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(54) Titre : SOURIS KNOCKOUT CONDITIONNELLE ABI1/HSSH3BP1
(54) Title: ABI1/HSSH3BP1 CONDITIONAL KNOCKOUT MOUSE

(57) **Abrégé/Abstract:**

Genetically engineered conditional knock-out mice having conditional disruption of the Abi1/Hssh3bp1 gene are disclosed along with methods of making and using same.



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ABI1/HSSH3BP1 CONDITIONAL KNOCKOUT MOUSE**CROSS-REFERENCE TO RELATED APPLICATIONS**

[0001] The present application claims the benefit under 35 USC §119(e) to United States Provisional Patent Application 61/048,130 filed April 25, 2008, the entire contents of which are incorporated by reference herein.

FIELD OF THE INVENTION

[0002] The present disclosure relates to genetically engineered conditional knock-out mice having a conditional deletion in the Abi1/Hssh3bp1 gene and related methods.

BACKGROUND OF THE INVENTION

[0003] One of the common mechanisms in tumor formation is inactivation of one or more so-called tumor suppressor genes. Tumor suppressor genes (also known as “tumor-preventative” or “anti-tumor” genes) play an important role in the regulation of many basic cellular processes such as cell growth, division and proliferation, cell differentiation, and in communication of cells with other cells and with the extracellular environment. Inactivation of a tumor suppressor gene usually has devastating consequences on the regulation of cell growth within a specific tissues and usually results in tumor growth.

[0004] The selective growth advantage of tumor cells is often achieved by functional imbalance of opposing functions of tumor suppressors and oncogenes. Increased function of oncogenes such as growth factor receptors (such as epidermal growth factor receptor [EGFR] and platelet derived growth factor receptor [PDGFR]), or signaling molecule molecules (such as PI-3 kinase, Ras or Myc) promote proliferative potential of cells. When this is combined with decreased function of tumor suppressors and stabilized by inactivating mutations, cells may run out of protective responses such as apoptosis or senescence to balance the problem. Additional genomic instabilities including genetic events such as chromosomal translocations often stabilize effects of mutations subsequently leading to further amplification of anti-apoptotic, anti-senescence, and pro-proliferative signals.

[0005] The recently discovered TMPRSS2-ETS gene family chromosomal translocations and genetic alterations of tumor suppressor genes are the most common causes of neoplastic transformation leading to prostate tumorigenesis. Known prostate cancer tumor suppressor genes include Pten, p53, Rb, Nkx3.1, KLF6, and p27. However, it is clear that additional tumor suppressor genes are inactivated in primary prostate adenocarcinoma. According to the multi-hit/multi-gene hypothesis, several genes that control critical growth/survival/apoptotic pathways must be altered to lead to fully penetrant prostate cancer. For example, in mice, the loss of Pten must be accompanied by loss of p53 for progression from noninvasive to highly invasive tumors. Similar relationships have been found in other Pten double knockout models, which the second knockout gene is Nkx3.1 or p27.

[0006] A recently identified prostate cancer tumor suppressor gene is Hssh3bp1 which inhibits growth of prostate tumor cells in laboratory culture conditions. Expression of the Hssh3bp1 gene product, which is a protein, is lost in some patients with prostate tumors. Additionally Hssh3bp1 regulates the function of Abi1 kinase, which is implicated in malignant processes in leukemia. Inactivating mutations of Abi1/Hssh3bp1 have been found in primary tumors.

[0007] The successful development of novel therapies for cancer requires animal models which incorporate the unique anatomical and physiology characteristics of the target organ or tissue and appropriate stromal-tumor interactions and appropriate immunological responses. Genetically engineered mice provide these aspects. Tissue-specific developmental (through the use of developmentally regulated tissue-specific promoters driving Cre recombinase expression) or conditional (through the use of tamoxifen-responsive promoters driving Cre retroviral vectors) disruptions or overexpression of targeted genes resembles closely the mutation-driven inactivation of human tumor suppressors or activation of oncogenes, respectively, *in situ*. This allows evaluation of the process of tumorigenesis from early time points of gene inactivation, through early histopathological changes, and subsequently through tumor growth and metastases if such occur. The possibility of evaluation of different levels of tumor suppressor inactivation (through one- or two-allele knockouts, or

production of hypomorphic, as well as knock-in mutant strains) allows understanding of both cell signaling pathways as well as production of specific preclinical models.

SUMMARY OF THE INVENTION

[0008] The present disclosure encompasses genetically engineered mice having conditional disruption (knock-out) of the *Abi1/Hssh3bp1* gene.

[0009] A transgenic knock-out mouse whose genome is heterozygous for an engineered conditional disruption in the *Abi1/Hssh3bp1* gene, wherein said engineered conditional disruption in a homozygous state inhibits production of a functional *Abi1/Hssh3bp1* protein.

[0010] In one embodiment, a conditional knock-out mouse is provided whose somatic and germ cells comprise a conditionally disrupted *Abi1/Hssh3bp1* gene, wherein the disruption results in an inability of the mouse to produce detectable levels of the *Abi1/Hssh3bp1* protein.

[0011] In another embodiment, the conditional disruption is induced by breeding the mouse with a mouse expressing flippase or Cre recombinase. In another embodiment, the conditional knock-out mouse comprises a recombinant *Abi1/Hssh3bp1* allele containing a neomycin gene, frt sites and loxP sites flanking at least a portion of the *Abi1/Hssh3bp1* gene.

[0012] In another embodiment, the at least a portion of the *Abi1/Hssh3bp1* gene is exon 1 of the *Abi1/Hssh3bp1* gene. In yet another embodiment, the conditional disruption occurs in exon 1 of the *Abi1/Hssh3bp1* gene.

[0013] In another embodiment of the conditional knock-out mouse, the *Abi1/Hssh3bp1* gene is not expressed in all the mouse's tissues. In yet another embodiment, the *Abi1/Hssh3bp1* gene is not expressed in only a portion of the mouse's tissues, such as in the mouse's prostate tissue.

[0014] In another embodiment of the conditional knock-out mouse, the mouse exhibits at least one phenotype selected from the group consisting of disruption of cell motility, increased directional persistence, decreased migration distance, and decreased migration rate.

[0015] In one embodiment, a cell isolated from the disclosed conditional knock-out mouse is provided. In another embodiment, the cell is from the mouse's prostate tissue.

[0016] In one embodiment, a *Abi1/Hssh3bp1* gene conditional knock-out construct is provided comprising a portion of an *Abi1/Hssh3bp1* gene, wherein exon 1 of the *Abi1/Hssh3bp1* gene is flanked by a 5' loxP site and a 3' selectable marker cassette, wherein the selectable marker cassette comprises a selectable marker flanked by frt sites and loxP sites 3' to the 3' frt site and 3' to the 5' frt site. In another embodiment, the *Abi1/Hssh3bp1* gene conditional knock-out has the sequence of SEQ ID NO:14.

[0017] In one embodiment, a method is provided for producing a mouse with a targeted conditional disruption in an *Abi1/Hssh3bp1* gene, comprising the steps of transfecting the disclosed knockout gene construct into a population of murine embryonic stem (ES) cells; selecting a transfected ES cell which expresses the selectable marker; introducing the transfected ES cell into an embryo of an ancestor of the mouse; allowing the embryo to develop to term to produce a chimeric mouse with a conditional knock-out construct in its germ line; breeding the chimeric mouse to produce a heterozygous mouse with a conditionally disruptable *Abi1/Hssh3bp1* gene; and breeding the heterozygous mouse with a mouse expressing flippase or Cre recombinase to produce a mouse with a disruption in the *Abi1/Hssh3bp1* gene and does not contain the selectable marker.

BRIEF DESCRIPTION OF THE DRAWINGS

[0018] FIG. 1 depicts construction of the *Abi1/Hssh3bp1* conditional knock-out (CKO) mouse. FIG. 1A depicts one embodiment of a knock-out construct. FIG. 1B depicts the cloning strategy for generation of the *Abi1/Hssh3bp1* mouse. Approximately 11.8kb region used to construct the targeting vector was first subcloned from a positively identified BAC clone. The region was designed such that the short homology arm (SA) extends 1.9kb 3' to exon 1. The long homology arm (LA) ends on the 5' side of exon 1 and was approximately 9kb long. The single loxP site was inserted 5' to exon 1, and the loxP-flanked neomycin gene cassette was inserted 3' to exon 1. The neomycin gene cassette was bound by two frt sites, with one loxP site 3' to the 5' frt site. The target region was 0.9kb and included exon 1.

Locations of primers used for confirmation of the locations of loxP sites and for subsequent genotyping are indicated: a, mAbi1loxP35' (SEQ ID NO:3); b, DL75' (SEQ ID NO:7); c, mAbi1Intr15' (SEQ ID NO:15); d, LAN1 (SEQ ID NO:1); e, Neogene13' (SEQ ID NO:16); f, Flankneo13' (SEQ ID NO:4); g, A2 (SEQ ID NO:2); h, WT1 (SEQ ID NO:17); and i, SG1 (SEQ ID NO:18). The "h" and "i" primer set (arrows) are specific for the wild type Abi1/Hssh3bp1 gene sequence only.

[0019] FIG. 2 depicts sequences of exemplary genes and alleles disclosed herein. FIG. 2A depicts the DNA sequence of the Abi1 floxed allele sequence after removal of the neomycin gene with both 5' loxP (underlined) and 3' loxP (double underlined) sites and exon 1 (bold underline, coding strand). The forward sequencing primer DL75' (bold and underline, SEQ ID NO:7) and the reverse sequencing primer Flankneo13' (bold, underline and italic, SEQ ID NO:4) are indicated. Bases in lower case represent DNA sequence of the neomycin cassette remaining after flippase-mediated neomycin gene removal. FIG. 2B depicts the DNA sequence of the ABL-1 full-length conditional allele with all recombinant elements and including the neomycin gene. The long homology arm is indicated in bold, Exon 1 is highlighted, the short homology arm is underlined, the single loxP site is indicated in double underline and the loxP/FRT sites flanking the neo cassette are indicated in bold underline. FIG. 2C depicts the DNA sequence of the Abi1/Hssh3bp1 KO allele resulting from Cre recombinase-mediated recombination. As a result of the recombination exon 1 is deleted and it contains only one loxP site (underlined). The forward sequencing primer DL75' and the reverse sequencing primer Flankneo13' are indicated (bold and underline). Only the coding strand is presented in FIG. 2C.

[0020] FIG. 3 depicts genotyping of the F1 Abi1/Hssh3bp1 heterozygous strain by polymerase chain reaction (PCR) with primers LAN1 (5'-CCAGAGGCCACTTGTGTAGC-3'; SEQ ID NO:1) and A2 (5'-CTGGAAGCTGACAAGAGGATAG-3'; SEQ ID NO:2) for the neomycin gene cassette (Neo⁺/frt⁺/loxP⁺), with primers mAbi1loxP35' (5'-AATAATTTAATAGTTCTGGTGATAT GACAGC-3'; SEQ ID NO:3) and Flankneo13' (5'-GGGCAGACGGCGAGAAGCAGAG-3'; SEQ ID NO:4) for the wild type allele (Wt)

(upper panel, lower band) or the floxed *Abi1/Hssh3bp1* allele, which is lacking the neomycin gene and the 3' frt site ($\text{Neo}^-/\text{frt}^-/\text{loxP}^+$) (upper panel, upper band).

[0021] FIG. 4 depicts the *Abi1/Hssh3bp1* gene disruptions in primary mouse embryonic fibroblasts isolated from *Abi1/Hssh3bp1*^{loxP/+} (FIG. 4A) and *Abi1/Hssh3bp1*^{loxP/loxP} (*Abi1/Hssh3bp1*[fl/fl]; FIG. 4B) mice.

[0022] FIG. 5 depicts PCR-based genotyping to identify MEF cells homozygous for the recombinant *Abi1* floxed allele. FIG. 5A depicts the genotyping controls for MEF cell screening. Genomic DNA obtained from the frt deleter strain and expressing only wild type alleles (lower band), and heterozygous *Abi1/Hssh3bp1* (fl/+) animals expressing wild type (lower band) and *Abi1/Hssh3bp1* floxed alleles (upper band), were subjected to PCR genotyping. FIG. 5B depicts screening of MEF cells. MEF cell DNA samples (#1-34) were isolated from mouse embryos that resulted from breeding of heterozygous *Abi1/Hssh3bp1* (fl/+) animals. Upper band, floxed *Abi1/Hssh3bp1* allele (Floxed); Lower band, wild type allele (Wt). Genotyping was performed using primers m*Abi1loxP35'* and Flankneo13'.

[0023] FIG. 6 depicts Cre recombinase-mediated loss of *Abi1/Hssh3bp1* protein expression in MEF#3 cell line subclones. Western blot analysis of *Abi1/Hssh3bp1* expression in parental MEF#3 *Abi1*(fl/fl) and in exon 1 deleted *Abi1*(-/-) MEF cell lines is depicted in the lower panel. Cell lysates of the indicated cell lines were blotted with antibody 7B6 (specific for *Abi1/Hssh3bp1*). Clones #3-1 through #3-11 represent subclones of the parental MEF#3 obtained following transient Cre recombinase expression. *Abi1* (+/+) MEF Wt represents mouse embryonic cells expressing the wild type *Abi1/Hssh3bp1* gene. Loading control represents part of a protein-stained gel of the same samples as used for Western blotting analysis in the upper panel.

[0024] FIG. 7 depicts the localization of *Abi1/Hssh3bp1* in control and deficient MEF cells after platelet derived growth factor (PDGF)-stimulation. Control (#3) and *Abi1/Hssh3bp1*-KO (#3-11) cell lines were grown on glass-coverslips, starved and treated with PDGF, and immunostained with antibodies and phalloidin. Anti-*Abi1/2* antibody (W8.3) or anti *Abi1* (4E2) antibody were used.

[0025] FIG. 8 depicts the quantification of peripheral (FIG. 8A) and dorsal (FIG. 8B) ruffling. MEF control (fl/fl) and *Abi1/Hssh3bp1* KO were plated on glass

coverslips and serum-starved overnight. Cells were stimulated with PDGF, fixed and stained with Alexa Fluor 594 conjugated phalloidin to detect F-actin. The percentages of cells with different cell morphologies in response to PDGF treatment were quantified in the indicated MEF cell lines. Dorsal circular and peripheral PDGF-induced ruffles were independently evaluated. The following categories of morphologies of PDGF response were scored: with ruffles, without ruffles, or with ambiguous cell morphology. At least 100 cells were analyzed and categorized for each condition. Columns are percentage of cells with respective morphology displayed as means $\pm$ SEMs of at least three independent experiments. #3 control, indicates parental MEF#3 cell line; #3-6 KO, #3-8 KO, and #3-11 KO, indicate MEF#3 subclones lacking Abi1/Hssh3bp1 expression; #8 indicates parental MEF cell line; #8-7, #8-11, indicate MEF #8 subclones.

[0026] FIG. 9 depicts PDGF-induced Rac activation. The indicated parental Abi1/Hssh3bp1(fl/fl) and Abi1/Hssh3bp1 KO (-/-) cell lines were analyzed in the assay.

[0027] FIG. 10 depicts the evaluation of cell motility of mouse embryonic fibroblasts lacking Abi1/Hssh3bp1. The parameters of random cell motility, migration distance (FIG. 10A), rate (FIG. 10B), and directional persistence (FIG. 10C) were evaluated in Abi1/Hssh3bp1 null cell lines (clones #3-6 and #3-11) and Abi1 floxed cells (control #3, (fl/fl)) cells.

[0028] FIG. 11 depicts data from the wound-healing migration assay. The rate of wound closure was determined by measuring the area not covered by cells per unit of time. Data represent means $\pm$ SD of four independent assays of Abi1/Hssh3bp1 KO cell lines (#3-6 and #3-11) as compared with control #3 (fl/fl) MEF cells (FIG. 11A). FIG. 11B depicts representative micrographs from live cell observations.

[0029] FIG. 12 depicts the evaluation of Wave complex in Abi1/Hssh3bp1 KO cells. Western blot analysis of MEF cell lysates of Abi1/Hssh3bp1 KO cell lines. WAVE 2, Nap1, and Sra-1 protein levels were evaluated with specific antibodies in total cellular lysates obtained from 2 clones (#3-6 and #3-11) lacking Abi1/Hssh3bp1 expression and from the parental line MEF#3.

[0030] FIG. 13 depicts the activity of mitochondrial dehydrogenase in Abi1^{-/-} and Abi1^{+/+} MEF cells (**p<0.01).

[0031] FIG. 14 depicts the prostate-specific disruption of the *Abi1/Hssh3bp1* gene. Animals (males only) resulting from breeding of the probasin promoter driven Cre recombinase expressing strain [B6.D2-Tg(Pbsn-Cre)4Prb] with the *Abi1/Hssh3bp1* floxed (fl/fl) strain were genotyped for expression of the floxed *Abi1/Hssh3bp1* allele and Cre recombinase expression. Prostate tissue (anterior prostate and posterior prostate) from animals expressing Cre recombinase demonstrated exon 1 deletion (Deleted) in contrast to animals negative for expression of Cre (Floxed). Primary MEF (RARA1, RARA3 and RARA 7), parental MEF #8 (*Abi1* (fl/fl)) and its subcloned cell lines #8-7 and #8-11 and parental MEF#3 and its subcloned lines #3-6, #3-8 and #3-11 were also genotyped.

[0032] FIG. 15 depicts staining of normal (FIGs. 15A and 15C) and malignant (FIGs. 15B and 15D) prostate tissues from cases 398 (FIGs. 15A and 15B) and 400 (FIGs. 15C and 15D) with mAb 2G8 antibody to *Hssh3bp1*. Staining is intense in both normal tissues shown (FIGs. 15A and 15C) and in tumor tissue from case 400 (FIG. 15D), which was not deleted for 10p loci. Note the complete absence of staining in the malignant tissue from case 398 (FIG. 15B), which also demonstrated deletion of sequences adjacent to the *Hssh3bp1* locus on 10p. The large panels are shown at x100 magnification; insets are at x400 magnification.

[0033] FIG. 16 depicts protein truncation test of *Hssh3bp1* in prostate tumor cell lines by *in vitro* translation of *Hssh3bp1* cDNA using rabbit reticulocyte lysate. Reaction mixtures following *in vitro* translation of PCR products were separated on 7% Tricine SDS polyacrylamide gel; the gel was blotted with the polyclonal antibody Ab-2 to *Hssh3bp1*. Lane 1, reaction mixture without addition of exogenous DNA; lane 2, reaction mixture containing *Hssh3bp1* cDNA from LNCaP; lane 3, reaction mixture containing *Hssh3bp1* cDNA from PC3. Apparently the rabbit reticulocyte lysate contains an Ab-2 antibody reactive band (lane 1). Arrows indicate the full-length *Hssh3bp1* polypeptides representing isoforms 2 and 3 of *Hssh3bp1* as confirmed by PCR analysis (not shown). Asterisk indicates a truncated polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

[0034] The present disclosure encompasses genetically engineered mice having a conditional disruption of the *Abi1/Hssh3bp1* gene and mice lacking expression of *Abi1/Hssh3bp1* in at least one tissue. The term “*Hssh3bp1*” refers to a clone of the

spectrin SH3-binding protein 1 (SSH3BP1) gene. The term Abi1 refers to the Abl interactor 1 (Abi-1) protein which serves as a regulator of Abl function in transformation or in signal transduction. Abi-1 and Hssh3bp1 have been determined to be the same protein. Therefore the gene is referred to herein as the Abi1/Hssh3bp1 gene.

[0035] As used herein, the term “floxed” refers to the sandwiching of a DNA sequence between two *lox P* sites.

[0036] As used herein, the phrase “conditional knockout,” or “CKO,” when used to describe a mouse, refers to mice containing the knock-out construct comprising a selectable marker inserted adjacent to exon 1 of the Abi1/Hssh3bp1 gene and wherein the selectable marker is flanked by frt sites. Additionally, there are loxP sites 5' of exon 1 and 3' of the selectable marker 3' frt site. An additional loxP site is 3' to the selectable marker 5' frt site. The conditional knockout mouse retains a functional Abi1/Hssh3bp1 gene. The term “knock-out,” or “KO,” as used herein refers to a mouse, or a tissue within a mouse, in which exon 1 of the Abi1/Hssh3bp1 gene has been disrupted and this mouse, or the specific tissue, does not have a functional Abi1/Hssh3bp1 gene.

[0037] c-Abl tyrosine kinase is expressed in most human tissues and has been implicated in the regulation of cell growth and death. Mutated forms of c-Abl, such as BCR-Abl, have been implicated in some forms of cancer such as, but not limited to, chronic myeloid leukemia and some forms of acute lymphocytic leukemia.

[0038] Abi1/Hssh3bp1 is a physiological inhibitor of Abl kinase. Imatinib mesylate, an inhibitor of c-Abl kinase, is an effective therapeutic agent for chronic myelogenous leukemia and other types of cancer. However, certain patients with CML are resistant to therapy with imatinib mesylate. Therefore, new therapies targeting this enzyme are needed. Abi1/Hssh3bp1-based compounds have the potential to be used for the treatment of prostate cancer. Other types of cancer are likely to involve c-Abl tyrosine kinase or Arg tyrosine kinase (Arg tyrosine kinase is the second member of the Abl family of tyrosine kinases). The Abl family of tyrosine kinases regulate the actin- and microtubule-based cytoskeleton and through the cytoskeleton, regulate basic cellular processes such as cell proliferation, division, endocytosis and differentiation. Defective fidelity of these processes often underlies

tumorigenesis. Arg and Abl tyrosine kinases have highly conserved sequences, particularly in the SH3, SH2 and kinase domains. Thus Abi1/Hssh3bp1 is likely to be the source of inhibitors for multiple members of the Abl tyrosine kinase family.

[0039] Peptides, whose sequences are derived from the Abi1/Hssh3bp1 protein, inhibit c-Abl kinase activity *in vitro* (see US provisional patent application serial number 60/741,208, and subsequent non-provisional US patent application 12/095,728 and PCT patent application PCT/US2006/45570, the disclosures of which are incorporated herein in their entirety). Some of the Abi1/Hssh3bp1 peptides contain a specific phosphotyrosine residue that is phosphorylated by c-Abl kinase. Both phosphotyrosine-containing and non-phosphorylated peptides have inhibitory activity on c-Abl kinase but mechanisms of kinase inhibition by these peptides are different. The mechanism of c-Abl kinase inhibition by phosphopeptides involves binding to the c-Abl SH2 domain, or binding to both Abl SH2 and SH3 domains, depending on the peptide length. The critical role of the Abi1/Hssh3bp1 gene in c-Abl kinase activity is supported by inhibition of cell growth upon expression of Abi1/Hssh3bp1 in cells deficient in the region containing regulatory kinase.

[0040] The conditional knockout mice, and resultant cell lines, described herein are useful for the study the role of the Abi1Hssh3bp1 gene in the formation, progression and behavior of cancer. Furthermore, the CKO and KO mice, and the resultant cell lines, are useful in screening drugs or therapeutic modalities for the treatment of cancers, in a non-limiting example, prostate cancer.

[0041] The creation of a genetically engineered CKO mouse involves inserting specific DNA sequences, such as a knock-out construct, into the mouse DNA. The inserted sequences are recognized by two DNA specific enzymes, frt recombinase (also known as flippase) and Cre recombinase, not normally present in mice. Cre recombinase recognition sites are termed loxP sites and flippase recognition sites are termed frt sites. Each of these enzymes can cut and remove a DNA sequence that is flanked by its recognitions sites. This can lead to disruption of gene function if a functional DNA sequence of the gene of interest is removed. In addition, a selectable marker gene is inserted into the mouse, the introduction of which allows

selection of embryonic mouse cells (stem cells) that contain the Cre recombination or flippase recognition sites. The resultant mouse is a conditional knockout mouse.

[0042] A knock-out construct is a nucleic acid sequence, such as a DNA construct, which, when introduced into a cell, results in suppression (partial or complete) of expression of a polypeptide or protein encoded by endogenous DNA in the cell. An exemplary knock-out construct is provided herein. This construct contains a loxP site 5' to exon 1 of the *Abi1/Hssh3bp1*, a selectable marker cassette and a loxP site 3' to the selectable marker cassette. The selectable marker cassette comprises frt sites 5' and 3' to the selectable marker and an internal loxP site between the 5' frt site and the selectable marker gene. Suitable selectable markers include, but are not limited to, neomycin, puromycin and hygromycin. Suitable vectors include, but are not limited to, pBLUESCRIPT, pBR322, and pGEM7. Details for preparing the knock-out constructs are provided herein.

[0043] Embryonic stem (ES) cells are typically selected for their ability to integrate into and become part of the germ line of a developing embryo so as to create germ line transmission of the transgene. Thus, any ES cell line that can do so is suitable for use herein. For example, the 129SvEv ES cell line described herein may be used. Alternatively, suitable cell lines which may be used include, but are not limited to, the 129J ES cell line, the D3 ES or the J1 ES cell line. The cells are cultured and prepared for DNA insertion using methods well-known to the skilled artisan

[0044] Introduction of the knock-out construct into ES cells may be accomplished using a variety of methods well-known in the art, including, for example, electroporation, microinjection, and calcium phosphate treatment. For introduction of the DNA sequence, the knock-out construct DNA is added to the ES cells under appropriate conditions for the insertion method chosen. If the cells are to be electroporated, the ES cells and construct DNA are exposed to an electric pulse using an electroporation machine (electroporator) and following the manufacturer's guidelines for use. After electroporation, the cells are allowed to recover under suitable incubation conditions. The cells are then screened for the presence of the knockout construct.

[0045] Screening for cells which contain the transgene (homologous recombinants) may be done using a variety of methods. For example, as described herein, cells can be processed as needed to render DNA in them available for screening with specific probes by polymerase chain reaction (PCR).

[0046] Once appropriate ES cells are identified, they are introduced into an embryo using standard methods. They can be introduced using microinjection, for example. Embryos at the proper stage of development for integration of the ES cell to occur are obtained, such as by perfusion of the uterus of pregnant females. For example, mouse embryos at 3-4 days development can be obtained and injected with ES cells using a micropipet. After introduction of the ES cell into the embryo, the embryo is introduced into the uterus of a pseudopregnant female mouse. The stage of the pseudopregnancy is selected to enhance the chance of successful implantation. In mice, 2-3 days pseudopregnant females are appropriate.

[0047] Successful incorporation of ES cells into implanted embryos results in offspring termed chimeras. Chimeras capable of germline transmission of the mutant allele are identified by standard methods. Chimeras are bred and the resulting progeny are screened for the presence of the desired alteration (e.g., the modified recombinant *Abi/Hssh3bp1* allele). This may be done, for example, on the basis of coat color or by obtaining DNA from offspring (e.g., tail DNA) to assess for the transgene, using known methods (e.g., Southern analysis, dot blot analysis, PCR analysis). Transgene expression may also be assessed (e.g., to determine if a replacement construct is expressed) by known methods, such as northern analysis or PCR analysis. Southern hybridization or PCR analysis of progeny DNA (e.g., tail DNA) may be conducted to identify desired genotypes.

[0048] The present disclosure describes a CKO wherein the disrupted gene is the *Abi1/Hssh3bp1* gene. Conditional disruption of the *Abi1/Hssh3bp1* gene was obtained by breeding the CKO mice with mice that express flippase or Cre recombinase. The Jackson Laboratory (Bar Harbor, ME) sells over 70 strains of mice expressing flippase or Cre recombinase. The flippase or Cre recombinase-expressing mouse strains express these enzymes in all mouse tissues, or can express the enzymes under signals that cause them to be present only in specific tissues, such as in prostate tissue, or only in a specific cell type, such as astrocytes.

In addition to tissue- or cell-specific signals, development-specific signals (such as endogenous developmental factors or diet responsive gene promoters) can be used to control the time of flippase or Cre recombinase expression. In one embodiment of the instant mouse, the action of flippase removes the neomycin gene and the action of Cre recombinase removes a critical part of the targeted gene of interest, exon 1 of *Abi1/Hssh3bp1*. In another embodiment of the instant mouse, the action of Cre recombinase removes both the neomycin gene and exon 1 of *Abi1/Hssh3bp1*. Removal of exon 1 of *Abi1/Hssh3bp1* leads to inactivation of the gene due to lack of a start codon and thus no production of protein (FIG. 2C). In a knockout, preferably the target gene expression is undetectable or insignificant.

[0049] The *AbiHssh3bp1* knock-out mice exhibit one or more phenotypes including, but not limited to, disruption of cell motility, increased directional persistence, decreased migration distance and decreased migration rate.

[0050] The CKO mice disclosed herein include at least three elements: (1) at least two enzyme-specific recognition sites flanking a critical portion of the target gene; (2) a gene encoding a selection marker such as, but not limited to neomycin; and (3) at least two enzyme-specific recognition sites flanking a selection marker gene for easy removal upon breeding with specific mouse strains. In a non-limiting example, exon 1 of the target gene has been designated as the critical portion. In one embodiment the enzyme-specific recognition sites flanking the critical portion of the target gene are loxP sites. In another embodiment, the enzyme-specific recognition sites flanking the selection marker gene are frt sites. In another embodiment, both sets of recognition sites comprise the same the same. In additional embodiments, other exon(s) or portion(s) of the target gene can be designated at the critical portion. In additional embodiments include DNA modifying enzymes other than flippase and Cre recombinase which mimic their action. In another embodiment, any other method of gene activation can be used to inactivate the target gene can be used. Embryonic stem (ES) cells from alternative mouse strains may also be used for gene targeting.

[0051] As used herein, nucleotide sequences which are substantially the same share at least about 90% identity, and amino acid sequences which are substantially the same typically share more than 95% amino acid identity. It is recognized,

however, that proteins (and DNA or mRNA encoding such proteins) containing less than the above-described level of homology arising as splice variants or that are modified by conservative amino acid substitutions (or substitution of degenerate codons) are contemplated to be within the scope of the present disclosure. As readily recognized by those of skill in the art, various ways have been devised to align sequences for comparison, e.g., Blosum 62 scoring matrix, as described by Henikoff and Henikoff in Proc. Natl. Acad. Sci. USA 89:10915 (1992). Algorithms conveniently employed for this purpose are widely available (see, for example, Needleman and Wunsch in J. Mol. Bio. 48:443 (1970).

EXAMPLES

Example 1

Genetically Engineered Abi1/Hssh3bp1 Mice

[0052] Embryos of the Abi1/Hssh3bp1 heterozygote floxed mice (Abi1/Hssh3bp1^{loxP+/wt}; also called Abi1/Hssh3bp1(fl/+)) were deposited at the American Type Culture Collection (Rockville, MD) under Accession Number XXXXXX and identified as mouse embryos 9050671VF-1 through 9050671VF-10. These mice have the minimal amount of sequence required for conditional disruption of the gene (loxP sites around exon 1 of Abi1Hssh3bp1, hereinafter “exon 1”). These mice do not have the neomycin gene in the recombinant Abi1/Hssh3bp1 locus; there is a small amount of sequence from the neo cassette remaining (see FIG. 2A). Abi1/Hssh3bp1^{loxP+/wt} are bred to obtain Abi1/Hssh3bp1^{loxP+/loxP} (Abi1/Hssh3bp1 (fl/fl)) mice

[0053] An ABL-1 conditional targeting construct (SEQ ID NO:14, also referred to as the knock-out construct or the targeting vector) was constructed having a PGK-Neo cassette flanked by frt and loxP sites inserted into exon 1 of the mouse Abi-1 (accession numbers NM_007380 and ENSMUSG00000058835), the mouse orthologue of the human gene ABI-1 (accession number NM_005470).

[0054] A genomic bacterial artificial chromosome (BAC) clone was isolated and the conditional KO construct was generated. An approximately 11.8kb region used to construct the targeting vector was first subcloned from a positively identified BAC clone using a homologous recombination-based technique. The region was designed such that the short homology arm (SA) extends 1.9 kb 3' to exon 1. The long

homology arm (LA) ends on the 5' side of exon 1 and is approximately 9kb long. The single loxP site is inserted 5' to exon 1, and the loxP-flanked Neo cassette is inserted 3' to exon 1. The target region is 0.9kb and includes exon 1 (FIG. 1, FIG. 2). The targeting vector was confirmed by restriction analysis after each modification step and by sequencing using specific primers.

[0055] The conditional KO construct was transfected into 129SvEv embryonic stem (ES) cells, and approximately 300 antibiotic-resistant colonies were selected. After *in vitro* expansion, aliquots of cells were lysed, DNA was extracted, purified, and dried into 96-well tissue culture plates. The 96-well plates of DNA isolated from the homologous recombinant clones were screened using a PCR-based strategy utilizing PCR primers located in both the short homology arm and within the Neo cassette. Positive clones were then submitted for sequencing to confirm proper integration of all loxP and frt sites, and then finally expanded into cultured ES cells.

[0056] Two positive ES clones, 1-2D3 and 1-3D1, were microinjected into C57BL/6 blastocytes which were implanted into the uteri of pseudo-pregnant females. Pseudo-pregnant female mice then gave birth to the offspring. Upon reaching 4 weeks of age, chimerism in the offspring was analyzed by coat color observation. Five males of at least 90% agouti chimerism were obtained. Male mice having at least 90% agouti chimerism upon reaching 6 weeks of age were harem-mated with C57BL/6 wild-type female mice for the production of heterozygous offspring. Both F1 heterozygous male and female offspring were obtained.

[0057] Heterozygote mice with the initial recombinant DNA elements (i.e. neomycin gene, loxP, and frt sites (i.e. neo+/loxP+/frt+)) were found to be less fertile; breeding of these mice led to fewer pups, in the range of 2-4 (6-12 pups is normal). Homozygote mice with the neomycin gene in the recombinant gene cassette were not obtained. Homozygote floxed mice were obtained upon removal of the neomycin gene.

[0058] Following successful breeding of Abi1/Hssh3bp1 chimeric mice, the germline transmission of the modified recombinant Abi1/Hssh3bp1 allele (containing the neomycin gene, frt and loxP sequences) was achieved and subsequently led to production of F1 strain. The resultant offspring were genotyped by PCR to determine

the presence of the conditional knock-out (CKO) allele and were also sequenced for the presence of loxP and frt sites.

[0059] Mice heterozygous for the recombinant Abi1/Hssh3bp1 allele containing neomycin gene, frt sites and loxP sites were bred with the “frt deleter” strain 129S4/SvJaeSorGt(ROSA)26Sortm1(FLP1)Dym/J (Jackson Laboratories, Inc. stock number 003946). Flipase-mediated deletion of the neomycin gene from the recombinant gene cassette was confirmed by genotyping with specific primers. Heterozygous Abi1/Hssh3bp1 animals (Abi1/Hssh3bp1 (loxP⁺/wt) also called Abi1/Hssh3bp1 (fl/+) or (floxed/+)) (see FIG. 3) were subsequently bred to obtain homozygous Abi1/Hssh3bp1 (fl/fl) mice. Mouse embryonic fibroblast (MEF) cell lines were subsequently obtained from these mice.

Example 2

Cell Lines with Normal and Mutant Hssh3bp1 Genes

[0060] A cell line was isolated from the heterozygote mouse described in Example 1. The cell lines, termed MEF for mouse embryonic fibroblast, have one copy of the wild-type gene and one copy of the genetically recombined Abi1/Hssh3bp1 gene with loxP sequences flanking exon 1 (this cell line contained the neomycin gene). Following isolation of primary MEF, the cells were genotyped by PCR (FIG. 5). Several MEF cell lines were randomly selected. These included cell lines expressing wild type Abi1/Hssh3bp1 as well as lines expressing the desired homozygous floxed Abi1/Hssh3bp1 gene (FIG. 5).

[0061] MEF cell lines were immortalized by retroviral transduction of the SV40 large T antigen. Following genotype confirmation, homozygous Abi1/Hssh3bp1 (fl/fl) MEF cell lines (parental MEF #3 and parental MEF #8) were used to obtain syngeneic cell lines *in vitro* (i.e. for *in vitro* genetic knockout experiments). The Abi1/Hssh3bp1 (fl/fl) cell lines were either transiently transfected with a Cre recombinase-encoding plasmid in order to remove the floxed alleles, or with a control EGFP (enhanced green fluorescent protein) plasmid expressing puromycin. Both plasmids carried the puromycin resistance cassette. For transfection FuGene6 reagent was used according to the manual (Roche). Transfection medium was replaced after 24 hours by normal medium supplemented with 5 µg/ml puromycin. Cells were cultured with puromycin for six days (the appropriate puromycin

concentration was achieved by performing a killing curve). Cell lines were then cultured under normal conditions as described above. Single clones were obtained by limiting dilution subcloning. For each Abi1/Hssh3bp1 precursor cell line at least 10 individual Abi1 KO cell clones were established. The effective removal of the Abi1 floxed alleles in cells transfected with the Cre recombinase encoding plasmid was confirmed by PCR, by evaluation of protein expression levels, and by RNA-array analysis.

[0062] Clones #3 and clone #8 were used for production of Abi1/Hssh3bp1 deletion lines. Disruption of the Abi1/Hssh3bp1 gene by deletion of exon 1 was achieved by transient transfection with Cre recombinase using a plasmid conferring resistance to puromycin. Genomic deletion of Abi1/Hssh3bp1 exon 1 was confirmed by genotyping with several PCR primer sets, including primers DL75' (SEQ ID NO:7), Neogene 13' (SEQ ID NO:16), and mAbi1loxP35' (SEQ ID NO:3) (FIG. 4), and by sequencing PCR products. Western blot analysis (FIG. 6) demonstrated the lack of Abi1/Hssh3bp1 protein expression in the clones. Representative data from 11 subclones of the parental MEF clone #3 are presented in (FIG. 6).

Example 3

Morphology of Cells Lacking Abi1/Hssh3bp1 Gene Expression

[0063] Abi1/Hssh3bp1 is localized to PDGF (platelet derived growth factor)-stimulated peripheral and dorsal ruffles in precursor (fl/fl) cells, but is absent from knockout MEF cells. Abi1/Hssh3bp1 is known to be involved in actin reorganization resulting in lamellipodia, and in actin-rich peripheral and dorsal ruffle formation. Therefore, it was determined whether Abi1/Hssh3bp1 localizes to these structures in isolated MEF cells and whether any defect in these structures is observed in cells lacking expression of a functional Abi1/Hssh3bp1 gene.

[0064] Upon PDGF treatment, both Abi1/Hssh3bp1 (fl/fl) control (#3) and Abi1/Hssh3bp1 deficient (clones #3-11) cells display peripheral as well as dorsal ruffle formation, although dorsal ruffling is less prominent in the Abi1/Hssh3bp1 KO cell line. Abi1 is highly enriched in dorsal ruffles and localizes at the tip of ruffles in the cell periphery in Abi1/Hssh3bp1 control cells, while it cannot be detected in the Abi1/Hssh3bp1 knockout cell line. Abi2 is also present in both cell lines, but in the Abi1/Hssh3bp1 control cells, it cannot be distinguished from Abi1/Hssh3bp1

localization (FIG. 7). Thus, we have confirmed the participation of Abi1/Hssh3bp1 in the formation of circular and peripheral ruffles in control (fl/fl) MEF cells and the absence of Abi1/Hssh3bp1 in knockout MEF cells.

[0065] PDGF stimulation of Abi1/Hssh3bp1 MEF cell lines led to the formation of both peripheral and dorsal ruffling in Abi1/Hssh3bp1 control and Abi1/Hssh3bp1-deficient cells. Multiple cell morphologies were observed, and were quantified and classified according to the following categories: with ruffles, without ruffles, or with ambiguous cell morphology (FIG. 8). Remarkably, lack of Abi1/Hssh3bp1 did not affect peripheral ruffle formation in a quantifiable manner, whereas dorsal ruffling was significantly reduced in all tested Abi1/Hssh3bp1 KO cell lines as compared to their respective parental controls. Abi1/Hssh3bp1 KO clone # 3-11 showed the most severe phenotype in response to PDGF treatment. Notably, the Abi1/Hssh3bp1 # 3 control cell line was stimulated to a greater extent by PDGF as compared to the Abi1/Hssh3bp1 # 8 control cell line (FIG. 8).

[0066] No change in Rac activity was observed in cells lacking a functional Abi1/Hssh3bp1 gene. Rac activity was assayed in Abi1/Hssh3bp1 MEF cell lines following PDGF treatment using the G-LISA kit (Cytoskeleton, Inc.) according to manufacturer's instructions. The PDGF treatment induced strong Rac activation in both Abi1/Hssh3bp1 control and Abi1/Hssh3bp1-deficient cell lines (FIG. 9). However, no significant effects were observed in the Abi1/Hssh3bp1 knockout cells. This observation suggested that Abi1/Hssh3bp1 acts either downstream of Rac or that Abi1/Hssh3bp1 function is compensated for by another protein, for instance Abi2.

[0067] Cells lacking Abi1/Hssh3bp1 exhibit cell motility defects. Abi1/Hssh3bp1 has been implicated as a regulator of actin cytoskeleton-dependent cell motility as part of the Wave 2 complex. Therefore, Abi1/Hssh3bp1 KO MEF cell lines were examined in a series of motility assays. For random migration analysis, cells were seeded in 6-well plates at a density of 10^4 cells/well in regular growth medium, and placed in a temperature- and CO₂-controlled microscope chamber (Axiovert 200, Carl Zeiss, Microimaging Inc.). Time lapse recording started 6 hours after plating. Images were collected with a 10x objective at 15-minutes intervals over an 8 hour period, using an AxioCam MRm camera (Zeiss) and Axiovision software. Motility

parameters including migration path, distance, rate and directional persistence were obtained from time-lapse movies. To track the migration path of individual cells, cells were manually located in each frame using ImageJ software (NIH ImageJ, software Version 1.41n); nuclei were used as geographical centers for tracking. The migration paths were expressed as graphs. The rates of cell migration were calculated as a ratio of the total length of migration paths and the duration of migration. Migration distances were determined as the net translocation during an 8-hour period. Directional persistence was calculated as a ratio of the direct distance during an 8-hour period and the total length of the migration path. These assays indicated reduced random cell motility (migration rate and migration distance), but increased directional persistence of cells lacking Abi1/Hssh3bp1 (FIG. 10).

[0068] To determine the effects of Abi1Hssh3bp1 on wound healing, cells were seeded in 6-well plates at a density of 1×10^6 cells/well in regular growth medium. After 6 hours, the confluent monolayer of cells was scratched with a fine pipette tip, and migration was visualized by time-lapse imaging as described above. The rate of wound closure was determined by measuring the area not covered by cells per unit of time. Each assay was repeated at least four times. In this assay, subtle but statistically significant impairment of wound closure of cells lacking Abi1/Hssh3bp1 (FIG. 11).

[0069] Cell motility assays indicated defects in cell motility in Abi1/Hssh3bp1 KO cells and suggested downregulation of Wave 2 dependent actin polymerization. It is assumed that Abi1/Hssh3bp1 is a vital part of the Wave 2-Arp 2/3 activating complex, which is regulated by Rac1 activation. Interaction between Rac1, Wave complex and Abi1 is mediated by Nap1 and Sra-1. Data from RNA silencing experiments indicated that upon downregulation of individual subunits, all major components of the Wave 2 complex are coordinately down regulated. How gene disruption-mediated (i.e. genetic) knockout of Abi1/Hssh3bp1 affects the stability of the WAVE2 complex components was studied. Western blot analysis demonstrated that Wave 2, Sra-1 and Nap1 expression levels were lower in Abi1 (-/-) null cells but were not completely abrogated (FIG. 12).

Example 4

Sequencing of Abi1/Hssh3bp1 Knock-out Mouse Genome

[0070] Total genomic DNA was isolated from the indicated sources below and subjected to PCR amplification using the indicated primers (PCR primers). PCR fragments were separated on 1% agarose gel (FIG. 14). Sequencing of the PCR product bands was performed using primer DL75' (forward sequencing primer; SEQ ID NO:7), which is located upstream of 5'loxP site, and with primer Flankneo13' (reverse sequencing primer; SEQ ID NO:4), which is located downstream of 3'loxP site. Names of MEF cell lines and mice are indicated.

[0071] Primary MEF cell lines

[0072] "RARA1" is the obtained from a mouse embryo resulting from breeding of heterozygous Abi1/Hssh3bp1 (loxP/+) strain and genotyped to be negative for the loxP allele. Sequencing data confirms the lack of a 5'loxP site and lack of a 3'loxP site in the WT sequence of the Abi1/Hssh3bp1 gene.

[0073] "RARA3" is obtained from a mouse embryo resulting from breeding of heterozygous Abi1/Hssh3bp1 (loxP/+) strain and genotyped to be homozygous for the loxP allele. Sequencing confirms the presence of a 5'loxP site and a 3'loxP site in the recombinant Abi1/Hssh3bp1 gene.

[0074] "RARA7" is obtained from mouse embryo resulting from breeding of heterozygous Abi1/Hssh3bp1 (loxP/+) strain and genotyped to be heterozygous for the loxP allele and the wild type allele. Sequencing confirms the presence of both 5' and 3' loxP sites. Also, the WT sequence was confirmed with the DL75' and Flankneo13' primers.

[0075] Where indicated, the term "upper band" refers to sequence data from the recombinant Abi1/Hssh3bp1 floxed allele and the term "lower band" refers to sequence data from the wild type Abi1/Hssh3bp1 gene allele.

[0076] Sequencing data from primary MEF cell lines confirmed the presence of 5'loxP and 3'loxP sites and the lack of neomycin gene in the recombinant Abi1/Hssh3bp1 floxed gene.

[0077] Immortalized MEF cell lines

[0078] MEF#3 (parental #3 MEF Abi1/Hssh3bp1 floxed cell line): Sequencing confirmed the presence of both 5' and 3' loxP sites in the recombinant Abi1/Hssh3bp1 gene.

[0079] MEF#3 clones #3-6, #3-8 and #3-11: Sequencing confirmed the deletion of exon 1 and the presence of only one loxP site in the recombinant Abi1/Hssh3bp1 gene.

[0080] MEF#8 (parental #8 MEF Abi1/Hssh3bp1 floxed cell line): Sequencing confirmed the presence of both 5' and 3' loxP sites in the recombinant Abi1/Hssh3bp1 gene.

[0081] MEF#* clones #8-7 and #8-11: Sequencing confirmed the deletion of exon 1 and the presence of only one loxP site in the recombinant Abi1/Hssh3bp1 gene.

[0082] Sequencing data from the immortalized MEF cell lines confirmed the presence of 5'loxP and 3'loxP sites and the lack of neomycin gene in the recombinant Abi1/Hssh3bp1 floxed gene allele in parental #3 and #8 cell lines. In cell lines subcloned following transient Cre recombinase transfection (#3-6, #3-8, #3-11 from the parental MEF #3 and #8-7 and #8-11 from the parental MEF #8), the Abi1/Hssh3bp1 gene sequence located between loxP sites including exon 1 and including one loxP site is deleted from the recombinant allele. This resulted in disruption of Abi1/Hssh3bp1 protein expression (see the FIG. 6 for protein expression data from #3 subclones).

[0083] Prostate tissue from Abi1/Hssh3bp1 floxed mouse crossed with PbCre mice and positive for Cre recombinase expression

[0084] Mouse #418 anterior and posterior prostate: Sequencing confirmed the presence of both 5' and 3' loxP sites in the recombinant Abi1/Hssh3bp1 gene.

[0085] Prostate tissue from control Abi1/Hssh3bp1 floxed mouse crossed with PbCre mice but negative for Cre recombinase expression

[0086] Mouse #419 anterior and posterior prostate: Sequencing confirmed the presence of both 5' and 3' loxP sites in the recombinant Abi1/Hssh3bp1 gene.

[0087] For these tissues the term “upper band” refers to sequence data from the floxed allele and the term “lower band” refers to sequence data from the exon 1 deleted allele.

[0088] Sequencing data from the mouse prostate tissue confirmed the presence of 5'loxP and 3'loxP sites and the lack of neomycin gene in the recombinant Abi1/Hssh3bp1 floxed gene allele in anterior and posterior prostate tissues in animals #418 and #419. In prostate tissues obtained from the mouse expressing probasin-driven (i.e. prostate specific) Cre recombinase (mouse #418), Cre recombinase-mediated deletion of the Abi1/Hssh3bp1 gene sequences was observed located between loxP sites and including exon 1 and one loxP site.

Example 5

Abi1/Hssh3bp1 Knock-out Mouse

[0089] Mice homozygous for the recombinant floxed Abi1/Hssh3bp1 allele were bred with a probasin promoter driven Cre recombinase (Pb-Cre) expressing strain: B6.D2-Tg(Pbsn-Cre)4Prb (National Cancer Institute-Frederick; the Mouse Repository of the Mouse Models of Human Cancers Consortium). In these transgenic mice, the prostate-specific promoter of the rat probasin gene (Pb) regulates expression of Cre recombinase, hence the enzyme is expected to be expressed only in mature prostate-tissue. The Pb-Cre strain is maintained in the hemizygous state by breeding to C57BL/6J females. Cre must be transmitted through the male mice to avoid small, but significant oocyte-mediated recombination. Breeding pairs were supplied as a hemizygous male and a female C57BL/6N mate. Successive generations of Pb-Cre mice were bred to C57BL/6J mice to generate sufficient Pb-Cre mice for experiments. Mice were genotyped using tail-obtained DNA.

[0090] Prostate specific deletion of Abi1/Hssh3bp1 exon 1 was confirmed in prostate tissue by genotyping with primers DL75' and Flankneo13' (FIG. 13). This result confirms the functionality of the loxP sites *in vivo*, and demonstrates the suitability of these mice for studies of Abi1/Hssh3bp1 gene function.

Example 6

Proliferation of Cells Lacking Abi1/Hssh3bp1

[0091] The proliferation rates of cells lacking Abi1/Hssh3bp1 are higher than control Abi1/Hssh3bp1(fl/fl) MEF cells. Loss of Abi1/Hsshb3p1 in primary prostate tumors and subsequent identification of primary tumor mutations that lead to disruption of Abi1/Hsshb3p1 function suggested that loss of Abi1/Hsshb3p1 protein leads to dysregulation of cell growth. This was tested using MEF cells isolated from the Abi1/Hssh3bp1 CKO mice. Consistent with the tumor suppressor hypothesis, enhanced proliferation rates as determined by activity of mitochondrial dehydrogenase were observed in MEF Abi1/Hsshb3p1 (-/-) cells (clone #3-11) in comparison to parental clone #3 Abi1 (+/+) (FIG. 13). Primers DL75' and Flankneo13' were used for genotyping.

Example 7

Role of Abi1/Hssh3bp1 in Prostate Cancer

[0092] The deletion of specific chromosomal regions has been reported in human prostatic tumors. For chromosome 10, both the 10p and 10q arms have been reported as frequently deleted. Deletions on 10q often involve the 10q23–24 region, including sequences mapped to the candidate prostate tumor suppressor gene, PTEN or MMAC1. Loss of heterozygosity (LOH) on the short arm of chromosome 10, 10p, has also been observed in prostate tumors. Several studies performed using polymorphic markers indicated high rates of LOH specifically in the 10p11.2 region. The rate of LOH varies among the studies, dependent upon the marker used and the stages of the cancers examined. Genetic alterations on 10p are often present in conjunction with the changes on 10q. An extensive deletion mapping of 10p in human prostate tumors at 13 highly polymorphic loci has been performed. In this study, 57% of 35 tumors examined demonstrated loss of 10p sequences. The highest concentration of allelic losses on 10p spanned a 4- to 7-cM region and included loci D10S211, D10S89, and D10S111, which defined a minimal common region of deletion on 10p in human prostate tumors. Moreover, this study suggested that one or more deletion domains may map to 10p, as some tumors were deleted exclusively at D10S211 or D10S89–D10S111. These studies were confirmed by the observation that the LOH of 3.2% in localized (Stage B) and LOH of 27% in

advanced prostate cancer (Stages C and D) using the marker D10S111. Taken together, these allelotyping studies suggest that one or more tumor suppressor genes map to 10p in human prostate tumors. Functional studies supporting this hypothesis were provided by studies in prostate cell lines supplemented with portions of chromosome 10p. The introduction of subchromosomal fragments encompassing 10pter-q11 into the PC3 prostate adenocarcinoma cell line reduced tumorigenicity following injection of hybrid clones in nude mice. Similar results were obtained by another group using the PPC-1 cell line, a subline of PC3, in which decreased colony formation in soft agar was observed following introduction of 10p sequences.

[0093] Thus, both allelotyping and functional studies suggest that one or more tumor suppressor genes critical for prostate tumorigenesis map to 10p inclusive of the D10S89 and D10S111 loci. The minimal common region of deletion on 10p in human prostate tumors contains a gene encoding a candidate human spectrin SH3 domain binding protein 1, Hssh3bp1. Hssh3bp1 binds to SH3 domains of spectrin and Abl tyrosine kinase, associates with macropinocytic vesicles in cultured cells, and is a potential regulator of macropinocytosis. E3b1, a protein identified independently by another group as Eps8 binding protein and which is identical to isoform 2 of Hssh3bp1, was recently implicated in transmission of signals from Ras to Rac. Hssh3bp1 maps near loci D10S89 and D10S111 within the 10p minimal region of deletion observed in prostate cancer, and all three sequences localize to a single YAC, 961C7. Moreover, Hssh3bp1 protein expression is downregulated in prostate tumors deleted for D10S89 or D10S111. Two prostate tumor cell lines contain a mutation in Hssh3bp1 gene leading to expression of the aberrant form of Hssh3bp1. These data are consistent with a role for Hssh3bp1 as a candidate tumor suppressor gene inactivated during prostate tumorigenesis.

[0094] DNA Analysis

[0095] Colonies from each of 11 CEPH YACs (965D10, 746D9, 815C7, 747H10, 857C9, 934E11, 796F8, 899E10, 875B4, 746G7, and 961C7), comprising a complete contig of the 10p minimal region of deletion, were picked and incubated in 10 μ l of lyticase solution (1.2 M sorbitol, 10 mM sodium phosphate, pH 7.4 [1:4 v/v monobasic: dibasic from 1 M stocks]) and 2.5 mg/ml lyticase (Sigma) at 37°C for 5

min. Five microliters of each digestion mixture was used in subsequent polymerase chain reaction (PCR) comprising 200 μ M each dGTP, dATP, dTTP, and dCTP; 1x PCR buffer (50 mM KCl, 10 mM Tris-HCl, pH 8.3, 2.5 mM $MgCl_2$); 1 μ M each forward and reverse primers, and 0.6 U Taq Polymerase (Life Technologies) using an annealing temperature of 55°C. The linkage order of these markers has been reported as: pter-D10S211 - WI4906 - 10S553 - D10S1789 - D10S550 - WI4133 - D10S582 - D10S1673-D10S586-D10S1749-D10S1747-D10S572-D10S89-D10S111-centromere.

[0096] Primer sequences and linkage information were obtained from databases maintained by the Human Genome Data Base E-mail: (<http://gdbwww-w.gdb.org/>), Center for Genome Research at the Whitehead Institute for Biomedical Research E-mail: (<http://www-genome.wi.mit.edu/>), and the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). The Hssh3bp1 forward primer used was PROM 35' (5'-CTGCAGAGACCCATGATTGTGCC-3', SEQ ID NO:8), and the reverse primer used was PROM 53' (5'-CAAGTTGAGTACGAATACTCCGTAC-3', SEQ ID NO:9). Reaction products were electrophoresed on 2.5% agarose and visualized after ethidium bromide staining.

[0097] The Hssh3bp1 exon 6 sequences were amplified from genomic DNA isolated from prostate cell lines using forward primer Ex615' (5'-CAAAGGGAGACTCACATA TTTT TGG-3', SEQ ID NO:10), and the reverse primer Ex613' (5'-TCCATAGGAGT TTGTCGCCAGTCAG-3' (SEQ ID NO:11) and sequenced. The primer sequences were derived from Contig NT 008730 (Gen-Bank) containing the entire Hssh3bp1 gene (see also AceView of the gene at NCBI web site at the address indicated above).

[0098] Analysis of Hssh3bp1 Expression

[0100] Frozen paired normal and tumor prostatic tissues previously characterized for 10p dosage status were utilized. Monoclonal antibody (mAb) 2G8 was raised to the recombinant C-terminal portion of Hssh3bp1, plasmid C5 at the Institute for Basic Research in Developmental Disabilities Antibody Facility using standard techniques. Immunohistochemistry was performed in 5 micron sections, which were cut from paired frozen normal and malignant tissues from radical prostatectomy specimens, fixed for 10 minutes in ice-cold acetone, then air-dried

briefly at 4°C. The slides were stained with a 1:2000 dilution of mAb 2G8 using a Ventana 320 ES Automatic Immunohistochemistry/IPOX Staining Station according to manufacturer's protocols. The antibody staining was evaluated by a pathologist, and the degree of staining was assessed as 0 (absent), 1 (weak), 2 (moderate), or 3 (strong).

[0101] Protein Truncation Test (PTT)

[0102] Prostate cell lines LNCAP.FGC-10 (CRL-10995), LNCaP.FGC (CRL-1740), and PC3 (CRL 1435) were obtained from ATCC and were grown according to ATCC instructions. RNA from cultured cells was prepared using Tri-Reagent (Molecular Research Center). RT-PCR was performed using Hssh3bp1-specific primers T7-M (5'-GATTAATACGACTCACTATAGGGACGCGAGAGGAAGCGATGCAGAG-3', 5' primer; SEQ ID NO:12) and P3 (5'-CTTGAATTCAAGCAAATCAGTGAAGGAAAGGAC-3', 3' primer; SEQ ID NO:13). *In vitro* translation of gel-purified PCR products (200 ng) was performed using T7-h1 primer and T7 TNT System (Promega). SDS-PAGE protein electrophoresis and Western blotting were performed. Polyclonal antibody Ab-2 to Hssh3bp1 was used in the analysis.

[0103] Hssh3bp1 Maps to the 10p Minimal Common Region of Deletion in Prostate Tumors

[0104] Each of 11 CEPH YACs was amplified for 14 loci mapping within the 10p minimal common region of deletion. These experiments ordered the YACs into a contig spanning this region (Table 1). The Hssh3bp1 gene localized exclusively to YAC 961C7, which also contains sequences specific for markers D10S89 and D10S111. Because D10S89 also localizes to a more telomeric YAC, 875B4, the likely sequence order is: 10pter-D10S89-Hssh3bp1/D10S111-10cen, where "/" indicates that the actual orientation is unclear (Table 1). The relatively small size of YAC 961C7, which is 1.67 Mb, suggested the possibility that the Hssh3bp1 gene may be co-deleted in tumors deleted for D10S89 or D10S111.

Table 1. YAC Contig of 10p Prostate Cancer Minimal Deletion Region.

YAC Designation	Chromosome 10p Loci																
	D10S211	WI-4906	D10S553	D10S1789	D10S550	WI-4133	D10S582	D10S1673	D10S586	D10S1749	D10S1747	D10S572	D10S89	<i>Hssh3bp1</i>	D10S111		
965-D-10	+																
746-D-9	+																
815-C-7	+	+															
747-H-10		+	+														
857-C-9		+	+	+	+	+	+	+	+								
934-E-11			+	+	+	+	+	+	+	+							
796-F-8			+	+	+	+	+	+									
899-E-10								+	+	+							
875-B-4											+		+				
746-G-7													+				
961-C-7													+	+	+	+	

YAC clones are listed on the left and chromosome 10p loci are listed on the top. YAC 961-C-7 contains D10S89, *Hssh3bp1*, and D10S111. The analysis was done by PCR using specific primers.

[0105] Hssh3bp1 Expression is Downregulated in Prostate Tumors Deleted for Adjacent 10p Sequences

[0106] Immunohistochemical analysis of prostate tissues using a mAb to Hssh3bp1 was performed to determine whether Hssh3bp1 protein expression correlated with D10S89 or D10S111 dosage in prostate tumors. Seventeen paired normal and malignant prostate specimens previously characterized for dosage at D10S89 and D10S211 were utilized for these studies. Of the 17 tumor tissues, six were characterized by deletions at D10S89 or D10S111 (Table 2). The remaining 11 tumors retained normal diploid dosage at D10S89, D10S111, or both loci (Table 2). Immunohistochemical staining of epithelial cytoplasm was graded into four groups: absent (0), weak (1), moderate (2), or strong (3). Moderate or strong expression of Hsshb3p1 was detected in 82% (14/17) of normal tissues examined (Table 2). In contrast, moderate or strong expression of Hssh3bp1 was detected in only 41% (7/17) of malignant tissues examined. Moreover, 4/6 (67%) tumors deleted for 10p sequences at D10S89 or D10S111, within the minimal common region of deletion, failed to express Hssh3bp1 protein compared to 5/11 (46%) tumors that retained normal diploid dosage at these loci. An example of Hssh3bp1 staining in normal and malignant is shown in Figure 16.

Table 2. Expression of Hssh3bp1 in Prostate Tumors.

Case Number	10p Deletion [*]	Antibody Staining [†]		Correlation with 10p Status	Tumor Grade [‡]	Tumor Stage [§]
		Normal	Tumor			
404	yes	3	3	no	3+3	T2b
334	yes	2	0	yes	3+3	T2b
340	yes	2	0, 2 [¶]	yes	3+4	T2b
398	yes	1-2	0	yes	3+3	T2
408	yes	3	0	yes	3+4	T2
394	yes	2	3	no	3+3	T1b
344	no	1	1	yes	3+3	T2
402	no	3	3	yes	4+3	T3N1
244	no	0	2	no	3+3	T3
390	no	3	3	yes	3+3	T3
260	no	2-3	1	no	3+4	T2b
392	no	1	0	no	3+3	T2
400	no	3	3	yes	3+3	T3

386	no	3	0	no	3+3	T3N1
380	no	2	1	no	3+4	T3
320	no	2	2	yes	3+4	T2
268	no	3	1, 3 [†]	no	3+3	T2b

* 10p deletion was characterized as described [6]. "no" indicates that the tumors were not deleted at 10p or were uninformative at one or more loci.

[†]Mab 2G8 was used in all cases. (0) Absent; (1) weak; (2) moderate; (3) strong.

[‡]According to Gleason score.

[§]According to TNM system.

[0107] Taken together, these experimental results show that the loss of Hssh3bp1 protein expression was clearly associated with the deletion of adjacent loci on 10p deletion in human prostate tumors.

[0108] Prostate Tumor Cell Lines Contain Mutations in Hssh3bp1

[0109] PTT was performed in two prostate tumor cell lines, LNCaP (CRL-10995) and PC3 (CRL-1435). The PTT test used an antibody to the C-terminus of Hssh3bp1 and indicated the presence of a truncated polypeptide in LNCaP cell line in comparison to two polypeptides in the PC3 cell line (FIG. 16). As determined by DNA sequencing, the LNCaP cell line, but not the PC3 cell line, contains deletion of nucleotides 660–800 (total of 141 nucleotides) of the Hssh3bp1 cDNA. This results in the in-frame deletion of amino residues 194 through 240 of Hssh3bp1 and is consistent with the observation of a smaller translation of product in the PTT. Identical deletion of Hssh3bp1 sequences was observed in another tumor cell line, CRL-1740. Sequencing of Hssh3bp1 gene from these cell lines revealed the presence of a heterozygous point mutation in exon 6 of the gene located near the 3' splice junction of the preceding intron: the sequence *TAG↓ACGG* is now *TAG↓ACAG*, where italic indicates intronic sequence, an arrow splice site, and underline/bold mutated residue. The mutation causes codon 194 change from R (CGG) to Q (CAG). This missense mutation apparently led to exon 6 skipping in the splicing of Hssh3bp1 mRNA, which may be explained by at least two independent mechanisms: a missense-induced exon skipping or by a conformational change in Hssh3bp1 mRNA near the 3' splice site. PCR analysis of Hssh3bp1 cDNA in PC3 cells using isoform-specific primers revealed expression of isoforms 2 and 3 of Hssh3bp1, which is consistent with the observation of two closely spaced polypeptides (FIG. 16). Apparent migration of the polypeptide from LnCAP cells

corresponds to migration of isoform 5 of Hssh3bp1 lacking amino acid sequence encoded by exon 6.

[0110] Previous allelotyping and functional studies suggested that one or more tumor suppressor genes important for prostate tumorigenesis mapped to the 10p chromosomal region. The Hssh3bp1 gene was mapped adjacent to loci D10S89 and D10S111 within the 10p minimal region of deletion previously defined by our laboratory for prostate tumors. Moreover, expression of the Hssh3bp1 protein was reduced in the majority of prostate tumors deleted for either D10S89 or D10S111. These studies suggest that the observed reduction of Hssh3bp1 protein expression may be due to the allelic inactivation of the gene through the deletion of one copy and mutation of the remaining copy. This mechanism is consistent with that of the “two-hit” model originally proposed for the “prototype” tumor suppressor gene, retinoblastoma. Therefore, Hssh3bp1 is a candidate tumor suppressor gene important for prostate tumorigenesis.

[0111] The co-localization of Hssh3bp1 sequences with D10S89 and D10S111 within the 10p minimal common region of deletion in prostate cancer suggests that expression of Hssh3bp1 may be lost in prostate tumors. This is supported by the immunohistochemical studies presented here which show that Hssh3bp1 protein expression is absent or reduced in the majority (5/6, 83%) of prostate tumors examined with deletions of D10S89 or D10S111, but is expressed in the majority of normal tissues and prostate tumors intact at these loci.

[0112] Two mechanisms that may account for the observed reduced expression of Hssh3bp1 protein in conjunction with the deletion of adjacent 10p loci include deletion and/or mutation of Hssh3bp1 sequences. Other mechanisms may also be involved, however. For example, five tumors (cases 344, 260, 392, 386, and 380) failed to express Hssh3bp1 protein, though they did not exhibit deletion of D10S89 or D10S111. In these cases, it is possible that Hssh3bp1 expression was downregulated through other means, e.g., small interstitial deletions, mutations involving both Hssh3bp1 alleles, transcriptional downregulation, or reduced protein stability. Significantly, these proposed events are apparently specific to prostate tumors, as the vast majority of normal prostate epithelial specimens (14/17, 82%) exhibited moderate or strong Hssh3bp1 protein expression. It should also be noted,

as an exception, that one tumor (case 404), deleted for one allele at both D10S89 and D10S111, expressed high levels of Hssh3bp1 protein. It is possible that deletion affected only one allele of Hssh3bp1 in this tumor, allowing normal expression of the remaining allele.

[0113] Two prostate tumor LnCAP cell lines, CRL-10995 and CRL-1740, contain a missense mutation in exon 6 of Hssh3bp1. These cell lines are derivative of each other, which is why the same mutation in the gene was observed. This mutation leads to an apparent exon 6 skipping resulting in expression of aberrant form of Hssh3bp1 mRNA and protein. Although the exon 6 mutation is observed in one allele of Hsshb3p1 gene, only expression of the truncated polypeptide is observed in these cells, suggesting downregulation of the normal allele by mechanisms mentioned in the previous paragraph. Exon skipping was demonstrated to be due to nonsense or missense mutations located in exonic splice enhancers present in both constitutively and alternatively spliced exons in genes such as BRCA1 and others. The identified mutation may also affect RNA secondary structure and conformation required for appropriate splicing of exon 6 since it is located at the +3 position from the 3' splice junction of the preceding intron. The presence of exon 6 sequences is invariably observed in Hssh3bp1 cDNA obtained from various tissues including primary prostate cells, PC3 cells, human brain, as well as several cultured cell lines. Alternative splicing of Hssh3bp1 in brain leads to five isoforms of the mRNA coding region with additional possibility of alternative splicing of the 3' untranslated region. Expression of specific Hssh3bp1 isoforms in different cells may be functionally significant and is different in PC3 than in LnCAP cell lines.

[0114] Lack of exon 6 sequences that encode amino residues 194 through 240 of Hssh3bp1 results in the loss of a portion of Abl tyrosine kinase SH3 domain binding site (amino residues 144–260 of Hssh3bp1) in Hssh3bp1 in LnCAP cell lines. Such deletion may affect subcellular localization of Abl tyrosine kinase and alter its kinase activity, resulting in cellular transformation. This hypothesis is consistent with the fact that mutations of the Abl SH3 domain lead to the increased transformation ability of Abl. Consistent with the proposed tumor suppressor function, Hssh3bp1 may be a negative regulator of the function of Abl tyrosine kinase, an oncogene.

[0115] Previous studies identified Hssh3bp1 as a marker of macropinocytic vesicles. In addition, overexpression of Hssh3bp1 decreased endocytosis of a fluorescent dye, suggesting a potential negative regulatory role of Hssh3bp1 in macropinocytosis. Macropinocytosis is upregulated in tumor cell lines by stimulation with growth factors, and PI-3 kinase is a positive regulator of the process. LY294002, a specific inhibitor of PI-3 kinase, blocks endocytosis of fluorescent dyes into Hssh3bp1 macropinosomes and dramatically affects their morphology. This suggests that Hssh3bp1 is involved in a transduction pathway involving PI-3 kinase. PI-3 kinase function is, in turn, opposed by PTEN/MMAC, a tumor suppressor gene implicated in prostate tumorigenesis. Thus, Hssh3bp1 and PTEN may be located in the same signal transduction pathway affected in prostate cancer. Thus, down-regulation of Hssh3bp1 may be a downstream event of aberrant regulation of PTEN or PI-3 kinase. Downregulation of Hssh3bp1 protein expression may also occur independently through a deletion and, possibly, mutation mechanism.

[0116] Unless otherwise indicated, all numbers expressing quantities of ingredients, properties such as molecular weight, reaction conditions, and so forth used in the specification and claims are to be understood as being modified in all instances by the term “about.” Accordingly, unless indicated to the contrary, the numerical parameters set forth in the specification and attached claims are approximations that may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of the claims, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques. Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the invention are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently contains certain errors necessarily resulting from the standard deviation found in their respective testing measurements.

[0117] The terms “a,” “an,” “the” and similar referents used in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein

or clearly contradicted by context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., “such as”) provided herein is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention otherwise claimed. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the invention.

[0118] Groupings of alternative elements or embodiments of the invention disclosed herein are not to be construed as limitations. Each group member may be referred to and claimed individually or in any combination with other members of the group or other elements found herein. It is anticipated that one or more members of a group may be included in, or deleted from, a group for reasons of convenience and/or patentability. When any such inclusion or deletion occurs, the specification is deemed to contain the group as modified thus fulfilling the written description of all Markush groups used in the appended claims.

[0119] Certain embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Of course, variations on these described embodiments will become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventor expects skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

[0120] Specific embodiments disclosed herein may be further limited in the claims using consisting of or consisting essentially of language. When used in the

claims, whether as filed or added per amendment, the transition term “consisting of” excludes any element, step, or ingredient not specified in the claims. The transition term “consisting essentially of” limits the scope of a claim to the specified materials or steps and those that do not materially affect the basic and novel characteristic(s). Embodiments of the invention so claimed are inherently or expressly described and enabled herein.

[0121] Furthermore, numerous references have been made to patents and printed publications throughout this specification. Each of the above-cited references and printed publications are individually incorporated herein by reference in their entirety.

[0122] In closing, it is to be understood that the embodiments of the invention disclosed herein are illustrative of the principles of the present invention. Other modifications that may be employed are within the scope of the invention. Thus, by way of example, but not of limitation, alternative configurations of the present invention may be utilized in accordance with the teachings herein. Accordingly, the present invention is not limited to that precisely as shown and described.

I claim:

1. A conditional knock-out mouse whose somatic and germ cells comprise a conditionally disrupted *Abi1/Hssh3bp1* gene, wherein the disruption results in an inability of said mouse to produce detectable levels of the *Abi1/Hssh3bp1* protein.
2. The conditional knock-out mouse of claim 1 wherein said conditional disruption is induced by breeding said mouse with a mouse expressing flippase or Cre recombinase.
3. The conditional knock-out mouse of claim 1 comprising a recombinant *Abi1/Hssh3bp1* allele containing a neomycin gene, frt sites and loxP sites flanking at least a portion of the *Abi1/Hssh3bp1* gene.
4. The conditional knock-out mouse of claim 3 wherein said at least a portion of the *Abi1/Hssh3bp1* gene is exon 1 of the *Abi1/Hssh3bp1* gene.
5. The conditional knock-out mouse of claim 1 wherein said conditional disruption occurs in exon 1 of the *Abi1/Hssh3bp1* gene.
6. The conditional knock-out mouse of claim 1 wherein said *Abi1/Hssh3bp1* gene is not expressed in all the mouse's tissues.
7. The conditional knock-out mouse of claim 1 wherein said *Abi1/Hssh3bp1* gene is not expressed in only a portion of the mouse's tissues.
8. The conditional knock-out mouse of claim 1 wherein said *Abi1/Hssh3bp1* gene is not expressed in the mouse's prostate tissue.
9. The conditional knock-out mouse of claim 1 wherein said mouse exhibits at least one phenotype selected from the group consisting of disruption of cell motility, increased directional persistence, decreased migration distance, and decreased migration rate.
10. A cell isolated from the mouse of claim 1.
11. The cell of claim 10 wherein the cell is from the mouse's prostate tissue.
12. An *Abi1/Hssh3bp1* gene conditional knock-out construct comprising a portion of an *Abi1/Hssh3bp1* gene, wherein exon 1 of said *Abi1/Hssh3bp1* gene is

flanked by a 5' loxP site and a 3' selectable marker cassette, wherein said selectable marker cassette comprises a selectable marker flanked by frt sites and loxP sites 3' to the 3' frt site and 3' to the 5' frt site.

13. The Abi1/Hssh3bp1 gene conditional knock-out construct of claim 12 having the sequence of SEQ ID NO:14.

14. A method of producing a mouse with a targeted conditional disruption in an Abi1/Hssh3bp1 gene, comprising the steps of:

transfecting the knockout gene construct of claim 12 into a population of murine embryonic stem (ES) cells;

selecting a transfected ES cell which expresses said selectable marker;

introducing said transfected ES cell into an embryo of an ancestor of said mouse;

allowing said embryo to develop to term to produce a chimeric mouse with a conditional knock-out construct in its germ line;

breeding said chimeric mouse to produce a heterozygous mouse with a conditionally disruptable Abi1/Hssh3bp1 gene; and

breeding said heterozygous mouse with a mouse expressing flippase or Cre recombinase to produce a mouse with a disruption in the Abi1/Hssh3bp1 gene and does not contain said selectable marker.

FIG. 1A

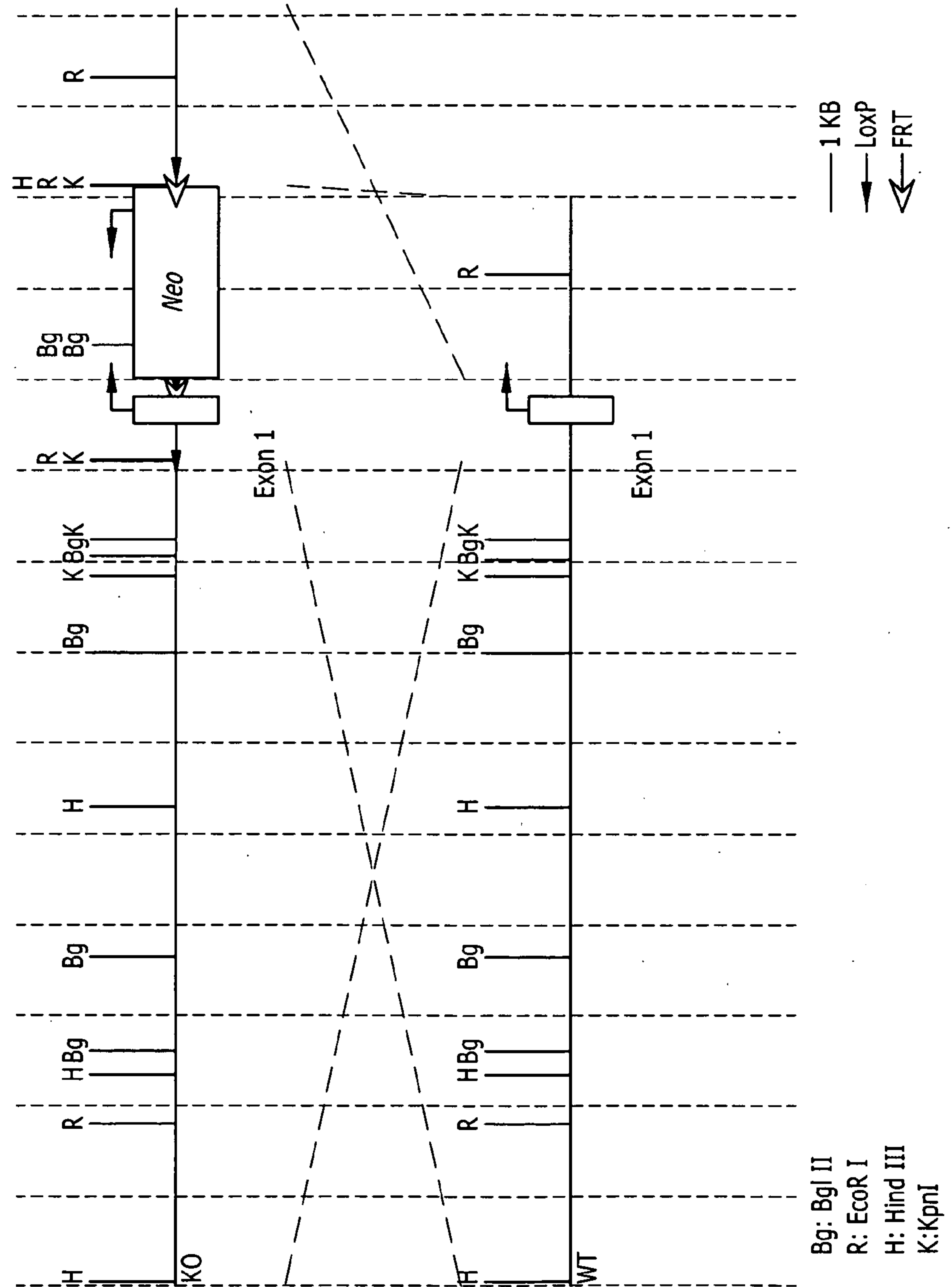


FIG. 1B

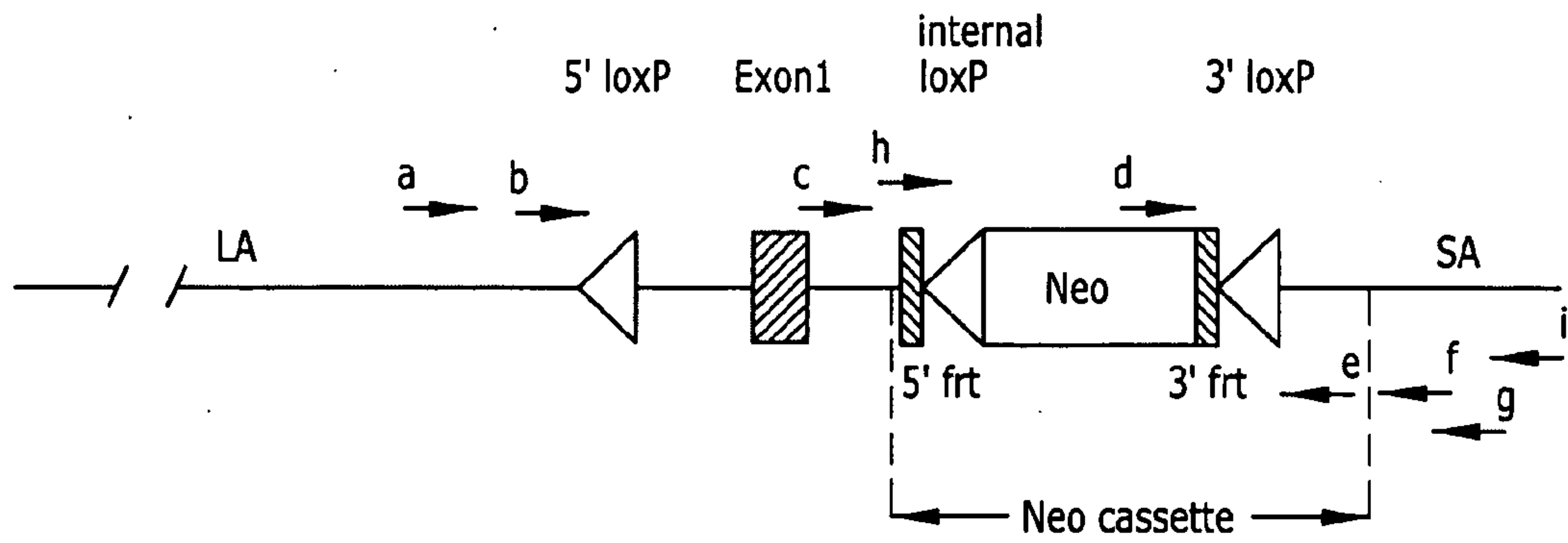


FIG. 6

Abi1(-/-) MEF Subclones of #3:

FIG. 6

Abi1(-/-) MEF Subclones of #3:

#3-1 #3-2 #3-3 #3-4 #3-5 #3-6 #3-7 #3-8 #3-9 #3-10 #3-11 Abi1(f/f) MEF #3 Abi1(+/-) MEF Wt

Anti-Abi1

Loading control

Abi1

Lane	Sample	Anti-Abi1	Loading control
1	#3-1	No band	Band
2	#3-2	No band	Band
3	#3-3	No band	Band
4	#3-4	No band	Band
5	#3-5	No band	Band
6	#3-6	No band	Band
7	#3-7	No band	Band
8	#3-8	No band	Band
9	#3-9	No band	Band
10	#3-10	No band	Band
11	#3-11	No band	Band
12	Abi1(f/f) MEF #3	Band	Band
13	Abi1(+/-) MEF Wt	Band	Band

FIG. 2A**SEQ ID NO: 19 - Abi1/Hssh3bp1 floxed allele**

TCACTGCTCTTAACCACTGAGCCATCTCGCCAGCTCCCTCTTTCAATTCTTTAGGGTACAAA
TTATCCTTGCTTCATTTGTTTCTGCAATATCAAGCACTACTGCATGATGTACATCTGCCGTG
GTACCATAACTTCGTATAGCATAACATTATACGAAGTTATGAATTCGTGCCACCGCGAGAAT
TGATAGTTTTTCAGGGTTTTAAATGAATTGGGGCATAAGTTAAGAAGGCAAAGTCTCTCTTAC
AAAATTGAGGAAGTCAGGATTCAGATTTCTATTTTAAATCGTTATCTGATTGGATGCCTTTG
ACTTACTGACTTTCCTAAGTAAGTTCTGCCAATTTTCAATGTTCTCATAGGAAAAATTCGT
TGTCTAGATCAACTTGTGGCGCCATCTTCTGGGGCCTTAAGAAGACTCTCAAGATTTAAAC
TGTATTGGTTTTTTTTAAAGTCTTCCTAGTTTTTGAAGTTCCTTAGACGCATGCGCGGCCTA
GCCAGGAAGAACTACAATTCAGAAAGCATTGCTATAGTGGATGGGTGGGGGACTCCCGT
TGTCATGGGGGAAATGATTCTCGCGAGAAAGTGAGCCTGTGGCGGCTGTGCGTCCTGGGTGG
AGGGGGTGGGGGGGAGGAGGCGGGGAGAGTAAGGAGGAAGAGGAGGAGGTGCAGTCCCACAA
TACCCGGCGGAGGGAGGGTGGGTGGTGGCGTCTGGTCTGTGCGGAGCTCGGGTCCCCGGCG
GACTCAGCTTCCTCTGTCTCTTTAATGCGAGAGGAAGCGATGCGGAGGGGTGGAAAATGGCA
GAGCTGCAGATGTTACTAGAGGAGGAGATCCCGTCTGGCAAGAGGGCGCTGATAGAGAGTTA
CCAGAACCTGACCCGGGTGGCGGACTACTGTGAAAACAACCTATATACAGGTGAGGAGCTTGA
GCGGCCGGCGGGGGCGGCTGGGACGACAGGCAGGCTGGGCGCCGTGGGGACTGCCCTACTCC
GCCACCCTCCGCCCCAGCCCGAGCGGCGGCCGCGCGGCGATACAGGAAGTGGCCGCCTTGA
GAAAATGGGTGAGGAGCAGGGCCCGCGGGCGCGCTGACCCGATGCCGCTCCCCGcgtac
gccggcttaagtgtacacgcgtactagtctagcgaagttcctatactttctagagaatagga
acttcgttcgaacataacttcgtatagcatatacgaagtatatggtacctgcagaatt
catgacataagcttggatccgttcttcggacgcctcgtcaacaccgtacgCAGCCTGCCCGG
GGCCGCCTGTGCTCCCCACAGCCTGCCCGGGCGTTGCTCCCTAAAGCCTACCCCGGCCGAGC
TCTGCTTCTCGCCGTCTGCCCGGCCAGCTGTGCTCCCCACCACCTGCCCTGGCTGAGGTCT
GCGCCTAAACCCCGCCGCTTTCC

FIG. 2B**SEQ ID NO: 14 - Abi1/Hssh3bp1 conditional allele**

GTACTTTGCTTTTGGCTACACTTGGAGTTAGATTTTAAAGATAAGTAAGTAAGGTAAAAATGA
AATGATTAGACTAGGGCCCTAATTAAATACAGCTGAGGTTTTTGTGTCATTATAAAAAGAGG
AAAAGATACAAGGGTTGGATATGTGAAGAGAAAATGCCGGGTGAGGGCACACAGATTATCAT
GCAAGGTGAGAGCCTCAGGAGAAACCTTGTTTGGGACTTGTGTCACCCAGAACTATGAGAAA
AACCTTTCTGTTGTCTGAGCTACCTTTCAGAGAGGGGAGAATGGGCGGTTTCAGCTATAAAGA
CGTGTGAAGAAAAGGCCATGTGCCCTGACTCTCTTACTTCTTCCTGAGTGGGTGCCTGCATC
ACTGAGGCTGTCATCAGACTTCAGATTCTCTAGCCTTGCAACAGGAATTGAATCCTTGTGGT
TCTCCAGGGAGCTTCCTGGACAGACTGCGGCTGCGCCTCCAGCCTTGTGGCCCAAGCAGTTG
GTGAGTTCTCTTCCTCTTCTGTGCCGACAGCTGTTGGTACACAACCCCCAACTTCTGTCCTT
TGCCAATCAAATAACTTTCTTACTGTTCTTTTCGCTGTGAAGAAACACCATGACCATGGCAAC
TCTTAAAAAAGAAAGCCTTTAACTAGGGGCTTGCCCTATAGTTTCAGAAAGTTAGTCCATTAC
CATCGCAGGAGGGGAGCATGGCAGCAGGCAGGCATGGTGCTGGAGAGATAGCTGATAACTAC
ATCCTGATCCTTGGGGGTGGGGGGAGAGGGGGAGAGAGAGAGGAGGAAGGGGGAGGGGGAGAGG
GAGGAGAGGGAGAGGGGAGAGACTAAGTCTTGTGTGGGCTTTTAAAACCTGAAAGCCCACCCC
CATTGACATATTTCTCCAACAAGACCACACCTCCTAATCTTTCTATTGCTTTCAGACAGTT
CCATTCCCTGGTGATGAAGCATTCAAATATATGAGCCTCTGGGGGCATTCTTATTGAAACCA
TCACACTACACATTATGTATTTTCCTTTCAGTCTATTTCTCTACATAACCCTCCCTAACATG
AGAAATTATGCCATATGGGGATGGTGGCAATGCAAGTGGTGGGAGTATTTTGGAGGGTGTCAG
GACAGATGGGGGAGTGGTTCTGCCTTCCTGACTGCTAGTTTCTTTCCAGTATATCACGTGCG
CATTCTGGATTCTAGCTTGCTGACCACCTACTTAGCATCCTGGTACACAGTGCTGTGAATTA
TCTACACAGAAAGTAAAAACAAAAACAAACAGAAAGCAGAGTTCTGAAGTTTTTTTCAGTGT
AATGTGCCAGATAATATCAGCAATTATGTACCAAATAATCCAAATTATAATTTTTTTGCCT
GTCACATCACACATCTCTTTTTGTAGACATGATTTTTTGATGAAATCATTTGTTTTGTAACCC
AGGCTGACTTCCAACAGGCAAATCTACTGGTTCAACCTCCCAAGTGCTAGAGTTGTAATGGC
ATATTACCAGGCTTAGCTACATAGCTGATCTCTTTATCTCTCTGAAGCAACGTCCATCATTG
TCAGCTATCTACTGTCTTAAAACTCAACCTGTAAAATGTTTTCCCATCTGTCCAGAATGTGC
ACTTCACAAACTTTTTTATTACCAAATTAATTTGCTTATGTCCATTAAAAGAAGGGTACAGG
TGCTAGGGAATCTAGCTTAGCTGGATTAGTGCCTGGTATGCATAAAGCCTAGCTTTAGCCCC
CAGCACTTCATAAAGCAAGATGTGGTGGCACATATCTGTAATCCCAGTACTGAGAAGATGGA
AGCAGGAGGATCAGTTCAAGGCTACCATTGGGTACATACTAAGTTTGAGGCTAGCCTAGACT
ACAACAGACTTTGTCTCATTAAATAAGTAAATAAATAAATGGTTGGATTTACAGGTTGAACA
CTGGCAAAGTCATTACATTTAATACAAACACTGTTACTCTTTATTTTATTGCAATTTTCATT
TTCTTTTATTTTATTCTGGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGATCACATGTGG
GAACATGTGTGGGTACATGTACAGGTATACTTCCCTATAGATATCTTAAGGTACTATAGAAT
GTCTTCTTCAATCACATTCCATTTTACTTTTTTGTGTTGTTGTTGTTTGGTTTTTCAAGACAG
GGTTTCTCTGTGTAGCCCTGGCTGTCTGGAACCTCACTCTGTAGACCAGGCTGGCCTCAGAA
GTCCACCTGCTTTAGCACAAATACTCTTTAATACTTGCTTAAATGAGGCATGGCAGAAATCAG
CCTGTGATCCTAGCACTTGAGCCTTGGAGGATGGTTCAAGGTTGCTGGAGATAACTATGTTA
AGAGAAATAAATCAGGAACAGAAAGGGAAAAAACAACAGTGTGTACTTAGCTATAGA
GAGGTTCAAGTCCACAGTGGATATGAGACCCTCTCTCAAGAACAAGCTAAGTTATTAGATGC
TATTAGTATTTTAACTTGTCAAAAAACAAAACAAACATGGAAAGCCATCAGTTATAATG
TGGTACCTTGTCTTATGGTTATCTTCTACAGGCTGGCTGTGAATGCAGGAAACTCCTTGTC
TCTAGCTCTCAGTTAGTTATTTCTTCTTTTCTTTAGATTTATTTTGAGTGTTTTGCCTGTG
TGTATGTCTCTGTACCACACCCATGTCTTCTGTCTGCAGAGGTCAGAAGAGGGTTTCAGATC
CCCTGGGACTGGGAATTAGGAATAATTGTGAACCATTTGTGTGGACACTAGGAACCAAAACAC
AGGTTATTTGCACCTCATTCTTTGGGATGTGTTGTTTTCTTTCTTTGTTGTTGCATTGGCA

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ATAGTTTCTCCATACGCTGTCTGTCTGGGACTTTTCTATATGCACCAGACCTTCCTCAAACCT
TTCAGTGATCGTCCTGCCTCTGCCTCACCAGTGCTGGGGCGACAGGTATGTGCAACCATGCT
AGCATTTAATTTCTTTTTGATTAGTATGCAAAGTAATGAGTTTCACTGTAACACTTTCATGT
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CTCCCTCCCTCCCTCCCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC
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TTCCTGCCCCAACTACCACTAGTTCATCTTGGGTGTGTGTATTTGTGTTGGGAGGGAGAGA
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CCTTTGACGGTTTGTCCATTCTTTTACTGTGGTCTGATGATTATTCTGGGTTTCAGGTTAT
TAGGCTTTCACTGTCCAGCAGTTTCTCTGCTGAACATATTTTCAGCCTCCCTTCATCCCCAT
TAATTCTTCTTAAGTGGCTTAAATAATTCTTTTGTTTTATTTATTATGTTTTTGAGACAAT
CTCACTGTGTAGCTCAGGCTGACCTGAACTCATGGGTGGCAATGTCTTCCCTTTATCTCCC
GAGTGTTGGGACTGTAGTGTGAAACACCTCACCTGTGGGTTTTTTTTTTTTTTAATGGACTA
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GTCACCTTTAAAAAAGCAATCTGTTGGAATTCTGGCCTGCTCAACAAGAGGGAAAGCATGTTT
AGTACTGGAAACCTAGCCAACCTACCCAGAACTAGTGAAGTCATGGATCTTGGAAAGAGAACCT
ACAATCAACCGCCACTTCTAAACCAGCATAATCCTTAACTACATTTAAATTTTTTTTTCAT
ACAGAATACTTTGATCTGATTATTTGCCTTCTTCCAACCTCCTCCCAGGTTTTTCTTAACTCC
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CCACTTAGCATCAGTCAGAGTAGTACCTCTACTGGGGACAGCGCTAGCTCTCTGACCAAGGT
GGCAGTAGTTGCAGGGGACCTAGAGTCCCTCAGGGCATGTGATAGCAAAAGCCTGGTACCA
GCTATTCCAGACAGCCCTGGCTGAGCTGGTTCCTTTAGGAGCGGCAGTCTTAGTGTGATTAC
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TGTAGCTGAGGGTGATCTTGAACACGATGTCCTCCTGTTACATTTCAAGTGCTGGGATTACA
GGAGAGCATTTATTAAATCCTGGCTTCTATTACATTTTAAAAAACATTTTGTATTTTTATGT
GTATGCATGTTTTGCCTGCATCTGTGTCTGCATACCACATGCCTGCTTGATGCCCAGTGATG
CCAGAAAAGGTGCCAGATCCCTGGAAGTGGAGTTATGAATAGTTGTGAGCCATCATGTGGG
TGCTAGACTGAATCTGGGTCTCTGCAAGAGCAATAATTGCACTTAATTTCTTTCCAGTTCT
CTACCCACCCACACCTGGCTTTTACATCTTAAGTTTGTCTATTCTATATCCATTGCATTAA
CTGTTGAGTAGACATTTGCTATAGCTTCCCAATGATCCTTTTGTCTCTTCCACACATCTTCC
TTTGACCAATTATCCCTCCTGAGCTTTTGTGCAATACTGTGGTACTTTCAAAGTAGAAATC
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TCTTTGGGATCCATGTGGTACAAGGAGAGAATTTACTATCACCAGTTGTTCTCTGATTTTCA
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CGTGGGGATTCTGTCCTCAGAAATGGGGTAGTACTTAAAGGTTAGAGGGAATGAGTTTAGCT
TGTTTGGCCTTTGGCCTTTTGCCATATGAGGATATAGCAAGAGACTATCACTACACAAAATA
AATGTCCACAACCTTTCTTTTTGGCTCTTTTTTTTTTTTCTTTGAGATAGGGTTTTTCTGTG
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CTGCCTCTGCCTCCTGAGTGCTGAGATTAAAGGCATCAGCCACCACTGCTTGACAAGTATCC
TAGATTTTAAAGTGAATAAGGGGCTGGTGAGGTGGTAGAGCACTTGCTGCTTTTCTCTAG
GACTCAGGTTTATTCTTAGCACCCACATACTGGTTTACAGCAGTAAGTCTAGTTCCAGAAGA
TTGGAACATTCTCTTAGCCTCTGCAGGCACCATACACATGTAGTATACAGATATACTTGC
AGTCAAAATACCTTACACATAAATTGTAAAGTTTGTGTTTTTTAATGTGTGTGTGTATG
TGTGTGTATGTATGTGTGTGTATATATAAAATCACAGCCTGTGATATTTTGTGTGTAAC
AGCACACATTAAGATATGTTTCAGTGAGGTCTGGAAAGGTCTGTATGTATAGGTGGATTGGC
CATACTGACTTCTTAAGTACCTTTAGTGAGGTGTGACAAAGCACTGTGACCAAGAAGGCACC
TTATGGAAGGAAGTGCTTATGGTGGCTTGCAAGTGTGAGGGGTGAGTTTGTATTTATCATTG
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TTACAAGCAAGAGGCACACGCTCGAATGCTCACACGCACACACACACACACACACACACA
CACACACACACACATACACACACACACACACACAGGGGGGGGGGAGAGAGAGAGAGAGAGG
GAGGGGCATTTGAAACCTCAAAGCCTGCTTTTAGTGATATACCTTCTCCAACAAGGTCCCAC
CTCTTAATCTTCCCCAACAGTTTAAACCGACTGTGGACCAAGTATTCAAGTACATGGGCCTA
TGGGAGTCATTCTCATTAGACCATCACATTGGCTTTAGTATTCTAGTTTCTTTTAA
CTCACTTTAATTCCTTAGTAGTATCCTCTAATTTGATTTGTTTCTTTTGATGGATATTACTC
ACCCATGAGGGCTTTCTTGTCTAGATGGAAAATTGTCATATTCTTCCATACATTAATACTT
AACTTAATTGTGTATCTATTTTGCTCCAGAGATAATAATGACTGAGACAAAGACTATATA
TCCTTAGGAAATTTTCGTTATGGGGACAAGGGAACATGCTGAGTATGCACACACACACCTCG
CGCACACACACCCACACCCACACGCACATAACCAAACACCAAACTAAAACCCCTCATTTCA
AATAGATAAGGAAGTAGTAAGATGGGAGCTAGAAAACAGGATTTGGAAGAAGGGGCTTCTT

[illegible]

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[illegible]

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FIG. 2C

SEQ ID NO: 20 - Abi1/Hssh3bp1 KO allele resulting from Cre recombinase-mediated recombination.

TCACTGCTCTTAACCACTGAGCCATCTCGCCAGCTCCCTCTTTCAATTCTTTTAGGGTACAAA
TTATCCTTGCTTCATTTGTTTCTGCAATATCAAGCACTACTGCATGATGTACATCTGCGGTG
GTACCATAACTTCGTATAGCATAACATTATACGAAGTTATGGTACCTGCAGAATTCATGACAT
AAGCTTGGATCCGTTCTTCGGACGCCTCGTCAACACCGTACGCAGCCTGCCCCGGGGCCGCCT
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TCGCCGTCTGCCCGGCCAGCTGTGCTCCCCACCACCTGCCCTG

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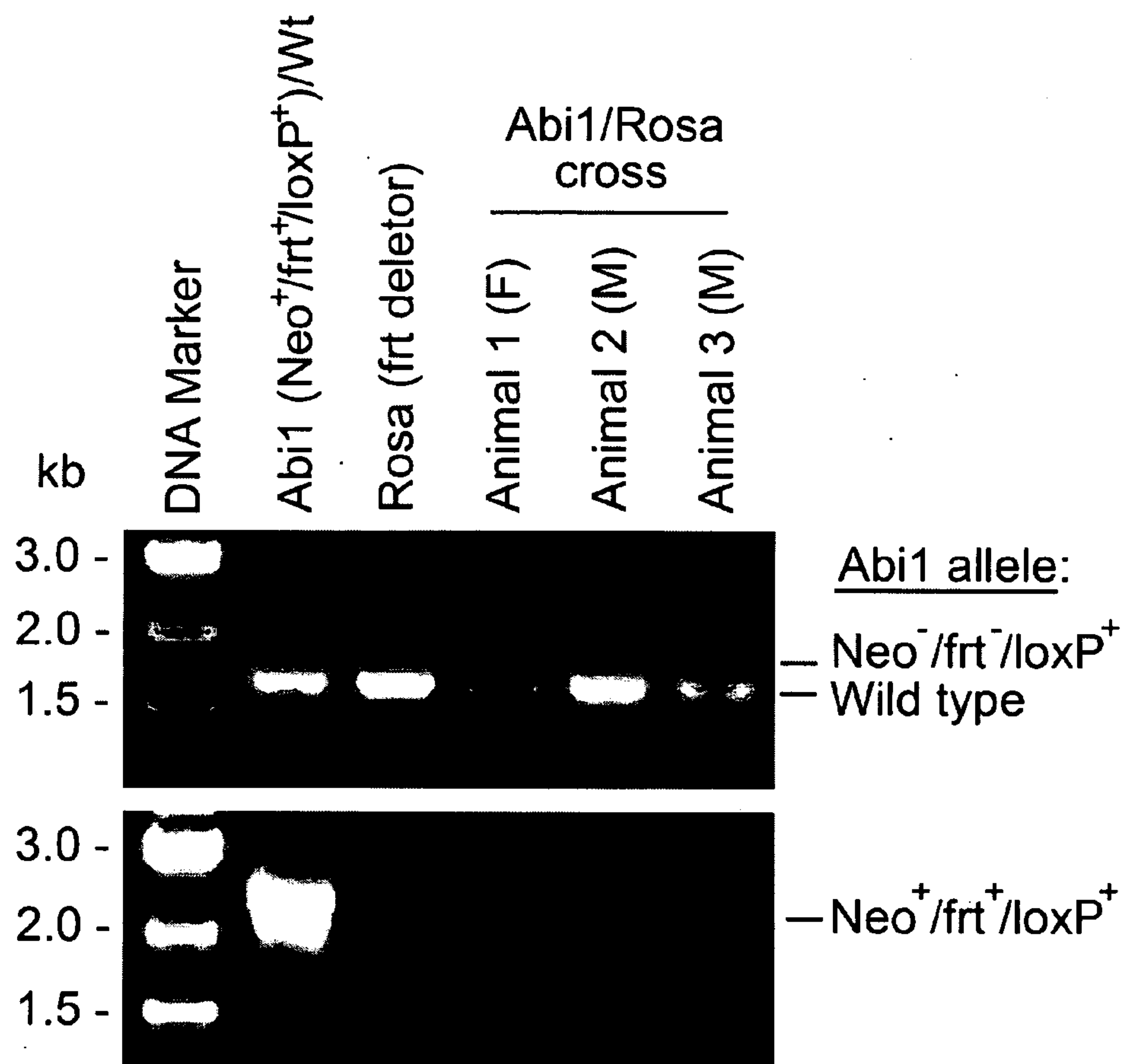
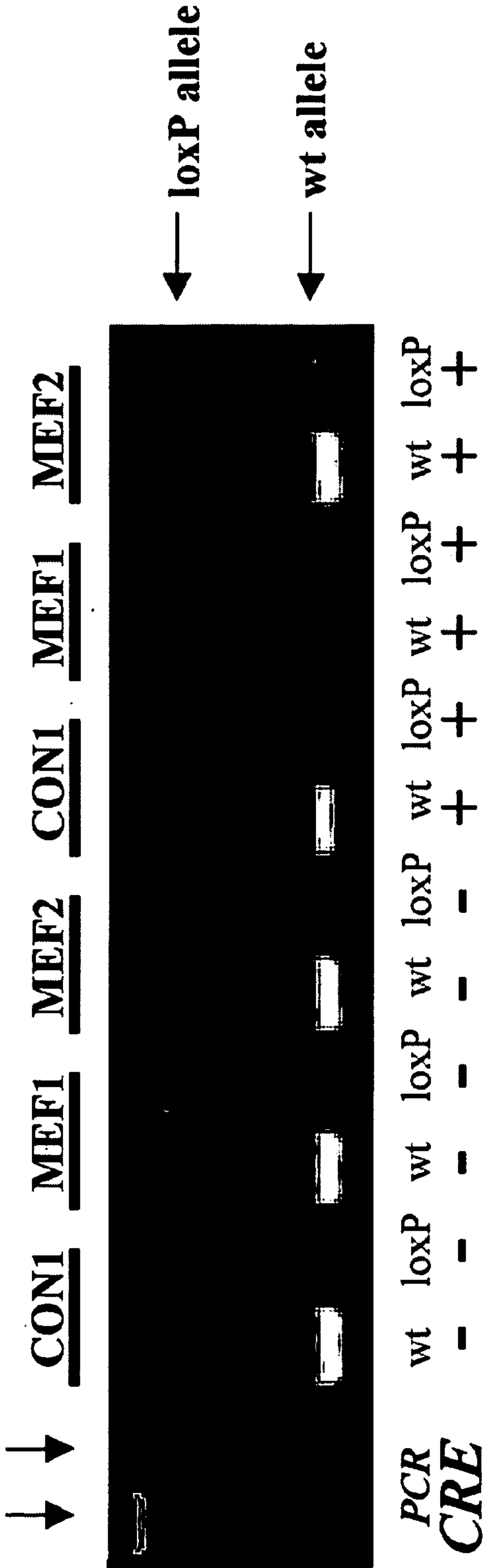
FIG. 3

FIG. 4A



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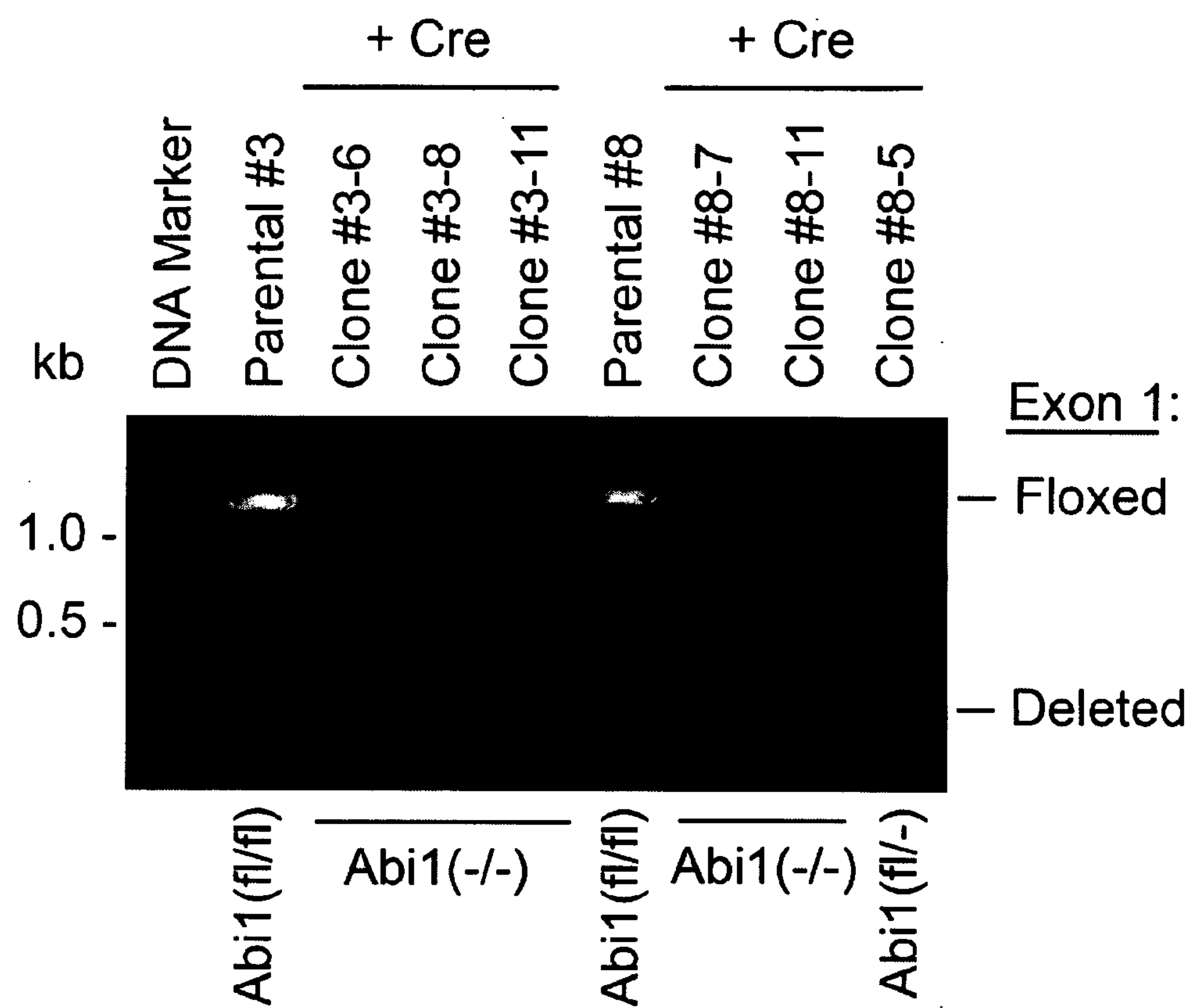
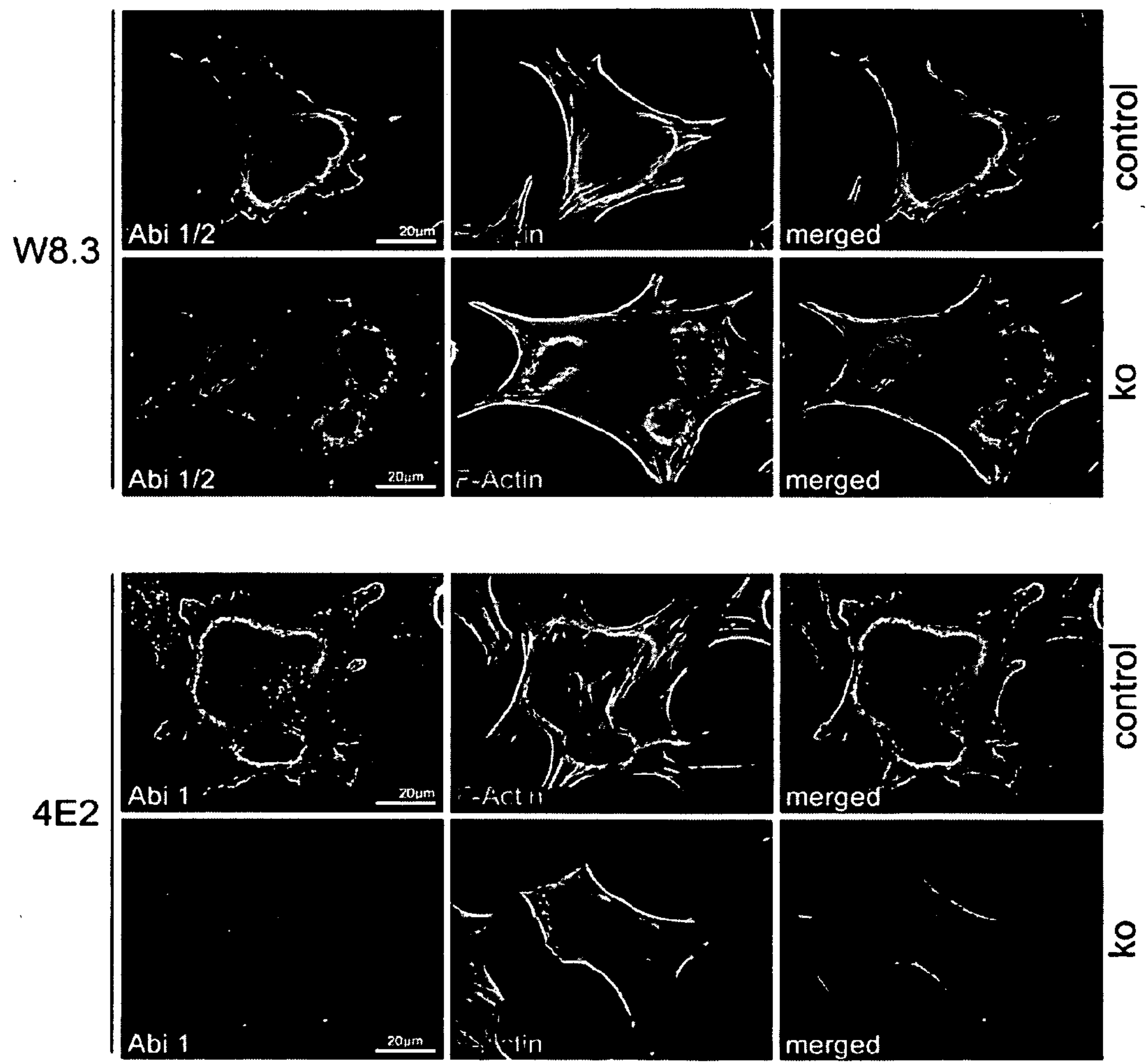
FIG. 4B

FIG. 5



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FIG. 7

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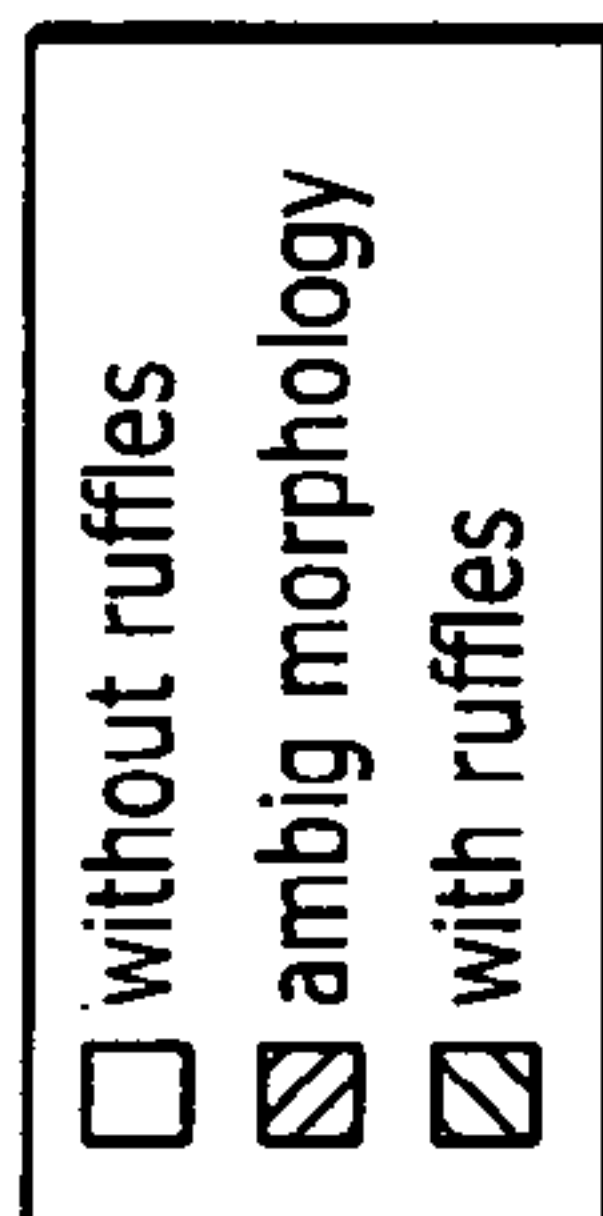


FIG. 8B

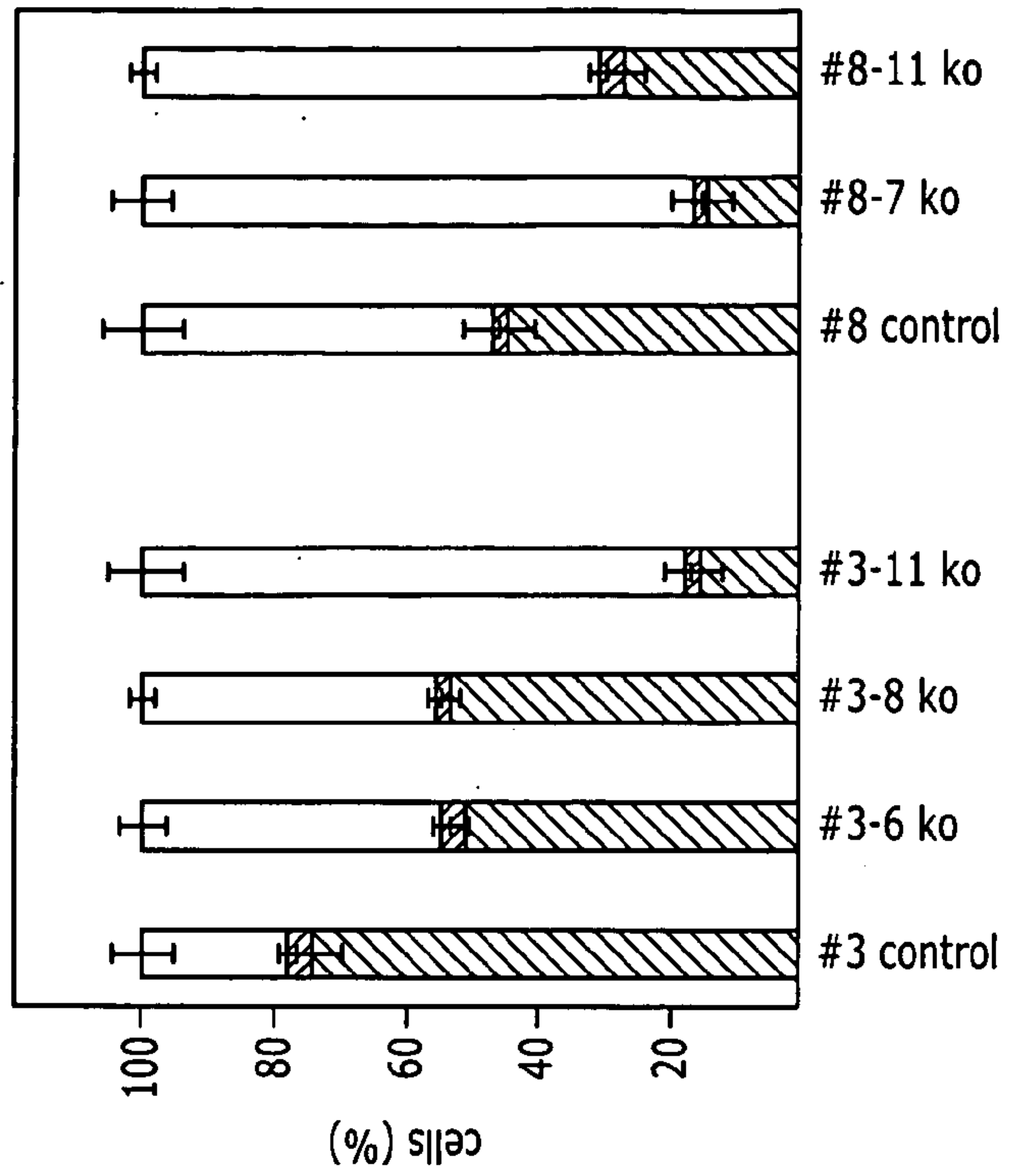
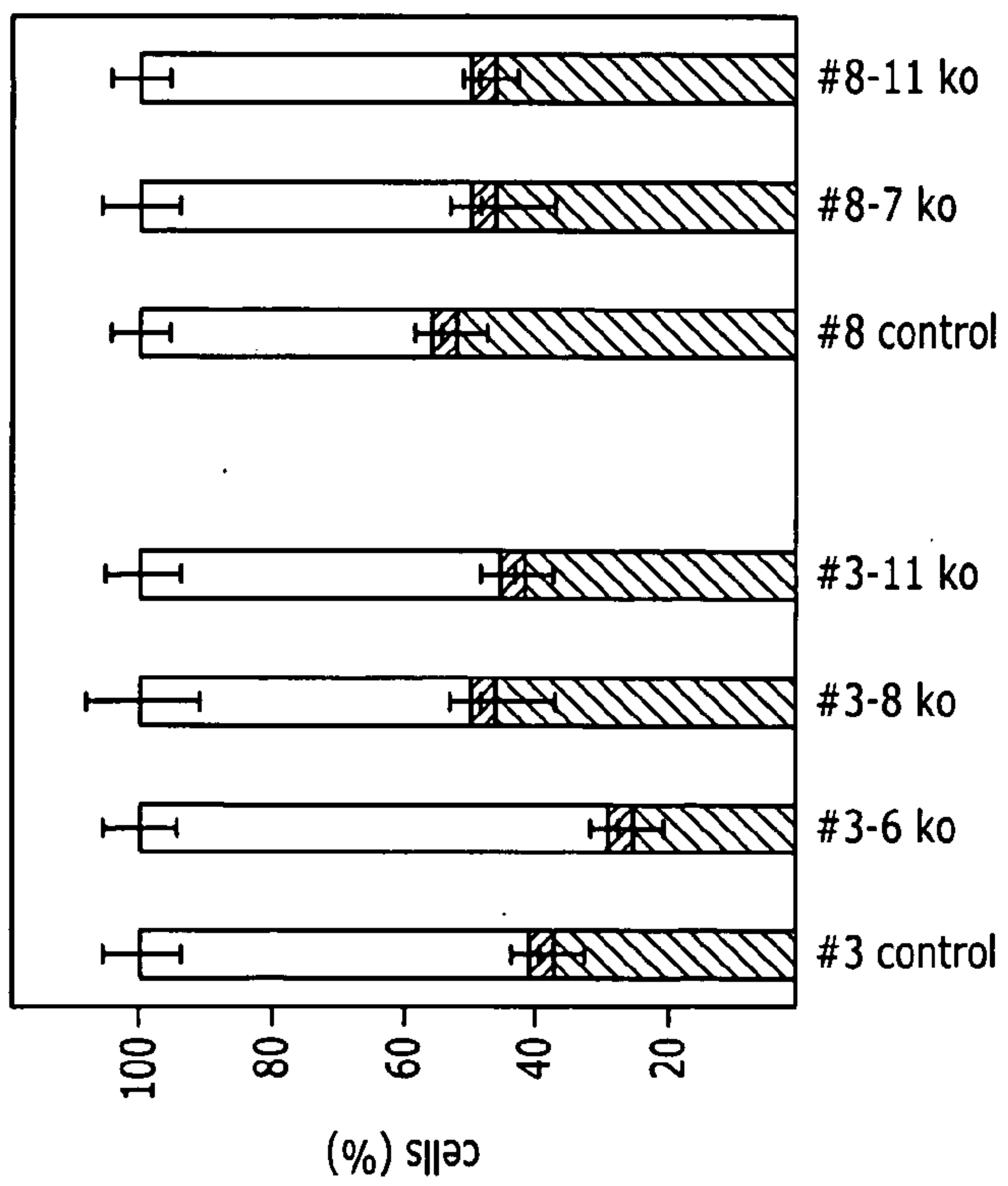
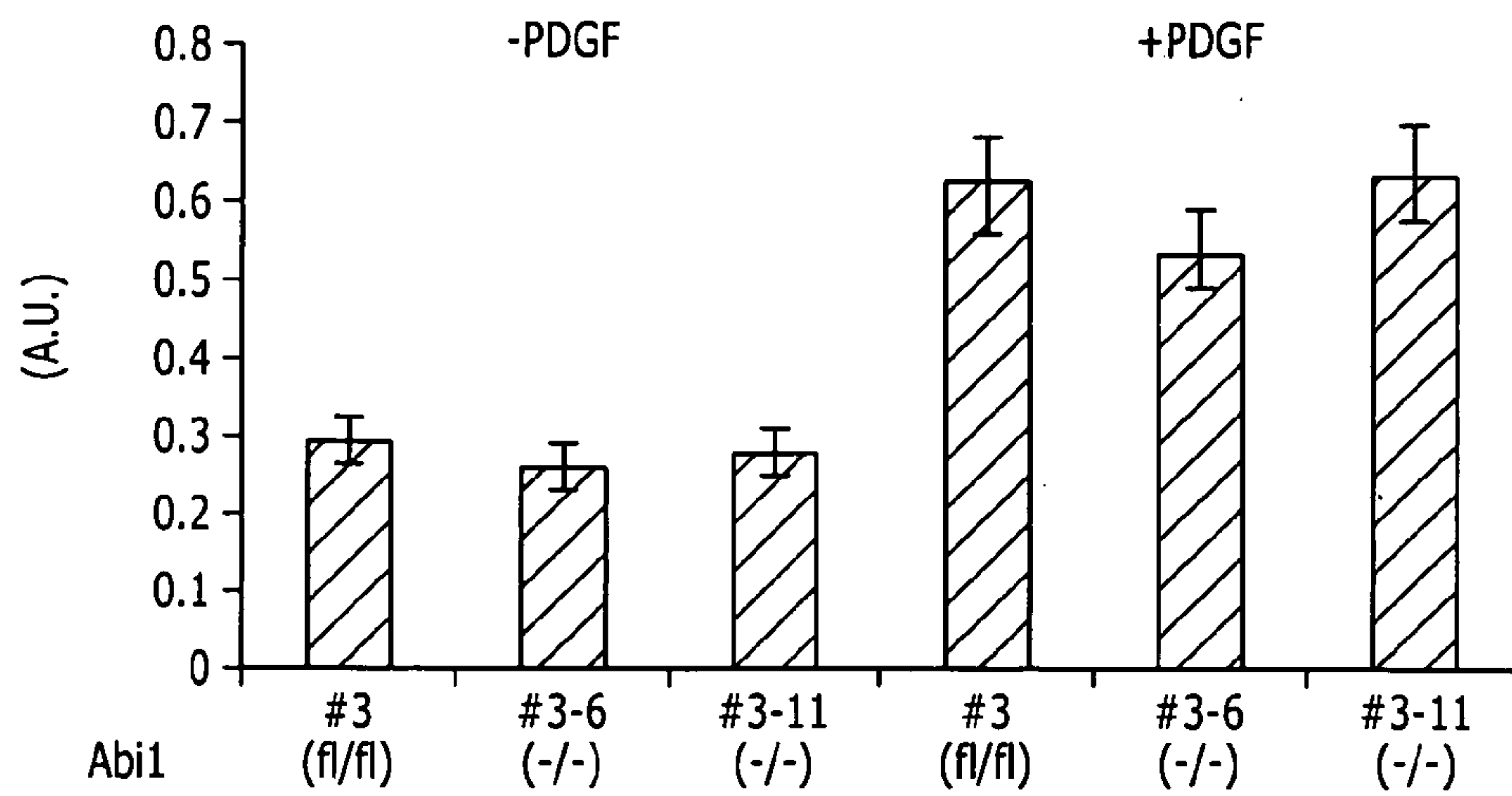
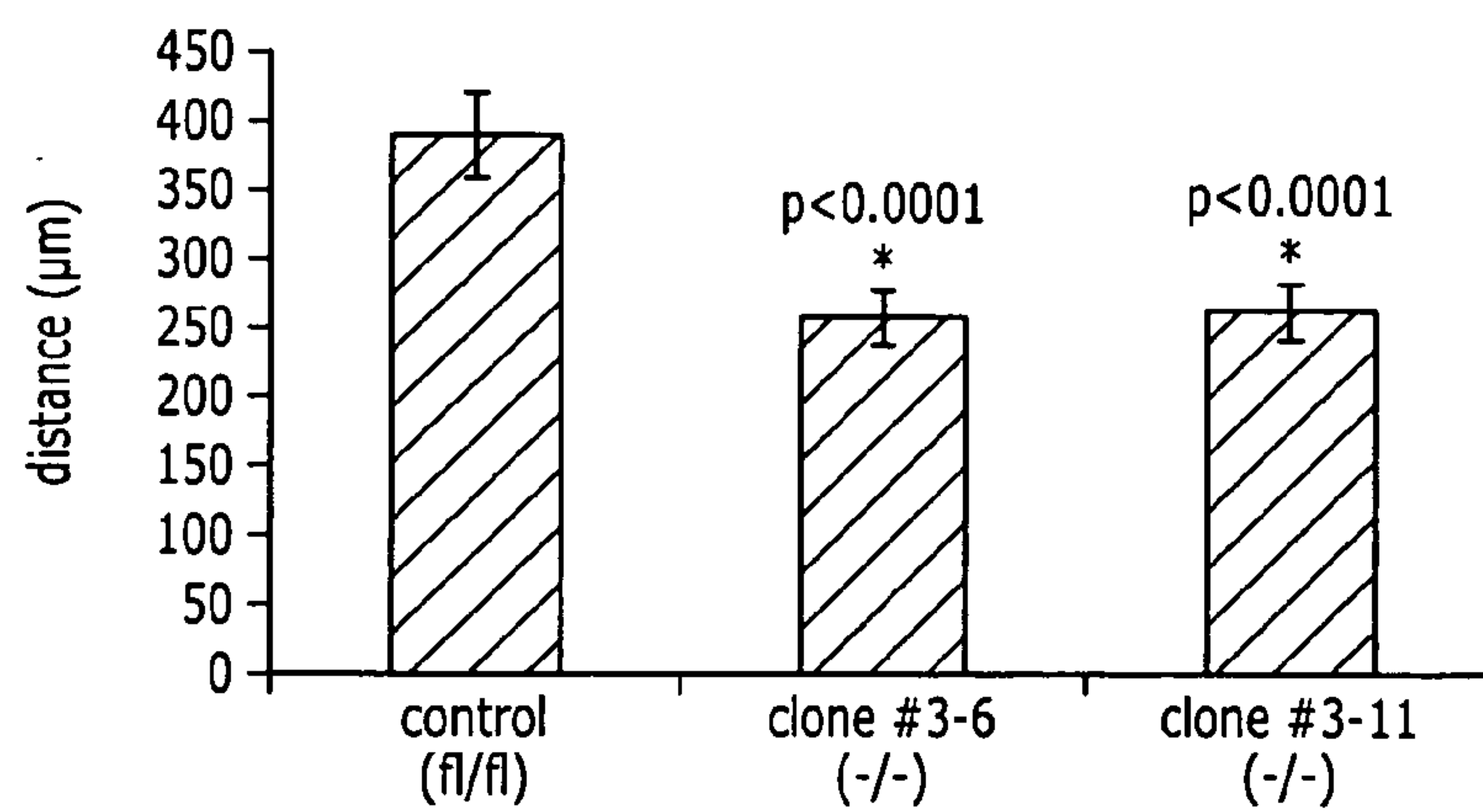


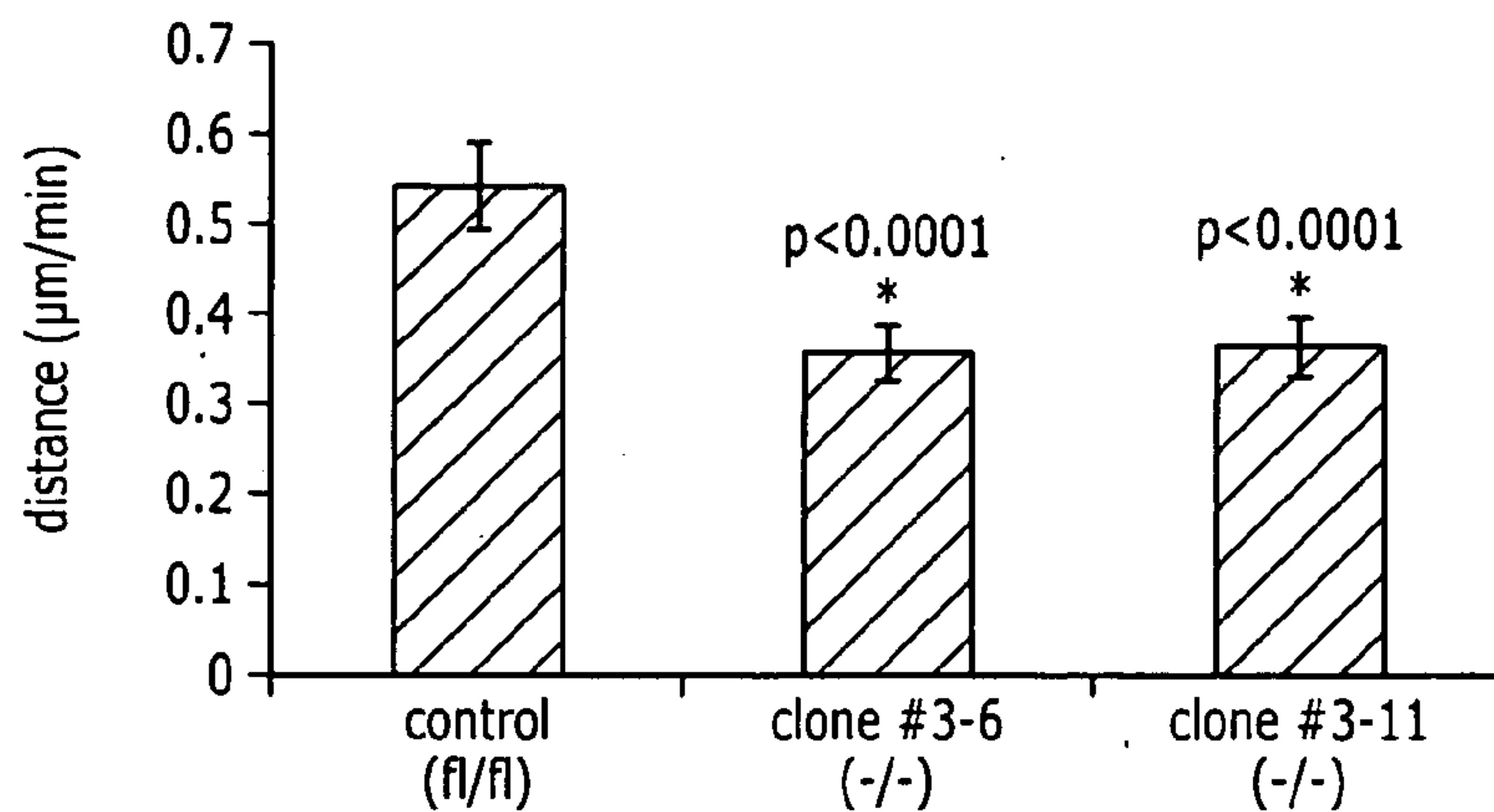
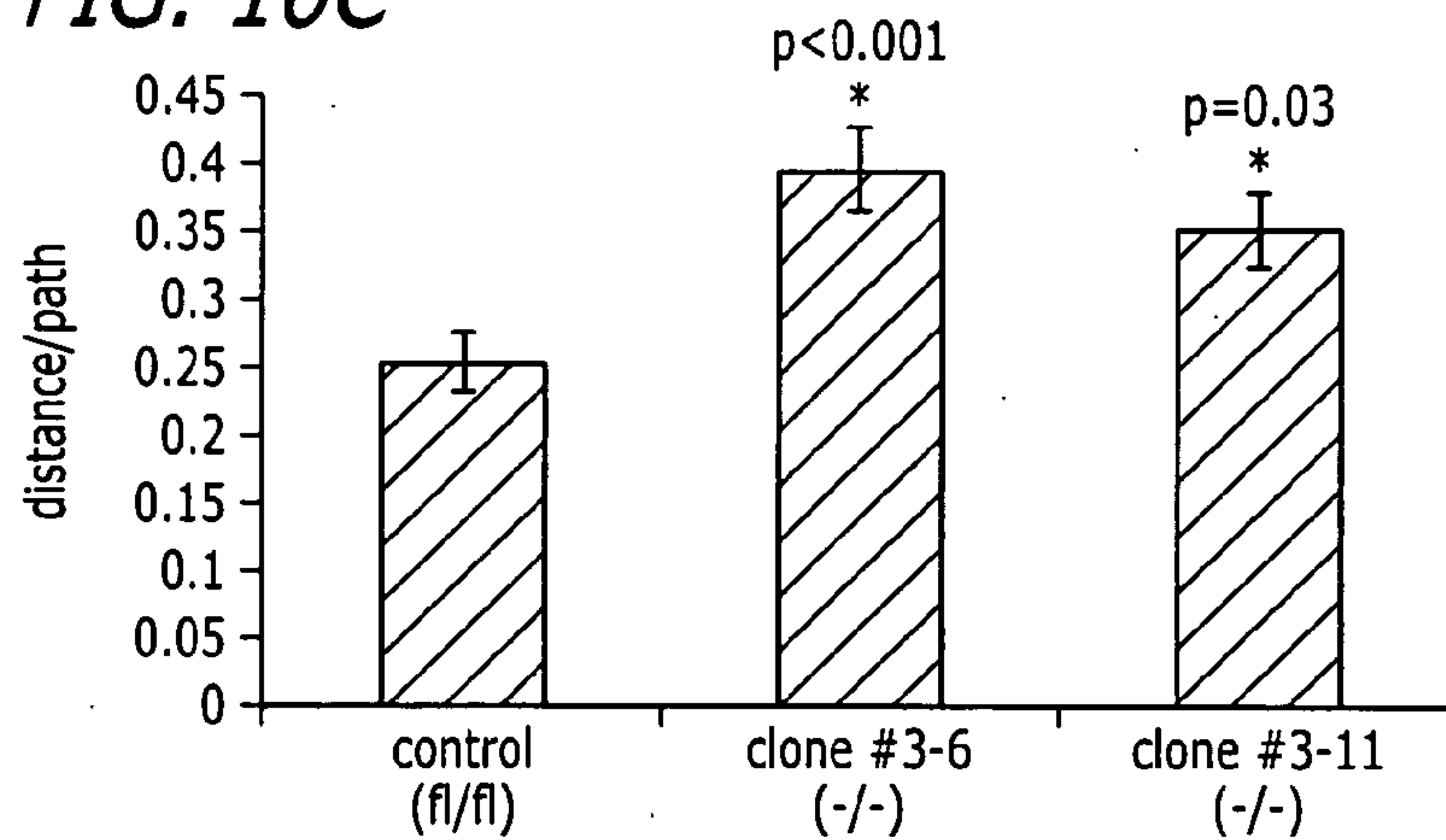
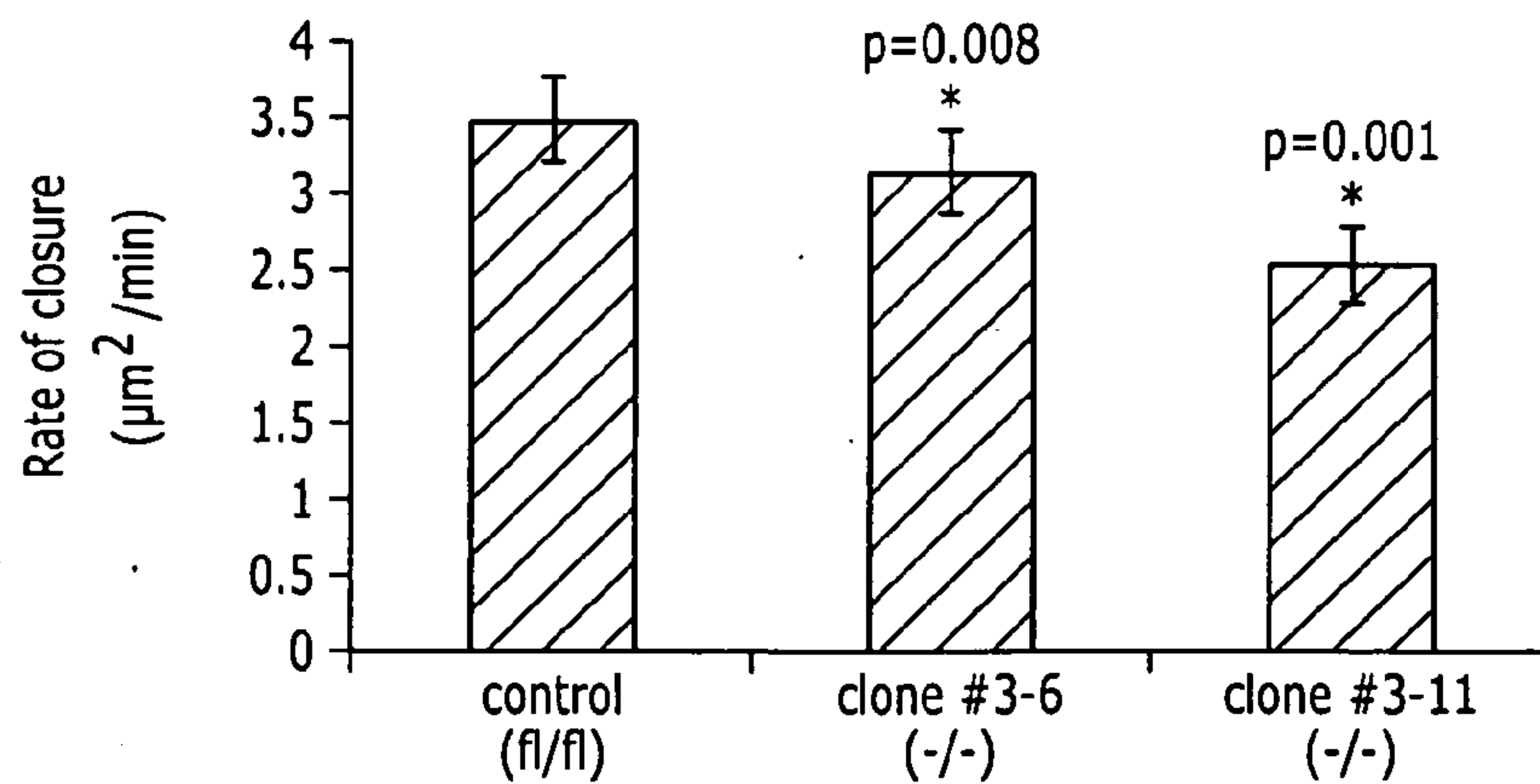
FIG. 8A



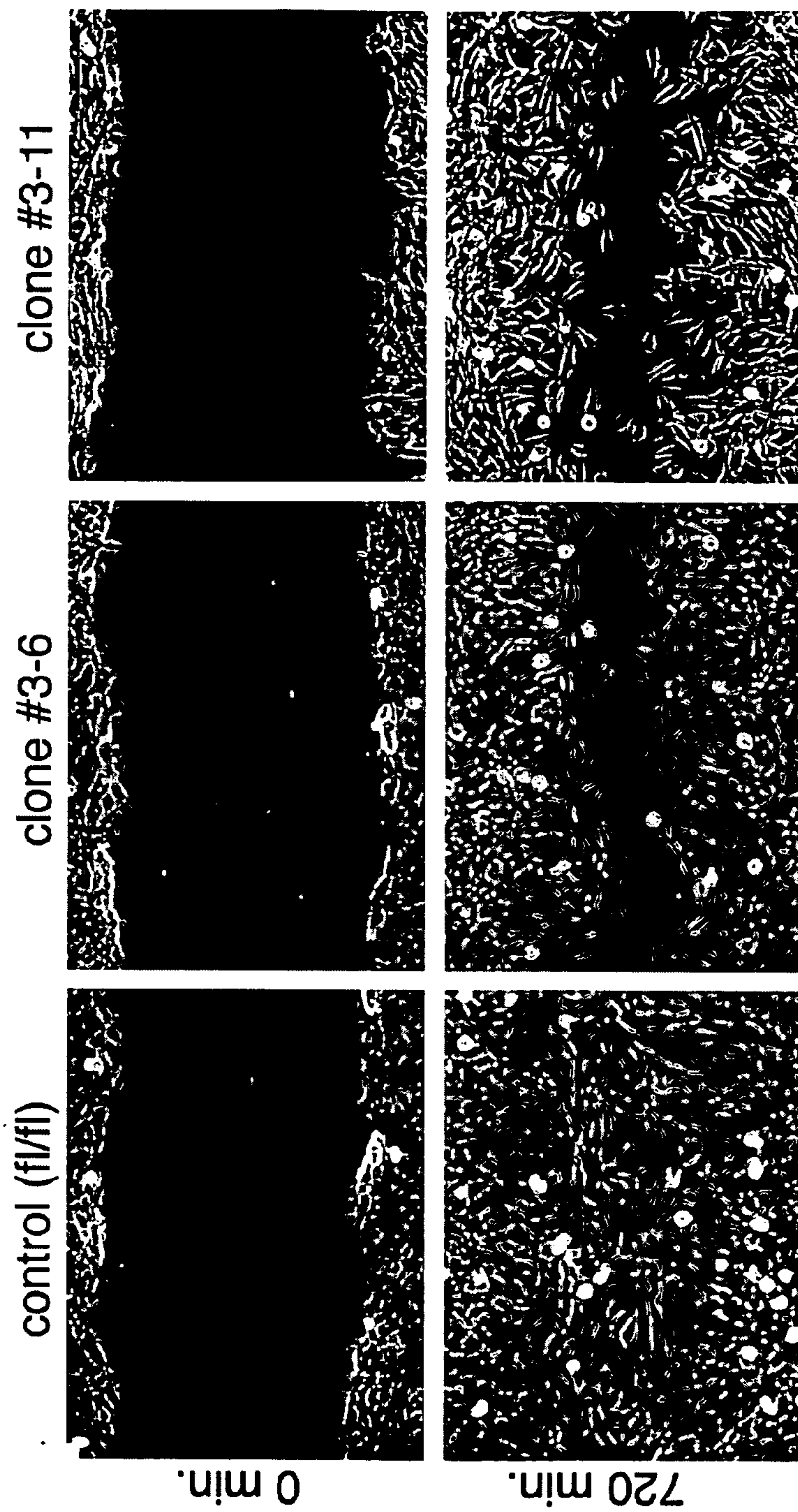
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FIG. 9**FIG. 10A**

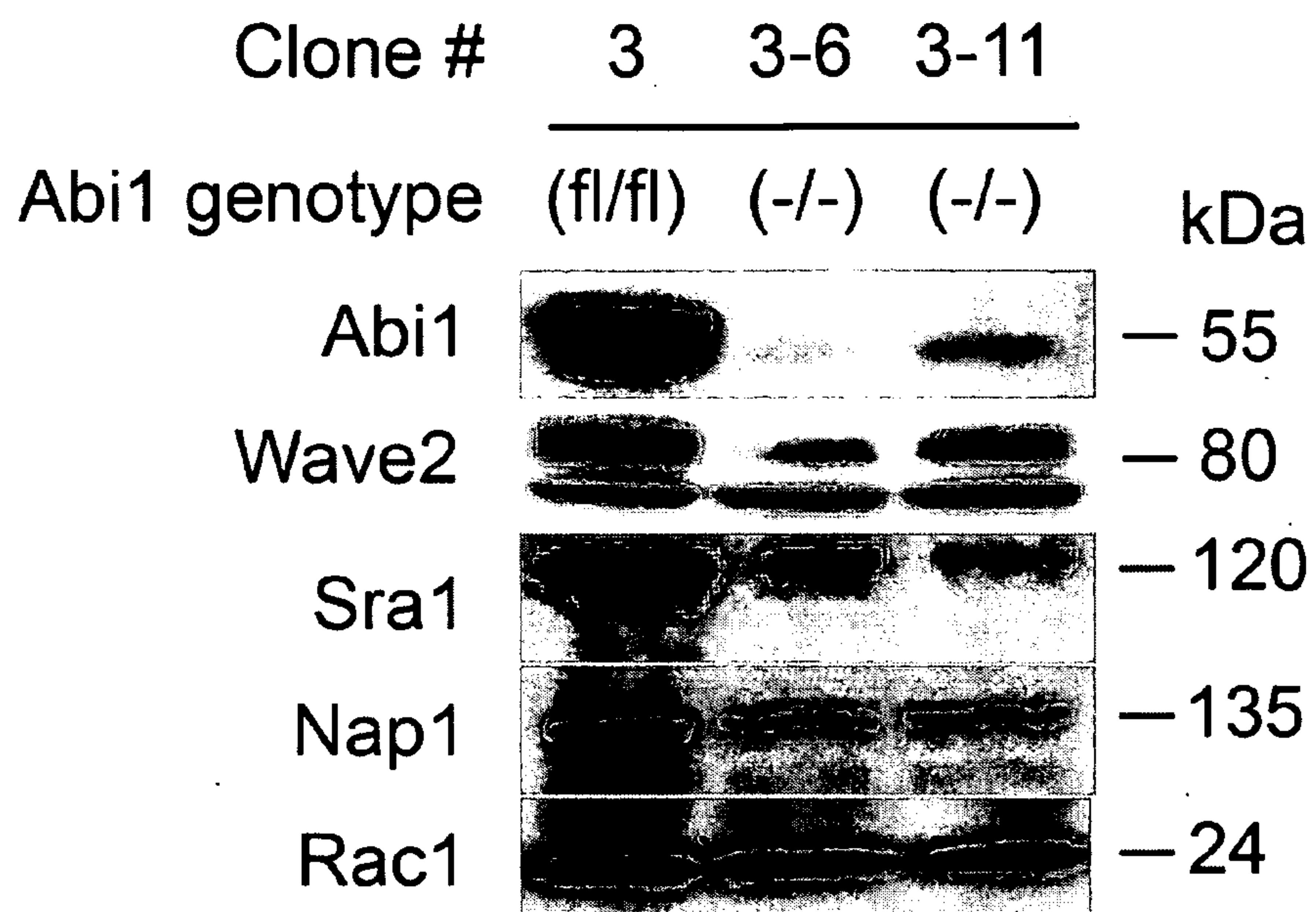
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FIG. 10B**FIG. 10C****FIG. 11A**

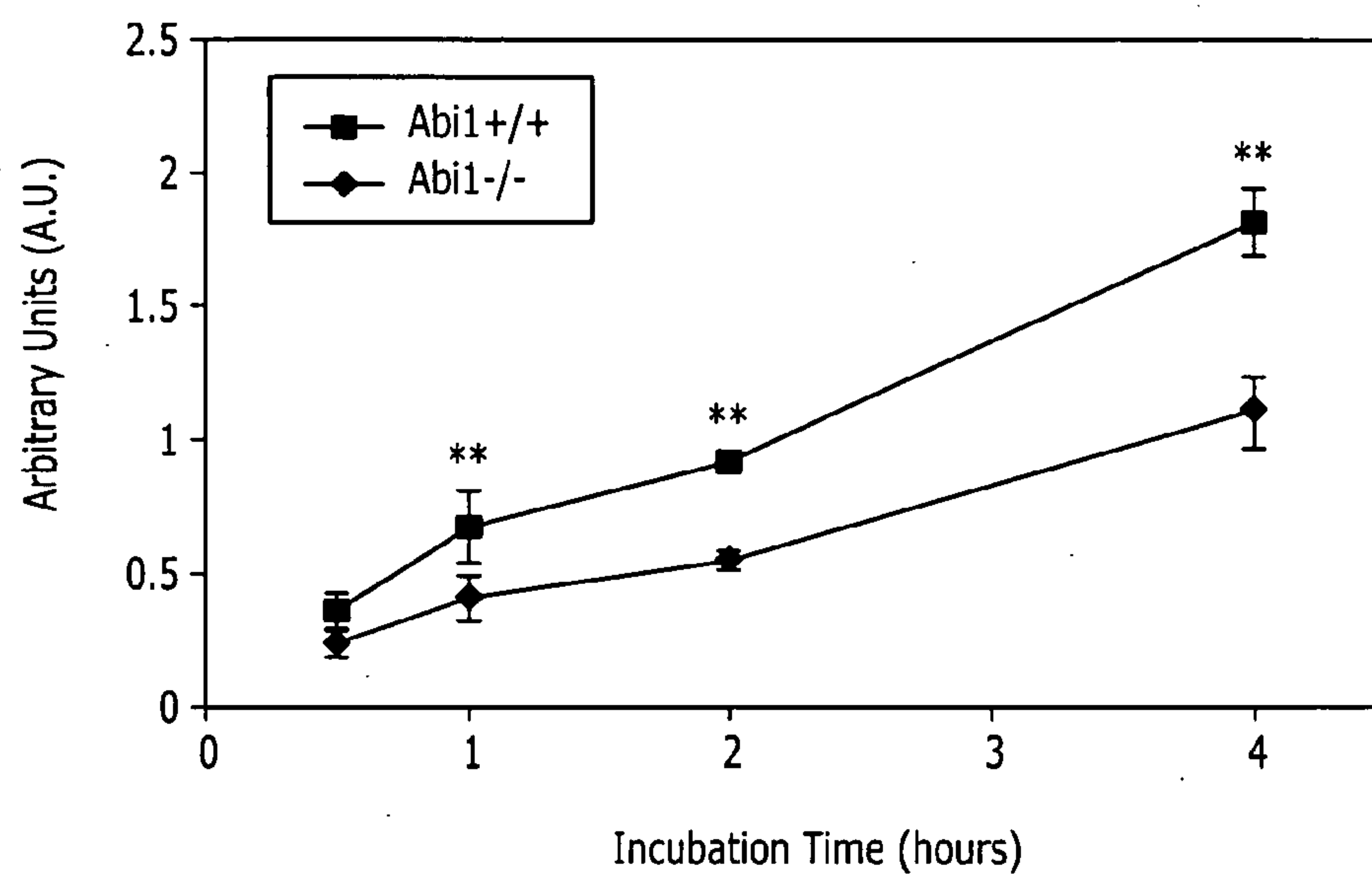
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FIG. 11B

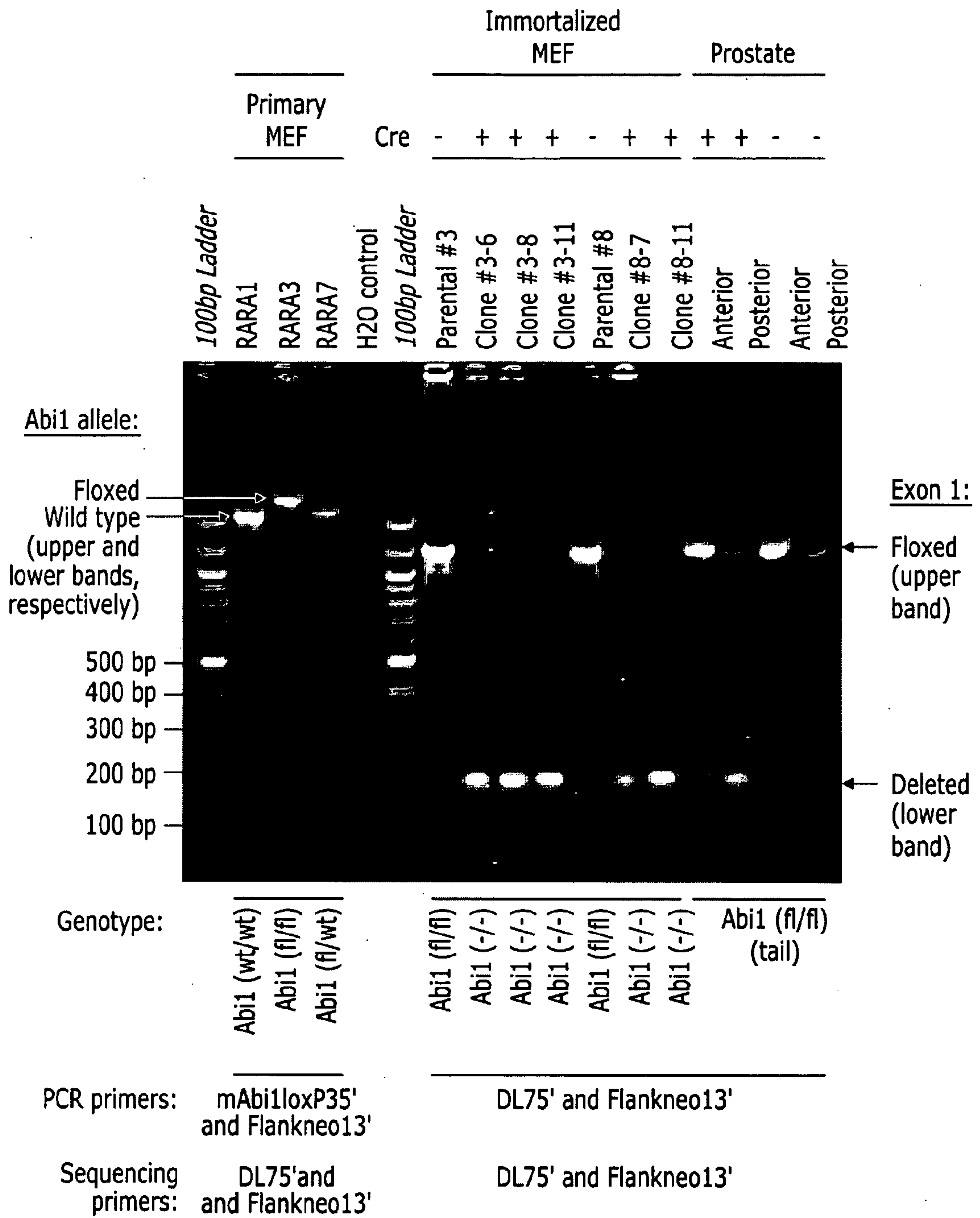
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FIG. 12

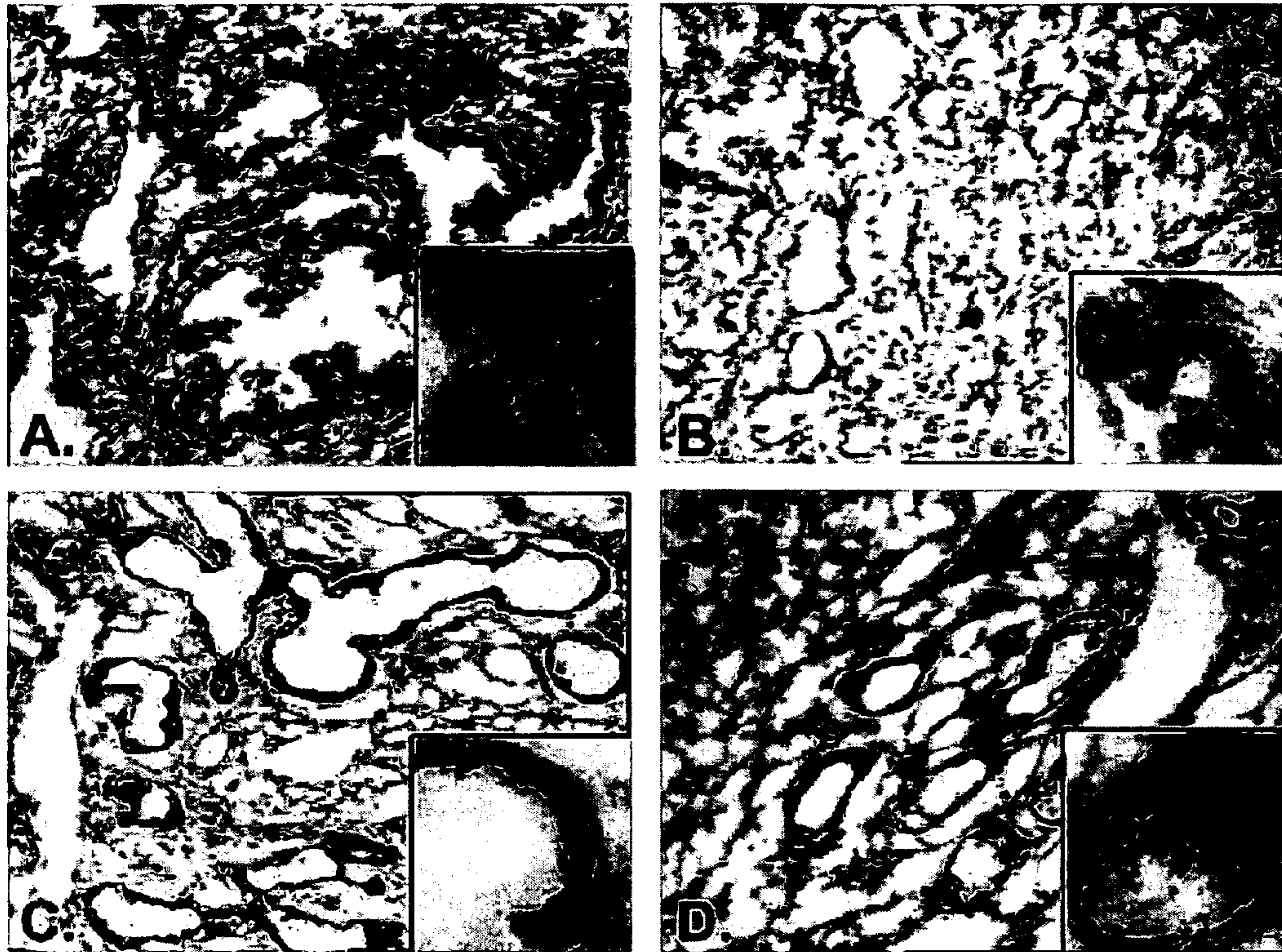
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FIG. 13

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FIG. 14

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FIG. 15**FIG. 16**