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(54) Titre : MODELE DE CANCER DE LA PROSTATE CHEZ LE RONGEUR
(54) Title: RODENT MODEL OF PROSTATE CANCER

(57) Abrégé/Abstract:
This disclosure provides a rodent model of prostate cancer. The rodents disclosed herein comprise a transgene that provides prostate-specific expression of an oncogenic protein (e.g, an SV40 tumor antigen) under the control of 5' and 3' regulatory regions of a mouse probasin gene. The rodents develop progressive forms of prostate tumor that resemble the development of human prostate cancer.

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(54) Title: RODENT MODEL OF PROSTATE CANCER

(57) Abstract: This disclosure provides a rodent model of prostate cancer. The rodents disclosed herein comprise a transgene that provides prostate-specific expression of an oncogenic protein (e.g, an SV40 tumor antigen) under the control of 5' and 3' regulatory regions of a mouse probasin gene. The rodents develop progressive forms of prostate tumor that resemble the development of human prostate cancer.

RODENT MODEL OF PROSTATE CANCER

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of priority of U.S. Provisional Application No. 62/213,389 filed September 2, 2015, the entire contents of which are incorporated herein by reference.

FIELD OF THE DISCLOSURE

[0002] This disclosure relates to a rodent model of prostate cancer. The rodents disclosed herein comprise a transgene that includes an SV40 tumor antigen coding sequence, operably linked to 5' and 3' regulatory regions of a mouse probasin gene. The rodents disclosed herein display prostate-specific expression of the transgene and develop progressive forms of prostate tumor that resemble the development of human prostate cancer.

INCORPORATION BY REFERENCE OF SEQUENCE LISTING

[0003] The sequence listing in the ASCII text file, named as 32350_10161US01_SequenceListing.txt of 440 KB, created on August 24, 2016, and submitted to the United States Patent and Trademark Office via EFS-Web, is incorporated herein by reference.

BACKGROUND

[0004] Animal models of human diseases are important tools for understanding the pathological mechanisms underlying the diseases and for developing effective therapies. Prostate cancer will likely claim the lives of about 30,000 men in the United States this year alone, and more than 200,000 men will be newly diagnosed with the disease. Although mouse models of prostate cancer have been described in the art, they each have limitations. For example, transgenic mice that express an SV40 tumor antigen under the control of a rat probasin promoter exhibited a rapid disease progression, typically displaying prostate intraepithelial neoplasia ("PIN") by 6-12 weeks of age, and invasive

carcinoma by 18-22 weeks of age. Such results differ from the characteristically slow development of carcinomas in humans. Further, prominent expression of the transgene has been detected in the ventral lobes in some of the mouse models, an area not analogous to the peripheral zone where human prostate carcinoma typically arises. In addition, the prevalence of neuroendocrine carcinomas in some of the mouse models also limits the relevance of those models to the small subpopulation of patients with neuroendocrine disease.

[0005] Therefore, there is a need for improved animal models of prostate cancer that faithfully recapitulate the pathological features of human prostate cancer.

SUMMARY

[0006] This disclosure provides a novel rodent model of prostate cancer. The rodents disclosed herein utilize 5' and 3' regulatory regions of a mouse probasin gene to direct prostate-specific expression of an oncogenic protein such as an SV40 tumor antigen or Myc. The rodents develop progressive forms of prostate tumor that recapitulate the development and progression of human prostate cancer.

[0007] In one aspect, this disclosure provides a rodent comprising a transgene in the genome, wherein the transgene comprises, from 5' to 3', a 5' regulatory region of a mouse probasin gene, a nucleic acid comprising a first nucleotide sequence encoding an oncogenic protein such as an SV40 tumor antigen or Myc, and a 3' regulatory region of a mouse probasin gene. The 5' regulatory region, the nucleic acid comprising a first nucleotide sequence encoding an oncogenic protein such as an SV40 tumor antigen, and the 3' regulatory region are operably linked to each other to effect prostate-specific expression of the oncogenic protein such as the SV40 tumor antigen or Myc in the rodent.

[0008] In some embodiments, the 5' regulatory region in a transgene includes a nucleotide sequence from a mouse probasin locus upstream of the transcriptional initiation site of the mouse probasin gene. In some embodiments, the 5' regulatory region in a transgene includes a nucleotide sequence from a mouse probasin locus immediately upstream of the transcriptional initiation site of the mouse probasin gene. In certain embodiments, the 5' regulatory region in a transgene includes a sequence of at least about 5 kb, 10 kb, or 25 kb

upstream (e.g., immediately upstream) of the transcriptional initiation site of the mouse probasin gene. In some embodiments, the 5' regulatory region includes a 5' untranslated region (UTR) of a mouse probasin gene. In specific embodiments, the 5' regulatory region comprises the nucleotide sequence as set forth in SEQ ID NO: 6.

[0009] In some embodiments, the 3' regulatory region in a transgene includes a nucleotide sequence from a mouse probasin locus downstream of the transcriptional termination site of the mouse probasin gene. In some embodiments, the 3' regulatory region in a transgene includes a nucleotide sequence from a mouse probasin locus immediately downstream of the transcriptional termination site of the mouse probasin gene. In certain embodiments, the 3' regulatory region includes a sequence of at least about 5 kb, 25 kb, or 50 kb downstream (e.g., immediately downstream) of the transcriptional termination site of a mouse probasin gene. In some embodiments, the 3' regulatory region includes a 3' untranslated region (UTR) of a mouse probasin gene. In specific embodiments, the 3' regulatory region comprises the nucleotide sequence as set forth in SEQ ID NO: 7.

[0010] In some embodiments, the nucleic acid sequence encoding an SV40 tumor antigen in a transgene encodes an SV40 large T antigen or a functionally active fragment thereof. In some embodiments, the nucleic acid sequence encoding an SV40 tumor antigen in a transgene encodes an SV40 small t antigen or a functionally active fragment thereof. In other embodiments, the nucleotide sequence encoding an SV40 tumor antigen encodes an SV40 large T antigen or a functional active fragment thereof, and also encodes an SV40 small t antigen or a functional active fragment thereof. In specific embodiments, the nucleotide sequence encoding an SV40 tumor antigen comprises the sequence as set forth in SEQ ID NO: 1.

[0011] In some embodiments, the transgene further comprises a reporter gene. In specific embodiments, the reporter is a luciferase. In a particular embodiment, the reporter gene comprises the nucleotide sequence as set forth in SEQ ID NO: 3.

[0012] The reporter gene is operably linked to the oncogenic protein (e.g., an SV40 tumor antigen or Myc) coding sequence such that the expression of the reporter protein reflects the expression of the oncogenic protein (such as the SV40 tumor antigen or Myc). In some embodiments, the oncogenic protein (e.g., SV40 tumor antigen) coding sequence in

a transgene is linked to a reporter gene in frame via a nucleotide sequence encoding a 2A peptide. In specific embodiments, the 2A peptide is selected from the group consisting of an F2A peptide, an E2A peptide, a P2A peptide and a T2A peptide. In particular embodiments, the 2A peptide is a T2A peptide that comprises the amino acid sequence of SEQ ID NO: 13.

[0013] In some embodiments, the transgene can include additional elements, for example, a selectable marker gene or cassette which permits selection and identification of a rodent cell that harbors the transgene.

[0014] In some embodiments, the transgene is integrated into an ectopic locus of the rodent gene. In certain embodiments, at least 1-10 copies (i.e., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more copies) of the transgene are integrated in one or more ectopic loci in the genome. In specific embodiments, multiple copies (2, 3, 4, 5, 6, 7, 8, 9, 10 or more copies) of the transgene are integrated in tandem in one ectopic locus in the genome. In a particular embodiment, 5 copies of the transgene are integrated in tandem in one ectopic locus in the genome. In other embodiments, the transgene is integrated into a target locus, e.g., an endogenous probasin locus.

[0015] In some embodiments, the rodent provided herein is a mouse or a rat. In specific embodiments, the rodent is a mouse. In some embodiments, the rodent is a mouse of a strain selected from a C57BL strain, a 129 strain, or a hybrid thereof. In specific embodiments, the rodent is a mouse of an F1H4 strain, which is a hybrid of C57BL/6 and 129.

[0016] In some embodiments, the rodents provided herein exhibit a combination of any of the expression and pathological features of human prostate cancer described herein, including, for example, the areas where the transgene encoding a reporter (e.g., luciferase) and an oncogenic protein (e.g., SV40 T antigen or Myc) is expressed, the period of time it takes to develop prostate intraepithelial neoplasia (PIN), the areas in the prostate where PIN develops, the period of time it takes to develop prostate adenocarcinoma, the areas in the prostate where adenocarcinoma develops, and the feature that the adenocarcinoma developed is not neuroendocrine carcinoma. In specific embodiments, the rodent begins to display prostate intraepithelial neoplasia in the prostate tissue at about 4-6 months of

age. In some embodiments, the rodent begins to display adenocarcinoma at about 7-9 months of age. In certain embodiments, the adenocarcinoma developed in the rodent is not neuroendocrine carcinoma.

[0017] In another aspect, this disclosure provides a cell or tissue isolated from the rodent provided herein. Rodent tissues from which a cell can be isolated include, for example, thymus, spleen, gastrointestine, liver, lung, bladder, and prostate.

[0018] In still another aspect, this disclosure provides a rodent embryonic stem (ES) cell comprising a transgene in the genome, wherein the transgene comprises, from 5' to 3', a 5' regulatory region of a mouse probasin gene, a nucleic acid encoding an oncogenic protein such as an SV40 tumor antigen or Myc, and a 3' regulatory region of the mouse probasin gene, wherein the 5' regulatory region, the nucleic acid encoding an oncogenic protein such as an SV40 tumor antigen or Myc, and the 3' regulatory region are operably linked to each other. In some embodiments, the rodent ES cell is a mouse ES cell or a rat ES cell.

[0019] In a further aspect, this disclosure provides a method for making a rodent model of prostate cancer, comprising introducing into the genome of a rodent ES cell a transgene which comprises, from 5' to 3', a 5' regulatory region of a mouse probasin gene, a nucleic acid encoding an oncogenic protein such as an SV40 tumor antigen or Myc, and a 3' regulatory region of the mouse probasin gene, wherein the 5' regulatory region, the nucleic acid encoding an oncogenic protein such as an SV40 tumor antigen or Myc, and the 3' regulatory region are operably linked to each other, and selecting a modified rodent ES cell comprising the transgene in the genome; introducing the modified rodent ES cell into a host embryo of the rodent at a premorula stage; implanting the host embryo into a surrogate mother; and obtaining the rodent model of prostate cancer.

BRIEF DESCRIPTION OF THE DRAWINGS

[0020] The file of this application contains at least one drawing executed in color. Copies of this patent with color drawing(s) will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

[0021] Figure 1 depicts an example of a transgene and its components used in making a mouse model of prostate cancer. The transgene comprises, from 5' to 3', a 5' regulatory region of about 51kb from a mouse probasin gene, a nucleic acid sequence encoding an SV40 tumor antigen, a nucleic acid sequence encoding a T2A peptide, a nucleic acid sequence encoding a luciferase reporter, a neomycin selection cassette, and a 3' regulatory region of about 107 kb from a mouse probasin gene.

[0022] Figure 2 illustrates identification of Luci-TRAMP ES clone A-C10 (5x) and prostate-specific expression of the transgene in mice derived from the ES clone. Transgene mRNA was evaluated using quantitative PCR (qPCR) with assays designed against the T-antigen and the luciferase transgenes. Tissues from mice of 8 weeks old were harvested and immersed immediately in RNALater reagent. Total RNA was extracted by the Regeneron DNA Core, and qPCR was performed according to PerkinElmer's instructions with minor modifications. WT, hybrid non-transgenic control mouse; A-B1, mouse with low/no-transgene expression; A-B8, mouse with moderate but mis-expressing the transgene; A-C10, Luci-TRAMP mouse with ~5 copies of the transgene expressed in only the dorsolateral prostate (DLP) and the anterior prostate (AP) and seminal vesicles (SV). The order of tissues represented by the bars in the graph is, from left to right, DLP, AP & SV, bladder, liver, lung, kidney, heart, thymus, and salivary gland.

[0023] Figures 3A–3C show the longitudinal *in vivo* bioluminescence imaging of Luci-TRAMP mice at several ages over their life. In Figure 3A, the F1H4 WT control mice did not exhibit any bioluminescence as they aged, while the luci-TRAMP mice showed increasing bioluminescence in their abdominal area as they aged. Figure 3B is a representative example (mouse ID#1255743) of this abdominal bioluminescence, and, at 11 months of age, the bilateral urogenital expression of the luciferase gene is very obvious. The WT F1H4 control showed no bioluminescence, while the second control

mice (R26-L-Luc2) showed bioluminescence in all organs and at all ages because the luciferase gene was expressed from the ubiquitous ROSA26 (R26) promoter. Figure 3C shows detection of the luciferase gene in the lung and possibly liver and bone marrow (BM). qPCR assays (same as described in Figure 2) were performed using indicated tissues, and the results showed that there was significant T-antigen transgene signal detected in the Luci-TRAMP lungs compared with either control strain lungs. The signals from Luci-TRAMP BM and liver were lower than the lungs, but statistically significant as compared with control tissues. The Luciferase qPCR results demonstrated statistically significant signals from the Luci-TRAMP lungs compared with F1H4 lungs. BM and liver signals were elevated from WT tissues but did not reach statistical significance. The results from R26-L-Luc2 mouse overwhelmed the signals from the Luci-TRAMP mice, and were omitted from the graph.

[0024] Figures 4A-4B are representative hematoxylin/eosin staining images of paraffin sections of dorsal lateral lobes of Luci-TRAMP and wild type mice. Figure 4A shows prostatic intraepithelial neoplasia (PIN grades are listed in the labels for each sub-panel) from dorsolateral prostate lobes of luci-TRAMP mice. By 8 months of age, the hyperplasia have progressed to adenocarcinoma, albeit with intact basal borders. By 11 months of age, the stroma of the prostate became more and more infiltrated with stromal cells (possibly immune in character). In contrast, the WT F1H4 prostates showed some age-related hyperplasia at 11-16 months of age, but never to the point of luci-TRAMP prostates. Figure 4B shows similar progression of luci-TRAMP anterior lobes from high-grade PIN to adenocarcinoma, compared with similar normal prostate epithelium in the WT control mice.

[0025] Figures 5A-5B demonstrate that the prostate tumors developed in Luci-TRAMP mice are epithelial tumors and not neuroendocrine tumors. Figure 5A shows immunostaining of prostate tissue samples using an anti-E-cadherin antibody. The brown-black deposition indicates where the antibody was specifically reacting with the protein which is expressed by luminal epithelial cells. Figure 5B shows immunostaining of prostate tissue samples using an anti-synaptophysin antibody. The brown reaction product in the pancreas indicates islet cells which are neuroendocrine in nature. In contrast, neither the F1H4 WT nor the luci-TRAMP prostates of either lobe (DLP or AP) showed

specific brown reaction product. The immunohistochemical protocol was performed according to standard procedures: paraffin sections were cut, deparaffinized, and reacted with the indicated antibody. A secondary antibody, against the host of the primary antibody and coupled to horseradish peroxidase was used to amplify the specific interaction. DAB [Figure 5B] was used to visualize the immune complex.

[0026] SEQ ID NOS: 1-17 are summarized below, and the sequences are set forth at the end of this disclosure.

1 SV-40 T antigen coding sequence (encoding large T and small t antigens)

2 T2A coding sequence

3 Luciferase coding sequence

4 SV-40 late poly (A) sequence

5 Neomycin selection cassette

6 51kb 5' regulatory region sequence of a mouse probasin gene

7 107 kb 3' regulatory region sequence of a mouse probasin gene

8 Amino acid sequence of SV40 Large T Antigen (GenBank: AAB59924.1)

9 Amino acid sequence of SV40 small t antigen (GenBank: AAB59925.1)

10 Amino acid sequence of peptide F2A

11 Amino acid sequence of peptide E2A

12 Amino acid sequence of peptide P2A

13 Amino acid sequence of peptide T2A

14 The LXCXE motif

15 Complete nucleotide sequence of a SV40 Tag-T2A-Luciferse transgene

16 5' sequence including the 5' untranslated region (5' UTR) of a mouse probasin gene

17 3' sequence including the 3' untranslated region (3' UTR) of a mouse probasin gene

DETAILED DESCRIPTION

[0027] This disclosure provides a novel rodent model of prostate cancer. The rodents disclosed herein contain a transgene that includes an oncogene or a nucleotide sequence encoding an oncogenic protein (such as an SV40 tumor antigen or Myc), operably linked to 5' and 3' regulatory regions of a mouse probasin gene. The rodents display prostate-specific expression of the transgene, and develop progressive forms of prostate tumor that resemble the development of human prostate cancer.

[0028] Transgenic mouse models of prostate cancer based on expression of SV40 tumor antigens driven by a rat probasin promoter have been described in the art. However, these transgenic mouse models have a number of limitations. For example, the transgenic mice generally have a rapid disease progression, typically displaying prostate intraepithelial neoplasia ("PIN") by 6-12 weeks of age, and invasive carcinoma by 18-22 weeks of age. The results differ from the characteristically slow development of carcinomas in humans. Further, prominent expression of the transgene has been detected in the ventral lobes in some of the mouse models, an area not analogous to the peripheral zone where human prostate carcinoma typically arises. In addition, the prevalence of neuroendocrine carcinomas in some of the mouse models also limits the relevance of those models to the small subpopulation of patients with neuroendocrine disease.

[0029] The rodents disclosed herein better recapitulate the pathological events occurring in human prostate cancer than the existing mouse models. For example, predominant expression of the transgene is detected in the dorsolateral lobes of the prostate in the rodents provided herein, an area analogous to the peripheral zone of human prostate where human prostate adenocarcinoma typically arises. Furthermore, the rodents provided herein develop progressive forms of prostate tumor that resemble the various stages of human prostate tumor, ranging from hyperplasia to high grade prostate intraepithelial neoplasia (or "HGPIN") to invasive adenocarcinoma, with a much slower rate of disease progression and longer life span than the transgenic mice reported in the art. In addition, adenocarcinoma developed in the rodent disclosed herein is not neuroendocrine in nature.

[0030] Without intending to be bound by any particular theory, it is believed that a 5' regulatory region and/or a 3' regulatory region of a mouse probasin gene, included in the transgene to direct the expression of an SV40 tumor antigen, may be an important factor for the observed advantages of the rodent model of this disclosure.

Transgene

[0031] The term "transgene" includes a nucleic acid molecule that is genetically engineered for introduction into a chromosome or extrachromosomal DNA of a recipient organism. "Transgene" also includes an exogenous nucleic acid integrated into a chromosomal or extrachromosomal DNA of an organism.

[0032] The transgenes disclosed herein for purposes of generating a transgenic rodent include from 5' to 3', a 5' regulatory region of a mouse probasin gene, a nucleic acid sequence encoding an SV40 tumor antigen, and a 3' regulatory region of a mouse probasin gene, operably linked to one another to effect prostate-specific expression of the SV40 tumor antigen in the rodent.

[0033] In some embodiments, the transgene includes additional elements, such as a reporter gene and a selectable marker gene, among others.

[0034] The term "operably linked" includes a linkage of nucleic acid elements in a functional relationship. A nucleic acid sequence is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For instance, a promoter or enhancer, or a 5' regulatory region containing a promoter or enhancer, is operably linked to a coding sequence if it effects the transcription of the coding sequence. In the context of this disclosure, a 5' regulatory region of a mouse probasin gene and a 3' regulatory region of a mouse probasin gene are operably linked to a nucleic acid sequence encoding an SV40 tumor antigen to effect the initiation and termination of transcription of the nucleic acid encoding the SV40 tumor antigen.

[0035] The transgenes disclosed herein can be made using known methods. For example, a transgene can be assembled using bacterial homologous recombination and VELOCIGENE® technology (see, e.g., U.S. 6,586,251 and Valenzuela *et al.*, High-throughput engineering of the mouse genome coupled with high-resolution expression

analysis, 2003, *Nature Biotech*. 21(6):652-659). An example of a transgene provided herein comprises the nucleotide sequence as set forth in SEQ ID NO: 15.

[0036] The various elements of transgenes suitable for use in generating a rodent model of prostate cancer are described in further details below.

5' and 3' regulatory regions of a mouse probasin gene

[0037] Probasin is a prostate-specific gene originally isolated from rat. The promoter of the rat probasin (rPB) gene has been shown to be capable of targeting heterologous genes specifically to the prostate in transgenic mice (Greenberg et al., *Proc. Natl. Acad. Sci. USA* 92: 3439-3443, 1995; Kasper et al., *Lab. Invest.* 78 (3): i-xv, 1998; Hill et al., *Cancer Res.* 65(22): 10243-10254, 2005). In these studies, the promoter region utilized is limited to a relatively short segment from the 5' region of the rat probasin gene (a 454 bp fragment (-426/+28) in Greenberg et al. (1995); a 11.5 kb fragment in Kasper et al. (1998); and a 458 bp fragment (-458) in Hill et al. (2005)).

[0038] In accordance with this disclosure, a 5' regulatory region and a 3' regulatory region from a mouse probasin gene are included in a transgene to direct prostate-specific expression of an SV40 tumor antigen.

[0039] By "prostate-specific expression" it is meant that the expression in the prostate is substantially higher than the expression in non-prostate tissues and organs, or the expression in non-prostate tissues and organs is insignificant compared to the expression in the prostate. By "substantially higher" it is meant that the expression in the prostate is at least 50%, 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, or 1000%, higher than the expression in other tissues and organs. By "insignificant" it is meant that the expression in each such other tissue is not more than 20%, 10%, 5%, or 1% of the expression in the prostate.

[0040] The 5' and the 3' regulatory regions for use in a transgene herein include regulatory elements found in the 5' upstream region and the 3' downstream region of a mouse probasin gene and are sufficient to confer prostate-specific expression of a heterologous gene such as an SV40 tumor antigen coding sequence.

[0041] The term "regulatory elements" includes transcriptional regulatory sequences, which include both 5' transcriptional regulatory sequences such as promoter, enhancer, and suppressor elements, and 3' transcriptional regulatory sequences such as a transcriptional termination sequence. The term "regulatory elements" also includes regulatory sequences in the 5' untranslated region (5' UTR) and the 3' UTR that may affect the efficiency of transcription and the stability of transcript, as well the initiation of translation.

[0042] In accordance with this disclosure, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene includes a nucleotide sequence from a mouse probasin locus upstream of the translational start (or start codon ATG) of the mouse probasin gene. In some embodiments, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene includes a nucleotide sequence from a mouse probasin locus immediately upstream of the transcriptional start (or transcription initiation site) of the mouse probasin gene. The phrase "immediately upstream of the transcriptional start" means that the sequence (e.g., the 5' regulatory sequence) is upstream and within 35, 30, 25, 20, 15, 10, 5, 2, or 1 bp of the transcriptional start site of a mouse probasin gene. In some embodiments, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene includes a sequence of about 1 kb, 2 kb, 3 kb, 4 kb, 5 kb, 6 kb, 7 kb, 8 kb, 9 kb, or 10 kb upstream (e.g., immediately upstream) of the transcriptional start of a mouse probasin gene. In other embodiments, the 5' sequence flanking the SV40 tumor antigen coding sequence includes a sequence of at least 10 kb, 11 kb, 12 kb, 13 kb, 14 kb, 15 kb, 16 kb, 17 kb, 18 kb, 19 kb, or 20 kb upstream (e.g., immediately upstream) of the transcriptional start of a mouse probasin gene. In still other embodiments, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence includes a sequence of at least 15 kb, 20 kb, 25 kb, 30 kb, 35 kb, 40 kb, 45 kb, or 50 kb upstream (e.g., immediately upstream) of the transcriptional start of a mouse probasin gene. In specific embodiments, the 5' sequence flanking the SV40 tumor antigen coding sequence includes a sequence of at least about 45 kb, 46 kb, 47 kb, 48 kb, 49 kb, or 50 kb upstream (e.g., immediately upstream) of the transcriptional start of a mouse probasin gene.

[0043] In some embodiments, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene also includes a 5' UTR sequence of a mouse probasin gene.

In certain embodiments, the 5' sequence flanking the SV40 tumor antigen coding sequence includes the entire 5' UTR sequence of a mouse probasin gene. In specific embodiments, the 5' UTR sequence of a mouse probasin gene included in the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence comprises the nucleotide sequence as set forth in nucleotides 329-469 or 427-469 of SEQ ID NO: 16.

[0044] In specific embodiments, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene comprises the polynucleotide sequence as set forth in SEQ ID NO: 6, a sequence having a substantial identity thereto, or a fragment thereof.

[0045] By "substantially identical" in the context of comparing two sequences, it is meant that the subject sequence has a sequence identity of at least 75%, 80%, 85%, 90%, 95%, 98% or greater to a reference sequence.

[0046] In certain embodiments, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene comprises the polynucleotide sequence as set forth in SEQ ID NO: 6. In other embodiments, the 5' regulatory sequence flanking the SV40 tumor antigen coding sequence comprises a fragment of at least 15 kb, 20 kb, 25 kb, 30 kb, 35 kb, 40 kb, 45 kb, or 50 kb in length of SEQ ID NO: 6, preferably a fragment of any of the above mentioned lengths measured from the 3' end of SEQ ID NO: 6.

[0047] In accordance with this disclosure, the 3' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene includes a nucleotide sequence from a mouse probasin locus downstream of the translational termination site of the mouse probasin gene. In some embodiments, the 3' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene includes a nucleotide sequence from a mouse probasin locus immediately downstream of the transcriptional termination site of the mouse probasin gene. The phrase "immediately downstream of the transcriptional termination site" means that the sequence (e.g., the 3' regulatory sequence) is downstream and within 35, 30, 25, 20, 15, 10, 5, 2, or 1 bp of the transcriptional termination site of a mouse probasin gene.

[0048] In some embodiments, the 3' regulatory sequence flanking the SV40 tumor antigen coding sequence in a transgene includes a sequence of at least 500 bp, 1 kb, 2 kb, 3 kb, 4

kb, 5 kb, 6 kb, 7 kb, 8 kb, 9 kb, or 10 kb downstream (e.g., immediately downstream) of the transcriptional termination of a mouse probasin gene. In specific embodiments, the 3' sequence flanking the SV40 tumor antigen coding sequence includes a sequence of at least 10 kb, 20 kb, 30 kb, 40 kb, 50 kb, 60 kb, 70 kb, 80 kb, 90 kb or 100 kb downstream (e.g., immediately downstream) of the transcriptional termination of a mouse probasin gene. In other embodiments, the 3' sequence flanking the SV40 tumor antigen coding sequence includes a sequence of about 100 kb, 101 kb, 102 kb, 103 kb, 104 kb, 105 kb, 106 kb, or 107 kb downstream (e.g., immediately downstream) of the transcriptional termination of a mouse probasin gene.

[0049] In some embodiments, the 3' sequence flanking the SV40 tumor antigen coding sequence also includes a 3' UTR sequence of a mouse probasin gene. In certain embodiments, the 3' sequence flanking the SV40 tumor antigen coding sequence includes the entire 3' UTR sequence and an intron of a mouse probasin gene. In specific embodiments, the 3' sequence that includes the 3' UTR and an intronic sequence of a mouse probasin gene is set forth in nucleotides 4-3982 of SEQ ID NO: 17.

[0050] In specific embodiments, the 3' sequence flanking the SV40 tumor antigen coding sequence comprises the polynucleotide sequence as set forth in SEQ ID NO: 7, a sequence having a substantial identity thereto, or a fragment thereof.

[0051] In certain embodiments, the 3' sequence flanking the SV40 tumor antigen coding sequence comprises the polynucleotide sequence as set forth in SEQ ID NO: 7. In other embodiments, the 3' sequence flanking the SV40 tumor antigen coding sequence comprises a fragment of at least 20 kb, 30 kb, 40 kb, 50 kb, 60 kb, 70 kb, 80 kb, 90 kb, 100 kb, or 105 kb in length of SEQ ID NO: 7, preferably a fragment of any of the above mentioned lengths measured from the 5' end of SEQ ID NO: 7.

SV40 tumor antigen

[0052] In many embodiments, an oncogene or a nucleic acid encoding an oncogenic protein is used in this disclosure. In some embodiments, the oncogene is Myc (Grabowska et al., *Cancer Metastasis Rev.* 2014 September ; 33(0): 377–397). In other embodiments, the oncogenic protein is an SV40 tumor antigen.

[0053] The simian virus 40 (SV40) genome consists of 5243 bp (see, e.g., GenBank Accession No. J02400.1) and is divided into three regions: an early coding region, a late coding region, and a regulatory region (Ahuja et al., *Oncogene* 24: 7729-7745 (2005)). The early coding region encodes three proteins that are expressed early in a productive infection: the large T antigen, the small t antigen, and the 17K T antigen (Ahuja et al. (2005), *supra*). The large T antigen and the small t antigen are produced from two mRNAs generated through alternative splicing from a common pre-mRNA transcript (van Santen et al., *Nucleic Acid Res.* 14 (24): 9911-9926 (1986). It has been established that the inhibition by the SV40 large T antigen of the p53 and retinoblastoma (Rb) family of tumor suppressors, and the action by the SV40 small t antigen on the pp2A phosphatase, are important to SV40 induced transformation (Ahuja et al. (2005), *supra*). Expression of SV40 tumor antigens, including truncated large T antigens, in transgenic mice, results in development of hyperplasia and carcinoma (Ahuja et al. (2005), *supra*; Hill et al., *Cancer Res.* 65: 10243-54, 2005).

[0054] The SV40 large T antigen consists of 708 amino acids, and the small t antigen consists of 174 amino acids. Both the large T and small t antigens share a J domain located in the N-terminal region of the proteins. The large T antigen has a number of additional domains including a Rb-protein-binding motif (LXCXE, SEQ ID NO: 14), and a nuclear localization signal (NLS). The small t antigen has a pp2A binding domain following the J domain. See Ahuja et al. (2005), *supra.*

[0055] The term "SV40 tumor antigen" includes a full-length (i.e., wild type) SV40 large T antigen or a functional active fragment thereof, a full-length (i.e., wild type) SV40 small t-antigen or a functional active fragment thereof, or a combination thereof. In other words, the nucleic acid sequence in a transgene encoding an SV40 tumor antigen can encode a full-length SV40 large T antigen or a functionally active fragment thereof (without a small t antigen), a full-length SV40 small t-antigen or a functionally active fragment thereof (without a large T antigen), or a combination thereof (e.g., the nucleic acid sequence codes for both an SV40 large T antigen and an SV40 small t antigen).

[0056] The term "functionally active fragment" refers to a fragment of a T antigen having one or more functions associated with a full-length (wild type) T antigen; for example, the function of a full-length T antigen associated with inducing transformation, or with

initiating, promoting or sustaining tumor formation; the function of a large T antigen in inhibiting the activity of p53 or Rb; or the function of a small t antigen in binding and acting on pp2A. An example of a functional active fragment of a T antigen is the truncated large T antigen described in Hill et al. (2005), *supra*, which includes only the N-terminal 121 amino acids of a wild type large T antigen (without a small t antigen), also referred to as "T121." The T121 mutant antigen, which includes the J domain and the pRb-binding domain, is found sufficient to inactivate the pRb family proteins and to produce PIN and adenocarcinoma in mice (Hill et al. (2005), *supra*).

[0057] Other mutant SV40 T antigens have been described that also maintain the function of a wild-type SV40 T antigen in initiating, promoting or sustaining tumor formation. For example, an SV40 gene deletion mutant described by Kasper et al. (*Lab Invest.* 78 (3): i-xv, 1998) expresses only the large T antigen without the small t antigen and was also found to induce PIN and adenocarcinoma in mice.

[0058] In accordance with some embodiments, the nucleic acid sequence encoding an SV40 tumor antigen in a transgene encodes a full-length SV40 large T antigen or a functional active fragment thereof, without also encoding a small t-antigen. In certain embodiments, the large T antigen comprises the amino acid sequence of SEQ ID NO: 8 or a sequence substantially identical thereto. In specific embodiments, the nucleic acid sequence encoding an SV40 tumor antigen encodes a large T antigen comprising the amino acid sequence of SEQ ID NO: 8. In other specific embodiments, the nucleic acid sequence encoding an SV40 tumor antigen codes for a truncated large T antigen comprising the first 121 amino acids of SEQ ID NO: 8.

[0059] In some embodiments, the nucleic acid sequence encoding an SV40 tumor antigen in a transgene encodes a full-length SV40 small t antigen or a functional active fragment thereof, without also encoding a large T antigen. In certain embodiments, the small t antigen comprises the amino acid sequence of SEQ ID NO: 9 or a sequence substantially identical thereto. In specific embodiments, the nucleic acid sequence encoding an SV40 tumor antigen encodes a small t antigen having the amino acid sequence of SEQ ID NO: 9.

[0060] In still other embodiments, the nucleic acid sequence encoding an SV40 tumor antigen in a transgene encodes both a full-length SV40 large T antigen or a functional

active fragment thereof, and a full-length SV40 small t-antigen or a functional active fragment thereof. In certain embodiments, the nucleic acid sequence encoding an SV40 tumor antigen encodes both a full-length SV40 large T antigen and a full-length SV40 small t-antigen. In a specific embodiment, the nucleic acid encoding an SV40 tumor antigen comprises the nucleotide sequence set forth in SEQ ID NO: 1 or a nucleotide sequence substantially identical thereto.

Reporter

[0061] In some embodiments, the transgenes disclosed herein also include a reporter gene encoding a reporter protein (or "reporter") that provides or is capable of generating a detectable signal. Suitable reporters for use in this disclosure include β-galactosidase, mPlum, mCherry, tdTomato, mStrawberry, J-Red, DsRed, mOrange, mKO, mCitrine, Venus, YPet, yellow fluorescent protein (YFP), enhanced yellow fluorescent protein (EYFP), Emerald, green fluorescent protein (GFP), enhanced green fluorescent protein (EGFP), CyPet, cyan fluorescent protein (CFP), Cerulean, T-Sapphire, luciferase, alkaline phosphatase, or a combination thereof.

[0062] In certain embodiments, the reporter is a luciferase. The term "luciferase" includes the class of oxidative enzymes that catalyze an oxidation reaction of the substrate, luciferin, and bioluminescence is emitted as a result of the oxidation reaction. Luciferases suitable for use herein include firefly luciferase from the firefly species *Photinus pyralis*, luciferases from other organisms, and functional derivatives thereof (such as functional derivatives made by genetic engineering techniques). A "functional derivative" of a wild type (or naturally-occurring) luciferase includes proteins that differ from a wild type luciferase by having one or more amino acid modifications (e.g., additions, deletions, or substitutions) and that substantially retain the enzymatic activity of the wild type luciferase. The phrase "substantially retain the enzymatic activity of the wild type luciferase" includes a difference in both directions of not more than 30%, 25%, 20%, 15%, 10%, 5, 2% or 1% when a functional derivative and a wild type luciferase are compared in their enzymatic activities. In some embodiments, a functional derivative of a wild type luciferase has an amino acid sequence substantially identical to the amino acid sequence of the wild type luciferase. In a specific embodiment, the reporter gene encodes a luciferase

and comprises the nucleotide sequence as set forth in SEQ ID NO: 3 or a nucleotide sequence substantially identical to SEQ ID NO: 3.

Linkage between an SV40 tumor antigen coding sequence and a reporter gene

[0063] A reporter gene sequence is placed in a transgene in operable linkage with a nucleic acid sequence encoding an SV40 tumor antigen, such that the expression of the reporter reflects and coincides with the expression of the SV40 tumor antigen. Operable linkage between an SV40 tumor antigen coding sequence and a reporter nucleic acid can be achieved in a number of ways known in the art, such as through the use of multicistronic expression strategies. Multicistronic expression vectors simultaneously express two or more separate proteins from the same mRNA (i.e., a transcript produced from the same promoter). Suitable strategies for multicistronic expression of proteins include the use of a 2A peptide and the use of an internal ribosome entry site ("IRES").

[0064] In some embodiments, an SV40 tumor antigen coding sequence and a reporter gene are linked to each other via a nucleic acid sequence encoding a 2A peptide. The SV40 tumor antigen coding sequence can be placed at the N-terminus of a 2A peptide coding sequence, and the reporter gene is placed at the C-terminus of the 2A peptide coding sequence. Alternatively, the SV40 tumor antigen coding sequence can be placed at the C-terminus of a 2A peptide coding sequence, and the reporter gene is placed at the N-terminus of the 2A peptide coding sequence.

[0065] 2A peptides are small "self-cleaving" peptides, generally having 18–22 amino acids in length. It has been demonstrated that ribosomes skip the synthesis of a glycyl-prolyl peptide bond at the C-terminus of a 2A peptide, leading to the cleavage between a 2A peptide and its immediate downstream peptide (Kim et al., *PLoS One* 2011; 6(4): e18556). As a result, the "cleaved-off" downstream peptide has proline at its N-terminus. 2A-mediated cleavage is a universal phenomenon in all eukaryotic cells. 2A peptides have been identified from picornaviruses, insect viruses and type C rotaviruses (Szymczak et al., "*Development of 2A peptide-based strategies in the design of multicistronic vectors*," *Expert Opin Biol Ther* 5: 627–638 (2005)) and are suitable for use in this disclosure. In certain embodiments, the 2A peptide used in linking the SV40 tumor antigen and the reporter protein is a 2A peptide selected from FMDV 2A ("F2A"), equine

rhinitis A virus (ERAV) 2A ("E2A"), porcine teschovirus-1 2A ("P2A"), or *Thoseaasigna* virus 2A ("T2A"). In particular embodiments, these 2A peptides have the following sequences:

F2A VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 10)
E2A QCTNYALLKLAGDVESNPGP (SEQ ID NO: 11)
P2A ATNFSLLKQAGDVEENPGP (SEQ ID NO: 12)
T2A EGRGSLLTCGDVEENPGP (SEQ ID NO: 13)

[0066] In some embodiments, a T2A peptide is used to provide a linkage between an SV40 tumor antigen and a reporter protein. In one embodiment, the T2A peptide used herein comprises the amino acid sequence of SEQ ID NO: 13. In a specific embodiment, the T2A peptide is encoded by the nucleotide sequence of SEQ ID NO: 2.

[0067] In other embodiments, an SV40 tumor antigen coding sequence and a reporter nucleic acid sequence are linked to each other via an Internal Ribosome Entry Site (IRES). An IRES is a nucleotide sequence well documented in the art that allows for translation initiation in the middle of a mRNA, thereby providing translation of two or more protein products from a single mRNA molecule.

Other elements in a transgene

[0068] In some embodiments, the transgenes provided herein also include a nucleic acid sequence encoding a selection marker. Such selection markers include, but are not limited to, neomycin phosphotransferase (neo^r), hygromycin B phosphotransferase (hyg^r), puromycin-N-acetyltransferase ($puro^r$), blasticidin S deaminase (bsr^r), xanthine/guanine phosphoribosyl transferase (gpt), or herpes simplex virus thymidine kinase (HSV-k), or a combination thereof.

[0069] The selection marker nucleic acid can be contained in an expression cassette, wherein the nucleic acid sequence encoding the selection marker is operably linked to one or more promoters active in desired cells - for example, two promoters, with one active in a rodent cell such as a rodent ES cell, and the other active in a bacterial cell.

[0070] In some embodiments, the nucleic acid sequence encoding the selection marker is flanked with site-specific recombination target sequences that permit removal of the nucleic acid sequence between the site-specific recombination target sequences (e.g., the selection marker nucleic acid) following integration of a transgene. Site-specific recombination target sequences, which can flank the selection marker nucleic acid or any polynucleotide of interest can include, but are not limited to, loxP, lox511, lox2272, lox66, lox71, loxM2, lox5171, FRT, FRT11, FRT71, attp, att, rox, and a combination thereof.

[0071] In particular embodiments, the transgenes provided herein include a neomycin selection cassette that contains, from 5' to 3', a loxP (5') sequence, a TATA box-hUb (human ubiquitin promoter, an EM7 promoter, a neomycin phosphotransferase coding sequence, a polyA sequence, and a loxP (3') sequence. In a specific embodiment, the neomycin selection cassette comprises the nucleotide sequence as set forth in SEQ ID NO: 5 or a sequence substantially identical thereto. Once an ES cell clone comprising the transgene is selected, the neomycin selection cassette can be excised by introducing a Cre recombinase, e.g., via electroporation. Alternatively, the neomycin selection cassette can be removed by crossing the progeny generated from the ES clone with a deletor rodent strain that expresses a Cre recombinase.

[0072] In some embodiments, the transgenes provided herein also include an SV40 late region poly A sequence, placed at the 3' side of the SV40 tumor antigen coding sequence; and if a reporter nucleic acid is present, at the 3' side of the reporter nucleic acid. In a specific embodiment, the SV40 late region poly A sequence comprises the nucleotide sequence as set forth in SEQ ID NO: 4 or a sequence substantially identical thereto.

Rodent Models of Prostate Cancer

[0073] Rodents are provided that contain in their genome a transgene encoding an SV40 tumor antigen, operably linked to 5' and 3' regulatory regions of a mouse probasin gene. Such rodents express the transgene specifically in the prostate and display progressive forms of prostate tumors that resemble the development of human prostate cancer.

[0074] Transgenic mouse models of prostate cancer have been described in the art. For example, a transgenic adenocarcinoma of the mouse prostate (TRAMP) model has been

described by Greenberg et al. (1995), *supra*, and Gingrich et al. (*Cancer Res.* 56: 4096-4102, 1996), and utilizes a prostate-specific rat probasin minimal promoter (-427/+28 bp) to drive expression of SV40 large T- and small t-antigens. The transgene is specifically expressed in the prostatic epithelium of TRAMP mice, with expression at significantly higher levels in the ventral lobes as compared to the dorsal, lateral and anterior lobes of the prostate (Figure 1 of Greenberg et al. (1995)). TRAMP mice develop prostate intraepithelial neoplasia (PIN) by 6-12 weeks of age, which progresses to poorly differentiated and invasive adenocarcinoma in the dorsolateral lobes of the prostate by 20-24 weeks of age (Greenberg et al. (1995)). Adenocarcinomas formed in TRAMP mice develop metastases to distant sites (e.g., lymph nodes and lungs) (Gingrich et al. (1996), *supra*), but rarely to bone. A majority of adenocarcinomas developed in TRAMP mice are neuroendocrine in origin (Chiaverotti et al., *Am J Pathol.* 172(1): 236–246, 2008), a type of carcinoma representing only 10% of human prostate cancer patients. A TRAMP model derivative is described by Hill et al. (2005), *supra*, and utilizes a truncated rat probasin promoter segment (-458 bp) with two adenine and uridine-rich elements (or "AREs") replaced to drive expression of a truncated SV40 large T antigen. The transgene is expressed in the dorsal, anterior and ventral lobes of the prostate. Such TRAMP derivative mice develop PIN by 2 months of age, which progresses to carcinoma by 4 months of age. A LADY transgenic mouse model of prostate cancer is described by Kasper et al. (1998), *supra*, and utilizes a larger (11.5 kb) rat probasin promoter segment to drive a truncated SV40 large T-antigen, which leads to transgene expression in the prostate. LADY mice develop glandular hyperplasia and PIN by 5-10 weeks of age, followed by high-grade epithelial dysplasia and poorly undifferentiated adenocarcinoma by 20 weeks, primarily in the dorsolateral and anterior lobes of the prostate. LADY mice rarely develop metastasis to other organs. All of these transgenic mouse models have a rapid rate of disease progression, which differs from the characteristically slow development of carcinomas in humans. The prevalence of neuroendocrine carcinomas in TRAMP mice also limits the relevance of this mouse model to the small subpopulation of patients with neuroendocrine disease.

[0075] The rodents provided herein better recapitulate the pathological features of human prostate cancer than the models described in the art. For example, predominant expression of the transgene is detected in the dorsolateral lobes of the rodents, the area analogous to

the peripheral zone of human prostate where human prostate adenocarcinoma typically arises. Furthermore, the rodents provided herein develop progressive forms of prostate tumors that resemble the various stages of human prostate cancer, ranging from hyperplasia to high grade prostate intraepithelial neoplasia (or "HGPIN") to adenocarcinoma, with a much slower rate of disease progression and longer life span as compared to TRAMP and LADY mice reported in the art. In addition, adenocarcinoma developed in the rodents disclosed herein is not neuroendocrine in nature.

[0076] In some embodiments, the transgene is expressed in the dorsolateral lobes and/or anterior lobes of the prostate of rodents. In some embodiments, the expression of the transgene in the dorsolateral lobes and/or anterior lobes is higher than in the ventral lobes of the prostate. In specific embodiments, the expression of the transgene in the dorsolateral lobes, the anterior lobes, or in the dorsolateral and anterior lobes combined, is substantially higher (i.e., at least 30%, 40%, 50%, 75%, 100% or greater) than the expression in the ventral lobes.

[0077] The rodents provided herein develop prostate intraepithelial neoplasia, or "PIN". PIN is typically characterized by proliferation of atypical cells within pre-existing glandular spaces without invasion (i.e., the basement membrane has not been breached). In some embodiments, the rodents begin to display PIN at about 3-7 months of age, or about 4-6 months of age. In certain embodiments, the rodents do not display PIN until at least about 2, 3, 4, 5 or 6 months of age. In some embodiments, the PIN developed in the rodents is in the dorsolateral lobes, or the dorsolateral and anterior lobes of the prostate. In specific embodiments, the PIN developed in the rodents is substantially in the dorsolateral and/or anterior lobes of the prostate, but substantially not in the ventral lobes of the prostate. The term "substantially" means that at least 50%, 60%, 70%, 80%, 90% or greater of areas displaying PIN are in the dorsolateral and/or anterior lobes of the prostate, with not more than 50%, 40%, 30%, 20%, 10% or less of areas displaying PIN are in the ventral lobes of the prostate.

[0078] The rodents provided herein develop prostate adenocarcinoma. Adenocarcinoma is generally characterized by infiltrative and/or destructive proliferation of atypical cells. Generally speaking, the atypical cells have some degree of glandular differentiation. In some embodiments, the rodents begin to display prostate adenocarcinoma at about 7-9

months of age, or at about 8 months of age. In certain embodiments, the rodents do not display adenocarcinoma until at least about 6, 7, 8, 9 or 10 months of age. In some embodiments, the adenocarcinoma developed in the rodents is in the dorsolateral lobes, or dorsolateral and anterior lobes of the prostate. In specific embodiments, the adenocarcinoma developed in the rodents is substantially in the dorsolateral and/or anterior lobes of the prostate, but substantially not in the ventral lobes of the prostate. The term "substantially" means that at least 50%, 60%, 70%, 80%, 90% or greater of areas displaying adenocarcinoma are in the dorsolateral and/or anterior lobes of the prostate, with not more than 50%, 40%, 30%, 20%, 10% or less of areas in the prostate displaying adenocarcinoma being in the ventral lobes of the prostate.

[0079] In some embodiments, the reporter gene (e.g., a luciferase gene) is detected in another organ. In specific embodiments, the reporter gene is detected in an organ selected from bladder, liver, lung, kidney, heart, thymus, salivary gland, bone, or a combination thereof.

[0080] In some embodiments, the adenocarcinoma developed in the rodents provided herein is not neuroendocrine carcinoma. Neuroendocrine (NE) carcinoma is associated with distinct morphology and marker expression pattern (Chiaverotti et al. (2008), *supra*). For example, NE carcinomas are characterized by poorly differentiated and highly invasive lesions; form large masses that distort the ductal architecture, entrap normal or hyperplastic glands, usually involve multiple lobes; and often have large areas of necrosis. In immunostaining assays, NE carcinoma typically stains negative for androgen receptor (AR) or shows weak and diffuse cytoplasmic staining for AR, but stains positive for synaptophysin, contrasting sharply with normal and hyperplastic prostatic epithelia which stain negative for synaptophysin with strong nuclear staining for AR. In specific embodiments, the adenocarcinoma developed in the rodents provided herein does not express synaptophysin, i.e., stains negative for synaptophysin as determined by immunostaining for example, although positive for the epithelial marker, E-cadherin.

[0081] In some embodiments, the rodents provided herein exhibit a combination of any of the expression and pathological features described above, including, for example, the areas where the transgene is expressed, the period of time it takes to develop PIN, the areas in the prostate where PIN develops, the period of time it takes to develop prostate

adenocarcinoma, the areas in the prostate where adenocarcinoma develops, and the feature that the adenocarcinoma developed is not neuroendocrine carcinoma. In many embodiments, the rodents may exhibit a combination of any one of the following features: (i) transgene expression in the dorsolateral lobes and/or anterior lobes of the prostate; (ii) not displaying PIN until at least about 2, 3, 4, 5 or 6 months of age, and in specific embodiments, beginning to display PIN at about 3-7 months of age, or about 4-6 months of age; (iii) displaying PIN in the dorsolateral lobes, or the dorsolateral and anterior lobes of the prostate, and in some embodiments, substantially in the dorsolateral and/or anterior lobes of the prostate, but substantially not in the ventral lobes of the prostate; (iv) not displaying adenocarcinoma until at least about 6, 7, 8, 9 or 10 months of age, and in specific embodiments, beginning to display prostate adenocarcinoma at about 7-9 months of age, or at about 8 months of age; (v) displaying adenocarcinoma in the dorsolateral lobes, or dorsolateral and anterior lobes of the prostate, and in specific embodiments, substantially in the dorsolateral and/or anterior lobes of the prostate, but substantially not in the ventral lobes of the prostate. In particular embodiments, disclosed herein is a rodent that begins to display PIN in the prostate tissue at about 4-6 months of age, and begins to display adenocarcinoma at about 7-9 months of age, wherein the adenocarcinoma developed in the rodent is not neuroendocrine carcinoma.

[0082] The rodents provided herein have a longer survival time as compared to TRAMP and LADY mice reported in the art, possibly because the rodents provided herein have a slower rate of disease progression and do not develop the more aggressive, neuroendocrine carcinoma. In some embodiments, the rodents provided herein live at least to 16, 18, 20, 22, or 24 months of age. In specific embodiments, the rodents live longer than 24 months of age.

[0083] The rodents provided herein include, for example, mice, rats, and hamsters. In some embodiments, the rodent is a mouse or a rat. In specific embodiments, the rodent is a mouse.

[0084] In some embodiments, the rodent is a mouse of a C57BL strain, for example, a C57BL strain selected from C57BL/A, C57BL/An, C57BL/GrFa, C57BL/KaLwN, C57BL/6, C57BL/6J, C57BL/6ByJ, C57BL/6NJ, C57BL/10, C57BL/10ScSn, C57BL/10Cr, and C57BL/Ola. In other embodiments, the rodent is a mouse of a 129

strain, for example, a 129 strain selected from the group consisting of 129P1, 129P2, 129P3, 129X1, 129S1 (e.g., 129S1/SV, 129S1/SvIm), 129S2, 129S4, 129S5, 129S9/SvEvH, 129/SvJae, 129S6 (129/SvEvTac), 129S7, 129S8, 129T1, 129T2 (see, e.g., Festing et al. (1999), *Mammalian Genome* 10:836; Auerbach et al. (2000), *Biotechniques* 29(5):1024-1028, 1030, 1032). In some embodiments, the rodent is a mouse that is a mix of an aforementioned 129 strain and an aforementioned C57BL/6 strain. In certain embodiments, the mouse is a mix (i.e., hybrid) of aforementioned 129 strains, or a mix of aforementioned C57BL strains, or a mix of a C57BL strain and a 129 strain. In certain embodiments, the mouse is a mix of a C57BL/6 strain with a 129 strain. In specific embodiments, the mouse is a VGF1 strain, also known as F1H4, which is a hybrid of C57BL/6 and 129. In other embodiments, the mouse is a BALB strain, e.g., BALB/c strain. In some embodiments, the mouse is a mix of a BALB strain and another aforementioned strain.

[0085] In some embodiments, the rodent is a rat. In certain embodiments, the rat is selected from a Wistar rat, an LEA strain, a Sprague Dawley strain, a Fischer strain, F344, F6, and Dark Agouti. In other embodiments, the rat is a mix of two or more strains selected from the group consisting of Wistar, LEA, Sprague Dawley, Fischer, F344, F6, and Dark Agouti.

Methods Of Making A Transgenic Rodent

[0086] The rodents provided herein can be made using methods known in the art. In exemplary embodiments, a vector containing a transgene that encodes an SV40 tumor antigen operably linked to 5' and 3' regulatory regions of a mouse probasin gene can be constructed. For example, a BAC vector carrying a desirable transgene can be constructed utilizing bacterial artificial chromosome (BAC) clones and bacterial homologous recombination and VELOCIGENE® technology (see, e.g., U.S. 6,586,251 and Valenzuela *et al.* (2003), High-throughput engineering of the mouse genome coupled with high-resolution expression analysis, *Nature Biotech.* 21(6):652-659).

[0087] In some embodiments, a BAC vector carrying a transgene can be introduced into rodent embryonic stem (ES) by, e.g., electroporation. Both mouse ES cells and rat ES cells have been described in the art. See, e.g., US 7,576,259, US 7,659,442, US

7,294,754, and US 2008-0078000 A1 (all of which are incorporated herein by reference) describe mouse ES cells and the VELOCIMOUSE® method for making a genetically modified mouse; and US 2014/0235933 A1 and US 2014/0310828 A1 (all of which are incorporated herein by reference) describe rat ES cells and methods for making a genetically modified rat.

[0088] ES cells having the transgene integrated in the genome can be selected. In some embodiments, ES cells having the transgene integrated into a target locus of a rodent are selected. Target loci include, for example, an endogenous rodent probasin locus (via homologous recombination mediated integration, for example). Targeting vectors that facilitate targeted integration can be designed and used for generating ES cells having targeted integration of the transgene. In other embodiments, ES cells having the transgene integrated into the genome are selected irrespective of the site(s) where the integration occurs; in other words, one or more copies of the transgene may be integrated at one or more ectopic sites (i.e., sites other than a target locus). In some embodiments, at least 1-10 copies copy of a transgene are integrated in the genome of an ES cell. In certain embodiments, multiple copies of a transgene, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more copies of a transgene, are integrated in the genome of an ES cell. The multiple copies of the transgene can be integrated into one locus or multiple loci of the genome. In specific embodiments, multiple copies (i.e., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more copies) of a transgene are integrated in tandem into one locus of the genome. ES cells having the transgene integrated in the genome are then used as donor ES cells for injection into a pre-morula stage embryo (e.g., 8-cell stage embryo) by using the VELOCIMOUSE® method (see, e.g., US 7,576,259, US 7,659,442, US 7,294,754, and US 2008-0078000 A1), or methods described in US 2014/0235933 A1 and US 2014/0310828 A1. The embryo comprising the donor ES cells is incubated until blastocyst stage and then implanted into a surrogate mother to produce an F0 rodent fully derived from the donor ES cells. Rodent pups bearing the transgene can be identified by genotyping of DNA isolated from tail snips using a modification of allele (MOA) assay (Valenzuela *et al.*, *supra*) that detects the presence of the transgene sequence. Pups positive for the transgene can be further screened based on prostate-specific expression of the transgene (e.g., the level of expression in the prostate relative to other tissues and organs, and the expression in various sections of the prostate such as in dorsal, lateral, anterior, and ventral lobes),

and/or based on development and progression of prostate carcinoma (e.g., the onset and progression of PIN and carcinoma).

[0089] ES clones capable of generating rodents that demonstrate desirable phenotypes as described above can be identified. Desirable phenotypes include, e.g., prostate-specific expression of the transgene substantially in the dorsolateral and anterior lobes of the prostate, and having an onset of PIN at about 4-6 months of age and an onset of carcinoma at about 8 months of age. Such ES clones can be cultured and stored. In some embodiments, an ES clone contains at least one copy of the transgene integrated at a target locus (e.g., an endogenous probasin locus). In other embodiments, at least 1-10 copies of a transgene are integrated at one or more ectopic sites in the genome. In some embodiments, an ES clone contains multiple copies of a transgene, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more copies of the transgene, integrated in the genome. In certain embodiments, multiple copies (2, 3, 4, 5, 6, 7, 8, 9, 10 or more copies) of a transgene are integrated into multiple loci of the genome. In certain other embodiments, multiple copies of the transgene are integrated in tandem into one locus, e.g., one ectopic locus, of the genome. In a specific embodiment, a mouse ES clone designated as Clone A-C10 (5x) is provided herein that have five copies of a transgene integrated in tandom into one locus of the genome, wherein the transgene includes a coding sequence for SV40Tag-T2A- luciferase, flanked by 5' and 3' regulatory regions of a mouse probasin gene.

[0090] In other embodiments, a transgenic rodent can be made without using ES cells. For example, the genome of a non-ES cell of a rodent (e.g., a fibroblast or an induced pluripotent cell) can be modified based on conventional transformation methods (e.g., electroporation), and the modified genome of such non-ES cell can be transferred to a suitable recipient cell, e.g., an oocyte, by employing the nuclear transfer technique. The modified cell (e.g., the modified oocyte) is then gestated under suitable conditions to form an embryo. See, e.g., Han et al., "*Nuclear Transfer in Mouse Oocytes and Embryos*", *Methods in Enzymology* 476: 171-184 (2010), and Zhou et al., "*Generation of Fertile Cloned Rats by Regulating Oocyte Activation*", *Science* 302: 1179 (2003).

Methods of Using the Transgenic Rodents

[0091] The rodents provided herein permit the development of methodologies for the identification, diagnosis and staging of prostate cancer, as well as a better understanding of the molecular mechanisms underlying the progression of prostate cancer. In addition, such rodents may be used in the screening and development of therapeutic agents for the prevention and treatment of prostate cancer.

[0092] The present description is further illustrated by the following examples, which should not be construed as limiting in any way. The contents of all cited references (including literature references, issued patents, and published patent applications as cited throughout this application) are hereby expressly incorporated by reference.

Example 1. Generation of Luci-TRAMP Mice

[0093] This example illustrates generation of transgenic mice, also referred to herein as Luci-TRAMP mice, which contain a transgene that includes a nucleic acid coding sequence for an SV40 tumor antigen-T2A-luciferase polypeptide, flanked by a 5' regulatory region and a 3' regulatory region of a mouse probasin gene.

[0094] A vector containing the transgene was constructed via bacterial homologous recombination and VELOCIGENE® technology (see, e.g., U.S. 6,586,251 and Valenzuela *et al.*, High-throughput engineering of the mouse genome coupled with high-resolution expression analysis, 2003, *Nature Biotech.* 21(6):652-659). Briefly, a bacterial artificial chromosome (BAC) clone RP23-417B18, which contains a mouse probasin gene, was utilized and modified as follows. One fragment, comprised of 75 base pairs (bps) of the mouse 5'-UTR, the SV40-T-antigen (without a stop codon), followed by the T2A sequence, NcoI/XhoI/NheI restriction sites, and a stop codon and 89 bps of the mouse 3'-UTR, was synthesized by GenScript and cloned into the R6K backbone for propagation. The luciferase2 cDNA sequence and its own pA, was amplified from the Promega plasmid (pGL4) using primers that add flanking NcoI and XhoI restriction sites. The neomycin resistance cassette, flanked by XhoI and NheI sites, were co-ligated with the luciferase amplicon into the synthesized fragment. Bacterial homologous recombination to replace the mouse Pbsn gene (from start ATG codon to stop TAG codon) was mediated by the

homologous sequences up- (75 bps) and down-stream (89 bps). After sequencing the junctions to ensure the recombination was seamless and restriction fragment analysis to ascertain expected size of the modified BAC, the BacVec was linearized and purified for electroporation.

[0095] The resulting modified BAC vector is graphically depicted in **Figure 1**. The nucleotide sequences of the components of the modified BAC vector are set forth in SEQ ID NOs: 1-7.

[0096] This modified BAC vector was electroporated into VGF1 (also known as F1H4) C57BL6/129 F1 hybrid embryonic stem (ES) cells to create modified ES cells having the SV40-T2A-luciferase transgene integrated in the genome. Modified ES cells containing the SV40-T2A-luciferase transgene were selected based on their resistance to geneticin (G418).

[0097] Selected ES cell clones were then used as donor ES cells and microinjected into a pre-morula stage mouse embryo by the VELOCIMOUSE® method (see, e.g., US 7,576,259, US 7,659,442, US 7,294,754, and US 2008-0078000 A1). The mouse embryo comprising the donor ES cells was incubated until blastocyst stage and then implanted into a surrogate mother to produce an F0 mouse fully derived form the donor ES cells. Mice bearing the transgene were identified by genotyping of DNA isolated from tail snips using a modification of allele (MOA) assay (Valenzuela *et al.*, *supra*) that detected the presence of the transgene sequence. Pups positive for the transgene were further screened for prostate-specific expression of T-antigen and luciferase.

[0098] Clone A-C10 (5x) was identified as an ES clone that produced mice which showed prostate-specific transgene expression at 8 weeks (**Figure 2**). Transgene mRNA was evaluated using quantitative PCR (qPCR) with assays designed against the T-antigen and the luciferase transgenes. Tissues from mice at age 8 weeks were harvested and immersed immediately in RNALater reagent. Total RNA was extracted by the Regeneron DNA Core, and qPCR was performed according to PerkinElmer's instructions with minor modifications. WT, hybrid non-transgenic control mouse; A-B1, mouse with low/no-transgene expression; A-B8, mouse with moderate but mis-expressing the transgene; A-C10, Luci-TRAMP mouse with ~5 copies of the trasnsgene expressed in only the dorsolateral prostate (DLP) and the anterior prostate (AP and seminal vesicles (SV).

Example 2. Longitudinal Analysis of Luci-TRAMP Cohort

[0099] Luci-TRAMP mice generated from ES clone A-C10 (5x) were designated as MAID 2319 and used in the experiments described in this example. Mice designated as MAID 2363 contain the transgene "R26-L-luc2" at the Rosa 26 locus in the genome (which expresses a luciferase reporter in a non-tissue specific manner and wild type F1H4 mice, were used as controls.

[00100] A cohort of 35 MAID2319 mice (Luci-TRAMP) were kept to allow prostate tumor to develop, in parallel with an equivalent number of MAID 2363 mice (R26-L-Luc2) and F1H4 mice. 5 mice were removed from each group at 2, 4, 6, 8, 11, and 16 months, respectively, for *in vivo* luciferase imaging, μCT scan (to assess lean/fat/bone mass), histopathology analysis (starting from 4 months), and molecule phenotyping (RNA-seq and qPCR).

[00101] For the longitudinal study, at each indicated time point (inset below), all animals were given luciferin subcutaneously (150mg/kg PerkinElmer), anesthetized by isofluorane, and scanned on a Lumina XR *in vivo* imaging system after 12-14 min. Living software was used to automatically draw ROIs with a contour perimeter and compute intensity signal (total flux) at a 5% threshold.

[00102] qPCR probes were designed using BioSearch Technologies and Regeneron in-house search parameters. Tissues were homogenized in TRIzol and chloroform was used for phase separation. The aqueous phase, containing total RNA, was purified using miRNeasy Mini Kit (Qiagen, Cat #217004) according to manufacturer's specifications. Genomic DNA was removed using MagMAX™Turbo™DNase Buffer and TURBO DNase reagents (Ambion by Life Technologies). mRNA was reverse-transcribed into cDNA using SuperScript® VILO™ Master Mix reagent (Invitrogen by Life Technologies, Cat# 11755500). cDNA was amplified with the TaqMan® Gene Expression Master Mix reagent (Applied Biosystems by Life Technologies, Cat# 4370074) using the ABI 7900HT Sequence Detection System (Applied Biosystems). Beta-actin was used as the internal control gene to normalize any cDNA input differences. WT (F1H4) lung was used as a reference sample to calculate the fold difference of mRNA between samples. N=5 males per tissue per genotype. Statistical and graphical analyses were performed using

GraphPad Prism software (version 3.0). Data were analyzed using Student's unpaired t-test. Results were considered statistically significant at P values <0.05. Error bars depict SD.

[00103] Results are shown in **Figures 3A-3C**. Prostate cancer progression revealed from the histopathology analysis was summarized in **Table 1**. The assignment of mPIN and adenocarcinoma was based on the following guideline.

[00104] mPIN: Proliferation of atypical cells within pre-existing glandular spaces, but lacking invasion (i.e., the basement membrane has not been breached). mPIN is differentiated from epithelial hyperplasia based on morphology (atypical) compatible with the particular GEM model. Progression of mPIN is associated with age, and has been demonstrated to advance to invasive carcinomas. Grading is based on increasing degrees of architectural or cytological abnormalities on a scale of 1-4:

mPIN1 (epithelial hyperplasia) = mild nuclear and/or cytoplasm atypia (independent of inflammation) with cells arranged single or double layers.

mPIN2 = two or more layers of cells with nuclear atypia in tufts or papillary branches.

mPIN3 = increased/more frequent atypia, with more extensive papillary branching that partially to completely fills the lumen.

mPIN4 = marked/frequent atypia, with exuberant branching and distention of the gland spaces, but lacking clear invasion.

Adenocarcinoma: Infiltrative and/or destructive proliferation of atypical cells that have some degree of glandular differentiation. In mice, stromal desmoplasia and varying degrees of interstitial inflammation are associated with more advanced lesions.

[00105] Representative pathology staining images are provided in **Figures 4A-4B**. Immunohistochemistry analysis of prostate tumor from Luci-TRAMP mice is shown in **Figures 5A-5B**. Tissues were fixed in freshly prepared 4% paraformaldehyde overnight,

then paraffin embedded, sectioned, and stained with hematoxylin and eosin for staging. Some sections were assayed for neuroendocrine or epithelial antigens using antibodies against synaptophysin (Abcam #32127) or E-cadherin (Cell Signaling clone 64E10), respectively.

[00106] These studies have revealed the following.

- Starting from 4 month of age, prostate tumor development was visible in all Luci-TRAMP prostates (5/5 mice each age group) under dissection microscope (solid whitish spots/areas within otherwise transparent prostatic glands), no abnormality detected in controls.
- At 4 and 6 month, 3/3 Luci-TRAMP mice analyzed in each age demonstrated *non-invasive prostate tumors* in both dorsal lateral and anterior lobes. 4/4 control mice analyzed in each age group showed no abnormality in any lobes.
- At 8 and 11 month, 3/3 Luci-TRAMP mice of each group demonstrated *prostate adenocarcinoma* in both dorsal lateral and anterior lobes. 3/3 control mice analyzed in each age group showed little abnormality in any lobes.
- At 16 month, 5/5 Luci-TRAMP mice demonstrated *prostate adenocarcinoma* in anterior lobe and 4/4 detected for prostate adenocarcinoma in dorsal lateral lobes.
- Ventral lobe showed minor changes (limited to epithelial hyperplasia) in Luci-TRAMP mice.
- Although micro-invasion was observed starting 8 months of age, there was no evidence of vascular invasion by age of 16 month.
- IHC analysis showed that Luci-TRAMP prostate tumor were stained positive for epithelial marker E-cadherin and negative for neuroendocrine marker Synaptophysin.

Table 1. Luci-TRAMP Mice Prostate Pathology Overview

	LOBE	Mouse ID	Dorsolateral (DLP)	Anterior (CG)	Ventral
4 Month	F1H4	M6	WNL	WNL	WNL
		M8	WNL	WNL	NI
	ROSA: 2319	1258782	WNL	WNL	WNL
		1258784	WNL	WNL	NI
	Luci-TRAMP	M6	epithelial hyperplasia	mPIN-3, focal	epithelial hyperplasia
		M8	epithelial hyperplasia	mPIN-2, focal	epithelial hyperplasia
		M10*	epithelial hyperplasia, focal	epithelial hyperplasia, focal	NI
6 Month	F1H4	M12	WNL	epithelial hyperplasia, diffuse	WNL
		M14	WNL	WNL	WNL
	ROSA: 2314	M12	WNL	WNL	WNL (scant present)
		M14	WNL	WNL	NI
	Luci-TRAMP	M11	epithelial hyperplasia	mPIN-3, focal	WNL
		M13	epithelial hyperplasia	mPIN-3, diffuse	EH; dilated gland lumens
		M15	epithelial hyperplasia	mPIN-3, diffuse	dilated glands, WNL
8 Month	F1H4	16	WNL	WNL	WNL
		18	WNL	WNL	NI
		20	WNL	WNL	WNL
	Luci-TRAMP	M16	adenocarcinoma	adenocarcinoma	epithelial hyperplasia (NI)
		M18	adenocarcinoma	adenocarcinoma	epithelial hyperplasia

		M20	adenocarcinoma	adenocarcinoma	NI
11 Month	F1H4	21	WNL	epithelial hyperplasia, focal	NI
		22	WNL	WNL	NI
		23	WNL	WNL	WNL
	Luci-TRAMP	M21	adenocarcinoma	adenocarcinoma	NI
		M22	adenocarcinoma	adenocarcinoma	NI
		M23	adenocarcinoma	adenocarcinoma	NI
16 Month	F1H4	26	WNL (dilated lateral)	epithelial hyperplasia, focal	WNL
		27	WNL	WNL	NI
		28	WNL	epithelial hyperplasia, focal	WNL (dilated)
		29	WNL (dilated lateral)	WNL	WNL (dilated)
		30	WNL (dilated)	epithelial hyperplasia, focal	NI
	Luci-TRAMP	M26	adenocarcinoma	adenocarcinoma	NI
		M27	*Very few specimen*	adenocarcinoma	NI
		M28	adenocarcinoma	adenocarcinoma	NI
		M29	adenocarcinoma	adenocarcinoma	NI
		M30	adenocarcinoma	adenocarcinoma	NI

WNL = Within Normal Limits; NI = Not IDENTIFIED

WHAT IS CLAIMED IS:

1. A rodent comprising in its genome a transgene comprising:

(a) a 5' regulatory region of a mouse probasin gene,

(b) a nucleic acid comprising a first nucleotide sequence encoding an oncogenic protein, and

(c) a 3' regulatory region of the mouse probasin gene,

wherein the 5' regulatory region, the nucleic acid, and the 3' regulatory region are operably linked to each other.

2. The rodent of claim 1, wherein the 5' regulatory region comprises a nucleic acid sequence of at least 5 kb upstream of the transcription initiation site of the mouse probasin gene.

3. The rodent of claim 1, wherein the 5' regulatory region comprises a nucleic acid sequence of at least 10 kb upstream of the transcription initiation site of the mouse probasin gene.

4. The rodent of claim 1, wherein the 5' regulatory region comprises a nucleic acid sequence of at least 25 kb upstream of the transcription initiation site of the mouse probasin gene.

5. The rodent of claim 1, wherein the 5' regulatory region comprises a 5' untranslated region (UTR) of the mouse probasin gene.

6. The rodent of claim 1, wherein the 5' regulatory region comprises the nucleotide sequence as set forth in SEQ ID NO: 6.

7. The rodent according to any one of claims 1-6, wherein the 3' regulatory region comprises a nucleic acid sequence of at least 5 kb downstream of the transcription termination site of the mouse probasin gene.

8. The rodent according to any one of claims 1-6, wherein the 3' regulatory region comprises a nucleic acid sequence of at least 25 kb downstream of the transcription termination site of the mouse probasin gene.

9. The rodent according to any one of claims 1-6, wherein the 3' regulatory region comprises a nucleic acid sequence of at least 50 kb downstream of the transcription termination site of the mouse probasin gene.

10. The rodent according to any one of claims 1-6, wherein the 3' regulatory region comprises a 3' untranslated region of the mouse probasin gene.

11. The rodent according to any one of claims 1-6, wherein the 3' regulatory region comprises the nucleotide sequence as set forth in SEQ ID NO: 7.

12. The rodent according to any one of claims 1-11, wherein the oncogenic protein comprises an SV40 tumor antigen or Myc.

13. The rodent of claim 12, wherein the SV40 tumor antigen comprises an SV40 large T antigen or a functionally active fragment thereof.

14. The rodent of claim 12, wherein the SV40 tumor antigen comprises an SV40 small t antigen or a functionally active fragment thereof.

15. The rodent according to any one of claims 1-11, wherein the first nucleotide sequence encodes both an SV40 large T antigen or a functional active fragment thereof and also an SV40 small t antigen or a functional active fragment thereof.

16. The rodent according to any one of claims 1-11, wherein the first nucleotide sequence comprises the sequence as set forth in SEQ ID NO: 1.

17. The rodent according to any one of claims 1-16, wherein the nucleic acid further comprises a second nucleotide sequence encoding a reporter.

18. The rodent of claim 17, wherein the reporter is a luciferase.

19. The rodent according to claim 17 or 18, wherein the first nucleotide sequence is linked to the second nucleotide sequence in frame via a third nucleotide sequence encoding a 2A peptide.

20. The rodent of claim 19, wherein the 2A peptide is selected from the group consisting of an F2A peptide comprising the amino acid sequence of SEQ ID NO: 10, an

E2A peptide comprising the amino acid sequence of SEQ ID NO: 11, a P2A peptide comprising the amino acid sequence of SEQ ID NO: 12, and a T2A peptide comprising the amino acid sequence of SEQ ID NO: 13.

21. The rodent of claim 19, wherein the 2A peptide is a T2A peptide comprising the amino acid sequence of SEQ ID NO: 13.

22. The rodent according to any one of claims 1-21, wherein the nucleic acid further comprises a fourth nucleotide sequence encoding a selectable marker operably linked to a promoter active in the rodent cell.

23. The rodent according to any one of claims 1-22, wherein the transgene is integrated at an ectopic locus in the genome.

24. The rodent of claim 23, wherein at least one to ten copies of the transgene are integrated in tandem at the ectopic locus.

25. The rodent according to any one of claims 1-24, wherein the rodent is a mouse or a rat.

26. The rodent of claim 1-24, wherein the rodent is a mouse.

27. The rodent of claim 26, wherein the mouse is of a strain selected from the group consisting of a C57BL/6 strain, a 129 strain, or a hybrid thereof.

28. The rodent of claim 27, wherein the mouse is of an F1H4 strain.

29. The rodent according to any one of claims 1-28, wherein the oncogenic protein is expressed specifically in the prostate.

30. The rodent of claim 29, wherein the oncogenic protein is expressed in the dorsolateral lobes, the anterior lobes, or the dorsolateral and anterior lobes of the prostate.

31. The rodent according to any one of claims 1-30, wherein the rodent is characterized by at least one phenotype selected from the group consisting of (i) the rodent begins to display prostate intraepithelial neoplasia (PIN) in the prostate tissue after at least about 2 months of age; (ii) the rodent displays PIN in the dorsolateral lobes, or the

dorsolateral and anterior lobes of the prostate; (iii) the rodent displays PIN substantially in the dorsolateral lobes, the anterior lobes, or both the dorsolateral and anterior lobes of the prostate, but substantially not in the ventral lobes of the prostate; (iv) the rodent begins to display adenocarcinoma after at least about 6 months of age; (v) the rodent displays adenocarcinoma in the dorsolateral lobes, the anterior lobes, or both the dorsolateral and anterior lobes of the prostate; (vi) the rodent displays adenocarcinoma substantially in the dorsolateral lobes, the anterior lobes, or both the dorsolateral and anterior lobes of the prostate, but substantially not in the ventral lobes of the prostate.

32. The rodent of claim 31, wherein the rodent begins to display PIN at about 4-6 months of age.

33. The rodent of claim 31, wherein the rodent begins to display adenocarcinoma at about 7-9 months of age.

34. The rodent of claim 31 or 33, wherein the adenocarcinoma is not neuroendocrine carcinoma.

35. The rodent of claim 1, wherein displays adenocarcinoma in the prostate and wherein the adenocarcinoma is not neuroendocrine carcinoma.

36. The rodent of claim 31, wherein the rodent begins to display PIN at about 4-6 months of age in the dorsolateral and/or anterior lobes of the prostate, and begins to display adenocarcinoma at about 7-9 months of age in the dorsolateral and/or anterior lobes of the prostate.

37. An isolated cell or tissue of the rodent according to any one of claims 1-36.

38. A rodent embryonic stem (ES) cell comprising a transgene in the genome, wherein the transgene comprises:

(a) a 5' regulatory region of a mouse probasin gene,

(b) a nucleic acid comprising a first nucleotide sequence encoding an oncogenic protein, and

(c) a 3' regulatory region of a mouse probasin gene,

wherein the 5' regulatory region, the nucleic acid, and the 3' regulatory region are operably linked to each other.

39. The rodent ES cell of claim 38, wherein the rodent ES cell is a mouse ES cell or a rat ES cell.

40. The rodent ES cell of claim 38, wherein the oncogenic protein comprises an SV40 tumor antigen or Myc.

41. A method of making a rodent model of prostate cancer, comprising

(a) introducing into a rodent ES cell a transgene that comprises:

(i) a 5' regulatory region of a mouse probasin gene,

(ii) a nucleic acid comprising a first nucleotide sequence which codes for an oncogenic protein, and

(iii) a 3' regulatory region of the mouse probasin gene,

wherein the 5' regulatory region, the nucleic acid, and the 3' regulatory region are operably linked;

(b) selecting a modified rodent ES cell comprising the transgene in the genome;

(c) introducing the modified rodent ES cell into a host embryo of the rodent at a premorula stage;

(d) implanting the host embryo into a surrogate mother; and,

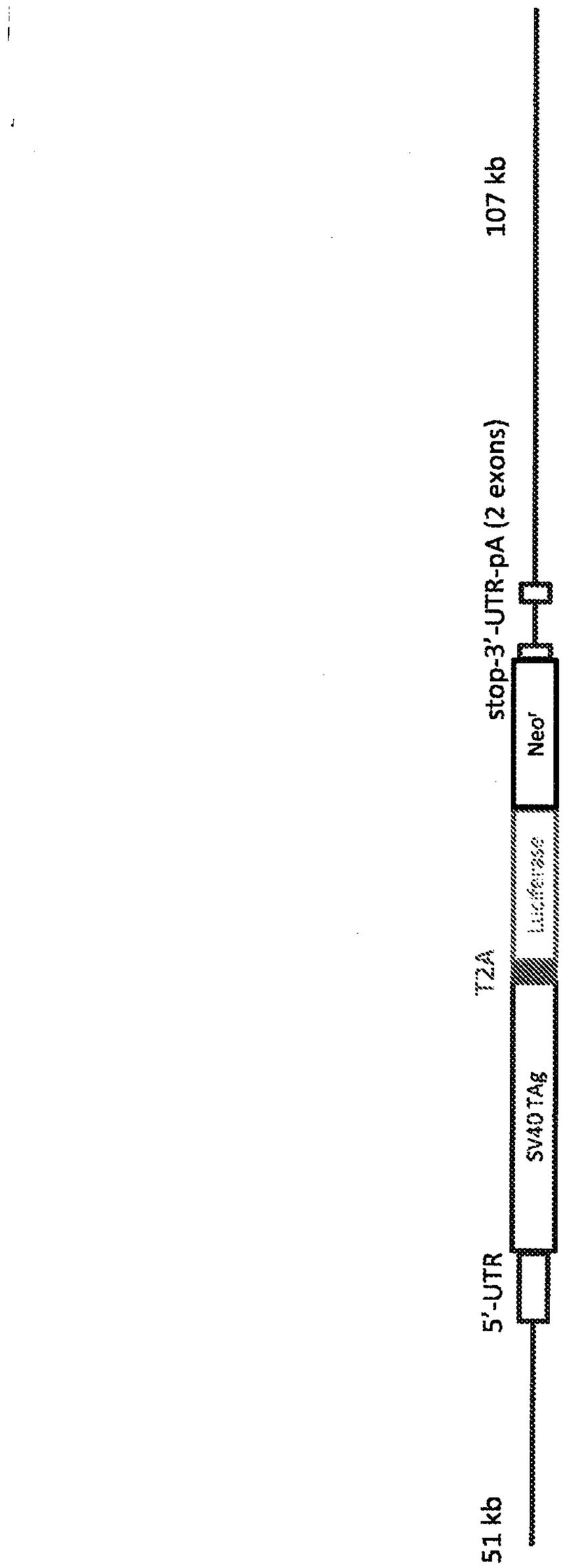
(e) obtaining the rodent model of prostate cancer.

42. The method of claim 41, wherein the transgene is integrated into an ectopic locus.

43. The method of claim 41, wherein the rodent is a mouse or a rat.

44. The method of claim 41, wherein the oncogenic protein comprises an SV40 tumor antigen or Myc.

45. The method of claim 41, wherein the oncogenic protein is specifically expressed in the prostate of the rodent.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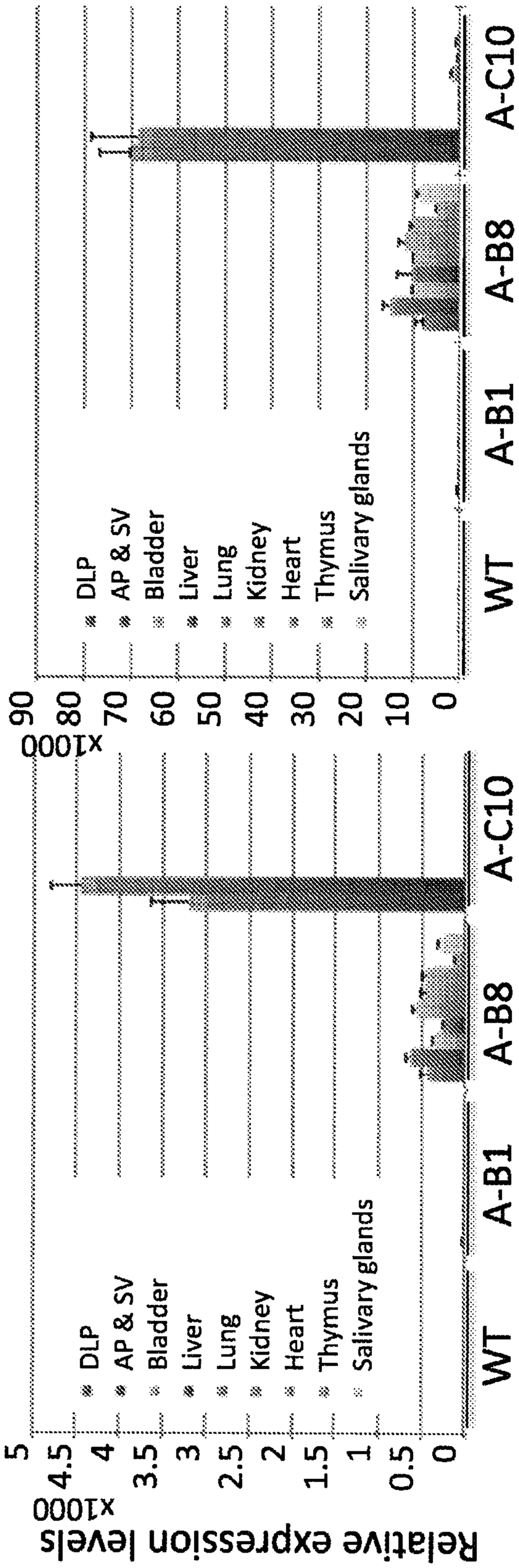
Neo^r
T2A
Luciferase
SV40 TAg
5'-UTR
51 kb

Figure 1


Luc2
90
80
70
60
50
40
30
20
10
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DLP
AP & SV
Bladder
Liver
Lung
Kidney
Heart
Thymus
Salivary glands
WT
A-B1
A-B8
A-C10
SV40 TAg
x1000
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4
3.5
3
2.5
2
1.5
1
0.5
0
Relative expression levels

Figure 2

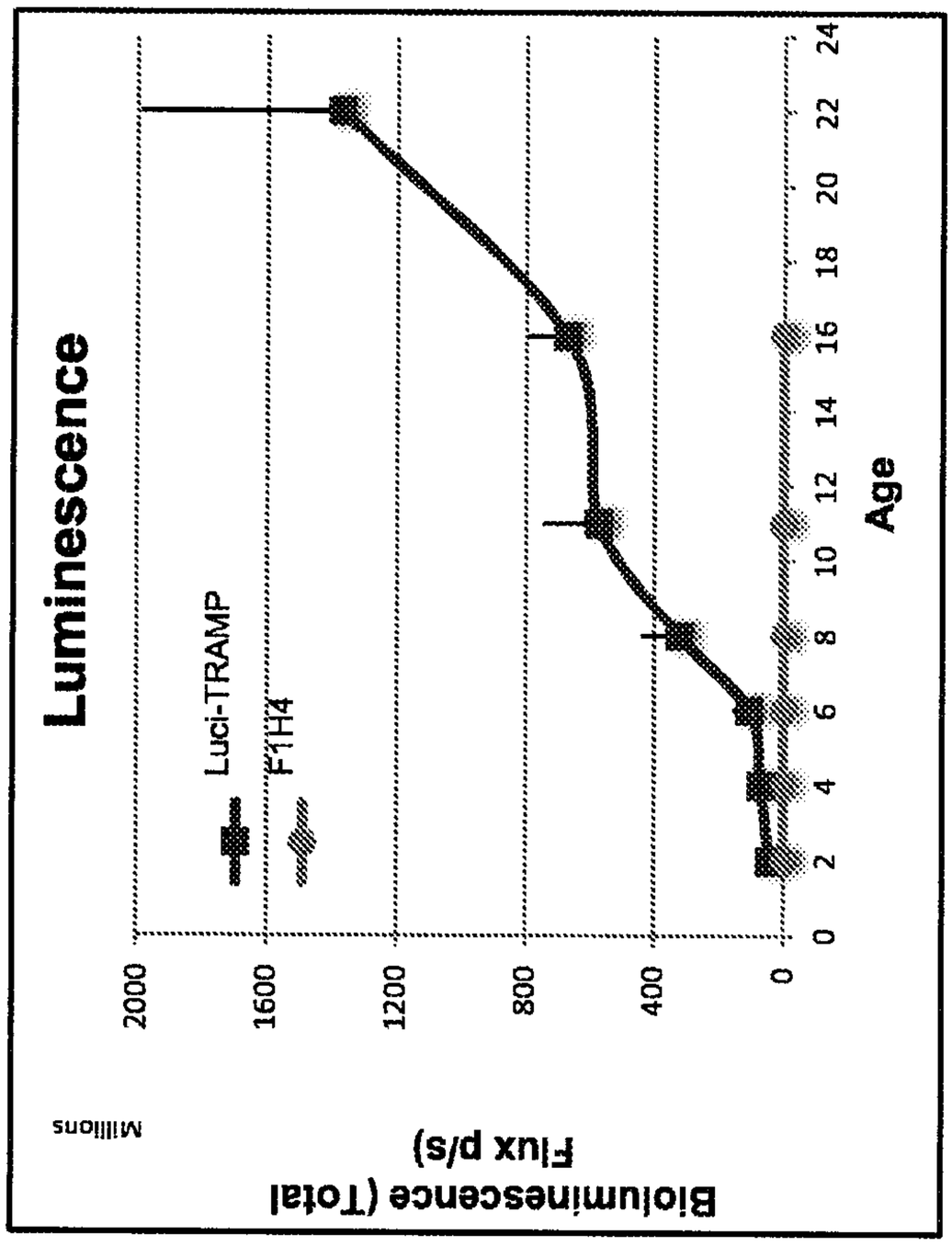
Luminescence
Luci-TRAMP
F1H4
Bioluminescence (Total Flux p/s)
Millions
2000
1600
1200
800
400
0
0
2
4
6
8
10
12
14
16
18
20
22
24
Age

Figure 3A

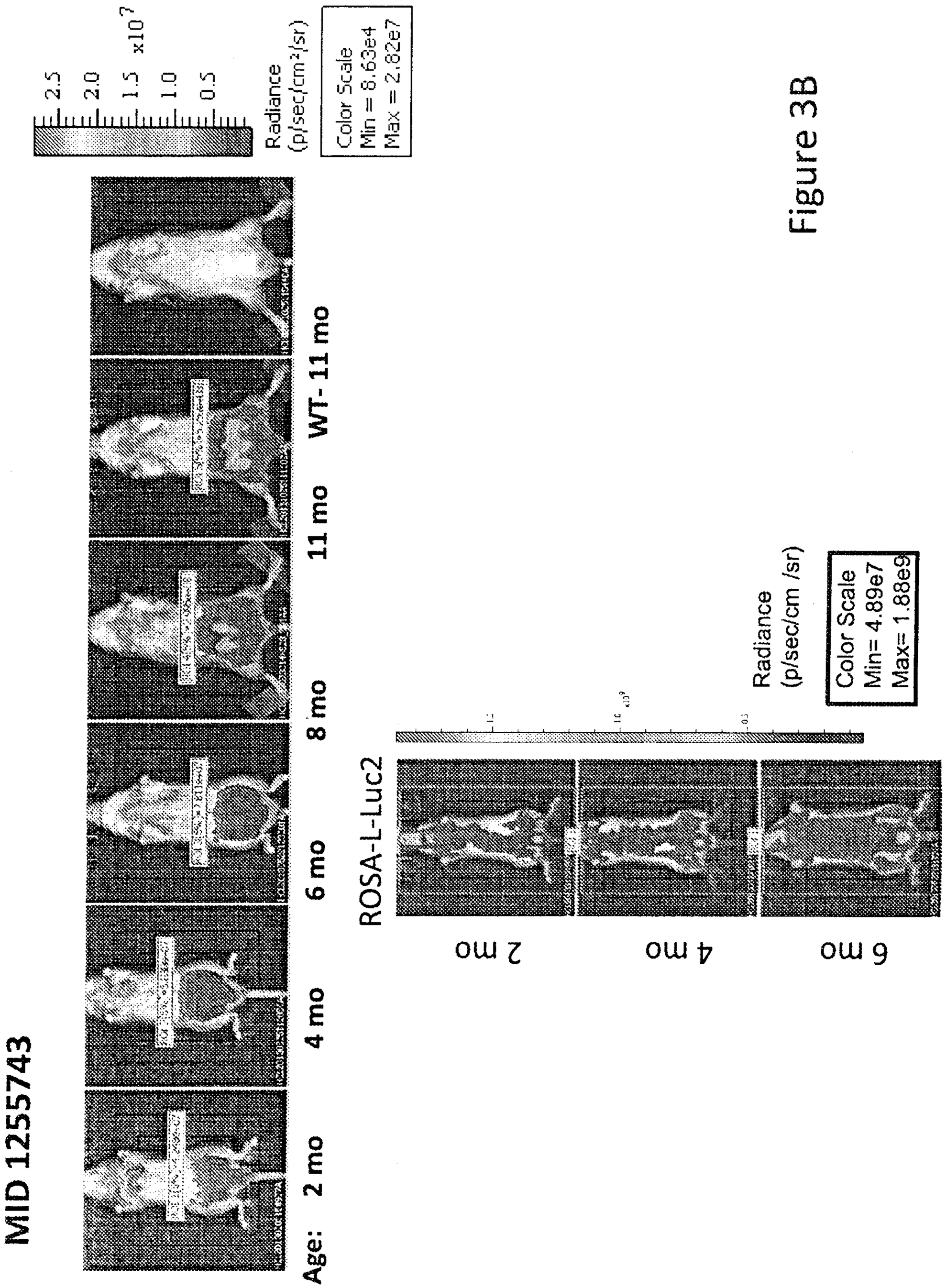

Figure 3B

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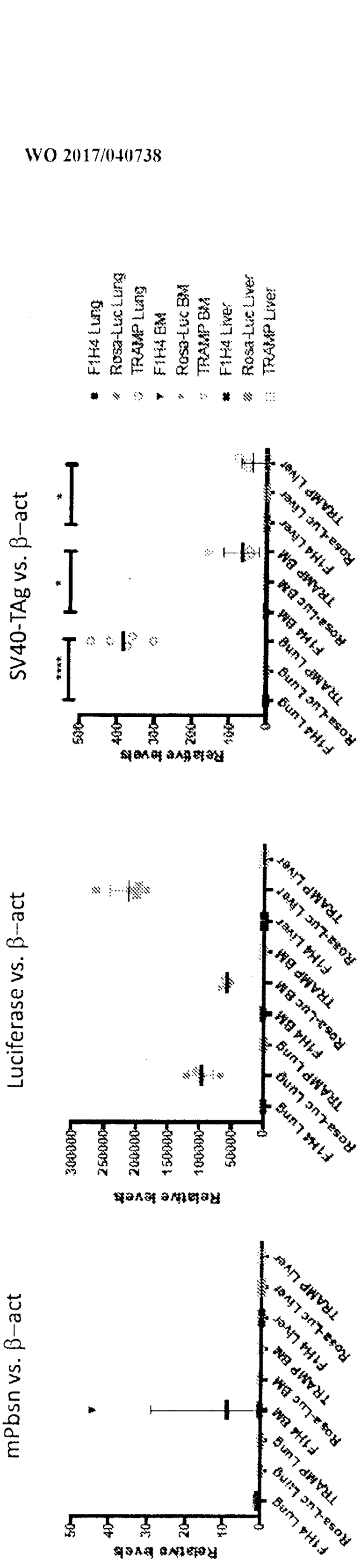

Figure 3C

CA 02995248 2018-02-08

Figure 4A

Representative prostate pathology in dorsal lateral lobes of Luci-TRAMP mice

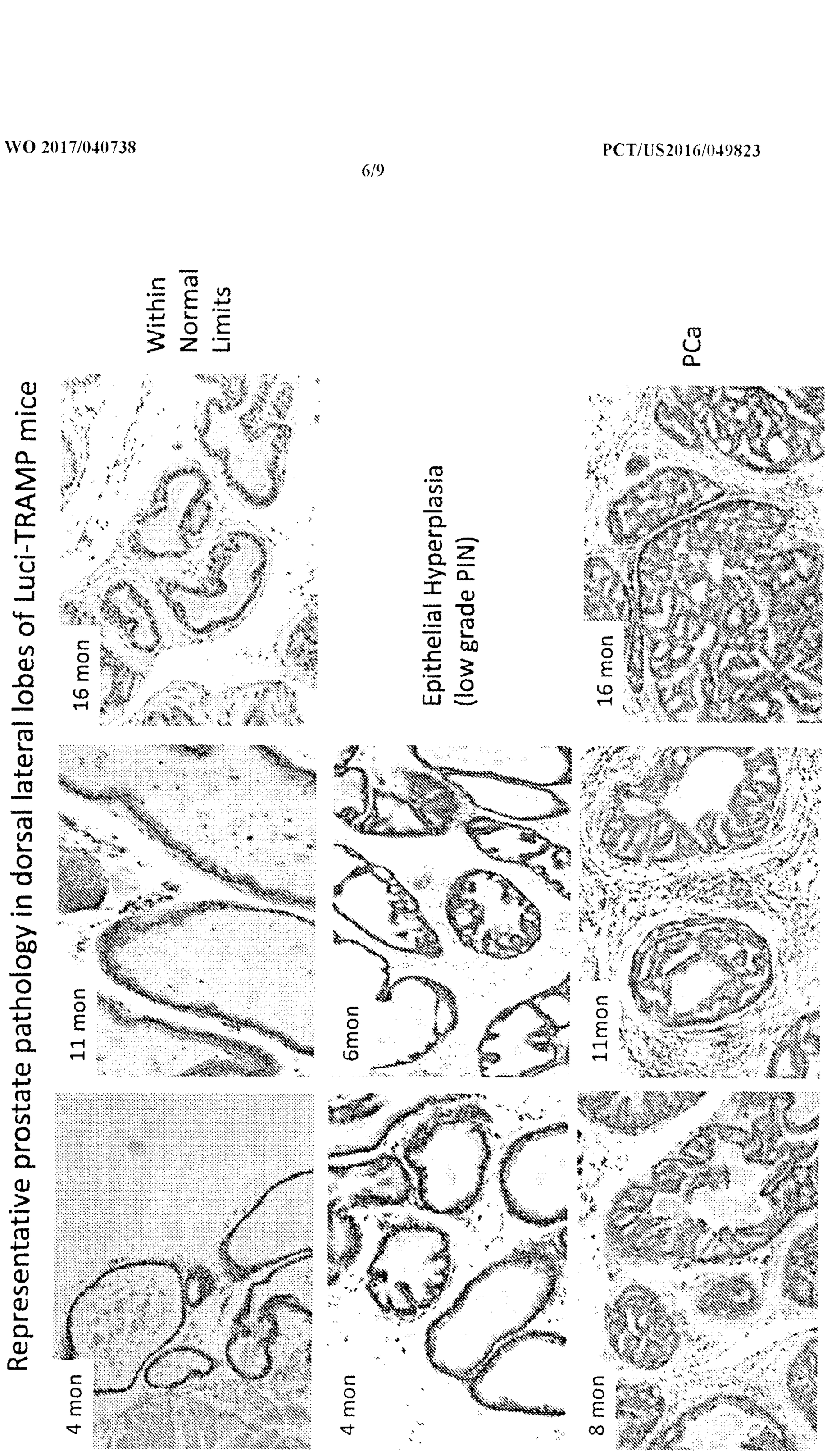

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Figure 4B

Prostate pathology in anterior lobes of Luci-TRAMP mice

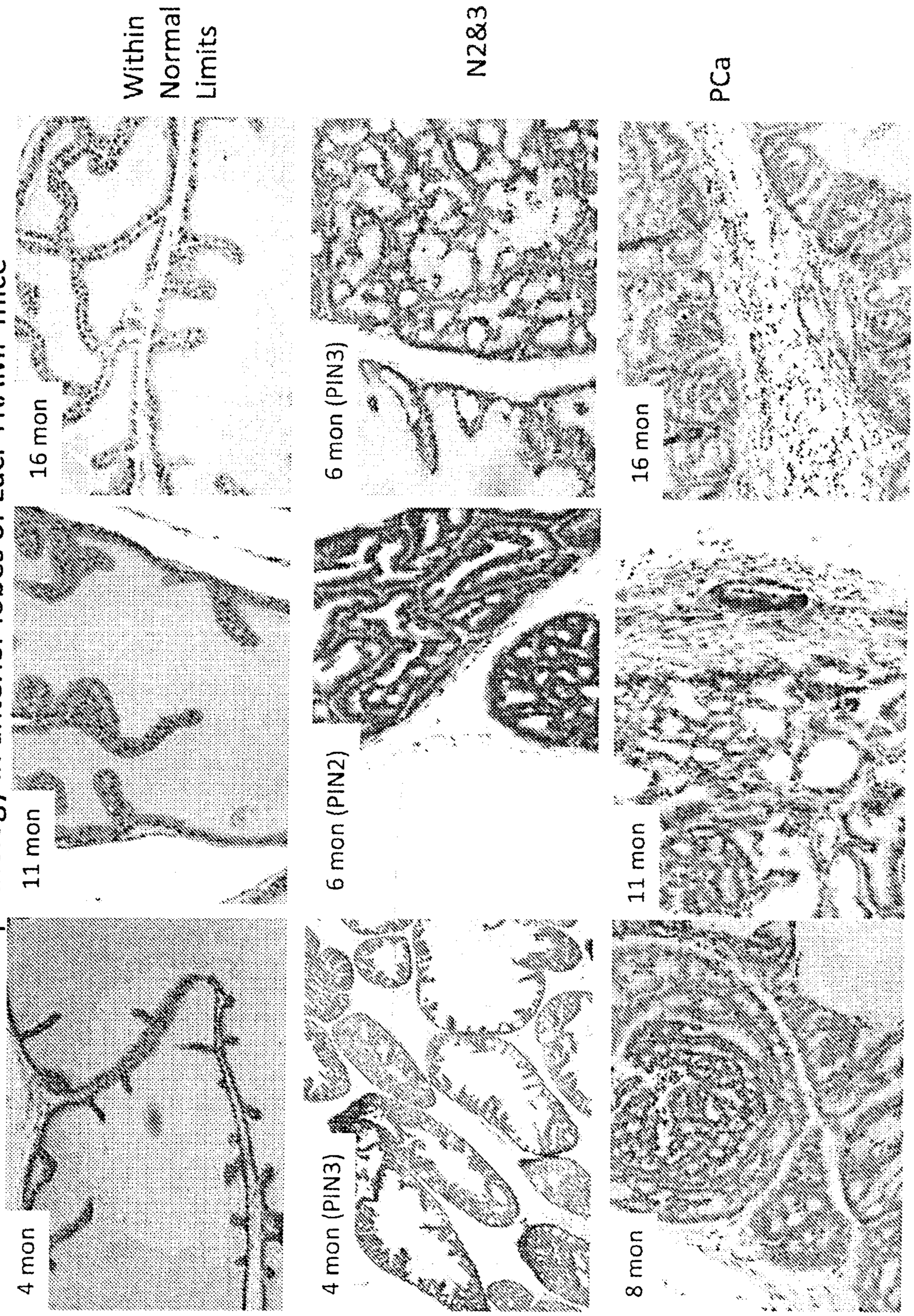

Figure 5A

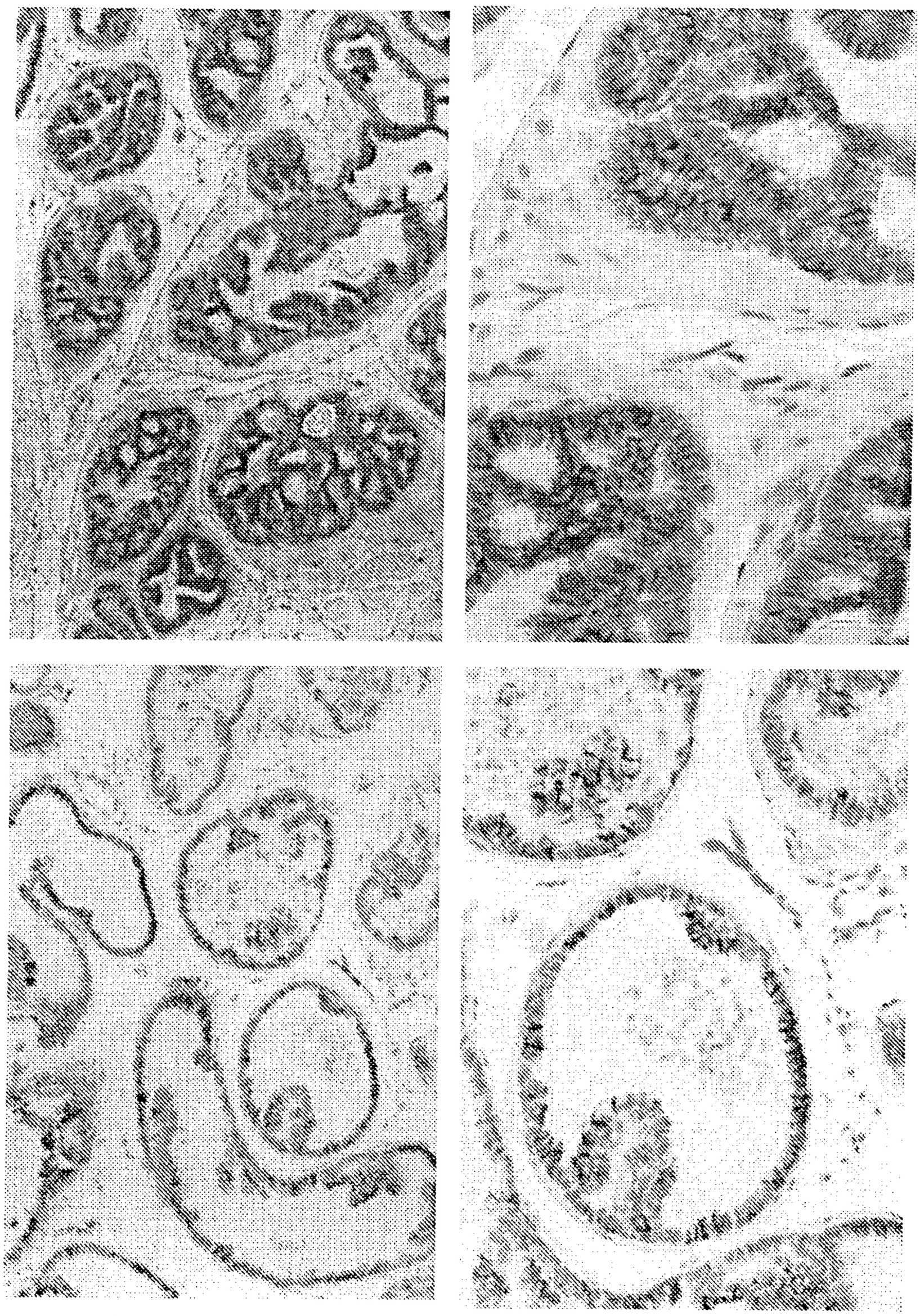

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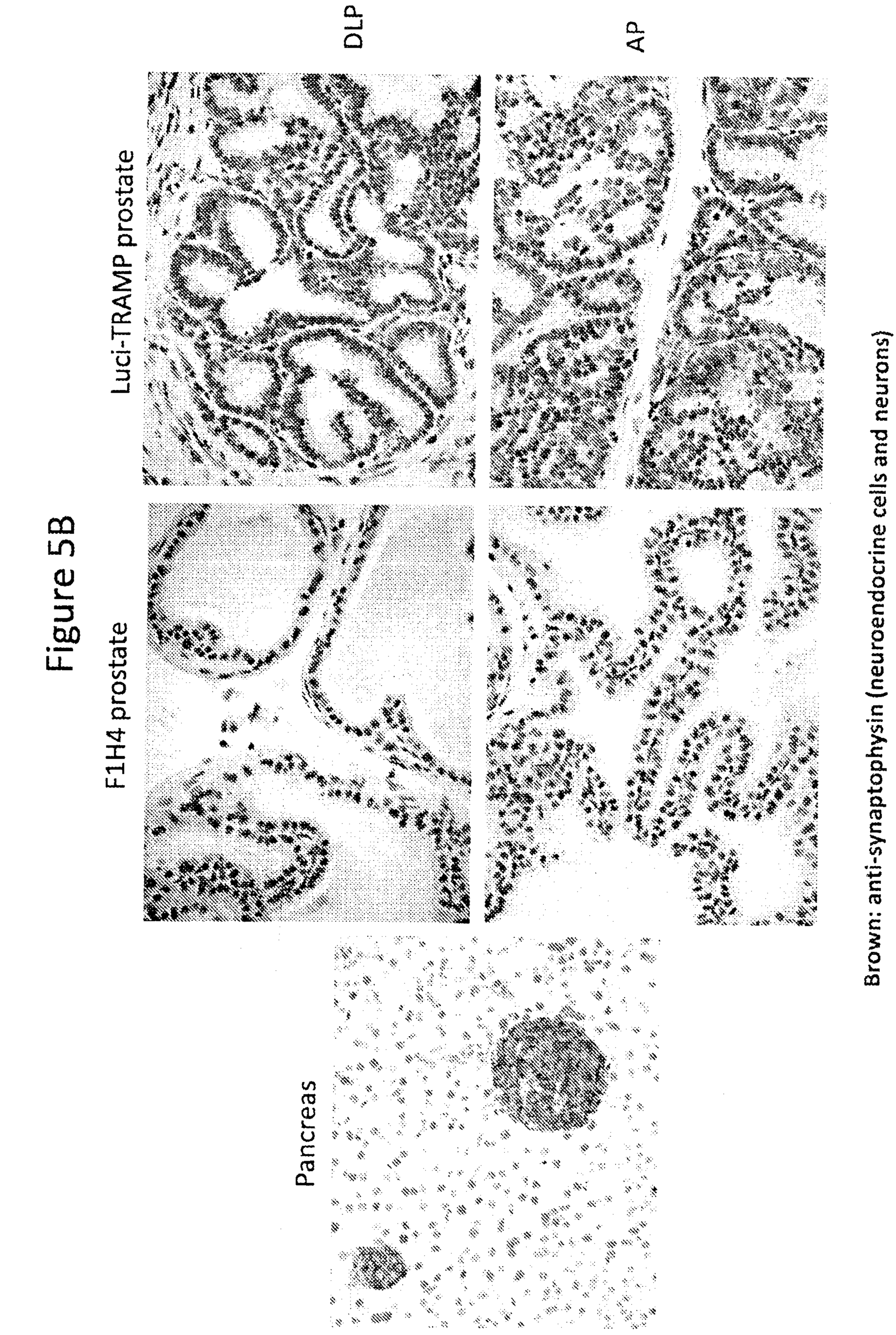
Figure 5B



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