO: 1 and SEQ ID NO: 2 or the complement thereof.

9. The method of any one of claims 1-5, wherein the agent is a CDK19 targeting shRNA or siRNA complementary or substantially complementary to the 5' UTR of CDK19, but not to the 5' UTR of CDK8.

10. The method of any one of claims 1-5, wherein the agent is a CDK19 targeting shRNA or siRNA complementary or substantially complementary to the 3' UTR of CDK19, but not to the 3'UTR CDK8.

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11. The method of any one of claims 1-5, wherein the agent is a CDK19 targeting shRNA or siRNA complementary or substantially complementary to the coding region of CDK19, but not to the coding region of CDK8.

12. The method of any one of claims 1-5, wherein the agent binds CDK19 in the cytoplasm of a breast epithelial cell.

13. The method of claim 1, wherein the inhibitory nucleic acid is an shRNA or siRNA that hybridizes to a portion of a CDK19 RNA transcript and decreases CDK19 gene expression.

14. The method of claim 1, wherein the RNA is an shRNA administered using an expression vector encoding the shRNA.

15. The method of claim 2, wherein the RNA is an shRNA administered using an expression vector encoding the shRNA.

16. The method of claim 1, wherein the agent is an RNAse H dependent antisense oligonucleotide.

17. The method of claim 1, wherein the agent is a guide RNA complexed to a Cas protein.

18. A method of predicting the likely therapeutic responsiveness of a subject with TNBC to a CDK19 targeting agent comprising:

(a) quantitating $EpCAM^{med/high}/CD10^{-/low}$ cells in a tumor sample obtained from the subject;

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(b) comparing the quantity of $EpCAM^{med/high}/CD10^{-/low}$ cells in (a) to a reference value characteristic of tumors responsive to a CDK19 targeting therapy, and

(c) treating the patient with an inhibitor of CDK19 expression or activity if the quantity of $EpCAM^{med/high}/CD10^{-/low}$ cells is equal to or exceeds the reference value.

FIG. 1A

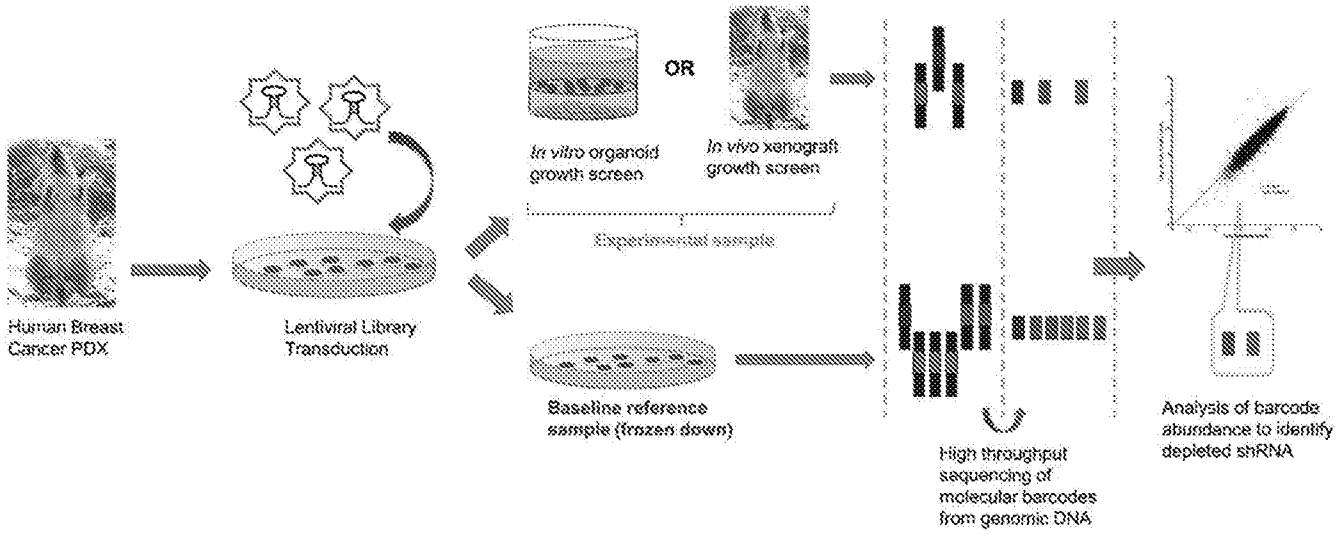

Human Breast Cancer PDX
Lentiviral Library Transduction
OR
In vitro organoid growth screen
In vivo xenograft growth screen
Experimental sample
Baseline reference sample (frozen down)
High throughput sequencing of molecular barcodes from genomic DNA
Analysis of barcode abundance to identify depleted shRNA

FIG. 1B

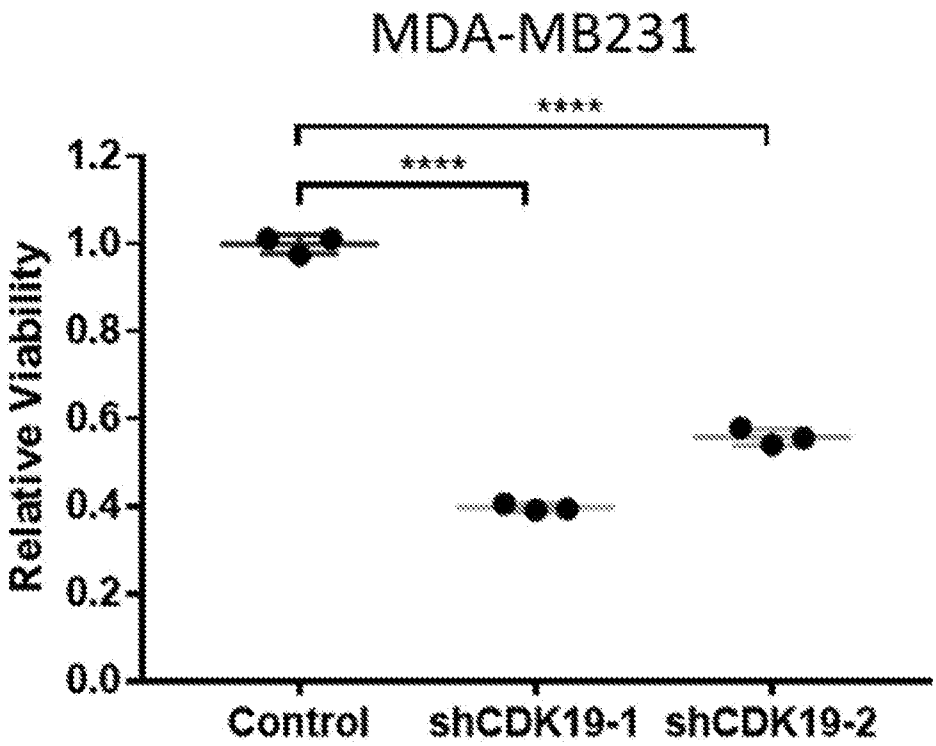

MDA-MB231
****
****
Relative Viability
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control
shCDK19-1
shCDK19-2

FIG. 1C

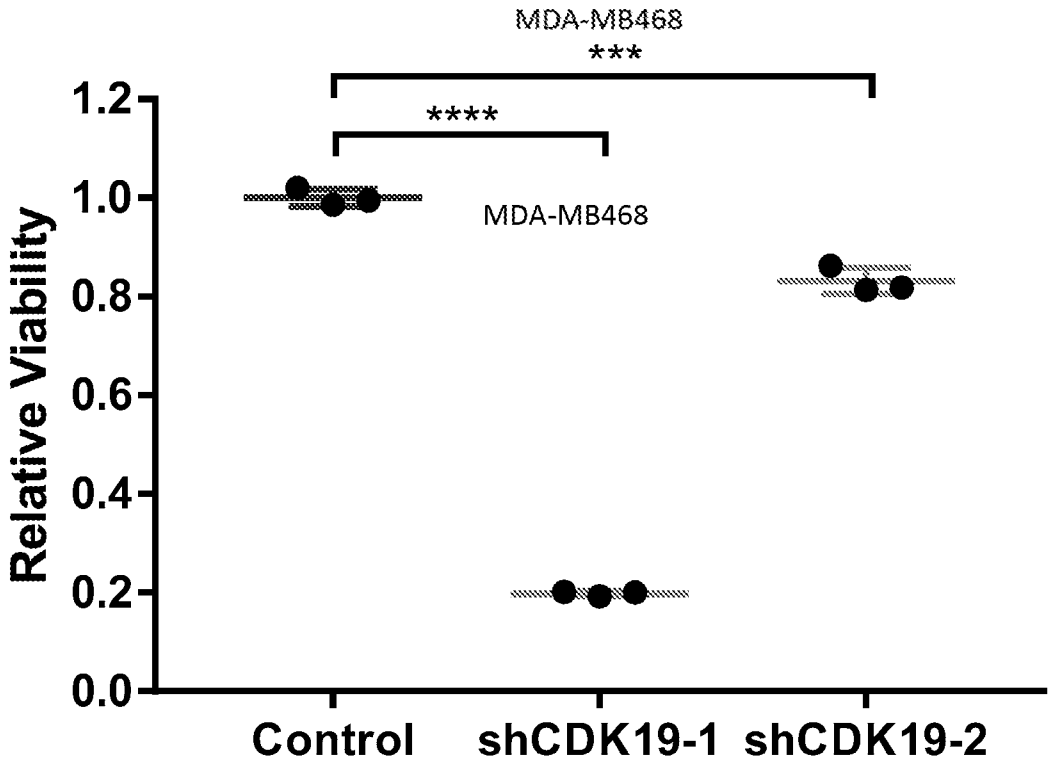

MDA-MB468
***
****
MDA-MB468
Relative Viability
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control
shCDK19-1
shCDK19-2

FIG. 1D

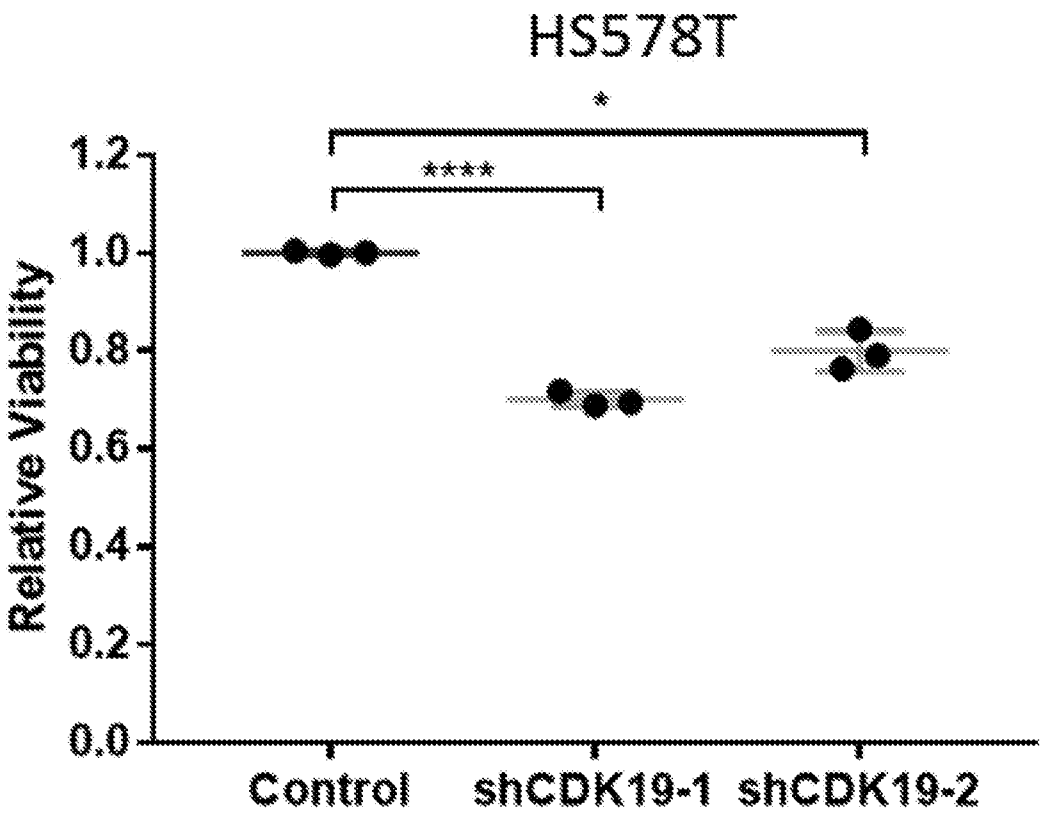

HS578T
*
****
Relative Viability
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control
shCDK19-1
shCDK19-2

FIG. 1E

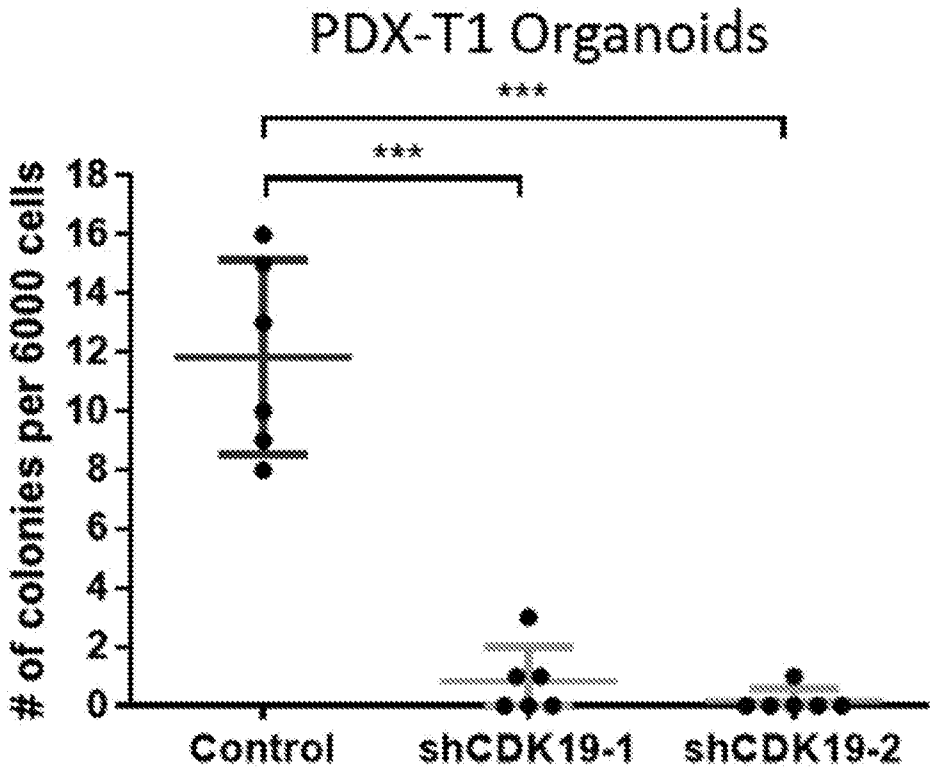

PDX-T1 Organoids
***
***
# of colonies per 6000 cells
18
16
14
12
10
8
6
4
2
0
Control
shCDK19-1
shCDK19-2

FIG. 1F

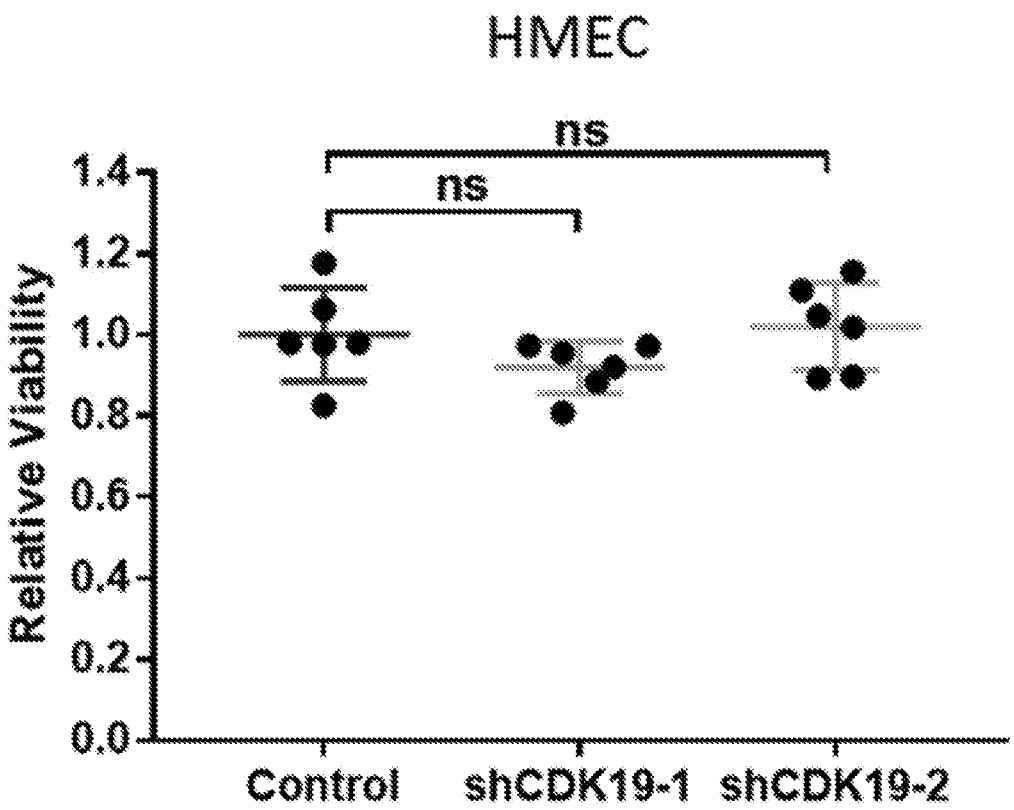

HMEC
ns
ns
Relative Viability
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control
shCDK19-1
shCDK19-2

FIG. 1G

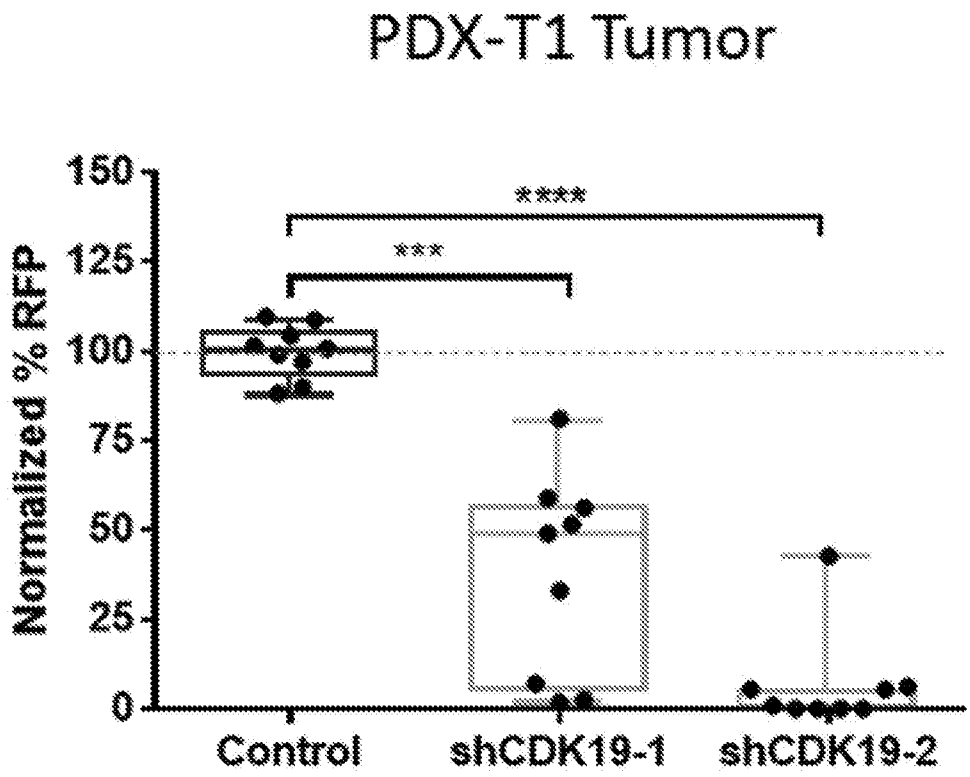

PDX-T1 Tumor
Normalized % RFP
150
125
100
75
50
25
0
****
***
Control
shCDK19-1
shCDK19-2

FIG. 1H

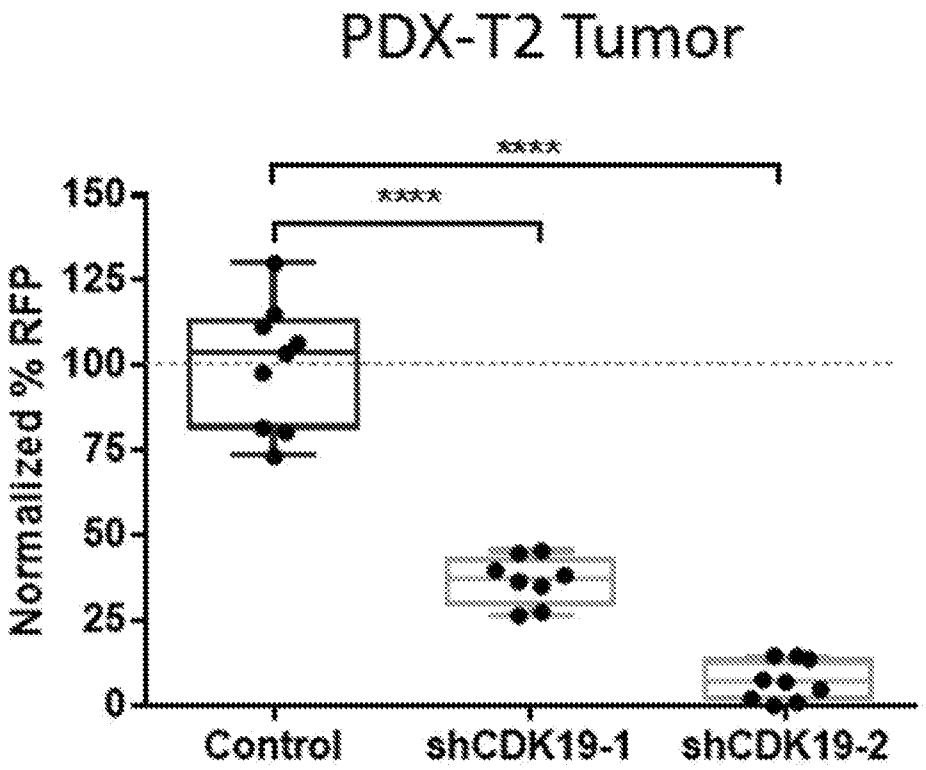

PDX-T2 Tumor
****
****
Normalized % RFP
150
125
100
75
50
25
0
Control
shCDK19-1
shCDK19-2

FIG. 1I

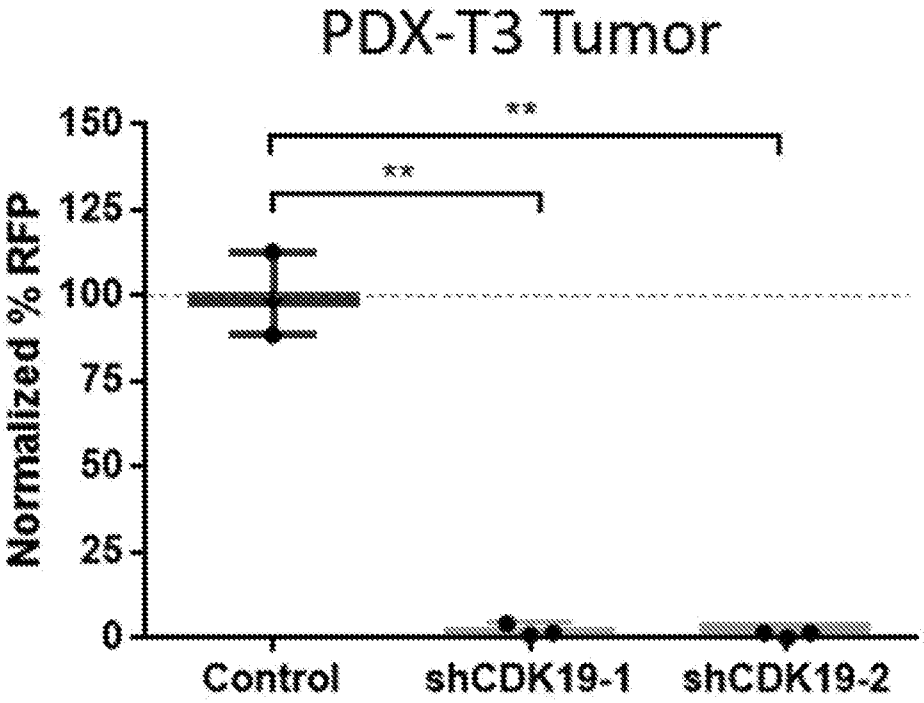

PDX-T3 Tumor
**
**
150
125
100
75
50
25
0
Normalized % RFP
Control
shCDK19-1
shCDK19-2

FIG. 1J

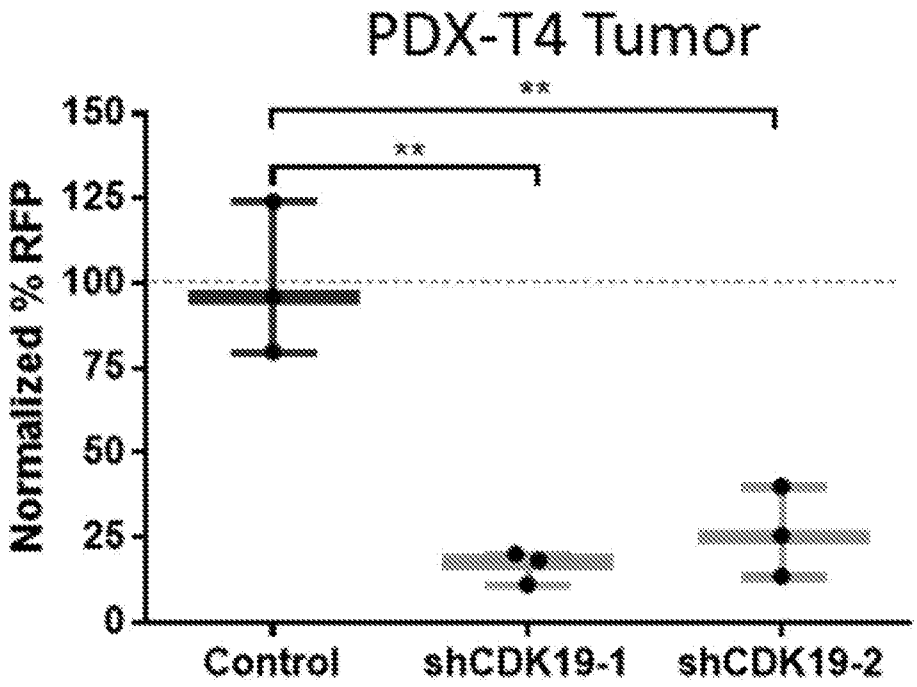

PDX-T4 Tumor
**
**
Normalized % RFP
150
125
100
75
50
25
0
Control
shCDK19-1
shCDK19-2

FIG. 1K

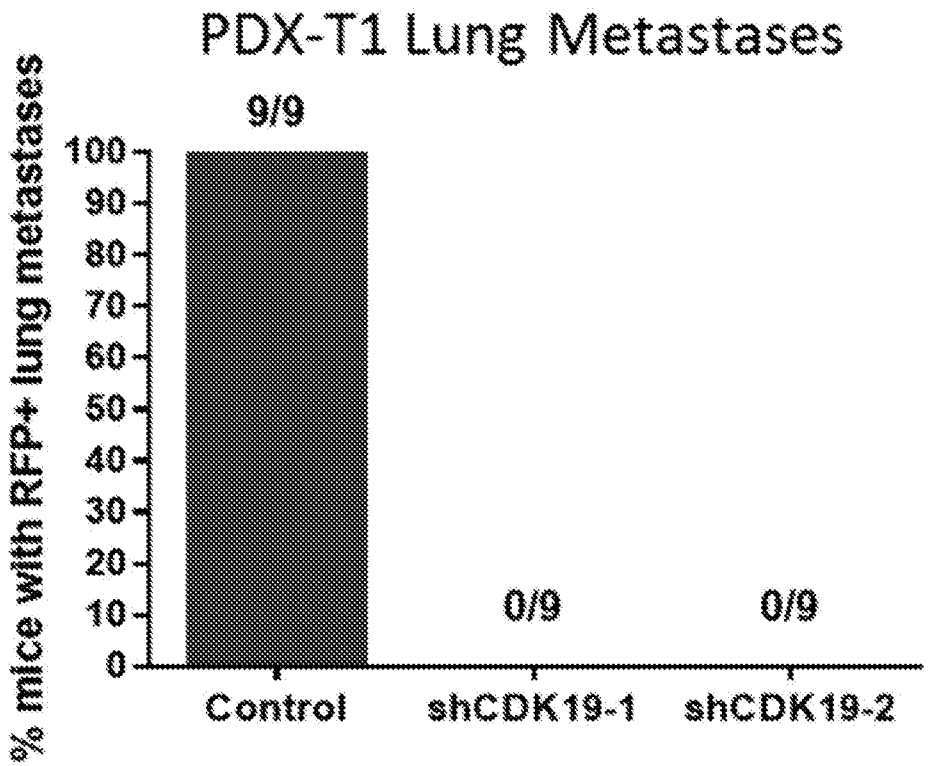

PDX-T1 Lung Metastases
% mice with RFP+ lung metastases
100
90
80
70
60
50
40
30
20
10
0
9/9
0/9
0/9
Control
shCDK19-1
shCDK19-2

FIG. 1L

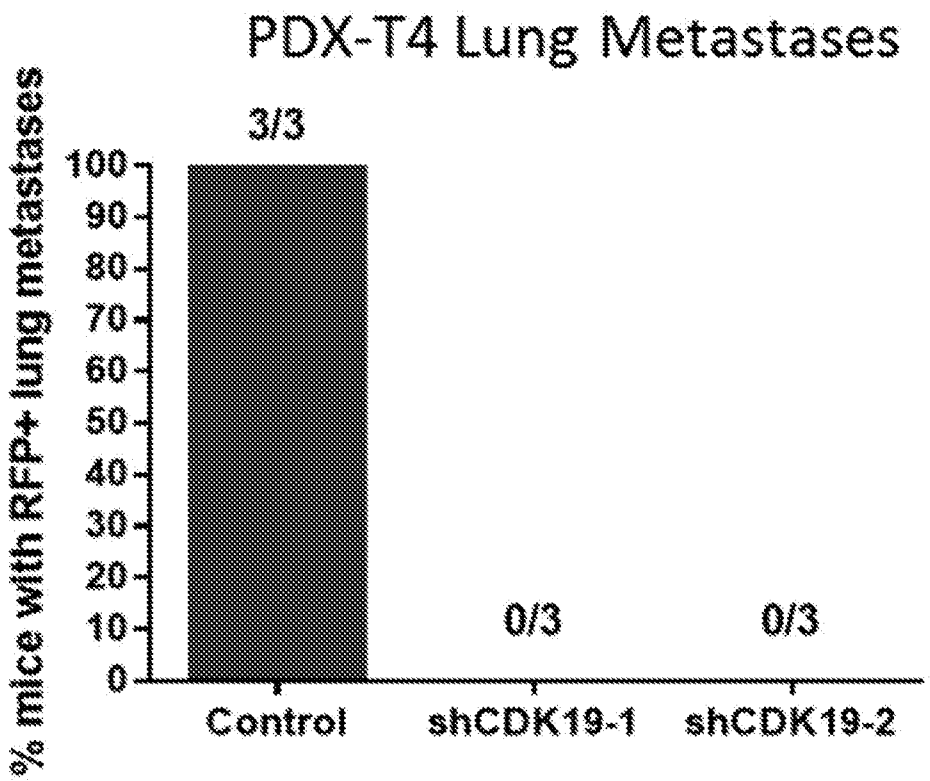

PDX-T4 Lung Metastases
% mice with RFP+ lung metastases
100
90
80
70
60
50
40
30
20
10
0
3/3
0/3
0/3
Control
shCDK19-1
shCDK19-2

FIG. 1M

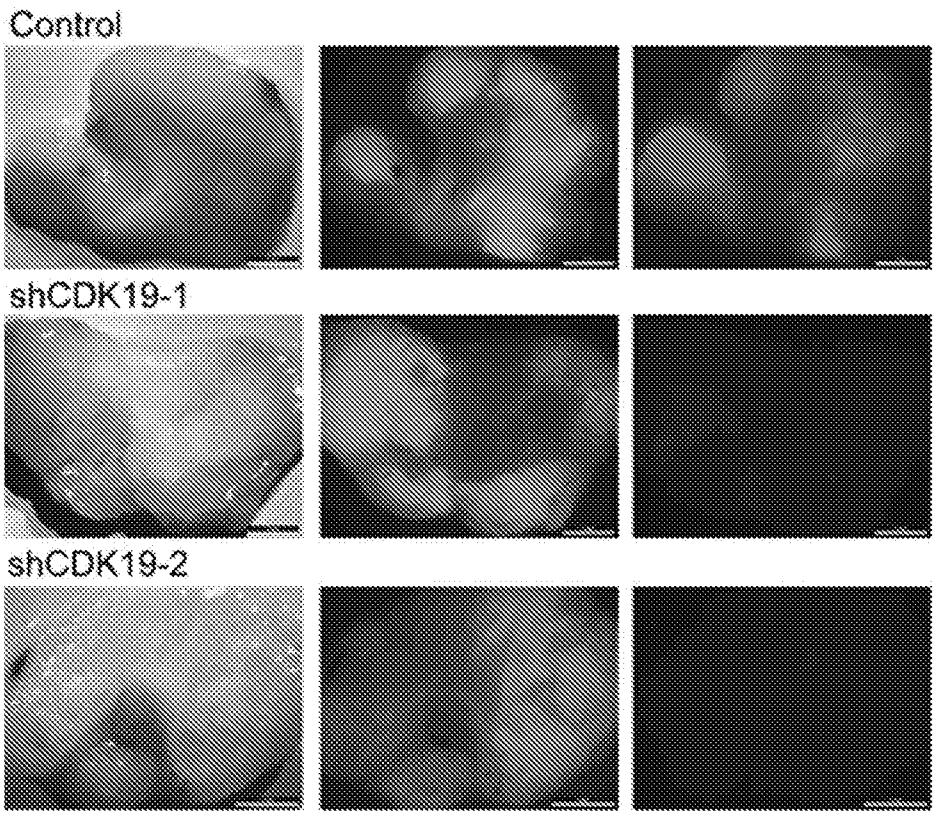


FIG. 1N

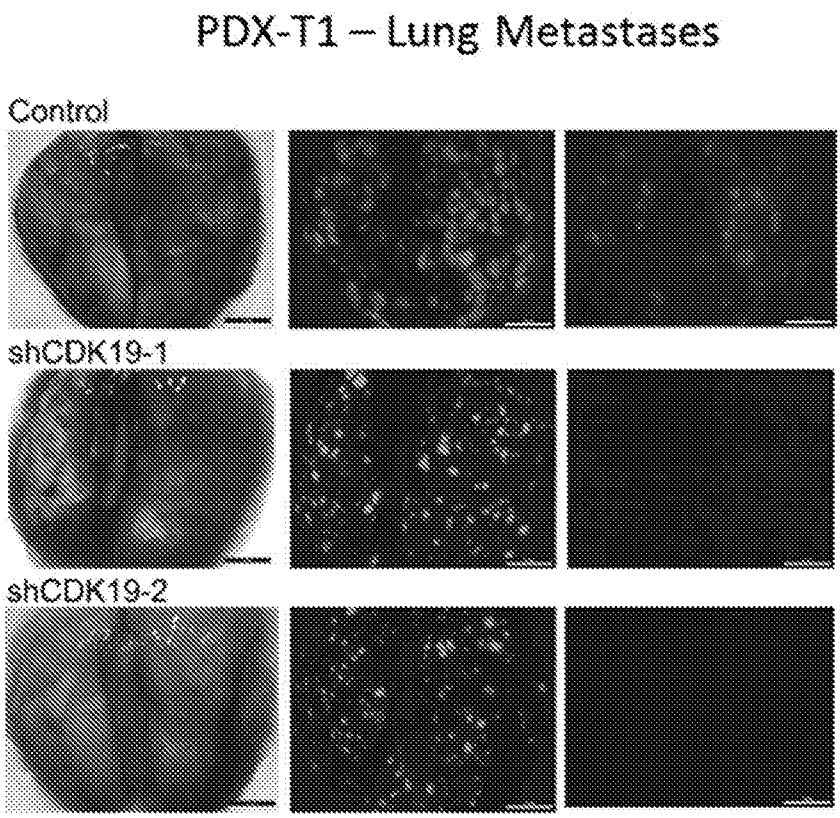


FIG. 2A

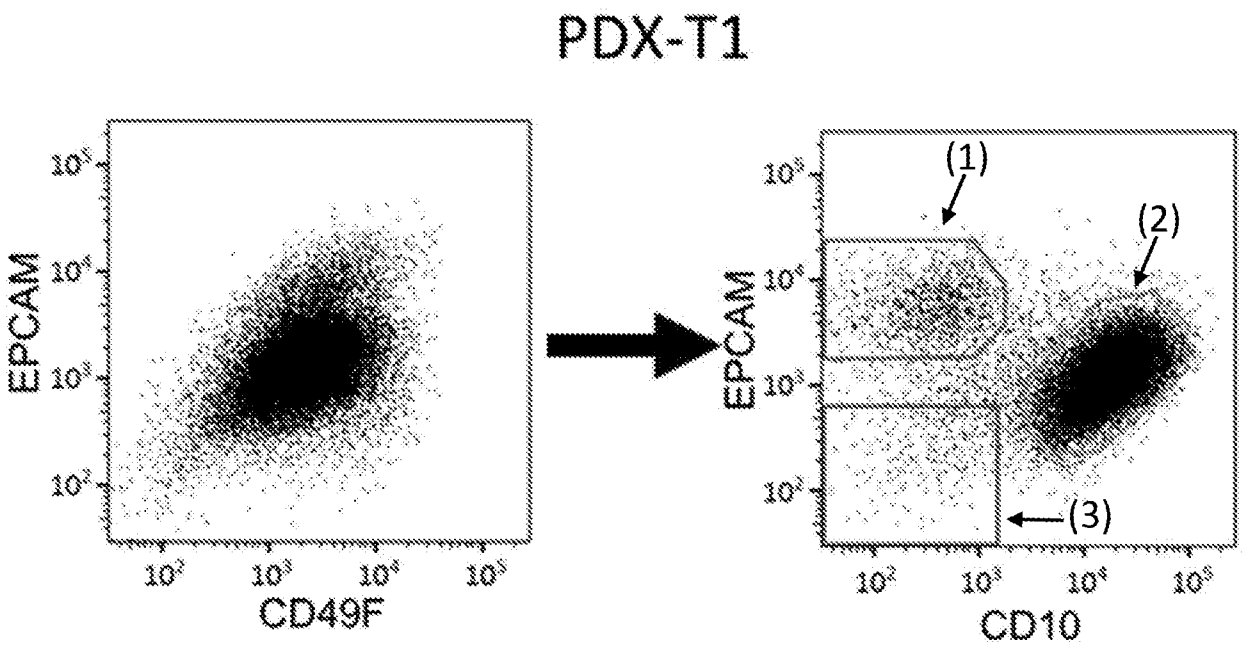


FIG. 2B

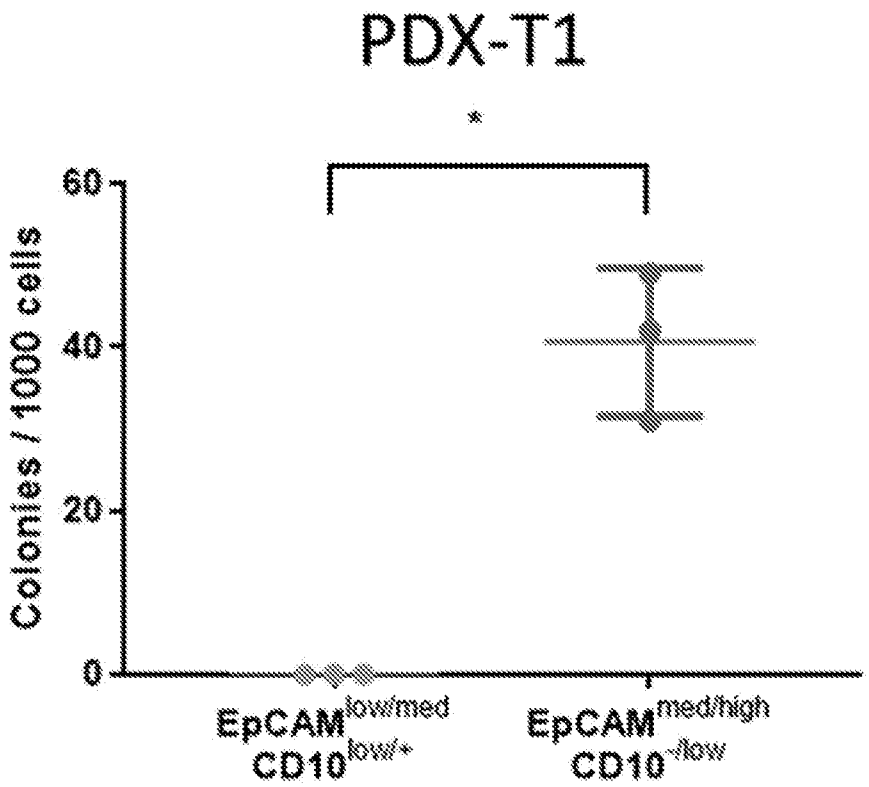
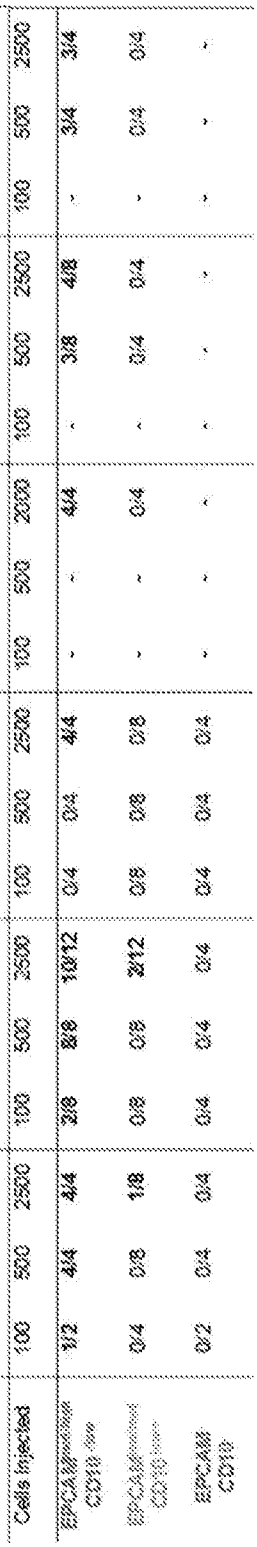

PDX-T1
*
Colonies / 1000 cells
60
40
20
0
EpCAM low/med CD10 low/+
EpCAM med/high CD10 -/low

FIG. 2C



Cells injected	PDX-T1			PDX-T2			PDX-T5			PDX-T4			PDX-T6			PDX-T7		
	100	500	2500	100	500	2500	100	500	2500	100	500	2000	100	500	2500	100	500	2500
EPCAM^{pos} CD19^{neg}	1/2	4/4	4/4	2/8	8/8	10/12	0/4	0/4	4/4	-	-	4/4	-	3/8	4/8	-	3/4	3/4
EPCAM^{pos} CD19^{neg}	0/4	0/8	1/8	0/8	0/8	2/12	0/8	0/8	0/8	-	-	0/4	-	0/4	0/4	-	0/4	0/4
EPCAM^{neg} CD19^{neg}	0/2	0/4	0/4	0/4	0/4	0/4	0/4	0/4	0/4	-	-	-	-	-	-	-	-	-

FIG. 2D

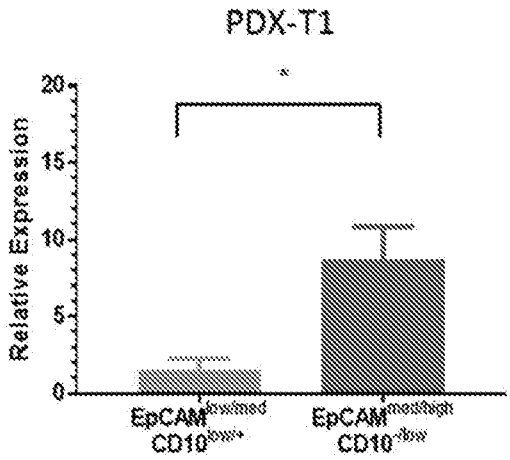


FIG. 2E

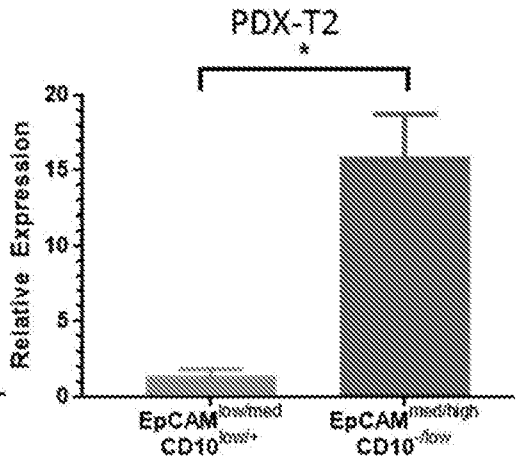


FIG. 2F

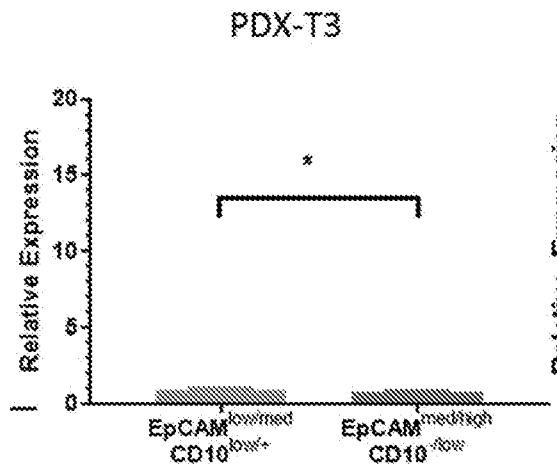


FIG. 2G

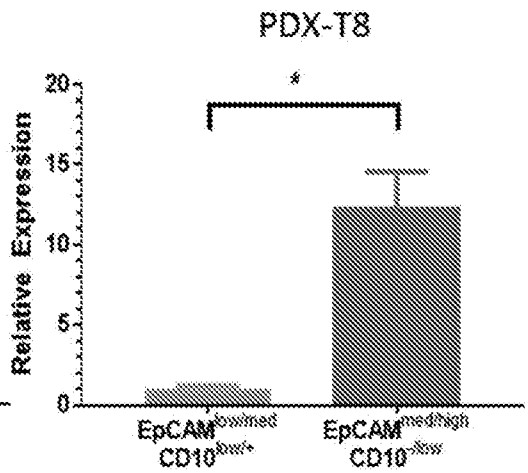


FIG. 3A

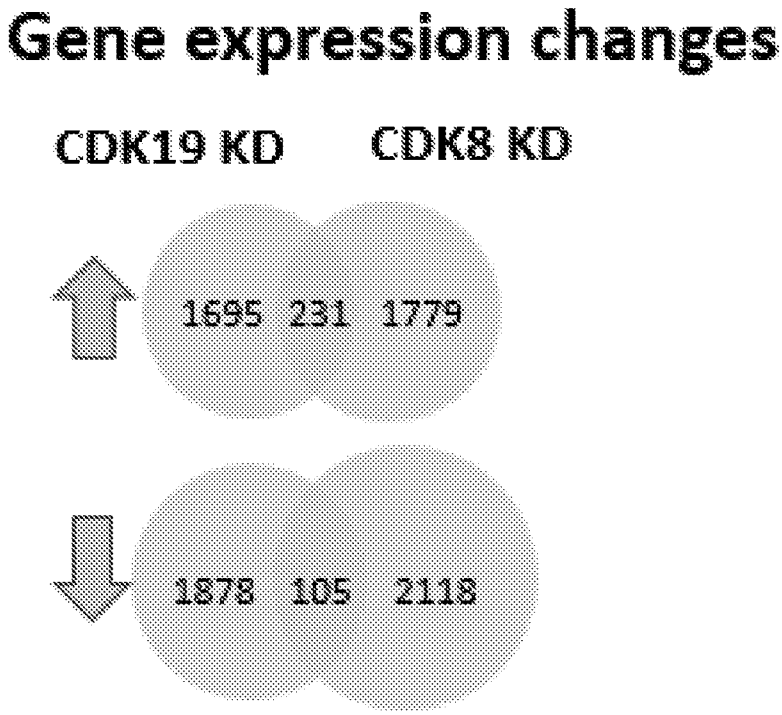

Gene expression changes
CDK19 KD
CDK8 KD
1695 231 1779
1878 105 2118

FIG. 3B

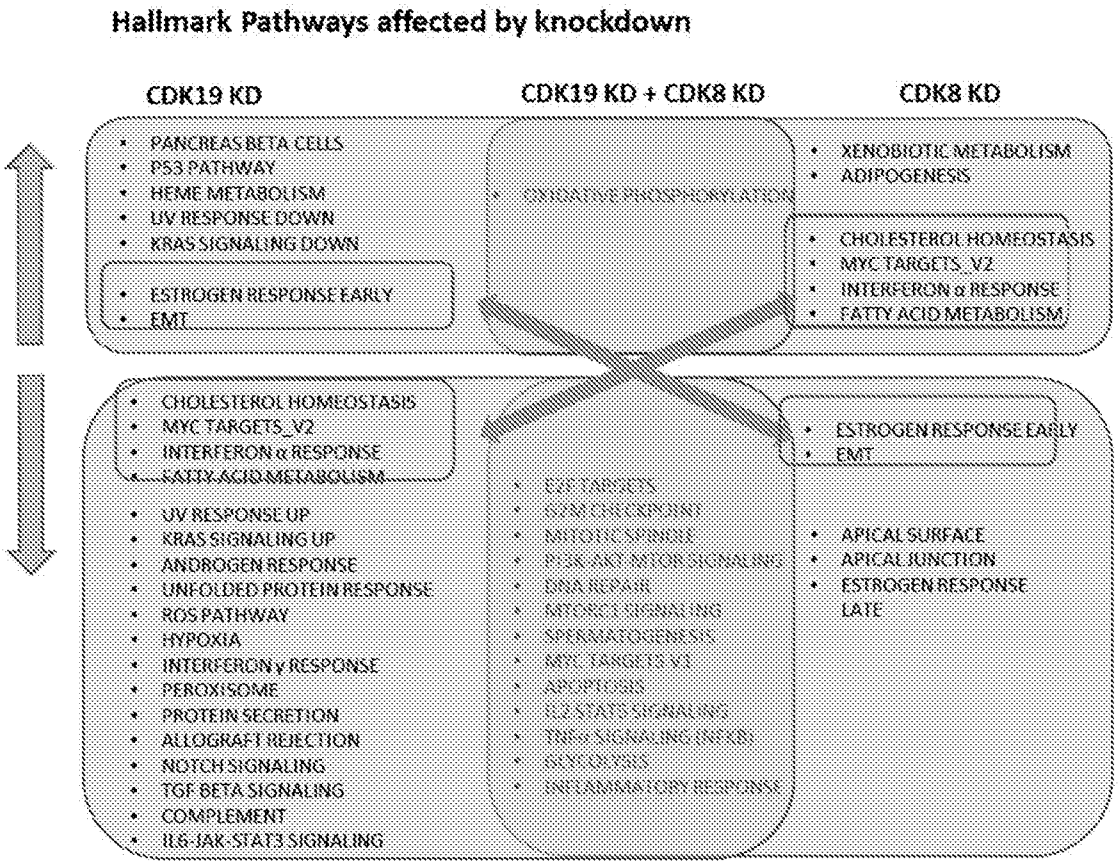

Hallmark Pathways affected by knockdown
CDK19 KD
CDK19 KD + CDK8 KD
CDK8 KD
PANCREAS BETA CELLS
P53 PATHWAY
HEME METABOLISM
UV RESPONSE DOWN
KRAS SIGNALING DOWN
ESTROGEN RESPONSE EARLY
EMT
OXIDATIVE PHOSPHORYLATION
XENOBIOTIC METABOLISM
ADIPOGENESIS
CHOLESTEROL HOMEOSTASIS
MYC TARGETS_V2
INTERFERON α RESPONSE
FATTY ACID METABOLISM
CHOLESTEROL HOMEOSTASIS
MYC TARGETS_V2
INTERFERON α RESPONSE
FATTY ACID METABOLISM
UV RESPONSE UP
KRAS SIGNALING UP
ANDROGEN RESPONSE
UNFOLDED PROTEIN RESPONSE
ROS PATHWAY
HYPOXIA
INTERFERON γ RESPONSE
PEROXISOME
PROTEIN SECRETION
ALLOGRAFT REJECTION
NOTCH SIGNALING
TGF BETA SIGNALING
COMPLEMENT
IL6-JAK-STAT3 SIGNALING
E2F TARGETS
G2M CHECKPOINT
MITOTIC SPINDLE
PI3K AKT MTOR SIGNALING
DNA REPAIR
MTORC1 SIGNALING
SPERMATOGENESIS
MYC TARGETS V1
APOPTOSIS
IL2 STAT5 SIGNALING
TNFα SIGNALING VIA NFKB
GLYCOLYSIS
INFLAMMATORY RESPONSE
ESTROGEN RESPONSE EARLY
EMT
APICAL SURFACE
APICAL JUNCTION
ESTROGEN RESPONSE LATE

FIG. 3C

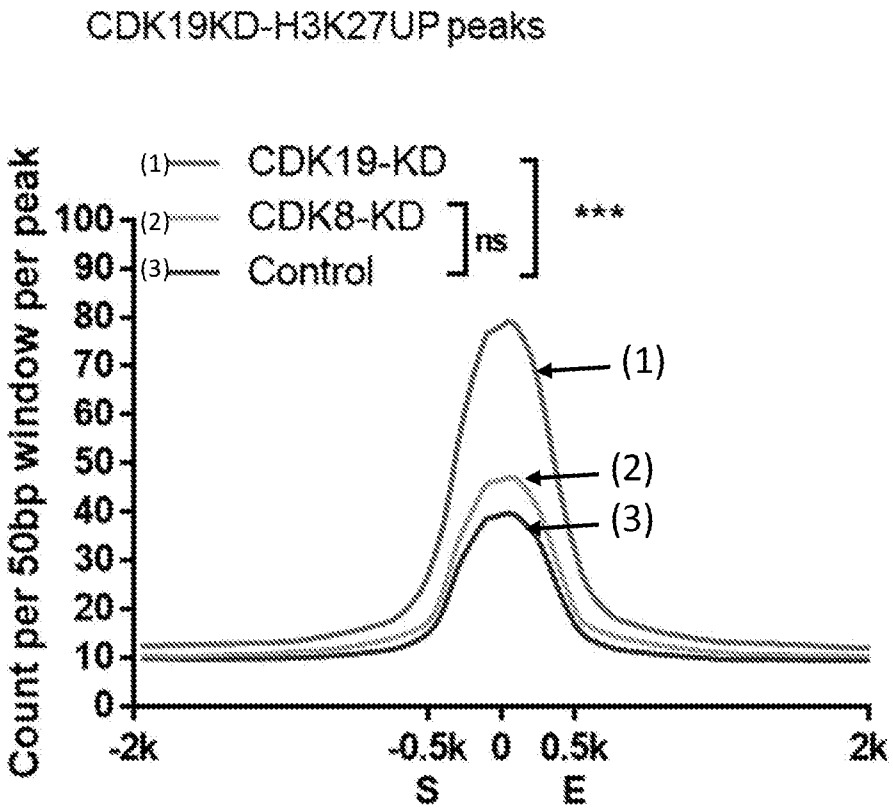

CDK19KD-H3K27UP peaks
(1) CDK19-KD
(2) CDK8-KD
(3) Control
ns
***
Count per 50bp window per peak
100
90
80
70
60
50
40
30
20
10
0
(1)
(2)
(3)
-2k
-0.5k
S
0
0.5k
E
2k

FIG. 3D

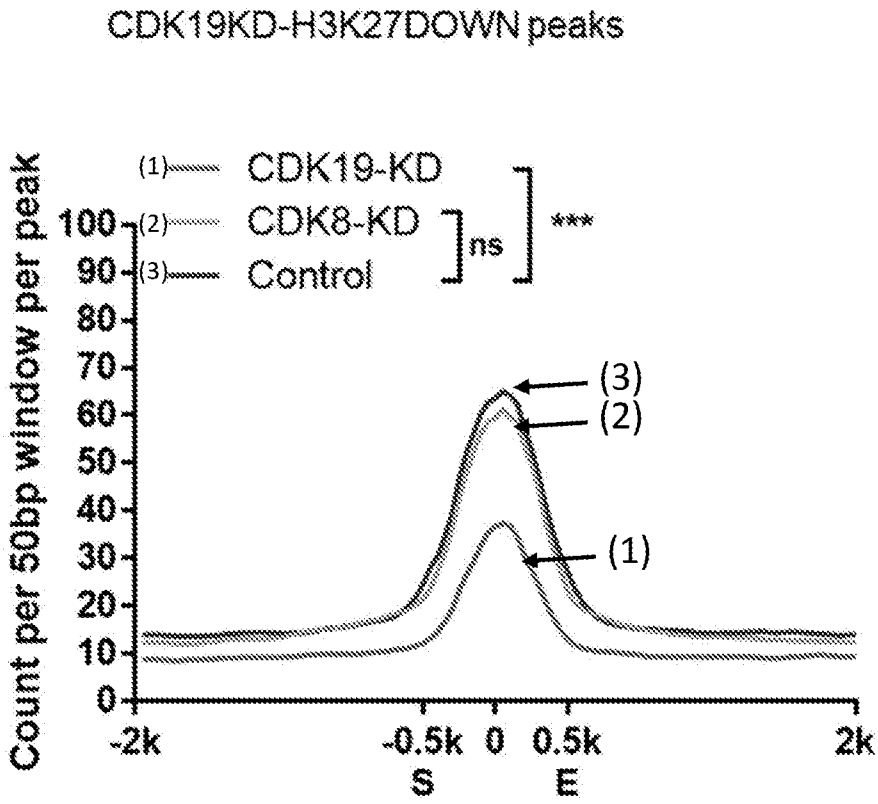

CDK19KD-H3K27DOWN peaks
(1) CDK19-KD
(2) CDK8-KD
(3) Control
ns
***
Count per 50bp window per peak
100
90
80
70
60
50
40
30
20
10
0
(3)
(2)
(1)
-2k
-0.5k
S
0
0.5k
E
2k

FIG. 3E

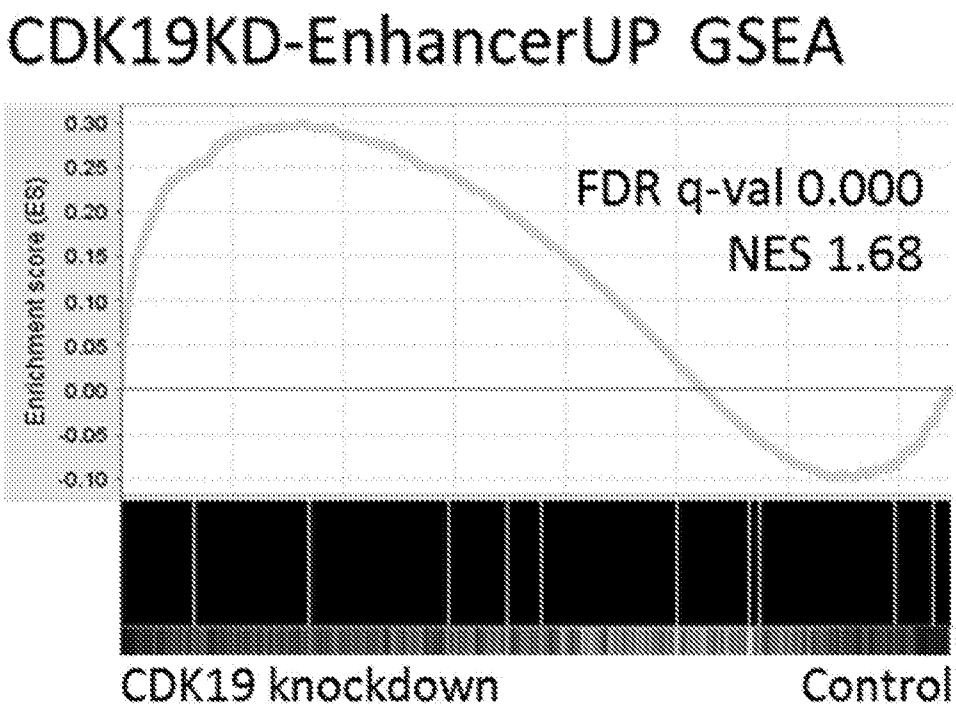

CDK19KD-EnhancerUP GSEA
Enrichment score (ES)
0.30
0.25
0.20
0.15
0.10
0.05
0.00
-0.05
-0.10
FDR q-val 0.000
NES 1.68
CDK19 knockdown
Control

FIG. 3F

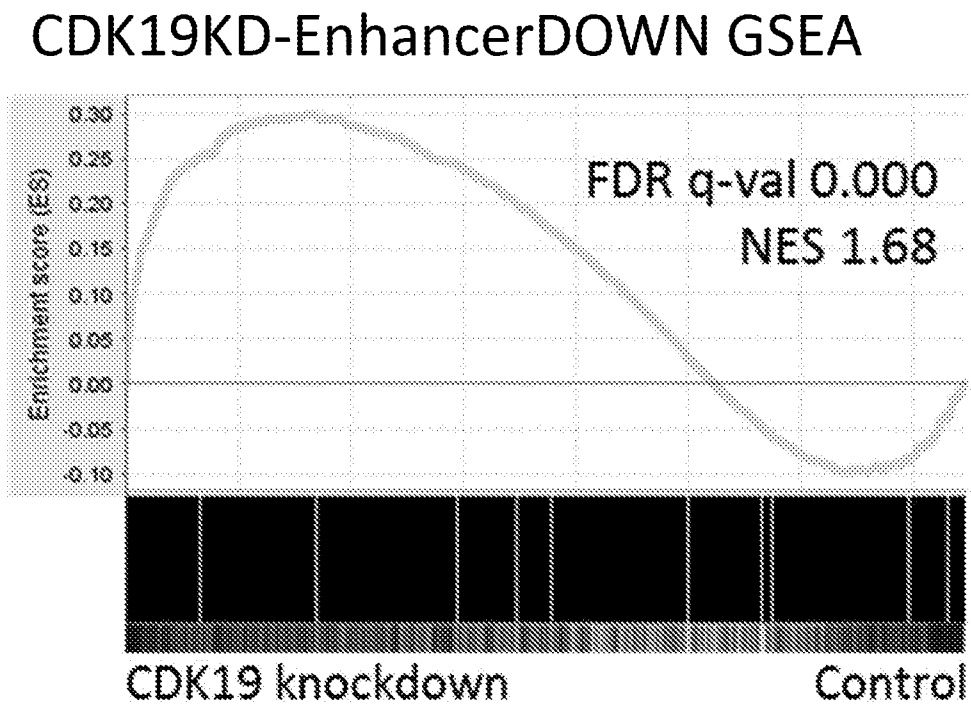
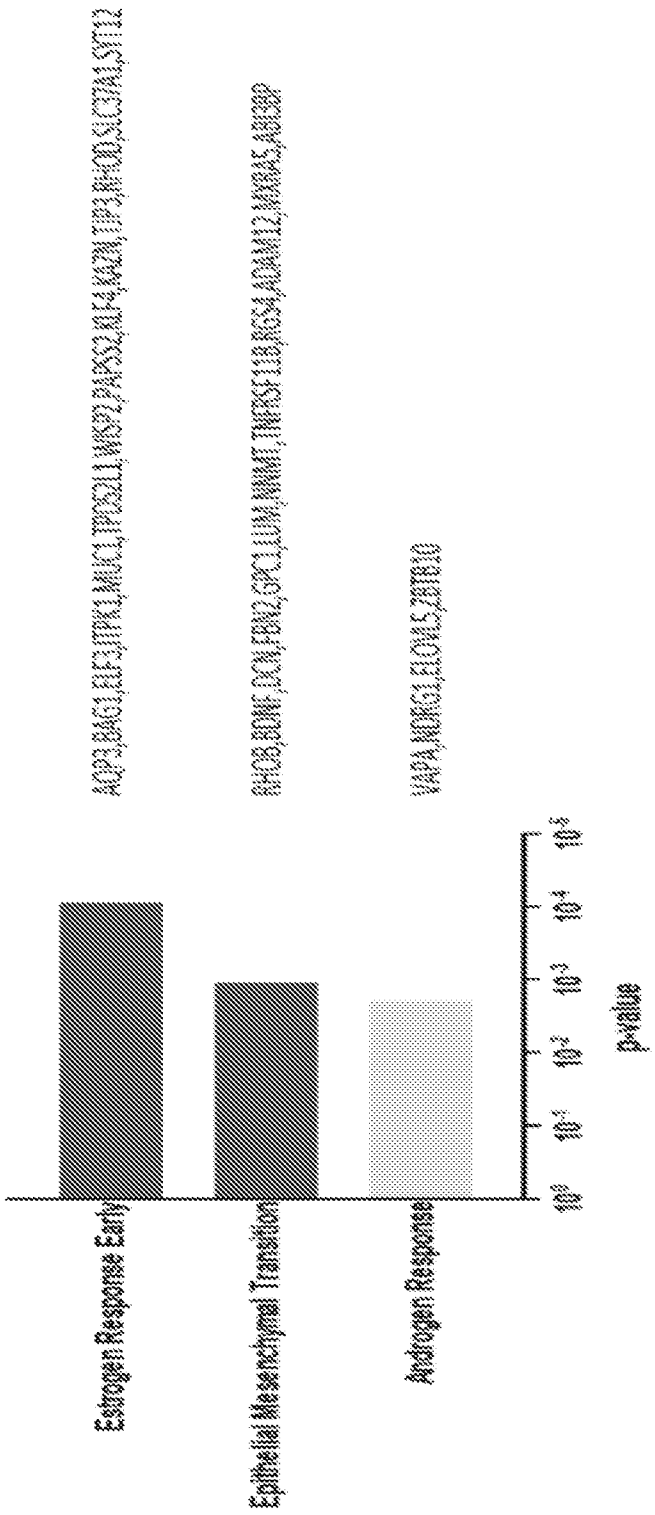

CDK19KD-EnhancerDOWN GSEA
Enrichment score (ES)
0.30
0.25
0.20
0.15
0.10
0.05
0.00
-0.05
-0.10
FDR q-val 0.000
NES 1.68
CDK19 knockdown
Control

FIG. 3G


AQP3,BAG1,ELF3,ITPK1,MUC1,TPD52L1,WSP2,PAPSS2,KLF4,NAZN,TJP3,RHOD,SLC3A1,SYT12
RHOB,BDNF,DCN,FBN2,GPC1,LUM,NNMT,TNFRSF11B,RGS4,ADAM12,MXRA5,ABI3BP
VAPA,NDRG1,ELOVL5,ZBTB10
Estrogen Response Early
Epithelial Mesenchymal Transition
Androgen Response
p-value

inducCDK19KD-PDX-T1 Organoids

FIG. 4A

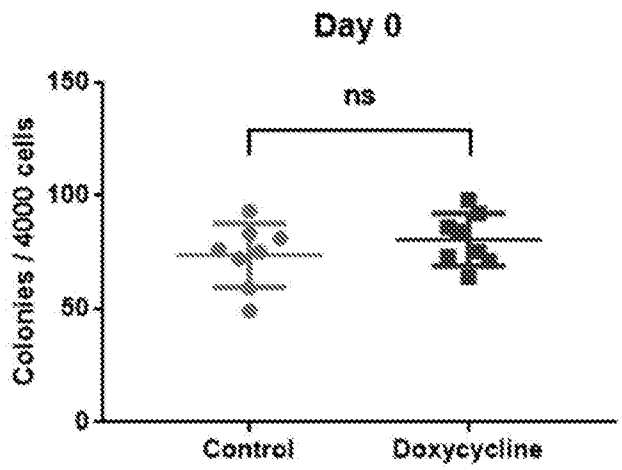


FIG. 4B

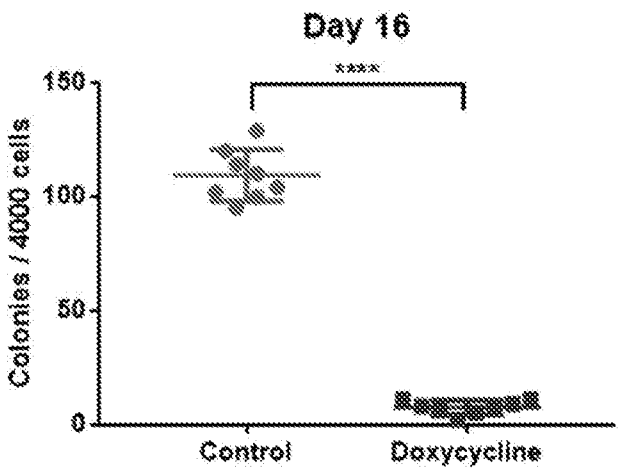


FIG. 4C

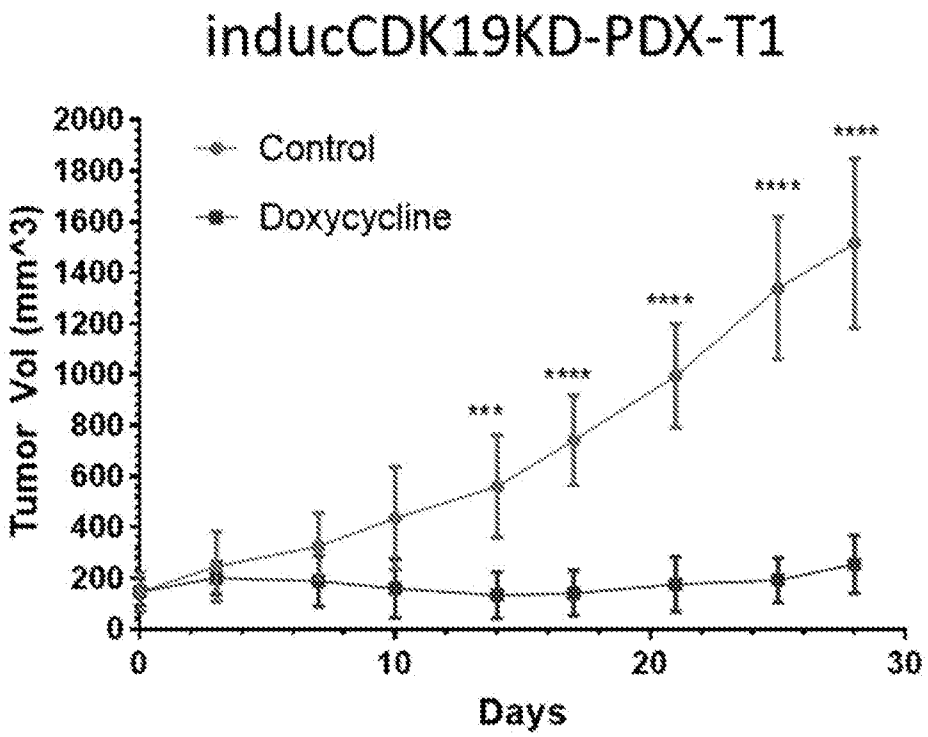

inducCDK19KD-PDX-T1
Control
Doxycycline
Tumor Vol (mm^3)
2000
1800
1600
1400
1200
1000
800
600
400
200
0
0
10
20
30
Days
***
****
****
****
****

FIG. 4D

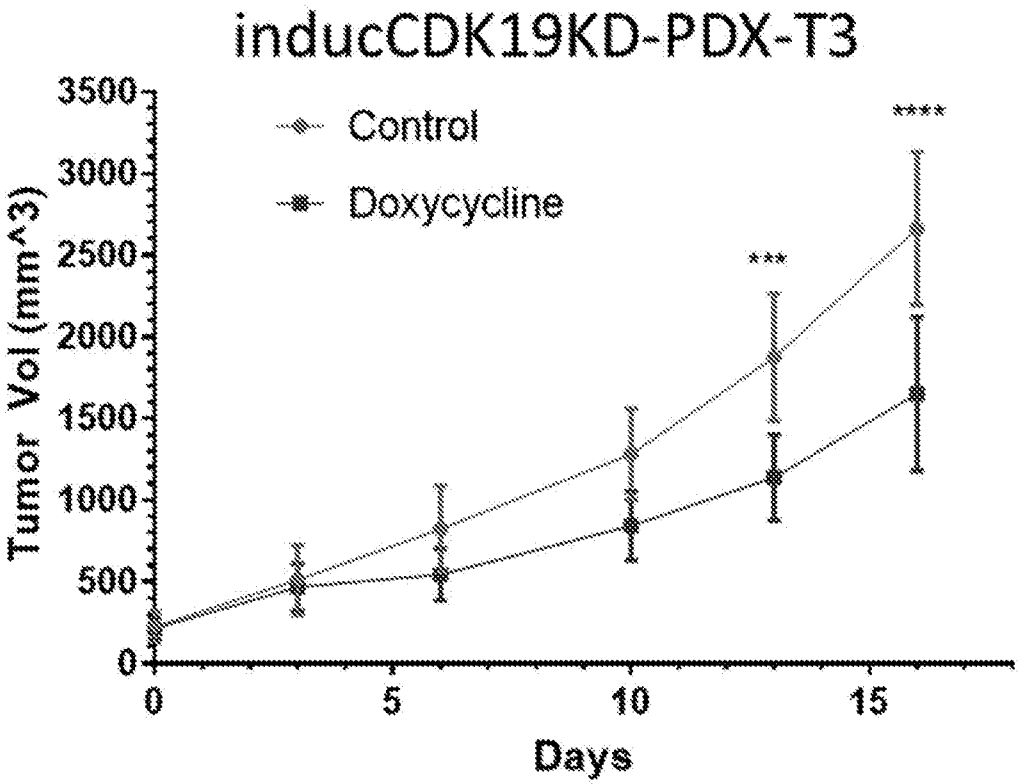

inducCDK19KD-PDX-T3
Control
Doxycycline
Tumor Vol (mm^3)
3500
3000
2500
2000
1500
1000
500
0
0
5
10
15
Days
***
****

FIG. 4E

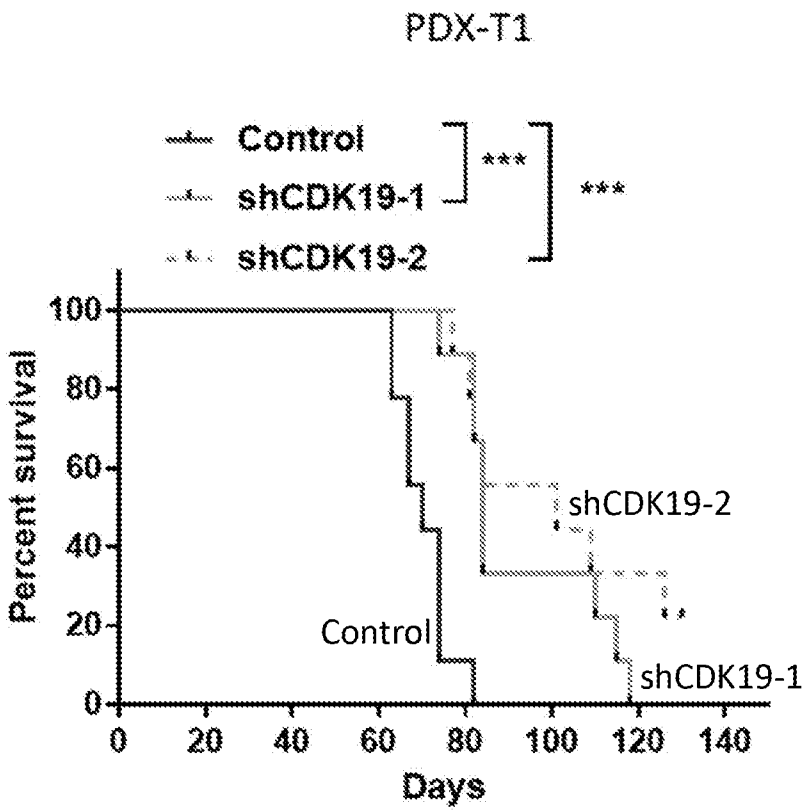
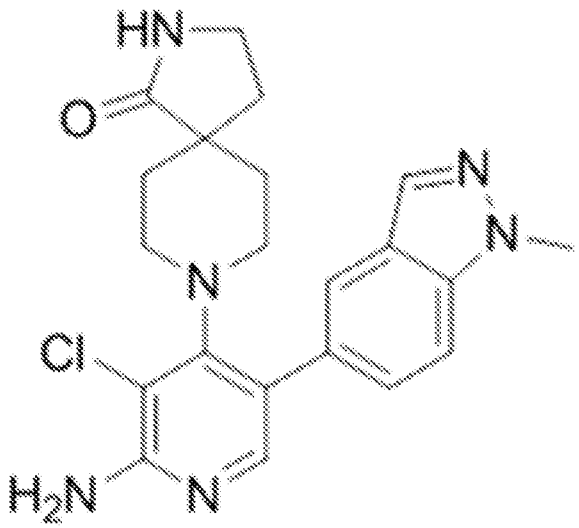

PDX-T1
Control
shCDK19-1
shCDK19-2
***
***
Percent survival
100
80
60
40
20
0
0
20
40
60
80
100
120
140
Days
shCDK19-2
Control
shCDK19-1

FIG. 4F



CCT251921

FIG. 4G

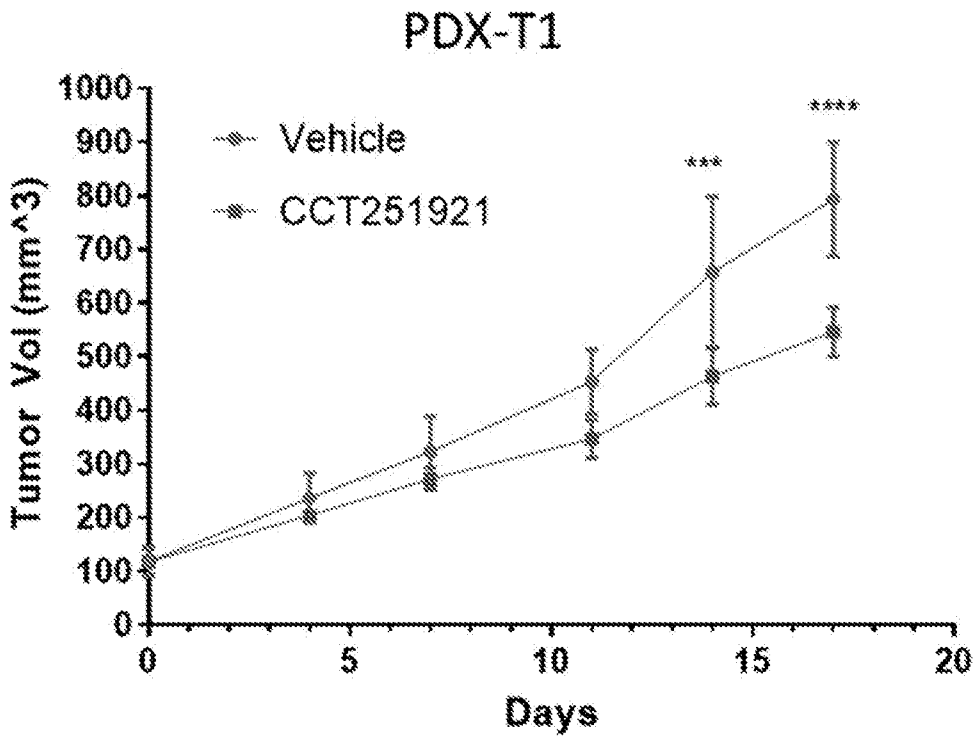

PDX-T1
Vehicle
CCT251921
***
****
Tumor Vol (mm^3)
1000
900
800
700
600
500
400
300
200
100
0
0
5
10
15
20
Days

FIG. 5A

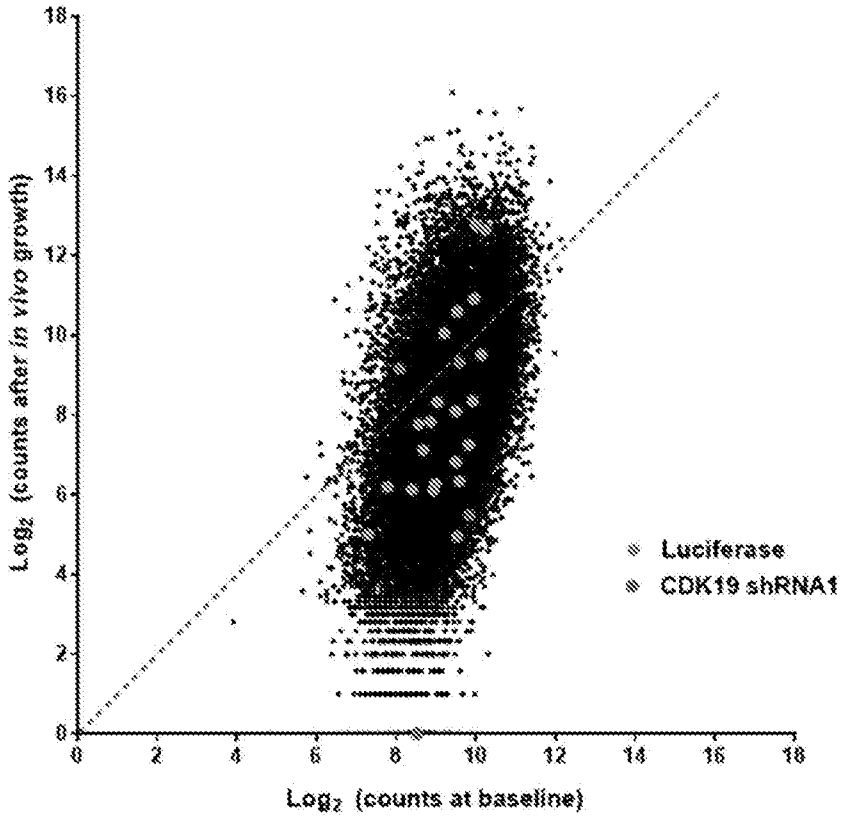

Log2 (counts after in vivo growth)
Log2 (counts at baseline)
Luciferase
CDK19 shRNA1
0
2
4
6
8
10
12
14
16
18

FIG. 5B

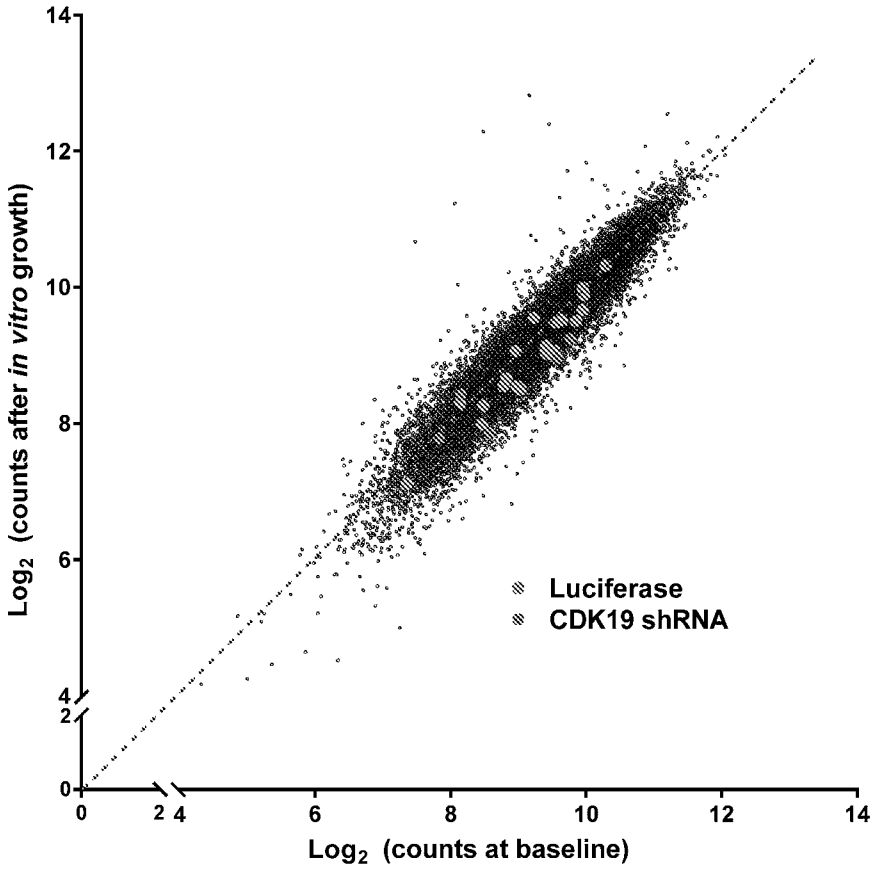

14
12
10
8
6
4
2
0
0
2
4
6
8
10
12
14
Log2 (counts after in vitro growth)
Log2 (counts at baseline)
Luciferase
CDK19 shRNA

FIG. 5C

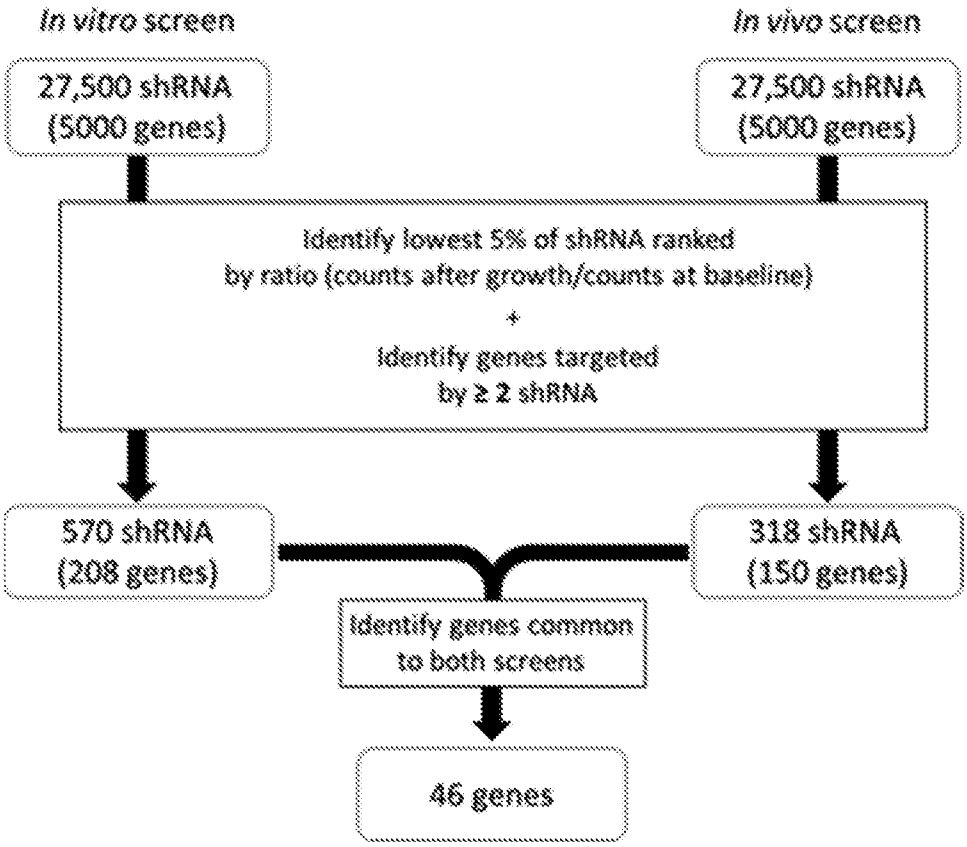

In vitro screen
27,500 shRNA
(5000 genes)
In vivo screen
27,500 shRNA
(5000 genes)
Identify lowest 5% of shRNA ranked
by ratio (counts after growth/counts at baseline)
+
Identify genes targeted
by ≥ 2 shRNA
570 shRNA
(208 genes)
318 shRNA
(150 genes)
Identify genes common
to both screens
46 genes

FIG. 5D

ARD1A/NAA10	EIF2S2	PSMA2	RPL13A
ASCC3L1	HGF	PSMA6	RPL14
C15ORF15	HNRNPC	PSMB3	RPL4
CDC2/CDK1	KARS	PSMB6	RPL6
CDC2L1/CDK11B	KLRK1	PSMC3	RRM1
CDC2L6/CDK19	KPNB1	PSMD1	RRM2
CSE1L	NEDD8	PSMD13	SEC22B
DTYMK	POLA	PSMD3	SH3GLB2
DUT	POLR2A	RBX1	TUBA1A
EEF2	POLR2F	RPA1	TUBA1C
EFTUD2	PSMA1	RPA2	WBSCR17
EIF1AX		RPA3	

FIG. 6A

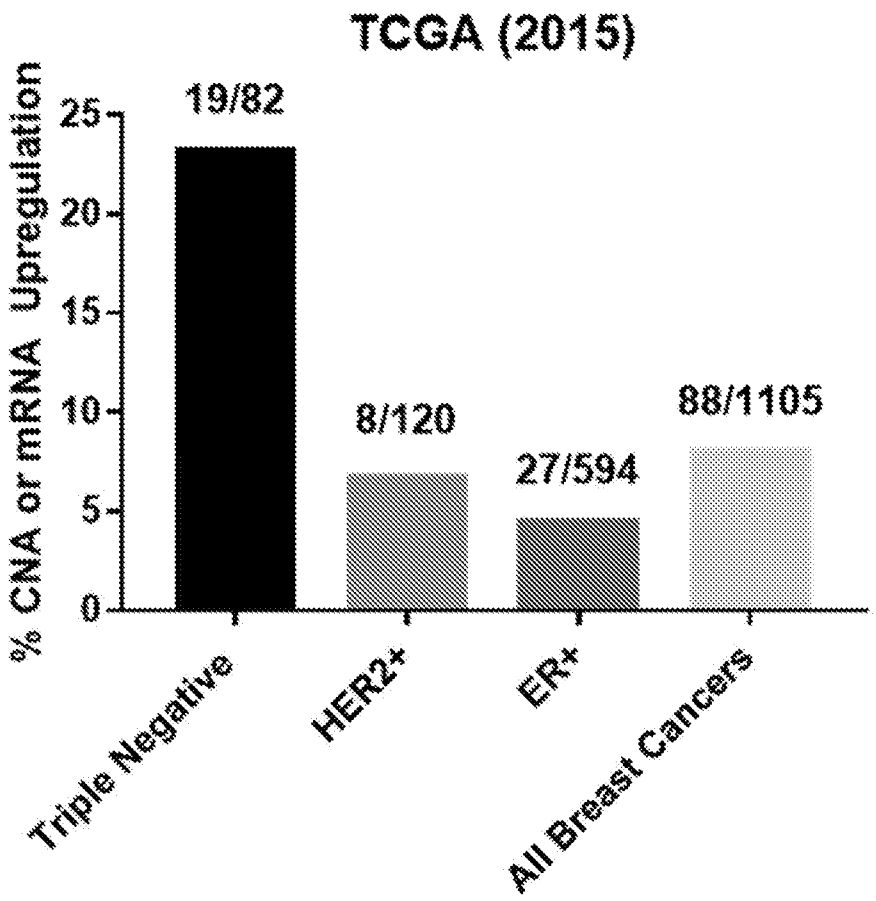

TCGA (2015)
% CNA or mRNA Upregulation
25
20
15
10
5
0
19/82
8/120
27/594
88/1105
Triple Negative
HER2+
ER+
All Breast Cancers

FIG. 6B

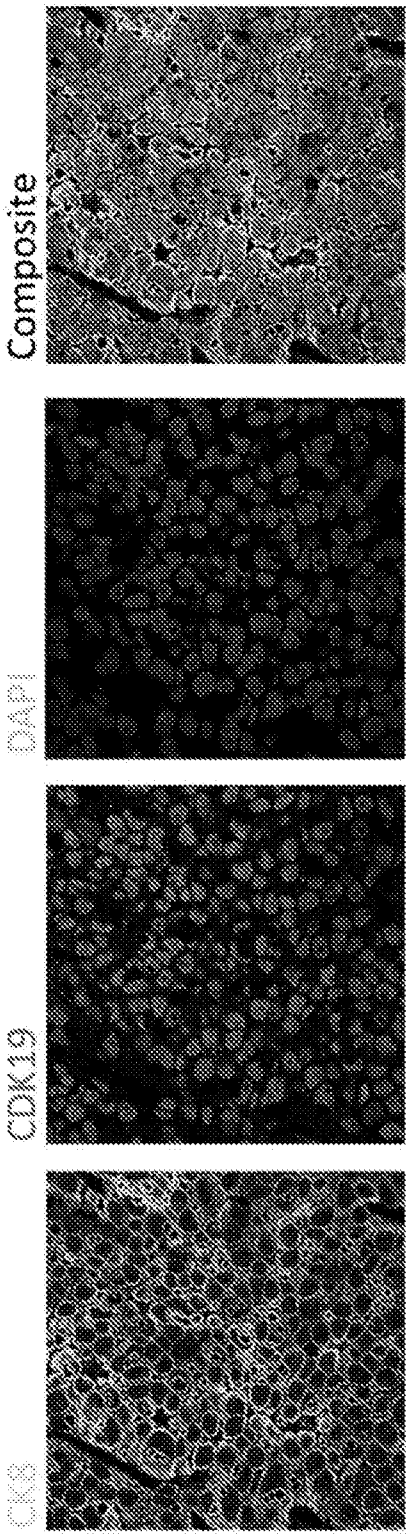


FIG. 7A

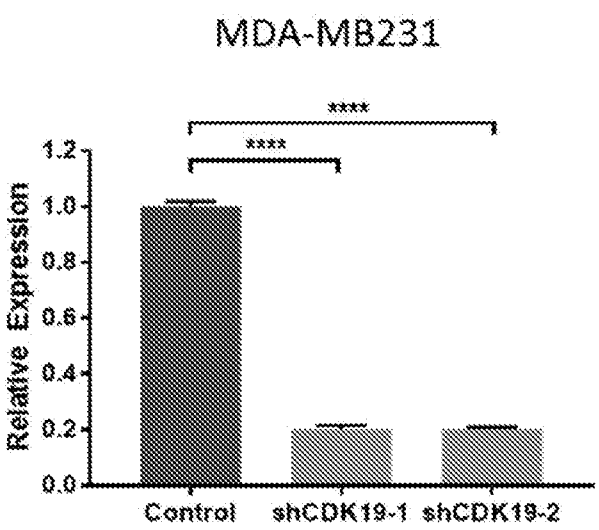

MDA-MB231
****
****
Relative Expression
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control
shCDK19-1
shCDK19-2

FIG. 7B

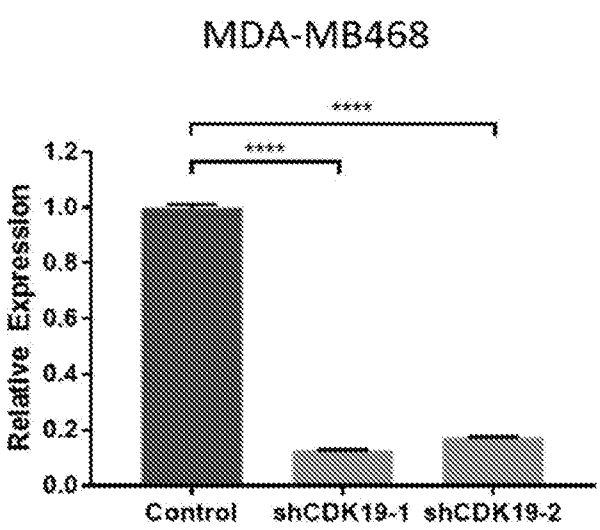

MDA-MB468
****
****
Relative Expression
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control
shCDK19-1
shCDK19-2

FIG. 7C

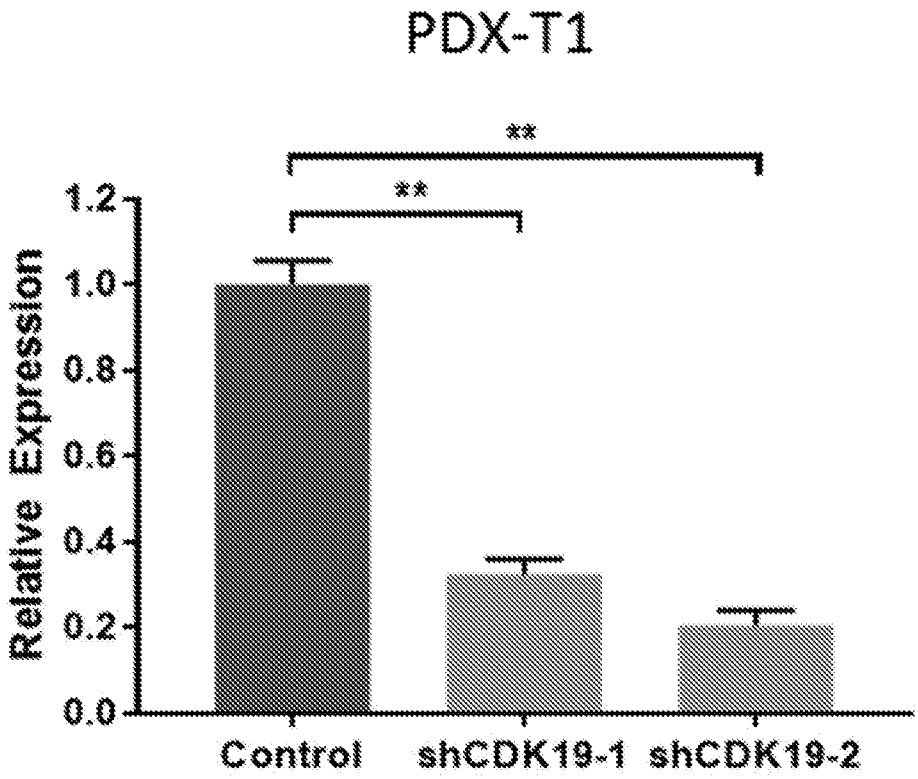

PDX-T1
**
**
Relative Expression
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Control
shCDK19-1
shCDK19-2

FIG. 7D

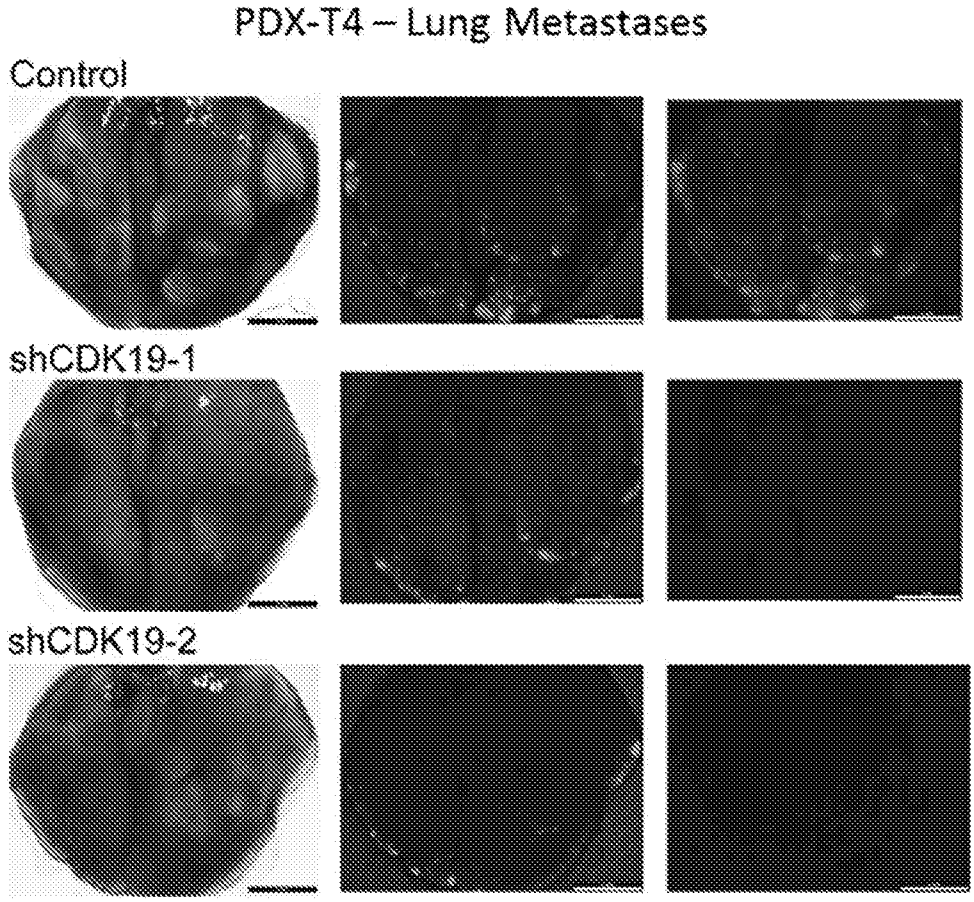


FIG. 8A

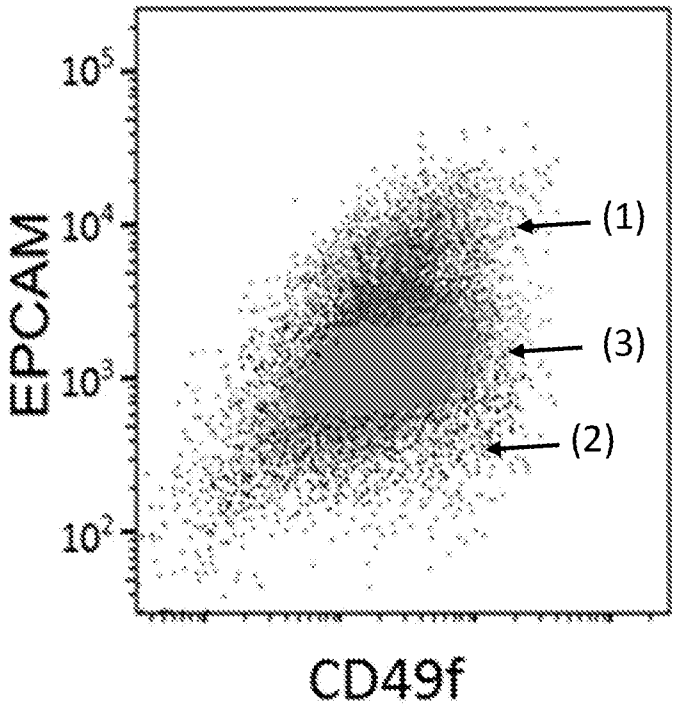


FIG. 8B

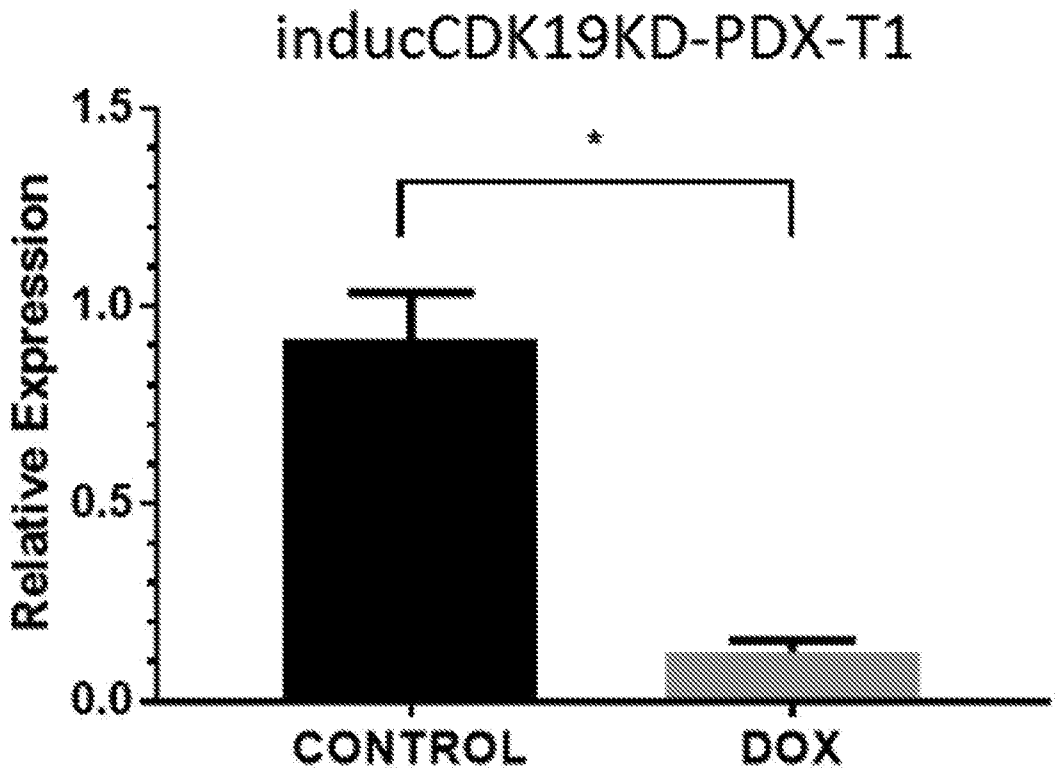

inducCDK19KD-PDX-T1
Relative Expression
1.5
1.0
0.5
0.0
*
CONTROL
DOX

FIG. 8C

	50 cells	250 cells	1250 cells
+ Dox	0/5	0/5	0/5

	50 cells	250 cells	1250 cells
No Dox	1/5	2/5	5/5

FIG. 8D

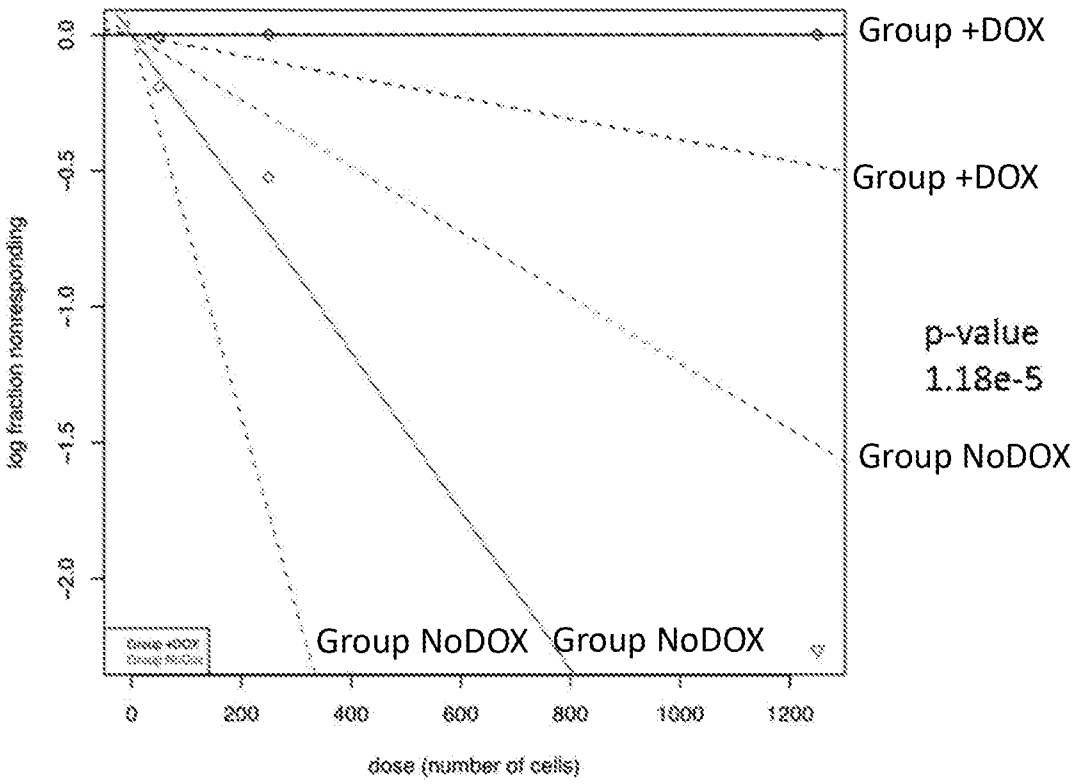

Group +DOX
Group +DOX
p-value
1.18e-5
Group NoDOX
Group NoDOX
Group NoDOX
log fraction nonresponding
0.0
-0.5
-1.0
-1.5
-2.0
0
200
400
600
800
1000
1200
dose (number of cells)

FIG. 9

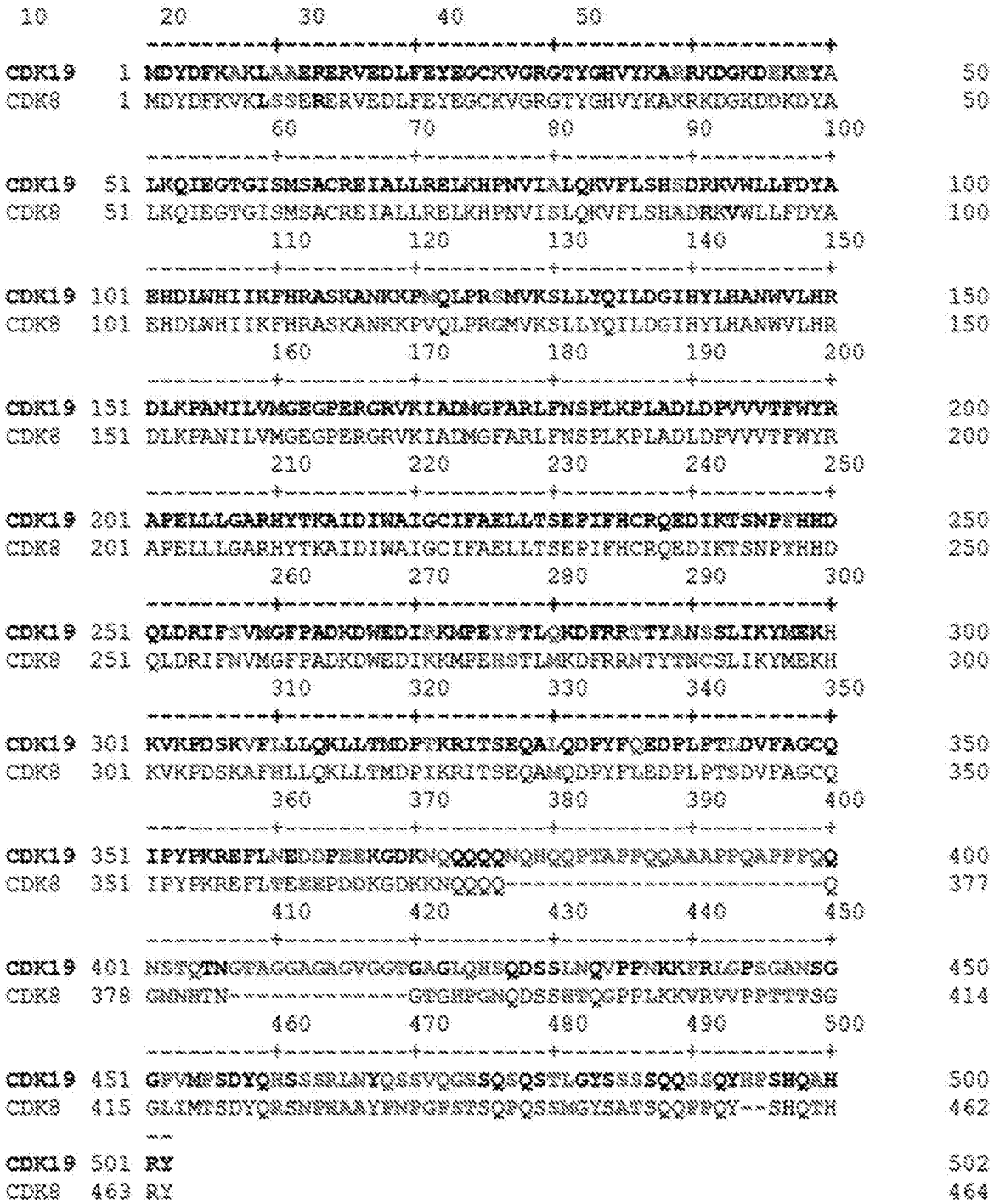


FIG. 10

Upregulated with CDK19 Knockdown		
	NES	FOR q-val
OXIDATIVE PHOSPHORYLATION	1.663	0.019
PANCREAS_BETA_CELLS	1.529	0.036
UV_RSPOLNSE_DN	1.374	0.110
KRAS_SIGNALING_DN	1.295	0.167
ESTROGEN_RESPONSE_EARLY **	1.278	0.153
EPITHELIAL_MESENCHYMAL_TRANSITION **	1.260	0.152
P53_PATHWAY	1.208	0.197
HEME_METABOLISM	1.181	0.210

Downregulated with CDK19 Knockdown		
	NES	FOR q-val
E2F_TARGETS *	-3.495	0.000
G2M_CHECKPOINT *	-3.292	0.000
MYC_TARGETS_V1 *	-2.646	0.000
MTORC1_SIGNALING *	-2.632	0.000
MITOTIC_SPINDLE *	-2.331	0.000
ANDROGEN_RESPONSE	-2.045	0.000
GLYCOLYSIS *	-1.977	0.000
KRAS_SIGNALING_UP	-1.928	0.001
DNA_REPAIR *	-1.900	0.001
UNFOLDED_PROTEIN_RESPONSE	-1.855	0.001
CHOLESTEROL_HOMEOSTASIS **	-1.804	0.002
TNFA_SIGNALING_VIA_NFKB *	-1.779	0.003
REACTIVE_OXIGEN_SPECIES_PATHWAY	-1.686	0.005
HYPOXIA	-1.681	0.004
SPERMATOGENESIS *	-1.676	0.004
APOPTOSIS *	-1.654	0.006
IL2_STAT 5_SIGNALING	-1.613	0.008
INTERFERON_GAMMA_RESPONSE	-1.609	0.008
PEROXISOME	-1.423	0.043
MYC_TARGETS_V2 **	-1.366	0.070
PROTEIN_SECRETION	-1.359	0.071
ALLOGRAFT_REJECTION	-1.251	0.163
NOTCH_SIGNALING	-1.246	0.161
INTERFERON_ALPHA_RESPONSE **	-1.238	0.163
TGF_BETA_SIGNALING	-1.225	0.173
COMPLEMENT	-1.210	0.185
IL6_JAK_STAT3_SIGNALING	-1.180	0.219
FATTY_ACID_METABOLISM	-1.180	0.212
INFLAMMATORY_RESPONSE	-1.177	0.208
UV_RESPONSE_UP	-1.175	0.204
P3K_AKT_MTOR_SIGNALING *	-1.144	0.244

Upregulated with CDK8 Knockdown		
	NES	FOR q-val
OXIDATIVE PHOSPHORYLATION *	2.529	0.000
XENOBIOTIC_METABOLISM	1.937	0.000
MYC_TARGETS_V2 **	1.664	0.013
FATTY_ACID_METABOLISM	1.596	0.019
ADIPOGENESIS	1.508	0.031
INTERFERON_ALPHA_RESPONSE **	1.205	0.232
CHOLESTEROL_HOMEOSTASIS **	1.190	0.0224

Downregulated with CDK8 Knockdown		
	NES	FOR q-val
E2F_TARGETS *	-2.930	0.000
G2M_CHECKPOINT *	-2.895	0.000
MITOTIC_SPINDLE *	-2.217	0.000
APICAL_SURFACE	1.720	0.005
PI3K_AKT_MMTOR_SIGNALING *	1.667	0.007
DNA_REPAIR *	1.641	0.008
MTORC1_SIGNALING *	1.597	0.012
SPERMATOGENESIS *	1.500	0.033
MYC_TRGETS_V1 *	1.467	0.042
APICAL_JUNCTION	1.453	0.045
INFLAMMATORY_RESPONSE	1.447	0.043
ESTROGEN_RESPONSE_LATE	1.407	0.063
EPITHDELIAL_MESENCHYMAL_TRANSITION **	1.405	0.060
GLYCOLYSIS	1.382	0.071
APOPTOSIS *	1.307	0.139
IL2_STAT5_SIGNALING *	1.298	0.142
ESTROGEN_RESPONSE_EARLY **	1.282	0.154
TNFA_SIGNALING_VIA_NFKB *	1.233	0.222

FIG. 11

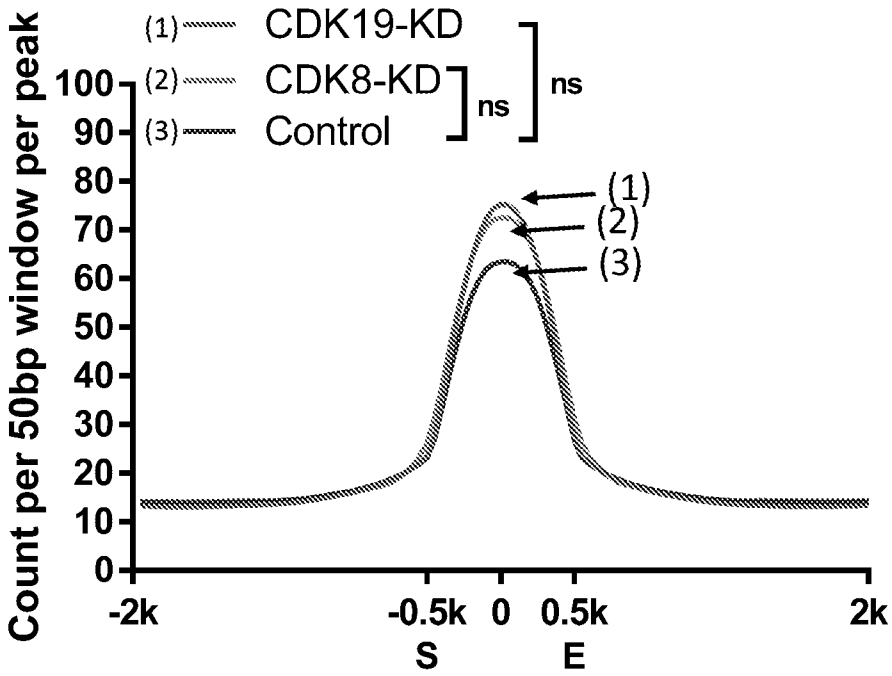

(1) CDK19-KD
(2) CDK8-KD
(3) Control
ns
ns
Count per 50bp window per peak
100
90
80
70
60
50
40
30
20
10
0
(1)
(2)
(3)
-2k
-0.5k
S
0
0.5k
E
2k

FIG. 12A

CDK19KD-
EnhancerUP leading edge 'core' genes

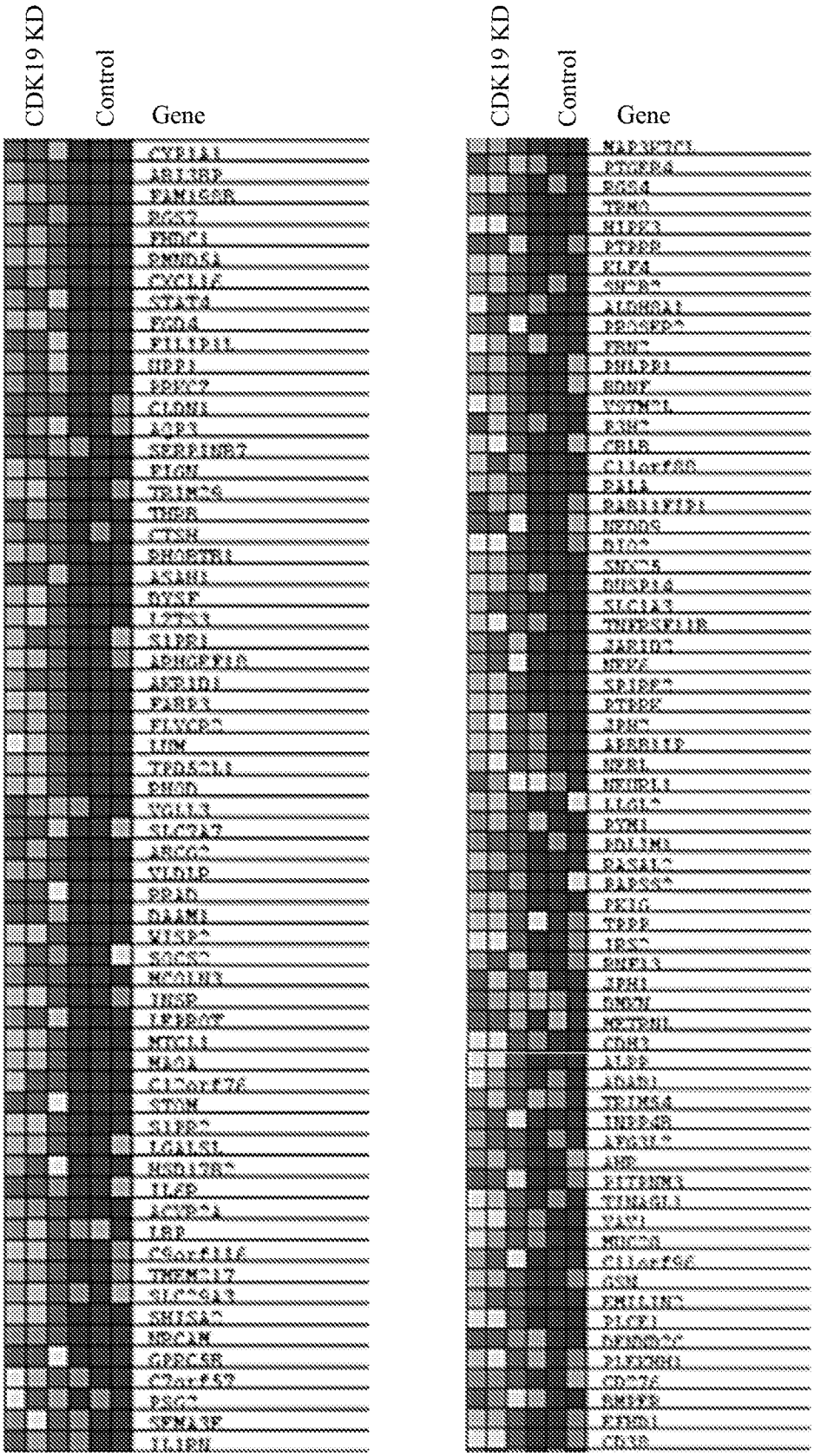


FIG. 12A (cont'd)

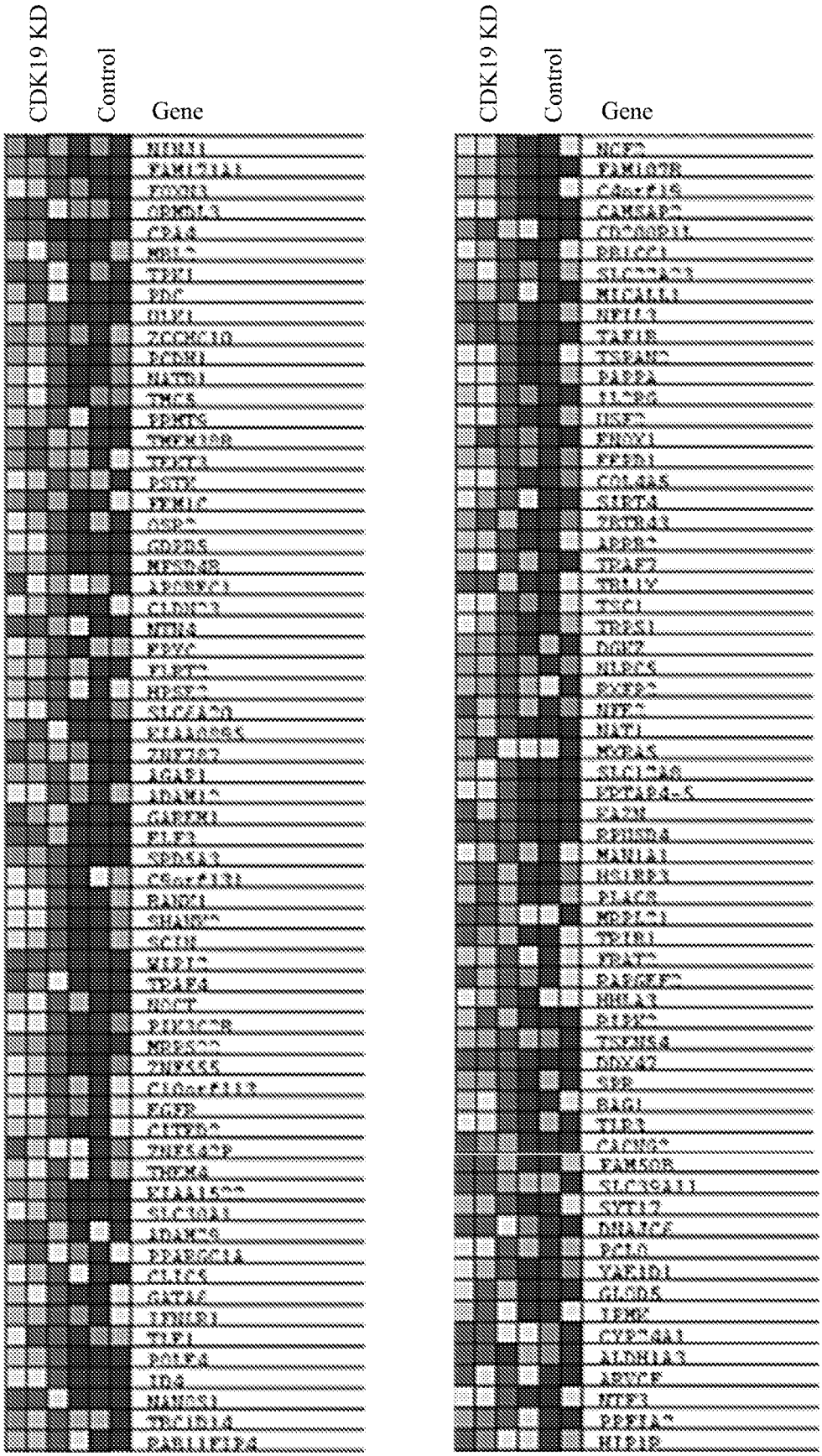


FIG. 12A (cont'd)

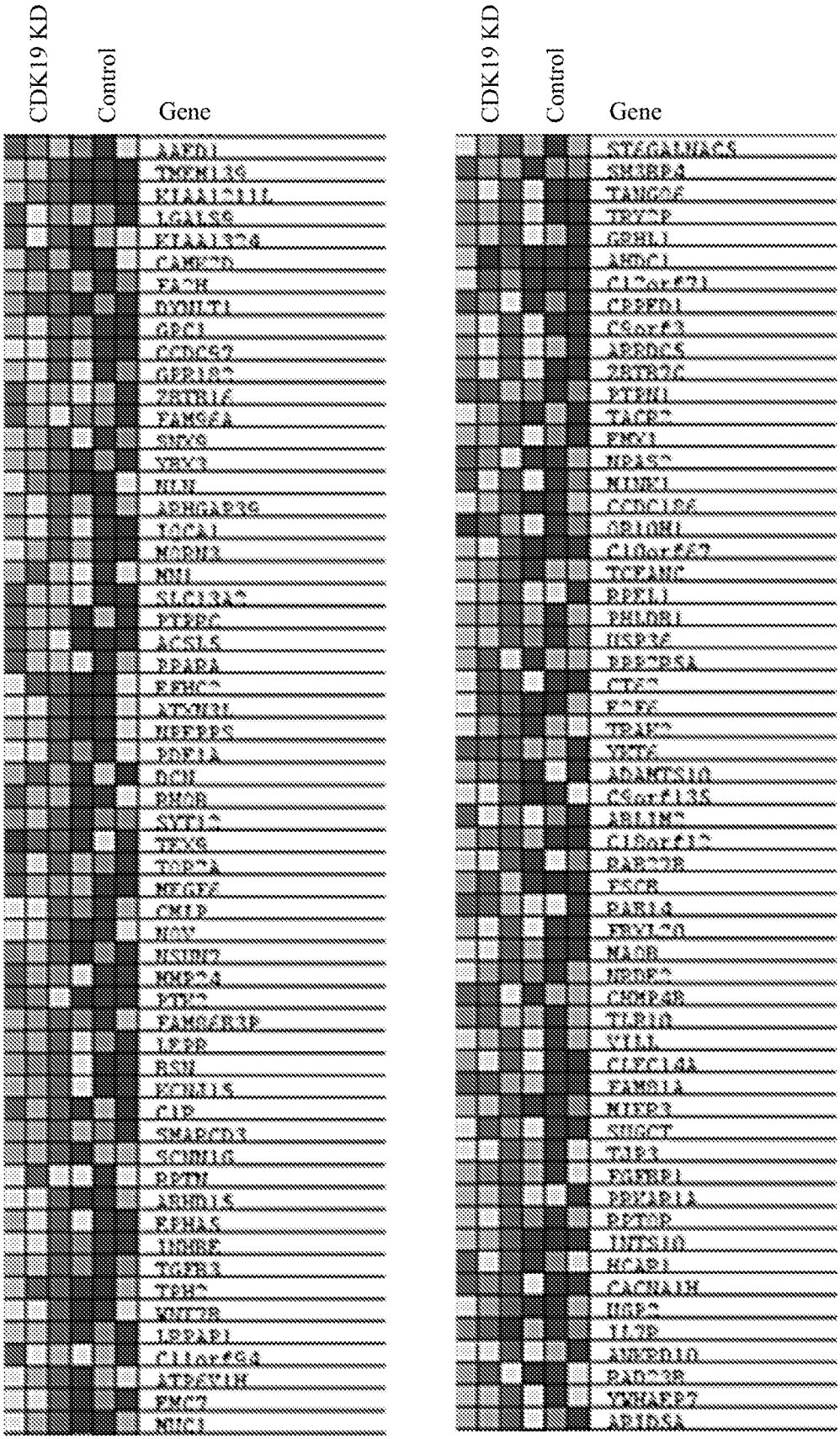


FIG. 12A (cont'd)

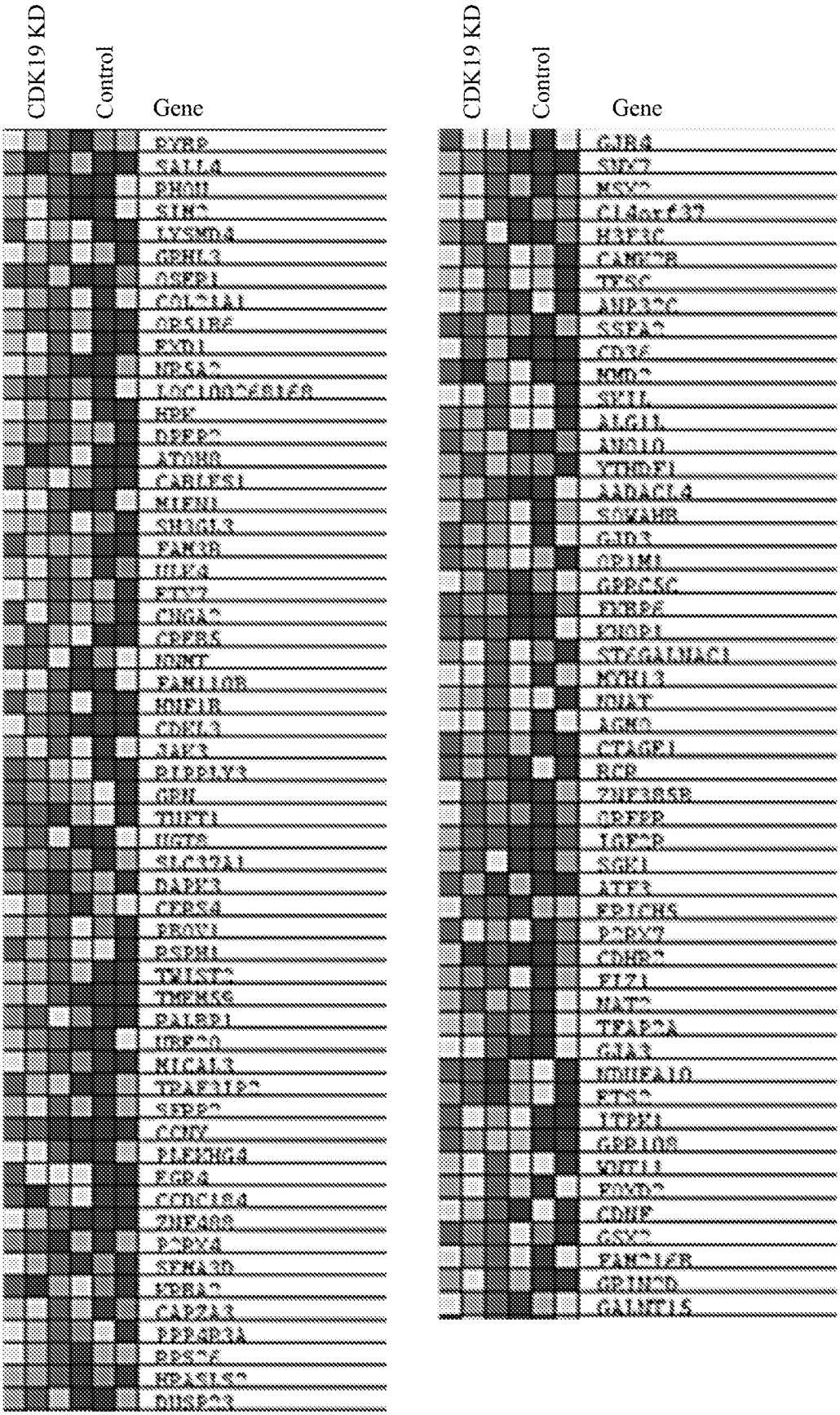


FIG. 12B

CDK19KD-EnhancerDOWN leading edge 'core' genes

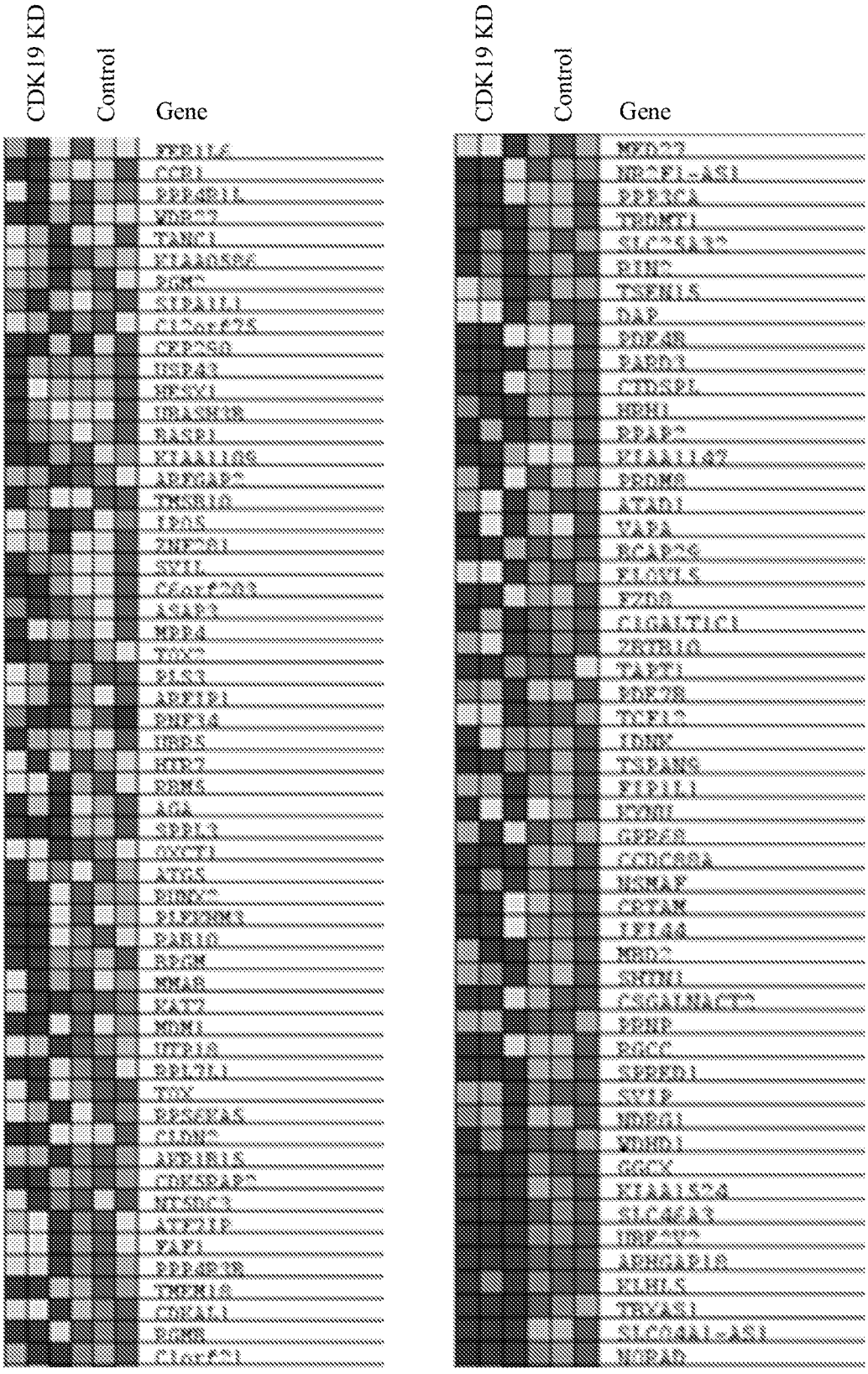


FIG. 12B (cont'd)

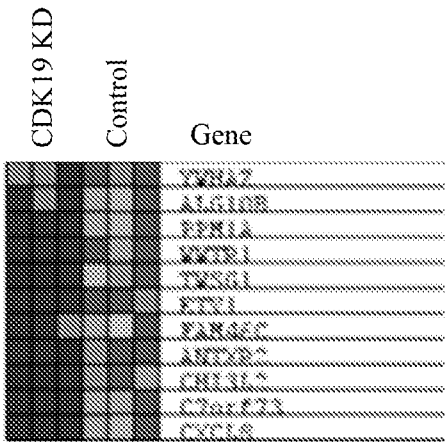


FIG. 13A

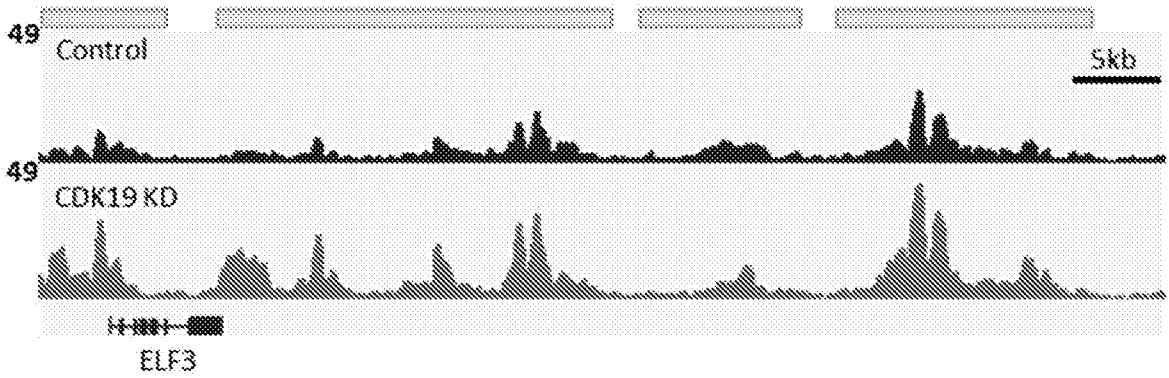


FIG. 13B

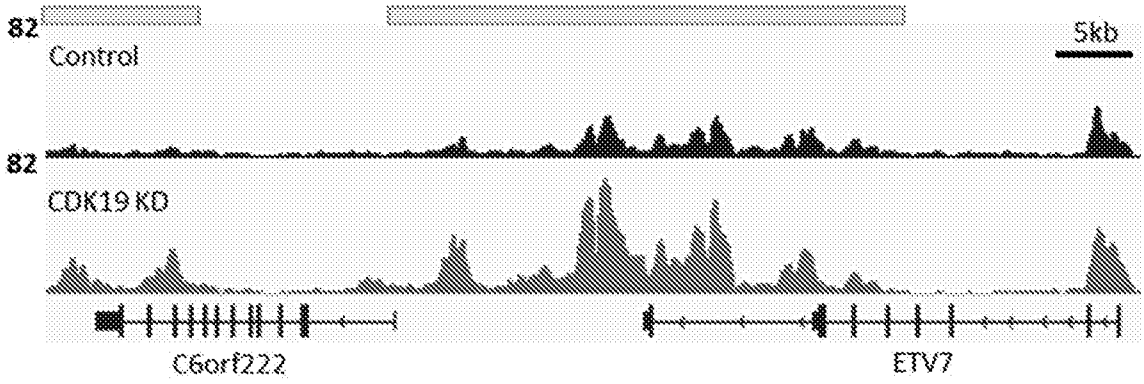


FIG. 13C

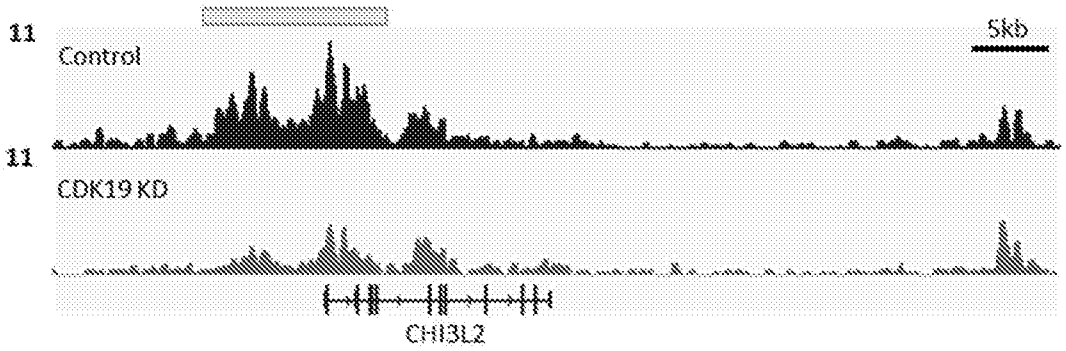


FIG. 13D

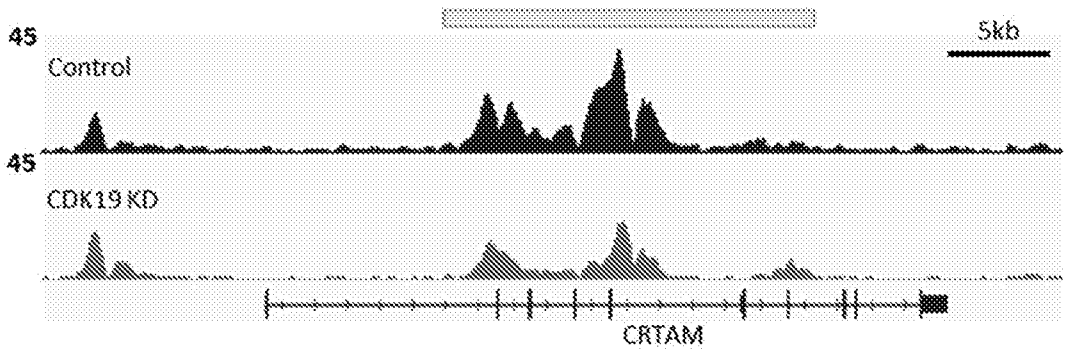


FIG. 13E

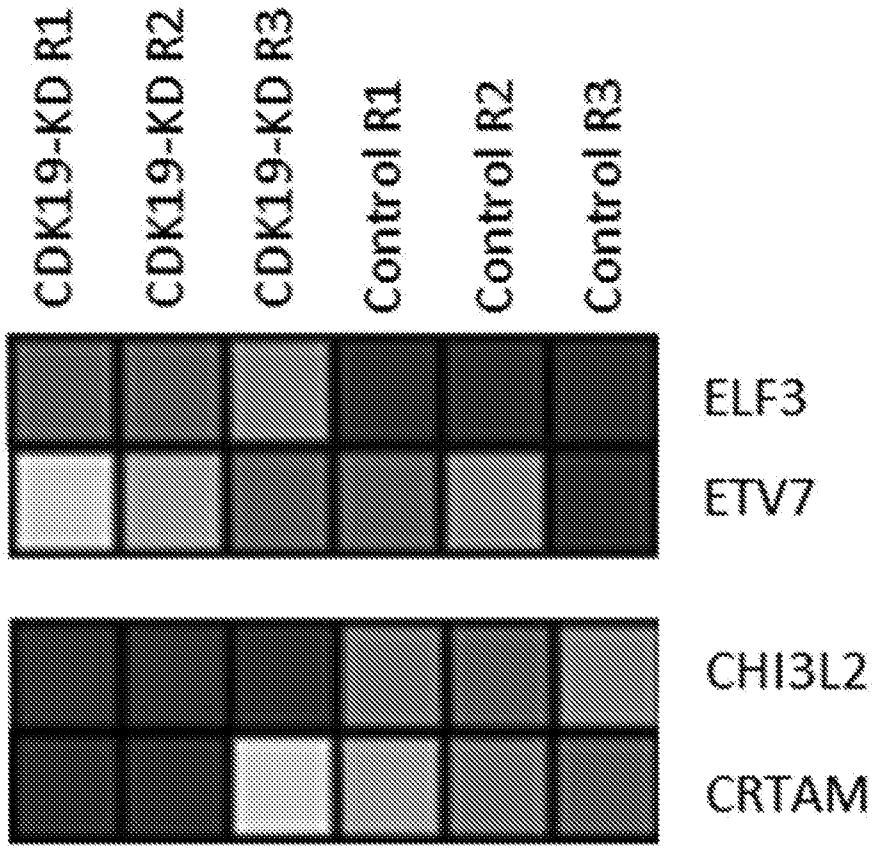

CDK19-KD R1
CDK19-KD R2
CDK19-KD R3
Control R1
Control R2
Control R3
ELF3
ETV7
CHI3L2
CRTAM

FIG. 14A

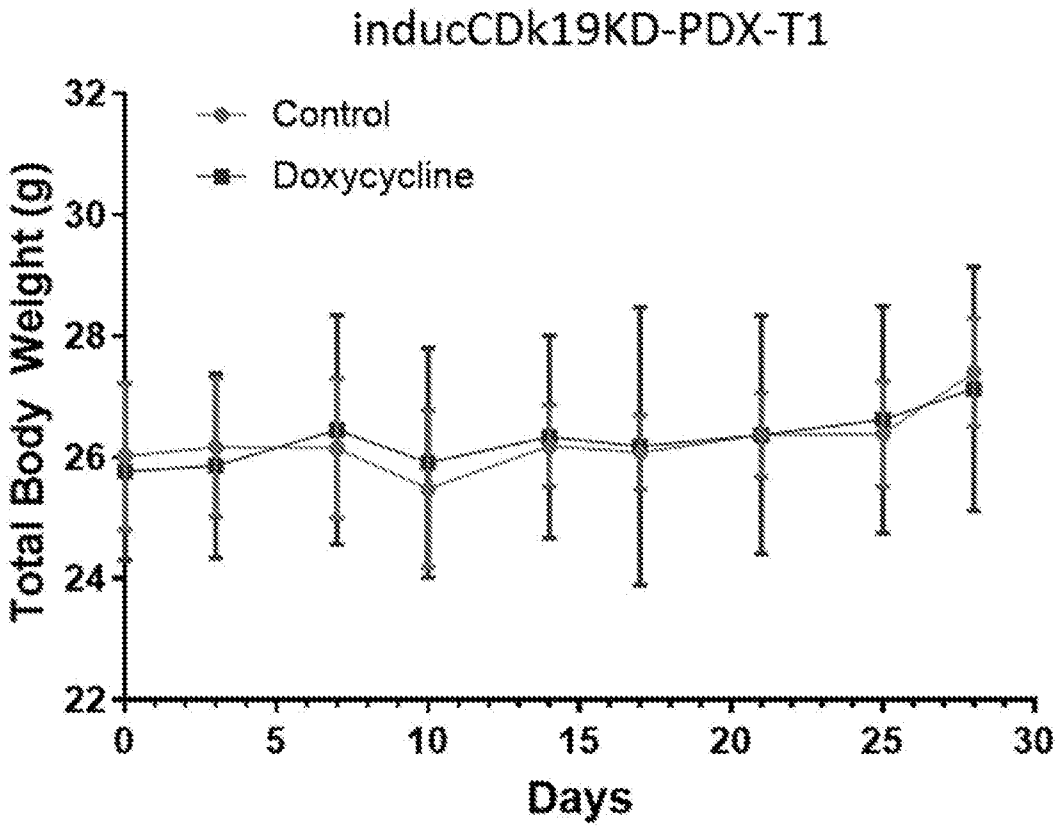

inducCDk19KD-PDX-T1
Control
Doxycycline
Total Body Weight (g)
32
30
28
26
24
22
0
5
10
15
20
25
30
Days

FIG. 14B

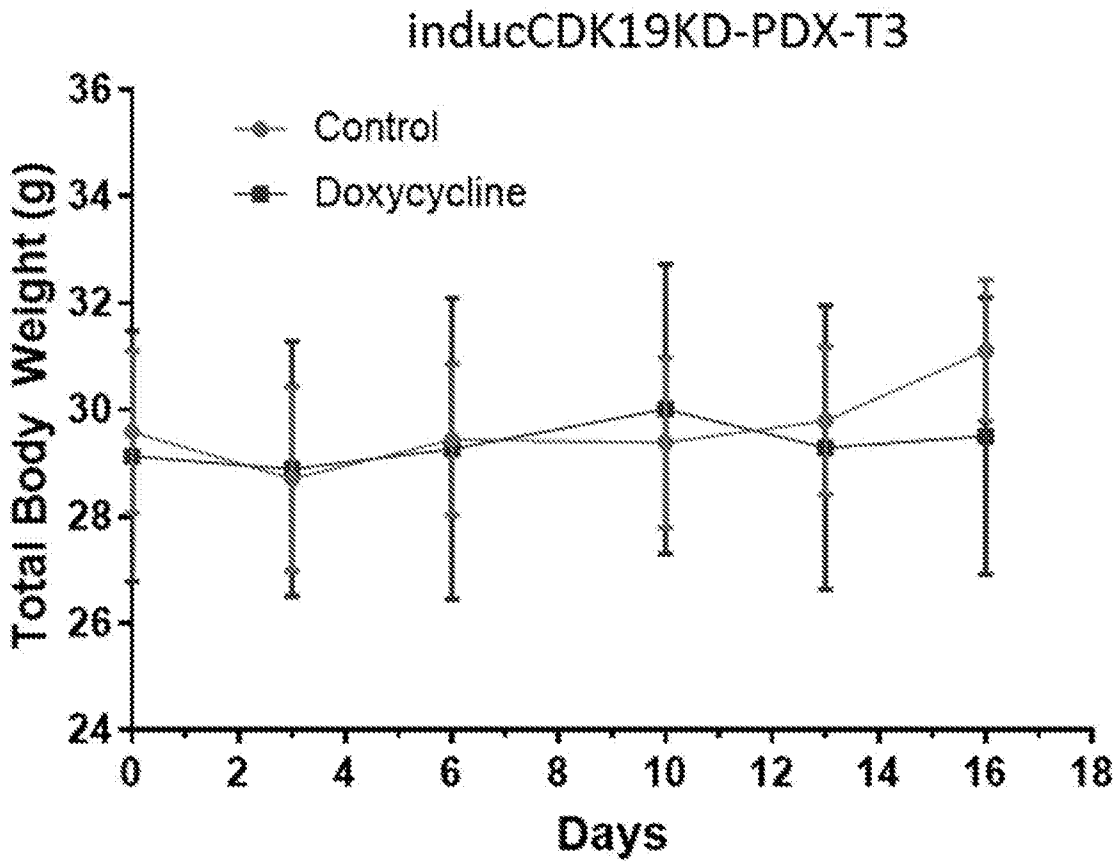
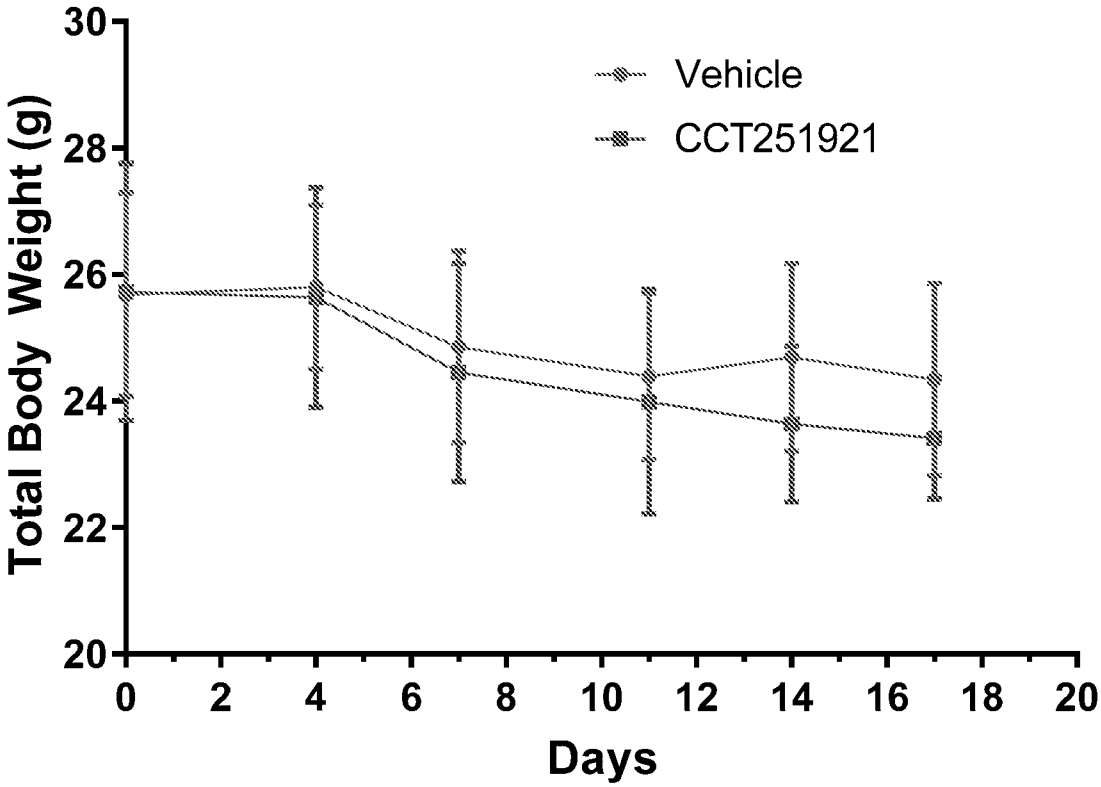

inducCDK19KD-PDX-T3
Control
Doxycycline
Total Body Weight (g)
36
34
32
30
28
26
24
0
2
4
6
8
10
12
14
16
18
Days

FIG. 14C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26
24
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20
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2
4
6
8
10
12
14
16
18
20
Days
Vehicle
CCT251921

FIG. 15

Tumor	Origin	ER/PR/HER2 status	Diagnosis	Treatment Status
PDX-T1 (C69)	Breast Primary	-/-/-	IDC	Radiation
PDX-T2 (C70)	Breast Primary	-/-/-	IDC	Not treated
PDX-T3 (S58T)	Breast Primary	-/-/-	IDC	Not treated
PDX-T4 (C87)	Brain metastases	-/-/-	Inflammatory Breast CA	Neo-adjuvant chemotherapy
PDX-T5 (C51)	Breast Primary	-/-/+	Inflammatory Breast CA	Neo-adjuvant chemotherapy
PDX-T6 (C64)	Breast Primary	-/-/-	IDC	Neo-adjuvant chemotherapy
PDX-T7 (C74)	Breast Primary	+/+/+	IDC	Unknown
PDX-T8 (S11T)	Breast Primary	+/+/-	IDC	Neoadjuvant chemotherapy

FIG. 16A

FIG. 16B

FIG. 16C

CDK8-3primeUTR
Majority
CDK19-3primeUTR
CDK8-3primeUTR
Majority
CDK19-3primeUTR
CDK8-3primeUTR
Majority
CDK19-3primeUTR
CDK8-3prim

FIG. 16D

Majority
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FIG. 17

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SEQUENCE LISTING

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Board of Trustees of the Leland Stanford Junior University

<120> METHODS FOR TREATING TRIPLE-NEGATIVE BREAST CANCER

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<150> US 62/560,140
<151> 2017-09-18

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<213> Homo sapiens

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acctttcttt ttagtgtctt atcagtgggc tgattcattt tctacattaa tcagtgtttt 540

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<212> PRT
<213> Homo sapiens

<400> 45

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Glu Asp Leu Phe Glu Tyr Glu Gly Cys Lys Val Gly Arg Gly Thr Tyr
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Gly His Val Tyr Lys Ala Arg Arg Lys Asp Gly Lys Asp Glu Lys Glu
35 40 45

Tyr Ala Leu Lys Gln Ile Glu Gly Thr Gly Ile Ser Met Ser Ala Cys
50 55 60

Arg Glu Ile Ala Leu Leu Arg Glu Leu Lys His Pro Asn Val Ile Ala
65 70 75 80

Leu Gln Lys Val Phe Leu Ser His Ser Asp Arg Lys Val Trp Leu Leu
85 90 95

Phe Asp Tyr Ala Glu His Asp Leu Trp His Ile Ile Lys Phe His Arg
100 105 110

Ala Ser Lys Ala Asn Lys Lys Pro Met Gln Leu Pro Arg Ser Met Val
115 120 125

Lys Ser Leu Leu Tyr Gln Ile Leu Asp Gly Ile His Tyr Leu His Ala
130 135 140

Asn Trp Val Leu His Arg Asp Leu Lys Pro Ala Asn Ile Leu Val Met
145 150 155 160

Gly Glu Gly Pro Glu Arg Gly Arg Val Lys Ile Ala Asp Met Gly Phe
165 170 175

Ala Arg Leu Phe Asn Ser Pro Leu Lys Pro Leu Ala Asp Leu Asp Pro
180 185 190

Val Val Val Thr Phe Trp Tyr Arg Ala Pro Glu Leu Leu Leu Gly Ala
195 200 205

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Arg His Tyr Thr Lys Ala Ile Asp Ile Trp Ala Ile Gly Cys Ile Phe
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Ala Glu Leu Leu Thr Ser Glu Pro Ile Phe His Cys Arg Gln Glu Asp
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Ile Lys Thr Ser Asn Pro Phe His His Asp Gln Leu Asp Arg Ile Phe
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Ser Val Met Gly Phe Pro Ala Asp Lys Asp Trp Glu Asp Ile Arg Lys
            260                 265                 270

Met Pro Glu Tyr Pro Thr Leu Gln Lys Asp Phe Arg Arg Thr Thr Tyr
        275                 280                 285

Ala Asn Ser Ser Leu Ile Lys Tyr Met Glu Lys His Lys Val Lys Pro
    290                 295                 300

Asp Ser Lys Val Phe Leu Leu Leu Gln Lys Leu Leu Thr Met Asp Pro
305                 310                 315                 320

Thr Lys Arg Ile Thr Ser Glu Gln Ala Leu Gln Asp Pro Tyr Phe Gln
                325                 330                 335

Glu Asp Pro Leu Pro Thr Leu Asp Val Phe Ala Gly Cys Gln Ile Pro
            340                 345                 350

Tyr Pro Lys Arg Glu Phe Leu Asn Glu Asp Asp Pro Glu Glu Lys Gly
        355                 360                 365

Asp Lys Asn Gln Gln Gln Gln Gln Asn Gln His Gln Gln Pro Thr Ala
    370                 375                 380

Pro Pro Gln Gln Ala Ala Ala Pro Pro Gln Ala Pro Pro Pro Gln Gln
385                 390                 395                 400

Asn Ser Thr Gln Thr Asn Gly Thr Ala Gly Gly Ala Gly Ala Gly Val
                405                 410                 415

Gly Gly Thr Gly Ala Gly Leu Gln His Ser Gln Asp Ser Ser Leu Asn
            420                 425                 430

Gln Val Pro Pro Asn Lys Lys Pro Arg Leu Gly Pro Ser Gly Ala Asn
        435                 440                 445

Ser Gly Gly Pro Val Met Pro Ser Asp Tyr Gln His Ser Ser Ser Arg
    450                 455                 460

Leu Asn Tyr Gln Ser Ser Val Gln Gly Ser Ser Gln Ser Gln Ser Thr
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His Gln Ala His Arg Tyr
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<212> PRT
<213> Homo sapiens

<400> 46

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Glu Asp Leu Phe Glu Tyr Glu Gly Cys Lys Val Gly Arg Gly Thr Tyr
20 25 30

Gly His Val Tyr Lys Ala Lys Arg Lys Asp Gly Lys Asp Asp Lys Asp
35 40 45

Tyr Ala Leu Lys Gln Ile Glu Gly Thr Gly Ile Ser Met Ser Ala Cys
50 55 60

Arg Glu Ile Ala Leu Leu Arg Glu Leu Lys His Pro Asn Val Ile Ser
65 70 75 80

Leu Gln Lys Val Phe Leu Ser His Ala Asp Arg Lys Val Trp Leu Leu
85 90 95

Phe Asp Tyr Ala Glu His Asp Leu Trp His Ile Ile Lys Phe His Arg
100 105 110

Ala Ser Lys Ala Asn Lys Lys Pro Val Gln Leu Pro Arg Gly Met Val
115 120 125

Lys Ser Leu Leu Tyr Gln Ile Leu Asp Gly Ile His Tyr Leu His Ala
130 135 140

Asn Trp Val Leu His Arg Asp Leu Lys Pro Ala Asn Ile Leu Val Met
145 150 155 160

Gly Glu Gly Pro Glu Arg Gly Arg Val Lys Ile Ala Asp Met Gly Phe
165 170 175

Ala Arg Leu Phe Asn Ser Pro Leu Lys Pro Leu Ala Asp Leu Asp Pro
180 185 190

Val Val Val Thr Phe Trp Tyr Arg Ala Pro Glu Leu Leu Leu Gly Ala
195 200 205

Arg His Tyr Thr Lys Ala Ile Asp Ile Trp Ala Ile Gly Cys Ile Phe
210 215 220

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Ala Glu Leu Leu Thr Ser Glu Pro Ile Phe His Cys Arg Gln Glu Asp
225                 230                 235                 240

Ile Lys Thr Ser Asn Pro Tyr His His Asp Gln Leu Asp Arg Ile Phe
                245                 250                 255

Asn Val Met Gly Phe Pro Ala Asp Lys Asp Trp Glu Asp Ile Lys Lys
            260                 265                 270

Met Pro Glu His Ser Thr Leu Met Lys Asp Phe Arg Arg Asn Thr Tyr
        275                 280                 285

Thr Asn Cys Ser Leu Ile Lys Tyr Met Glu Lys His Lys Val Lys Pro
    290                 295                 300

Asp Ser Lys Ala Phe His Leu Leu Gln Lys Leu Leu Thr Met Asp Pro
305                 310                 315                 320

Ile Lys Arg Ile Thr Ser Glu Gln Ala Met Gln Asp Pro Tyr Phe Leu
                325                 330                 335

Glu Asp Pro Leu Pro Thr Ser Asp Val Phe Ala Gly Cys Gln Ile Pro
            340                 345                 350

Tyr Pro Lys Arg Glu Phe Leu Thr Glu Glu Glu Pro Asp Asp Lys Gly
        355                 360                 365

Asp Lys Lys Asn Gln Gln Gln Gln Gln Gly Asn Asn His Thr Asn Gly
    370                 375                 380

Thr Gly His Pro Gly Asn Gln Asp Ser Ser His Thr Gln Gly Pro Pro
385                 390                 395                 400

Leu Lys Lys Val Arg Val Val Pro Pro Thr Thr Thr Ser Gly Gly Leu
                405                 410                 415

Ile Met Thr Ser Asp Tyr Gln Arg Ser Asn Pro His Ala Ala Tyr Pro
            420                 425                 430

Asn Pro Gly Pro Ser Thr Ser Gln Pro Gln Ser Ser Met Gly Tyr Ser
        435                 440                 445

Ala Thr Ser Gln Gln Pro Pro Gln Tyr Ser His Gln Thr His Arg Tyr
    450                 455                 460
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