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(54) **Title:** RECURRENT GENE FUSIONS IN PROSTATE CANCER

(57) **Abstract:** Recurrent gene fusions of androgen regulated genes and ETS family member genes in prostate cancer are described. Compositions and methods having utility in prostate cancer diagnosis, research, and therapy are also provided.

WO 2007/033187 A2

RECURRENT GENE FUSIONS IN PROSTATE CANCER

This Application claims priority to provisional patent application serial numbers 60/716,436, filed 9/12/05, 60/779,041, filed 3/3/06, 60/730,358, filed 10/27/05, and 60/795,590, filed 4/28/06, each of which is herein incorporated by reference in its entirety.

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FIELD OF THE INVENTION

The present invention relates to compositions and methods for cancer diagnosis, research and therapy, including but not limited to, cancer markers. In particular, the present invention relates to recurrent gene fusions as diagnostic markers and clinical targets for prostate cancer.

BACKGROUND OF THE INVENTION

A central aim in cancer research is to identify altered genes that are causally implicated in oncogenesis. Several types of somatic mutations have been identified including base substitutions, insertions, deletions, translocations, and chromosomal gains and losses, all of which result in altered activity of an oncogene or tumor suppressor gene. First hypothesized in the early 1900's, there is now compelling evidence for a causal role for chromosomal rearrangements in cancer (Rowley, *Nat Rev Cancer* 1: 245 (2001)). Reccurent chromosomal aberrations were thought to be primarily characteristic of leukemias, lymphomas, and sarcomas. Epithelial tumors (carcinomas), which are much more common and contribute to a relatively large fraction of the morbidity and mortality associated with human cancer, comprise less than 1% of the known, disease-specific chromosomal rearrangements (Mitelman, *Mutat Res* 462: 247 (2000)). While hematological malignancies are often characterized by balanced, disease-specific chromosomal rearrangements, most solid tumors have a plethora of non-specific chromosomal aberrations. It is thought that the karyotypic complexity of solid tumors is due to secondary alterations acquired through cancer evolution or progression.

Two primary mechanisms of chromosomal rearangments have been described. In one mechanism, promoter/enhancer elements of one gene are rearranged adjacent to a proto-oncogene, thus causing altered expression of an oncogenic protein. This type of translocation is exemplified by the apposition of immunoglobulin (IG) and T-cell receptor (TCR) genes to MYC leading to activation of this oncogene in B- and T-cell malignancies, respectively (Rabbitts, *Nature* 372: 143 (1994)). In the second mechanism, rearrangement results in the fusion of two genes, which produces a fusion protein that may have a new function or altered activity. The prototypic example of this translocation is the BCR-ABL gene fusion in chronic myelogenous leukemia (CML) (Rowley, *Nature* 243: 290 (1973); de Klein et al., *Nature* 300: 765 (1982)). Importantly, this finding led to the rational development of imatinib mesylate (Gleevec), which successfully targets the BCR-ABL kinase (Deininger et al., *Blood* 105: 2640 (2005)). Thus, identifying recurrent gene rearrangements in common epithelial tumors may have profound implications for cancer drug discovery efforts as well as patient treatment.

SUMMARY OF THE INVENTION

The present invention provides, but is not limited to, methods for diagnosing prostate cancer in a patient comprising: providing a sample from the patient; and, detecting the presence or absence in the sample of a gene fusion having a 5' portion from a transcriptional regulatory region of an androgen regulated gene (ARG) and a 3' portion from an ETS family member gene, wherein the presence in the sample of the gene fusion is indicative of prostate cancer in the patient. The ARG may be TMPRSS2 or PSA. The ETS family member gene may be ERG, ETV1 (ER81), FLI1, ETS1, ETS2, ELK1, ETV6 (TEL1), ETV7 (TEL2), GABPα, ELF1, ETV4 (E1AF; PEA3), ETV5 (ERM), ERF, PEA3/E1AF, PU.1, ESE1/ESX, SAP1 (ELK4), ETV3 (METS), EWS/FLI1, ESE1, ESE2 (ELF5), ESE3, PDEF, NET (ELK3; SAP2), NERF (ELF2), or FEV. The transcriptional regulatory region of the ARG may comprise a promoter region of the ARG. The promoter region of the ARG may further comprise an androgen response element (ARE) of the ARG.

Detecting the presence or absence in the sample of a gene fusion may comprise detecting chromosomal rearrangements of genomic DNA having a 5' portion from a transcriptional regulatory region of an ARG and a 3' portion from an ETS family member gene. A variety of techniques may be used for detecting the chromosomal rearrangements of genomic DNA, including nucleic acid sequencing, nucleic acid hybridization, and,

nucleic acid amplification. Nucleic acid hybridization techniques include *in situ* hybridization (ISH), microarray, and Southern blot. Nucleic acid amplification techniques include polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), transcription-mediated amplification (TMA), ligase chain reaction (LCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

Detecting the presence or absence in the sample of a gene fusion may alternatively comprise detecting chimeric mRNA transcripts having a 5' portion from a transcriptional regulatory region of an ARG and a 3' portion from an ETS family member gene. A variety of techniques may be used for detecting the chimeric mRNA, including nucleic acid sequencing, nucleic acid hybridization, and, nucleic acid amplification. Nucleic acid hybridization techniques include *in situ* hybridization (ISH) (*e.g.*, Fluorescence *in situ* hybridization (FISH)), microarray, and Northern blot). Nucleic acid amplification techniques include, polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), transcription-mediated amplification (TMA), ligase chain reaction (LCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

Detecting the presence or absence in the sample of a gene fusion may also alternatively comprise detecting an amino-terminally truncated ETS family member protein resulting from a fusion of a transcriptional regulatory region of an ARG to an ETS family member gene, or detecting a chimeric protein having an amino-terminal portion from a transcriptional regulatory region of an ARG and a carboxy-terminal portion from an ETS family member gene. A variety of techniques may be used for detecting the truncated ETS family member protein or chimeric protein: protein sequencing; and, immunoassay. Immunoassay techniques include immunoprecipitation, Western blot, ELISA, immunohistochemistry, immunocytochemistry, flow cytometry, and immuno-PCR.

The present invention further provides, but is not limited to, compositions and kits for diagnosing prostate cancer in a patient. The compositions and kits may comprise: a single labeled probe comprising a sequence that hybridizes to the junction at which a 5' portion from a transcriptional regulatory region of an ARG fuses to a 3' portion from an ETS family member gene; a pair of labeled probes wherein the first labeled probe comprises a sequence that hybridizes to a transcriptional regulatory region of an ARG and the second labeled probe comprises a sequence that hybridizes to an ETS family member gene; a pair

of amplification oligonucleotides wherein the first amplification oligonucleotide comprises a sequence that hybridizes to a transcriptional regulatory region of an ARG and the second amplification oligonucleotide comprises a sequence that hybridizes to an ETS family member gene; an antibody to an amino-terminally truncated ETS family member protein resulting from a fusion of a transcriptional regulatory region of an ARG to an ETS family member gene; or, an antibody to a chimeric protein having an amino-terminal portion from a transcriptional regulatory region of an ARG and a carboxy-terminal portion from an ETS family member gene.

The present invention also provides, but is not limited to, methods for treating prostate cancer in a patient comprising: administering to the patient an agent that inhibits at least one biological activity of a gene fusion having a 5' portion from a transcriptional regulatory region of an androgen regulated gene (ARG) and a 3' portion from an ETS family member gene. The ARG may be TMPRSS2 or PSA. The ETS family member gene may be ERG, ETV1 (ER81), FLI1, ETS1, ETS2, ELK1, ETV6 (TEL1), ETV7 (TEL2), GABPα, ELF1, ETV4 (E1AF; PEA3), ETV5 (ERM), ERF, PEA3/E1AF, PU.1, ESE1/ESX, SAP1 (ELK4), ETV3 (METS), EWS/FLI1, ESE1, ESE2 (ELF5), ESE3, PDEF, NET (ELK3; SAP2), NERF (ELF2), and FEV. The transcriptional regulatory region of the ARG may comprise a promoter region of the ARG. The promoter region of the ARG may further comprise an androgen response element (ARE) of the ARG. The agent may be a small molecule, an siRNA, an antisense nucleic acid, or an antibody.

Additional embodiments of the present invention are provided in the description and examples below.

DESCRIPTION OF THE FIGURES

Figure 1 shows the Cancer Outlier Profile Analysis (COPA) of microarray data. (A) ETV1 (left panels) and ERG (middle panels) expression (normalized expression units) are shown from all profiled samples in two large scale gene expression studies. (B) As in (A), except data from laser capture microdissected samples were used. (C) As in (A), except oncogenes (FGFR3 and CCND1) with known translocations to the immunoglobulin heavy chain promoter (IgH) in multiple myeloma were examined.

Figure 2 shows the identification and characterization of TMPRSS2:ETV1 and TMPRSS2:ERG gene fusions in prostate cancer (PCA). (A) Prostate cancer cell lines (DuCaP, LnCaP and VCaP) and hormone refractory metastatic (MET) prostate cancer

tissues were analyzed for ERG (■) and ETV1 (□) mRNA expression by quantitative PCR (QPCR). (B) Loss of over-expression of ETV1 exons 2 and 3 in MET26 compared to LNCaP cells. (C) Schematic of 5' RNA ligase-mediated rapid amplification of cDNA ends (RLM-RACE) results for ETV1 in MET26-LN and ERG in MET28-LN revealing gene fusions with TMPRSS2. (D) Validation of TMPRSS2:ETV1 expression using translocation-specific QPCR in MET26-LN and MET26-RP. (E) Validation of TMPRSS2:ERG expression using translocation-specific QPCR in cell lines and PCA specimens.

Figure 3 shows interphase fluorescence *in situ* hybridization (FISH) on formalin-fixed paraffin embedded tissue sections that confirms TMPRSS2:ETV1 gene fusion and ERG gene rearrangement. (A and B) show two-color, fusion-signal approach to detect the fusion of TMPRSS2 (green signal) and ETV1 (red signal). (C and D) Detection of ERG gene rearrangements using a two-color split-signal approach with two probes spanning the 5' (green signal) and 3' (red signal) regions of ERG. (E) Matrix representation of FISH results using the same probes as (A-D) on an independent tissue microarray containing cores from 13 cases of clinically localized prostate cancer (PCA) and 16 cases of metastatic prostate cancer (MET).

Figure 4 shows androgen regulation of ERG in prostate cancer cells carrying the TMPRSS2:ERG translocation.

Figure 5 shows Cancer Outlier Profile Analysis (COPA). Figure 5A shows a schematic of COPA analysis. Figure 5B shows that RUNX1T1 (ETO) had the highest scoring outlier profile at the 90th percentile in the Valk et al. acute myeloid leukemia dataset (n = 293).

Figure 6 shows a schematic of RNA ligase-mediated rapid amplification of cDNA ends (RLM-RACE) results for ETV1 in MET26-LN and ERG in PCA4 revealing gene fusions with TMPRSS2 (TMPRSS2:ERGb fusion).

Figure 7 shows over-expression of ETS family members in prostate cancer. Expression of all monitored ETS family members in profiled benign prostate, prostatic intraepithelial neoplasia (PIN), clinically localized prostate cancer and metastatic prostate cancer from grossly dissected tissue (A) or tissue isolated by laser capture microdissection (B) was visualized using Oncomine.

Figure 8 shows over expression of TMPRSS2 and ETV4 loci in a prostate cancer case that over-expresses ETV4. A. Expression of the indicated exons or region of ETV4 in

pooled benign prostate tissue (CPP), prostate cancers that did not over-express ETV4 and were either TMPRSS2:ERG positive (PCA1-2) or negative (PCA3-4), and the prostate cancer case from our LCM cohort with ETV4 over-overexpression (PCA5). B. RLM-RACE reveals fusion of sequences upstream of TMPRSS2 with ETV4 in PCA5. C. Expression of TMPRSS2:ETV4a and TMPRSS2:ETV4b in PCA5 by QPCR. D. Interphase fluorescence *in situ* hybridization on formalin-fixed paraffin-embedded tissue confirms fusion of TMPRSS2 and ETV4 loci in PCA5.

Figure 9 shows mRNA sequences of exemplary ETS family genes.

Figure 10 shows the mRNA sequence of TMPRSS2.

Figure 11 shows *TMPRSS2:ERG* gene fusion analysis by FISH. Panel A: Ideogram, depicting a break apart assay for the indirect detection of *TMPRSS2:ERG* fusion. Panel B: Interphase nuclei of a stromal cell (left) and a prostate cancer gland (right). Panel C: Interphase nuclei of prostate cancer glands showing break apart and simultaneous deletion as indicated by loss of the telomeric probe (100x oil immersion objective magnification). Panel D. Magnified view of boxed area in C demonstrating two nuclei with break apart and loss of the telomeric probe. (60x oil immersion objective magnification).

Figure 12 shows Genomic deletions on chromosome 21 between *ERG* and *TMPRSS2*. Panel A: Samples, including 6 cell lines, 13 xenografts and 11 metastatic PCA samples, were characterized for *TMPRSS2:ERG* and *TMPRSS2:ETV1* status (gray bars for negative and blue bar for positive status), by qPCR and/or by FISH. Panel B: Magnification of the green framed box in A. Panel C: Magnification of the black framed box in A.

Figure 13 shows *TMPRSS2:ERG* rearrangement in clinically localized prostate cancer and association with pathological parameters. Panel A. The *TMPRSS2:ERG* rearrangement was identified in 49.2% of the primary PCA samples and 41.2% in the hormone naïve metastatic LN samples. Panel B. *TMPRSS2:ERG* rearranged tumors with deletions tended to be observed in a higher percentage of PCA cases with advanced tumor stage ($p=0.03$).

Figure 14 shows known genes located on 21q22-23 between *ERG* (centromeric) and *TMPRSS2* (telomeric). Genes above the black line are oriented 5'-centromeric to 3'-telomeric and genes below the black line are oriented 5'-telomeric to 3'-centromeric. In the lower half of the image, a magnification of the ERG locus is depicted with FISH probes.

Figure 15 shows 'heterogenous' prostate cancer case predominantly showing *TMPRSS2:ERG* rearrangement with the deletion (nucleus on the right) and only small areas showing the *TMPRSS2:ERG* rearrangement without the deletion (nucleus on the left).

Figure 16 shows meta-analysis of genes located between TMPRSS2 and ERG across 8 published expression array datasets.

Figure 17 shows that the FISH assay detects the characteristic deletion associated with TMPRSS2:ERG gene fusion, which is associated with disease progression. Panels A and B: For analyzing the ERG rearrangement on chromosome 21q22.2, a break apart probe system was applied, consisting of the Biotin-14-dCTP labeled BAC clone RP11-24A11 (eventually conjugated to produce a red signal) and the Digoxigenin-dUTP labeled BAC clone RP11-137J13 (eventually conjugated to produce a green signal), spanning the neighboring centromeric and telomeric region of the ERG locus, respectively. Using this break apart probe system, a nucleus without ERG rearrangement exhibits two pairs of juxtaposed red and green signals. Juxtaposed red-green signals form a yellow fusion signal (Panel B, arrow). Panel C: In a cumulative incidence regression model, TMPRSS2:ERG was evaluated as a determinant for the cumulative incidence or metastases or prostate cancer-specific death.

Figure 18 shows FLI1 overexpression without fusion transcript.

Figure 19 shows induction of ERG protein expression by androgen in TMPRSS2-ERG+ cells.

Figure 20 shows a schematic of the endogenous and fusion ERG polypeptides.

Figure 21 shows Nuclear interactors for ERG2.

Figure 22 shows sequences for peptide antibody and aqua probe generation against ERG1.

Figure 23 shows sequences for peptide antibody and aqua probe generation against ETV1.

Figure 24 shows sequences for peptide antibody and aqua probe generation against FLI1.

Figure 25 shows sequences for peptide antibody and aqua probe generation against ETV4.

Figure 26 shows the over-expression and androgen regulation of ETV1 in the LNCaP prostate cancer cell line. Figure 26A shows expression signature of androgen-regulated genes in VCaP and LNCaP prostate cancer cell lines. Figure 26B shows

confirmation of PSA induction by androgen in both VCaP and LNCaP cells by quantitative PCR (QPCR). Figure 26C shows ETV1 induction by androgen in LNCaP cells. Figure 26D shows that ETV1 is markedly over-expressed in LNCaP cells.

Figure 27 shows rearrangement of ETV1 in LNCaP cells. Figure 27A shows a schematic of BACs used as probes for fluorescence *in situ* hybridization (FISH). Figure 27B shows that RP11-124L22 and RP11-1149J13 co-localize to chromosome 7 in normal peripheral lymphocytes (NPLs). Figure 27C shows localization of BAC #1 and BAC #4 on metaphase spreads (top panel) and interphase cells (bottom panel) was determined in the near tetraploid LNCaP cell line. Figure 27D shows signal from RP11-124L22 localizes to chromosome 14 in LNCaP cells.

Figure 28 shoes that the entire ETV1 locus is inserted into chromosome 14 in LNCaP cells. Figure 28A shows a schematic of BACs used in this experiment. Figure 28B shows localization of RP11-124L22 (BAC #1) and RP11-313C20 (BAC #2) on metaphase spreads (top panel) and interphase cells (bottom panel) was determined by FISH in LNCaP cells.

Figure 29 shows siRNA knockdown of ETV1 in LnCaP.

Figure 30 shows siRNA knockdown of ERG in VCAP.

Figure 31 shows viral overexpression systems.

Figure 32 shows a schematic of transgenic mice.

Figure 33 shows detection of ERG and ETV1 transcripts in urine. Figure 33A shows detection of ERG and ETV1 in LNCaP (high *ETV1* expression) or VCaP (high *ERG* and *TMPRSS2:ERG* expression) prostate cancer cells. Figure 33B shows detection of ERG and ETV1 in urine of patients suspected of having prostate cancer.

Figure 34 shows assays used to detect TMPRSS2:ETS gene fusions in prostate cancer. Figure 34A shows break apart assays for TMPRSS2 and ERG. An ERG rearrangement positive case (without deletion), as indicated by one pair of split 5' and 3' signals, is shown in the left panel. A TMPRSS2 rearranegment positive case (with deletion), as indicated by a loss of one 3' signal, is shown in the right panel. Figure 34B shows a fusion assay for TMPRSS2:ETV1 gene fusions. Figure 34C shows a break apart assay for ETV4.

Figure 35 shows TMPRSS2, ERG, ETV1 and ETV4 rearrangements as detected by FISH. Figure 35A shows a Table of results for rearrangements in TMPRSS2, ERG, ETV1 and ETV4 as detected by the assays shown in Figure 34. Figure 34B shows a heat map

representation of the TMPRSS2, ERG, ETV1 and ETV4 status from the 38 cases where all four assays were evaluable as described in A. Figure 34C shows a heat map representation of cases with discordant TMPRSS2 and ETS rearrangement status.

Figure 36 shows the sequences of gene fusions of the present invention.

Figure 37 shows primers and probes for FLI-1 expression analysis.

DEFINITIONS

To facilitate an understanding of the present invention, a number of terms and phrases are defined below:

As used herein, the term "gene fusion" refers to a chimeric genomic DNA, a chimeric messenger RNA, a truncated protein or a chimeric protein resulting from the fusion of at least a portion of a first gene to at least a portion of a second gene. The gene fusion need not include entire genes or exons of genes.

As used herein, the term "transcriptional regulatory region" refers to the non-coding upstream regulatory sequence of a gene, also called the 5' untranslated region (5'UTR).

As used herein, the term "androgen regulated gene" refers to a gene or portion of a gene whose expression is initiated or enhanced by an androgen (*e.g.*, testosterone). The promoter region of an androgen regulated gene may contain an "androgen response element" that interacts with androgens or androgen signaling molecules (*e.g.*, downstream signaling molecules).

As used herein, the terms "detect", "detecting", or "detection" may describe either the general act of discovering or discerning or the specific observation of a detectably labeled composition.

As used herein, the term "inhibits at least one biological activity of a gene fusion" refers to any agent that decreases any activity of a gene fusion of the present invention (*e.g.*, including, but not limited to, the activities described herein), via directly contacting gene fusion protein, contacting gene fusion mRNA or genomic DNA, causing conformational changes of gene fusion polypeptides, decreasing gene fusion protein levels, or interfering with gene fusion interactions with signaling partners, and affecting the expression of gene fusion target genes. Inhibitors also include molecules that indirectly regulate gene fusion biological activity by intercepting upstream signaling molecules.

As used herein, the term "siRNAs" refers to small interfering RNAs. In some embodiments, siRNAs comprise a duplex, or double-stranded region, of about 18-25 nucleotides long; often siRNAs contain from about two to four unpaired nucleotides at the 3' end of each strand. At least one strand of the duplex or double-stranded region of a siRNA is substantially homologous to, or substantially complementary to, a target RNA molecule. The strand complementary to a target RNA molecule is the "antisense strand;" the strand homologous to the target RNA molecule is the "sense strand," and is also complementary to the siRNA antisense strand. siRNAs may also contain additional sequences; non-limiting examples of such sequences include linking sequences, or loops, as well as stem and other folded structures. siRNAs appear to function as key intermediaries in triggering RNA interference in invertebrates and in vertebrates, and in triggering sequence-specific RNA degradation during posttranscriptional gene silencing in plants.

The term "RNA interference" or "RNAi" refers to the silencing or decreasing of gene expression by siRNAs. It is the process of sequence-specific, post-transcriptional gene silencing in animals and plants, initiated by siRNA that is homologous in its duplex region to the sequence of the silenced gene. The gene may be endogenous or exogenous to the organism, present integrated into a chromosome or present in a transfection vector that is not integrated into the genome. The expression of the gene is either completely or partially inhibited. RNAi may also be considered to inhibit the function of a target RNA; the function of the target RNA may be complete or partial.

As used herein, the term "stage of cancer" refers to a qualitative or quantitative assessment of the level of advancement of a cancer. Criteria used to determine the stage of a cancer include, but are not limited to, the size of the tumor and the extent of metastases (*e.g.*, localized or distant).

As used herein, the term "gene transfer system" refers to any means of delivering a composition comprising a nucleic acid sequence to a cell or tissue. For example, gene transfer systems include, but are not limited to, vectors (*e.g.*, retroviral, adenoviral, adeno-associated viral, and other nucleic acid-based delivery systems), microinjection of naked nucleic acid, polymer-based delivery systems (*e.g.*, liposome-based and metallic particle-based systems), biolistic injection, and the like. As used herein, the term "viral gene transfer system" refers to gene transfer systems comprising viral elements (*e.g.*, intact viruses, modified viruses and viral components such as nucleic acids or proteins) to facilitate delivery of the sample to a desired cell or tissue. As used herein, the term

"adenovirus gene transfer system" refers to gene transfer systems comprising intact or altered viruses belonging to the family Adenoviridae.

As used herein, the term "site-specific recombination target sequences" refers to nucleic acid sequences that provide recognition sequences for recombination factors and the location where recombination takes place.

As used herein, the term "nucleic acid molecule" refers to any nucleic acid containing molecule, including but not limited to, DNA or RNA. The term encompasses sequences that include any of the known base analogs of DNA and RNA including, but not limited to, 4-acetylcytosine, 8-hydroxy-N6-methyladenosine, aziridinylcytosine, pseudoisocytosine, 5-(carboxyhydroxylmethyl) uracil, 5-fluorouracil, 5-bromouracil, 5-carboxymethylaminomethyl-2-thiouracil, 5-carboxymethylaminomethyluracil, dihydrouracil, inosine, N6-isopentenyladenine, 1-methyladenine, 1-methylpseudouracil, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-methyladenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarbonylmethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, oxybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, N-uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, and 2,6-diaminopurine.

The term "gene" refers to a nucleic acid (*e.g.*, DNA) sequence that comprises coding sequences necessary for the production of a polypeptide, precursor, or RNA (*e.g.*, rRNA, tRNA). The polypeptide can be encoded by a full length coding sequence or by any portion of the coding sequence so long as the desired activity or functional properties (*e.g.*, enzymatic activity, ligand binding, signal transduction, immunogenicity, etc.) of the full-length or fragment are retained. The term also encompasses the coding region of a structural gene and the sequences located adjacent to the coding region on both the 5' and 3' ends for a distance of about 1 kb or more on either end such that the gene corresponds to the length of the full-length mRNA. Sequences located 5' of the coding region and present on the mRNA are referred to as 5' non-translated sequences. Sequences located 3' or downstream of the coding region and present on the mRNA are referred to as 3' non-translated sequences. The term "gene" encompasses both cDNA and genomic forms of a

gene. A genomic form or clone of a gene contains the coding region interrupted with non-coding sequences termed "introns" or "intervening regions" or "intervening sequences." Introns are segments of a gene that are transcribed into nuclear RNA (hnRNA); introns may contain regulatory elements such as enhancers. Introns are removed or "spliced out" from the nuclear or primary transcript; introns therefore are absent in the messenger RNA (mRNA) transcript. The mRNA functions during translation to specify the sequence or order of amino acids in a nascent polypeptide.

As used herein, the term "heterologous gene" refers to a gene that is not in its natural environment. For example, a heterologous gene includes a gene from one species introduced into another species. A heterologous gene also includes a gene native to an organism that has been altered in some way (*e.g.*, mutated, added in multiple copies, linked to non-native regulatory sequences, etc). Heterologous genes are distinguished from endogenous genes in that the heterologous gene sequences are typically joined to DNA sequences that are not found naturally associated with the gene sequences in the chromosome or are associated with portions of the chromosome not found in nature (*e.g.*, genes expressed in loci where the gene is not normally expressed).

As used herein, the term "oligonucleotide," refers to a short length of single-stranded polynucleotide chain. Oligonucleotides are typically less than 200 residues long (*e.g.*, between 15 and 100), however, as used herein, the term is also intended to encompass longer polynucleotide chains. Oligonucleotides are often referred to by their length. For example a 24 residue oligonucleotide is referred to as a "24-mer". Oligonucleotides can form secondary and tertiary structures by self-hybridizing or by hybridizing to other polynucleotides. Such structures can include, but are not limited to, duplexes, hairpins, cruciforms, bends, and triplexes.

As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (*i.e.*, a sequence of nucleotides) related by the base-pairing rules. For example, the sequence "5'-A-G-T-3'," is complementary to the sequence "3'-T-C-A-5'." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods that depend upon binding between nucleic acids.

The term "homology" refers to a degree of complementarity. There may be partial homology or complete homology (*i.e.*, identity). A partially complementary sequence is a nucleic acid molecule that at least partially inhibits a completely complementary nucleic acid molecule from hybridizing to a target nucleic acid is "substantially homologous." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or Northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe will compete for and inhibit the binding (*i.e.*, the hybridization) of a completely homologous nucleic acid molecule to a target under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to one another be a specific (*i.e.*, selective) interaction. The absence of non-specific binding may be tested by the use of a second target that is substantially non-complementary (*e.g.*, less than about 30% identity); in the absence of non-specific binding the probe will not hybridize to the second non-complementary target.

When used in reference to a double-stranded nucleic acid sequence such as a cDNA or genomic clone, the term "substantially homologous" refers to any probe that can hybridize to either or both strands of the double-stranded nucleic acid sequence under conditions of low stringency as described above.

A gene may produce multiple RNA species that are generated by differential splicing of the primary RNA transcript. cDNAs that are splice variants of the same gene will contain regions of sequence identity or complete homology (representing the presence of the same exon or portion of the same exon on both cDNAs) and regions of complete non-identity (for example, representing the presence of exon "A" on cDNA 1 wherein cDNA 2 contains exon "B" instead). Because the two cDNAs contain regions of sequence identity they will both hybridize to a probe derived from the entire gene or portions of the gene containing sequences found on both cDNAs; the two splice variants are therefore substantially homologous to such a probe and to each other.

When used in reference to a single-stranded nucleic acid sequence, the term "substantially homologous" refers to any probe that can hybridize (*i.e.*, it is the complement of) the single-stranded nucleic acid sequence under conditions of low stringency as described above.

As used herein, the term "hybridization" is used in reference to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (*i.e.*, the strength of the association between the nucleic acids) is impacted by such factors as the degree of complementary between the nucleic acids, stringency of the conditions involved, the T_m of the formed hybrid, and the G:C ratio within the nucleic acids. A single molecule that contains pairing of complementary nucleic acids within its structure is said to be "self-hybridized."

As used herein the term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds such as organic solvents, under which nucleic acid hybridizations are conducted. Under "low stringency conditions" a nucleic acid sequence of interest will hybridize to its exact complement, sequences with single base mismatches, closely related sequences (*e.g.*, sequences with 90% or greater homology), and sequences having only partial homology (*e.g.*, sequences with 50-90% homology). Under 'medium stringency conditions," a nucleic acid sequence of interest will hybridize only to its exact complement, sequences with single base mismatches, and closely relation sequences (*e.g.*, 90% or greater homology). Under "high stringency conditions," a nucleic acid sequence of interest will hybridize only to its exact complement, and (depending on conditions such a temperature) sequences with single base mismatches. In other words, under conditions of high stringency the temperature can be raised so as to exclude hybridization to sequences with single base mismatches.

"High stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42°C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH_2PO_4 H_2O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 0.1X SSPE, 1.0% SDS at 42°C when a probe of about 500 nucleotides in length is employed.

"Medium stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42°C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH_2PO_4 H_2O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 1.0X SSPE, 1.0% SDS at 42°C when a probe of about 500 nucleotides in length is employed.

"Low stringency conditions" comprise conditions equivalent to binding or hybridization at 42°C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l NaH_2PO_4 H_2O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.1% SDS, 5X Denhardt's reagent [50X Denhardt's contains per 500 ml: 5 g Ficoll (Type 400, Pharamcia), 5 g BSA (Fraction V; Sigma)] and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 5X SSPE, 0.1% SDS at 42°C when a probe of about 500 nucleotides in length is employed.

The art knows well that numerous equivalent conditions may be employed to comprise low stringency conditions; factors such as the length and nature (DNA, RNA, base composition) of the probe and nature of the target (DNA, RNA, base composition, present in solution or immobilized, etc.) and the concentration of the salts and other components (*e.g.*, the presence or absence of formamide, dextran sulfate, polyethylene glycol) are considered and the hybridization solution may be varied to generate conditions of low stringency hybridization different from, but equivalent to, the above listed conditions. In addition, the art knows conditions that promote hybridization under conditions of high stringency (*e.g.*, increasing the temperature of the hybridization and/or wash steps, the use of formamide in the hybridization solution, etc.) (see definition above for "stringency").

As used herein, the term "amplification oligonucleotide" refers to an oligonucleotide that hybridizes to a target nucleic acid, or its complement, and participates in a nucleic acid amplification reaction. An example of an amplification oligonucleotide is a "primer" that hybridizes to a template nucleic acid and contains a 3' OH end that is extended by a polymerase in an amplification process. Another example of an amplification oligonucleotide is an oligonucleotide that is not extended by a polymerase (*e.g.*, because it has a 3' blocked end) but participates in or facilitates amplification. Amplification oligonucleotides may optionally include modified nucleotides or analogs, or additional nucleotides that participate in an amplification reaction but are not complementary to or contained in the target nucleic acid. Amplification oligonucleotides may contain a sequence that is not complementary to the target or template sequence. For example, the 5' region of a primer may include a promoter sequence that is non-complementary to the target nucleic acid (referred to as a "promoter-primer"). Those skilled in the art will understand that an amplification oligonucleotide that functions as a primer may be modified to include a 5' promoter sequence, and thus function as a promoter-primer. Similarly, a promoter-primer may be modified by removal of, or synthesis without, a promoter sequence and still function

as a primer. A 3' blocked amplification oligonucleotide may provide a promoter sequence and serve as a template for polymerization (referred to as a "promoter-provider").

As used herein, the term "primer" refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, that is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product that is complementary to a nucleic acid strand is induced, (*i.e.*, in the presence of nucleotides and an inducing agent such as DNA polymerase and at a suitable temperature and pH). The primer is preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. Preferably, the primer is an oligodeoxyribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the inducing agent. The exact lengths of the primers will depend on many factors, including temperature, source of primer and the use of the method.

As used herein, the term "probe" refers to an oligonucleotide (*i.e.*, a sequence of nucleotides), whether occurring naturally as in a purified restriction digest or produced synthetically, recombinantly or by PCR amplification, that is capable of hybridizing to at least a portion of another oligonucleotide of interest. A probe may be single-stranded or double-stranded. Probes are useful in the detection, identification and isolation of particular gene sequences. It is contemplated that any probe used in the present invention will be labeled with any "reporter molecule," so that is detectable in any detection system, including, but not limited to enzyme (*e.g.*, ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems. It is not intended that the present invention be limited to any particular detection system or label.

The term "isolated" when used in relation to a nucleic acid, as in "an isolated oligonucleotide" or "isolated polynucleotide" refers to a nucleic acid sequence that is identified and separated from at least one component or contaminant with which it is ordinarily associated in its natural source. Isolated nucleic acid is such present in a form or setting that is different from that in which it is found in nature. In contrast, non-isolated nucleic acids as nucleic acids such as DNA and RNA found in the state they exist in nature. For example, a given DNA sequence (*e.g.*, a gene) is found on the host cell chromosome in proximity to neighboring genes; RNA sequences, such as a specific mRNA sequence encoding a specific protein, are found in the cell as a mixture with numerous other mRNAs

that encode a multitude of proteins. However, isolated nucleic acid encoding a given protein includes, by way of example, such nucleic acid in cells ordinarily expressing the given protein where the nucleic acid is in a chromosomal location different from that of natural cells, or is otherwise flanked by a different nucleic acid sequence than that found in nature. The isolated nucleic acid, oligonucleotide, or polynucleotide may be present in single-stranded or double-stranded form. When an isolated nucleic acid, oligonucleotide or polynucleotide is to be utilized to express a protein, the oligonucleotide or polynucleotide will contain at a minimum the sense or coding strand (*i.e.*, the oligonucleotide or polynucleotide may be single-stranded), but may contain both the sense and anti-sense strands (*i.e.*, the oligonucleotide or polynucleotide may be double-stranded).

As used herein, the term "purified" or "to purify" refers to the removal of components (*e.g.*, contaminants) from a sample. For example, antibodies are purified by removal of contaminating non-immunoglobulin proteins; they are also purified by the removal of immunoglobulin that does not bind to the target molecule. The removal of non-immunoglobulin proteins and/or the removal of immunoglobulins that do not bind to the target molecule results in an increase in the percent of target-reactive immunoglobulins in the sample. In another example, recombinant polypeptides are expressed in bacterial host cells and the polypeptides are purified by the removal of host cell proteins; the percent of recombinant polypeptides is thereby increased in the sample.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based on the discovery of recurrent gene fusions in prostate cancer. The present invention provides diagnostic, research, and therapeutic methods that either directly or indirectly detect or target the gene fusions. The present invention also provides compositions for diagnostic, research, and therapeutic purposes.

I. Gene Fusions

The present invention identifies recurrent gene fusions indicative of prostate cancer. The gene fusions are the result of a chromosomal rearrangement of an androgen regulated gene (ARG) and an ETS family member gene. Despite their recurrence, the junction where the ARG fuses to the ETS family member gene varies. The gene fusions typically comprise a 5' portion from a transcriptional regulatory region of an ARG and a 3' portion from an

ETS family member gene. The recurrent gene fusions have use as diagnostic markers and clinical targets for prostate cancer.

A. Androgen Regulated Genes

Genes regulated by androgenic hormones are of critical importance for the normal physiological function of the human prostate gland. They also contribute to the development and progression of prostate carcinoma. Recognized ARGs include, but are not limited to: TMPRSS2; PSA; PSMA; KLK2; SNRK; Seladin-1; and, FKBP51 (Paoloni-Giacobino et al., *Genomics* 44: 309 (1997); Velasco et al., *Endocrinology* 145(8): 3913 (2004)). TMPRSS2 (NM_005656), in particular, has been demonstrated to be highly expressed in prostate epithelium relative to other normal human tissues (Lin et al., *Cancer Research* 59: 4180 (1999)). The TMPRSS2 gene is located on chromosome 21. This gene is located at 41,750,797 – 41,801,948 bp from the pter (51,151 total bp; minus strand orientation). The human TMPRSS2 protein sequence may be found at GenBank accession no. AAC51784 (Swiss Protein accession no. O15393)) and the corresponding cDNA at GenBank accession no. U75329 (see also, Paoloni-Giacobino, et al., *Genomics* 44: 309 (1997)).

The transcriptional regulatory region of an ARG may contain coding or non-coding regions of the ARG, including the promoter region. The promoter region of the ARG may further contain an androgen response element (ARE) of the ARG. The promoter region for TMPRSS2, in particular, is provided by GenBank accession number AJ276404.

B. ETS Family Member Genes

The ETS family of transcription factors regulate the intra-cellular signaling pathways controlling gene expression. As downstream effectors, they activate or repress specific target genes. As upstream effectors, they are responsible for the spacial and temporal expression of numerous growth factor receptors. Almost 30 members of this family have been identified and implicated in a wide range of physiological and pathological processes. These include, but are not limited to: ERG; ETV1 (ER81); FLI1; ETS1; ETS2; ELK1; ETV6 (TEL1); ETV7 (TEL2); GABPα; ELF1; ETV4 (E1AF; PEA3); ETV5 (ERM); ERF; PEA3/E1AF; PU.1; ESE1/ESX; SAP1 (ELK4); ETV3 (METS); EWS/FLI1; ESE1; ESE2 (ELF5); ESE3; PDEF; NET (ELK3; SAP2); NERF (ELF2); and FEV. Exemplary ETS family member gene sequences are given in Figure 9.

ERG (NM_004449), in particular, has been demonstrated to be highly expressed in prostate epithelium relative to other normal human tissues. The ERG gene is located on chromosome 21. The gene is located at 38,675,671– 38,955,488 base pairs from the pter. The ERG gene is 279,817 total bp; minus strand orientation. The corresponding ERG cDNA and protein sequences are given at GenBank accesssion no. M17254 and GenBank accession no. NP04440 (Swiss Protein acc. no. P11308), respectively.

The ETV1 gene is located on chromosome 7 (GenBank accession nos. NC_000007.11; NC_086703.11; and NT_007819.15). The gene is located at 13,708330 – 13,803,555 base pairs from the pter. The ETV1 gene is 95,225 bp total, minus strand orientation. The corresponding ETV1 cDNA and protein sequences are given at GenBank accession no. NM_004956 and GenBank accession no. NP_004947 (Swiss protein acc. no. P50549), respectively.

The human ETV4 gene is located on chromosome 14 (GenBank accession nos. NC_000017.9; NT_010783.14; and NT_086880.1). The gene is at 38,960,740 – 38,979,228 base pairs from the pter. The ETV4 gene is 18,488 bp total, minus strand orientation. The corresponding ETV4 cDNA and protein sequences are given at GenBank accession no. NM_001986 and GenBank accession no. NP_01977 (Swiss protein acc. no. P43268), respectively.

C. ARG/ETS Gene Fusions

As described above, the present invention provides fusions of an ARG to an ETS family member gene. Exemplary gene fusion sequences are given in Figure 36. For all involved genes (TMPRSS2, ERG, ETV1 and ETV4), the GenBank reference sequence ID's are provided and the exons are aligned using the May 2004 assembly of the UCSC Human Genome. For all identified fusions, Figure 36 provides a complete sequence from the beginning of the TMPRSS2 gene through the fusion and the stop codon of the ETS family member gene. The deposited GenBank sequence for each of the published variants is also provided. Some TMPRSS2:ERG and TMPRSS2:ETV1 fusions are described by the breakpoint exons of TMPRSS2 and the ETS family member gene. For example, TMPRSS2:ERGa, which fuses exon 1 of TMPRSS2 to exons 4 through 11 of ERG, is identified as TMPRSS2:ERG(1,4).

The fusion of an ARG to an ETS family member gene is detectable as DNA, RNA or protein. Initially, the gene fusion is detectable as a chromosomal rearrangement of

genomic DNA having a 5' portion from a transcriptional regulatory region of the ARG and a 3' portion from the ETS family member gene. Once transcribed, the gene fusion is detectable as a chimeric mRNA having a 5' portion from the transcriptional regulatory region of the ARG and a 3' portion from the ETS family member gene. Once translated, the gene fusion is detectable as an amino-terminally truncated ETS family member protein resulting from the fusion of the transcriptional regulatory region of the ARG to the ETS family member gene; a chimeric protein having an amino-terminal portion from the transcriptional regulatory region of the ARG and a carboxy-terminal portion from the ETS family member gene; or, an upregulated, but otherwise indistinguishable, native ETS family member protein. The truncated ETS family member protein and chimeric protein may differ from their respective native proteins in amino acid sequence, post-translational processing and/or secondary, tertiary or quaternary structure. Such differences, if present, can be used to identify the presence of the gene fusion. Specific methods of detection are described in more detail below.

Certain gene fusions are more common than others in prostate cancer. The present invention identifies 50-80% of prostate cancers as having recurrent gene fusions of TMPRSS2 with ERG, ETV1, ETV4, or FLI1. Of those, 50-70% are TMPRSS2-ERG, 50%-60% of which result from the deletion of genetic information between the TMPRSS2 and ERG locus on chromosome 21 (described in more detail below), 5-10% are TMPRSS2-ETV1, 1-2% are TMPRSS2-ETV4, and 1-2% are TMPRSS2-FLI1.

Experiments conducted during the course of development of the present invention indicated that certain fusion genes express fusion transcripts, while others do not express a functional transcript (Tomlins et al., *Science*, 310: 644-648 (2005); Tomlins et al., *Cancer Research* 66: 3396-3400 (2006)).

Further experiments conducted during the course of development of the present invention identified significant genomic deletions located between *TMPRSS2* and *ERG* on chromosome 21q22.2-3. Deletions were seen in *TMPRSS2:ERG* fusion positive PCA samples. The deletions appear in a consensus area but show variability within this area. In previously published work by Paris *et al.* (*Hum. Mol. Genet. 13:*1303-13 (2004)), CGH analysis detected deletions in the CTD-2103O7 BAC that is 6 kb centromeric from *TMPRSS2.* These deletions were observed in 12.5% (9/72) of clinically localized PCA samples and 33% (5/15) of the metastatic PCA samples. These results support the SNP array data from the current study and suggests that either PCA deletions become more

common with progression or that deletions are identified more often in PCA that tend to progress more rapidly. Given the striking intra-tumoral homogeneity of the *TMPRSS2:ERG* rearrangements, it is more likely that these molecular sub-types are associated with different disease progression characteristics.

One hundred eighteen clinically localized PCA cases with 49.2% harboring rearrangement of *ERG* were evaluated. Intronic deletions were observed in 60.3% of these *TMPRSS2:ERG* fusion positive cases. Almost all PCA samples with marked over expression of ERG have a rearrangement, and the over expression occurs in about the same number of cases as the rearrangement. Using Oncomine, a publicly available compendium of gene expression data, 4 significantly down regulated genes located in the area of the common deletion site were identified (Figure 16).

The present invention is not limited to a particular mechanism. Indeed, an understanding of the mechanism is not necessary to practice the present invention. Nonetheless, the results suggest that nearly half of all PCAs can be defined by the *TMPRSS2:ERG* rearrangement. The majority of these tumors demonstrate an intronic deletion, which according to the oligonucleotide SNP array genomic analysis is variable in size. However, approximately 30-40% did not demonstrate a deletion and thus might harbor a balanced translocation of *TMRPSS2* and *ERG*. This variability in the extent of the deletion may be associated with disease progression as has been observed with CML. The current study identified significant clinical associations with tumor stage and lymph node status. *TMPRSS2:ERG* rearranged tumors with deletion also showed a trend towards higher rates of PSA biochemical failure.

Additional experiments conducted during the course of development of the present invention explored the risk of developing metastases or prostate cancer specific death based on the presence of the TMPRSS2:ERG gene fusion in a watchful waiting cohort of early prostate cancers with long term follow-up. The frequency of the TMPRSS2:ERG gene fusion was assessed using 92 cases. The frequency of TMPRSS2:ERG gene fusion in this population-based cohort was 15.2% (14/92), lower than the 50% frequency observed in two hospital-based cohorts. The present invention is not limited to a particular mechanism. Indeed, an understanding of the mechanism is not necessary to practice the present invention. Nonetheless, this difference in TMPRSS2:ERG gene fusion prostate cancers may be due to ethnic and racial genetic differences. These differences may also be

explained by the lower percentage of high grade cases in this watchful waiting cohort as compared to the other non-population based studies.

A significant association between TMPRSS2:ERG gene fusion and development of distant metastases and prostate cancer specific death was observed with a cumulative incidence ratio of 3.6 (P = .004, 95% confidence interval=1.5 to 8.9). These data suggest that TMPRSS2:ERG gene fusion prostate cancers have a more aggressive phenotype. Further experiments indicated that genomic deletions in the TMPRSS2:ERG gene fusion were correlated with advanced and/or metastatic prostate cancer (See *e.g.*, Example 5).

The present invention has also demonstrated that androgen can induce the overexpression of ERG, presumably through AREs, in a TMPRSS2-ERG-positive cell line. The present invention is not limited to a particular mechanism. Indeed, an understanding of the mechanism is not necessary to practice the present invention. Nonetheless, collectively, the results suggest that dysregulation of ETS family activity through AREs upstream of TMPRSS2 may drive prostate cancer development.

It is contemplated that the presence, molecular sub-type or amount of gene fusion expression is correlated with the stage, aggressiveness or progression of the disease, or the presence or risk of metastasis. It is further contemplated that similar recurrent gene fusions involving ETS family member genes occur in other epithelial cancers.

II. Antibodies

The gene fusion proteins of the present invention, including fragments, derivatives and analogs thereof, may be used as immunogens to produce antibodies having use in the diagnostic, research, and therapeutic methods described below. The antibodies may be polyclonal or monoclonal, chimeric, humanized, single chain or Fab fragments. Various procedures known to those of ordinary skill in the art may be used for the production and labeling of such antibodies and fragments. *See, e.g.*, Burns, ed., *Immunochemical Protocols*, 3rd ed., Humana Press (2005); Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988); Kozbor et al., *Immunology Today* 4: 72 (1983); Köhler and Milstein, *Nature* 256: 495 (1975). Antibodies or fragments exploiting the differences between the truncated ETS family member protein or chimeric protein and their respective native proteins are particularly preferred.

III. Diagnostic Applications

The present invention provides DNA, RNA and protein based diagnostic methods that either directly or indirectly detect the gene fusions. The present invention also provides compositions and kits for diagnostic purposes.

The diagnostic methods of the present invention may be qualitative or quantitative. Quantitative diagnostic methods may be used, for example, to discriminate between indolent and aggressive cancers via a cutoff or threshold level. Where applicable, qualitative or quantitative diagnostic methods may also include amplification of target, signal or intermediary (*e.g.*, a universal primer).

An initial assay may confirm the presence of a gene fusion but not identify the specific fusion. A secondary assay is then performed to determine the identity of the particular fusion, if desired. The second assay may use a different detection technology than the initial assay.

The gene fusions of the present invention may be detected along with other markers in a multiplex or panel format. Markers are selected for their predictive value alone or in combination with the gene fusions. Exemplary prostate cancer markers include, but are not limited to: AMACR/P504S (U.S. Pat. No. 6,262,245); PCA3 (U.S. Pat. No. 7,008,765); PCGEM1 (U.S. Pat. No. 6,828,429); prostein/P501S, P503S, P504S, P509S, P510S, prostase/P703P, P710P (U.S. Publication No. 20030185830); and, those disclosed in U.S. Pat. Nos. 5,854,206 and 6,034,218, and U.S. Publication No. 20030175736, each of which is herein incorporated by reference in its entirety. Markers for other cancers, diseases, infections, and metabolic conditions are also contemplated for includsion in a multiplex of panel format.

The diagnostic methods of the present invention may also be modified with reference to data correlating particular gene fusions with the stage, aggressiveness or progression of the disease or the presence or risk of metastasis. Ultimately, the information provided by the methods of the present invention will assist a physician in choosing the best course of treatment for a particular patient.

A. Sample

Any patient sample suspected of containing the gene fusions may be tested according to the methods of the present invention. By way of non-limiting examples, the sample may be tissue (*e.g.*, a prostate biopsy sample or a tissue sample obtained by prostatectomy), blood, urine, semen, prostatic secretions or a fraction thereof (*e.g.*, plasma, serum, urine supernatant, urine cell pellet or prostate cells). A urine sample is preferably collected immediately following an attentive digital rectal examination (DRE), which causes prostate cells from the prostate gland to shed into the urinary tract.

The patient sample typically requires preliminary processing designed to isolate or enrich the sample for the gene fusions or cells that contain the gene fusions. A variety of techniques known to those of ordinary skill in the art may be used for this purpose, including but not limited: centrifugation; immunocapture; cell lysis; and, nucleic acid target capture (*See, e.g.*, EP Pat. No. 1 409 727, herein incorporated by reference in its entirety).

B. DNA and RNA Detection

The gene fusions of the present invention may be detected as chromosomal rearrangements of genomic DNA or chimeric mRNA using a variety of nucleic acid techniques known to those of ordinary skill in the art, including but not limited to: nucleic acid sequencing; nucleic acid hybridization; and, nucleic acid amplification.

1. Sequencing

Illustrative non-limiting examples of nucleic acid sequencing techniques include, but are not limited to, chain terminator (Sanger) sequencing and dye terminator sequencing. Those of ordinary skill in the art will recognize that because RNA is less stable in the cell and more prone to nuclease attack experimentally RNA is usually reverse transcribed to DNA before sequencing.

Chain terminator sequencing uses sequence-specific termination of a DNA synthesis reaction using modified nucleotide substrates. Extension is initiated at a specific site on the template DNA by using a short radioactive, or other labeled, oligonucleotide primer complementary to the template at that region. The oligonucleotide primer is extended using a DNA polymerase, standard four deoxynucleotide bases, and a low concentration of one chain terminating nucleotide, most commonly a di-deoxynucleotide. This reaction is repeated in four separate tubes with each of the bases taking turns as the di-deoxynucleotide. Limited incorporation of the chain terminating nucleotide by the DNA

polymerase results in a series of related DNA fragments that are terminated only at positions where that particular di-deoxynucleotide is used. For each reaction tube, the fragments are size-separated by electrophoresis in a slab polyacrylamide gel or a capillary tube filled with a viscous polymer. The sequence is determined by reading which lane produces a visualized mark from the labeled primer as you scan from the top of the gel to the bottom.

Dye terminator sequencing alternatively labels the terminators. Complete sequencing can be performed in a single reaction by labeling each of the di-deoxynucleotide chain-terminators with a separate fluorescent dye, which fluoresces at a different wavelength.

2. Hybridization

Illustrative non-limiting examples of nucleic acid hybridization techniques include, but are not limited to, *in situ* hybridization (ISH), microarray, and Southern or Northern blot.

In situ hybridization (ISH) is a type of hybridization that uses a labeled complementary DNA or RNA strand as a probe to localize a specific DNA or RNA sequence in a portion or section of tissue (*in situ*), or, if the tissue is small enough, the entire tissue (whole mount ISH). DNA ISH can be used to determine the structure of chromosomes. RNA ISH is used to measure and localize mRNAs and other transcripts within tissue sections or whole mounts. Sample cells and tissues are usually treated to fix the target transcripts in place and to increase access of the probe. The probe hybridizes to the target sequence at elevated temperature, and then the excess probe is washed away. The probe that was labeled with either radio-, fluorescent- or antigen-labeled bases is localized and quantitated in the tissue using either autoradiography, fluorescence microscopy or immunohistochemistry, respectively. ISH can also use two or more probes, labeled with radioactivity or the other non-radioactive labels, to simultaneously detect two or more transcripts.

2.1 FISH

In some embodiments, fusion sequences are detected using fluorescence *in situ* hybridization (FISH). The preferred FISH assays for the present invention utilize bacterial artificial chromosomes (BACs). These have been used extensively in the human genome

sequencing project (see *Nature* 409: 953-958 (2001)) and clones containing specific BACs are available through distributors that can be located through many sources, *e.g.*, NCBI. Each BAC clone from the human genome has been given a reference name that unambiguously identifies it. These names can be used to find a corresponding GenBank sequence and to order copies of the clone from a distributor.

In some embodiments, the detection assay is a FISH assay utilizing a probe for ETV1 (*e.g.*, bac RP11-692L4), a set of probes for c-ERG:t-ERG break apart (*e.g.*, bac RP11-24A11 and as a probe for t-ERG RP11-372O17 or RP11-137J13). In other embodiments, the FISH assay is performed by testing for ETV1 deletion or amplification with a set of probes, wherein one probe spans the ETV1 locus (*e.g.*, bac RP11-692L4) and the other probe hybridizes to chromosome 7 (*e.g.*, a probe on the centromere of the chromosome). In still further embodiments, the method is performed by testing for ERG deletion or amplification with a set of probes, one spanning the ERG locus (*e.g.*, bac RP11-476D17) and one reference probe on chromosome 21 (*e.g.*, PR11-32L6; RP11-752M23; RP11-1107H21; RP11-639A7 or RP11-1077M21). In yet other embodiments, the method is performed by testing for TMPRSS2 deletion/amplification with a set of probes, one spanning the TMPRSS2 (*e.g.*, RP11-121A5; RP11-120C17; PR11-814F13; or RR11-535H11) locus and one reference probe on chromosome 21(*e.g.*, PR11-32L6; RP11-752M23; RP11-1107H21; RP11-639A7 or RP11-1077M21). In some embodiments, the method further comprises a hybridization using a probe selected from the group including, but not limited to RP11-121A5; RP11-120C17; PR11-814F13; and RR11-535H11.

The present invention further provides a method of performing a FISH assay on human prostate cells, human prostate tissue or on the fluid surrounding said human prostate cells or human prostate tissue. In some embodiments, the assay comprises a hybridization step utilizing a probe selected from the group including, but not limited to, RP11-372O17; RP11-137J13; RP11-692L4; RP11-476D17; PR11-32L6; RP11-752M23; RP11-1107H21; RP11-639A7; RP11-1077M21; RP11-121A5; RP11-120C17; PR11-814F13; and RR11-535H11.

Specific BAC clones that can be used in FISH protocols to detect rearrangements relevant to the present invention are as follows:

- For testing for an ETV1-TMPRSS2 fusion, one probe spanning the ETV1 and one spanning the TMPRSS2 locus may be used:

BAC for ETV1: RP11-692L4

BAC for TMPRSS2: RP11-121A5, (RP11-120C17, PR11-814F13, RR11-535H11)

- Testing ERG translocation with set of probes for c-ERG:t-ERG break apart:
  BAC for c-ERG: RP11-24A11
  BACs for t-ERG: RP11-372O17, RP11-137J13
- Testing ETV1 deletion/amplification with set of probes, one spanning the ETV1 locus and one reference probe on chromosome 7:
  BAC for ETV1: RP11-692L4

Testing ERG deletion/amplification with set of probes, one spanning the ERG locus and one reference probe on chromosome 21:

BAC for ERG: RP11-476D17

BACs for reference probe on chromosome 21: *

- Testing TMPRSS2 deletion/amplification with set of probes, one spanning the TMPRSS2 locus and one reference probe on chromosome 21:
  BACs for TMPRSS2: RP11-121A5, (RP11-120C17, PR11-814F13, RR11-535H11)
  BACs for reference probe on chromosome 21: *PR11-32L6, RP11-752M23, RP11-1107H21, RP11-639A7, (RP11-1077M21).*

The most preferred probes for detecting a deletion mutation resulting in a fusion between TMPRSS2 and ERG are RP11-24A11 and RP11-137J13. These probes, or those described above, are labeled with appropriate fluorescent or other markers and then used in hybridizations. The Examples section provided herein sets forth one particular protocol that is effective for measuring deletions but one of skill in the art will recognize that many variations of this assay can be used equally well. Specific protocols are well known in the art and can be readily adapted for the present invention. Guidance regarding methodology may be obtained from many references including: *In situ* Hybridization: Medical Applications (eds. G. R. Coulton and J. de Belleroche), Kluwer Academic Publishers, Boston (1992); *In situ* Hybridization: In Neurobiology; Advances in Methodology (eds. J. H. Eberwine, K. L. Valentino, and J. D. Barchas), Oxford University Press Inc., England (1994); *In situ* Hybridization: A Practical Approach (ed. D. G. Wilkinson), Oxford

University Press Inc., England (1992)); Kuo, *et al.*, *Am. J. Hum. Genet. 49*:112-119 (1991); Klinger, *et al.*, *Am. J. Hum. Genet. 51*:55-65 (1992); and Ward, *et al.*, *Am. J. Hum. Genet. 52*:854-865 (1993)). There are also kits that are commercially available and that provide protocols for performing FISH assays (available from *e.g.*, Oncor, Inc., Gaithersburg, MD). Patents providing guidance on methodology include U.S. 5,225,326; 5,545,524; 6,121,489 and 6,573,043. All of these references are hereby incorporated by reference in their entirety and may be used along with similar references in the art and with the information provided in the Examples section herein to establish procedural steps convenient for a particular laboratory.

Table 13 below shows additional BAC clones that find use as FISH probes.

Table 13

Gene	Chromosome	RefSeq	5' BAC	3' BAC	Paired
EHF	11p13	NM_012153	RP5-1135K18	RP5-1002E13	2
ELF1	13q14	NM_172373	RP11-88n4	RP11-53f19	
ELF2	4q28	NM_201999.1	RP11-22o8	RP11-375P1	
ELF3	1q32	NM_004433	RP11-25B7	RP11-246J15	
ELF4	Xq25	NM_001421	RP5-875H3	RP4-753P9	
ELF5	11p13	NM_001422.2	RP5-1002E13	RP5-1135K18	2
ELK1	Xp11	NM_005229	RP1-54B20	RP1-306D1	
ELK3	12q22	NM_005230	RP11-69E3	RP11-510I5	
ELK4	1q32	NM_001973.2	RP11-131E5	RP11-249h15	
ERF	19q13	NM_006494.1	RP11-208I3	RP11-317E13	
ERG	21q22	NM_004449.3	RP11-137J13	RP11-24A11	1
ETS1	11q24	NM_005238.2	RP11-254C5	RP11-112m22	
ETS2	21q22	NM_005239.4	RP11-24A11	RP11-137J13	1
ETV1	7p21	NM_004956.3	RP11-1149J13	RP11-34C22	
ETV2	19q13	NM_014209.1	RP11-32h17	RP11-92j4	
ETV3	1q23	NM_005240.1	RP11-91G5	RP11-1038N13	3
ETV4	17q21	NM_001986.1	RP11-436J4	RP11-100E5	
ETV5	3q27	NM_004454.1	RP11-379C23	RP11-1144N13	
ETV6	12p13	NM_001987.3	RP11-90N7	RP11-59h1	
ETV7	6p21	NM_016135.2	RP3-431A14	RP1-179N16	
FEV	2q35	NM_017521.2	RP11-316O14	RP11-129D2	
FLI1	11q24	NM_002017.2	RP11-112M22	RP11-75P14	
FLJ16478	1q23	NM_001004341	RP11-91G5	RP11-1038N13	3
SPDEF	6p21	NM_012391.1	RP11-79j23	RP11-119c22	
SPI1	11p11	NM_016135.2	RP11-56e13	RP11-29o22	
SPIB	19q13	NM_003121.2	RP11-510I16	RP11-26P14	
SPIC	12q23	NM_152323.1	RP11-426H24	RP11-938C1	
TMPRSS2	21q22	NM_005656.2	RP11-35C4	RP11-120C17	

2.2 Microarrays

Different kinds of biological assays are called microarrays including, but not limited to: DNA microarrays (*e.g.*, cDNA microarrays and oligonucleotide microarrays); protein microarrays; tissue microarrays; transfection or cell microarrays; chemical compound microarrays; and, antibody microarrays. A DNA microarray, commonly known as gene chip, DNA chip, or biochip, is a collection of microscopic DNA spots attached to a solid surface (*e.g.*, glass, plastic or silicon chip) forming an array for the purpose of expression profiling or monitoring expression levels for thousands of genes simultaneously. The affixed DNA segments are known as probes, thousands of which can be used in a single DNA microarray. Microarrays can be used to identify disease genes by comparing gene expression in disease and normal cells. Microarrays can be fabricated using a variety of technologies, including but not limiting: printing with fine-pointed pins onto glass slides; photolithography using pre-made masks; photolithography using dynamic micromirror devices; ink-jet printing; or, electrochemistry on microelectrode arrays.

Southern and Northern blotting is used to detect specific DNA or RNA sequences, respectively. DNA or RNA extracted from a sample is fragmented, electrophoretically separated on a matrix gel, and transferred to a membrane filter. The filter bound DNA or RNA is subject to hybridization with a labeled probe complementary to the sequence of interest. Hybridized probe bound to the filter is detected. A variant of the procedure is the reverse Northern blot, in which the substrate nucleic acid that is affixed to the membrane is a collection of isolated DNA fragments and the probe is RNA extracted from a tissue and labeled.

3. Amplification

Chromosomal rearrangements of genomic DNA and chimeric mRNA may be amplified prior to or simultaneous with detection. Illustrative non-limiting examples of nucleic acid amplification techniques include, but are not limited to, polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), transcription-mediated amplification (TMA), ligase chain reaction (LCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA). Those of ordinary skill in the art will recognize that certain amplification techniques (*e.g.*, PCR) require that RNA be reversed transcribed to DNA prior to amplification (*e.g.*, RT-PCR), whereas other amplification techniques directly amplify RNA (*e.g.*, TMA and NASBA).

The polymerase chain reaction (U.S. Pat. Nos. 4,683,195, 4,683,202, 4,800,159 and 4,965,188, each of which is herein incorporated by reference in its entirety), commonly referred to as PCR, uses multiple cycles of denaturation, annealing of primer pairs to opposite strands, and primer extension to exponentially increase copy numbers of a target nucleic acid sequence. In a variation called RT-PCR, reverse transcriptase (RT) is used to make a complementary DNA (cDNA) from mRNA, and the cDNA is then amplified by PCR to produce multiple copies of DNA. For other various permutations of PCR *see, e.g.*, U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,800,159; Mullis et al., *Meth. Enzymol.* 155: 335 (1987); and, Murakawa et al., *DNA* 7: 287 (1988), each of which is herein incorporated by reference in its entirety.

Transcription mediated amplification (U.S. Pat. Nos. 5,480,784 and 5,399,491, each of which is herein incorporated by reference in its entirety), commonly referred to as TMA, synthesizes multiple copies of a target nucleic acid sequence autocatalytically under conditions of substantially constant temperature, ionic strength, and pH in which multiple RNA copies of the target sequence autocatalytically generate additional copies. *See, e.g.*, U.S. Pat. Nos. 5,399,491 and 5,824,518, each of which is herein incorporated by reference in its entirety. In a variation described in U.S. Publ. No. 20060046265 (herein incorporated by reference in its entirety), TMA optionally incorporates the use of blocking moieties, terminating moieties, and other modifying moieties to improve TMA process sensitivity and accuracy.

The ligase chain reaction (Weiss, R., *Science* 254: 1292 (1991), herein incorporated by reference in its entirety), commonly referred to as LCR, uses two sets of complementary DNA oligonucleotides that hybridize to adjacent regions of the target nucleic acid. The DNA oligonucleotides are covalently linked by a DNA ligase in repeated cycles of thermal denaturation, hybridization and ligation to produce a detectable double-stranded ligated oligonucleotide product.

Strand displacement amplification (Walker, G. et al., *Proc. Natl. Acad. Sci. USA* 89: 392-396 (1992); U.S. Pat. Nos. 5,270,184 and 5,455,166, each of which is herein incorporated by reference in its entirety), commonly referred to as SDA, uses cycles of annealing pairs of primer sequences to opposite strands of a target sequence, primer extension in the presence of a dNTPαS to produce a duplex hemiphosphorothioated primer extension product, endonuclease-mediated nicking of a hemimodified restriction endonuclease recognition site, and polymerase-mediated primer extension from the 3' end of

the nick to displace an existing strand and produce a strand for the next round of primer annealing, nicking and strand displacement, resulting in geometric amplification of product. Thermophilic SDA (tSDA) uses thermophilic endonucleases and polymerases at higher temperatures in essentially the same method (EP Pat. No. 0 684 315).

Other amplification methods include, for example: nucleic acid sequence based amplification (U.S. Pat. No. 5,130,238, herein incorporated by reference in its entirety), commonly referred to as NASBA; one that uses an RNA replicase to amplify the probe molecule itself (Lizardi et al., *BioTechnol.* 6: 1197 (1988), herein incorporated by reference in its entirety), commonly referred to as Qβ replicase; a transcription based amplification method (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)); and, self-sustained sequence replication (Guatelli et al., *Proc. Natl. Acad. Sci. USA* 87: 1874 (1990), each of which is herein incorporated by reference in its entirety). For further discussion of known amplification methods *see* Persing, David H., "In Vitro Nucleic Acid Amplification Techniques" in *Diagnostic Medical Microbiology: Principles and Applications* (Persing et al., Eds.), pp. 51-87 (American Society for Microbiology, Washington, DC (1993)).

4. Detection Methods

Non-amplified or amplified gene fusion nucleic acids can be detected by any conventional means. For example, the gene fusions can be detected by hybridization with a detectably labeled probe and measurement of the resulting hybrids. Illustrative non-limiting examples of detection methods are described below.

One illustrative detection method, the Hybridization Protection Assay (HPA) involves hybridizing a chemiluminescent oligonucleotide probe (*e.g.*, an acridinium ester-labeled (AE) probe) to the target sequence, selectively hydrolyzing the chemiluminescent label present on unhybridized probe, and measuring the chemiluminescence produced from the remaining probe in a luminometer. *See, e.g.*, U.S. Pat. No. 5,283,174 and Norman C. Nelson et al., Nonisotopic Probing, Blotting, and Sequencing, ch. 17 (Larry J. Kricka ed., 2d ed. 1995, each of which is herein incorporated by reference in its entirety).

Another illustrative detection method provides for quantitative evaluation of the amplification process in real-time. Evaluation of an amplification process in "real-time" involves determining the amount of amplicon in the reaction mixture either continuously or periodically during the amplification reaction, and using the determined values to calculate the amount of target sequence initially present in the sample. A variety of methods for

determining the amount of initial target sequence present in a sample based on real-time amplification are well known in the art. These include methods disclosed in U.S. Pat. Nos. 6,303,305 and 6,541,205, each of which is herein incorporated by reference in its entirety. Another method for determining the quantity of target sequence initially present in a sample, but which is not based on a real-time amplification, is disclosed in U.S. Pat. No. 5,710,029, herein incorporated by reference in its entirety.

Amplification products may be detected in real-time through the use of various self-hybridizing probes, most of which have a stem-loop structure. Such self-hybridizing probes are labeled so that they emit differently detectable signals, depending on whether the probes are in a self-hybridized state or an altered state through hybridization to a target sequence. By way of non-limiting example, "molecular torches" are a type of self-hybridizing probe that includes distinct regions of self-complementarity (referred to as "the target binding domain" and "the target closing domain") which are connected by a joining region (*e.g.*, non-nucleotide linker) and which hybridize to each other under predetermined hybridization assay conditions. In a preferred embodiment, molecular torches contain single-stranded base regions in the target binding domain that are from 1 to about 20 bases in length and are accessible for hybridization to a target sequence present in an amplification reaction under strand displacement conditions. Under strand displacement conditions, hybridization of the two complementary regions, which may be fully or partially complementary, of the molecular torch is favored, except in the presence of the target sequence, which will bind to the single-stranded region present in the target binding domain and displace all or a portion of the target closing domain. The target binding domain and the target closing domain of a molecular torch include a detectable label or a pair of interacting labels (*e.g.*, luminescent/quencher) positioned so that a different signal is produced when the molecular torch is self-hybridized than when the molecular torch is hybridized to the target sequence, thereby permitting detection of probe:target duplexes in a test sample in the presence of unhybridized molecular torches. Molecular torches and a variety of types of interacting label pairs are disclosed in U.S. Pat. No. 6,534,274, herein incorporated by reference in its entirety.

Another example of a detection probe having self-complementarity is a "molecular beacon." Molecular beacons include nucleic acid molecules having a target complementary sequence, an affinity pair (or nucleic acid arms) holding the probe in a closed conformation in the absence of a target sequence present in an amplification reaction, and a label pair that

interacts when the probe is in a closed conformation. Hybridization of the target sequence and the target complementary sequence separates the members of the affinity pair, thereby shifting the probe to an open conformation. The shift to the open conformation is detectable due to reduced interaction of the label pair, which may be, for example, a fluorophore and a quencher (*e.g.*, DABCYL and EDANS). Molecular beacons are disclosed in U.S. Pat. Nos. 5,925,517 and 6,150,097, herein incorporated by reference in its entirety.

Other self-hybridizing probes are well known to those of ordinary skill in the art. By way of non-limiting example, probe binding pairs having interacting labels, such as those disclosed in U.S. Pat. No. 5,928,862 (herein incorporated by reference in its entirety) might be adapted for use in the present invention. Probe systems used to detect single nucleotide polymorphisms (SNPs) might also be utilized in the present invention. Additional detection systems include "molecular switches," as disclosed in U.S. Publ. No. 20050042638, herein incorporated by reference in its entirety. Other probes, such as those comprising intercalating dyes and/or fluorochromes, are also useful for detection of amplification products in the present invention. *See, e.g.*, U.S. Pat. No. 5,814,447 (herein incorporated by reference in its entirety).

C. Protein Detection

The gene fusions of the present invention may be detected as truncated ETS family member proteins or chimeric proteins using a variety of protein techniques known to those of ordinary skill in the art, including but not limited to: protein sequencing; and, immunoassays.

1. Sequencing

Illustrative non-limiting examples of protein sequencing techniques include, but are not limited to, mass spectrometry and Edman degradation.

Mass spectrometry can, in principle, sequence any size protein but becomes computationally more difficult as size increases. A protein is digested by an endoprotease, and the resulting solution is passed through a high pressure liquid chromatography column. At the end of this column, the solution is sprayed out of a narrow nozzle charged to a high positive potential into the mass spectrometer. The charge on the droplets causes them to fragment until only single ions remain. The peptides are then fragmented and the mass-charge ratios of the fragments measured. The mass spectrum is analyzed by computer and

often compared against a database of previously sequenced proteins in order to determine the sequences of the fragments. The process is then repeated with a different digestion enzyme, and the overlaps in sequences are used to construct a sequence for the protein.

In the Edman degradation reaction, the peptide to be sequenced is adsorbed onto a solid surface (*e.g.*, a glass fiber coated with polybrene). The Edman reagent, phenylisothiocyanate (PTC), is added to the adsorbed peptide, together with a mildly basic buffer solution of 12% trimethylamine, and reacts with the amine group of the N-terminal amino acid. The terminal amino acid derivative can then be selectively detached by the addition of anhydrous acid. The derivative isomerizes to give a substituted phenylthiohydantoin, which can be washed off and identified by chromatography, and the cycle can be repeated. The efficiency of each step is about 98%, which allows about 50 amino acids to be reliably determined.

2. Immunoassays

Illustrative non-limiting examples of immunoassays include, but are not limited to: immunoprecipitation; Western blot; ELISA; immunohistochemistry; immunocytochemistry; flow cytometry; and, immuno-PCR. Polyclonal or monoclonal antibodies detectably labeled using various techniques known to those of ordinary skill in the art (*e.g.*, colorimetric, fluorescent, chemiluminescent or radioactive) are suitable for use in the immunoassays.

Immunoprecipitation is the technique of precipitating an antigen out of solution using an antibody specific to that antigen. The process can be used to identify protein complexes present in cell extracts by targeting a protein believed to be in the complex. The complexes are brought out of solution by insoluble antibody-binding proteins isolated initially from bacteria, such as Protein A and Protein G. The antibodies can also be coupled to sepharose beads that can easily be isolated out of solution. After washing, the precipitate can be analyzed using mass spectrometry, Western blotting, or any number of other methods for identifying constituents in the complex.

A Western blot, or immunoblot, is a method to detect protein in a given sample of tissue homogenate or extract. It uses gel electrophoresis to separate denatured proteins by mass. The proteins are then transferred out of the gel and onto a membrane, typically polyvinyldiflroride or nitrocellulose, where they are probed using antibodies specific to the

protein of interest. As a result, researchers can examine the amount of protein in a given sample and compare levels between several groups.

An ELISA, short for Enzyme-Linked ImmunoSorbent Assay, is a biochemical technique to detect the presence of an antibody or an antigen in a sample. It utilizes a minimum of two antibodies, one of which is specific to the antigen and the other of which is coupled to an enzyme. The second antibody will cause a chromogenic or fluorogenic substrate to produce a signal. Variations of ELISA include sandwich ELISA, competitive ELISA, and ELISPOT. Because the ELISA can be performed to evaluate either the presence of antigen or the presence of antibody in a sample, it is a useful tool both for determining serum antibody concentrations and also for detecting the presence of antigen.

Immunohistochemistry and immunocytochemistry refer to the process of localizing proteins in a tissue section or cell, respectively, via the principle of antigens in tissue or cells binding to their respective antibodies. Visualization is enabled by tagging the antibody with color producing or fluorescent tags. Typical examples of color tags include, but are not limited to, horseradish peroxidase and alkaline phosphatase. Typical examples of fluorophore tags include, but are not limited to, fluorescein isothiocyanate (FITC) or phycoerythrin (PE).

Flow cytometry is a technique for counting, examining and sorting microscopic particles suspended in a stream of fluid. It allows simultaneous multiparametric analysis of the physical and/or chemical characteristics of single cells flowing through an optical/electronic detection apparatus. A beam of light (*e.g.*, a laser) of a single frequency or color is directed onto a hydrodynamically focused stream of fluid. A number of detectors are aimed at the point where the stream passes through the light beam; one in line with the light beam (Forward Scatter or FSC) and several perpendicular to it (Side Scatter (SSC) and one or more fluorescent detectors). Each suspended particle passing through the beam scatters the light in some way, and fluorescent chemicals in the particle may be excited into emitting light at a lower frequency than the light source. The combination of scattered and fluorescent light is picked up by the detectors, and by analyzing fluctuations in brightness at each detector, one for each fluorescent emission peak, it is possible to deduce various facts about the physical and chemical structure of each individual particle. FSC correlates with the cell volume and SSC correlates with the density or inner complexity of the particle (*e.g.*, shape of the nucleus, the amount and type of cytoplasmic granules or the membrane roughness).

Immuno-polymerase chain reaction (IPCR) utilizes nucleic acid amplification techniques to increase signal generation in antibody-based immunoassays. Because no protein equivalence of PCR exists, that is, proteins cannot be replicated in the same manner that nucleic acid is replicated during PCR, the only way to increase detection sensitivity is by signal amplification. The target proteins are bound to antibodies which are directly or indirectly conjugated to oligonucleotides. Unbound antibodies are washed away and the remaining bound antibodies have their oligonucleotides amplified. Protein detection occurs via detection of amplified oligonucleotides using standard nucleic acid detection methods, including real-time methods.

D. Data Analysis

In some embodiments, a computer-based analysis program is used to translate the raw data generated by the detection assay (*e.g.*, the presence, absence, or amount of a given marker or markers) into data of predictive value for a clinician. The clinician can access the predictive data using any suitable means. Thus, in some preferred embodiments, the present invention provides the further benefit that the clinician, who is not likely to be trained in genetics or molecular biology, need not understand the raw data. The data is presented directly to the clinician in its most useful form. The clinician is then able to immediately utilize the information in order to optimize the care of the subject.

The present invention contemplates any method capable of receiving, processing, and transmitting the information to and from laboratories conducting the assays, information provides, medical personal, and subjects. For example, in some embodiments of the present invention, a sample (*e.g.*, a biopsy or a serum or urine sample) is obtained from a subject and submitted to a profiling service (*e.g.*, clinical lab at a medical facility, genomic profiling business, etc.), located in any part of the world (*e.g.*, in a country different than the country where the subject resides or where the information is ultimately used) to generate raw data. Where the sample comprises a tissue or other biological sample, the subject may visit a medical center to have the sample obtained and sent to the profiling center, or subjects may collect the sample themselves (*e.g.*, a urine sample) and directly send it to a profiling center. Where the sample comprises previously determined biological information, the information may be directly sent to the profiling service by the subject (*e.g.*, an information card containing the information may be scanned by a computer and the data transmitted to a computer of the profiling center using an electronic communication

systems). Once received by the profiling service, the sample is processed and a profile is produced (*i.e.*, expression data), specific for the diagnostic or prognostic information desired for the subject.

The profile data is then prepared in a format suitable for interpretation by a treating clinician. For example, rather than providing raw expression data, the prepared format may represent a diagnosis or risk assessment (*e.g.*, likelihood of cancer being present) for the subject, along with recommendations for particular treatment options. The data may be displayed to the clinician by any suitable method. For example, in some embodiments, the profiling service generates a report that can be printed for the clinician (*e.g.*, at the point of care) or displayed to the clinician on a computer monitor.

In some embodiments, the information is first analyzed at the point of care or at a regional facility. The raw data is then sent to a central processing facility for further analysis and/or to convert the raw data to information useful for a clinician or patient. The central processing facility provides the advantage of privacy (all data is stored in a central facility with uniform security protocols), speed, and uniformity of data analysis. The central processing facility can then control the fate of the data following treatment of the subject. For example, using an electronic communication system, the central facility can provide data to the clinician, the subject, or researchers.

In some embodiments, the subject is able to directly access the data using the electronic communication system. The subject may chose further intervention or counseling based on the results. In some embodiments, the data is used for research use. For example, the data may be used to further optimize the inclusion or elimination of markers as useful indicators of a particular condition or stage of disease.

E. *In vivo* Imaging

The gene fusions of the present invention may also be detected using *in vivo* imaging techniques, including but not limited to: radionuclide imaging; positron emission tomography (PET); computerized axial tomography, X-ray or magnetic resonance imaging method, fluorescence detection, and chemiluminescent detection. In some embodiments, *in vivo* imaging techniques are used to visualize the presence of or expression of cancer markers in an animal (*e.g.*, a human or non-human mammal). For example, in some embodiments, cancer marker mRNA or protein is labeled using a labeled antibody specific for the cancer marker. A specifically bound and labeled antibody can be detected in an

individual using an *in vivo* imaging method, including, but not limited to, radionuclide imaging, positron emission tomography, computerized axial tomography, X-ray or magnetic resonance imaging method, fluorescence detection, and chemiluminescent detection. Methods for generating antibodies to the cancer markers of the present invention are described below.

The *in vivo* imaging methods of the present invention are useful in the diagnosis of cancers that express the cancer markers of the present invention (*e.g.*, prostate cancer). *In vivo* imaging is used to visualize the presence of a marker indicative of the cancer. Such techniques allow for diagnosis without the use of an unpleasant biopsy. The *in vivo* imaging methods of the present invention are also useful for providing prognoses to cancer patients. For example, the presence of a marker indicative of cancers likely to metastasize can be detected. The *in vivo* imaging methods of the present invention can further be used to detect metastatic cancers in other parts of the body.

In some embodiments, reagents (*e.g.*, antibodies) specific for the cancer markers of the present invention are fluorescently labeled. The labeled antibodies are introduced into a subject (*e.g.*, orally or parenterally). Fluorescently labeled antibodies are detected using any suitable method (*e.g.*, using the apparatus described in U.S. Pat. No. 6,198,107, herein incorporated by reference).

In other embodiments, antibodies are radioactively labeled. The use of antibodies for *in vivo* diagnosis is well known in the art. Sumerdon *et al.*, (Nucl. Med. Biol 17:247-254 [1990] have described an optimized antibody-chelator for the radioimmunoscintographic imaging of tumors using Indium-111 as the label. Griffin *et al.*, (J Clin Onc 9:631-640 [1991]) have described the use of this agent in detecting tumors in patients suspected of having recurrent colorectal cancer. The use of similar agents with paramagnetic ions as labels for magnetic resonance imaging is known in the art (Lauffer, Magnetic Resonance in Medicine 22:339-342 [1991]). The label used will depend on the imaging modality chosen. Radioactive labels such as Indium-111, Technetium-99m, or Iodine-131 can be used for planar scans or single photon emission computed tomography (SPECT). Positron emitting labels such as Fluorine-19 can also be used for positron emission tomography (PET). For MRI, paramagnetic ions such as Gadolinium (III) or Manganese (II) can be used.

Radioactive metals with half-lives ranging from 1 hour to 3.5 days are available for conjugation to antibodies, such as scandium-47 (3.5 days) gallium-67 (2.8 days), gallium-68

(68 minutes), technetiium-99m (6 hours), and indium-111 (3.2 days), of which gallium-67, technetium-99m, and indium-111 are preferable for gamma camera imaging, gallium-68 is preferable for positron emission tomography.

A useful method of labeling antibodies with such radiometals is by means of a bifunctional chelating agent, such as diethylenetriaminepentaacetic acid (DTPA), as described, for example, by Khaw *et al.* (Science 209:295 [1980]) for In-111 and Tc-99m, and by Scheinberg *et al.* (Science 215:1511 [1982]). Other chelating agents may also be used, but the 1-(p-carboxymethoxybenzyl)EDTA and the carboxycarbonic anhydride of DTPA are advantageous because their use permits conjugation without affecting the antibody's immunoreactivity substantially.

Another method for coupling DPTA to proteins is by use of the cyclic anhydride of DTPA, as described by Hnatowich *et al.* (Int. J. Appl. Radiat. Isot. 33:327 [1982]) for labeling of albumin with In-111, but which can be adapted for labeling of antibodies. A suitable method of labeling antibodies with Tc-99m which does not use chelation with DPTA is the pretinning method of Crockford *et al.*, (U.S. Pat. No. 4,323,546, herein incorporated by reference).

A preferred method of labeling immunoglobulins with Tc-99m is that described by Wong *et al.* (Int. J. Appl. Radiat. Isot., 29:251 [1978]) for plasma protein, and recently applied successfully by Wong *et al.* (J. Nucl. Med., 23:229 [1981]) for labeling antibodies.

In the case of the radiometals conjugated to the specific antibody, it is likewise desirable to introduce as high a proportion of the radiolabel as possible into the antibody molecule without destroying its immunospecificity. A further improvement may be achieved by effecting radiolabeling in the presence of the specific cancer marker of the present invention, to insure that the antigen binding site on the antibody will be protected. The antigen is separated after labeling.

In still further embodiments, *in vivo* biophotonic imaging (Xenogen, Almeda, CA) is utilized for *in vivo* imaging. This real-time *in vivo* imaging utilizes luciferase. The luciferase gene is incorporated into cells, microorganisms, and animals (*e.g.*, as a fusion protein with a cancer marker of the present invention). When active, it leads to a reaction that emits light. A CCD camera and software is used to capture the image and analyze it.

F. Compositions & Kits

Compositions for use in the diagnostic methods of the present invention include, but are not limited to, probes, amplification oligonucleotides, and antibodies. Particularly preferred compositions detect a product only when an ARG fuses to ETS family member gene. These compositions include: a single labeled probe comprising a sequence that hybridizes to the junction at which a 5' portion from a transcriptional regulatory region of an ARG fuses to a 3' portion from an ETS family member gene (*i.e.*, spans the gene fusion junction); a pair of amplification oligonucleotides wherein the first amplification oligonucleotide comprises a sequence that hybridizes to a transcriptional regulatory region of an ARG and the second amplification oligonucleotide comprises a sequence that hybridizes to an ETS family member gene; an antibody to an amino-terminally truncated ETS family member protein resulting from a fusion of a transcriptional regulatory region of an ARG to an ETS family member gene; or, an antibody to a chimeric protein having an amino-terminal portion from a transcriptional regulatory region of an ARG and a carboxy-terminal portion from an ETS family member gene.

Other useful compositions, however, include: a pair of labeled probes wherein the first labeled probe comprises a sequence that hybridizes to a transcriptional regulatory region of an ARG and the second labeled probe comprises a sequence that hybridizes to an ETS family member gene.

Any of these compositions, alone or in combination with other compositions of the present invention, may be provided in the form of a kit. For example, the single labeled probe and pair of amplification oligonucleotides may be provided in a kit for the amplification and detection of gene fusions of the present invention. Kits may further comprise appropriate controls and/or detection reagents.

The probe and antibody compositions of the present invention may also be provided in the form of an array.

IV. Prognostic Applications

Experiments conducted during the course of development of the present invention demonstrated a close correlation between gene fusions of the present invention and the prognosis of patients with prostate cancer (See *e.g.*, Example 5 below). Especially in cases where a fusion results from a deletion of the genomic DNA lying between TMPRSS2 and ERG, it has been found that cancer cells assume a more aggressive phenotype. Thus, in

some embodiments, assays that are capable of detecting gene fusions between TMPRSS2 and ERG in which there has been a deletion of intervening DNA are used to provide prognoses and help physicians decide on an appropriate therapeutic strategy. For example, in some embodiments, patients with tumors having this particular rearrangement are treated more intensively since their prognosis is significantly worse than patients that lack the rearrangement.

Any assay may be used to determine whether cells are present having a rearrangement of the type discussed above (*e.g.*, those described above).

Although the present invention will most preferably be used in connection with obtaining a prognosis for prostate cancer patients, other epithelial cell tumors may also be examined and the assays and probes described herein may be used in determining whether cancerous cells from these tumors have rearrangements that are likely to make them particularly aggressive, *i.e.*, likely to be invasive and metastatic. Examples of tumors that may be characterized using this procedure include tumors of the breast, lung, colon, ovary, uterus, esophagus, stomach, liver, kidney, brain, skin and muscle. The assays will also be of value to researchers studying these cancers in cell lines and animal models.

Further experiments conducted during the course of development of the present invention demonstrated that chromosomal deletions can be detected by assaying samples to determine whether there is a loss of expression of one or more genes located in the deleted region. For example, approximately 2.8 megabases of genomic DNA is typically deleted in forming a fusion between TMPRSS2 and ERG and at least four genes lying in this area are lost when this occurs. These are the ETS2 gene, the WRB gene, the PCP4 gene and the MX1 gene. A decrease in one or more of these in cancerous prostate cells suggests a poor prognosis.

Accordingly, in some embodiments, the present invention provides a method of assaying epithelial cells for the deletion of chromosomal DNA indicative of a cancer-associated rearrangement, comprising performing a FISH assay using at least a first and a second probe, wherein the first probe is at least 15 nucleotides in length (*e.g.*, at least 15, 20, 35, etc.); is bound to a first fluorescent label; and hybridizes under stringent conditions to a first sequence in the human genome wherein the first sequence includes at least a portion of either an androgen responsive gene (*e.g.*, the TMPRSS2 gene) or a ETS family gene (*e.g.*, the ERG gene, the ETV1 gene, or the ETV4 gene); and the second probe: is at least 15 nucleotides in length; is bound to a second fluorescent label that is different from the first

fluorescent label; and hybridizes under stringent conditions to a second sequence in the human genome that is different from the first sequence and which includes at least a portion of an androgen responsive gene (*e.g.*, the TMPRSS2 gene) or a ETS family gene (*e.g.*, the ERG gene, the ETV1 gene, or the ETV4 gene).

In further embodiments, the present invention provides a method for assaying epithelial cells (*e.g.*, prostate cells) for a deletion of genomic DNA indicative of a cancer-associated rearrangement, comprising: obtaining a test sample of epithelial cells; assaying the sample of epithelial cells to determine the level of expression of one or more genes selected from the group including, but not limited to, ETS2; WRB; PCP4; and MX1; comparing the expression level determined in step b) with the level in a control sample; and concluding that a deletion has occurred if the level of expression determined for the gene in the test sample is lower than that for a control sample.

V. Drug Screening Applications

In some embodiments, the present invention provides drug screening assays (*e.g.*, to screen for anticancer drugs). The screening methods of the present invention utilize cancer markers identified using the methods of the present invention (*e.g.*, including but not limited to, ERG, ETV1, ETV4, and FLI1 gene fusions with TMPRSS2). For example, in some embodiments, the present invention provides methods of screening for compounds that alter (*e.g.*, decrease) the expression of cancer marker genes. The compounds or agents may interfere with transcription, by interacting, for example, with the promoter region. The compounds or agents may interfere with mRNA produced from the fusion (*e.g.*, by RNA interference, antisense technologies, etc.). The compounds or agents may interfere with pathways that are upstream or downstream of the biological activity of the fusion. In some embodiments, candidate compounds are antisense or interfering RNA agents (*e.g.*, oligonucleotides) directed against cancer markers. In other embodiments, candidate compounds are antibodies or small molecules that specifically bind to a cancer marker regulator or expression products of the present invention and inhibit its biological function.

In one screening method, candidate compounds are evaluated for their ability to alter cancer marker expression by contacting a compound with a cell expressing a cancer marker and then assaying for the effect of the candidate compounds on expression. In some embodiments, the effect of candidate compounds on expression of a cancer marker gene is assayed for by detecting the level of cancer marker mRNA expressed by the cell. mRNA expression can be detected by any suitable method. In other embodiments, the effect of

candidate compounds on expression of cancer marker genes is assayed by measuring the level of polypeptide encoded by the cancer markers. The level of polypeptide expressed can be measured using any suitable method, including but not limited to, those disclosed herein.

Specifically, the present invention provides screening methods for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, proteins, peptides, peptidomimetics, peptoids, small molecules or other drugs) which bind to cancer markers of the present invention, have an inhibitory (or stimulatory) effect on, for example, cancer marker expression or cancer marker activity, or have a stimulatory or inhibitory effect on, for example, the expression or activity of a cancer marker substrate. Compounds thus identified can be used to modulate the activity of target gene products (*e.g.*, cancer marker genes) either directly or indirectly in a therapeutic protocol, to elaborate the biological function of the target gene product, or to identify compounds that disrupt normal target gene interactions. Compounds that inhibit the activity or expression of cancer markers are useful in the treatment of proliferative disorders, *e.g.*, cancer, particularly prostate cancer.

In one embodiment, the invention provides assays for screening candidate or test compounds that are substrates of a cancer marker protein or polypeptide or a biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds that bind to or modulate the activity of a cancer marker protein or polypeptide or a biologically active portion thereof.

The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone, which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, *e.g.*, Zuckennann *et al.*, J. Med. Chem. 37: 2678-85 [1994]); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are preferred for use with peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) Anticancer Drug Des. 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.*, Proc. Natl. Acad. Sci. U.S.A. 90:6909 [1993]; Erb *et al.*, Proc. Nad. Acad. Sci. USA 91:11422 [1994]; Zuckermann *et al.*, J. Med. Chem. 37:2678 [1994];

Cho *et al.,* Science 261:1303 [1993]; Carrell *et al.,* Angew. Chem. Int. Ed. Engl. 33.2059 [1994]; Carell *et al.,* Angew. Chem. Int. Ed. Engl. 33:2061 [1994]; and Gallop *et al.,* J. Med. Chem. 37:1233 [1994].

Libraries of compounds may be presented in solution (*e.g.*, Houghten, Biotechniques 13:412-421 [1992]), or on beads (Lam, Nature 354:82-84 [1991]), chips (Fodor, Nature 364:555-556 [1993]), bacteria or spores (U.S. Pat. No. 5,223,409; herein incorporated by reference), plasmids (Cull *et al.,* Proc. Nad. Acad. Sci. USA 89:18651869 [1992]) or on phage (Scott and Smith, Science 249:386-390 [1990]; Devlin Science 249:404-406 [1990]; Cwirla *et al.,* Proc. NatI. Acad. Sci. 87:6378-6382 [1990]; Felici, J. Mol. Biol. 222:301 [1991]).

In one embodiment, an assay is a cell-based assay in which a cell that expresses a cancer marker mRNA or protein or biologically active portion thereof is contacted with a test compound, and the ability of the test compound to the modulate cancer marker's activity is determined. Determining the ability of the test compound to modulate cancer marker activity can be accomplished by monitoring, for example, changes in enzymatic activity, destruction or mRNA, or the like.

The ability of the test compound to modulate cancer marker binding to a compound, *e.g.*, a cancer marker substrate or modulator, can also be evaluated. This can be accomplished, for example, by coupling the compound, *e.g.*, the substrate, with a radioisotope or enzymatic label such that binding of the compound, *e.g.*, the substrate, to a cancer marker can be determined by detecting the labeled compound, *e.g.*, substrate, in a complex.

Alternatively, the cancer marker is coupled with a radioisotope or enzymatic label to monitor the ability of a test compound to modulate cancer marker binding to a cancer marker substrate in a complex. For example, compounds (*e.g.*, substrates) can be labeled with ^{125}I, ^{35}S ^{14}C or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

The ability of a compound (*e.g.*, a cancer marker substrate) to interact with a cancer marker with or without the labeling of any of the interactants can be evaluated. For example, a microphysiorneter can be used to detect the interaction of a compound with a

cancer marker without the labeling of either the compound or the cancer marker (McConnell *et al.* Science 257:1906-1912 [1992]). As used herein, a "microphysiometer" (*e.g.*, Cytosensor) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between a compound and cancer markers.

In yet another embodiment, a cell-free assay is provided in which a cancer marker protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to bind to the cancer marker protein, mRNA, or biologically active portion thereof is evaluated. Preferred biologically active portions of the cancer marker proteins or mRNA to be used in assays of the present invention include fragments that participate in interactions with substrates or other proteins, *e.g.*, fragments with high surface probability scores.

Cell-free assays involve preparing a reaction mixture of the target gene protein and the test compound under conditions and for a time sufficient to allow the two components to interact and bind, thus forming a complex that can be removed and/or detected.

The interaction between two molecules can also be detected, *e.g.*, using fluorescence energy transfer (FRET) (see, for example, Lakowicz *et al.*, U.S. Pat. No. 5,631,169; Stavrianopoulos *et al.*, U.S. Pat. No. 4,968,103; each of which is herein incorporated by reference). A fluorophore label is selected such that a first donor molecule's emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy.

Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, the spatial relationship between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label should be maximal. A FRET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

In another embodiment, determining the ability of the cancer marker protein or mRNA to bind to a target molecule can be accomplished using real-time Biomolecular

Interaction Analysis (BIA) (*see, e.g.*, Sjolander and Urbaniczky, Anal. Chem. 63:2338-2345 [1991] and Szabo *et al.* Curr. Opin. Struct. Biol. 5:699-705 [1995]). "Surface plasmon resonance" or "BIA" detects biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BlAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal that can be used as an indication of real-time reactions between biological molecules.

In one embodiment, the target gene product or the test substance is anchored onto a solid phase. The target gene product/test compound complexes anchored on the solid phase can be detected at the end of the reaction. Preferably, the target gene product can be anchored onto a solid surface, and the test compound, (which is not anchored), can be labeled, either directly or indirectly, with detectable labels discussed herein.

It may be desirable to immobilize cancer markers, an anti-cancer marker antibody or its target molecule to facilitate separation of complexed from non-complexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to a cancer marker protein, or interaction of a cancer marker protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase-cancer marker fusion proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione Sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione-derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed target protein or cancer marker protein, and the mixture incubated under conditions conducive for complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above.

Alternatively, the complexes can be dissociated from the matrix, and the level of cancer markers binding or activity determined using standard techniques. Other techniques for immobilizing either cancer markers protein or a target molecule on matrices include using conjugation of biotin and streptavidin. Biotinylated cancer marker protein or target

molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, EL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical).

In order to conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; *e.g.*, using a labeled antibody specific for the immobilized component (the antibody, in turn, can be directly labeled or indirectly labeled with, *e.g.*, a labeled anti-IgG antibody).

This assay is performed utilizing antibodies reactive with cancer marker protein or target molecules but which do not interfere with binding of the cancer markers protein to its target molecule. Such antibodies can be derivatized to the wells of the plate, and unbound target or cancer markers protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the cancer marker protein or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the cancer marker protein or target molecule.

Alternatively, cell free assays can be conducted in a liquid phase. In such an assay, the reaction products are separated from unreacted components, by any of a number of standard techniques, including, but not limited to: differential centrifugation (see, for example, Rivas and Minton, Trends Biochem Sci 18:284-7 [1993]); chromatography (gel filtration chromatography, ion-exchange chromatography); electrophoresis (*see, e.g.*, Ausubel *et al.*, eds. Current Protocols in Molecular Biology 1999, J. Wiley: New York.); and immunoprecipitation (*see*, for example, Ausubel *et al.*, eds. Current Protocols in Molecular Biology 1999, J. Wiley: New York). Such resins and chromatographic techniques are known to one skilled in the art (*See e.g.*, Heegaard J. Mol. Recognit 11:141-8 [1998]; Hageand Tweed J. Chromatogr. Biomed. Sci. Appl 699:499-525 [1997]). Further,

fluorescence energy transfer may also be conveniently utilized, as described herein, to detect binding without further purification of the complex from solution.

The assay can include contacting the cancer markers protein, mRNA, or biologically active portion thereof with a known compound that binds the cancer marker to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a cancer marker protein or mRNA, wherein determining the ability of the test compound to interact with a cancer marker protein or mRNA includes determining the ability of the test compound to preferentially bind to cancer markers or biologically active portion thereof, or to modulate the activity of a target molecule, as compared to the known compound.

To the extent that cancer markers can, *in vivo*, interact with one or more cellular or extracellular macromolecules, such as proteins, inhibitors of such an interaction are useful. A homogeneous assay can be used can be used to identify inhibitors.

For example, a preformed complex of the target gene product and the interactive cellular or extracellular binding partner product is prepared such that either the target gene products or their binding partners are labeled, but the signal generated by the label is quenched due to complex formation (see, *e.g.*, U.S. Pat. No. 4,109,496, herein incorporated by reference, that utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances that disrupt target gene product-binding partner interaction can be identified. Alternatively, cancer markers protein can be used as a "bait protein" in a two-hybrid assay or three-hybrid assay (*see*, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.*, Cell 72:223-232 [1993]; Madura *et al.*, J. Biol. Chem. 268.12046-12054 [1993]; Bartel *et al.*, Biotechniques 14:920-924 [1993]; Iwabuchi *et al.*, Oncogene 8:1693-1696 [1993]; and Brent W0 94/10300; each of which is herein incorporated by reference), to identify other proteins, that bind to or interact with cancer markers ("cancer marker-binding proteins" or "cancer marker-bp") and are involved in cancer marker activity. Such cancer marker-bps can be activators or inhibitors of signals by the cancer marker proteins or targets as, for example, downstream elements of a cancer markers-mediated signaling pathway.

Modulators of cancer markers expression can also be identified. For example, a cell or cell free mixture is contacted with a candidate compound and the expression of cancer marker mRNA or protein evaluated relative to the level of expression of cancer marker

mRNA or protein in the absence of the candidate compound. When expression of cancer marker mRNA or protein is greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of cancer marker mRNA or protein expression. Alternatively, when expression of cancer marker mRNA or protein is less (i.e., statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of cancer marker mRNA or protein expression. The level of cancer markers mRNA or protein expression can be determined by methods described herein for detecting cancer markers mRNA or protein.

A modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a cancer markers protein can be confirmed *in vivo*, *e.g.*, in an animal such as an animal model for a disease (*e.g.*, an animal with prostate cancer or metastatic prostate cancer; or an animal harboring a xenograft of a prostate cancer from an animal (*e.g.*, human) or cells from a cancer resulting from metastasis of a prostate cancer (*e.g.*, to a lymph node, bone, or liver), or cells from a prostate cancer cell line.

This invention further pertains to novel agents identified by the above-described screening assays (*See e.g.*, below description of cancer therapies). Accordingly, it is within the scope of this invention to further use an agent identified as described herein (*e.g.*, a cancer marker modulating agent, an antisense cancer marker nucleic acid molecule, a siRNA molecule, a cancer marker specific antibody, or a cancer marker-binding partner) in an appropriate animal model (such as those described herein) to determine the efficacy, toxicity, side effects, or mechanism of action, of treatment with such an agent. Furthermore, novel agents identified by the above-described screening assays can be, *e.g.*, used for treatments as described herein.

VI. Therapeutic Applications

In some embodiments, the present invention provides therapies for cancer (*e.g.*, prostate cancer). In some embodiments, therapies directly or indirectly target cancer markers (*e.g.*, including but not limited to, ERG, ETV1, and ETV4 gene fusions with TMPRSS2).

A. RNA Interference and Antisense Therapies

In some embodiments, the present invention targets the expression of cancer markers. For example, in some embodiments, the present invention employs compositions

comprising oligomeric antisense or RNAi compounds, particularly oligonucleotides (*e.g.*, those identified in the drug screening methods described above), for use in modulating the function of nucleic acid molecules encoding cancer markers of the present invention, ultimately modulating the amount of cancer marker expressed.

1. RNA Interference (RNAi)

In some embodiments, RNAi is utilized to inhibit fusion protein function. RNAi represents an evolutionary conserved cellular defense for controlling the expression of foreign genes in most eukaryotes, including humans. RNAi is typically triggered by double-stranded RNA (dsRNA) and causes sequence-specific mRNA degradation of single-stranded target RNAs homologous in response to dsRNA. The mediators of mRNA degradation are small interfering RNA duplexes (siRNAs), which are normally produced from long dsRNA by enzymatic cleavage in the cell. siRNAs are generally approximately twenty-one nucleotides in length (*e.g.* 21-23 nucleotides in length), and have a base-paired structure characterized by two nucleotide 3'-overhangs. Following the introduction of a small RNA, or RNAi, into the cell, it is believed the sequence is delivered to an enzyme complex called RISC (RNA-induced silencing complex). RISC recognizes the target and cleaves it with an endonuclease. It is noted that if larger RNA sequences are delivered to a cell, RNase III enzyme (Dicer) converts longer dsRNA into 21-23 nt ds siRNA fragments. In some embodiments, RNAi oligonucleotides are designed to target the junction region of fusion proteins.

Chemically synthesized siRNAs have become powerful reagents for genome-wide analysis of mammalian gene function in cultured somatic cells. Beyond their value for validation of gene function, siRNAs also hold great potential as gene-specific therapeutic agents (Tuschl and Borkhardt, Molecular Intervent. 2002; 2(3):158-67, herein incorporated by reference).

The transfection of siRNAs into animal cells results in the potent, long-lasting post-transcriptional silencing of specific genes (Caplen et al, Proc Natl Acad Sci U.S.A. 2001; 98: 9742–7; Elbashir et al., Nature. 2001; 411:494–8; Elbashir et al., Genes Dev. 2001;15: 188–200; and Elbashir et al., EMBO J. 2001; 20: 6877–88, all of which are herein incorporated by reference). Methods and compositions for performing RNAi with siRNAs are described, for example, in U.S. Pat. 6,506,559, herein incorporated by reference.

siRNAs are extraordinarily effective at lowering the amounts of targeted RNA, and by extension proteins, frequently to undetectable levels. The silencing effect can last several months, and is extraordinarily specific, because one nucleotide mismatch between the target RNA and the central region of the siRNA is frequently sufficient to prevent silencing (Brummelkamp et al, Science 2002; 296:550–3; and Holen et al, Nucleic Acids Res. 2002; 30:1757–66, both of which are herein incorporated by reference).
An important factor in the design of siRNAs is the presence of accessible sites for siRNA binding. Bahoia et al., (J. Biol. Chem., 2003; 278: 15991-15997; herein incorporated by reference) describe the use of a type of DNA array called a scanning array to find accessible sites in mRNAs for designing effective siRNAs. These arrays comprise oligonucleotides ranging in size from monomers to a certain maximum, usually Comers, synthesized using a physical barrier (mask) by stepwise addition of each base in the sequence. Thus the arrays represent a full oligonucleotide complement of a region of the target gene. Hybridization of the target mRNA to these arrays provides an exhaustive accessibility profile of this region of the target mRNA. Such data are useful in the design of antisense oligonucleotides (ranging from 7mers to 25mers), where it is important to achieve a compromise between oligonucleotide length and binding affinity, to retain efficacy and target specificity (Sohail et al, Nucleic Acids Res., 2001; 29(10): 2041- 2045). Additional methods and concerns for selecting siRNAs are described for example, in WO 05054270, WO05038054A1, WO03070966A2, J Mol Biol. 2005 May 13;348(4):883-93, J Mol Biol. 2005 May 13;348(4):871-81, and Nucleic Acids Res. 2003 Aug 1;31(15):4417-24, each of which is herein incorporated by reference in its entirety. In addition, software (*e.g.*, the MWG online siMAX siRNA design tool) is commercially or publicly available for use in the selection of siRNAs.

2. Antisense

In other embodiments, fusion protein expression is modulated using antisense compounds that specifically hybridize with one or more nucleic acids encoding cancer markers of the present invention. The specific hybridization of an oligomeric compound with its target nucleic acid interferes with the normal function of the nucleic acid. This modulation of function of a target nucleic acid by compounds that specifically hybridize to it is generally referred to as "antisense." The functions of DNA to be interfered with include replication and transcription. The functions of RNA to be interfered with include all

vital functions such as, for example, translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity that may be engaged in or facilitated by the RNA. The overall effect of such interference with target nucleic acid function is modulation of the expression of cancer markers of the present invention. In the context of the present invention, "modulation" means either an increase (stimulation) or a decrease (inhibition) in the expression of a gene. For example, expression may be inhibited to potentially prevent tumor proliferation.

It is preferred to target specific nucleic acids for antisense. "Targeting" an antisense compound to a particular nucleic acid, in the context of the present invention, is a multistep process. The process usually begins with the identification of a nucleic acid sequence whose function is to be modulated. This may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. In the present invention, the target is a nucleic acid molecule encoding a cancer marker of the present invention. The targeting process also includes determination of a site or sites within this gene for the antisense interaction to occur such that the desired effect, *e.g.*, detection or modulation of expression of the protein, will result. Within the context of the present invention, a preferred intragenic site is the region encompassing the translation initiation or termination codon of the open reading frame (ORF) of the gene. Since the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon". A minority of genes have a translation initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function *in vivo*. Thus, the terms "translation initiation codon" and "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (in prokaryotes). Eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the present invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used *in vivo* to initiate translation of an mRNA molecule transcribed from a gene encoding a tumor antigen of the present invention, regardless of the sequence(s) of such codons.

Translation termination codon (or "stop codon") of a gene may have one of three sequences (*i.e.*, 5'-UAA, 5'-UAG and 5'-UGA; the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively). The terms "start codon region" and "translation initiation codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (*i.e.*, 5' or 3') from a translation initiation codon. Similarly, the terms "stop codon region" and "translation termination codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (*i.e.*, 5' or 3') from a translation termination codon.

The open reading frame (ORF) or "coding region," which refers to the region between the translation initiation codon and the translation termination codon, is also a region that may be targeted effectively. Other target regions include the 5' untranslated region (5' UTR), referring to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene, and the 3' untranslated region (3' UTR), referring to the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene. The 5' cap of an mRNA comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage. The 5' cap region of an mRNA is considered to include the 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap. The cap region may also be a preferred target region.

Although some eukaryotic mRNA transcripts are directly translated, many contain one or more regions, known as "introns," that are excised from a transcript before it is translated. The remaining (and therefore translated) regions are known as "exons" and are spliced together to form a continuous mRNA sequence. mRNA splice sites (*i.e.*, intron-exon junctions) may also be preferred target regions, and are particularly useful *in situ*ations where aberrant splicing is implicated in disease, or where an overproduction of a particular mRNA splice product is implicated in disease. Aberrant fusion junctions due to rearrangements or deletions are also preferred targets. It has also been found that introns can also be effective, and therefore preferred, target regions for antisense compounds targeted, for example, to DNA or pre-mRNA.

In some embodiments, target sites for antisense inhibition are identified using commercially available software programs (*e.g.*, Biognostik, Gottingen, Germany; SysArris Software, Bangalore, India; Antisense Research Group, University of Liverpool, Liverpool, England; GeneTrove, Carlsbad, CA). In other embodiments, target sites for antisense inhibition are identified using the accessible site method described in PCT Publ. No. WO0198537A2, herein incorporated by reference.

Once one or more target sites have been identified, oligonucleotides are chosen that are sufficiently complementary to the target (*i.e.*, hybridize sufficiently well and with sufficient specificity) to give the desired effect. For example, in preferred embodiments of the present invention, antisense oligonucleotides are targeted to or near the start codon.

In the context of this invention, "hybridization," with respect to antisense compositions and methods, means hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleoside or nucleotide bases. For example, adenine and thymine are complementary nucleobases that pair through the formation of hydrogen bonds. It is understood that the sequence of an antisense compound need not be 100% complementary to that of its target nucleic acid to be specifically hybridizable. An antisense compound is specifically hybridizable when binding of the compound to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA to cause a loss of utility, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target sequences under conditions in which specific binding is desired (*i.e.*, under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and in the case of *in vitro* assays, under conditions in which the assays are performed).

Antisense compounds are commonly used as research reagents and diagnostics. For example, antisense oligonucleotides, which are able to inhibit gene expression with specificity, can be used to elucidate the function of particular genes. Antisense compounds are also used, for example, to distinguish between functions of various members of a biological pathway.

The specificity and sensitivity of antisense is also applied for therapeutic uses. For example, antisense oligonucleotides have been employed as therapeutic moieties in the treatment of disease states in animals and man. Antisense oligonucleotides have been safely and effectively administered to humans and numerous clinical trials are presently underway. It is thus established that oligonucleotides are useful therapeutic modalities that can be

configured to be useful in treatment regimes for treatment of cells, tissues, and animals, especially humans.

While antisense oligonucleotides are a preferred form of antisense compound, the present invention comprehends other oligomeric antisense compounds, including but not limited to oligonucleotide mimetics such as are described below. The antisense compounds in accordance with this invention preferably comprise from about 8 to about 30 nucleobases (*i.e.*, from about 8 to about 30 linked bases), although both longer and shorter sequences may find use with the present invention. Particularly preferred antisense compounds are antisense oligonucleotides, even more preferably those comprising from about 12 to about 25 nucleobases.

Specific examples of preferred antisense compounds useful with the present invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene

containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

In other preferred oligonucleotide mimetics, both the sugar and the internucleoside linkage (*i.e.*, the backbone) of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen *et al.*, Science 254:1497 (1991).

Most preferred embodiments of the invention are oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular --CH_2, --NH--O--CH_2--, --CH_2--N(CH_3)--O--CH_2-- [known as a methylene (methylimino) or MMI backbone], --CH_2--O--N(CH_3)--CH_2--, --CH_2--N(CH_3)--N(CH_3)--CH_2--, and --O--N(CH_3)--CH_2--CH_2-- [wherein the native phosphodiester backbone is represented as --O--P--O--CH_2--] of the above referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above referenced U.S. Pat. No. 5,602,240. Also preferred are oligonucleotides having morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkaryl, aralkyl,

O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O--$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, Helv. Chim. Acta 78:486 [1995]) *i.e.*, an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy (*i.e.*, a $O(CH_2)_2ON(CH_3)_2$ group), also known as 2'-DMAOE, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), *i.e.*, 2'-O--CH_2--O--CH_2--$N(CH_2)_2$.

Other preferred modifications include 2'-methoxy(2'-O--CH_3), 2'-aminopropoxy(2'-$OCH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar.

Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These

include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2. °C and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Another modification of the oligonucleotides of the present invention involves chemically linking to the oligonucleotide one or more moieties or conjugates that enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety, cholic acid, a thioether, (*e.g.*, hexyl-S-tritylthiol), a thiocholesterol, an aliphatic chain, (*e.g.*, dodecandiol or undecyl residues), a phospholipid, (*e.g.*, di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate), a polyamine or a polyethylene glycol chain or adamantane acetic acid, a palmityl moiety, or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety.

One skilled in the relevant art knows well how to generate oligonucleotides containing the above-described modifications. The present invention is not limited to the antisense oligonucleotides described above. Any suitable modification or substitution may be utilized.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds that are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of the present invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, *i.e.*, a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNaseH is a cellular endonuclease that cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression.

Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

Chimeric antisense compounds of the present invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above.

The present invention also includes pharmaceutical compositions and formulations that include the antisense compounds of the present invention as described below.

B. Gene Therapy

The present invention contemplates the use of any genetic manipulation for use in modulating the expression of cancer markers of the present invention. Examples of genetic manipulation include, but are not limited to, gene knockout (*e.g.*, removing the fusion gene from the chromosome using, for example, recombination), expression of antisense constructs with or without inducible promoters, and the like. Delivery of nucleic acid construct to cells *in vitro* or *in vivo* may be conducted using any suitable method. A suitable method is one that introduces the nucleic acid construct into the cell such that the desired event occurs (*e.g.*, expression of an antisense construct). Genetic therapy may also be used to deliver siRNA or other interfering molecules that are expressed *in vivo* (*e.g.*, upon stimulation by an inducible promoter (*e.g.*, an androgen-responsive promoter)).

Introduction of molecules carrying genetic information into cells is achieved by any of various methods including, but not limited to, directed injection of naked DNA constructs, bombardment with gold particles loaded with said constructs, and macromolecule mediated gene transfer using, for example, liposomes, biopolymers, and the like. Preferred methods use gene delivery vehicles derived from viruses, including, but not limited to, adenoviruses, retroviruses, vaccinia viruses, and adeno-associated viruses. Because of the higher efficiency as compared to retroviruses, vectors derived from adenoviruses are the preferred gene delivery vehicles for transferring nucleic acid molecules into host cells *in vivo*. Adenoviral vectors have been shown to provide very efficient *in vivo* gene transfer into a variety of solid tumors in animal models and into human solid tumor xenografts in immune-deficient mice. Examples of adenoviral vectors and methods for

gene transfer are described in PCT publications WO 00/12738 and WO 00/09675 and U.S. Pat. Appl. Nos. 6,033,908, 6,019,978, 6,001,557, 5,994,132, 5,994,128, 5,994,106, 5,981,225, 5,885,808, 5,872,154, 5,830,730, and 5,824,544, each of which is herein incorporated by reference in its entirety.

Vectors may be administered to subject in a variety of ways. For example, in some embodiments of the present invention, vectors are administered into tumors or tissue associated with tumors using direct injection. In other embodiments, administration is via the blood or lymphatic circulation (*See e.g.*, PCT publication 99/02685 herein incorporated by reference in its entirety). Exemplary dose levels of adenoviral vector are preferably 10^8 to 10^{11} vector particles added to the perfusate.

C. Antibody Therapy

In some embodiments, the present invention provides antibodies that target prostate tumors that express a cancer marker of the present invention (*e.g.*, ERG, ETV1, or ETV4 fusions with TMPRSS2). Any suitable antibody (*e.g.*, monoclonal, polyclonal, or synthetic) may be utilized in the therapeutic methods disclosed herein. In preferred embodiments, the antibodies used for cancer therapy are humanized antibodies. Methods for humanizing antibodies are well known in the art (*See e.g.*, U.S. Pat. Nos. 6,180,370, 5,585,089, 6,054,297, and 5,565,332; each of which is herein incorporated by reference).

In some embodiments, the therapeutic antibodies comprise an antibody generated against a cancer marker of the present invention (*e.g.*, ERG, ETV1, or ETV4 fusions with TMPRSS2), wherein the antibody is conjugated to a cytotoxic agent. In such embodiments, a tumor specific therapeutic agent is generated that does not target normal cells, thus reducing many of the detrimental side effects of traditional chemotherapy. For certain applications, it is envisioned that the therapeutic agents will be pharmacologic agents that will serve as useful agents for attachment to antibodies, particularly cytotoxic or otherwise anticellular agents having the ability to kill or suppress the growth or cell division of endothelial cells. The present invention contemplates the use of any pharmacologic agent that can be conjugated to an antibody, and delivered in active form. Exemplary anticellular agents include chemotherapeutic agents, radioisotopes, and cytotoxins. The therapeutic antibodies of the present invention may include a variety of cytotoxic moieties, including but not limited to, radioactive isotopes (*e.g.*, iodine-131, iodine-123, technicium-99m, indium-111, rhenium-188, rhenium-186, gallium-67, copper-67, yttrium-90, iodine-125 or

astatine-211), hormones such as a steroid, antimetabolites such as cytosines (*e.g.*, arabinoside, fluorouracil, methotrexate or aminopterin; an anthracycline; mitomycin C), vinca alkaloids (*e.g.*, demecolcine; etoposide; mithramycin), and antitumor alkylating agent such as chlorambucil or melphalan. Other embodiments may include agents such as a coagulant, a cytokine, growth factor, bacterial endotoxin or the lipid A moiety of bacterial endotoxin. For example, in some embodiments, therapeutic agents will include plant-, fungus- or bacteria-derived toxin, such as an A chain toxins, a ribosome inactivating protein, α-sarcin, aspergillin, restrictocin, a ribonuclease, diphtheria toxin or pseudomonas exotoxin, to mention just a few examples. In some preferred embodiments, deglycosylated ricin A chain is utilized.

In any event, it is proposed that agents such as these may, if desired, be successfully conjugated to an antibody, in a manner that will allow their targeting, internalization, release or presentation to blood components at the site of the targeted tumor cells as required using known conjugation technology (*See, e.g.*, Ghose *et al.*, Methods Enzymol., 93:280 [1983]).

For example, in some embodiments the present invention provides immunotoxins targeted a cancer marker of the present invention (*e.g.*, ERG or ETV1 fusions). Immunotoxins are conjugates of a specific targeting agent typically a tumor-directed antibody or fragment, with a cytotoxic agent, such as a toxin moiety. The targeting agent directs the toxin to, and thereby selectively kills, cells carrying the targeted antigen. In some embodiments, therapeutic antibodies employ crosslinkers that provide high *in vivo* stability (Thorpe *et al.*, Cancer Res., 48:6396 [1988]).

In other embodiments, particularly those involving treatment of solid tumors, antibodies are designed to have a cytotoxic or otherwise anticellular effect against the tumor vasculature, by suppressing the growth or cell division of the vascular endothelial cells. This attack is intended to lead to a tumor-localized vascular collapse, depriving the tumor cells, particularly those tumor cells distal of the vasculature, of oxygen and nutrients, ultimately leading to cell death and tumor necrosis.

In preferred embodiments, antibody based therapeutics are formulated as pharmaceutical compositions as described below. In preferred embodiments, administration of an antibody composition of the present invention results in a measurable decrease in cancer (*e.g.*, decrease or elimination of tumor).

D. Pharmaceutical Compositions

The present invention further provides pharmaceutical compositions (*e.g.*, comprising pharmaceutical agents that modulate the expression or activity of gene fusions of the present invention). The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic and to mucous membranes including vaginal and rectal delivery), pulmonary (*e.g.*, by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, *e.g.*, intrathecal or intraventricular, administration.

Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable.

Compositions and formulations for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets or tablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable.

Compositions and formulations for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions that may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions may be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids.

The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general the formulations are prepared by uniformly and intimately bringing into association

the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

In one embodiment of the present invention the pharmaceutical compositions may be formulated and used as foams. Pharmaceutical foams include formulations such as, but not limited to, emulsions, microemulsions, creams, jellies and liposomes. While basically similar in nature these formulations vary in the components and the consistency of the final product.

Agents that enhance uptake of oligonucleotides at the cellular level may also be added to the pharmaceutical and other compositions of the present invention. For example, cationic lipids, such as lipofectin (U.S. Pat. No. 5,705,188), cationic glycerol derivatives, and polycationic molecules, such as polylysine (WO 97/30731), also enhance the cellular uptake of oligonucleotides.

The compositions of the present invention may additionally contain other adjunct components conventionally found in pharmaceutical compositions. Thus, for example, the compositions may contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the compositions of the present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the present invention. The formulations can be sterilized and, if desired, mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavorings and/or aromatic substances and the like which do not deleteriously interact with the nucleic acid(s) of the formulation.

Certain embodiments of the invention provide pharmaceutical compositions containing (a) one or more antisense compounds and (b) one or more other chemotherapeutic agents that function by a non-antisense mechanism. Examples of such chemotherapeutic agents include, but are not limited to, anticancer drugs such as daunorubicin, dactinomycin, doxorubicin, bleomycin, mitomycin, nitrogen mustard, chlorambucil, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine (CA), 5-fluorouracil (5-FU), floxuridine (5-FUdR), methotrexate (MTX), colchicine, vincristine, vinblastine, etoposide, teniposide, cisplatin and diethylstilbestrol (DES). Anti-inflammatory drugs, including but not limited to nonsteroidal anti-inflammatory drugs and corticosteroids, and antiviral drugs, including but not limited to ribivirin, vidarabine, acyclovir and ganciclovir, may also be combined in compositions of the invention. Other non-antisense chemotherapeutic agents are also within the scope of this invention. Two or more combined compounds may be used together or sequentially.

Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. The administering physician can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on EC_{50}s found to be effective in *in vitro* and *in vivo* animal models or based on the examples described herein. In general, dosage is from 0.01 μg to 100 g per kg of body weight, and may be given once or more daily, weekly, monthly or yearly. The treating physician can estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the subject undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 μg to 100 g per kg of body weight, once or more daily, to once every 20 years.

VII. Transgenic Animals

The present invention contemplates the generation of transgenic animals comprising an exogenous cancer marker gene (*e.g.*, gene fusion) of the present invention or mutants and variants thereof (*e.g.*, truncations or single nucleotide polymorphisms). In preferred

embodiments, the transgenic animal displays an altered phenotype (*e.g.*, increased or decreased presence of markers) as compared to wild-type animals. Methods for analyzing the presence or absence of such phenotypes include but are not limited to, those disclosed herein. In some preferred embodiments, the transgenic animals further display an increased or decreased growth of tumors or evidence of cancer.

The transgenic animals of the present invention find use in drug (*e.g.*, cancer therapy) screens. In some embodiments, test compounds (*e.g.*, a drug that is suspected of being useful to treat cancer) and control compounds (*e.g.*, a placebo) are administered to the transgenic animals and the control animals and the effects evaluated.

The transgenic animals can be generated via a variety of methods. In some embodiments, embryonal cells at various developmental stages are used to introduce transgenes for the production of transgenic animals. Different methods are used depending on the stage of development of the embryonal cell. The zygote is the best target for micro-injection. In the mouse, the male pronucleus reaches the size of approximately 20 micrometers in diameter that allows reproducible injection of 1-2 picoliters (pl) of DNA solution. The use of zygotes as a target for gene transfer has a major advantage in that in most cases the injected DNA will be incorporated into the host genome before the first cleavage (Brinster *et al.,* Proc. Natl. Acad. Sci. USA 82:4438-4442 [1985]). As a consequence, all cells of the transgenic non-human animal will carry the incorporated transgene. This will in general also be reflected in the efficient transmission of the transgene to offspring of the founder since 50% of the germ cells will harbor the transgene. U.S. Pat. No. 4,873,191 describes a method for the micro-injection of zygotes; the disclosure of this patent is incorporated herein in its entirety.

In other embodiments, retroviral infection is used to introduce transgenes into a non-human animal. In some embodiments, the retroviral vector is utilized to transfect oocytes by injecting the retroviral vector into the perivitelline space of the oocyte (U.S. Pat. No. 6,080,912, incorporated herein by reference). In other embodiments, the developing non-human embryo can be cultured *in vitro* to the blastocyst stage. During this time, the blastomeres can be targets for retroviral infection (Janenich, Proc. Natl. Acad. Sci. USA 73:1260 [1976]). Efficient infection of the blastomeres is obtained by enzymatic treatment to remove the zona pellucida (Hogan *et al.*, in *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. [1986]). The viral vector system used to introduce the transgene is typically a replication-defective retrovirus

carrying the transgene (Jahner *et al.,* Proc. Natl. Acad Sci. USA 82:6927 [1985]). Transfection is easily and efficiently obtained by culturing the blastomeres on a monolayer of virus-producing cells (Stewart, *et al.,* EMBO J., 6:383 [1987]). Alternatively, infection can be performed at a later stage. Virus or virus-producing cells can be injected into the blastocoele (Jahner *et al.,* Nature 298:623 [1982]). Most of the founders will be mosaic for the transgene since incorporation occurs only in a subset of cells that form the transgenic animal. Further, the founder may contain various retroviral insertions of the transgene at different positions in the genome that generally will segregate in the offspring. In addition, it is also possible to introduce transgenes into the germline, albeit with low efficiency, by intrauterine retroviral infection of the midgestation embryo (Jahner *et al., supra* [1982]). Additional means of using retroviruses or retroviral vectors to create transgenic animals known to the art involve the micro-injection of retroviral particles or mitomycin C-treated cells producing retrovirus into the perivitelline space of fertilized eggs or early embryos (PCT International Application WO 90/08832 [1990], and Haskell and Bowen, Mol. Reprod. Dev., 40:386 [1995]).

In other embodiments, the transgene is introduced into embryonic stem cells and the transfected stem cells are utilized to form an embryo. ES cells are obtained by culturing pre-implantation embryos *in vitro* under appropriate conditions (Evans *et al.,* Nature 292:154 [1981]; Bradley *et al.,* Nature 309:255 [1984]; Gossler *et al.*, Proc. Acad. Sci. USA 83:9065 [1986]; and Robertson *et al.*, Nature 322:445 [1986]). Transgenes can be efficiently introduced into the ES cells by DNA transfection by a variety of methods known to the art including calcium phosphate co-precipitation, protoplast or spheroplast fusion, lipofection and DEAE-dextran-mediated transfection. Transgenes may also be introduced into ES cells by retrovirus-mediated transduction or by micro-injection. Such transfected ES cells can thereafter colonize an embryo following their introduction into the blastocoel of a blastocyst-stage embryo and contribute to the germ line of the resulting chimeric animal (for review, *See*, Jaenisch, Science 240:1468 [1988]). Prior to the introduction of transfected ES cells into the blastocoel, the transfected ES cells may be subjected to various selection protocols to enrich for ES cells which have integrated the transgene assuming that the transgene provides a means for such selection. Alternatively, the polymerase chain reaction may be used to screen for ES cells that have integrated the transgene. This technique obviates the need for growth of the transfected ES cells under appropriate selective conditions prior to transfer into the blastocoel.

In still other embodiments, homologous recombination is utilized to knock-out gene function or create deletion mutants (*e.g.*, truncation mutants). Methods for homologous recombination are described in U.S. Pat. No. 5,614,396, incorporated herein by reference.

EXPERIMENTAL

The following examples are provided in order to demonstrate and further illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

Example 1
ERG and ETV1 Gene Fusions

A. Materials and Methods

Cancer Outlier Profile Analysis (COPA)

COPA analysis was performed on 132 gene expression data sets in Oncomine 3.0 comprising 10,486 microarray experiments. In addition, data from 99 amplified laser-capture microdissected prostate tissue samples were included in the COPA analysis. COPA has three steps. First, gene expression values are median centered, setting each gene's median expression value to zero. Second, the median absolute deviation (MAD) is calculated and scaled to 1 by dividing each gene expression value by its MAD. Median and MAD were used for transformation as opposed to mean and standard deviation so that outlier expression values do not unduly influence the distribution estimates, and are thus preserved post-normalization. Third, the 75th, 90th, and 95th percentiles of the transformed expression values are tabulated for each gene and then genes are rank-ordered by their percentile scores, providing a prioritized list of outlier profiles.

Samples

Tissues utilized were from the radical prostatectomy series at the University of Michigan and from the Rapid Autopsy Program (Shah et al., Cancer Res 64, 9209 (Dec 15,

2004)), which are both part of University of Michigan Prostate Cancer Specialized Program of Research Excellence (S.P.O.R.E.) Tissue Core.

Tissues were also obtained from a radical prostatectomy series at the University Hospital Ulm (Ulm, Germany). All samples were collected from consented patients with prior institutional review board approval at each respective institution. Total RNA from all samples was isolated with Trizol (Invitrogen) according to the manufacturer's instructions. Total RNA was also isolated from RWPE, PC3 , PC3+AR (Dai et al., Steroids 61, 531 (1996)), LNCaP, VCaP and DuCaP cell lines. RNA integrity was verified by denaturing formaldehyde gel electrophoresis or the Agilent Bioanalyzer 2100. A commercially available pool of benign prostate tissue total RNA (CPP, Clontech) was also used.

Quantitative PCR (QPCR)

Quantitative PCR (QPCR) was performed using SYBR Green dye on an Applied Biosystems 7300 Real Time PCR system essentially as described (Chinnaiyan et al., Cancer Res 65, 3328 (2005); Rubin et al., Cancer Res 64, 3814 (2004)). Briefly, 1-5 μg of total RNA was reverse transcribed into cDNA using SuperScript III (Invitrogen) in the presence of random primers or random primers and oligo dT primers. All reactions were performed with SYBR Green Master Mix (Applied Biosystems) and 25 ng of both the forward and reverse primer using the manufacturer's recommended thermocycling conditions. All reactions were subjected to melt curve analysis and products from selected experiments were resolved by electrophoreses on 1.5% agarose gels. For each experiment, threshold levels were set during the exponential phase of the QPCR reaction using Sequence Detection Software version 1.2.2 (Applied Biosystems). The amount of each target gene relative to the housekeeping gene glyceraldehyde-3-phosphate dehydrogenase (GAPDH) for each sample was determined using the comparative threshold cycle (Ct) method (Applied Biosystems User Bulletin #2), with the cDNA sample serving as the calibrator for each experiment described in the figure legend. All oligonucleotide primers were synthesized by Integrated DNA Technologies.

GAPDH primers were as described (Vandesompele et al., Genome Biol 3, RESEARCH0034 (2002)) and all other primers are listed (Table 4).

Approximately equal efficiencies of the primers were confirmed using serial dilutions of prostate cancer cDNA or plasmid templates in order to use the comparative Ct method.

RNA ligase mediated rapid amplification of cDNA ends (RLM-RACE)

RNA ligase mediated rapid amplification of cDNA ends was performed using the GeneRacer RLM-RACE kit (Invitrogen), according to the manufacturer's instructions. Initially, samples were selected based on expression of ERG or ETV1 by QPCR. Five micrograms of total RNA was treated with calf intestinal phosphatase to remove 5' phosphates from truncated mRNA and non-mRNA and decapped with tobacco acid phyrophosphatase. The GeneRace RNA Oligo was ligated to full length transcripts and reverse transcribed using SuperScript III. To obtain 5' ends, first-strand cDNA was amplified with Platinum Taq High Fidelity (Invitrogen) using the GeneRacer 5' Primer and ETV1 exon 4-5_r for ETV1 or the GeneRacer 5' Primer and ERG exon 4a_r or ERG exon 4b_r for ERG. Primer sequences are given (Table S2). Products were resolved by electrophoresis on 1.5% agarose gels and bands were excised, purified and TOPO TA cloned into pCR 4-TOPO. Purified plasmid DNA from at least 4 colonies was sequenced bi-directionally using M13 Reverse and M13 Forward (-20) primers or T3 and T7 primers on an ABI Model 3730 automated sequencer by the University of Michigan DNA Sequencing Core. RLM-RACEd cDNA was not used for the other assays.

Reverse-transcription PCR for TMPRSS2:ERG fusion

After identifying TMPRSS2:ERG positive cases using QPCR as described above, the same cDNA samples were PCR amplified with Platinum Taq High Fidelity and TPRSS2:ERG primers. Products were resolved by electrophoresis, cloned into pCR 4-TOPO and sequenced as described above.

In vitro androgen responsiveness

RWPE, LNCaP, VCap DuCaP, PC3 and PC3 cells stably transfected with the human androgen receptor (PC3+AR) (3) were treated for 24 h with 1% ethanol control or 1 nM of the synthetic androgen R1881. Total RNA was isolated and subjected to reverse transcription and QPCR as described above with ERG exon 5-6_f and _r primers. The relative amount of ERG/GAPDH for each sample was calibrated to the RWPE control sample.

Fluorescence in situ hybridization (FISH)

Formalin- fixed paraffin-embedded (FFPE) tissue sections from normal peripheral lymphocytes and the metastatic prostate cancer samples MET-26 and MET-28 were used for interphase fluorescence *in situ* hybridization (FISH) analysis. In addition, interphase FISH was performed on a tissue microarray containing cores from FFPE sections of 13 clinically localized prostate cancer and 16 metastatic prostate cancer samples. A two-color, two-signal approach was employed to evaluate the fusion of TMPRSS2 and ETV1, with probes spanning most of the respective gene loci. The biotin-14-dCTP BAC clone RP11-124L22 was used for the ETV1 locus and the digoxin-dUTP lableled BAC clone RPP11-35CD was used for the TMPRSS2 locus. For analyzing gene rearrangements involving ERG, a split-signal probe strategy was used, with two probes spanning the ERG locus (biotin-14-dCTP labeled BAC clone RP11-476D17 and digoxin-dUTP labeled BAC clone RP11-95I21). All BAC clones were obtained from the Children's Hospital of Oakland Research Institute (CHORI). Prior to tissue analysis, the integrity and purity of all probes were verified by hybridization to metaphase spreads of normal peripheral lymphocytes. Tissue hybridization, washing and color detection were performed as described (Rubin et al., Cancer Res 64, 3814 (2004); Garraway et al., Nature 436, 117 (2005)).

B. Results

Cancer Outlier Profile Analysis

In recent years, gene expression profiling with DNA microarrays has become a common method to study the cancer transcriptome. Microarray studies have provided great insight into the molecular heterogeneity of cancer, often identifying novel molecular subtypes of disease that correspond to tumor histology, patient outcome, and treatment response (Valk et al., N Engl J Med 350, 1617 (2004)). However, in general, transcriptome analysis has not led to the discovery of novel causal cancer genes. It was hypothesized that rearrangements and highlevel copy number changes that result in marked over-expression of an oncogene should be evident in transcriptome data, but not necessarily by traditional analytical approaches.

In the majority of cancer types, heterogeneous patterns of oncogene activation have been observed, thus traditional analytical methods that search for common activation of genes across a class of cancer samples (*e.g.*, t-test or signal-to-noise ratio) will fail to find such oncogene expression profiles. Instead, a method that searches for marked over-

expression in a subset of cases is needed. Experiments conducted during the course of development of the present invention resulted in the development of Cancer Outlier Profile Analysis (COPA). COPA seeks to accentuate and identify outlier profiles by applying a simple numerical transformation based on the median and median absolute deviation of a gene expression profile (Ross et al., Blood 102, 2951 (2003)). This approach is illustrated in Figure 5A. COPA was applied to the Oncomine database (Bittner et al., Nature 406, 536 (2000)), which comprised a compendium of 132 gene expression datasets representing 10,486 microarray experiments. COPA correctly identified several outlier profiles for genes in specific cancer types in which a recurrent rearrangement or high- level amplification is known to occur. The analysis was focused on outlier profiles of known causal cancer genes, as defined by the Cancer Gene Census (Vasselli et al., Proc Natl Acad Sci U S A 100, 6958 (2003)), that ranked in the top 10 outlier profiles in an Oncomine dataset (Table 1 and Table 3). For example, in the Valk et al. acute myeloid leukemia (AML) dataset, RUNX1T1 (ETO) had the strongest outlier profile at the 95th percentile, consistent with this gene's known translocation and oncogenic activity in a subset of AML (Davis et al., Proc Natl Acad Sci U S A 100, 6051 (2003)) (Table 1). The outlier profile precisely associated with cases that had a documented t(8;21) translocation which fuses RUNX1 (AML1) and RUNX1T1 (ETO) (Fig. 5B). Similarly, in the Ross et al. acute lymphoblastic leukemia (ALL) dataset, PBX1 showed the strongest outlier profile at the 90th percentile, consistent with the E2A-PBX1 translocation known to occur in a subset of ALL (Segal et al., J Clin Oncol 21, 1775 (2003)) (Table 1). Again, the outlier expression profile perfectly correlated with the characterized t(1;19) E2A-PBX1 translocation in this panel of ALLs (Fig. S1C).

Identification of outlier profiles for ETS family members ERG and ETV1 in prostate cancer

Novel COPA predictions were next examined. In several independent datasets, COPA identified strong outlier profiles in prostate cancer for ERG and ETV1, two ETS family transcription factors that are known to be involved in oncogenic translocations in Ewing's sarcoma and myeloid leukemias (Lapointe et al., Proc Natl Acad Sci U S A 101, 811 (2004); Tian et al., N Engl J Med 349, 2483 (2003)). In the Dhanasekaran et al. (Keats et al., Blood 105, 4060 (2005)), Welsh et al. (Dhanasekaran et al., Faseb J 19, 243 (2005)) and Lapointe et al. (Wang et al., Lancet 365, 671 (2005)) prostate cancer gene expression datasets, ERG had the highest scoring outlier profile at the 75th percentile (Table 1), while in the Lapointe et al. and Tomlins et al. (Welsh et al., Cancer Res 61, 5974 (2001)) datasets,

ETV1 had the highest scoring outlier profile at the 90th percentile (Table 1). In total, COPA ranked ERG or ETV1 within the top ten outlier genes nine times in seven independent prostate cancer profiling studies. Both ERG and ETV1 are involved in oncogenic translocations in Ewing's sarcoma. Fusion of the 5' activation domain of the EWS gene to the highly conserved 3' DNA binding domain of an ETS family member, such as ERG (t(21;22)(q22;q12)) or ETV1 (t(7;22)(p21;q12)), is characteristic of Ewing's sarcoma (Lapoint et al., supra; Zhan et al., Blood 99, 1745 (2002); Fonseca et al., Cancer Res 64, 1546 (2004)). Because translocations involving ETS family members are functionally redundant in oncogenic transformation, only one type of translocation is typically observed in each case of Ewing's sarcoma.

It was contemplated that if ERG and ETV1 are similarly involved in the development of prostate cancer, their outlier profiles should be mutually exclusive, that is, each case should over-express only one of the two genes. Mutations in functionally redundant genes, or genes in the same oncogenic pathway, are unlikely to be co-selected for in neoplastic progression. The joint expression profiles of ERG and ETV1 was examined across several prostate cancer datasets and it was found that they showed mutually exclusive outlier profiles. ERG and ETV1 expression profiles from two large-scale transcriptome studies (Wang et al., supra; Cheok et al., Nat Genet 34, 85 (2003)), which profiled grossly dissected prostate tissues using different microarray platforms, were identified (Fig. 1A, left and middle panels). The study by Lapointe et al. profiled benign prostate tissue, clinically localized prostate cancer, and metastatic prostate cancer, with ERG and ETV1 outlier expression restricted to prostate cancer and metastatic prostate cancer, while the study by Glinsky et al. profiled clinically localized prostate cancer samples only. In both studies, prostate cancers exclusively expressed ERG or ETV1 (Fig. 1A, right panel). Similar results were found in a profiling study of 99 prostate tissue samples obtained by laser capture microdissection (LCM) (Welsh et al., supra). In addition to exclusive outlier expression of either ERG or ETV1 (Fig. 1B, right panel), results from the LCM study demonstrated that ETV1 and ERG are only over-expressed in epithelial cells from prostate cancer or metastatic prostate cancer, but not in the putative precursor lesion prostatic intraepithelial neoplasia (PIN) or adjacent benign epithelia. To directly determine whether the observed exclusive outlier pattern is consistent with other translocations where an activating gene can fuse with multiple partners, the Zhan et al. multiple myeloma dataset (Dhanasekaran et al., Nature 412, 822 (2001)) was examined. Recurrent fusions of the immunoglobulin heavy

chain promoter to CCND1 or FGFR3, t(11,14) or t(4,14) respectively, characterize specific subsets of multiple myeloma (Wigle et al., Cancer Res 62, 3005 (2002)). These translocations were reflected in the outlier profile analysis (Fig. 1C), as CCND1 was the highest scoring outlier at the 75th percentile and FGFR3 was the third highest scoring outlier at the 95th percentile (Table 1). Except for two cases, myeloma samples showed exclusive over-expression of CCND1 or FGFR3 (Fig. 1C, right panel). Taken together, the outlier profiles of ERG and ETV1 across multiple prostate cancer data sets are consistent with other causal mutations in various human malignancies. The exclusive over-expression of ERG or ETV1 in individual prostate cancer samples is consistent with other neoplasms in which an activating gene can fuse with biologically redundant partner genes, such as in multiple myeloma.

Discovery of a recurrent gene fusion of TMPRSS2 to ERG or ETV1 in prostate cancer.

The mechanism of ERG and ETV1 over-expression in individual prostate cancer samples was next determined. Prostate cancer cell lines and clinical specimens that over-expressed ERG or ETV1 were identified by performing quantitative PCR (QPCR) (Fig. 2A). The LNCaP prostate cancer cell line and two specimens obtained from a patient who died of hormone refractory metastatic prostate cancer (MET-26RP, residual primary carcinoma in the prostate and MET-26LN, a lymph node metastasis) markedly over-expressed ETV1 by QPCR (Fig. 2A). Five independent metastatic foci from different anatomical locations as well as the residual carcinoma in the prostate from this patient also over-expressed ETV1 by DNA microarray analysis (Welsh et al., supra), suggesting that ETV1 activation occurred in the primary tumor before widespread metastasis. A lymph node metastasis was also identified from a second patient who died of hormone refractory metastatic prostate cancer (MET-28LN) and two prostate cancer cell lines, VCaP and DuCaP, that over-expressed ERG (Fig. 2A). These cell lines were independently isolated from a vertebral metastasis (VCaP) and a dural metastasis (DuCaP) from a third patient with hormone-refractory prostate cancer (Golub et al., Science 286, 531 (1999); Rosenwald et al., Cancer Cell 3, 185 (2003)). The common over-expression of ERG in these two cell lines again suggests that ERG activation occurred before widespread metastasis. Taken together, these results suggest that specific genetic events may activate ERG or ETV1 in individual samples during prostate tumorigenesis.

In an effort to characterize these genetic events, samples with high ERG or ETV1 expression were tested for chromosomal amplifications at their respective loci (7p21.2 and 21q22.3). By QPCR on genomic DNA, amplification of ERG or ETV1 in samples with respective transcript over-expression (Sotiriou et al., Proc Natl Acad Sci U S A 100, 10393 (2003)) was not found. Next, the occurrence of DNA rearrangements was assayed. Because the primers used for the QPCR described above were located 5' to the known breakpoints for ERG and ETV1 in Ewing's sarcoma, it was unlikely that the same translocations occur in prostate cancer. Accordingly, the expression level of ETV1 exons was measured by exonwalking QPCR in the samples identified above that displayed ETV1 over-expression. Five primer pairs spanning ETV1 exons 2 through 7 were used and LNCaP cells showed essentially uniform over-expression of all measured ETV1 exons, and both MET26 specimens showed > 90% reduction in the expression of ETV1 exons 2 and 3 compared to exons 4-7 (Fig. 2B). Potential explanations for this result include alternative splicing, a novel cancer-specific isoform or an unreported rearrangement.

In order to characterize the full length ETV1 transcript, 5' RNA ligase-mediated rapid amplification of cDNA ends (RLM-RACE) was performed on LNCaP cells and MET26-LN. In addition, RLM-RACE was performed to obtain the full length transcript of ERG in MET28-LN. For PCR amplification of ETV1 from the RLM-RACE cDNA, a forward primer complementary to the RNA-oligonucleotide ligated to the 5' end of complete transcripts and a reverse primer in exon 4, the 5'- most exon that was over-expressed in both LNCaP cells and MET26-LN was used. Utilizing a similar strategy as described above, it was determined that exon 4 of ERG was over-expressed in MET28-LN. A reverse primer in this exon was utilized for PCR amplification of RLM-RACE cDNA. Sequencing of the cloned products revealed fusions of the prostate specific gene TMPRSS2 (28) (21q22.2) with ETV1 in MET26-LN and with ERG in MET28-LN (Fig. 2C). In MET26-LN, two RLM-RACE PCR products were identified.

The first product, TMPRSS2:ETV1a, resulted in a fusion of the complete exon 1 of TMPRSS2 with the beginning of exon 4 of ETV1 (Fig. 2C). The second product, TMPRSS2:ETV1b, resulted in a fusion of exons 1 and 2 of TMPRSS2 with the beginning of exon 4 of ETV1 (Fig. 6). Both products are consistent with the exon-walking QPCR described above, where MET26-LN showed loss of over-expression in exons 2 and 3. In

MET28-LN, a single RLM-RACE PCR product was identified and sequencing revealed a fusion of the complete exon 1 of TMPRSS2 with the beginning of exon 4 of ERG (TMPRSS2:ERGa) (Fig. 2C).

Validation of TMPRSS2:ERG and TMPRSS2:ETV1 gene fusions in prostate cancer

Based on these results, QPCR primer pairs were designed with forward primers in TMPRSS2 and reverse primers in exon 4 of ERG and ETV1. SYBR Green QPCR was performed using both primer pairs across a panel of samples from 42 cases of clinically localized prostate cancer and metastatic prostate cancer, with representative results depicted (Fig. 2, D and E). These results demonstrate that only samples with high levels of ETV1 or ERG express the respective fusion product with TMPRSS2. Although QPCR resulted in measurable product after 35 cycles in some negative samples, melt curve analysis revealed distinct products in positive and negative samples, and gel electrophoresis of products after the 40 cycle QPCR analysis revealed only primer dimmers in negative fusion samples (Fig. 2, D and E). The formation of primer dimers may in part be explained by the difficulty in designing primers entirely in exon 1 of TMPRSS2 due to the high GC content (80.3%). However, the specific expression of TMPRSS2:ERGa, TMPRSS2:ETV1a and TMPRSS2:ETV1b fusions was confirmed using Taqman QPCR, with the forward primer spanning the respective fusion, and in each case, products were only detected in the same cases as the SYBR Green QPCR (Sotiriou et al., supra). To further confirm the specificity of the primers used for SYBR Green QPCR and the amplicons, standard reverse-transcription PCR was performed with the same primers as the SYBR Green QPCR on a panel of samples that expressed TMPRSS2:ERGa. Similar sized products were obtained and sequencing of cloned products confirmed the presence of TMPRSS2:ERGa. Two cases, PCA16 and PCA17, which expressed high levels of ETV1 or ERG respectively, but showed no evidence of the translocation by QPCR (Fig. 2, D and E) were identified. RLM-RACE supported these results, as sequencing of the product produced with ETV1 primers in PCA16 revealed no evidence of a fusion transcript and no product could be obtained with ERG primers in PCA17. Similar results were obtained for LNCaP cells, with no evidence of a fusion by RLMRACE or QPCR, consistent with the exon walking QPCR described above.

Summary of evidence for TMPRSS2 fusion transcripts with ETS family members in prostate cancer samples

Results from three different assays for the TMPRSS2:ERG and TMPRSS2:ETV1 fusion transcripts including sequencing of RLM-RACE products, QPCR and sequencing of RT-PCR products are summarized in Table 2. In addition to QPCR for TMPRSS2 fusions being performed in all samples, the existence of these fusions was confirmed using several techniques on selected samples. For example, in PCA1 (prostate cancer sample 1), TMPRSS2:ERGa was identified using sequencing of RLMRACE products, QPCR and sequencing of RT-PCR products. By QPCR melt curve analysis and gel electrophoresis of QPCR products, PCA4 produced a larger amplicon than expected. Subsequent RLM-RACE analysis confirmed a fusion of the complete exon 1 of TMPRSS2 with the beginning of exon 2 of ERG (TMPRSS2:ERGb) (Fig. 6). Taqman QPCR with the forward primer spanning the TMPRSS2:ERGb junction confirmed the presence of TMPRSS2:ERGb only in PCA4 and Taqman QPCR with the forward primer spanning the TMPRSS2:ERGa junction did not produce a product in this specimen (27). Evidence for the TMPRSS2:ERG and TMPRSS2:ETV1 fusions were only found in cases that over-expressed ERG or ETV1 respectively, by QPCR or DNA microarray. These results are in agreement with the exclusive expression observed in the outlier analysis.

Fluorescence in situ hybridization (FISH) confirms TMPRSS2:ETV1 translocation and ERG rearrangement

After confirming the existence of the TMPRSS2:ETV1 and TMPRSS2:ERG fusion transcripts, evidence of these rearrangements at the chromosomal level was obtained using interphase fluorescence *in situ* hybridization (FISH) on formalin fixed paraffin embedded (FFPE) specimens. Two different probe strategies were employed: a twocolor, fusion-signal approach to detect TMPRSS2:ETV1 translocations and a two-color, split-signal approach to detect rearrangements of the ERG locus. These probe strategies were validated on the two cases initially used for RLM-RACE, MET26 and
MET28 (Fig. 3). Using probes for TMPRSS2 and ETV1, normal peripheral lymphocytes (NPLs) demonstrated a pair of red and a pair of green signals (Fig. 3A). MET26 showed fusion of one pair of signals, indicative of probe overlap (Fig. 3B, yellow arrowhead), consistent with the expression of the TMPRSS2:ETV1 transcript in this sample. In addition, consistent low- level amplification of the ETV1 locus was identified, as indicated by the two remaining signals for ETV1 (Fig. 3B, red arrowheads). Similarly, using probes spanning the 5' and 3' region of the ERG locus, a pair of yellow signals in NPLs was

observed (Fig. 3C). In MET28, one pair of probes split into separate green and red signals, indicative of a rearrangement at the ERG locus (Fig. 3D, green and red arrows). This result is consistent with the expression of the TMPRSS2:ERG transcript in this case. Based on these results, the individual FISH analyses described above were performed on serial tissue microarrays containing cores from 13 cases of localized prostate cancer and 16 cases of metastatic prostate cancer (Fig. 3E). As indicated by the matrix, 23 of 29 cases (79.3%) showed evidence of TMPRSS2:ETV1 fusion (7 cases) or ERG rearrangement (16 cases). In addition, 12 of 29 cases (41.4%) showed evidence of low level amplification at the ETV1 locus. Previous reports have identified the genomic location of ETV1, 7p, as one of the most commonly amplified regions in localized and metastatic prostate cancer (Slamon et al., Science 235, 177 (1987)). However it does not appear that 7p amplification drives ETV1 expression, as ETV1 amplification occurred in 6 cases with ERG rearrangements and our transcript data demonstrates that 0 of 19 samples with high ERG expression and the TMPRSS2:ERG fusion also have high ETV1 expression. Furthermore, when both ETV1 amplification and the TMPRSS2:ETV1 fusion were present by FISH, only the individual ETV1 signal was amplified and not the fused signal. Nevertheless, results from this FISH analysis demonstrate the presence of TMPRSS2:ETV1 and ERG rearrangements at the genomic level consistent with the transcript data described above.

TMPRSS2 is an androgen-regulated gene and fusion with ERG results in androgen regulation of ERG. TMPRSS2 was initially identified as a prostate-specific gene whose expression was increased by androgen in LNCaP cells and also contains androgen responsive elements (AREs) in its promoter (Huang et al., Lancet 361, 1590 (2003); Schwartz et al., Cancer Res 62, 4722 (2002)). Subsequent studies have confirmed high expression in normal and neoplastic prostate tissue and demonstrated that TMPRSS2 is androgen-regulated in androgen-sensitive prostate cell lines (Schwartz et al., Cancer Res 62, 4722 (2002); Ferrando et al., Cancer Cell 1, 75 (2002); Chen et al., Mol Biol Cell 14, 3208 (2003); LaTulippe et al., Cancer Res 62, 4499 (2002)). In addition, while androgen does not increase the expression of TMPRSS2 in the androgen insensitive prostate cancer cell line PC3, stable expression of the androgen receptor in PC3 cells resulted in TMPRSS2 becoming androgen responsive (Schwartz et al., supra; Ferrando et al., supra; Chen et al., supra; LaTulippe et al., supra). In contrast, microarray studies of LNCaP prostate cell lines treated with androgen have not identified ERG or

ETV1 as being androgen-responsive (Jain et al., Cancer Res 64, 3907 (2004)) and examination of their promoter sequences did not reveal consensus AREs (Sotiriou et al., supra). It was contemplated that the TMPRSS2:ERGa fusion in DuCaP and VCaP cell lines, which was confirmed by three independent assays in each cell line (Table 2), would result in the androgen regulation of ERG. Using QPCR to assay for ERG expression, it was confirmed that even though ERG was highly expressed in both VCaP and DuCaP cells, treatment with the synthetic androgen R1881 increased the expression of ERG 2.57 fold in DuCaP cells and 5.02 fold in VCaP cells compared to untreated controls (Fig. 4). Expression of ERG was minimal and essentially unchanged after R1881 treatment in RWPE (1.37 fold), LnCaP (0.86 fold), PC3 (1.28 fold) and PC3 cells expressing the androgen receptor (0.73 fold) compared to untreated controls.

Microarray analysis of the same samples confirmed that ERG was only up-regulated in response to androgen in DuCaP and VCaP cells (Sotiriou et al., supra). The present invention is not limited to a particular mechanism. Indeed, an understanding of the mechanism is not necessary to practice the present invention. Nonetheless, it is contemplated that these results suggest a possible mechanism for the aberrant expression of ERG or ETV1 in prostate cancer when respective fusions with TMPRSS2 are present.

Table 1. Cancer Outlier Profile Analysis (COPA). Genes known to undergo causal mutations in cancer that had strong outlier profiles. "X", signifies literature evidence for acquired pathogenomic translocation. "XX" signifies literature evidence for the specific translocation as well as the samples in the specific study that were characterized for that translocation. "Y" signifies consistent with known amplification. "**" signifies ERG and ETV1 outlier profiles in prostate cancer.

Table 1

Rank	%	Score	Study	Cancer	Gene	Evidence
1	95	20.056	Valk et al., N Engl J Med 350, 1617 (2004)	Leukemia	*RUNX1T1*	XX
1	95	15.4462	Vasselli et al., PNAS USA 100, 6958 (2003)	Renal	*PRO1073*	X

1	90	12.9581	Ross et al., Blood 102, 2951 (2003).	Leukemia	*PBX1*	XX
1	95	10.03795	Lapointe et al., PNAS USA 101, 811 (Jan 20, 2004)	Prostate	*ETV1*	**
1	90	9.1163		Prostate	*ETV1*	**
1	90	7.4557	Tian et al., N Engl J Med 349, 2483 (2003)	Myeloma	*WHSC1*	X
1	75	5.4071	Dhanasekaran et al., Nature 412, 822 (2001)	Prostate	*ERG*	**
1	75	4.3628	Welsh et al., Cancer Res 61, 5974 (2001)	Prostate	*ERG*	**
1	75	4.3425	Zhan et al., Blood 99, 1745 (2002)	Myeloma	*CCND1*	X
1	75	3.4414	Lapointe et al., supra	Prostate	*ERG*	**
1	75	3.3875	Dhanasekaran et al., Faseb J 19, 243 (2005)	Prostate	*ERG*	**
2	90	6.7029		Prostate	*ERG*	**
3	95	13.3478	Zhan et al., supra	Myeloma	*FGFR3*	X
4	75	2.5728	Huang et al., Lancet 361, 1590 (2003)	Breast	*ERBB2*	Y
6	90	6.6079	Sotiriou et al., PNAS USA 100, 10393 (2003)	Breast	*ERBB2*	Y
9	95	17.1698	Glinsky et al., J Clin Invest 113, 913 (2004)	Prostate	*ETV1*	**
9	90	6.60865	Nielsen et al.,	Sarcoma	*SSX1*	X

			Lancet 359, 1301 (2002)			
9	75	2.2218	Yu et al., J Clin Oncol 22, 2790 (2004)	Prostate	*ERG*	**

Table 2 shows a summary of TMPRSS2 fusion to ETS family member status in prostate cancer samples and cell lines. For all assays, positive results are indicated by "+" and negative results are indicated by "-". Blank cells indicate that the specific assay was not performed for that sample. Over-expression of ERG or ETV1 by quantitative PCR (QPCR) is indicated and samples marked with an asterisk indicate the sample was also assessed by cDNA microarray and over-expression was confirmed. In order to detect TMPRSS2:ERG or TMPRSS2:ETV1 gene fusions, selected samples were subjected to RLM-RACE for the over-expressed ETS family member and samples with the TMPRSS2 fusion after sequencing are indicated. All samples were assayed for TMPRSS2:ETV1 and TMPRSS2:ERG expression by QPCR. Selected cases were also amplified by standard reverse-transcription PCR (RT-PCR) using the same TMPRSS2 fusion primers as for QPCR and amplicons were sequenced. Samples with evidence for TMPRSS2:ETV1 or TMPRSS2:ERG fusion are indicated in the final column.

Table 2

			TMPRSS2:ETS family member gene fusion assays				**TMPRSS2 :ETS**
Case	**Sample**	**QPCR Expression**	**RLM-RACE sequencing**	**QPCR TMPRSS2: ETV1**	**QPCR TMPRSS2: ERG**	**RT-PCR sequencing**	**family member fusion**
1	MET26-LN	ETV1*	+	+	-		+
1	MET26-RP	ETV1*		+	-		+

2	MET28-B	ERG		-	+		+
2	MET28-PTLN	ERG		-	+		+
2	MET28-41	ERG		-	+		+
2	MET28-LN	ERG	+	-	+		+
3	MET16-44	ERG		-	+		+
3	MET16-47	ERG		-	+		+
4	MET3	ERG*		-	+		+
5	MET18-23	ERG*		-	+	+	+
6	PCA1	ERG*	+	-	+	+	+
7	PCA2	ERG*		-	+	+	+
8	PCA3	ERG*		-	+	+	+
9	PCA4	ERG*	+	-	+		+
10	PCA5	ERG*	+	-	+		+
11	PCA6	ERG*		-	+		+
12	PCA7	ERG*	+	-	+		+
13	PCA8	ERG*		-	+		+
14	PCA9	ERG*		-	+		+
15	PCA10	ERG*		-	+		+
16	PCA11	ERG*		-	+		+
17	PCA12	ERG*		-	+		+
18	PCA13	ERG*		-	+		+
19	PCA14	ERG*		-	+		+
20	PCA15	ERG*		-	+		+
21	PCA16	ETV1*	-	-	-		-
22	PCA17	ERG*	-	-	-		-
23	MET30-LN	-		-	-		-
24	MET17-12	-		-	-		-
25	MET20-76	-		-	-		-
26	MET22-61	-		-	-		-

27	MET5-7	-		-	-		-
28	PCA18	-		-	-		-
29	PCA19	-		-	-		-
30	PCA20	-		-	-		-
31	PCA21	-		-	-		-
32	PCA22	-		-	-		-
33	PCA23	-		-	-		-
34	PCA24	-		-	-		-
35	PCA25	-		-	-		-
36	PCA26	-		-	-		-
37	PCA27	-		-	-		-
38	PCA28	-		-	-		-
39	PCA29	-		-	-		-
40	PCA30	-		-	-		-
41	PCA31	-		-	-		-
42	PCA32	-		-	-		-
Cell line	VCap	ERG	+	-	+		+
Cell line	DUCaP	ERG		-	+	+	+
Cell line	LnCaP	ETV1	-	-	-		-
Cell line	DU145	-		-	-		-
Cell line	PC3	-		-	-		-
Cell line	RWPE	-		-	-		-

Table 3. Cancer Outlier Profile Analysis (COPA). Genes that are known to undergo causal mutations in cancer that had an outlier profile in the top 10 of a study in Oncomine are shown. "X", signifies literature evidence for acquired pathognomonic translocation. "XX" signifies literature evidence for the specific translocation as well as that the samples in the specific study were characterized for that translocation. "Y" signifies consistent with known amplification. "**" signifies ERG and ETV1 outlier profiles in prostate cancer.

Table 3

Rank	%	Score	Study	Cancer	Reference	Gene	Evidence

1	90	21.9346	Bittner et al.	Melanoma	Nature 406, 536 (2000)	CDH1	
1	95	20.056	Valk et al.	Leukemia	Nature 406, 536 (2000)	RUNX1T1	XX
1	95	15.4462	Vasselli et al.	Renal	PNAS USA 100, 6958 (2003)	PRO1073	X (*12*)
1	95	14.2008	Segal et al.	Sarcoma	J Clin Oncol 21, 1775 (2003)	MYH11	
1	90	12.9581	Ross et al.	Leukemia	Blood 102, 2951 (2003)	PBX1	XX
1	95	10.03795	Lapointe et al.	Prostate	PNAS USA 101, 811 (2004)	ETV1	**
1	90	9.1163		Prostate		ETV1	**
1	90	7.4557	Tian et al.	Myeloma	N Engl J Med 349, 2483 (2003)	WHSC1	X (*16*)
1	75	5.4071	Dhanasekaran et al.	Prostate	Faseb J 19, 243 (2005)	ERG	**
1	75	5.2067	Wang et al.	Breast	Lancet 365, 671 (2005)	FOXO3A	
1	75	4.3628	Welsh et al.	Prostate	Cancer Res 61, 5974 (2001)	ERG	**
1	75	4.3425	Zhan et al.	Myeloma	Blood 99, 1745 (2002)	CCND1	X (*21*)
1	75	3.724	Cheok et al.	Leukemia	Nat Genet	PCSK7	

					34, 85 (May, 2003)		
1	75	3.4414	Lapointe et al.	Prostate	PNAS USA 101, 811 (2004)	ERG	**
1	75	3.3875	Dhanasekaran et al.	Prostate	Nature 412, 822 (2001)	ERG	**
1	75	2.5913	Wigle et al.	Lung	Cancer Res 62, 3005 (2002)	IGH@	
2	90	12.7953	Ross et al.	Leukemia	Blood 102, 2951 (2003)	HOXA9	
2	95	9.2916	Golub et al.	Leukemia	Science 286, 531 (1999)	TRA@	
2	95	9.2916	Golub et al.	Leukemia	Science 286, 531 (1999)	TRD@	
2	90	8.2292	Cheok et al.	Leukemia	Nat Genet 34, 85 (May, 2003)	SSX2	
2	90	6.7029		Prostate		ERG	**
3	95	13.3478	Zhan et al.	Myeloma	Blood 99, 1745 (2002)	FGFR3	X (*21*)
3	95	10.2267	Cheok et al.	Leukemia	Nat Genet 34, 85 (May, 2003)	ARHGAP26	
3	90	5.9174		Prostate		REL	
3	75	2.6162	Rosenwald et al.	Lymphoma	Cancer Cell 3, 185 (2003)	TCL1A	

3	75	2.036	Sotiriou et al.	Breast	PNAS USA 100, 10393 (2003)	RAD51L1	
4	75	8.4985	Bittner et al.	Melanoma	Nature 406, 536 (2000)	TP53	
4	90	5.4881	Golub et al.	Leukemia	Science 286, 531 (1999)	LCK	
4	75	2.5728	Huang et al.	Breast	Lancet 361, 1590 (2003)	ERBB2	Y(*29*)
4	75	2.0229	Schwartz et al.	Ovarian	Cancer Res 62, 4722 (2002)	IGL@	
6	90	17.3733	Ferrando et al.	Leukemia	Cancer Cell 1, 75 (2002)	ZBTB16	
6	95	9.1267	Chen et al.	Gastric	Mol Biol Cell 14, 3208 (2003)	FGFR2	
6	90	6.6079	Sotiriou et al.	Breast	PNAS USA 100, 10393 (2003)	ERBB2	Y(*29*)
6	75	5.7213	LaTulippe et al.	Prostate	Cancer Res 62, 4499 (2002)	NF1	
6	75	5.2752	Jain et al.	Endocrine	Cancer Res 64, 3907 (2004)	PHOX2B	
6	90	4.8383	Lapointe et al.	Prostate	PNAS USA 101, 811	LAF4	

6	90	4.1779	Alizadeh et al.	Lymphoma	(2004) Nature 403, 503 (2000)	IRTA1	
6	90	3.6325	Rosenwald et al.	Lymphoma	N Engl J Med 346, 1937 (2002)	IRTA1	
6	75	1.85865	Chen et al.	Liver	Mol Biol Cell 13, 1929 (2002)	HMGA1	
7	95	4.7561	Alon et al.	Colon	Proc Natl Acad Sci U S A 96, 6745 (1999)	NONO	
7	75	1.8133	Chen et al.	Liver	Mol Biol Cell 13, 1929 (2002)	GPC3	
8	90	4.7068	Lacayo et al.	Leukemia	Blood 104, 2646 (2004)	EVI1	
8	90	4.7068	Lacayo et al.	Leukemia	Blood 104, 2646 (2004)	MDS1	
9	95	17.1698	Glinsky et al.	Prostate	J Clin Invest 113, 913 (2004)	ETV1	**
9	90	15.3889	Ferrando et al.	Leukemia	Ferrando et al., Cancer Cell 1, 75 (2002)	MN1	
9	90	6.60865	Nielsen et al.	Sarcoma	Lancet 359, 1301 (2002)	SSX1	X (*42*)
9	90	4.4875	Lapointe et al.	Prostate	PNAS	CHEK2	

9	75	2.2218	Yu et al.	Prostate	USA 101, 811 (2004) J Clin Oncol 22, 2790 (2004)	ERG	**
10	95	10.6036	Segal et al.	Sarcoma	Segal et al., J Clin Oncol 21, 1775 (2003)	KIT	

Table 4. Oligonucleotide primers used in this study. For all primers, the gene, bases and exons (according to alignment of the reference sequences described in the text with the May 2004 assembly of the human genome using the UCSC Genome Browser) are listed. Forward primers are indicated with "f" and reverse primers with "r".

Table 4

Gene	Bases	Exon(s)	Primer	Sequence 5' to 3'	SEQ ID NO
ETV1	193-216	2	Exon 2-3_f	AACAGAGATCTGGCTCATGATTCA	1
ETV1	268-245	3	Exon 2-3_r	CTTCTGCAAGCCATGTTTCCTGTA	2
ETV1	248-271	3-4	Exon 3-4_f	AGGAAACATGGCTTGCAGAAGCTC	3
ETV1	305-280	4	Exon 3-4_r	TCTGGTACAAACTGCTCATCATTGTC	4
ETV1	269-294	4	Exon 4-5_f	CTCAGGTACCTGACAATGATGAGCAG	5
ETV1	374-351	5	Exon 4-5_r	CATGGACTGTGGGGTTCTTTCTTG	6
ETV1	404-429	5	Exon 5-6_f	AACAGCCCTTTAAATTCAGCTATGGA	7
ETV1	492-472	6	Exon 5-6_r	GGAGGGCCTCATTCCCACTTG	8
ETV1	624-645	6-7	Exon 6-7_f	CTACCCCATGGACCACAGATTT	9

ETV1	771-750	7	Exon 6-7_r	CTTAAAGCCTTGTGGTGGGAAG	10
ERG	574-597	5-6	Exon 5-6_f	CGCAGAGTTATCGTGCCAGCAGAT	11
ERG	659-636	6	Exon 5-6_r	CCATATTCTTTCACCGCCCACTCC	12
NA	NA	NA	Generacer 5'_f	CGACTGGAGCACGAGGACACTGA	13
ETV1	374-351	5	Exon 4-5_r	CATGGACTGTGGGGTTCTTTCTTG	14
ERG	284-263	4	Exon 4a_r	GGCGTTCCGTAGGCACACTCAA	15
ERG	396-377	4	Exon 4b_r	CCTGGCTGGGGGTTGAGACA	16
TMPRSS2	-4 - 17	1	TMPRSS2:ERG_f	TAGGCGCGAGCTAAGCAGGAG	17
ERG	276-252	4	TMPRSS2:ERG_r	GTAGGCACACTCAAACAACGACTGG	18
TMPRSS2	1-19	1	TMPRSS2:ETV1_f	CGCGAGCTAAGCAGGAGGC	19
ETV1	339-318	4-5	TMPRSS2:ETV1_r	CAGGCCATGAAAAGCCAAACTT	20

Example 2

ETV4 Gene Fusions

A. Materials and Methods

ETS family expression in profiling studies

To investigate the expression of ETS family members in prostate cancer, two prostate cancer profiling studies were utilized (Lapointe et al., Proc Natl Acad Sci U S A 2004;101:811-6 and Tomlins et al., Science 2005;310:644-8) present in the Oncomine database (Rhodes et al., Neoplasia 2004;6:1-6). Genes with an ETS domain were identified by the Interpro filter 'Ets' (Interpro ID: IPR000418). Heatmap representations were generated in Oncomine using the 'median-center per gene' option, and the color contrast was set to accentuate ERG and ETV1 differential expression.

Samples

Prostate cancer tissues (PCA1-5) were from the radical prostatectomy series at the University of Michigan, which is part of the University of Michigan Prostate Cancer Specialized Program of Research Excellence (S.P.O.R.E.) Tissue Core. All samples were collected with informed consent of the patients and prior institutional review board approval. Total RNA was isolated with Trizol (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. A commercially available pool of benign prostate tissue total RNA (CPP, Clontech, Mountain View, CA) was also used.

Quantitative PCR (QPCR)

QPCR was performed using SYBR Green dye on an Applied Biosystems 7300 Real Time PCR system (Applied Biosystems, Foster City, CA) as described (Tomlins et al., *supra*). The amount of each target gene relative to the housekeeping gene glyceraldehyde-3-phosphate dehydrogenase (GAPDH) for each sample was reported. The relative amount of the target gene was calibrated to the relative amount from the pool of benign prostate tissue (CPP). All oligonucleotide primers were synthesized by Integrated DNA Technologies (Coralville, IA). GAPDH primers were as described (Vandesompele et al., Genome Biol 2002; 3:RESEARCH0034). Primers for exons of ETV4 were as follows (listed 5' to 3'): ETV4_exon2-f: CCGGATGGAGCGGAGGATGA (SEQ ID NO:21), ETV4_exon2-r: CGGGCGATTTGCTGCTGAAG (SEQ ID NO:22), ETV4_exon3-f: GCCGCCCCTCGACTCTGAA (SEQ ID NO:23), ETV4_exon4-r: GAGCCACGTCTCCTGGAAGTGACT (SEQ ID NO:24), ETV4_exon11-f: CTGGCCGGTTCTTCTGGATGC (SEQ ID NO:25), ETV4_exon12-r: CGGGCCGGGGAATGGAGT (SEQ ID NO:26), ETV4_3'UTR-f: CCTGGAGGGTACCGGTTTGTCA (SEQ ID NO:27), ETV4_3'UTR-r: CCGCCTGCCTCTGGGAACAC (SEQ ID NO:28). Exons were numbered by alignment of the RefSeq for ETV4 (NM_001986.1) with the May 2004 freeze of the human genome using the UCSC Genome Browser. For QPCR confirmation of TMPRSS2:ETV4 fusion transcripts, TMPRSS2:ETV4a-f (AAATAAGTTTGTAAGAGGAGCCTCAGCATC (SEQ ID NO:29)) and TMPRSS2:ETV4b-f (ATCGTAAAGAGCTTTTCTCCCCGC (SEQ ID NO:30)), which detects both TMPRSS2:ETV4a and TMPRSS2;ETV4b transcripts, were used with ETV4_exon4-r.

RNA ligase mediated rapid amplification of cDNA ends (RLM-RACE)

RLM-RACE was performed using the GeneRacer RLM-RACE kit (Invitrogen), according to the manufacturer's instructions as described (Tomlins et al., *supra*). To obtain the 5' end of ETV4, first-strand cDNA from PCA5 was amplified using the GeneRacer 5' Primer and ETV4_exon4-r or ETV4_exon7-r (GAAAGGGCTGTAGGGGCGACTGT (SEQ ID NO:31)). Products were cloned and sequenced as described (Tomlins et al., *supra*). Equivalent 5' ends of the TMPRSS2:ETV4 transcripts were obtained from both primer pairs.

Fluorescence in situ hybridization (FISH)

Formalin-fixed paraffin-embedded (FFPE) tissue sections were used for interphase FISH. Deparaffinized tissue was treated with 0.2 M HCl for 10 min, 2x SSC for 10 min at 80°C and digested with Proteinase K (Invitrogen) for 10 min. The tissues and BAC probes were co-denatured for 5 min at 94°C and hybridized overnight at 37°C. Post-hybridization washing was with 2x SSC with 0.1% Tween-20 for 5 min and fluorescent detection was performed using anti-digoxigenin conjugated to fluorescein (Roche Applied Science, Indianapolis, IN) and streptavidin conjugated to Alexa Fluor 594 (Invitrogen). Slides were counterstained and mounted in ProLong Gold Antifade Reagent with DAPI (Invitrogen). Slides were examined using a Leica DMRA fluorescence microscope (Leica, Deerfield, IL) and imaged with a CCD camera using the CytoVision software system (Applied Imaging, Santa Clara, CA).

All BACs were obtained from the BACPAC Resource Center (Oakland, CA) and probe locations were verified by hybridization to metaphase spreads of normal peripheral lymphocytes. For detection of TMPRSS2:ETV4 fusion, RP11-35C4 (5' to TMPRSS2) was used with multiple BACs located 3' to ETV4 (distal to ETV4 to proximal: RP11-266I24, RP11-242D8, and RP11-100E5). For detection of ETV4 rearrangements, RP11-436J4 (5' to ETV4) was used with the multiple BACs 3' to ETV4. For each hybridization, areas of cancerous cells were identified by a pathologist and 100 cells were counted per sample. The reported cell count for TMPRSS2:ETV4 fusions used RP11-242D8 and similar results were obtained with all 3' ETV4 BACs. To exclude additional rearrangements in PCA5, FISH was performed with two probes 3' to ETV4 (RP11-266I24 and RP11-242D8), ERG split signal probes (RP11-95I21 and RP11-476D17) and TMPRSS2:ETV1 fusion probes (RP11-35C4 and RP11-124L22). BAC DNA was isolated using a QIAFilter Maxi Prep kit

(Qiagen, Valencia, CA) and probes were synthesized using digoxigenin- or biotin-nick translation mixes (Roche Applied Science).

B. Results

The initial COPA screen led to the characterization of TMPRSS2 fusions with ERG or ETV1 (Example 1). It was further contemplated that prostate cancers negative for these gene fusions harbor rearrangements involving other ETS family members. By interrogating the expression of all ETS family members monitored in prostate cancer profiling studies from the Oncomine database (Rhodes et al., supra), marked over-expression of the ETS family member ETV4 was identified in a single prostate cancer case from each of two studies—one profiling grossly dissected tissues (Lapointe et al., supra) (Fig. 7A) and the other profiling laser capture microdissected (LCM) tissues1 (Fig. 7B). As these cases did not over-express ERG or ETV1, and no benign prostate tissues showed over-expression, it was contemplated that fusion with TMPRSS2 was responsible for the over-expression of ETV4 in these cases. Although ELF3 was also over-expressed in a fraction of prostate cancer cases, in both studies normal prostate tissue samples also showed marked ELF3 over-expression, indicating that a gene fusion driving expression in both benign and cancerous tissue is unlikely. Thus, the ETV4 over-expressing case (designated here as PCA5) was further analyzed.

Total RNA was isolated from PCA5 and exon-walking quantitative PCR was used (QPCR) to confirm the over-expression of ETV4. QPCR demonstrated that exons 3' to exon 2 of ETV4 were markedly over-expressed in this case compared to pooled benign prostate tissue (CPP) (~900 fold) and prostate cancers that did not over-express ETV4 and were either TMPRSS2:ERG positive (PCA1-2) or negative (PCA3-4) (Fig. 8A). However, a dramatic decrease (>99%) in the expression of exon 2 of ETV4 relative to distal regions in PCA5 was observed, indicating a possible fusion with TMPRSS2, as observed previously in TMPRSS2:ERG and TMPRSS2:ETV1 positive cases (Tomlins et al., supra).

To identify the 5' end of the ETV4 transcript in PCA5, RNA-ligase mediated rapid amplification of cDNA ends (RLM-RACE) was performed using a reverse primer in exon 7. RLM-RACE revealed two transcripts, each containing 5' ends consisting of sequence located approximately 8 kb upstream of TMPRSS2 fused to sequence from ETV4 (Fig 8B). Specifically, the 5' end of TMPRSS2:ETV4a has 47 base pairs from this region upstream of TMPRSS2, while the 5' end of TMPRSS2:ETV4b has the same terminal 13 base pairs.

These 5' ends of both transcripts were fused to the same contiguous stretch consisting of the 9 base pairs of the intron immediately 5' to exon 3 of ETV4 and the reported reference sequence of exons 3 through the reverse primer in exon 7 of ETV4.

The existence of both transcripts in PCA5 and their absence in CPP and PCA1-4 was confirmed using QPCR. To further exclude the presence of fusion transcripts involving known exons from TMPRSS2, QPCR was performed using a forward primer in exon 1 of TMPRSS2 and the ETV4 exon 4 reverse primer, and as expected, no product was detected in CPP or PCA1-5.

Whether other prostate cancers with ETV4 dysregulation might contain TMPRSS2:ETV4 fusion transcripts structurally more similar to TMPRSS2:ERG and TMPRSS2:ETV1 transcripts (which involve known exons from TMPRSS2) is unknown. The TMPRSS2:ETV4 fusions reported here do not contain the well characterized AREs immediately upstream of TMPRSS2. However, evidence exists for androgen responsive enhancers located upstream of the TMPRSS2 sequences present in the TMPRSS2:ETV4 transcripts described here (Rabbitts, Nature 1994;372:143-9). Nevertheless, the marked over-expression of only ETV4 exons involved in the fusion transcript strongly suggests that the gene fusion is responsible for the dysregulation of ETV4. Together, the structure of the TMPRSS2:ETV4 fusion transcripts supports the conclusion that the regulatory elements upstream of TMPRSS2, rather than transcribed TMPRSS2 sequences, drive the dysregulation of ETS family members.

To confirm the fusion of the genomic loci surrounding TMPRSS2 (21q22) and ETV4 (17q21) as demonstrated by RLM-RACE and QPCR, interphase fluorescence *in situ* hybridization (FISH) was used. Using probes 5' to TMPRSS2 and 3' to ETV4, fusion of TMPRSS2 and ETV4 loci was observed in 65% of cancerous cells from PCA5 (Fig. 8D). As further confirmation of the rearrangement of ETV4, using probes 5' and 3' to ETV4, 64% of cancerous cells from PCA5 showed split signals. FISH was also performed on PCA5 using two probes 3' to ETV4, ERG split signal probes and TMPRSS2:ETV1 fusion probes to exclude additional rearrangements, with negative results obtained for each hybridization.

Taken together, the results highlight the use of carefully examining outlier profiles in tumor gene expression data, as most analytical methods discount profiles that do not show consistent deregulation (Eisen et al., Proc Natl Acad Sci U S A 1998;95:14863-8; Golub et al., Science 1999;286:531-7; Tusher et al., Proc Natl Acad Sci U S A

2001;98:5116-21) and would thus fail to identify ETV4 in prostate cancer, which appears rare (2 of 98 cases). Combined with the identification of TMPRSS2:ERG and TMPRSS2:ETV1 fusions, the results presented here show that dysregulation of ETS family members mediated by subversion of AREs or enhancers upstream of TMPRSS2 is a hallmark of prostate tumorigenesis.

Example 3

Detection of Gene Fusion RNA

This example describes target capture, amplification and qualitative detection of RNA (IVT) containing the sequences of the four gene fusions in four separate qualitative assays: TMPRSS2:ETV1a, TMPRSS2:ETV1b, TMPRSS2:ERGa and TMPRSS2:ERGb with APTIMA formulation reagents and HPA detection each spiked with the appropriate target specific oligonucleotides, primers and probes. Table 5 shows sequences of oligonucleotides used in the assay.

Table 5

Gene Fusion	Sequence (5' to	SEQ ID NO
TMPRSS2 exon1/Target Capture	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTCUCGAUUCGUCCUCCG	59
TMPRSS2 exon1/Target Capture	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTAUCCGCGCUCGAUUCGUC	60
TMPRSS2 exon1/Non-T7	GAGGGCGAGGGGCGGGGAGCGCC	61
TMPRSS2 exon2/Non-T7	CCTATCATTACTCGATGCTGTTGATAACAGC	62
ETV1a/b exon4/T7	AATTTAATACGACTCACTATAGGGAGAAACTTTCAGCCTGATA	63
ERGb exon2/T7	AATTTAATACGACTCACTATAGGGAGACTCTGTGAGTCATTTGTCTTGCTT	64
ERGa exon4/T7	AATTTAATACGACTCACTATAGGGAGAGCACACTCAAACAACGACTG	65
TMPRSS2exon1:ETV1a Junction/AE	GCGCGGCAG-CUCAGGUACCUGAC	66
TMPRSS2exon2:ETV1b Junction/AE	GCUUUGAACUCA-CUCAGGUACCUGAC	67
TMPRSS2exon1:ERGa Junction/AE	GAGCGCGGCAG-GAAGCCUUAUCAGUUG	68
TMPRSS2exon1:ERGb Junction/AE	GAGCGCGGCAG-GUUAUUCCAGGAUCUUU	69

A. Materials and Methods

RNA Target Capture

Lysis buffer contained 15 mM sodium phosphate monobasic monohydrate, 15 mM sodium phosphate dibasic anhydrous, 1.0 mM EDTA disodium dihydrate, 1.0 mM EGTA free acid, and 110 mM lithium lauryl sulfate, pH 6.7.

Target capture reagent contained 250 mM HEPES, 310 mM lithium hydroxide, 1.88 M lithium chloride, 100 mM EDTA free acid, at pH 6.4, and 250 µg/ml 1 micron magnetic particles SERA-MAG MG-CM Carboxylate Modified (Seradyn, Inc., Indianapolis, Indiana) having $dT)_{14}$ oligomers covalently bound thereto.

Wash solution contained 10 mM HEPES, 6.5 mM sodium hydroxide, 1 mM EDTA, 0.3% (v/v) ethanol, 0.02% (w/v) methyl paraben, 0.01% (w/v) propyl paraben, 150 mM sodium chloride, 0.1% (w/v) lauryl sulfate, sodium (SDS), at pH 7.5.

RNA Amplification & Detection

Amplification reagent was a lyophilized form of a 3.6 mL solution containing 26.7 mM rATP, 5.0 mM rCTP, 33.3 mM rGTP and 5.0 mM rUTP, 125 mM HEPES, 8% (w/v) trehalose dihydrate, 1.33 mM dATP, 1.33 mM dCTP, 1.33 mM dGTP and 1.33 mM dTTP, at pH 7.5. The Amplification reagent was reconstituted in 9.7 mL of the amplification reagent reconstitution solution (see below). Before use, 15 pmol each of primer oligomers was added.

Amplification reagent reconstitution solution contained 0.4% (v/v) ethanol, 0.10% (w/v) methyl paraben, 0.02% (w/v) propyl paraben, 33 mM KCl, 30.6 mM $MgCl_2$, 0.003% phenol red.

Enzyme reagent was a lyophilized form of a 1.45 mL solution containing 20 mM HEPES, 125 mM N-acetyl-L-cysteine, 0.1 mM EDTA disodium dihydrate, 0.2% (v/v) TRITON7 X-100 detergent, 0.2 M trehalose dihydrate, 0.90 RTU/mL Moloney murine leukemia virus (MMLV) reverse transcriptase, and 0.20 U/mL T7 RNA polymerase, at pH 7.0. One unit (RTU) of activity is defined as the synthesis and release of 5.75 fmol cDNA in 15 minutes at 37°C for MMLV reverse transcriptase, and for T7 RNA polymerase, one unit (U) of activity is defined as the production of 5.0 fmol RNA transcript in 20 minutes at 37°C. Enzyme reagent was reconstituted in 3.6 mL of the enzyme reagent reconstitution solution (see below).

Enzyme reagent reconstitution solution contained 50 mM HEPES, 1 mM EDTA, 10% (v/v) TRITON7 X-100, 120 mM potassium chloride, 20% (v/v) glycerol anhydrous, at pH 7.0.

Hybridization reagent contained 100 mM succinic acid free acid, 2% (w/v) lithium lauryl sulfate, 100 mM lithium hydroxide, 15 mM aldrithiol-2, 1.2 M lithium chloride, 20 mM EDTA free acid, 3.0% (v/v) ethanol, at pH 4.7.

Selection reagent contained 600 mM boric acid, 182.5 mM sodium hydroxide, 1% (v/v) TRITON7 X-100, at pH 8.5.

The detection reagents comprised detect reagent I, which contained 1 mM nitric acid and 32 mM hydrogen peroxide, and detect reagent II, which contained 1.5 M sodium hydroxide.

B. Assay Protocol

Target Capture

1. Prepare samples by making dilutions of IVT stock solution into STM at indicated copy levels for 400 µL sample per reaction tube.
2. Using the repeat pipettor, add 100 µL of the TCR with the TCO to the appropriate reaction tube.
3. Using the micropipettor, add 400 µL of each sample to the properly labeled.
4. Cover the tubes with the sealing card(s) and shake the rack gently by hand. Do not vortex. Incubate the rack at 62°±1°C in a water bath for 30±5 minutes.
5. Remove the rack from the water bath and blot bottoms of tubes dry on absorbent material.
6. Ensure the sealing cards are firmly seated. If necessary, replace with new sealing cards and seal tightly.
7. Without removing sealing cards, incubate the rack at room temperature for 30±5 minutes.
8. Place the rack on the TCS magnetic base for 5 to 10 minutes.
9. Prime the dispense station pump lines by pumping APTIMA Wash Solution through the dispense manifold. Pump enough liquid through the system so that there are no air bubbles in the line and all 10 nozzles are delivering a steady stream of liquid.
10. Turn on the vacuum pump and disconnect the aspiration manifold at the first connector between the aspiration manifold and the trap bottle. Ensure that the vacuum gauge reads greater than 25 in. Hg. It may take 15 seconds to achieve this reading. Reconnect the manifold, and ensure the vacuum gauge is between 7 and 12 in. Hg. Leave the vacuum pump on until all target capture steps are completed.

11. Firmly attach the aspiration manifold to the first set of tips. Aspirate all liquid by lowering the tips into the first TTU until the tips come into brief contact with the bottoms of the tubes. Do not hold the tips in contact with the bottoms of the tubes.
12. After the aspiration is complete, eject the tips into their original tip cassette. Repeat the aspiration steps for the remaining TTUs, using a dedicated tip for each specimen.
13. Place the dispense manifold over each TTU and, using the dispense station pump, deliver 1.0 mL of APTIMA Wash Solution into each tube of the TTU.
14. Cover tubes with a sealing card and remove the rack from the TCS. Vortex once on the multi-tube vortex mixer.
15. Place rack on the TCS magnetic base for 5 to 10 minutes.
16. Aspirate all liquid as in steps 13 and 14.
17. After the final aspiration, remove the rack from the TCS base and visually inspect the tubes to ensure that all liquid has been aspirated. If any liquid is visible, place the rack back onto the TCS base for 2 minutes, and repeat the aspiration for that TTU using the same tips used previously for each specimen.

Primer Annealing and Amplification

1. Using the repeat pipettor, add 75 µL of the reconstituted Amplification Reagent containing the analyte specific primers to each reaction tube. All reaction mixtures in the rack should now be red in color.
2. Using the repeat pipettor, add 200 µL of Oil Reagent.
3. Cover the tubes with a sealing card and vortex on the multi-tube vortex mixer.
4. Incubate the rack in a water bath at 62°±1°C for 10±5 minutes.
5. Transfer the rack into a water bath at 42°±1°C for 5±2 minutes.
6. With the rack in the water bath, carefully remove the sealing card and, using the repeat pipettor, add 25 µL of the reconstituted Enzyme Reagent to each of the reaction mixtures. All reactions should now be orange in color.
7. Immediately cover the tubes with a fresh sealing card, remove from the water bath, and mix the reactions by gently shaking the rack by hand.
8. Incubate the rack at 42°±1°C for 60±15 minutes.

Hybridization

1. Remove the rack from the pre-amplification water bath and transfer to the post-amplification area. Add 100 µL of the reconstituted Probe Reagent with analyte specific probe, using the repeat pipettor. All reaction mixtures should now be yellow in color.
2. Cover tubes with a sealing card and vortex for 10 seconds on the multi-tube vortex mixer.
2. Incubate the rack in a 62°±1°C water bath for 20±5 minutes.
3. Remove the rack from the water bath and incubate at room temperature for 5±1 minutes

Selection

1. Using the repeat pipettor, add 250 µL of Selection Reagent to each tube. All reactions should now be red in color.
2. Cover tubes with a sealing card, vortex for 10 seconds or until the color is uniform, and incubate the rack in a water bath at 62°±1°C for 10±1 minutes.
3. Remove the rack from the water bath. Incubate the rack at room temperature for 15±3 minutes.

Reading the TTUs

1. Ensure there are sufficient volumes of Auto Detection Regents I and II to complete the tests.
2. Prepare the LEADER Luminometer by placing one empty TTU in cassette position number 1 and perform the WASH protocol.
3. Load the TTUs into the luminometer and run the HC+ Rev B protocol.

C. Results

The results are shown in Tables 6-9 for 4 assays with each of the TMPRSS2:ERG and TMPRSS2:ETV1 gene fusion IVTs spiked into TCR.

Table 6

TMPRSS2:ETV1a (copies IVT/reaction)	RLU
0	4,945
0	4,599
10	2,185,959
10	2,268,090
10	2,284,908
100	2,270,369
100	2,302,023
100	2,272,735
1,000	2,279,627
1,000	2,285,742

Table 7

TMPRSS2:ETV1b (copies IVT/reaction)	RLU
0	7,743
0	6,622
0	7,370
0	6,181
0	7,409
10	7,712
10	7,178
10	7,302
10	8,430
10	8,331
100	774,792
100	285,712
100	3,361,878
100	1,349,368
100	2,757,334
1,000	3,647,502
1,000	3,790,087
1,000	3,813,812
1,000	3,753,743
1,000	3,667,242

Table 8

TMPRSS2:ERGa (copies IVT/reaction)	RLU
0	7,938
0	7,505
10	2,043,379
10	387,408
10	978,457
100	2,332,764
100	2,445,544
100	2,530,239

Table 9

TMPRSS2:ERGb (copies IVT/reaction)	RLU
0	5,978
0	6,284
10	2,700,069
10	2,768,541
100	2,883,091
100	2,779,233
1,000	2,857,247
1,000	2,957,914

Example 4

FISH Assay for Gene Fusions

This Example describes the use of fluorescence *in situ* hybridization (FISH), to demonstrate that 23 of 29 prostate cancer samples harbor rearrangements in ERG or ETV1. Cell line experiments suggest that the androgen-responsive promoter elements of TMPRSS2 mediate the overexpression of ETS family members in prostate cancer. These results have implications in the development of carcinomas and the molecular diagnosis and treatment of prostate cancer.

Below is a list of the specific BAC probes used in FISH assays.

Clinical FISH assay for testing aberrations in ETS family members by FISH

- Testing ETV1-TMPRSS2 fusion with one probe spanning the ETV1 and one spanning the TMPRSS2 locus

  BAC for ETV1: RP11-692L4

  BAC for TMPRSS2: RP11-121A5, (RP11-120C17, PR11-814F13, RR11-535H11)

- Testing ERG translocation with set of probes for c-ERG:t-ERG break apart:
  BAC for c-ERG: RP11-24A11
  BACs for t-ERG: RP11-372O17, RP11-137J13

- Testing ETV1 deletion/amplification with set of probes, one spanning the ETV1 locus and one reference probe on chromosome 7:
  BAC for ETV1: RP11-692L4
  BAC for reference robe on chromosome 7: A commercial probe on centromere of chr.

- Testing ERG deletion/amplification with set of probes, one spanning the ERG locus and one reference probe on chromosome 21:
  BAC for ERG: RP11-476D17
  BACs for reference probe on chromosome 21: *

- Testing TMPRSS2 deletion/amplification with set of probes, one spanning the TMPRSS2 locus and one reference probe on chromosome 21:
  BACs for TMPRSS2: RP11-121A5, (RP11-120C17, PR11-814F13, RR11-535H11)
  BACs for reference probe on chromosome 21: *

**BACs for reference probe on chromosome 21: PR11-32L6, RP11-752M23, RP11-1107H21, RP11-639A7, (RP11-1077M21)*

Example 5

***TMPRSS2:ERG* Fusion Associated Deletions**

This example describes the presence of common deletions located between *ERG* and *TMPRSS2* on chromosome 21q22.2-3 associated with the *TMPRSS2:ERG* fusion. Associations between disease progression and clinical outcome were examined using a wide range of human PCA samples, 6 cell lines, and 13 xenografts.

A. Materials and Methods

Clinical Samples

Prostate samples used for this study were collected under an IRB approved protocol. All clinically localized PCA samples were characterized by one pathologist and assigned a Gleason score to eliminate inter-observer differences in pathology reporting. Clinically localized PCA samples were collected as part of an on-going research protocol at the University of Ulm. The hormone refractory samples were taken from the Rapid Autopsy Program of the University of Michigan.

The FISH experiments were conducted on two PCA outcome arrays, which were composed of 897 tissue cores (histospots) from 214 patients. A summary of the patient demographics is presented in Table 10. All patients had undergone radical prostatectomy with pelvic lymphadenectomy at the University of Ulm (Ulm, Germany) between 1989 and 2001. Pre-operative PSA ranged between 1 and 314 ng/ml (mean 36 ng/ml). Mean and maximum follow-up was 3.4 and 8.4 yrs, respectively.

Cell Lines and Xenografts

Androgen independent (PC-3, DU-145, HPV10, and 22Rvl) and androgen sensitive (LNCaP) PCA cell lines were purchased from the American Type Culture Collection (Manassas, VA) and maintained in their defined medium. HPV10 was derived from cells from a high-grade PCA (Gleason score 4+4=8), which were transformed by transfection with HPV18 DNA(18). 22Rv1 is a human PCA epithelial cell line derived from a xenograft that was serially propagated in mice after castration-induced regression and relapse of the parental, androgen-dependent CWR22 xenograft. The VCAP cell line was from a vertebral metastatic lesion as part of the Rapid Autopsy program at the University of Michigan.

LuCaP 23.1, 35, 73, 77, 81, 86.2, 92.1, and 105 were derived from patients with androgen independent hormone-refractory disease PCA. LuCaP 49 and 115 are from patients with androgen dependent PCA. LuCaP 58 is derived from an untreated patient with clinically advanced metastatic disease and LuCaP 96 was established from a prostate derived tumor growing in a patient with hormone refractory PCA. LuCaP 49 (established from an omental mass) and LuCaP 93 are hormone-insensitive (androgen receptor [AR]-negative) small cell PCAs. These two xenografts demonstrate a neuroendocrine phenotype.

LuCaP 23.1 is maintained in SCID mice, and other xenografts are maintained by implanting tumors in male BALB/c nu/nu mice.

Determining TMPRSS2:ERG Fusion Status using Interphase FISH

The FISH analysis for the translocation of *TMPRSS2:ERG* is described above and previously (Tomlins, *et al.*, *Science 310:*644-8 (2005)). This break apart assay is presented in Figures 11 and 14. For analyzing the *ERG* rearrangement on chromosome 21q22.2, a break apart probe system was applied, consisting of the Biotin-14-dCTP labeled BAC clone RP11-24A11 (eventually conjugated to produce a red signal) and the Digoxigenin-dUTP labeled BAC clone RP11-137J13 (eventually conjugated to produce a green signal), spanning the neighboring centromeric and telomeric region of the *ERG* locus, respectively. All BAC clones were obtained from the BACPAC Resource Center, Children's Hospital Oakland Research Institute (CHORI), Oakland, CA.

Using this break apart probe system, a nucleus without *ERG* rearrangement exhibits two pairs of juxtaposed red and green signals. Juxtaposed red-green signals form a yellow fusion signal. A nucleus with an *ERG* rearrangement shows break apart of one juxtaposed red-green signal pair resulting in a single red and green signal for the translocated allele and a combined yellow signal for the non-translocated allele in each cell. Prior to tissue analysis, the integrity and purity of all probes were verified by hybridization to normal peripheral lymphocyte metaphase spreads. Tissue hybridization, washing, and fluorescence detection were performed as described previously (Garraway, *et al.*, *Nature 436:*117-22 (2005); Rubin, *et al.*, *Cancer Res. 64*:3814-22 (2004)). At least one TMA core could be evaluated in 59% PCA cases from two TMAs. The technical difficulties with this assay included the absence of diagnostic material to evaluate, weak probe signals, and overlapping cells preventing an accurate diagnosis. The remainder of the analysis focused on the 118 cases of clinically localized PCA that could be evaluated. 15 cases had corresponding hormone naïve metastatic lymph node samples that could also be evaluated.

The samples were analyzed under a 100x oil immersion objective using an Olympus BX-51 fluorescence microscope equipped with appropriate filters, a CCD (charge-coupled device) camera and the CytoVision FISH imaging and capturing software (Applied Imaging, San Jose, CA). Evaluation of the tests was independently performed by two pathologists both with experience in analyzing interphase FISH experiments. For each case,

it was attempted to score at least 100 nuclei per case. If significant differences between the results of both pathologists were found, the case was refereed by a third pathologist.

Oligonucleotide SNP Array Analysis

Although SNP arrays were intended for genotyping alleles, the SNP array data can provide information on Loss-of-Heterozygosity (Lieberfarb, *et al.*, *Cancer Res 63*:4781-5 (2003); Lin, *et al.*, *Bioinformatics 20:*1233-40 (2004)) and detection of copy number alterations (Zhao, *et al.*, *Cancer Cell 3:*483-95 (2003)). Using SNP array analysis, it was possible to identify and validate amplified genes in various cancers including melanoma (*MITF*) (Garraway, *et al.*, *Nature 436:*117-22 (2005)) and PCA (*TPD52*) (Rubin, *et al.*, *Cancer Res. 64*:3814-22 (2004)).

SNP detection on the 100K array began with a reduction in genome representation. Two aliquots of 250 ng of genomic DNA were digested separately with XbaI HindIII. The digested fragments were independently ligated to an oligonucleotide linker. The resulting products were amplified using a single PCR primer under conditions in which 200-2000 bp PCR fragments were amplified. These fragments represent a sub-fraction of the genome. The SNPs tiled on the arrays have been pre-selected as they lie within these XbaI and HindIII fragments and have been validated as robustly detected on the arrays. The derived amplified pools of DNA were then labeled, fragmented further and hybridized to separate HindIII and XbaI oligonucleotide SNP arrays.

Arrays were scanned with a GeneChip Scanner 3000. Genotyping calls and signal quantification were obtained with GeneChip Operating System 1.1.1 and Affymetrix Genotyping Tools 2.0 software. Only arrays with genotyping call rates exceeding 90% were analyzed further. Raw data files were pre-processed and visualized in dChipSNP Lin, *et al.*, *Bioinformatics 20:*1233-40 (2004)). In particular, preprocessing included array data normalization to a baseline array using a set of invariant probes and subsequent processing to obtain single intensity values for each SNP on each sample using a model based (PM/MM) method (Li, *et al.*, *Proc. Nat'l Acad. Sci. USA 98:*31-6 (2001)).

Quantitative PCR for TMPRSS2:ERG and TMPRSS2:ETV1 Fusion Transcripts

QPCR was performed using SYBR Green dye (Qiagen) on a DNA engine Opticon 2 machine from MJ Research. Total RNA was reverse transcribed into cDNA using TAQMAN reverse transcription reagents (Applied Biosystems) in the presence of random

Hexamers. All QPCR reactions were performed with SYBR Green Master Mix (Qiagen). All Oligonucleotide primers were designed at Integrated DNA Technologies. Primers that were described by Tomlin *et al.* (*Science 310:*644-8 (2005)) and are specific for the fusion were utilized:

TMPRSS2:ERG_f:TAGGCGCGAGCTAAGCAGGAG (SEQ ID NO:55),
TMPRSS2:ERG_r: GTAGGCACACTCAAACAACGACTGG (SEQ ID NO:56),
TMPRSS2:ETV1_f CGCGAGCTAAGCAGGAGGC, (SEQ ID NO:57)
TMPRSS2:ETV-1_r: CAGGCCATGAAAAGCCAAACTT (SEQ ID NO:58).

GAPDH primers were previously described (Vandesompele, *et al.*, *Genome Biol 3*: RESEARCH 0034 (2002)). 10 μMol of forward and reverse primer were used and procedures were performed according to the manufacturer's recommended thermocycling conditions. Threshold levels were set during the exponential phase of the QPCR reaction using Opticon Monitor analysis software version 2.02. The amount of each target gene relative to the housekeeping gene glyceraldehyde-3-phosphate dehydrogenase (GAPDH) for each sample was determined using the comparative threshold cycle (Ct) method (Applied Biosystems User Bulletin #2). All reactions were subjected to melt curve analysis and products from selected experiments were resolved by electrophoreses on 2% agarose gel.

Statistics

The clinical and pathology parameters were explored for associations with rearrangement status and with the presence of the deletion. Chi-squared test and Fisher exact test were used appropriately. Kaplan-Meier analysis was used to generate prostate-specific antigen recurrence free survival curves of the pathology and the genomic alteration parameters. Log-rank test was used to evaluate statistical significance of associations. Patients with prior neo-adjuvant hormone ablation therapy were excluded. All statistics were performed using SPSS 13.0 for Windows (SPSS Inc., Chicago, IL) with a significance level of 0.05.

B. Results

Detection of Deletions on Chromosome 21 Associated with the TMPRSS2:ERG Gene Rearrangement

In order to characterize the frequency of the *TMPRSS2:ERG* rearrangement in PCA, a modified FISH assay from the assay described by Tomlins, *et al.* (*Science 310:*644-8 (2005)) was utilzed. The original FISH assay used two probes located on *ERG* at the centromeric 3' and telomeric 5' ends. The new assay moved the 5' probe in a telomeric direction (Figure 14). Using a PCA screening tissue microarray (TMA), it was observed that approximately 70% of PCA demonstrating *TMPRSS2:ERG* rearrangement (Figure 11A and 11B) also showed a loss of the green signal corresponding to the telomeric 5' *ERG* probe (Figure 11C and 11D), suggesting that this chromosomal region was deleted. 100K oligonucleotide SNP arrays were used to characterize the extent of these deletions. By interrogating 30 PCA samples, including cell lines, xenografts and hormone naïve and hormone refractory metastatic PCA samples, genomic loss between *ERG* and *TMPRSS2* on chromosome 21q23 was identified (Figure 12A-C).

The rearrangement status for *TMPRSS2:ERG* and *TMPRSS2:ETV1* was determined for these 30 PCA by FISH and/or qPCR (Figure 12A, gray and light blue bar). Discrete genomic loss was observed in *TMPRSS2:ERG* rearrangement positive samples involving an area between *TMPRSS2* and the *ERG* loci for LuCaP 49, LuCaP 93, ULM LN 13, MET6-9,MET18-2, MET24-28, and MET28-27. The extent of these discrete deletions was heterogeneous. More extensive genomic loss on chromosome 21 including the area between *TMPRSS2* and the *ERG* loci was observed in LuCaP 35, LuCaP 86.2, LuCaP 92.1, and MET3-81. The VCaP cell line and the xenograft LuCap 23.1 did not demonstrate loss in this region. For a subset of samples 45%(5 out of 11) the deletion occurs in proximity of *ERG* intron 3. For a majority of samples 64% (7 out of 11) the deletion ends in proximity of the SNP located on *TMPRSS2* (the next SNP in the telomeric direction is about 100K bp distant). The VCaP cell line shows copy number gain along the entire chromosome 21.

For *TMPRSS2:ERG* rearrangement positive tumors, 71% (5 of 7) hormone refractory PCA demonstrate a deletion between *TMPRSS2* and the *ERG* loci whereas deletion was only identified in 25%(1 of 4) hormone naïve metastatic PCA samples (ULM LN 13). There is significant homogeneity for the deletion borders with two distinct sub-classes, distinguished by the start point of the deletion—either at 38.765 Mb or 38.911 Mb.

None of the standard PCA cell lines (PC-3, LNCaP, DU-145, or CWR22 (22Rv1)) demonstrated the *TMPRSS2:ERG* or *TMPRSS2:ETV1* fusion. Several of the LuCap xenografts demonstrate *TMPRSS2:ERG* fusion with deletion including LuCaP 49 (established from an omental mass) and LuCaP 93, both hormone-insensitive (androgen receptor [AR]-negative) small-cell PCAs.

Copy number gain of *ERG* was observed in a small subset of cases both with and without the *TMPRSS2:ERG* rearrangement. The VCaP cell line derived from a hormone refractory PCA demonstrated significant copy number gain on chromosome 21 (Figure 12A-C), which was confirmed by FISH.

TMPRSS2:ERG rearrangement in Primary Prostate Cancer Samples and Hormone Naïve Lymph Node Metastases

To characterize the frequency and potential clinical significance of these observations, 118 clinically localized PCA cases were examined by FISH. The clinical and pathology demographics are presented in Table 10. This cohort of patients is at high risk of disease recurrence as demonstrated by high tumor grades (Gleason grade), pathology stage, and pre-treatment PSA levels. Using standard tissue sections from this cohort, where the large areas of the PCA could be studied microscopically, the *TMPRSS2:ERG* rearrangement was obsesrved to be homogeneous for a given tumor. The TMA experiments confirmed these observations. In PCA cases where 3-6 cores were taken from different areas of the tumor, 100% concordance was observed for *TMPRSS2:ERG* rearrangement status (*i.e.* present or absent). It was also observed that in cases with the *TMPRSS2:ERG* rearrangement with deletion, the deletion was observed in all of the TMA cores from the same patient in 97.9% (94/96) of the cases.

Table 10: Clinical and Pathological Demographics of 118 Men with Clinically Localized Prostate Cancer Treated by Radial Protatectomy*

		Count	**Column N %**
Age	<= median	55	50.0%
	> median	55	50.0%
Preoperative PSA (ng/ml)	<= 4	6	8.2%
	>4 and < 10	13	17.8%

	>= 10	54	74.0%
Gleason Score Sum	< 7	7	6.0%
	= 7	51	43.6%
	> 7	59	50.4%
Nuclear Grade	1	-	-
	2	38	35.5%
	3	69	64.5%
Pathology Stage (pT)	PT2	26	22.2%
	PT3a	34	29.1%
	PT3b	57	48.7%
Surgical Margins status	Negative	30	27.8%
	Positive	78	72.2%
Lymph Node Status (pN)	N_0	52	44.1%
	N_1	56	47.5%
	N_2	10	8.5%
PSA Recurrence	no	34	48.6%
	yes	36	51.4%

*Not all data points were available for all 118 cases

The *TMPRSS2:ERG* rearrangement was identified in 49.2% of the primary PCA samples and 41.2% in the hormone naïve metastatic LN samples (Figure 13A). Deletion of the telomeric probe (green signal) (Figure 1C-D) was observed in 60.3% (35/58) of the primary PCA samples and 42.9% (3/7) of the hormone naïve lymph node tumors with *TMPRSS2:ERG* rearrangement.

In the 15 cases where there was matched primary and hormone naïve lymph node tumors, there was 100% concordance for *TMPRSS2:ERG* rearrangement status with 47% (7 of 15) of the pairs demonstrating the rearrangement. Deletion of the telomeric (green signal) probe was concordantly seen in 42.9%(3 of 7) of the pairs.

TMPRSS2:ERG rearrangement status and Prostate Cancer Progression

The associations between rearrangement status and clinical and pathological parameters were observed (Figure 13). *TMPRSS2:ERG* rearrangement with deletion was observed in a higher percentage of PCA cases with advanced tumor stage (pT)(p=0.03) (Figure 13B), and the presence of metastatic disease to regional pelvic lymph nodes (pN_0 versus pN_{1-2}) (p=0.02). Associations between *TMPRSS2:ERG* rearrangement with and without deletion and clinical outcome as determined by prostate specific antigen (PSA) biochemical failure for 70 patients where follow up data was available were also assesed. Gleason grade, tumor stage, nuclear grade and lymph node status were good predictors of PSA biochemical failure (all p-values < 0.0005). A trend was observed at the univariate level suggesting a PSA recurrence free survival advantage in *TMPRSS2:ERG* rearranged PCA cases without deletion as determined by the FISH assay.

Example 6

TMPRSS2:ERG Gene Fusion Associated with Lethal Prostate Cancer

In previous studies, the gene fusions of the 5'-untranslated region of TMPRSS2 (21q22.3) with the ETS transcription factor family members, either ERG (21q22.2), ETV1 (7p21.2) (Tomlins, *et al.*, *Science 310:*644-8 (2005)), or ETV4 (Tomlins, *et al.*, *Cancer Res. 66(7)*:3396-400 (2006)) provide a mechanism for the over expression of the ETS genes in the majority of prostate cancers. Furthermore, the fusion of an androgen regulated gene, TMPRSS2, and an oncogene suggests that disease progression may vary based on these molecular subtypes. The most common mechanism for gene fusion is loss of about 2.8 megabases of genomic DNA between TMPRSS2 and ERG (Figure 17A and B). This example describes the risk of metastases or prostate cancer specific death based on the presence of the common TMPRSS2:ERG gene fusion.

A. Methods

The study population comprises men with early prostate cancer (T1a-b, Nx, M0) diagnosed at the Örebro University Hospital, Sweden, between 1977 and 1991 by transurethral resection of the prostate (TURP) or transvesical adenoma enucleation for symptomatic benign prostatic hyperplasia as described by Andrén *et al.* (*J. Urol. 175(4)*:1337-40 (2006)). Baseline evaluation at diagnosis included physical examination, chest radiography, bone scan and skeletal radiography (if needed). Nodal staging was not

carried out. Because this evaluation provided no evidence for distant metastases, patients were followed expectantly and received clinical exams, laboratory tests and bone scans every 6 months during the first 2 years after diagnosis and subsequently at 12-month intervals. Patients, who developed metastases, as determined by bone scan, were treated with androgen deprivation therapy if they exhibited symptoms.

The cause of death in the cohort was determined by review of medical records by the study investigators. A validation study regarding cause of death compared to the Swedish Death Register showed greater than 90% concordance, with no systematic under- or over-reporting of any cause of death (Johansson, *et al.*, *Lancet 1(8642)*:799-803 (1989)). Follow-up of the cohort with respect to mortality was 100% and no patients were lost to follow-up through October 2005. The study endpoint was defined as development of distant metastases or prostate cancer specific death (median follow-up time 9.1 years, maximum 27 years).

All TURP samples were reviewed by one pathologist to confirm a diagnosis of prostate cancer, determine the Gleason score and nuclear grade, and estimate the tumor burden as previously described (*J. Urol. 175(4)*:1337-40 (2006)). A tissue microarray was assembled using a manual arrayer (Rubin, *et al.*, *Cancer Epidemiol. Biomarkers Prev. 14(6)*:1424-32 (2005)). The frequency of the TMPRSS2:ERG rearrangement in prostate cancer was assessed using a modified florescence *in situ* hybridization (FISH) assay from the assay originally described by Tomlins et al (*Science 310:*644-8 (2005)). The new assay moved the 5' probe approximately 600kb in a telomeric direction. At least one TMA core could be evaluated in 92 of the prostate cancer cases.

B. Results

In this population-based cohort of men diagnosed with localized cancer, the frequency of TMPRSS2:ERG fusion was 15.2% (14/92) (Figures 17A and B). TMPRSS2:ERG fusion positive tumors were more likely to have a higher Gleason score (two-sided P =.014) (Table 11). To assess the relation of fusion status and lethal prostate cancer, cumulative incidence regression was used. A significant association between the presence of the TMPRSS2:ERG gene fusion and metastases or disease specific death (Figure 17C) with a cumulative incidence ratio (CIR) of 3.6 (P = .004, 95% confidence interval [CI] = 1.5 to 8.9) was observed. When adjusting for Gleason Score, the CIR was 2.4 (P = .07 and 95%CI = 0.9 to 6.1). The present invention is not limited to a particular

mechanism. Indeed, an understanding of the mechanism is not necessary to practive the present invention. Nonetheless, it is contemplated that, based on the homogeneity of the TMPRSS2:ERG gene fusion in cells in a given tumor and its presence only in invasive prostate cancers (compared to Prostatic Intraepithelial Neoplasia), it is contemplated that this is an early event, which might, in part, contribute to the biology behind the phenotype of the Gleason patterns.

Table 11: Prognostic Factors for a Cohort of Men Expectantly Managed for Localized Prostate Cancer Stratified by the TMPRSS2:ERG Gene Fusion Status

Variable	TMPRSS2:ERG Fusion Status		P value*
	Negative	Positive	
No. of patients	78	14	
Age at diagnosis, y	73 (60 to 103)	73 (58 to 90)	.683
Gleason Score**			
Gleason Score <7	48 (61.5%)	3 (21.4%)	.014
Gleason Score =7	20 (25.6%)	6 (42.9%)	
Gleason Score >7	10 (12.8%)	5 (35.7%)	
Pathologic Stage			
pT1a	28 (35.9%)	2 (14.3%)	.112
pT1b	50 (64.1%)	12 (85.7%)	
Nuclear grade***			
1	53 (67.9%)	7 (53.8%)	.585
2	18 (23.1%)	4 (30.8%)	
3	7 (9.0%)	2 (15.4%)	
Status****			
Survived 12 years without metastases or cancer death	20 (25.6%)	1 (7.1%)	.016
Death due to other causes within 12 years	45 (57.7%)	6 (42.9%)	
Distant metastases or death due to prostate Cancer	13 (16.7%)	7 (50.0%)	

* Clinical parameters of subjects having the TMPRSS2:ERG fusion and of subjects not having the TMPRSS2:ERG fusion were compared by use of *t* tests or chi-square tests for continuous variable and categorical variables, respectively.

** Gleason Score is obtained by summing the major and minor Gleason patterns.

*** For one case nuclear grade was not assessed.

**** Individuals who lived at least 12 years and have not developed metastases or died of prostate cancer as of October 2005 are classified as long-term survivors.

Individuals who lived less than 12 years and did not develop metastases are classified as short-term survivors.

Example 7

Detection of *TMPRSS2:ETS* fusions in the urine of patients with prostate cancer

A. Materials and Methods

Urine Collection, RNA isolation and amplification

Urine samples were obtained from patients following a digital rectal exam before either needle biopsy or radical prostatectomy. Urine was voided into urine collection cups containing DNA/RNA preservative (Sierra Diagnostics). For isolation of RNA, a minimum of 30ml of urine were centrifuged at 400 rpm for 15 min at 4° C. RNAlater (Ambion) was added to the urine sediments and stored at -20° C until RNA isolation. Total RNA was isolated using a Qiagen RNeasy Micro kit according to the manufacturer's instructions. Total RNA was amplified using an OmniPlex Whole Transcriptome Amplification (WTA) kit (Rubicon Genomics) according to the manufacturer's instructions (Tomlins et al., Neoplasia 8:153 [2006]). Twenty five nanograms of total RNA were used for WTA library synthesis and the cDNA library was subjected to one round of WTA PCR amplification. Amplified product was purified using a QIAquick PCR Purification kit (Qiagen). For cell line proof of concept experiments, the indicated number of VCaP or LNCaP cells was spiked into 1 ml of sterile urine and the samples were processed as for voided urine.

Quantitative PCR

Quantitative PCR (QPCR) was used to detect *ERG*, *ETV1* and *TMPRSS2:ERG* transcripts from WTA amplified cDNA essentially as described (Tomlins et al., Neoplasia 8:153 [2006], Tomlins et al., Science 310:644 [2005], Example 1 above). For each QPCR reaction, 10 ng of WTA amplified cDNA was used as template. Reactions for *ERG*, *ETV1*, *PSA* and *GAPDH* used 2x Power SYBR Green Master Mix (Applied Biosystems) and 25ng of both the forward and reverse primers. Reactions for *TMPRSS2:ERGa* used 2x Taqman Universal PCR Master Mix and a final concentration of 900 nM forward and reverse primers, and 250 nM probe. For the Taqman assay, samples with Ct values greater than 38 cycles were considered to show no amplification. For all samples, the amount of *ERG* and

ETV1 were normalized to the amount of *GAPDH*. Samples with inadequate amplification of *PSA*, indicating poor recovery of prostate cells in the urine, were excluded from further analysis. *ERG* (exon5_6 forward) and *ETV1* (exon6_7)[2], *GAPDH*[3], and *PSA*[4] primers were as described. The Taqman primers and probe (MGB labeled) specific for TMPRSS2:ERGa are as follows:

TM-ERGa2_MGB-f;CGCGGCAGGAAGCCTTA (SEQ ID NO:70)

TM-ERGa2_MGB-r;TCCGTAGGCACACTCAAACAAC (SEQ ID NO:71),

TM-ERGa2_MGB-probe;5'-MGB-CAGTTGTGAGTGAGGACC-NFQ-3' (SEQ ID NO:72)

Fluorescene in situ Hybridization (FISH)

Four μm thick formalin-fixed paraffin-embedded (FFPE) sections from matched needle biopsies were used for interphase fluorescence *in situ* hybridization (FISH), processed and hybridized as described previously (Example 2 and Tomlins et al., Cancer Res 66:3396 [2006]). BAC probes to detect ERG rearrangements, RP11-95I21 (5' to ERG) and RP11-476D17 (3' to ERG) were prepared as described previously (Tomlins et al., Cancer Res 66:3396 [2006]; Tomlins et al., Science 310:644 [2005]; Examples 1 and 2 above).

B. Results

This example describes a non-invasive method to detect prostate cancer by the presence of *TMPRSS2:ETS* fusion transcripts in prostate cancer cells shed into the urine after a digital rectal exam. Results are shown in Figure 33. As a proof of concept, sterile urine spiked with prostate cancer cell lines expressing high levels of *ERG* and *TMPRSS2:ERG* (VCaP) or high levels of *ETV1* (LNCaP) was used. As shown in Figure 33A, it was possible to detect *ERG* over-expression exclusively in VCaP at 1,600 cells and *ETV1* over-expression exclusively in LNCaP at 16,000 cells by quantitative PCR (QPCR).

By correlating the number of spiked VCaP and LNCaP cells to *GAPDH* C_t (threshold cycle) values, it was observed that, in some cases, urine obtained from patients after a digital rectal exam contained insufficient cell numbers to reliably detect *ERG* or *ETV1* over-expression. Thus, total RNA collected from the urine of patients suspected of having prostate cancer was amplified using OmniPlex Whole Transcriptome Amplification before QPCR analysis. Using this strategy, a cohort of 16 patients where urine was

obtained after a digital rectal exam before a needle biopsy to detect prostate cancer was assesed. Subsequent assessment of needle biopsies demonstrated that this cohort contained 4 patients with benign prostates, 1 with high grade prostatic intraepithelial neoplasia (HGPIN) and 11 with prostate cancer. In addition, a cohort of 3 patients with prostate cancer where urine was collected after a digital rectal exam before radical prostatectomy was assesed.

Cohort characteristics are presented in Table 12. Each urine specimen was from a unique patient and was assigned an ID. The source of the sample (pre biopsy or radical prostatectomy (RP) is indicated. The diagnosis following needle biopsy (including benign, high grade prostatic intraepithelial neoplasia (HGPIN), and prostate cancer (PCa)) is indicated. For patients diagnosed as having prostate cancer following needle biopsy, major Gleason, minor Gleason, and Gleason sum score are indicated. For all patients, pre biopsy PSA (ng/ml) and age are reported, if available.

Table 12

Sample source	Diagnosis	Biopsy Gleason Major	Biopsy Gleason Minor	Biopsy Gleason Score	Pre-Biopsy PSA (ng/ml)
Pre-Biopsy	Benign				4.7
Pre-Biopsy	Benign				8.3
Pre-Biopsy	Benign				6.7
Pre-Biopsy	Benign				4
Pre-Biopsy	HGPIN				9.7
Pre-Biopsy	Pca	3	4	7	3.3
Pre-Biopsy	Pca	3	3	6	5.99
Pre-Biopsy	Pca	3	3	6	2.8
Pre-Biopsy	Pca	3	3	6	5.9
Pre-Biopsy	Pca	4	4	8	10.6
Pre-Biopsy	Pca				
Pre-Biopsy	Pca	4	5	9	11.8
Pre-Biopsy	Pca	3	4	7	5.5
Pre-Biopsy	Pca	3	3	6	3.8
Pre-Biopsy	Pca	4	5	9	19.3
Pre-Biopsy	Pca-treated	3	3	6	
Pre-RP	Pca				
Pre-RP	Pca				
Pre-RP	Pca				

From the needle biopsy cohort, 5 patients were identified with marked over-expression of *ERG*, 1 of which was diagnosed by needle biopsy as having HGPIN, while the other 4 were diagnosed as having prostate cancer. From the radical prostatectomy cohort, 1 of 3 patients with prostate cancer were identified as having high *ERG* expression (Fig 33B). *ETV1* over-expression was not detected in any patients from either cohort. To confirm the expression of *TMPRSS2:ERG* in the samples which over-expressed *ERG*, a TaqMan primer/probe assay designed to specifically amplify *TMPRSS2:ERGa* was utilized. This assay robustly amplified product from VCaP cells, which express *TMPRSS2:ERGa* (Tomlins et al., Science 310:644 [2005]). In addition, 5 of the 6 urine samples from patients with prostate cancer that over-expressed *ERG* also expressed *TMPRSS2:ERGa* (Ct values 29.8-38.9), while 0 of the 10 samples from patients without *ERG* over-expression expressed *TMPRSS2:ERGa*. As one sample over-expressed *ERG* without expression of *TMPRSS2:ERGa*, it is likely that this sample expresses other isoforms of the fusion transcript, such as *TMPRSS2:ERGb* or more recently identified fusion transcripts (Soller et al., Genes Chromosomes Cancer 45:717 [2006]; Yoshimoto et al., Neoplasia 8:465:2006). To confirm that the presence of *TMPRSS2:ERG* fusion transcripts indicates the presence of *TMPRSS2:ERG* positive cancerous tissue, fluorescence *in situ* hybridization (FISH) was performed using probes designed to detect *ERG* rearrangements on matched tissue sections from representative cases. Matched tissue was obtained from three patients with detectable *TMPRSS2:ERG* transcripts in the urine and a diagnosis of cancer, one patient with detectable *TMPRSS2:ERG* transcripts in the urine and a diagnosis of high grade PIN, and two patients without detectable *TMPRSS2:ERG* transcripts and a diagnosis of cancer. As shown in Figure 33B, both patients diagnosed with cancer but without detectable *TMPRSS2:ERG* transcripts in their urine did not harbor *ERG* rearrangements in cancerous tissue by FISH. All three patients diagnosed with cancer and with detectable *TMPRSS2:ERG* transcripts in their urine also showed *ERG* rearrangements in cancerous tissue by FISH. Finally, the patient with a diagnosis of high grade PIN with detectable *TMPRSS2:ERG* in their urine did not show *ERG* rearrangements in high grade PIN tissue. This indicates that this patient may have undiagnosed cancer elsewhere in the prostate, resulting in the presence of detectable *TMPRSS2:ERG* transcripts in their urine.

Example 8

TMPRSS2 and *ETS* Family Genes Fusions in Prostate Cancer

This study describes a comprehensive analysis of the frequency for the *TMPRSS2* and *ETS* family genes rearrangements in a screening-based cohort of 111 American men surgically treated for clinically localized prostate cancer.

A. Materials and Methods

Study Population, Clinical data and Prostate Sample Collection:

As a source of clinically localized prostate cancers, a tissue microarray (TMA) containing -- cores representing cancer and benign tissue was constructed from 111 men who underwent radical prostatectomy at the University of Michigan as the primary monotherapy (i.e., no adjuvant or neoadjuvant hormonal or radiation therapy). The radical prostatectomy series is part of the University of Michigan Prostate Cancer Specialized Program of Research Excellence (SPORE) Tissue Core. Three cores (0.6 mm in diameter) were taken from each representive tissue block to construct the TMA. The TMA construction protocol has been described (Kononen et al., Nat. Med. 4:844 [1998]; Rubin et al., Am J surg Pathol 26:312 [2002]). Detailed clinical, pathological, and TMA data re maintained on a secure relational database as previously described (Manley et al., Am J. Pathol. 159:837 [2001]).

Assessment of TMPRSS2-ETS gene fusion using an interphase Fluorescence in situ hybridization assay

Four μm thick tissue micro array sections were used for interphase fluorescence *in situ* hybridization (FISH), processed and hybridized as described previously (Tomlins et al., Science 310:644 [2005]; Tomlins et al., Cancer Res 66:3396 [2006]). Slides were examined using an Axioplan ImagingZ1 microscope (Carl Zeiss) and imaged with a CCD camera using the ISIS software system in Metafer image analysis system (Meta Systems, Altlussheim, Germany). FISH signals were scored manually (100x oil immersion) by pathologists in morphologically intact and non-overlapping nuclei and a minimum of 30 cells or the maximum numbers of cancer cells available in three cores from a case were recorded. Cases without 30 evaluable cells were reported as insufficient hybridization. All BACs were obtained from the BACPAC Resource Center (Oakland, CA), and probe locations were verified by hybridization to metaphase spreads of normal peripheral lymphocytes. For detection of *TMPRSS2*, *ERG* and *ETV4* rearrangements we used the

following probes: RP11-35C4 (5' to *TMPRSS2*) and RP11-120C17 (3' to *TMPRSS2*), RP11-95I21 (5' to *ERG*) and RP11-476D17 (3' to *ERG*), and RP11-100E5 (5' to *ETV4*) and RP11-436J4 (3' to *ETV4*). For detection of *TMPSS2-ETV1* fusion, RP11-35C4 (5' to *TMPRSS2*) was used with RP11-124L22 (3'to *ETV1*). BAC DNA was isolated using a QIAFilter Maxi Prep kit (Qiagen, Valencia, CA), and probes were synthesized using digoxigenin- or biotin-nick translation mixes (Roche Applied Science, Indianapolis, IN). The digoxigenin and biotin labeled probes were detected using fluorescein conjugated anti-digoxigenin antibodies (Roche Applied Science) and Alexa 594 conjugated sptreptavidin (Invitrogen, Carlsbad, CA), respectively.

A break apart (*TMPRSS2, ERG, ETV4*) or fusion (*TMPRSS2-ETV1*) probe strategy was employed to detect rearrangements at the chromosomal level. Normal signal patterns for *TMPRSS2, ERG* and *ETV4* in DAPI stained nuclei were indicated by two pairs of colocalized green and red signals. For these probes, a rearrangement was confirmed by break apart of one of the two colocalized signals. For *TMPRSS2-ETV1* fusion, two pairs of separate red and green were recorded as normal, while one pair of separate and one pair of colocalized signals was recorded as a rearrangement.

B. Results and Discussion

This example describes a comprehensive analysis outlining the signature of *TMPRSS2* and *ETS* transcription factor genes rearrangement in a large screening-based cohort of American men surgically treated for clinically localized prostate cancer. A *TMPRSS2* split probe FISH assay approach was used to detect the overall frequency of gene rearrangement in prostate cancer with known *ETS* family partners *ERG, ETV1, ETV4* and other unknown partners, as shown in Figure 34. It was hypothesized that prostate cancers negative for three known *ETS* partners (*ERG, ETV1* and *ETV4*) may harbor rearrangements involving other *ETS* family members. The results demonstrate complex molecular signature of *TMPRSS* and *ETS* family genes rearrangement in clinically localized prostate cancer (Figure 35A and B). Overall *TMPRSS2* was rearranged in 65% of evaluable cases, while ERG, ETV1 and ETV4 were rearranged in 55%, 2% and 2% of evaluable cases (Figure 35A). In 40.5% of cases with TMPRSS2 rearrangement, loss of the 3' probe was observed, consistent with a chromosomal deletion between TMPRSS2 and ERG as a mechanism of gene fusion. These results confirm the high frequency of TMPRSS2:ETS fusions in prostate cancer and confirm previous studies showing that TMPRSS2:ERG are by far the most

common type (Tomlins et al., Science 310:644; Perner et al., Cancer Res 66:3396 [2006]; Yoshimoto et al., Neoplasia 8:4665 [2006]; Soller et al., Genes Chromosomes Cancer 45:717 [2006]; Wang et al., Cancer Res 66:8347 [2006] and above examples).

Similar results were observed when the cohort was limited to just those cases where all four probes were evaluable (Figure 35A and B). This analysis confirmed that TMPRSS2:ETS rearrangements are mutually exclusive, as no cases showed rearrangments of multiple ETS family members. This analysis also demonstrates that a single TMPRSS2 assay can effectively detect almost all ETS rearrangements, as 23 of the 24 cases with ERG, ETV1 or ETV4 rearrangement were detected by the TMPRSS2 assay. In all 9 cases where the 5' ERG probe was deleted, deletion of the 3' TMPRSS2 probe was identified.

Furthermore, two cases were identified with break apart of the TMPRSS2 probes, indicating a rearrangement, without rearrangement of ERG, ETV1 or ETV4 (cases 32 and 36) and cases with *TMPRSS2* rearrangement without *ERG* rearrarngement where *ETV1* and/or *ETV4* could not be evaluated. These cases suggest that *TMPRSS2* may be partnering with novel *ETS* family members or unrelated oncogenes in prostate cancer.

Together, these results suggest that a single TMPRSS2 assay can provide diagnostic and prognostic information in prostate cancer.

Example 9

PSA Gene Fusions

FISH experiments were used to identify cases that show a split signal by FISH for probes located 5' and 3' to PSA. The 5' and 3' BACs used to detect the PSA split are RP11-510I16 and RP11-26P14, respectively. A partner for the PSA gene fusion has not yet been identified. These same probes also pick up a split in the ETS family member SPIB, as it is located very close to PSA.

Example 10

FLI1 overexpression

FLI1 expression was assayed in different cell samples not harboring a FLI1 gene fusion. The expression of 5' and 3' exons of FLI1 was measured from a case with high FLI1expression. Results are shown in Figure 18. No difference in the 5' and 3' transcript abundance was detected. RACE also did not indicate a fusion transcript. FLI1 was

overexpressed in prostate cancer relative to control samples. Primers for Fli1 amplification, as well as TaqMan probes, are shown in Figure 37.

FISH was also used to identify samples that have split signals for FLI1, indicating a rearrangement, but these cases do not have TMPRSS2:FLI1 fusion by FISH. BAC probes are shown in Table 13. These cases also have high FLI1 expression.

Example 11

Tissue Microarrays

Tissue microarrays were used to assay for the presence of gene fusions. TMAs used included prostate cancer progression array, prostate cancer outcome array, warm autopsy array, prostate cancer screening array, Erg negative prostate cancer array, and individual prostate cancer cases. The following gene probes were used on tissue microarrays: TMPRSS2-ETV1 fusion probes, Erg split probes, TMPRSS2 split probes, ETV1 split probes, ETV4 split probes, and FL1 split probes.

In addition, Erg split probes were used on an outcome array. The results are as follows: negative cases: 30, positive case: 29, marginal cases: 1. There was a weak association of Erg positive cases with higher Gleason score ($\geq$7).

Protein arrays and mass spec were used to identify nuclear interactors for ERG2. The results are shown in Figure 21.

Example 12

Androgen regulation of Erg expression

This Example describes the androgen regulation of Erg expression. LNCap (TMPRSS2-ERG-) and VCaP (TMPRSS2-ERG+) cell lines were used. The cells were contacted with varying amounts of R1881 for 48 hrs. Expression of Erg, PSA (+ control) and beta-tubulin (- control) were assayed. The results are shown in Figure 19. ERG expression was found to be androgen dependent in the VCaP, but not the LNCap cells.

Example 13

Peptide Antibody and Aqua Probe Generation

Figures 22-25 shows sequences (underlined) of ERG1, ETV1, FLI-1, and ETV4 for use in peptide antibody generation and for making aqua probes. Primers are designed by Applied Biosystems for all ETS family members. Expression is monitored in prostate

cancer cases, with high expression being an indicator of a possible gene fusion and an indicator for FISH.

Example 14

ETV1 in LnCaP Cells

This Example describes an analysis of the transcriptional response to androgen in VCaP and LNCaP. In addition to detecting a number of transcripts differentially expressed in both cell lines were identified, such as PSA, a number of transcripts uniquely dysregulated in VCaP or LNCaP cells were also identfied. This analysis identified ETV1 as being exclusively responsive to androgen in LNCaP cells. Combined with the over-expression of ETV1 in LNCaP cells, FISH was used to interrogate the ETV1 loci in LNCaP cells.

A. Materials And Methods

Cell lines

The prostate cancer cell lines LNCaP (originally derived from a lymph node prostate cancer metastasis) and VCaP (Korenchuk, S. et al., *In vivo* 15, 163-8 (2001)) (originally derived from a vertebral prostate cancer metastasis) were used for this study. For microarray studies, VCaP and LNCaP cells were grown in charcoal-stripped serum containing media for 24 hours before treatment for 48 hours with 0.1% ethanol or 1 nM of the synthetic androgen methyltrienolone (R1881, NEN Life Science Products, Boston, MA) dissolved in ethanol. For quantitative PCR (QPCR) studies, cells were grown in charcoal-stripped serum containing media for 24 hours, preincubated with 0.1% ethanol, Casodex dissolved in acetone (10 uM, bicalutamide, AstraZeneca Pharmaceuticals, Wilmington, DE) or flutamide dissolved in ethanol (10 uM, Sigma, St. Louis, MO). After 2 hours, 0.1% ethanol or 0.5nM of R1881 was added and the cells were harvested after 48 hours. Total RNA was isolated from all samples with Trizol (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. RNA integrity was verified by denaturing formaldehyde gel electrophoresis or the Agilent Bioanalyzer 2100 (Agilent Technologies, Palo Alto, CA).

Microarray analysis

The cDNA microarrays used for this study were constructed essentially as described, except the array contains 32,448 features. Protocols for printing and postprocessing of arrays are available on the Internet. cDNA microarray analysis was done essentially as described. Briefly, total RNA from control and R1881 treated VCaP and LNCaP cell lines were reverse transcribed and labeled with cy5 fluorescent dye. Pooled total RNA from control VCaP or LNCaP samples were reverse transcribed and labeled with cy3 fluorescent dye for all hybridizations from the respective cell lines. The labeled products were then mixed and hybridized to the cDNA arrays. Images were flagged and normalized using the Genepix software package (Axon Instruments Inc., Union City, CA). Data were median-centered by arrays and only genes that had expression values in at least 80% of the samples were used in the analysis.

Quantitative PCR (QPCR)

QPCR was performed using SYBR Green dye on an Applied Biosystems 7300 Real Time PCR system (Applied Biosystems, Foster City, CA) as described (Tomlins et al., Cancer Res 66, 3396-400 (2006); Tomlins et al., Science 310, 644-8 (2005)). The amount of each target gene relative to the housekeeping gene glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) for each sample was reported. The relative amount of the target gene in each cell line and/or experiment was calibrated to controls. All oligonucleotide primers were synthesized by Integrated DNA Technologies (Coralville, IA). *GAPDH* (Vandesompele et al., Genome Biol 3, RESEARCH0034 (2002)), *PSA* (Specht et al., Am J Pathol 158, 419-29 (2001)), *ERG* (Exon 5-6_f and Exon 5-6_r) and *ETV1* (Exon 6-7_f and Exon 6-7_r) primers (Tomlins et al., Science 310, 644-8 (2005)) were as described.

Fluorescence in situ hybridization (FISH)

Metaphase spreads were prepared from normal peripheral lymphocytes (NPLs) and LNCaP cells using standard techniques. Slides were treated with 2x SSC for 2 min, 70% ethanol for 2 min and 100% ethanol for 2 min before addition of the probe. Slides were coverslipped and incubated at 75° for 2 min and hybridized overnight at 37° C. Post-hybridization washing was with 2x SSC at 42° C for 5 min, followed by 3 washes in PBST. Fluorescent detection was performed using anti-digoxigenin conjugated to fluorescein (Roche Applied Science, Indianapolis, IN) and streptavidin conjugated to Alexa Fluor 594 (Invitrogen, Carlsbad, CA). Slides were counterstained and mounted in ProLong Gold

Antifade Reagent with DAPI (Invitrogen). Slides were examined using a Zeiss Axio Imager Z1 fluorescence microscope (Zeiss, Thornwood, NY) and imaged with a CCD camera using ISIS software (Metasystems, Altlussheim, Germany).

All BACs were obtained from the BACPAC Resource Center (Oakland, CA) and probe locations were verified by hybridization to metaphase spreads of normal peripheral lymphocytes. For hybridization to the ETV1 region on chromosome 7p, four BACs were used (telomeric to centromeric): RP11-124L22, RP11-313C20, RP11-703A4 and RP11-1149J13. For localization to chromosome 14q, the FISH mapped BAC RP11-483K13, which we also confirmed as hybridizing to 14q using NPLs. BAC DNA was isolated using a QIAFilter Maxi Prep kit (Qiagen, Valencia, CA) and probes were synthesized using digoxigenin- or biotin-nick translation mixes (Roche Applied Science).

B. Results

Results are shown in Figures 26-28. Figure 26 shows the over-expression and androgen regulation of ETV1 in the LNCaP prostate cancer cell line. Figure 26A shows expression signature of androgen-regulated genes in VCaP and LNCaP prostate cancer cell lines. Heatmap of genes showing induction or repression in either cell line (3,499 features, $p < 0.05$ and fold change ratio>=1.5) by 1 nM synthetic androgen R1881 (green) compared to vehicle treatment (gray). Each row represents a gene; each column represents a sample. Yellow and blue cells indicate over- or under-expression, respectively, according to the color scale. Gray cells indicate missing data. Values for each cell line are centered on the corresponding control samples. The locations of PSA, ERG and ETV1 in the heatmap are indicated and their expression is shown in the inset. Figure 26B shows confirmation of PSA induction by androgen in both VCaP and LNCaP cells by quantitative PCR (QPCR). The relative expression of PSA (normalized to GAPDH) in LNCaP (red) and VCaP (blue) cell lines was determined by QPCR. Cells were treated with vehicle or 1 nM R1881 for 48 hours in the presence or absence of the anti-androgens Casodex or Flutamide as indicated. The relative amount of PSA in each sample was calibrated to the amount in the control sample for each cell line. Figure 26C shows ETV1 induction by androgen in LNCaP cells. Using the same samples as B, the relative amount of ETV1 was determined by QPCR. Figure 26D shows that ETV1 is markedly over-expressed in LNCaP cells. The relative expression of PSA, ETV1 and ERG were determined in the 48 hour control samples from each cell line by QPCR. The

relative amount of target gene in each sample was calibrated to the average amount of PSA from both cell lines. The fold difference in ERG and ETV1 expression between LNCaP and VCaP is indicated.

Figure 27 shows rearrangement of ETV1 in LNCaP cells. Figure 27A shows a schematic of BACs used as probes for fluorescence *in situ* hybridization (FISH). The location and coordinates at 7p21 (including the ETV1 locus and surrounding BACs) and 14q32 was determined on the May 2004 freeze of the human genome using the UCSC Genome Browser. BACs used in this study are indicated as numbered rectangles. The location of ETV1 and DGKB are shown with the arrowhead indicating the direction of transcription. Figure 27B shows that RP11-124L22 and RP11-1149J13 co-localize to chromosome 7 in normal peripheral lymphocytes (NPLs). Localization of RP11-124L22 (BAC #1) and RP11-1149J13 (BAC #4) on metaphase spreads (top panel) or interphase cells (bottom panel) was determined by FISH in NPLs. For all metaphase pictures, signals on chromosome 7 are indicated by arrows, while signals on chromosome 14 are indicated by arrowheads of the corresponding probe color. Higher magnification of informative regions of metaphase spreads are shown in boxes. Figure 27C shows localization of BAC #1 and BAC #4 on metaphase spreads (top panel) and interphase cells (bottom panel) was determined in the near tetraploid LNCaP cell line. Two co-localized signals on chromosome 7, two red signals on chromosome 7 and two green signals on a different chromosome were observed. Figure 27D shows signal from RP11-124L22 localizes to chromosome 14 in LNCaP cells. As in C, except RP11-124L22 (BAC #1) was co-hybridized with RP11-483K13 (BAC #5, FISH mapped to chromosome 14q) on LNCaP metaphase spreads. Four red signals from RP11-483K13 localize to chromosome 14q; two green signals localize to chromosome 7p and two green signals localize to chromosome 14q.

Figure 28 shoes that the entire ETV1 locus is inserted into chromosome 14 in LNCaP cells. Figure 28A shows a schematic of BACs used in this experiment. Figure 28B shows localization of RP11-124L22 (BAC #1) and RP11-313C20 (BAC #2) on metaphase spreads (top panel) and interphase cells (bottom panel) was determined by FISH in LNCaP cells. In metaphase spreads, two pairs of co-localized signals were observed on chromosome 7 (yellow arrows) and chromosome 14 (yellow arrowheads).

These results demonstrate that the entire ETV1 locus is translocated from chromosome 7 to chromosome 14. Although the genomic sequence upstream of the

insertion on chromosome 14 is unknown, it is likely that this region contains AREs, which drive the high level of ETV1 observed only in LNCaP cells and the androgen responsiveness. These results suggest that LNCaP cells find use as an in vitro model of ETS gene fusions seen in human prostate cancers.

Example 15

Knockdown of ETS Family Members in PCA

This Example describes the knockdown of ETS family members in prostate cancer. siRNAs were used to knockdown expression of ETV1 and ERG in LnCaP and VCAP. Quantitative PCR was used to confirm the knockdown. Results are shown in Figures 29 and 30. The knockdown did not affect proliferation. Lentivirus expressing shRNA are generated for stable knockdowns.

Microarrays were performed on Agilent 44K Whole Genome arrays to determine which genes were differentially expressed when ERG expression was knocked down in VCaP cells (which have the TMPRSS2:ERG fusion). For this experiment, three conditions were used: knockdown using Dharmacon siRNA for ERG (ERGsi), knockdown of luciferase (control), and untransfected (untrans) VCaP cells. Three hybridizations of ERG/untrans and two of control/untrans were performed. The genes were called as present in all five experiments, had standard deviations less than 0.5 (of the average for both conditions), and showed a fold difference between the ERG and control of < 0.75 or > 1.5. The ERGdif field indicates the fold difference between the ERG and control knockdown experiments, so value less than one means the gene is underexpressed in the ERG knockdown (ERG itself ranks 81st in this analysis).

Example 16

Transgenic Mice

Transgenic mice that over express gene fusions of the present invention, as well as ETS and androgen responsive genes are generated. Figure 31 shows viral overexpression systems for use in generating mice. Figure 32 shows a schematic of genomic insertions in transgenic mice. Such mice find use in research (*e.g.*, mechanistic studies) and drug screening applications.

Example 17

Identification of TMPRSS2:ERGa

As described above (Example 1), fusions of TMPRSS2 to ERG were observed. To determine the expressed protein from the TMPRSS2:ERGa gene fusion, PCR was used to amplify the portion of ERG (NM_004449) from the fusion breakpoint at the beginning of exon 4 to the presumed stop codon in exon 11, inserting a 3x Flag tag immediately upstream of the stop codon, from the VCaP prostate cancer cell line. The product was TA cloned into pCR8/GW/TOPO TA (Invitrogen) and bi directionally sequenced. Sequencing revealed the presence of two distinct isoforms, herein designated as ERG1 (includes exon 6 from ERG isoform 1 (NM_182918, GGGGTGCAGCTTTTATTTTCCCAAATACTTCAGTATATCCTGAAGCTACGCAAA GAATTACAACTAGGCCAG; SEQ ID NO:73) and ERG2 (does not include this exon). The product was Gateway cloned into the pLenti6/V5-DEST destination vector. This plasmid was transfected directly into PHINX cells for ERG protein production.

A. Methods

Transfection Assay: Phinx cells were transfected with either ERG2 or the empty vector using Fugene transfection reagent (Roche) as per manufacturer's instructions. A total of ten 150 mm diameter plates were used for each construct. The cells were harvested 48h post-transfection and used for immunoprecipitation assay as described below.

Protein Lysis and Immunoprecipitation: Cells were washed in ice cold PBS containing protease inhibitors and lysed by homogenization in TBS containing 1 % NP40. The supernantant containing proteins were estimated for their protein content using Bradfords Protein Assay (Biorad Laboratories, Hercules, CA) as per manufacturer's instructions. Equal amounts of protein (approximately 30 mg in 15 ml buffer) from all samples were used for immunoprecipitation studies. About 200 microlitres of a 50 % slurry of EZVIEW Red ANTI-FLAG M2 Affinity Gel (Sigma, St Louis, MO) was added to each sample and incubated overnight at 4C. The immunoprecipitate was washed thrice each with TBS containing 0.1 % NP40 and TBS alone. Bound proteins were eluted using FLAG peptide (Sigma, St Louis, MO) as per manufacturer's instruction. The elution was performed three times. Proteins in the eluate were preicipited using 50 % TCA (Sigma, St Louis, MO). The precipitate was washed thrice with ice cold acetone, resuspended in Laemmeli buffer and electrophoresed on 4-20 % BIS-TRIS gel (Invitrogen Corporation, Carlbad, CA). The gels were stained with mass spectrometry compatible silver stain (Silver

Quest, Invitrogen Corporation, Carsbad, CA). Bands corresponding to ERG2 and the corresponding region in the vector lane were excised into 6 pieces of 1cm each. Each of the gel pieces were labeled bands 1-6 starting from higher molecular weight region on the gel moving down. Thus Band 1 corresponds to the region containing high molecular weight proteins while band 6 correponds to region of low molecular weight. Based on its native molecular mass of ERG2 (approximately 55 KDa) would migrate in Bands 4 and 5. ERG2 sequence identification was repeated three times and the data was consolidated from all the experiments.

Protein Identification

The gel bands were collected, destained using the destaining solution provided in the Silver Stain Kit as per manufacturers instruction (Invitrogen Corporation, Carsbad, CA). In gel digestion was performed using Porcine Trypsin (1:50, Promega Corporation, Madison, WI) in 1M Ammonium Bicarbonate, pH 9. The digestion was performed for 16h at 37^0C. At the end of 24h the trypsin activity was stopped using 3 % formic acid. The peptides were extracted using 50 % Acetonitrile. The peptides were dried and resuspended in 2 % Acetonitrile containing 0.1 % formic acid and separated by reversed-phase chromatography using a 0.075 mm × 150 mm C18 column attached to a Paradigm HPLC pump (Michrome Bio Resources Inc.). Peptides were eluted using a 45-min gradient from 5 to 95% B (0.1% formic acid/95% acetonitrile), where solvent A was 0.1% formic acid/2% acetonitrile. A Finnigan LTQ mass spectrometer (Thermo Electron Corp.) was used to acquire spectra, the instrument operating in data-dependent mode with dynamic exclusion enabled. The MS/MS spectra on three most abundant peptide ions in full MS scan were obtained. The spectra are searched using the MASCOT search tool against the composite, non-identical NCBI human reference sequence database. These database search results are validated for peptide assignment accuracy using the PeptideProphet program. This is a mixture model; an expectation maximization evaluation assigning a probability of correct peptide identification based on search result scores and various peptide features including the number of typtic termini. A second program, ProteinProphet, is used to group peptides by protein and combine their probabilities to assign a probability of a correct protein assignment. Discriminatory power increases with the subsequent re-estimation of individual peptide probabilities by way of their NSP value, or number of sibling peptides,

which amounts to peptide grouping information and the status of a possible multi-hit protein.

Results:

Table 14
COVERAGE MAP (**ERG2**)
NOTE: E*BAND*-* represent ERG2 peptides in ERG1 experiments

MIQTVPDPAA HI... (SEQ ID NO:74)	NCBI N-terminal, BAND05-20060217	**SEQ ID NO**
MASTIKEALS VVSEDQSLFE CAYGTPHLAK TEMTASSSSD	40	74
SSSSD	BAND03-20060206	75
YGQTSKMSPR VPQQDWLSQP PARVTIKMEC NPSQVNGSRN	80	76
VPQQDWLSQP PAR	BAND01-20060217	77
VPQQDWLSQP PAR	BAND02-20060206	78
VPQQDWLSQP PAR	BAND02-20060209	79
VPQQDWLSQP PAR	BAND02-20060217	80
YGQTSKMS VPQQDWLSQP PAR	BAND03-20060206	81
VPQQDWLSQP PAR	BAND03-20060209	82
VPQQDWLSQP PAR	BAND03-20060217	83
VPQQDWLSQP PAR	BAND04-20060206	84
VPQQDWLSQP PAR MEC NPSQVNGSR	BAND04-20060209	85
VPQQDWLSQP PAR	BAND04-20060217	86
VPQQDWLSQP PAR	BAND05-20060217	87
SPDECSVAKG GKMVGSPDTV GMNYGSYMEE KHMPPPNMTT 120		88
HMPPPNMTT	BAND01-20060206	89
HMPPPNMTT	BAND02-20060206	90
HMPPPNMTT	BAND02-20060209	91
NYGSYMEE KHMP	BAND02-20060217	92
MVGSPDTV GMNYGSYMEE KHMPPPNMTT	BAND03-20060206	93
HMPPPNMTT	BAND03-20060209	94
HMPPPNMTT	BAND04-20060206	95
MVGSPDTV GMNYGSYMEE KHMPPPNMTT	BAND04-20060209	96
MVGSPDTV GMNYGSYMEE KHMPPPNMTT	BAND04-20060217	97
NERRVIVPAD PTLWSTDHVR QWLEWAVKEY GLPDVNILLF 160		98
NER VIVPAD PTLWSTDHVR QWLEWAVKEY GLPDVNILLF	BAND01-20060206	99
NER EY GLPDVNILLF	BAND02-20060206	100
NER	BAND02-20060209	101
NER VIVPAD PTLWSTDHVR QWLEWAVK	BAND03-20060206	102
NERRVIVPAD PTLWSTDHVR EY GLPDVNILLF	BAND03-20060209	103
NER VIVPAD PTLWSTDHVR QWLEWAVKEY GLPDVNILLF	BAND04-20060206	104
NERRVIVPAD PTLWSTDHVR QWLEWAVKEY GLPDVNILLF	BAND04-20060209	105
NERRVIVPAD PTLWSTDHVR	BAND04-20060217	106
EY GLPDVNILLF	BAND05-20060206	107
QNIDGKELCK MTKDDFQRLT PSYNADILLS HLHYLRETPL 200		108
QNIDGK LT PSYNADILLS HLHYLRETPL	BAND01-20060206	109
ETPL	BAND01-20060217	110
QNIDGK ETPL	BAND02-20060206	111
ETPL	BAND02-20060217	112
ETPL	BAND03-20060206	113
QNIDGK LT PSYNADILLS HLHYLRETPL	BAND03-20060209	114
ETPL	BAND03-20060217	115
QNIDGK LT PSYNADILLS HLHYLRETPL	BAND04-20060206	116
QNIDGK LT PSYNADILLS HLHYLRETPL	BAND04-20060209	117
LT PSYNADILLS HLHYLRETPL	BAND04-20060217	118
QNIDGK	BAND05-20060206	119
PSYNADILLS HLHYLRETPL	BAND05-20060217	120
PHLTSDDVDK ALQNSPRLMH ARNTGGAAFI FPNTSVYPEA 240		121
PRLMH ARNT	BAND01-20060206	122
PHLTSDDVDK	BAND01-20060206	123
PHLTSDDVDK ALQNSPR	BAND01-20060217	124

PHLTSDDVDK ALQNSPR	BAND02-20060206	125
PHLTSDDVDK ALQNSPR	BAND02-20060217	126
PHLTSDDVDK ALQNSPR	BAND03-20060206	127
PHLTSDDVDK	BAND03-20060209	128
PHLTSDDVDK ALQNSPR	BAND03-20060217	129
PHLTSDDVDK ALQNSPR	BAND04-20060206	130
PHLTSDDVDK ALQNSPR	BAND04-20060209	131
RNT	BAND04-20060209	132
PHLTSDDVDK ALQNSPR	BAND04-20060217	133
PHLTSDDVDK ALQNSPRL	BAND05-20060217	134
TQRITTRPDL PYEPPRRSAW TGHGHPTPQS KAAQPSPSTV	280	135
DLPYEPPR	BAND01-20060206	136
SAW TGHGHPTPQS KAAQPSPSTV	BAND01-20060206	137
PYEPPRR	BAND01-20060217	138
SAW TGHGHPTPQS KAAQPSPSTV	BAND02-20060206	139
SAW TGHGHPTPQS KAAQPSPSTV	BAND02-20060209	140
PYEPPRRSAW TGHGHPTPQS KAAQPSPSTV	BAND02-20060217	141
SAW TGHGHPTPQS KAAQPSPSTV	BAND03-20060206	142
SAW TGHGHPTPQS KAAQPSPSTV	BAND03-20060209	143
DL PYEPPRR	BAND03-20060217	144
PYEPPRRSAW TGHGHPTPQS KAAQPSPSTV	BAND04-20060206	145
DL PYEPPRRSAW TGHGHPTPQS KAAQPSPSTV	BAND04-20060209	146
DL PYEPPRR	BAND04-20060209	147
DL PYEPPRRSAW TGHGHPTPQS KAAQPSPSTV	BAND04-20060217	148
AAQPSPSTV	BAND05-20060206	149
SAW TGHGHPTPQS KAAQPSPSTV	BAND05-20060209	150
DL PYEPPRRSAW TGHGHPTPQS KAAQPSPSTV	BAND05-20060217	151
SAW TGHGHPTPQS KAAQPSPSTV	BAND06-20060209	
PKTEDQRPQL DPYQILGPTS SRLANPGSGQ IQLWQFLLEL	320	152
PK	BAND01-20060206	153
TEDQRPQL DPYQILGPTS SR	BAND01-20060217	154
PKTEDQRPQL DPYQILGPTS SR	BAND02-20060206	155
PKTEDQRPQL DPYQILGPTS SR	BAND02-20060209	156
PKTEDQRPQL DPYQILGPTS SR	BAND02-20060217	157
PKTEDQRPQL DPYQILGPTS SR	BAND03-20060206	158
PKTEDQRPQL DPYQILGPTS SR	BAND03-20060209	159
TEDQRPQL DPYQILGPTS SR	BAND03-20060217	160
PKTEDQRPQL DPYQILGPTS SR	BAND04-20060206	161
PKTEDQRPQL DPYQILGPTS SR	BAND04-20060209	162
PKTEDQRPQL DPYQILGPTS SR	BAND04-20060217	163
PK	BAND05-20060206	164
PKTEDQRPQL DPYQILGPTS SR	BAND05-20060209	165
PKTEDQRPQL DPYQILGPTS SR	BAND05-20060217	166
PK	BAND06-20060209	167
LSDSSNSSCI TWEGTNGEFK MTDPDEVARR WGERKSKPNM	360	168
MTDPDEVAR	BAND01-20060206	169
MTDPDEVAR	BAND02-20060206	170
MTDPDEVAR	BAND03-20060206	171
MTDPDEVAR	BAND03-20060209	172
MTDPDEVAR	BAND04-20060206	173
MTDPDEVARR	BAND04-20060209	174
TDPDEVARR KSKPNM	BAND04-20060217	175
MTDPDEVAR	BAND05-20060209	176
KSKPNM	BAND05-20060217	177
NYDKLSRALR YYYDKNIMTK VHGKRYAYKF DFHGIAQALQ	400	178
F DFHGIAQALQ	BAND02-20060206	179
F DFHGIAQALQ	BAND02-20060209	180
F DFHGIAQALQ	BAND03-20060206	181
F DFHGIAQALQ	BAND03-20060209	182
YYYDKNIMTK YAYKF DFHGIAQALQ	BAND04-20060209	183
NYDKLSR	BAND04-20060217	184
NYDKLSR YYYDKNIMTK	BAND05-20060217	185
PHPPESSLYK YPSDLPYMGS YHAHPQKMNF VAPHPPALPV	440	186

PHPPESSLYK	BAND02-20060206	187
PHPPESSLYK YPSDLPYMGS YHAH	BAND02-20060209	188
PHPPESSLYK YPSDLPYMGS YHAHPQK	BAND03-20060206	189
PHPPESSLYK YPSDLPYMGS YHAHPQK	BAND03-20060209	190
YPSDLPYMGS YHAHPQK	BAND04-20060206	191
PHPPESSLYK YPSDLPYMGS YHAHPQK	BAND04-20060209	192
TSSSFFAAPN PYWNSPTGGI YPNTRLPTSH MPSHLGTYY	479	193
NSPTG	BAND02-20060217	194
SPTGGI YPNTR	BAND04-20060209	195

The table shows the coverage map for ERG2 obtained over 3 different experiments.The underlined aminoacid sequence correponds to the in silico translated sequence of ERG1 that was cloned from VCAP cells. The aminoacid sequence GGAAFI FPNTSVYPEATQRITTRP (SEQ ID NO:196) corresponds to the exon that is specific to ERG1 and is missing in ERG2. The remaining amino acid sequence correspond to ERG2 sequence identified in each of the three experiments. ERG2 was identified in Bands 1-5 in all the experiments. The peptide sequences for ERG2 obtained in each of these bands is illustrated. A very high coverage of the ERG2 protein was observed over the three experiments. The coverage map showed that the coverage of peptides in the N-terminal region of the cloned protein, corresponding to the first 50 aminoacid residues were rarely observed in the mass spectrometry coverage map. However, the peptide VPQQDWLSQP (SEQ ID NO:197) that starts with aminoacid valine was found to be highly abundant and thus identified in all the experiments. Closer evaluation suggested that aminoacid in the 47th position was an in frame Methionine. The lack of any peptide upstream (Nterminus) of the 47 th methionine in multiple experiments confirms that it is the N-terminal aminoacid of ERG2. Further, the presence of a Arginine residue at the 50th position makes it a potential tryptic cleavage site. Digestion by trypsin at this site would result in a shorter N-terminal peptide MSPR, which is too small for identification by ion trap mass spectrometer and a longer C-terminal peptide VPQQDWLSQP (SEQ ID NO:198), which was identified in all the experiments. Also the peptide sequence MIQTVPDPAA HI (SEQ ID NO:199) was identified in a single experiment at a very low probablility score. This maps to the N-terminus of ERG as reported in NCBI. This sequence was not a part of the ectopically overexpressed construct that was cloned from the VCAP cells. This could have been obtained from the *in vivo* ERG that is expressed in PHINX cells and thus may represent part of the ERG associated with benign cells.

Thus, in summary, the results indicate that the third Methionine is the translational Start site for the TMPRSS2-ERG fusion product. MASTIKEALS VVSEDQSLFE CAYGTPHLAK TEMTA YGQTSK**M**SPR VPQQDWLSQP (SEQ ID NO:200)

The First Methionine is the translational START Site for endogenous ERG.
MIQTVPDPAA HI (SEQ ID NO:201)

Figure 20 shows a schematic of the endogenous and fusion polypeptides.

Example 18

FISH Analysis on Urine Samples

To isolate and prepare prostatic cells from urine, ~ 30 ml of urine is collected following an attentive digital rectal exam. Imediately, 15 ml of PreservCyt is added, and the sample is centrifuged at 4000 rpm in a 50 ml tube for 10 min at room temperature. The supernatant is discarded, the pellet is resuspended in 15 ml of 0.75 M KCl for 15 min at room temperature, and centrifuged at 4000 rpm in a 50 ml tube for 10 min at room temperature. The supernatant is discarded, and the pellet is resuspended in 10 ml of a 3:1 ratio of methanol: glacial acetic acid. This is then centrifuged at 4000 rpm for 8 min. The supernatant is discarded, except for 200 µl, and the pellet is resuspended. The resuspended pellet is then dropped onto glass slides and allowed to air dry. Hybridization and probe preparation are as in Example 2 abvove, with the ERG 5'/3' and TMPRSS 5'/3' probe pairs.

All publications, patents, patent applications and accession numbers mentioned in the above specification are herein incorporated by reference in their entirety. Although the invention has been described in connection with specific embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications and variations of the described compositions and methods of the invention will be apparent to those of ordinary skill in the art and are intended to be within the scope of the following claims.

CLAIMS

We claim:

1. A method for diagnosing prostate cancer in a patient comprising:
   (a) providing a sample from the patient; and
   (b) detecting the presence or absence in the sample of a gene fusion having a 5' portion from a transcriptional regulatory region of an androgen regulated gene and a 3' portion from an ETS family member gene,
   wherein the presence in the sample of the gene fusion is indicative of prostate cancer in the patient.

2. The method of claim 1, wherein the androgen regulated gene is selected from the group consisting of TMPRSS2 and PSA.

3. The method of claim 2, wherein the transcriptional regulatory region of the androgen regulated gene comprises a promoter region of the androgen regulated gene.

4. The method of claim 3, wherein the promoter region of the androgen regulated gene comprises an androgen response element (ARE) of the androgen regulated gene.

5. The method of claim 1, wherein the ETS family member gene is selected from the group consisting of ERG, ETV1 (ER81), FLI1, ETS1, ETS2, ELK1, ETV6 (TEL1), ETV7 (TEL2), GABPα, ELF1, ETV4 (E1AF; PEA3), ETV5 (ERM), ERF, PEA3/E1AF, PU.1, ESE1/ESX, SAP1 (ELK4), ETV3 (METS), EWS/FLI1, ESE1, ESE2 (ELF5), ESE3, PDEF, NET (ELK3; SAP2), NERF (ELF2), and FEV.

6. The method of claim 1, wherein step (b) comprises detecting chromosomal rearrangements of genomic DNA having a 5' portion from a transcriptional regulatory region of an androgen regulated gene and a 3' portion from an ETS family member gene.

7. The method of claim 6, wherein step (b) comprises detecting chromosomal rearrangements of genomic DNA using a nucleic acid sequencing technique.

8. The method of claim 6, wherein step (b) comprises detecting chromosomal rearrangements of genomic DNA using a nucleic acid hybridization technique.

9. The method of claim 8, wherein step (b) comprises detecting chromosomal rearrangements of genomic DNA using a nucleic acid hybridization technique selected from the group consisting of *in situ* hybridization (ISH), microarray and Southern blot.

10. The method of claim 6, wherein step (b) comprises detecting chromosomal rearrangements of genomic DNA using a nucleic acid amplification method.

11. The method of claim 10, wherein step (b) comprises detecting chromosomal rearrangements of genomic DNA using a nucleic acid amplification method selected from the group consisting of polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), transcription-mediated amplification (TMA), ligase chain reaction (LCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

12. The method of claim 1, wherein step (b) comprises detecting chimeric mRNA transcripts having a 5' portion from a transcriptional regulatory region of an androgen regulated gene and a 3' portion from an ETS family member gene.

13. The method of claim 12, wherein step (b) comprises detecting chimeric mRNA transcripts using a nucleic acid sequencing technique.

14. The method of claim 12, wherein step (b) comprises detecting chimeric mRNA transcripts using a nucleic acid hybridization technique.

15. The method of claim 14, wherein step (b) comprises detecting chimeric mRNA transcripts using a nucleic acid hybridization technique selected from the group consisting of *in situ* hybridization (ISH), microarray and Northern blot.

16. The method of claim 15, wherein said *in situ* hybridization is fluorescence *in situ* hybridization (FISH) utilizing a probe selected from the group consisting of: RP11-372O17;

RP11-137J13; RP11-692L4; RP11-476D17; PR11-32L6; RP11-752M23; RP11-1107H21; RP11-639A7; RP11-1077M21; RP11-121A5; RP11-120C17; PR11-814F13; and RR11-535H11.

17. The method of claim 12, wherein step (b) comprises detecting chimeric mRNA transcripts using a nucleic acid amplification method.

18. The method of claim 17, wherein step (b) comprises detecting chimeric mRNA transcripts using a nucleic acid amplification method selected from the group consisting of polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), transcription-mediated amplification (TMA), ligase chain reaction (LCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

19. The method of claim 1, wherein step (b) comprises detecting an amino-terminally truncated ETS family member protein resulting from a fusion of a transcriptional regulatory region of an androgen regulated gene to an ETS family member gene.

20. The method of claim 1, wherein step (b) comprises detecting a chimeric protein having an amino-terminal portion from a transcriptional regulatory region of an androgen regulated gene and a carboxy-terminal portion from an ETS family member gene.

21. The method of claim 19 or 20, wherein step (b) comprises detecting protein using a protein sequencing technique.

22. The method of claim 19 or 20, wherein step (b) comprises detecting protein using an immunoassay.

23. The method of claim 22, wherein step (b) comprises detecting protein using an immunoassay selected from the group consisting of immunoprecipitation; Western blot; ELISA; immunohistochemistry; immunocytochemistry; flow cytometry; and, immuno-PCR.

24. The method of claim 1, wherein the sample is selected from the group consisting of tissue, blood, urine, semen, prostatic secretions and prostate cells.

25. The method of claim 1, wherein the gene fusion is fusion of TMPRSS2 and ERG, and wherein the method further comprises the step of characterizing the prostate cells based on the presence or absensce of a genomic deletion in the gene fusion.

26. The method of claim 25, wherein said gene rearrangement is a deletion of genomic DNA between the TMPRSS2 and the ERG gene on chromosome 21.

27. The method of claim 26, wherein said deletion includes the deletion of exon 1 of the ERG gene.

28. The method of claim 26, wherein said deletion includes the deletion of exon 3 of the TMPRSS2 gene.

29. The method of claim 26, wherein between 2.8 and 2.85 megabases of genomic DNA are deleted.

30. The method of claim 29, wherein said deletion is detected using a FISH assay uses at least one fluorescently labeled probe selected from the group consisting of BAC clone RP11-137J13; and BAC clone RP11-24A11.

31. The method of claim 28, wherein said deletion is detected using the polymerase chain reaction (PCR).

32. The method of claim 31, wherein said PCR is performed using a primer selected from the group consisting of SEQ ID NO:55-SEQ ID NO:58.

33. The method of claim 26, wherein the presence of the deletion is indicative of metastatic prostate cancer in the patient

34. A composition for diagnosing prostate cancer in a patient comprising at least one of the following:

(a) a labeled probe comprising a sequence that hybridizes to the junction at which a 5' portion from a transcriptional regulatory region of an androgen regulated gene fuses to a 3' portion from an ETS family member gene;

(b) a first labeled probe comprising a sequence that hybridizes to a transcriptional regulatory region of an androgen regulated gene and a second labeled probe comprising a sequence that hybridizes to an ETS family member gene;

(c) a first amplification oligonucleotide comprising a sequence that hybridizes to a transcriptional regulatory region of an androgen regulated gene and a second amplification oligonucleotide comprising a sequence that hybridizes to an ETS family member gene;

(d) an antibody to an amino-terminally truncated ETS family member protein resulting from a fusion of a transcriptional regulatory region of an androgen regulated gene to an ETS family member gene; and,

(e) an antibody to a chimeric protein having an amino-terminal portion from a transcriptional regulatory region of an androgen regulated gene and a carboxy-terminal portion from an ETS family member gene.

35. A method for assaying prostate cells for a deletion of genomic DNA indicative of a cancer-associated rearrangement, comprising:

a) obtaining a test sample of the prostate cells;

b) assaying the sample of prostate cells to determine the level of expression of one or more genes selected from the group consisting of: ETS2; WRB; PCP4; and MX1;

c) comparing the expression level determined in step b) with the level in a control sample; and

d) determining that a deletion has occurred if the level of expression determined for said gene in said test sample is lower than that for the control sample.

36. A method for treating prostate cancer in a patient comprising:

administering to the patient an agent that inhibits at least one biological activity of a gene fusion having a 5' portion from a transcriptional regulatory region of an androgen regulated gene and a 3' portion from an ETS family member gene.

37. The method of claim 36, wherein the androgen regulated gene is selected from the group consisting of TMPRSS2 and PSA.

38. The method of claim 37, wherein the transcriptional regulatory region of the androgen regulated gene comprises a promoter region of the androgen regulated gene.

39. The method of claim 38, wherein the promoter region of the androgen regulated gene comprises an androgen response element of the androgen regulated gene.

40. The method of claim 36, wherein the ETS family member gene is selected from the group consisting of ERG, ETV1 (ER81), FLI1, ETS1, ETS2, ELK1, ETV6 (TEL1), ETV7 (TEL2), GABPα, ELF1, ETV4 (E1AF; PEA3), ETV5 (ERM), ERF, PEA3/E1AF, PU.1, ESE1/ESX, SAP1 (ELK4), ETV3 (METS), EWS/FLI1, ESE1, ESE2 (ELF5), ESE3, PDEF, NET (ELK3; SAP2), NERF (ELF2), and FEV.

41. The method of claim 36, wherein the agent is selected from the group consisting of a small molecule, an siRNA, an antisense nucleic acid, and an antibody.

Fig 1.

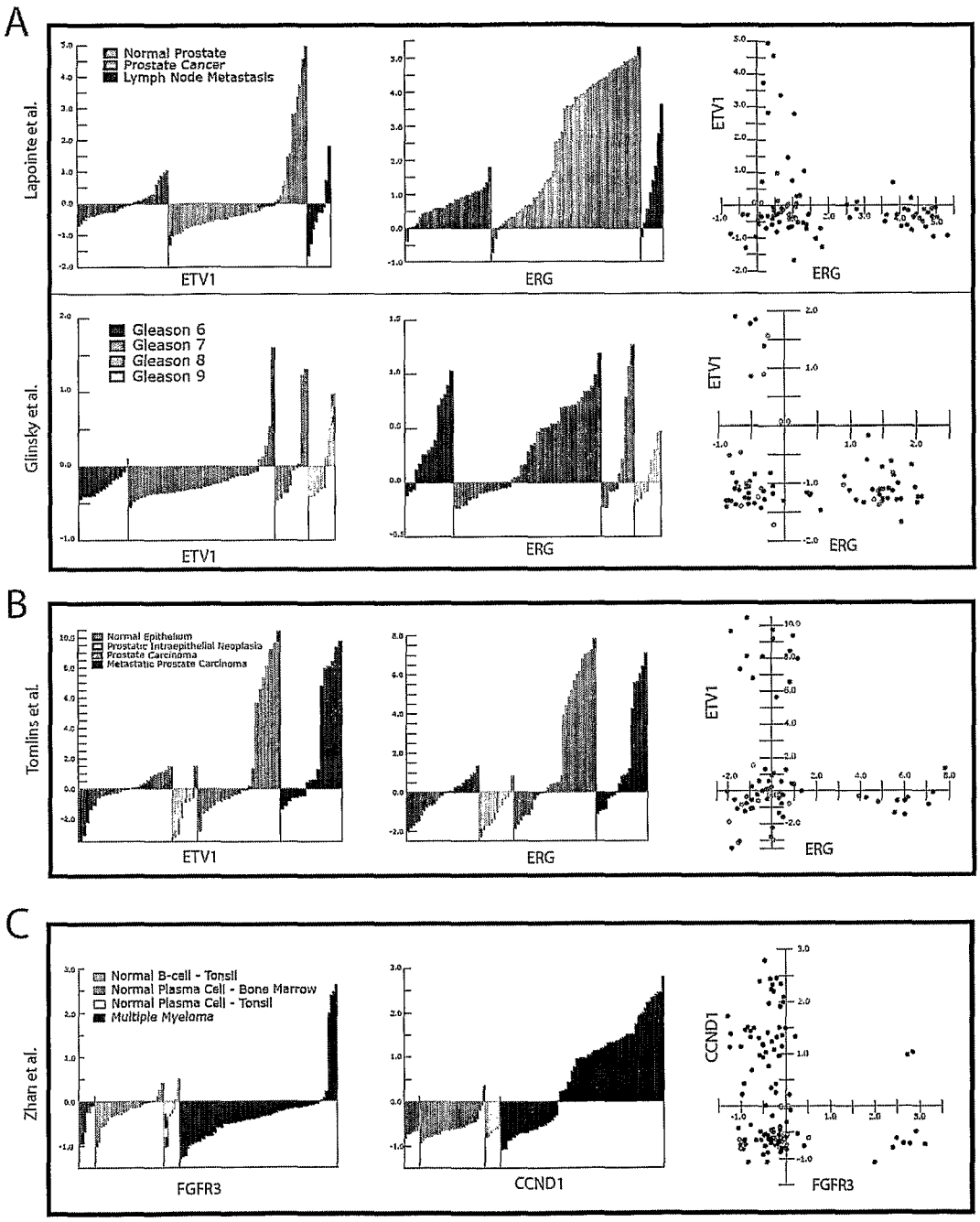

A
Lapointe et al.
Normal Prostate
Prostate Cancer
Lymph Node Metastasis
ETV1
ERG
ETV1
ERG
Glinsky et al.
Gleason 6
Gleason 7
Gleason 8
Gleason 9
ETV1
ERG
ETV1
ERG
B
Tomlins et al.
Normal Epithelium
Prostatic Intraepithelial Neoplasia
Prostate Carcinoma
Metastatic Prostate Carcinoma
ETV1
ERG
ETV1
ERG
C
Zhan et al.
Normal B-cell - Tonsil
Normal Plasma Cell - Bone Marrow
Normal Plasma Cell - Tonsil
Multiple Myeloma
FGFR3
CCND1
CCND1
FGFR3

Fig. 2

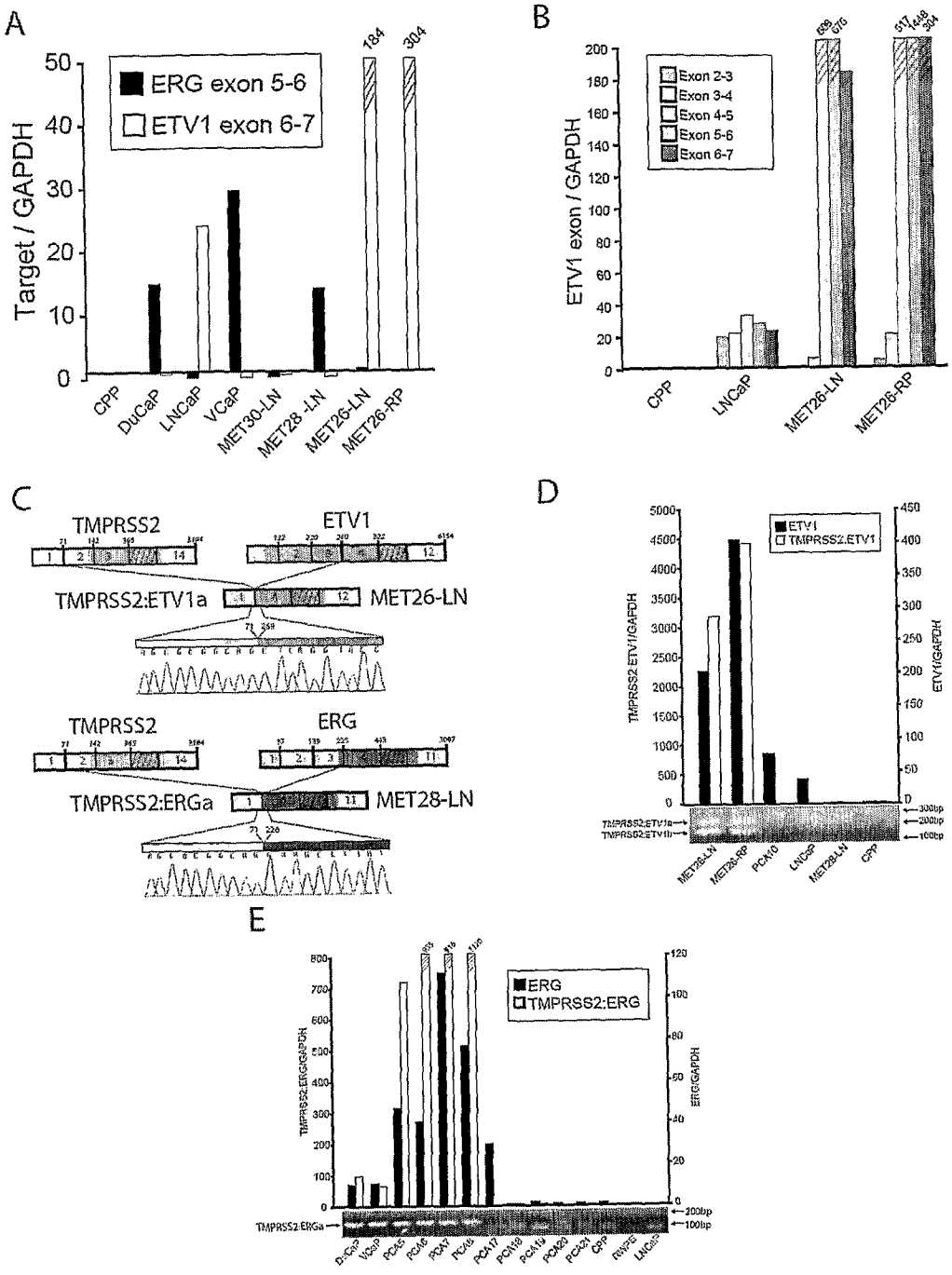
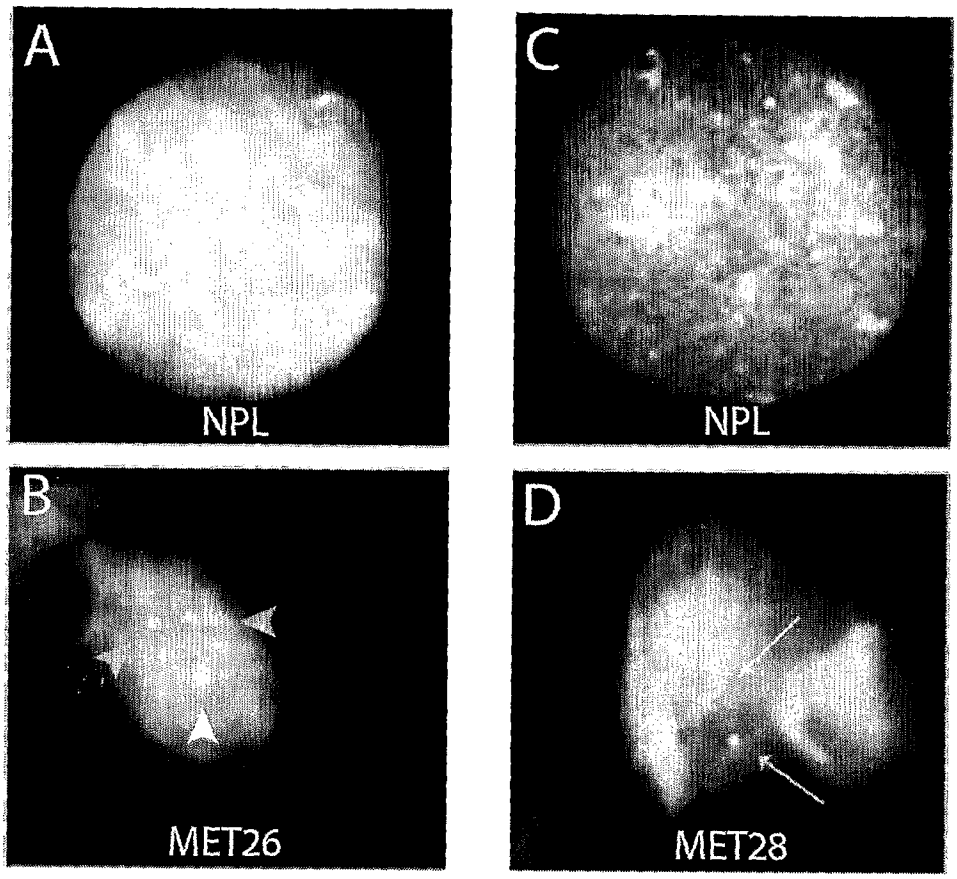

A
Target / GAPDH
ERG exon 5-6
ETV1 exon 6-7
184
304
CPP
DuCaP
LNCaP
VCaP
MET30-LN
MET28 -LN
MET26-LN
MET26-RP
B
ETV1 exon / GAPDH
Exon 2-3
Exon 3-4
Exon 4-5
Exon 5-6
Exon 6-7
CPP
LNCaP
MET26-LN
MET28-RP
C
TMPRSS2
ETV1
TMPRSS2:ETV1a
MET26-LN
TMPRSS2
ERG
TMPRSS2:ERGa
MET28-LN
D
ETV1
TMPRSS2.ETV1
TMPRSS2:ETV1/GAPDH
ETV1/GAPDH
TMPRSS2:ETV1a
TMPRSS2:ETV1b
MET26-LN
MET28-RP
PCA10
LNCaP
MET28-LN
CPP
E
ERG
TMPRSS2:ERG
TMPRSS2:ERG/GAPDH
ERG/GAPDH
TMPRSS2:ERGa
DuCaP
VCaP
PCA5
PCA6
PCA7
PCA15
PCA17
PCA18
PCA19
PCA20
PCA21
CPP
RWPE
LNCaP

Fig. 3


A
NPL
C
NPL
B
MET26
D
MET28

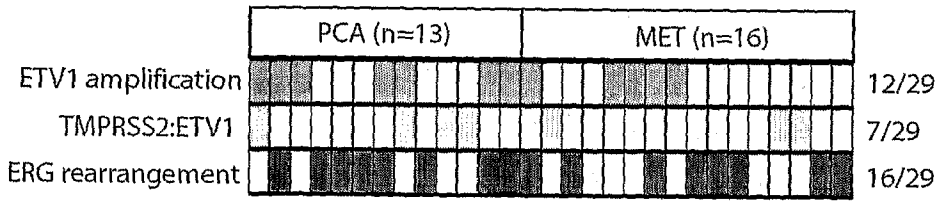

E
PCA (n=13)
MET (n=16)
ETV1 amplification
TMPRSS2:ETV1
ERG rearrangement
12/29
7/29
16/29

Fig. 4

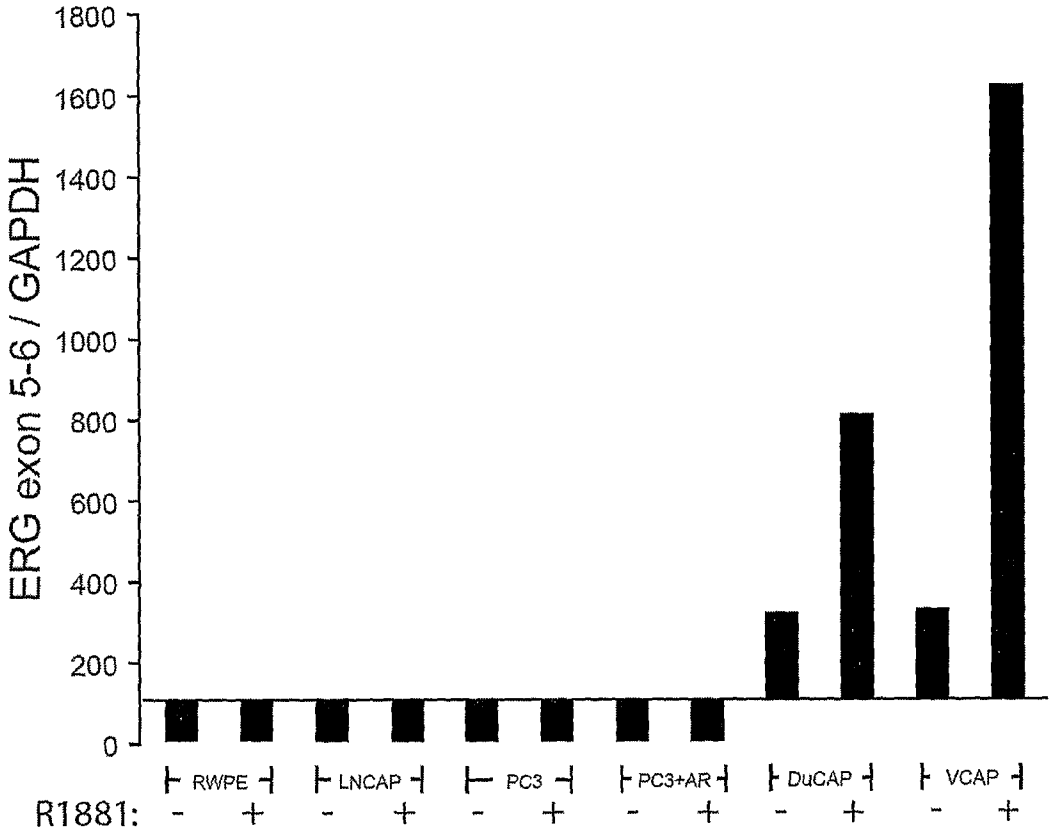

ERG exon 5-6 / GAPDH
1800
1600
1400
1200
1000
800
600
400
200
0
RWPE
LNCAP
PC3
PC3+AR
DuCAP
VCAP
R1881: - + - + - + - + - + - +

Figure 5

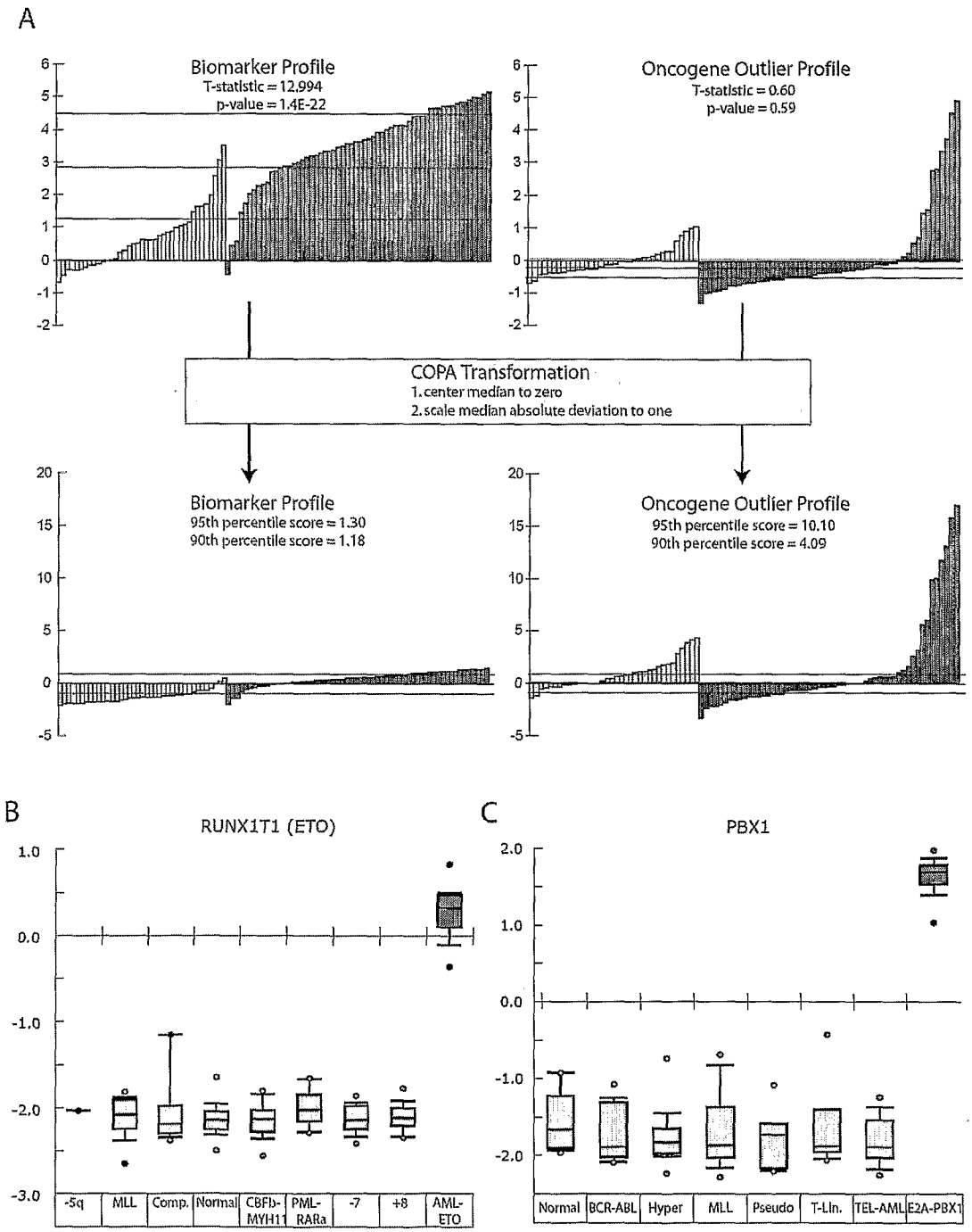

A
Biomarker Profile
T-statistic = 12.994
p-value = 1.4E-22
Oncogene Outlier Profile
T-statistic = 0.60
p-value = 0.59
COPA Transformation
1. center median to zero
2. scale median absolute deviation to one
Biomarker Profile
95th percentile score = 1.30
90th percentile score = 1.18
Oncogene Outlier Profile
95th percentile score = 10.10
90th percentile score = 4.09
B
RUNX1T1 (ETO)
-5q
MLL
Comp.
Normal
CBFb-MYH11
PML-RARa
-7
+8
AML-ETO
C
PBX1
Normal
BCR-ABL
Hyper
MLL
Pseudo
T-Lin.
TEL-AML
E2A-PBX1

Figure 6

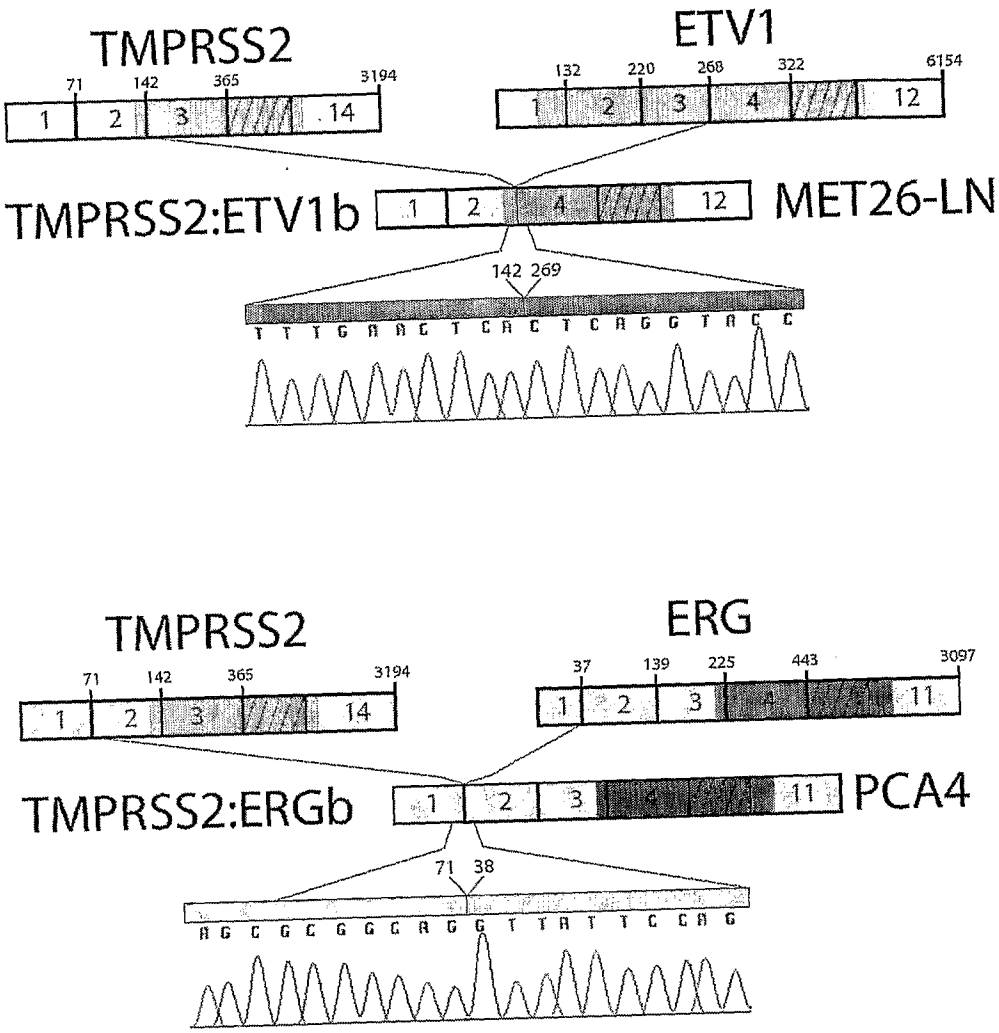

TMPRSS2
71
142
365
3194
1
2
3
14
ETV1
132
220
268
322
6154
1
2
3
4
12
TMPRSS2:ETV1b
1
2
4
12
MET26-LN
142 269
TMPRSS2
71
142
365
3194
1
2
3
14
ERG
37
139
225
443
3097
1
2
3
11
TMPRSS2:ERGb
1
2
3
11
PCA4
71 38

Figure 7

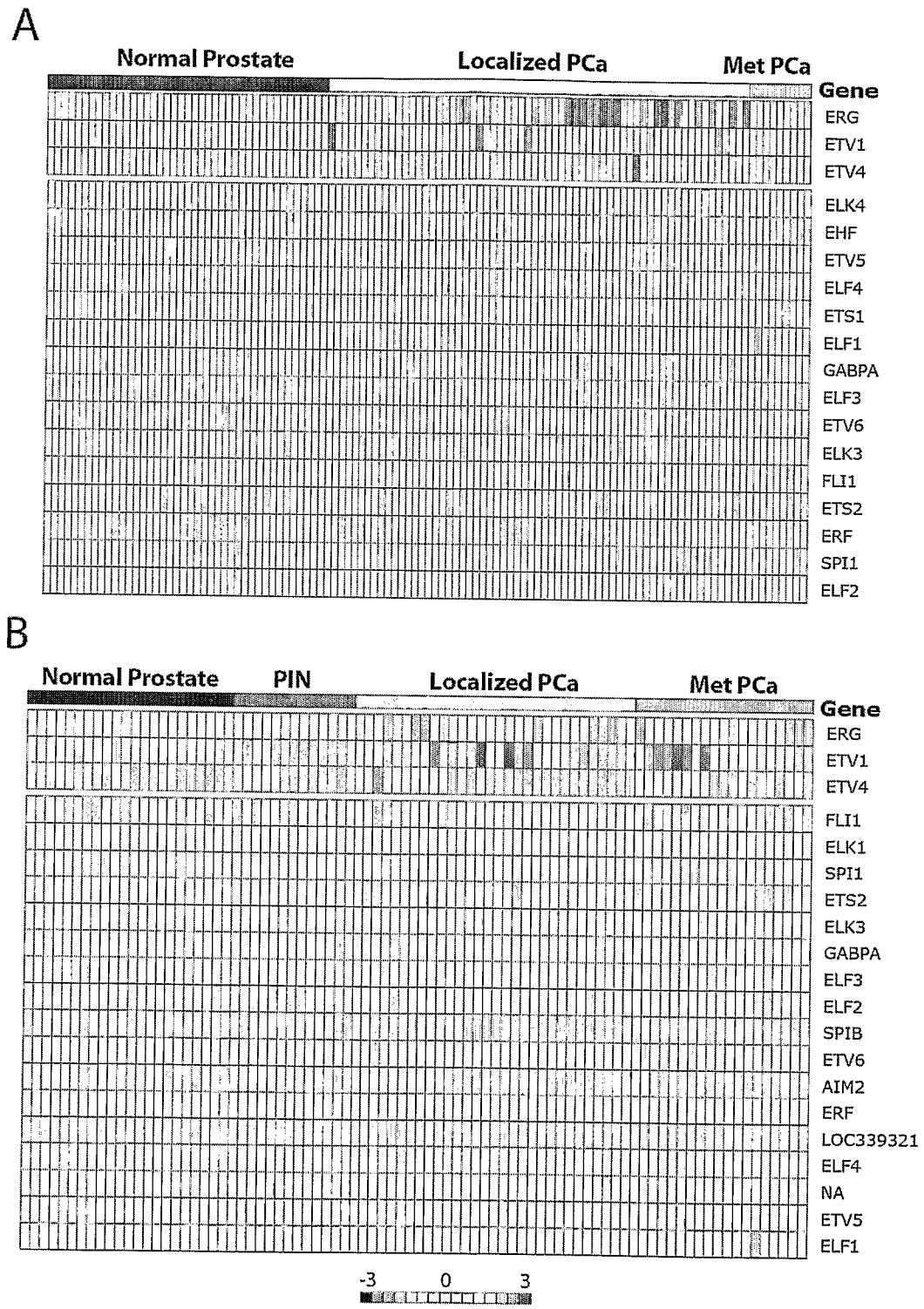

A
Normal Prostate
Localized PCa
Met PCa
Gene
ERG
ETV1
ETV4
ELK4
EHF
ETV5
ELF4
ETS1
ELF1
GABPA
ELF3
ETV6
ELK3
FLI1
ETS2
ERF
SPI1
ELF2
B
Normal Prostate
PIN
Localized PCa
Met PCa
Gene
ERG
ETV1
ETV4
FLI1
ELK1
SPI1
ETS2
ELK3
GABPA
ELF3
ELF2
SPIB
ETV6
AIM2
ERF
LOC339321
ELF4
NA
ETV5
ELF1
-3
0
3

Figure 8

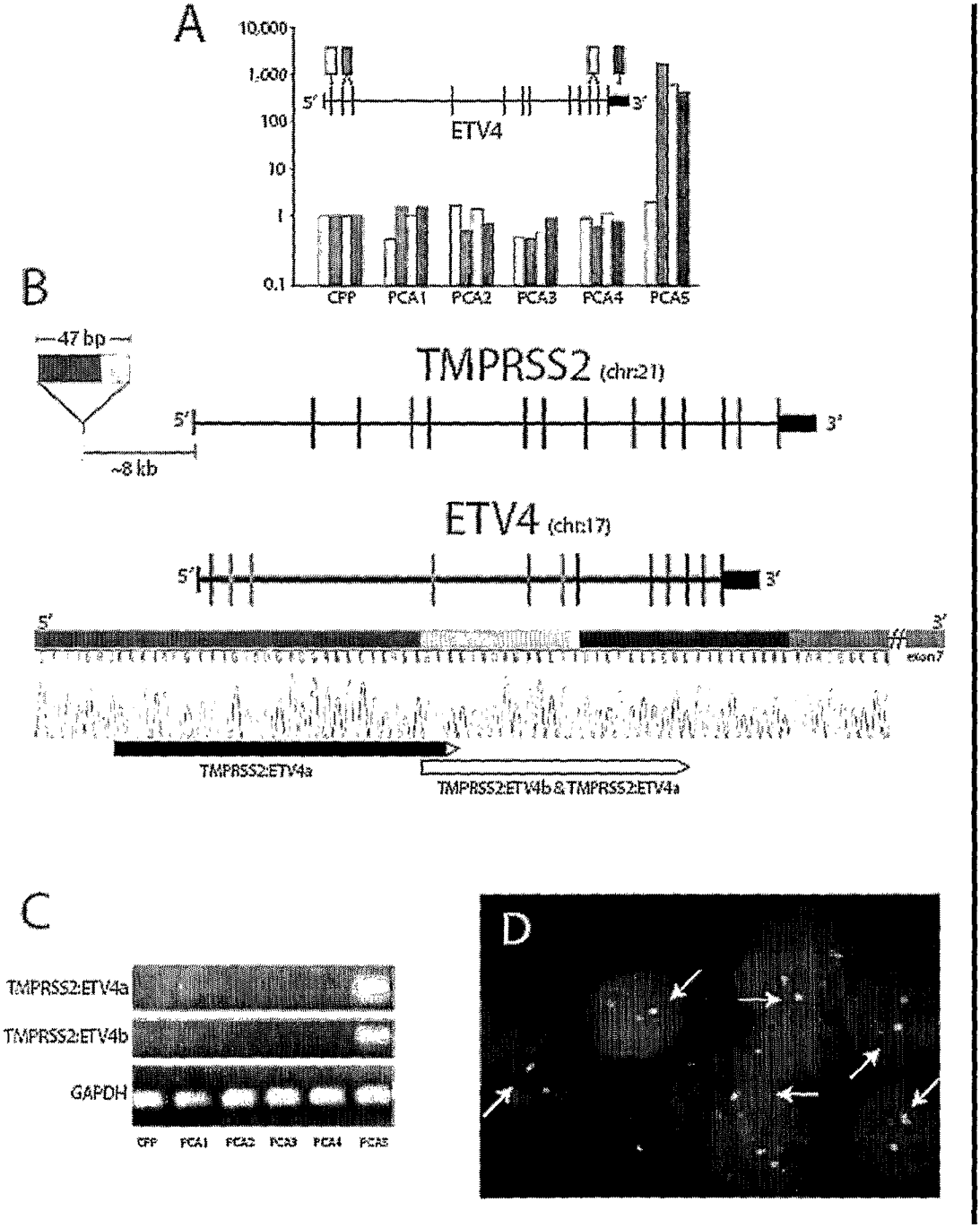

A
10,000
1,000
100
10
1
0.1
5'
3'
ETV4
CPP
PCA1
PCA2
PCA3
PCA4
PCA5
B
47 bp
~8 kb
TMPRSS2 (chr21)
5'
3'
ETV4 (chr17)
5'
3'
5'
3'
exon7
TMPRSS2:ETV4a
TMPRSS2:ETV4b & TMPRSS2:ETV4a
C
TMPRSS2:ETV4a
TMPRSS2:ETV4b
GAPDH
CPP
PCA1
PCA2
PCA3
PCA4
PCA5
D

Figure 9

AP001732 (ERG mRNA) SEQ ID NO:32

1 ccgtcggcgc cgagggagtt agtgcgaccc ggctcggcgc gcacggccaa ggcacgcgcg
61 ctggcacacg cgggcgcgga cacgcgcgga cacacacgtg cgggacacgc cctccccccga
121 cggcggcgct aacctctcgg ttattccagg atctttggag acccgaggaa agccgtgttg
181 accaaaagca agacaaatga ctcacagaga aaaaagatgg cagaaccaag ggcaactaaa
241 gccgtcaggt tctgaacagc tggtagatgg gctggcttac tgaaggacat gattcagact
301 gtcccggacc cagcagctca tatcaag

NM_004956 (ETV1 mRNA) SEQ ID NO:33

1 gttgatagaa gtccagatcc tgaggaaatc tccagctaaa tgctcaaaat ataaaatact
61 gagctgagat ttgcgaagag cagcagcatg gatggatttt atgaccagca agtgccttac
121 atggtcacca atagtcagcg tgggagaaat tgtaacgaga aaccaacaaa tgtcaggaaa
181 agaaaattca ttaacagaga tctggctcat gattcagaag aactctttca agatctaagt
241 caattacagg aaacatggct tgcagaagct caggtacctg acaatgatga gcagtttgta
301 ccagactatc aggctgaaag tttggctttt catggcctgc cactgaaaat caagaaagaa
361 ccccacagtc catgttcaga aatcagctct gcctgcagtc aagaacagcc ctttaaattc
421 agctatggag aaaagtgcct gtacaatgtc agtgcctatg atcagaagcc acaagtggga
481 atgaggccct ccaacccccc cacaccatcc agcacgccag tgtccccact gcatcatgca
541 tctccaaact caactcatac accgaaacct gaccgggcct tcccagctca cctccctcca
601 tcgcagtcca taccagatag cagctacccc atggaccaca gatttcgccg ccagctttct
661 gaaccctgta actcctttcc tcctttgccg acgatgccaa gggaaggacg tcctatgtac
721 caacgccaga tgtctgagcc aaacatcccc ttcccaccac aaggctttaa gcaggagtac
781 cacgacccag tgtatgaaca caacaccatg gttggcagtg cggccagcca aagctttccc
841 cctcctctga tgattaaaca ggaacccaga gattttgcat atgactcaga agtgcctagc
901 tgccactcca tttatatgag gcaagaaggc ttcctggctc atcccagcag aacagaaggc
961 tgtatgtttg aaaagggccc caggcagttt tatgatgaca cctgtgttgt cccagaaaaa
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1081 cgaggatcac ttcagctctg gcagtttttg gtagctcttc tggatgaccc ttcaaattct
1141 cattttattg cctggactgg tcgaggcatg gaatttaaac tgattgagcc tgaagaggtg
1201 gcccgacgtt ggggcattca gaaaaacagg ccagctatga actatgataa acttagccgt
1261 tcactccgct attactatga gaaaggaatt atgcaaaagg tggctggaga gagatatgtc
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1381 ccactgctga agacagacat ggaacgtcac atcaacgagg aggacacagt gcctctttct
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1561 ttttttctgc aagatacaga gaattgctga atctttgttt tatttctgtt gtttgtattt
1621 tatttttaaa taataataca caaaaagggg cttttcctgt tgcattattc tatggtctgc
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1801 ggatggggtc ctacaagttt tgagtatgat gaaactatat catgtctgtt tgatttcata
1861 acaacataag ataatgttta ttttatcggg gtatctatgg tacagttaat ttcacgttgt
1921 gtaaatatcc acttggagac tatttgcctt gggcattttc ccctgtcatt tatgagtctc
1981 tgcaggtgta caaaaaaacc ccaatctact gtaaatggca gtttaattgt tagaaatgac
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2221 ataggccagt agcattacgt gtatctggtg ccaccttgct gtttagatac aaatcatacc
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2581 tgtgttatgt tgataacata tataaatatt agataatgct aatgcttctg ctgctgtctt
2641 ttctgtaata ttctctttca tgctgaattt actatgacca tttataagca gtgcagttaa
2701 ctacagatag catttcagga caaaatagat gactcaaacc atttattgct taaaaaatag

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3961 tatttccaat acagaagggt tgaaaatatt acattataaa ctcttttgaa aaatgtatct
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aaatttaaaa
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agaaggcaaa
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agtactttta
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tcattctaaa
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attaaaatta
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aaatatgctc
6121 aaaatttaaa tctaaaataa aagcccagaa actgaaaa

NM_005238 (ETS1 mRNA) SEQ ID NO:34

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gtccgggcgc
121 gggggaaaga aaggcagcgg gaatttgaga tttttgggaa gaaagtcgga
tttccccgt
181 ccccttcccc ctgttactaa tcctcattaa aaagaaaaac aacagtaact
gcaaacttgc
241 taccatcccg tacgtccccc actcctggca ccatgaaggc ggccgtcgat
ctcaagccga
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ccggatatgg
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caagcattaa
421 aagctacttt cagtggtttc actaaagaac agcaacgact ggggatccca
aaagaccccc
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gaattcagcc
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gccctgggta
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gaacatctag
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ccagcctatc
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gataaatcct
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1981 aactgatgta aggcaattaa tttgcttctg tttttaggtc tgggagggca
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2761 cttttatgtc ttattttcca agagtcctcc atttttgca ccccctcacc
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attaagagag
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NM_016135 (TEL2 (ETV7) mRNA) SEQ ID NO:38

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NM_004454 ERM (ETV5) mRNA SEQ ID NO:39

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1261 agcggccccc actcggacgc cggcagcggg cagctgggga gaaggccgta gccgctgctg
1321 acaagagcgg tggcagtgca ggcgggctgg ctgagggggc aggggcgcta gccccaccgc
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1681 aggctggggg gcccctcacc ccaaggcggg tgagctctga cctccagcat gccacggccc
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2221 cctgccctgc ccctccaggg ggccatgagt gcctaggttt ctcatacccc acaaggtcac

2281 agcaggggag ggagggacaa ttttataatg aaccaaaaat tccatgtgtt
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2401 ccctctccca ctccccaccc cagcaccggt ccaacccctt catccccagc
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2581 tattctgtat tggggactga gggtgggggg agtagagggg ccgctggaga
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NM_003120 (PU.1) SEQ ID NO:43

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301 cccctatctc agcagtgatg gggagagcca tagcgaccat tactgggact
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gtcacccgcc
1141 cctccccca ctccaggccc cctccacatc ccgcttcgcc tccctccagg
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1261 tactgccttg ggagtctcaa gtccgtatgt aaatcagatc tcccctctca cccctcccac
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NM_001973 (ELK4, transcript variant a, mRNA) SEQ ID NO:44

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301 gtagagccac gaatggattt ctggtcgctg cctccatcgt cagggcaagc ttttcccacg
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1441 gatactatta tgtaaagaat atcatcaaaa aagtgaatgg tcagaagttt gtgtacaagt
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2281 tgagcccatc tctccctaca gcttctctta caccagcatt tttttcacag acacccatca
2341 tactgactcc aagccccttg ctctccagta tccacttctg gagtactctc agtcctgttg
2401 ctcccctaag tccagccaga ctgcaaggtg ctaacacact tttccagttt ccttctgtac
2461 tgaacagtca tgggccattc actctgtctg ggctggatgg accttccacc cctggcccat
2521 tttccccaga cctacagaag acataaccta tgcacttgtg gaatgagaga accgaggaac
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2641 tgataataga ctattgtgat ttttgccatt ccccattgaa aacatctttt taggattctc
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2881 caaaagcaat taagaacaaa gttactcctt ctggctattg ggacccttg gccaggaaaa
2941 attatgctta gaatctatta tttaaagaaa tatttgtgaa atgaaaaaaa aaaaaaaaaa
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NM_021795 (ELK4, transcript variant b, mRNA) SEQ ID NO:45

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241 tataaatgat gactgtttta gagaggttaa ggttgcttaa aattggtgag ttagtgaggg
301 gtagagccac gaatggattt ctggtcgctg cctccatcgt cagggcaagc ttttcccacg
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421 tatcaagcgt ttgtagtgtc ctgggatctg gcacttcgat gagaaagctg tgacggcccc
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NM_005240 (METS(ETV3)) SEQ ID NO:46

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1441 aaa

S72620 (EWS/Fli1) SEQ ID NO:47

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BC029743 (ESE2 (ELF5)) SEQ ID NO:48

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NM_012153 (ESE3) SEQ ID NO:49

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NM_006874 (NERF; ELF2) transcript variant 2 SEQ ID NO:52

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NM_ 201999 (NERF; ELF2) transcript variant 1 SEQ ID NO:53

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2881 ggtagctcta atacctggag ttttctttgt ttttttttct ttttttagt tgaagtttat
2941 gagggaaata ccagtgttca gttttgaact ataatagttt gtatattcaa catttgaagt
3001 atattctatt ttgttgtact cttgtttcaa agtgtattca agtaggtttt ctgaaatata
3061 gaaatgaaat ttatcttctg ttttggtctc tggtgatatt ttaaacaata tttaaaagtc
3121 agtatagaag tgttttagtt aggaagtgat aaaacatctc tcttctcctt cccaactact
3181 gcatgaagaa attctacttc cattatatta atatttgg

NM_017521 (FEV) SEQ ID NO:54

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1 gcggcgagtg gagcgggagc cgactggaag aagggctcta gggaggggc tgtggctgct
       61 ggggtccgag gtggggccgg gtacaccagc cccatcactg tttgcagaga
gtcagggagg
      121 cggaaaagac acgcgctcta ggctcccatc agggcacatg gcccgggccc
atcccccgcg
      181 cgtctccccg gctgcggggc gcgggggct gccgggtgcg cttggctgtg
gcgcggcgcg
      241 ttggagactt tattgcgatg ggacgataag aggggcgggg gcggggtcct
gggggccgag
      301 gcggcagcgc tttaattaaa acggaaattg cggccccggg ccgcgcgggg
gccggagggt
      361 tccaagcggc cccttagctg gaagcgtttc tccaggaccc ccccgcaacc
cccgccacgc
      421 ccgggctgcc ccctcccgcc aggccctgcc ggacccggcg ccgtcttctc
ctccttgtca
      481 cccgcggtcg cttcgggcgg ggatcggtgc caccgagcgc aaagcctgcc
tcgccccct
      541 tccccgtccc ccccatctcc caccgcccag tccccggcgg cgatgagaca
gagcggcgcc
      601 tcccagcccc tgctgatcaa catgtacctg ccagatcccg tcggagacgg
tctcttcaag
      661 gacgggaaga acccgagctg ggggccgctg agccccgcgg ttcagaaagg
cagcggacag
      721 atccagctgt ggcagtttct gctggagctg ctggctgacc gcgcgaacgc
cggctgcatc
      781 gcgtgggagg gcggtcacgg cgagttcaag ctcacggacc cggacgaggt
ggcgcggcgg
      841 tggggcgagc gcaagagcaa gcccaacatg aactacgaca agctgagccg
cgccctgcgc
      901 tactactacg acaagaacat catgagcaag gtgcatggca agcgctacgc
ctaccgcttc
      961 gacttccagg gcctggcgca ggcctgccag ccgccgcccg cgcacgctca
tgccgccgcc
     1021 gcagctgctg ccgccgccgc ggccgcccag gacggcgcgc tctacaagct
gcccgccggc
     1081 ctcgccccgc tgcccttccc cggcctctcc aaactcaacc tcatggccgc
ctcggccggg
     1141 gtcgcgcccg ccggcttctc ctactggccg ggcccgggcc ccgccgccac
cgctgccgcc
     1201 gccaccgccg cgctctaccc cagtcccagc ttgcagcccc cgcccgggcc
cttcggggcc
     1261 gtggccgcag cctcgcactt ggggggccat taccactaga cggggcggtc
gggtgcctgc
     1321 ggcctcgccc gcacgcctag agtctcgccc gatcccatcg gcatcccggg
gagggcccgg
     1381 gagcctccgt caaccgtcct ctaatccaga gtttactcca cctgccgcac
ttagcagggg
     1441 gacgggaccg aagctccctc aatccttgtc tggtactaga tttgctcctg
tcccaccccg
     1501 cagtcccctg aggagggcga tgtgcgccct ctttcacttt ttttcttcta
ggtctccagg
     1561 tcccggaggg gatttgtgga cctctcttgt ctccccacca ctccagtgca
tttccgcctg
```

1621 gctcctagaa gccccattca atatcactac tctttaacga gtgccaaatc ttttcccact
1681 tttgctcttc cccaaggaac tgctcccacc tcagcacgtg gaggcctctc acggtcctcc
1741 ttcctgggac ctgagcaggt ttggtgaaag ccaccgtcct ccgtgacaca cggccccctt
1801 cctcctgtcc ccacactccc aggagaaact cccggtgtgt ttctgaccct ttcagcccca
1861 ttaaagctcc tgagctctca aaaaaaaaaa aaaaaaaaaa a

Figure 10

NM_005656 mRNA (SEQ ID NO: 54)

1 cgcgagctaa gcaggaggcg gaggcggagg cggagggcga ggggcgggga gcgccgcctg
61 gagcgcggca ggtcatattg aacattccag atacctatca ttactcgatg
ctgttgataa
121 cagcaagatg gctttgaact cagggtcacc accagctatt ggaccttact
atgaaaacca
181 tggataccaa ccggaaaacc cctatcccgc acagcccact gtggtcccca
ctgtctacga
241 ggtgcatccg gctcagtact acccgtcccc cgtgccccag tacgccccga
gggtcctgac
301 gcaggcttcc aaccccgtcg tctgcacgca gcccaaatcc ccatccggga
cagtgtgcac
361 ctcaaagact aagaaagcac tgtgcatcac cttgaccctg gggaccttcc
tcgtgggagc
421 tgcgctggcc gctggcctac tctggaagtt catgggcagc aagtgctcca
actctgggat
481 agagtgcgac tcctcaggta cctgcatcaa cccctctaac tggtgtgatg
gcgtgtcaca
541 ctgccccggc ggggaggacg agaatcggtg tgttcgcctc tacggaccaa
acttcatcct
601 tcagatgtac tcatctcaga ggaagtcctg gcaccctgtg tgccaagacg
actggaacga
661 gaactacggg cgggcggcct gcagggacat gggctataag aataattttt
actctagcca
721 aggaatagtg gatgacagcg gatccaccag ctttatgaaa ctgaacacaa
gtgccggcaa
781 tgtcgatatc tataaaaaac tgtaccacag tgatgcctgt tcttcaaaag
cagtggtttc
841 tttacgctgt atagcctgcg gggtcaactt gaactcaagc cgccagagca
ggatcgtggg
901 cggtgagagc gcgctcccgg gggcctggcc ctggcaggtc agcctgcacg
tccagaacgt
961 ccacgtgtgc ggaggctcca tcatcacccc cgagtggatc gtgacagccg
cccactgcgt
1021 ggaaaaacct cttaacaatc catggcattg gacggcattt gcggggattt
tgagacaatc
1081 tttcatgttc tatggagccg gataccaagt agaaaaagtg atttctcatc
caaattatga
1141 ctccaagacc aagaacaatg acattgcgct gatgaagctg cagaagcctc
tgactttcaa
1201 cgacctagtg aaaccagtgt gtctgcccaa cccaggcatg atgctgcagc
cagaacagct
1261 ctgctggatt tccgggtggg gggccaccga ggagaaaggg aagacctcag
aagtgctgaa
1321 cgctgccaag gtgcttctca ttgagacaca gagatgcaac agcagatatg
tctatgacaa
1381 cctgatcaca ccagccatga tctgtgccgg cttcctgcag gggaacgtcg
attcttgcca
1441 gggtgacagt ggagggcctc tggtcacttc gaagaacaat atctggtggc
tgatagggga
1501 tacaagctgg ggttctggct gtgccaaagc ttacagacca ggagtgtacg
ggaatgtgat

1561 ggtattcacg gactggattt atcgacaaat gagggcagac ggctaatcca catggtcttc
1621 gtccttgacg tcgttttaca agaaaacaat ggggctggtt ttgcttcccc gtgcatgatt
1681 tactcttaga gatgattcag aggtcacttc atttttatta aacagtgaac ttgtctggct
1741 ttggcactct ctgccattct gtgcaggctg cagtggctcc cctgcccagc ctgctctccc
1801 taacccctttg tccgcaaggg gtgatggccg gctggttgtg ggcactggcg gtcaagtgtg
1861 gaggagaggg gtggaggctg ccccattgag atcttcctgc tgagtccttt ccaggggcca
1921 attttggatg agcatggagc tgtcacctct cagctgctgg atgacttgag atgaaaaagg
1981 agagacatgg aaagggagac agccaggtgg cacctgcagc ggctgccctc tggggccact
2041 tggtagtgtc cccagcctac ctctccacaa ggggattttg ctgatgggtt cttagagcct
2101 tagcagccct ggatggtggc cagaaataaa gggaccagcc cttcatgggt ggtgacgtgg
2161 tagtcacttg taaggggaac agaaacattt ttgttcttat ggggtgagaa tatagacagt
2221 gcccttggtg cgagggaagc aattgaaaag gaacttgccc tgagcactcc tggtgcaggt
2281 ctccacctgc acattgggtg gggctcctgg gagggagact cagccttcct cctcatcctc
2341 cctgaccctg ctcctagcac cctggagagt gcacatgccc cttggtcctg gcagggcgcc
2401 aagtctggca ccatgttggc ctcttcaggc ctgctagtca ctggaaattg aggtccatgg
2461 gggaaatcaa ggatgctcag tttaaggtac actgtttcca tgttatgttt ctacacattg
2521 ctacctcagt gctcctggaa acttagcttt tgatgtctcc aagtagtcca ccttcattta
2581 actctttgaa actgtatcac ctttgccaag taagagtggt ggcctatttc agctgctttg
2641 acaaaatgac tggctcctga cttaacgttc tataaatgaa tgtgctgaag caaagtgccc
2701 atggtggcgg cgaagaagag aaagatgtgt tttgttttgg actctctgtg gtcccttcca
2761 atgctgtggg tttccaacca ggggaagggt ccctttttgca ttgccaagtg ccataaccat
2821 gagcactact ctaccatggt tctgcctcct ggccaagcag gctggtttgc aagaatgaaa
2881 tgaatgattc tacagctagg acttaacctt gaaatggaaa gtcttgcaat cccatttgca
2941 ggatccgtct gtgcacatgc ctctgtagag agcagcattc ccagggacct tggaaacagt
3001 tggcactgta aggtgcttgc tccccaagac acatcctaaa aggtgttgta atggtgaaaa
3061 cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca actgtttgtc ttttttttgta
3121 tctttttttaa actgtaaagt tcaattgtga aaatgaatat catgcaaata aattatgcga
3181 ttttttttttc aaagcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa

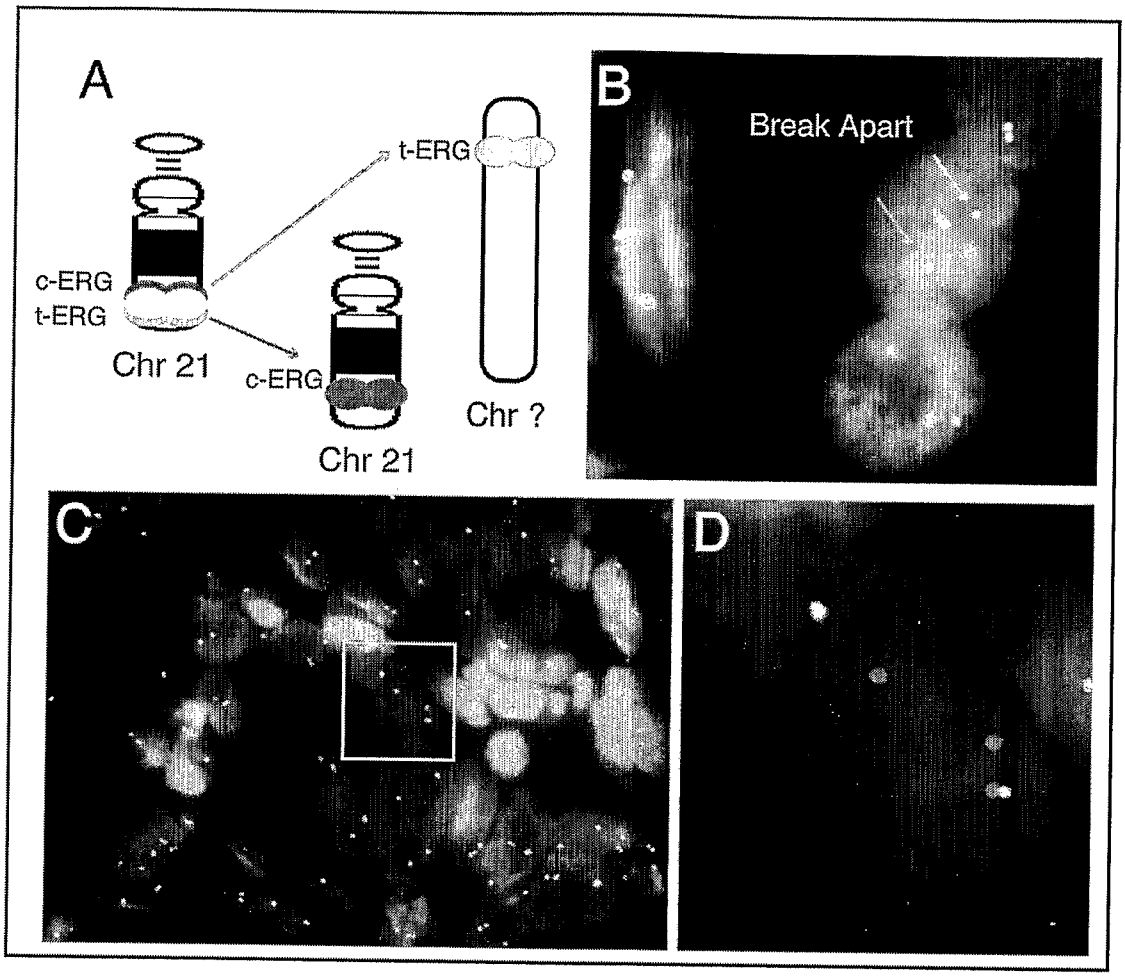


Figure 11

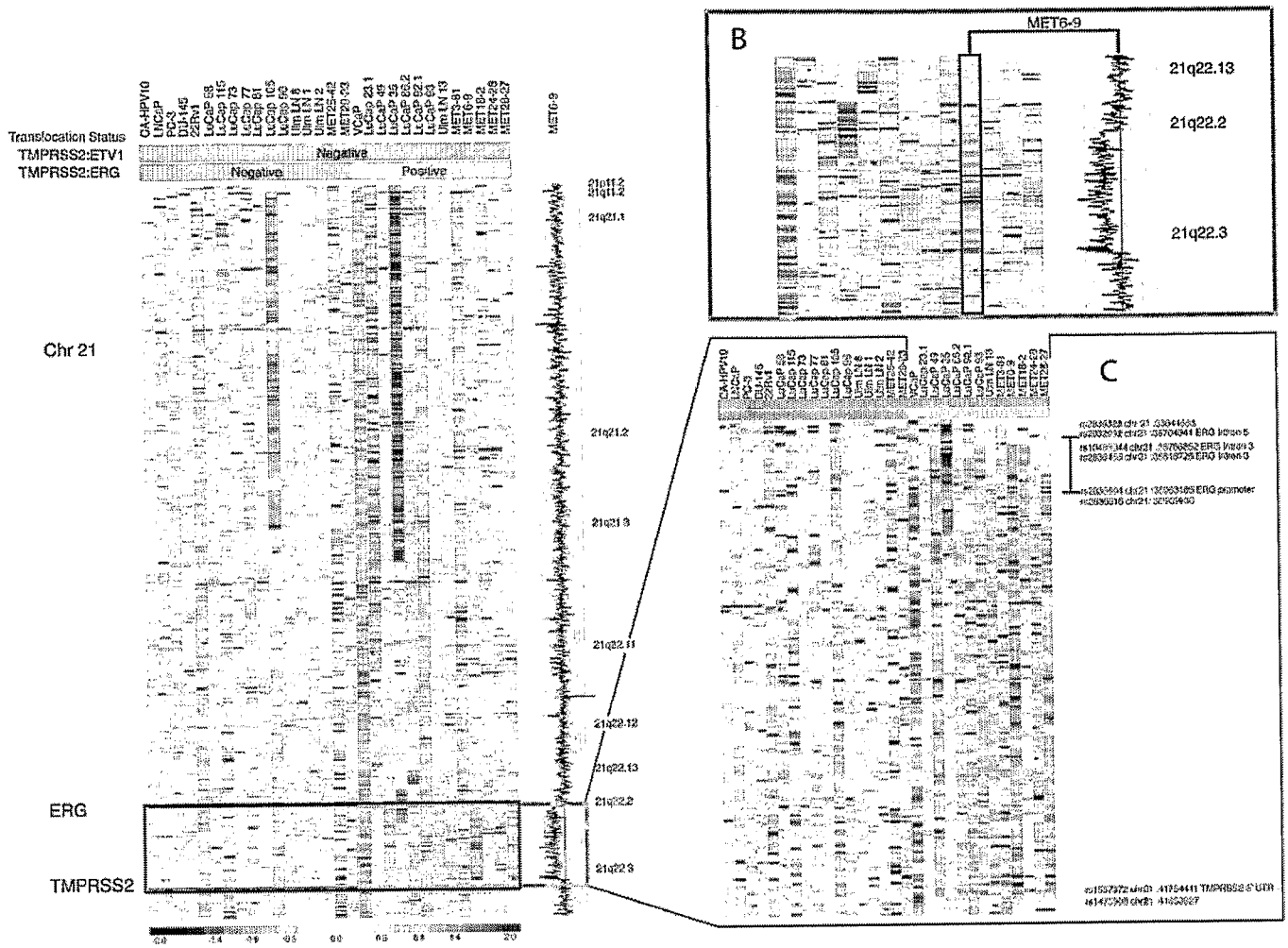

Translocation Status
TMPRSS2:ETV1
TMPRSS2:ERG
Negative
Negative
Positive
Chr 21
ERG
TMPRSS2
MET6-9
21q11.2
21q21.1
21q21.2
21q21.3
21q22.11
21q22.12
21q22.13
21q22.2
21q22.3
B
MET6-9
21q22.13
21q22.2
21q22.3
C

Figure 12

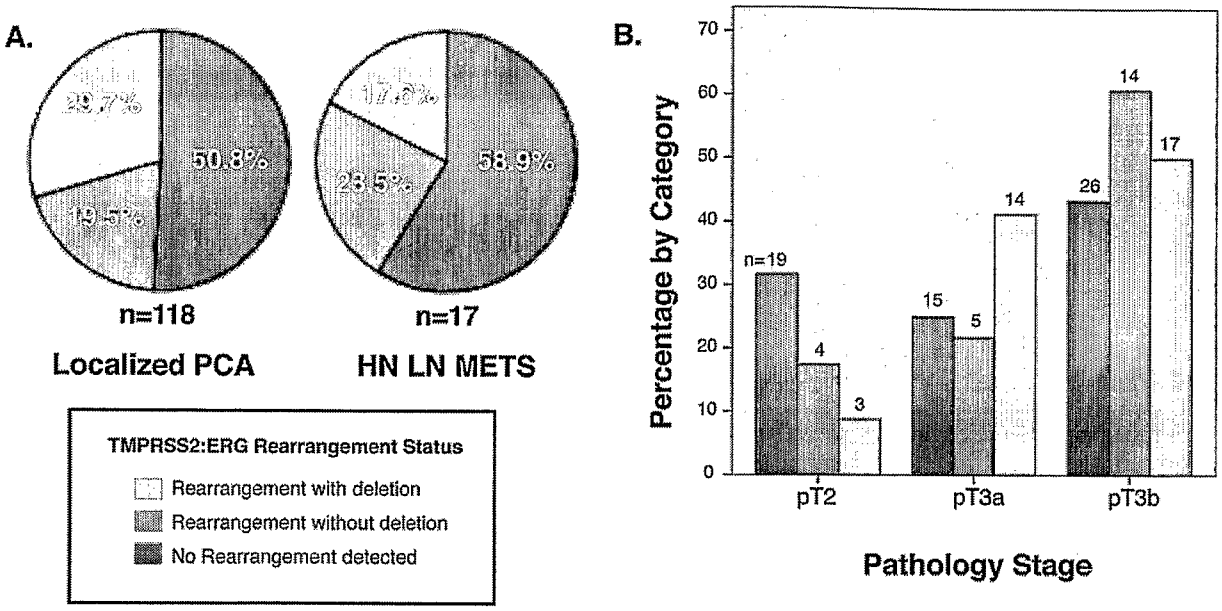

A.
29.7%
50.8%
19.5%
n=118
Localized PCA
17.6%
23.5%
58.9%
n=17
HN LN METS
TMPRSS2:ERG Rearrangement Status
Rearrangement with deletion
Rearrangement without deletion
No Rearrangement detected
B.
Percentage by Category
70
60
50
40
30
20
10
0
n=19
4
3
15
5
14
26
14
17
pT2
pT3a
pT3b
Pathology Stage

Figure 13

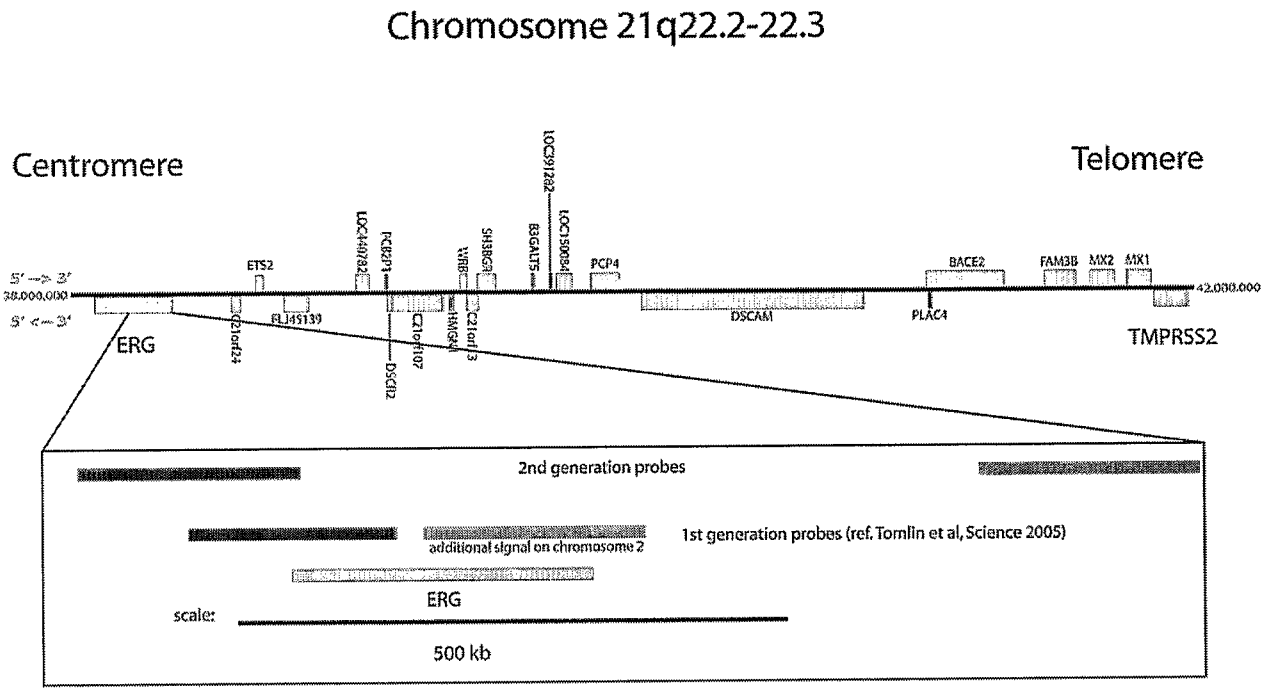

Chromosome 21q22.2-22.3
Centromere
Telomere
5' -> 3'
38,000,000
5' <- 3'
ETS2
LOC340782
PCBP3
LOC391282
LOC150084
SH3BGR
BACE2
FAM3B
MX2
MX1
PCP4
DSCAM
PLAC4
42,000,000
TMPRSS2
ERG
C21orf24
FLJ45139
DSCR2
C21orf107
C21orf13
2nd generation probes
1st generation probes (ref. Tomlin et al, Science 2005)
additional signal on chromosome 2
ERG
scale:
500 kb

Figure 14

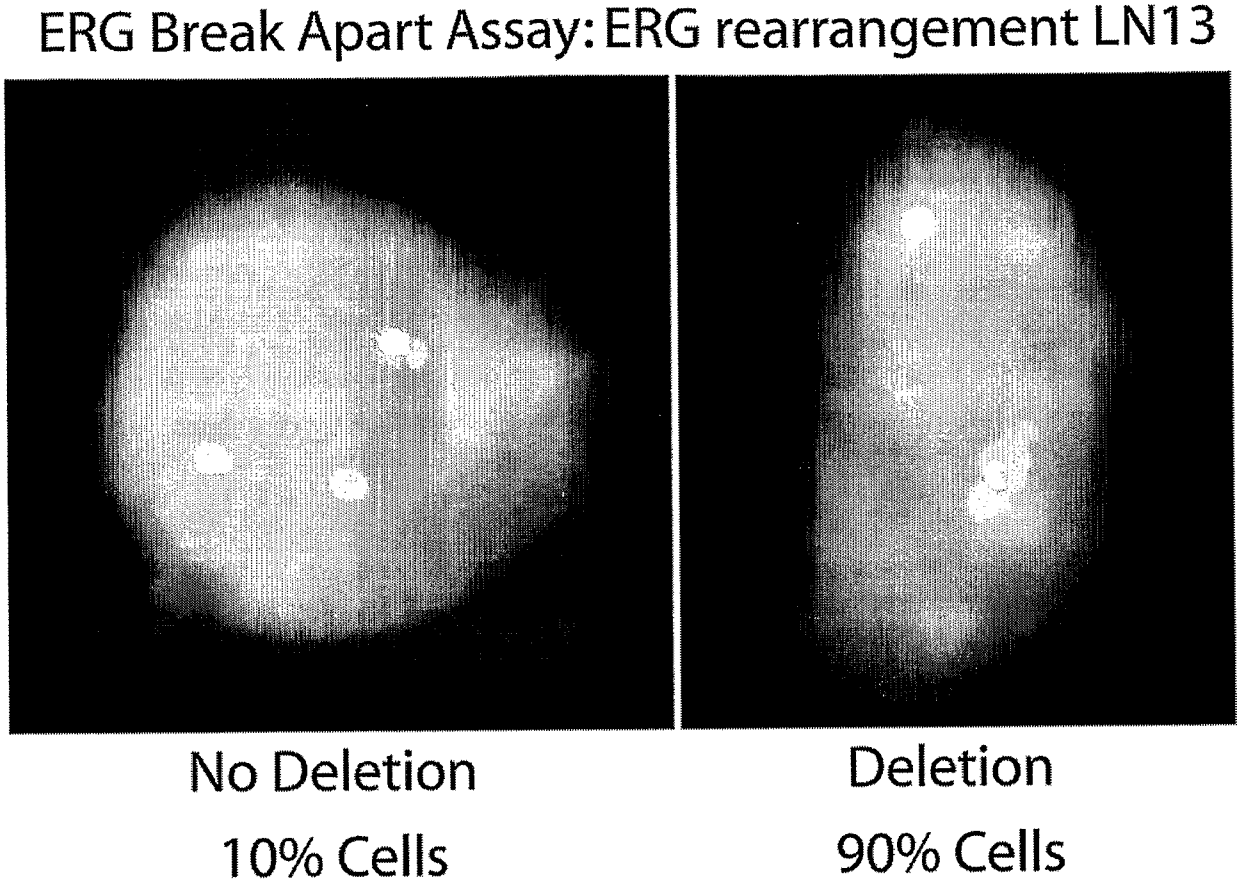

ERG Break Apart Assay: ERG rearrangement LN13
No Deletion
10% Cells
Deletion
90% Cells

Figure 15

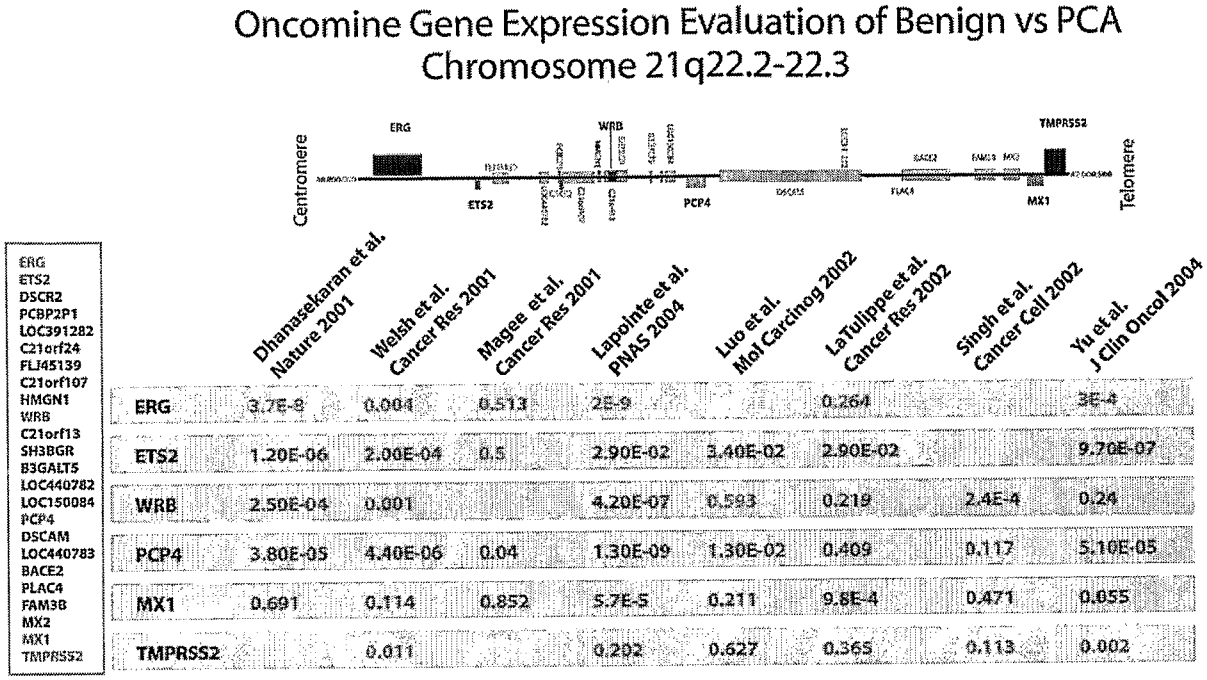

Oncomine Gene Expression Evaluation of Benign vs PCA
Chromosome 21q22.2-22.3
Centromere
ERG
ETS2
WRB
PCP4
TMPRSS2
MX1
Telomere
ERG
ETS2
DSCR2
PCBP2P1
LOC391282
C21orf24
FLJ45139
C21orf107
HMGN1
WRB
C21orf13
SH3BGR
B3GALT5
LOC440782
LOC150084
PCP4
DSCAM
LOC440783
BACE2
PLAC4
FAM3B
MX2
MX1
TMPRSS2
Dhanasekaran et al. Nature 2001
Welsh et al. Cancer Res 2001
Magee et al. Cancer Res 2001
Lapointe et al. PNAS 2004
Luo et al. Mol Carcinog 2002
LaTulippe et al. Cancer Res 2002
Singh et al. Cancer Cell 2002
Yu et al. J Clin Oncol 2004
ERG 3.7E-9 0.004 0.513 2E-9 0.264 3E-4
ETS2 1.20E-06 2.00E-04 0.5 2.90E-02 3.40E-02 2.90E-02 9.70E-07
WRB 2.50E-04 0.001 4.20E-07 0.593 0.219 2.4E-4 0.24
PCP4 3.80E-05 4.40E-06 0.04 1.30E-09 1.30E-02 0.409 0.117 5.10E-05
MX1 0.691 0.114 0.852 5.7E-5 0.211 9.8E-4 0.471 0.055
TMPRSS2 0.011 0.202 0.627 0.365 0.113 0.002

Figure 16

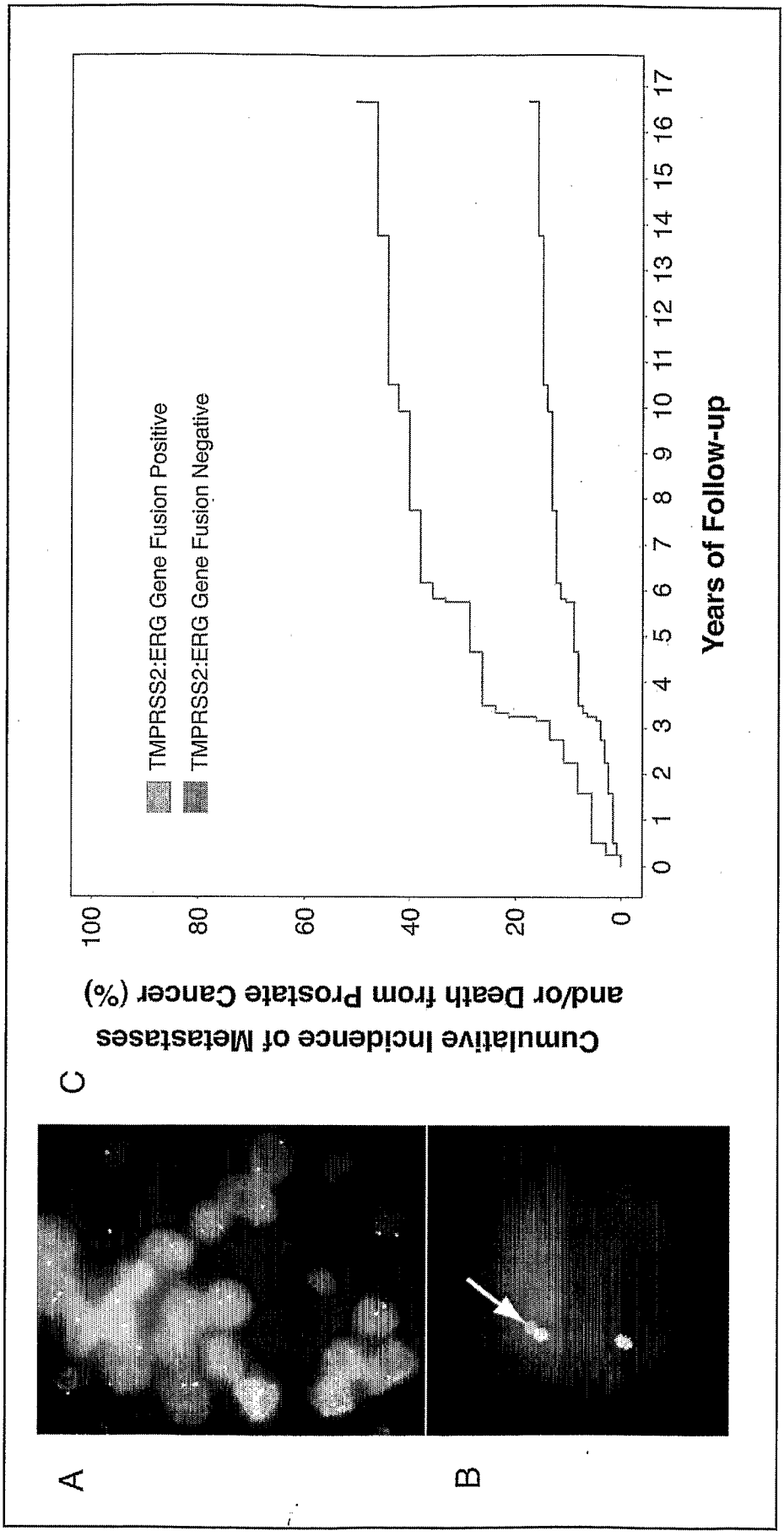

A
B
C
Cumulative Incidence of Metastases and/or Death from Prostate Cancer (%)
0
20
40
60
80
100
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
Years of Follow-up
TMPRSS2:ERG Gene Fusion Positive
TMPRSS2:ERG Gene Fusion Negative

Figure 17

Figure 18
FLI1 overexpression without fusion transcript

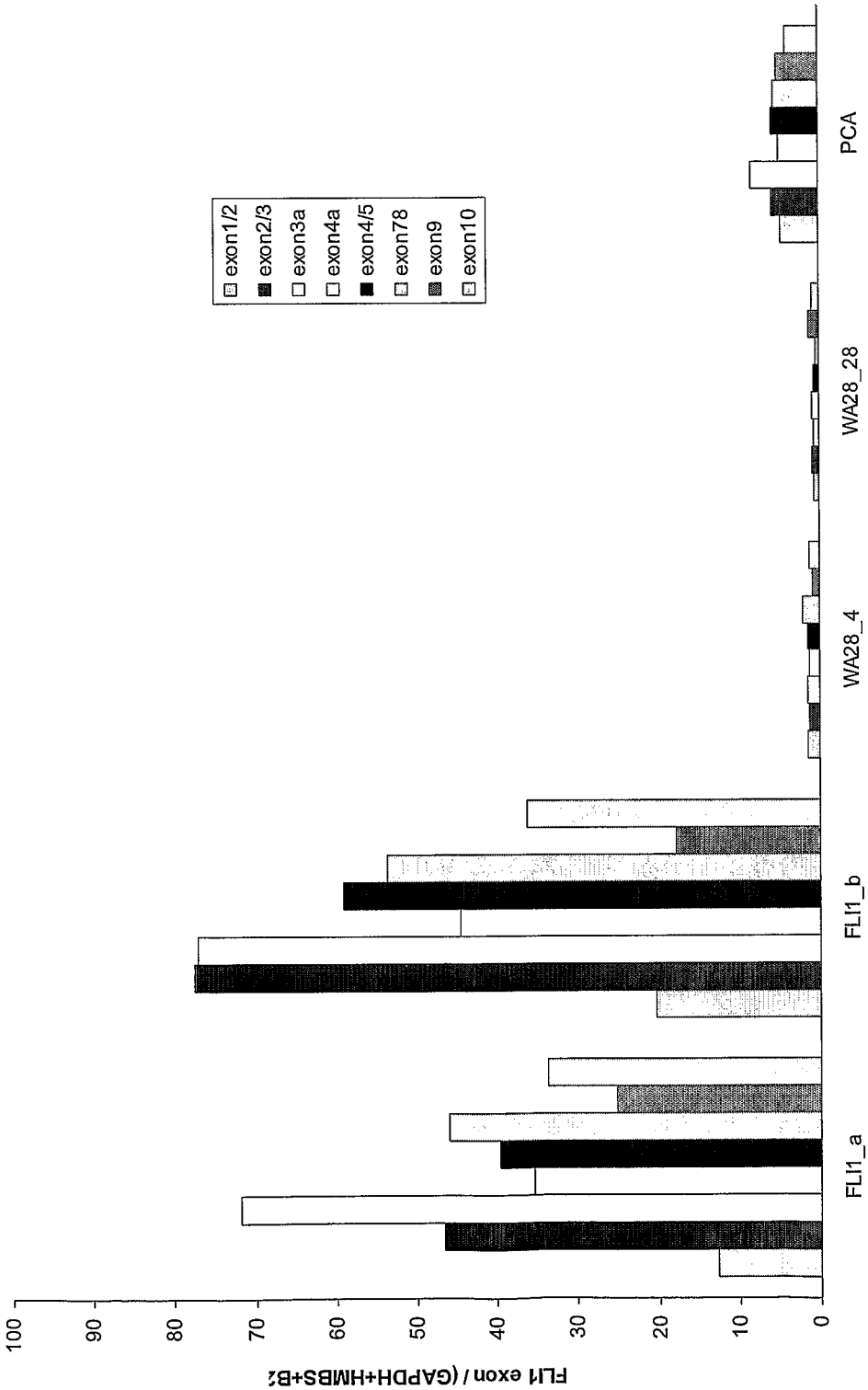


Figure 19
Induction of ERG protein by Androgen in TMPRSS2-ERG+ Cells

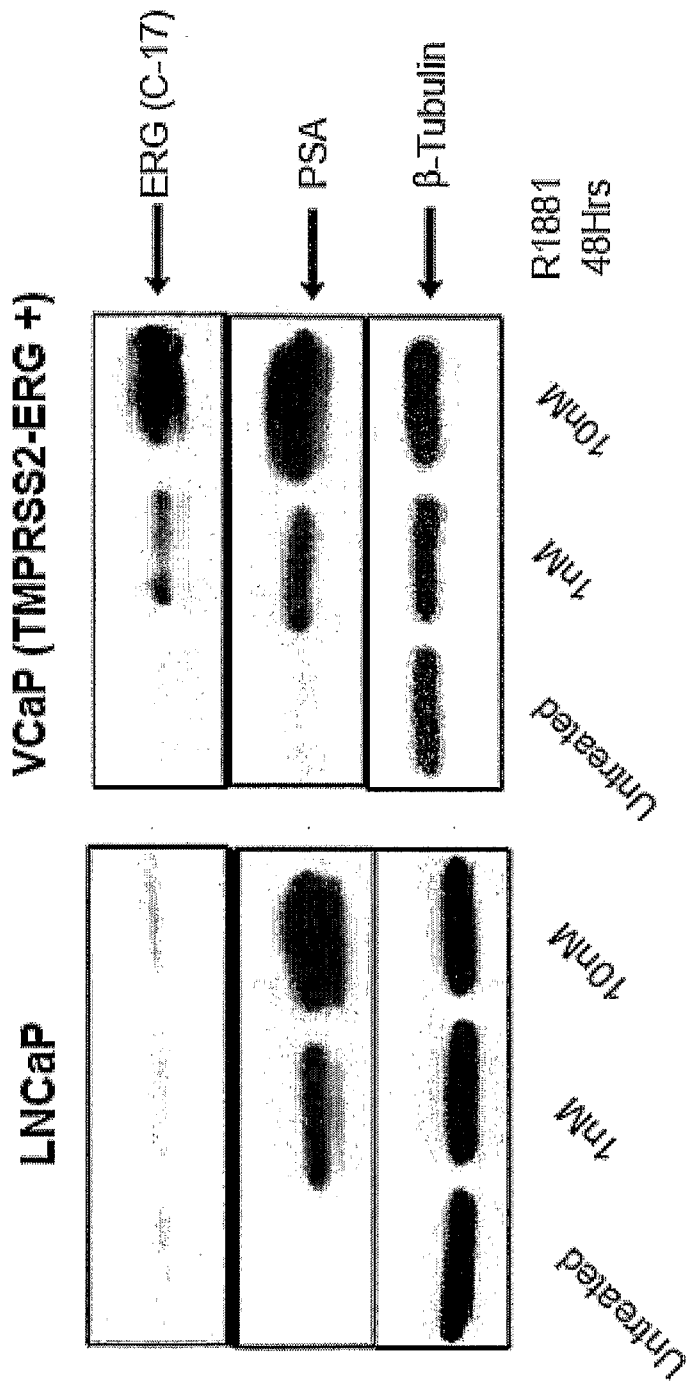
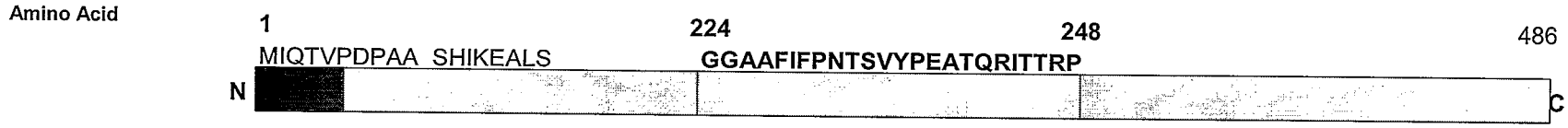
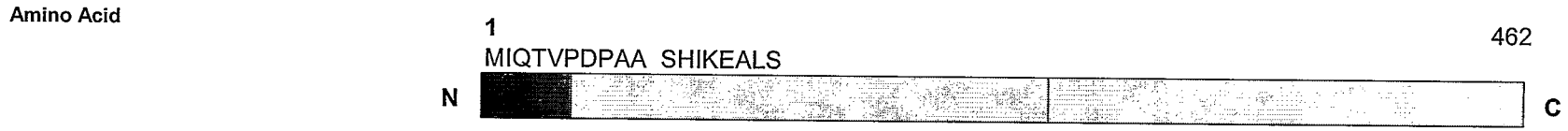


Figure 20

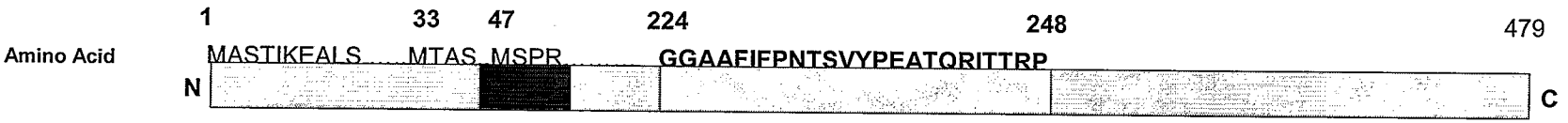
Endogenous ERG1



Endogenous ERG2



ERG1 Fusion Product



ERG2 Fusion Product

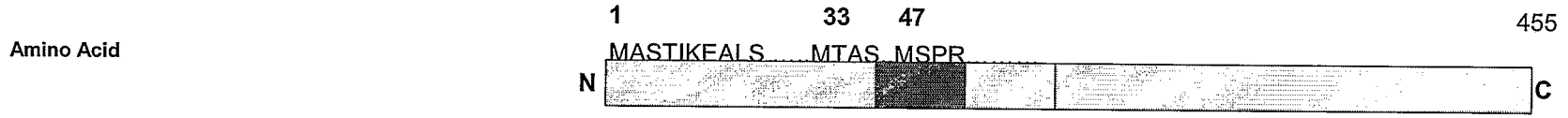


Figure 21
Nuclear Interactors for ERG2 (Mass spec and Protein Arrays)

PRP8 pre-mRNA processing factor 8 homolog (yeast)	PRPF8
T-box, brain, 1	TBR1
EBNA1 binding protein 2	EBNA1BP2
V-ets erythroblastosis virus E26 oncogene like (avian)	ERG
Fibrillarin	FBL
Exosome component 7	EXOSC7
Friend leukemia virus integration 1	FLI1
Nuclear mitotic apparatus protein 1	NUMA1
Poly(rC) binding protein 1	PCBP1
Small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	SNRP70
Lectin, galactoside-binding, soluble, 3 (galectin 3)	LGALS3
RNA binding motif protein 23	RBM23
TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	TAF6
Zinc finger protein 306	ZNF306
Ras association (RalGDS/AF-6) domain family 5	RASSF5
Calcium/calmodulin-dependent protein kinase I	CAMK1

Figure 22

ERG 1

```
MASTIKEALS VVSEDQSLFE CAYGTPHLAK TEMTASSSSD      40
YGQTSKMSPR VPQQDWLSQP PARVTIKMEC NPSQVNGSRN      80
SPDECSVAKG GKMVGSPDTV GMNYGSYMEE KHMPPPNMTT     120
NERRVIVPAD PTLWSTDHVR QWLEWAVKEY GLPDVNILLF     160
QNIDGKELCK MTKDDFQRLT PSYNADILLS HLHYLRETPL     200
PHLTSDDVDK ALQNSPRLMH ARNTGGAAFI FPNTSVYPEA     240
                          GAAFI FPNTSVYP
TQRITTRPDL PYEPPRRSAW TGHGHPTPQS KAAQPSPSTV     280
PKTEDQRPQL DPYQILGPTS SRLANPGSGQ IQLWQFLLEL     320
LSDSSNSSCI TWEGTNGEFK MTDPDEVARR WGERKSKPNM     360
NYDKLSRALR YYYDKNIMTK VHGKRYAYKF DFHGIAQALQ     400
PHPPESSLYK YPSDLPYMGS YHAHPQKMNF VAPHPPALPV     440
TSSSFFAAPN PYWNSPTGGI YPNTRLPTSH MPSHLGTYY      479
```

Figure 23

ETV1 (NCBI)

```
    MDGFYDQQVP YMVTNSQRGR NCNEKPTNVR KRKFINRDLA HDSEELFQDL SQLQETWLAE
 61 AQVPDNDEQF VPDYQAESLA FHGLPLKIKK EPHSPCSEIS SACSQEQPFK FSYGEKCLYN
                                    PHSPCSEIS SACSQ
121 VSAYDQKPQV GMRPSNPPTP SSTPVSPLHH ASPNSTHTPK PDRAFPAHLP PSQSIPDSSY
                         TP SSTPVSPLHH A              RAFPAHLP PSQSIPDS
181 PMDHRFRRQL SEPCNSFPPL PTMPREGRPM YQRQMSEPNI PFPPQGFKQE YHDPVYEHNT
241 MVGSAASQSF PPPLMIKQEP RDFAYDSEVP SCHSIYMRQE GFLAHPSRTE GCMFEKGPRQ
301 FYDDTCVVPE KFDGDIKQEP GMYREGPTYQ RRGSLQLWQF LVALLDDPSN SHFIAWTGRG
361 MEFKLIEPEE VARRWGIQKN RPAMNYDKLS RSLRYYYEKG IMQKVAGERY VYKFVCDPEA
421 LFSMAFPDNQ RPLLKTDMER HINEEDTVPL SHFDESMAYM PEGGCCNPHP YNEGYVY
```

Figure 24

FLI-1 (NCBI)

```
  1 MDGTIKEALS VVSDDQSLFD SAYGAAAHLP KADMTASGSP DYGQPHKINP LPPQQEWINQ
                    SLFD SAYGAAAHLP                    HKINP LPPQ   INQ
 61 PVRVNVKREY DHMNGSRESP VDCSVSKCSK LVGGGESNPM NYNSYMDEKN GPPPPNMTTN
    PVRVNV          RESP VDCSVSKCSK LVG
121 ERRVIVPADP TLWTQEHVRQ WLEWAIKEYS LMEIDTSFFQ NMDGKELCKM NKEDFLRATT
                   TQEHVRQ
181 LYNTEVLLSH LSYLRESSLL AYNTTSHTDQ SSRLSVKEDP SYDSVRRGAW GNNMNSGLNK
                                      SSRLSVKE
241 SPPLGGAQTI SKNTEQRPQP DPYQILGPTS SRLANPGSGQ IQLWQFLLEL LSDSANASCI
301 TWEGTNGEFK MTDPDEVARR WGERKSKPNM NYDKLSRALR YYYDKNIMTK VHGKRYAYKF
361 DFHGIAQALQ PHPTESSMYK YPSDISYMPS YHAHQQKVNF VPPHPSSMPV TSSSFFGAAS
421 QYWTSPTGGI YPNPNVPRHP NTHVPSHLGS YY
                         P NTHVPSHL
```

Figure 25

ETV-4 (NCBI)

```
       1 MERRMKAGYL DQQVPYTFSS KSPGNGSLRE ALIGPLGKLM DPGSLPPLDS EDLFQDLSHF
                 GYL DQQVPYTFS         LRE ALIGPLGK                 LFQDLSH
      61 QETWLAEAQV PDSDEQFVPD FHSENLAFHS PTTRIKKEPQ SPRTDPALSC SRKPPLPYHH
                                 SENLAFH                 TDPALSC SRKPPLPYHH
     121 GEQCLYSSAY DPPRQIAIKS PAPGALGQSP LQPFPRAEQR NFLRSSGTSQ PHPGHGYLGE
         GEQCLYSSAY DPPRQIAIKS PAPGALGQSP LQPFP               SQ PHPGH YLGE
     181 HSSVFQQPLD ICHSFTSQGG GREPLPAPYQ HQLSEPCPPY PQQSFKQEYH DPLYEQAGQP
         HSSVFQQPLD ICHSF         EPLPAPYQ HQLSEPCPPY PQQ      YH DPLYEQ GQP
     241 AVDQGGVNGH RYPGAGVVIK QEQTDFAYDS DVTGCASMYL HTEGFSGPSP GDGAMGYGYE
         AVDQ        RYPGAGVVIK         YDS DVTGCASMY                   YE
     301 KPLRPFPDDV CVVPEKFEGD IKQEGVGAFR EGPPYQRRGA LQLWQFLVAL LDDPTNAHFI
         KPLRPFPDDV CVVPE
     361 AWTGRGMEFK LIEPEEVARL WGIQKNRPAM NYDKLSRSLR YYYEKGIMQK VAGERYVYKF
     421 VCEPEALFSL AFPDNQRPAL KAEFDRPVSE EDTVPLSHLD ESPAYLPELA GPAQPFGPKG
     481 GYSY
```

Figure 26

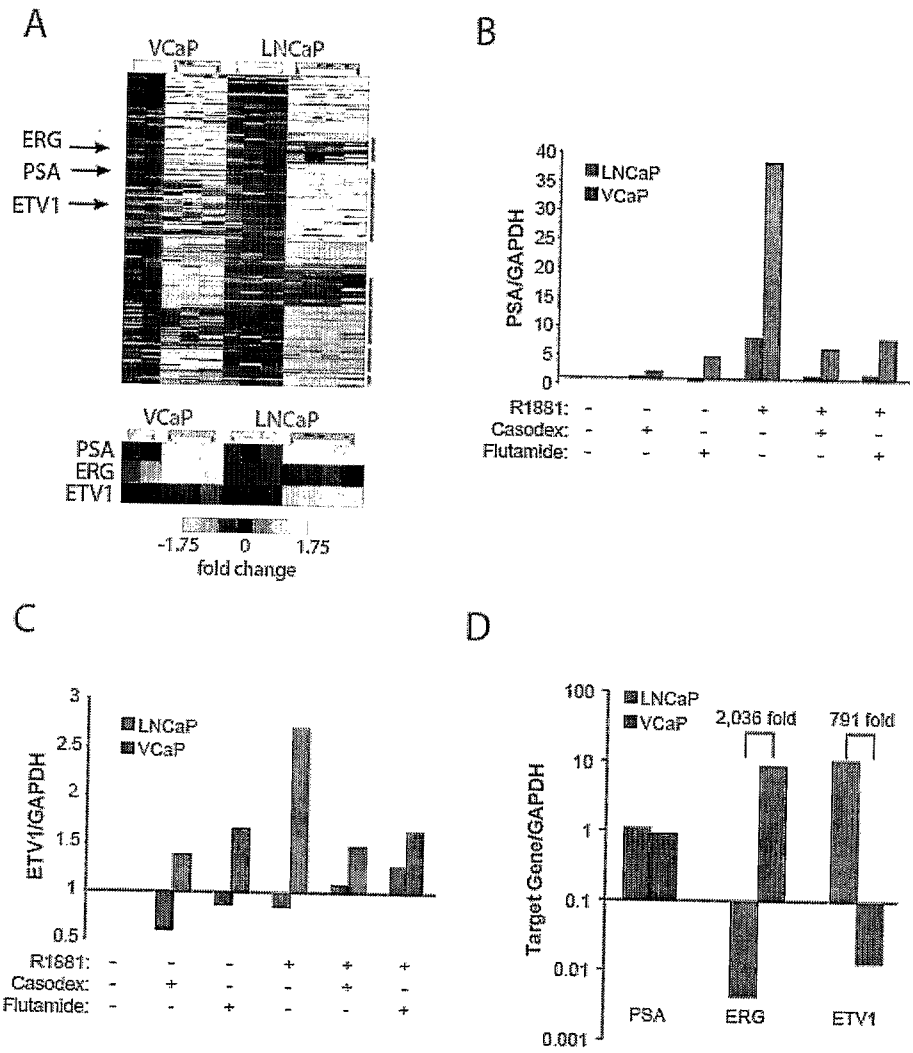

A
VCaP
LNCaP
ERG
PSA
ETV1
VCaP
LNCaP
PSA
ERG
ETV1
-1.75
0
1.75
fold change
B
LNCaP
VCaP
PSA/GAPDH
R1881:
Casodex:
Flutamide:
C
LNCaP
VCaP
ETV1/GAPDH
R1881:
Casodex:
Flutamide:
D
LNCaP
VCaP
2,036 fold
791 fold
Target Gene/GAPDH
PSA
ERG
ETV1

Figure 27

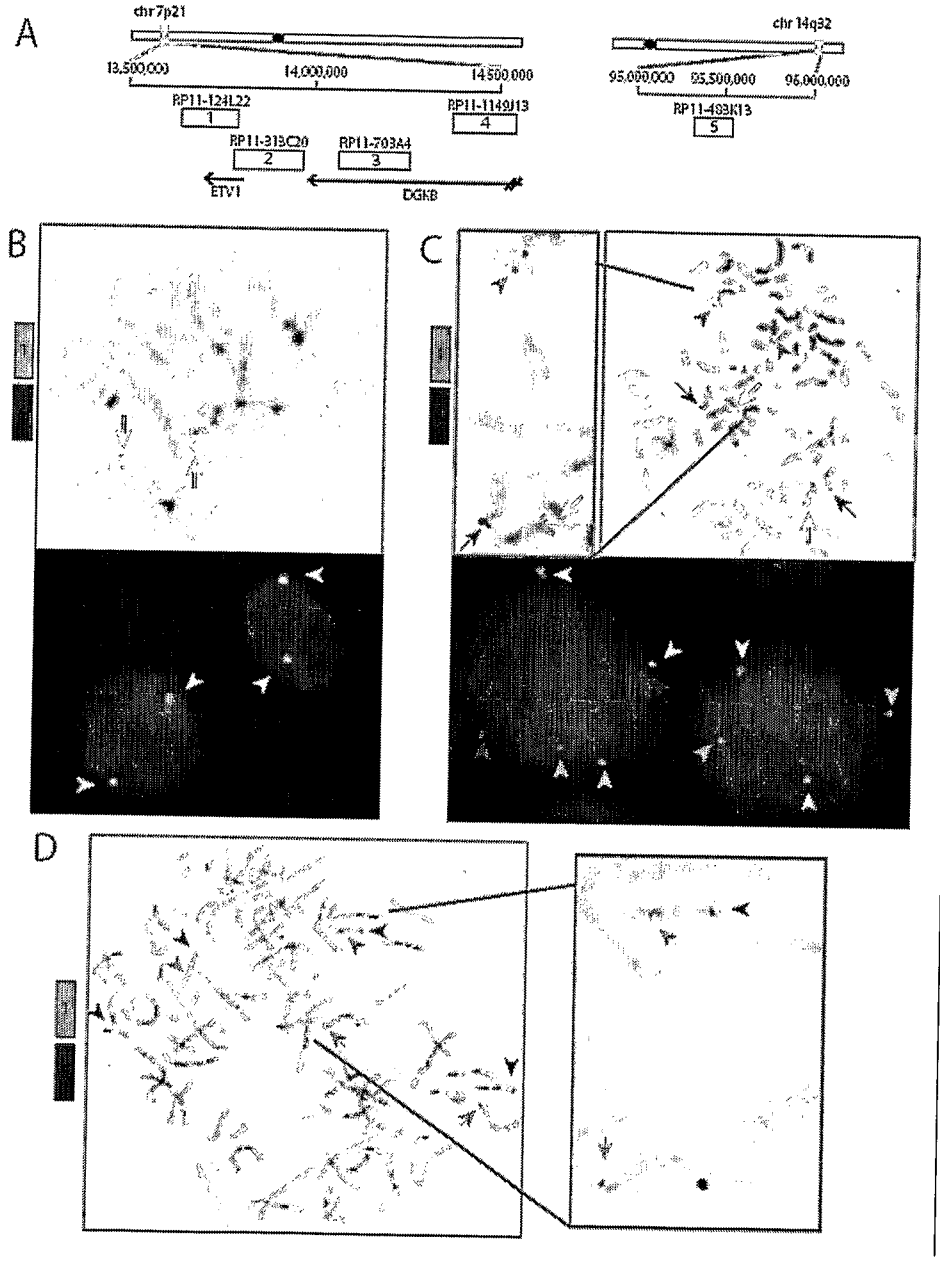

A
chr7p21
13,500,000
14,000,000
14,500,000
RP11-124L22
1
RP11-1149J13
4
RP11-313C20
2
RP11-703A4
3
ETV1
DGKB
chr 14q32
95,000,000
95,500,000
96,000,000
RP11-483K13
5
B
C
D

Figure 28

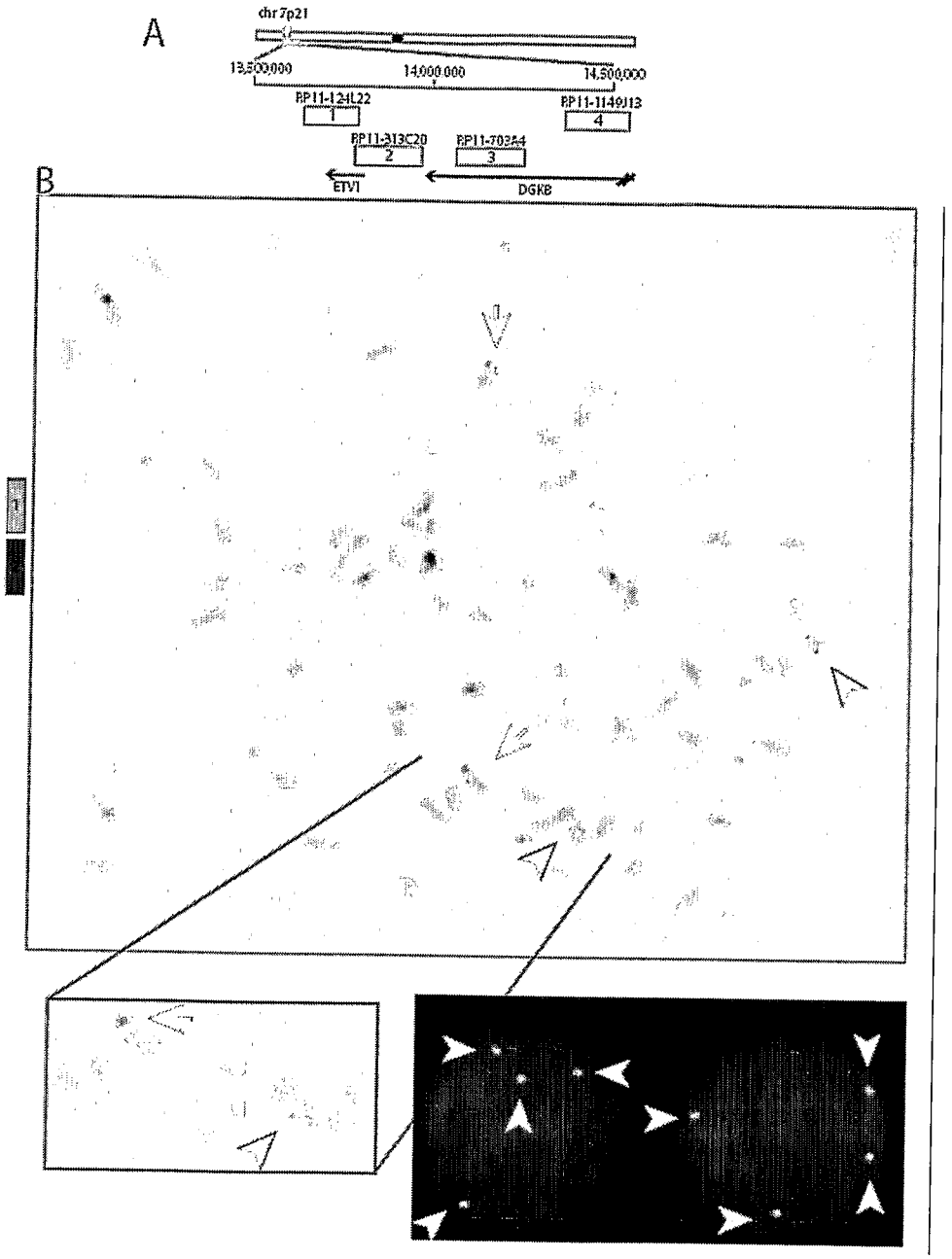

A
chr7p21
13,500,000
14,000,000
14,500,000
RP11-124L22
1
RP11-313C20
2
RP11-702A4
3
RP11-1149J13
4
ETV1
DGKB
B

Figure 29
SiRNA knockdown of ETV1 in LnCaP

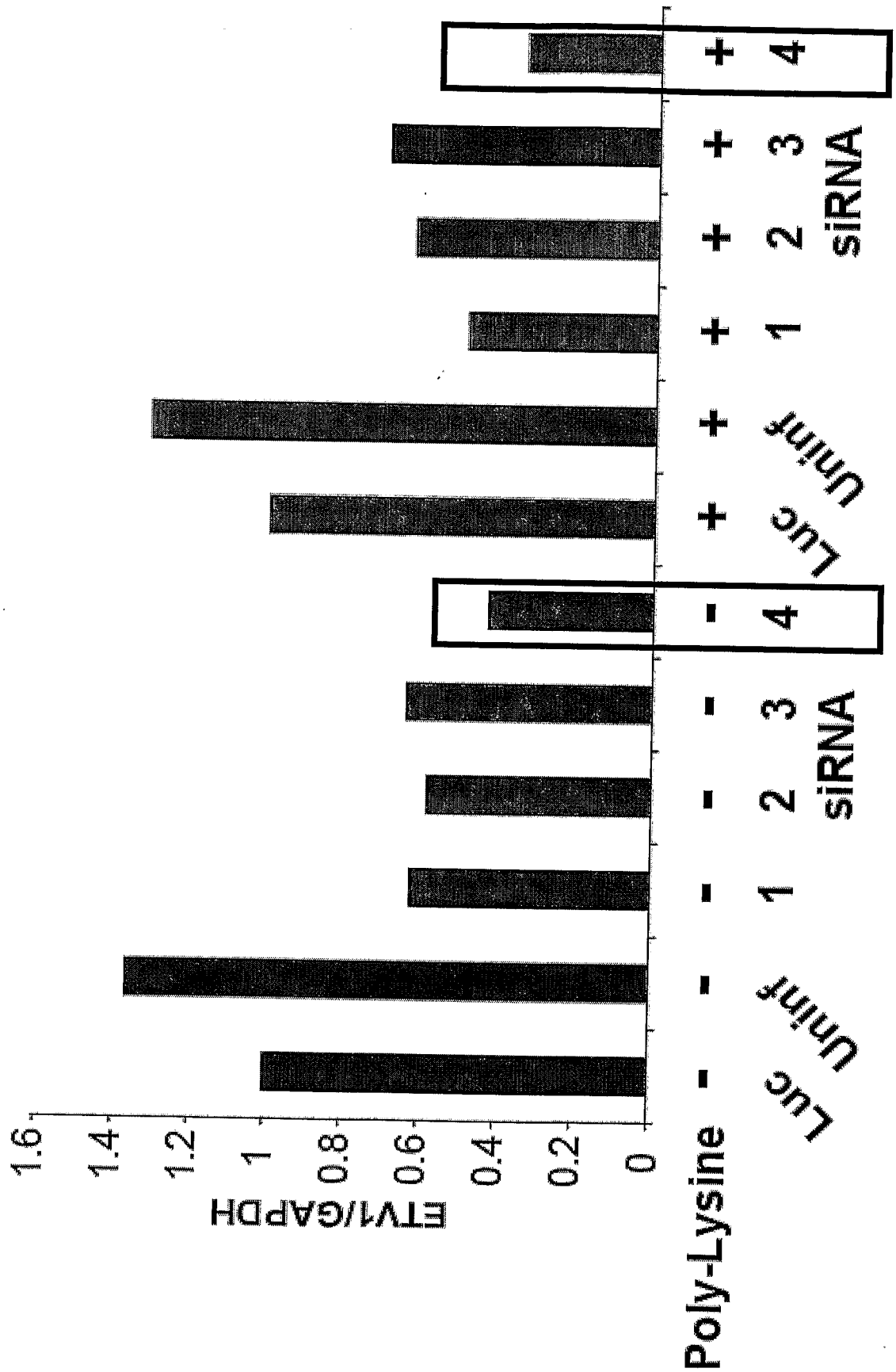


Figure 30
siRNA knockdown of ERG in VCAP

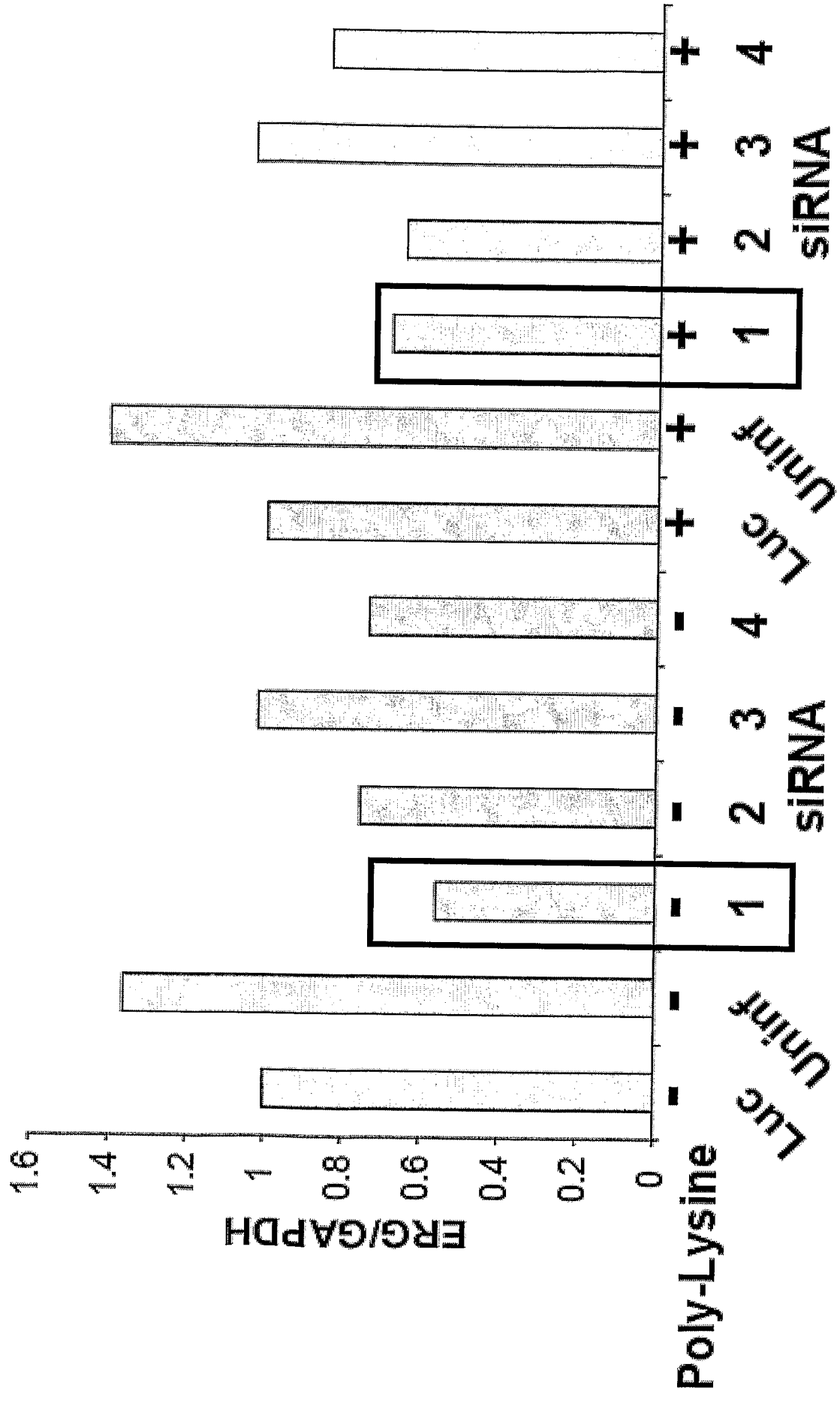
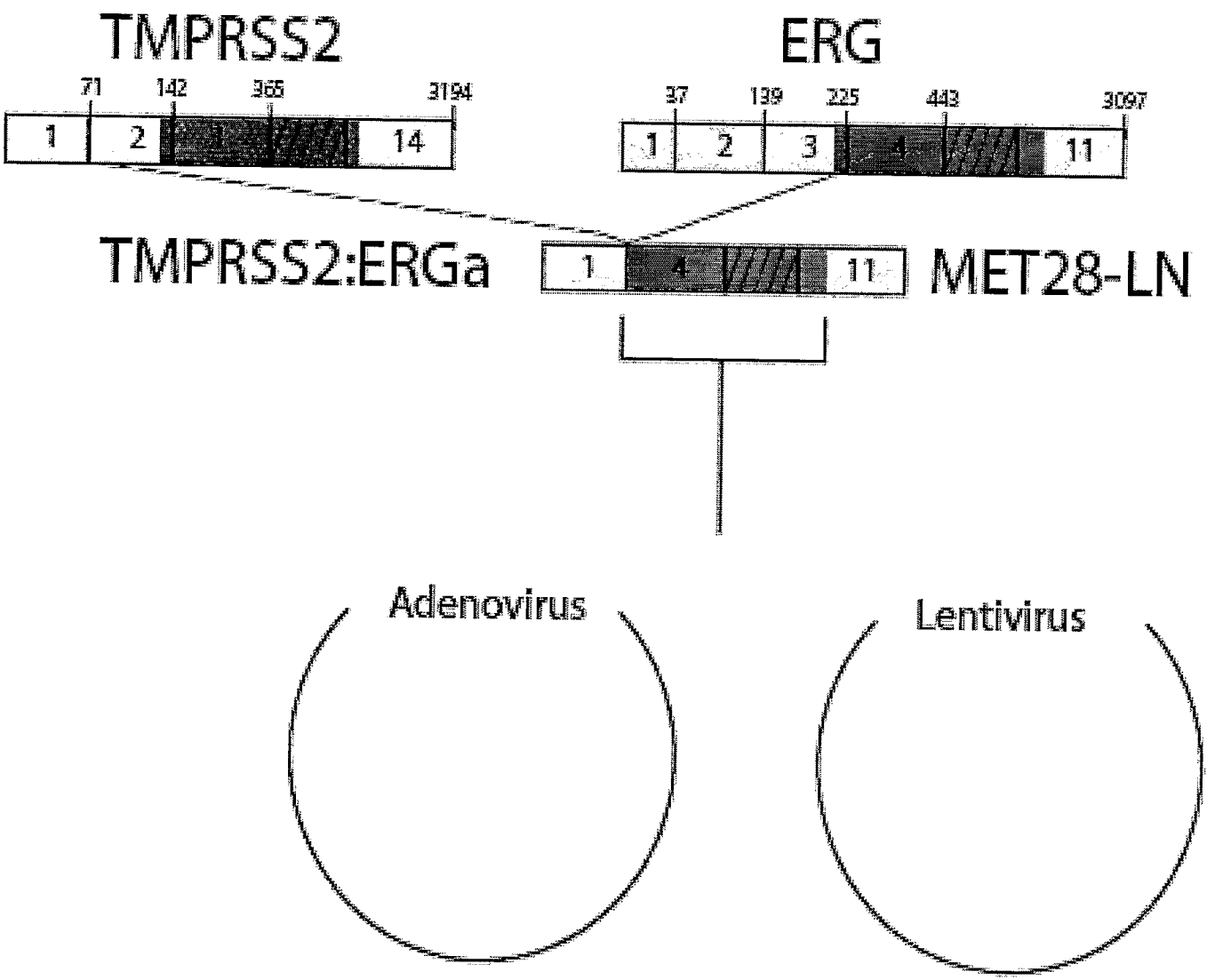


Figure 31
Viral Overexpression Systems



- ERG1
- ERG2
- ETV1

Figure 32
Transgenic Mice

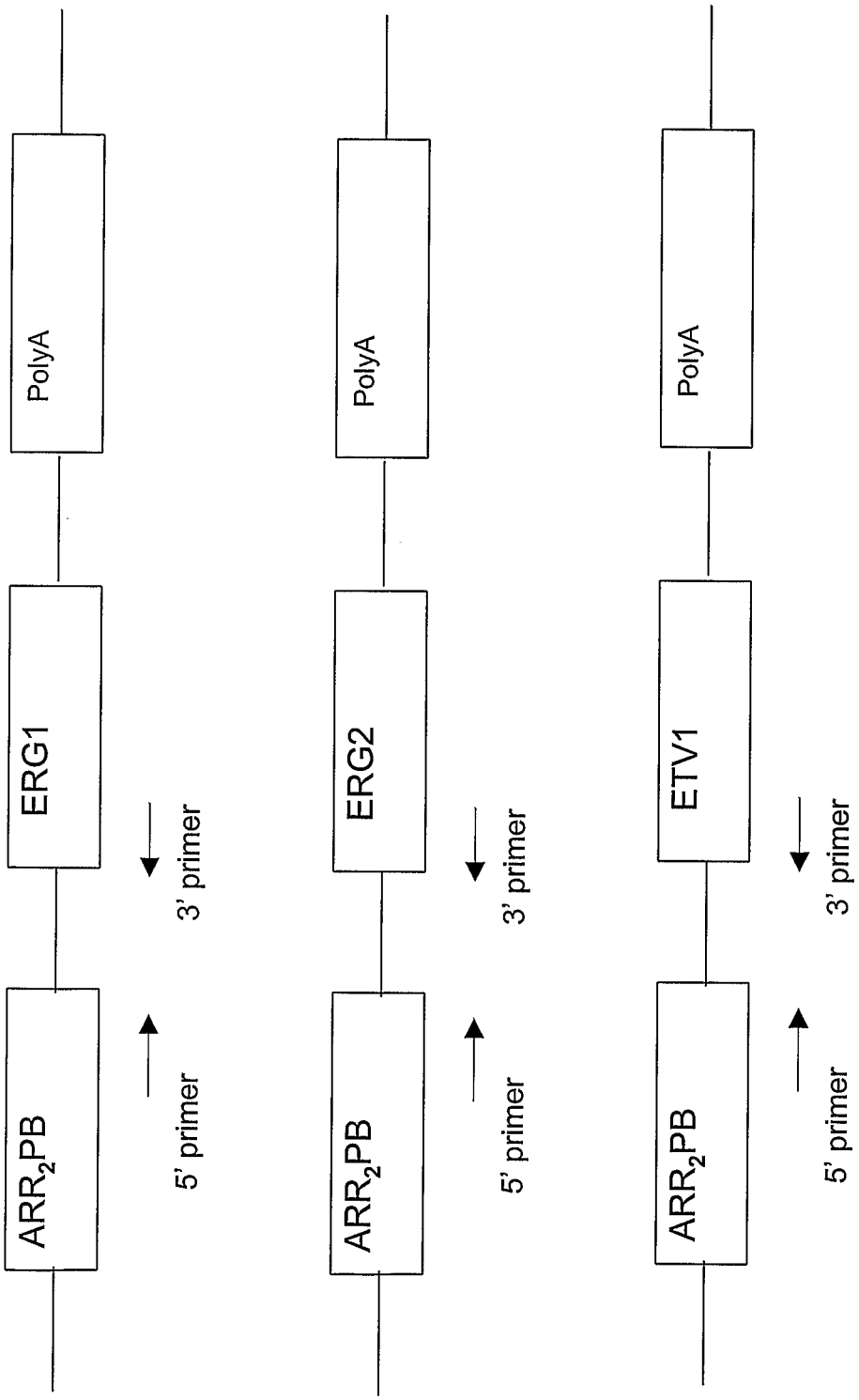


Figure 33A

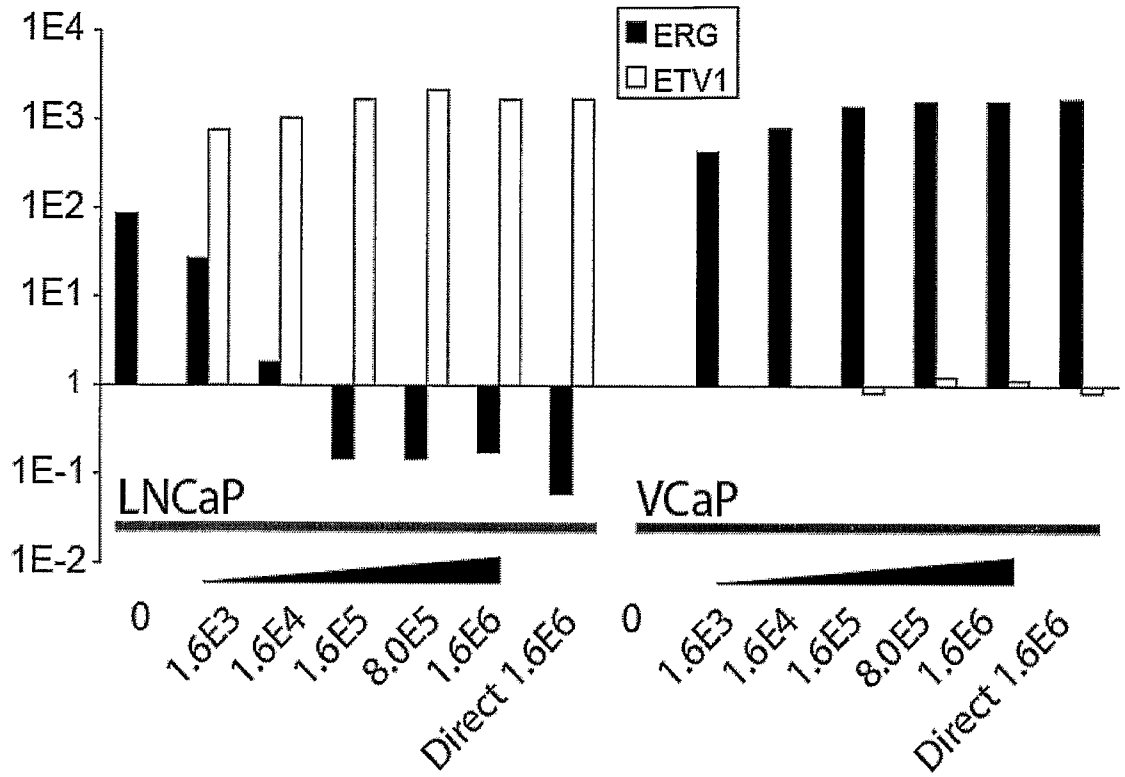

1E4
1E3
1E2
1E1
1
1E-1
1E-2
ERG
ETV1
LNCaP
VCaP
0
1.6E3
1.6E4
1.6E5
8.0E5
1.6E6
Direct 1.6E6
0
1.6E3
1.6E4
1.6E5
8.0E5
1.6E6
Direct 1.6E6

Figure 33B

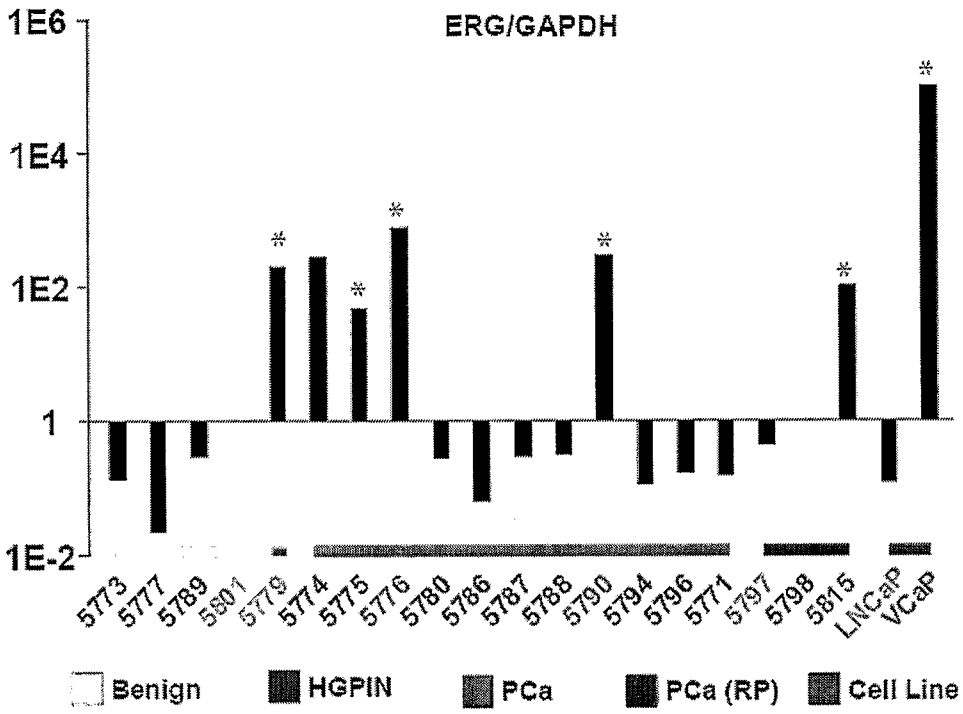

ERG/GAPDH
1E6
1E4
1E2
1
1E-2
5773
5777
5789
5501
5779
5774
5775
5776
5780
5786
5787
5788
5790
5794
5796
5771
5797
5798
5815
LNCaP
VCaP
Benign
HGPIN
PCa
PCa (RP)
Cell Line

Figure 34

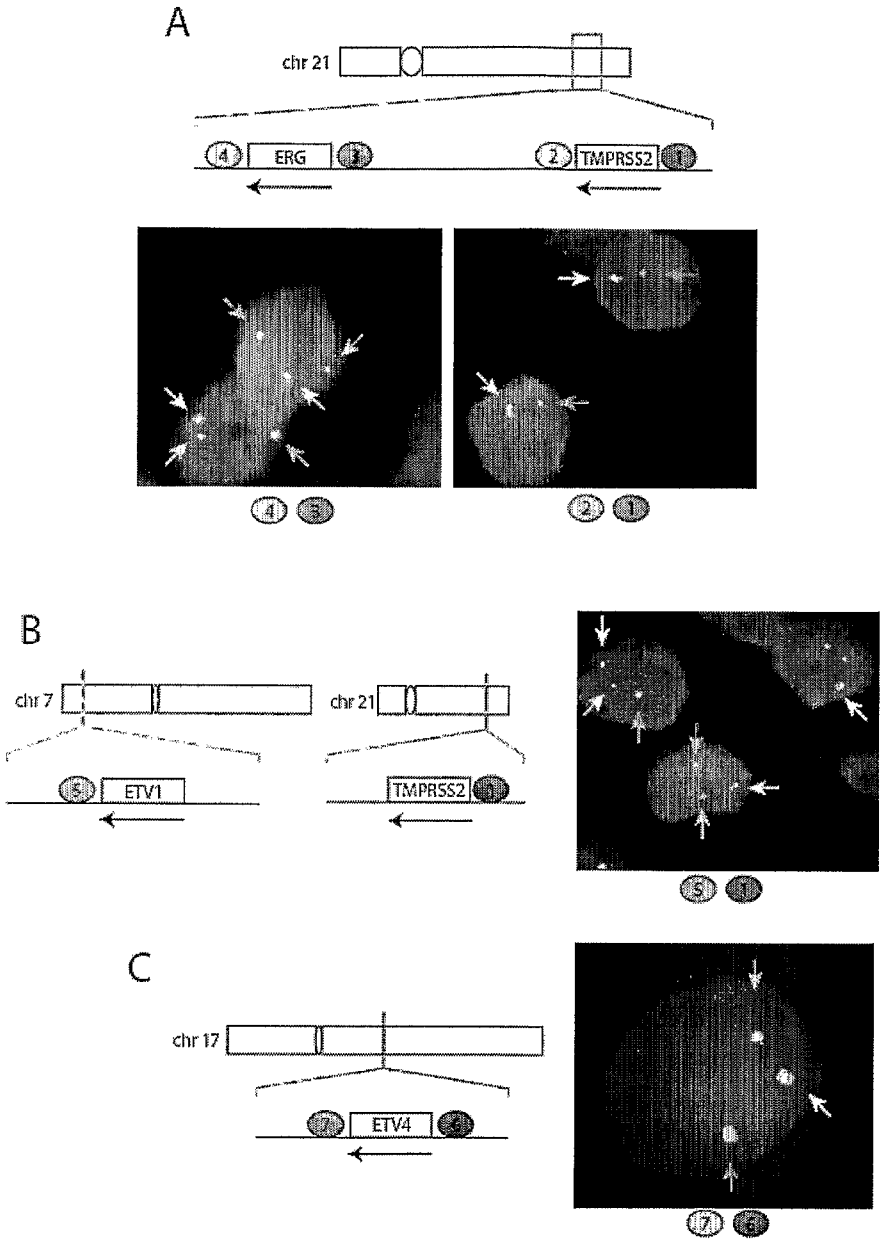

A
chr 21
4
ERG
3
2
TMPRSS2
1
4
5
2
1
B
chr 7
chr 21
5
ETV1
TMPRSS2
1
5
1
C
chr 17
7
ETV4
6
7
6

Figure 35

A

	TMPRSS2	ERG	ETV1	ETV4
# Evaluable cases (of 75):	57	65	53	58
# Rearranged (%):	37 (64.9%)	36 (55.4%)	1 (1.9%)	1 (1.7%)
# Deletion (%):	15 (40.5%)	14 (38.9%)		
# All 4 probes evaluable (of 75):	38	38	38	38
# Rearranged (%):	25 (65.8%)	22 (57.9%)	1 (2.6%)	1 (2.6%)
# Deletion (%):	10 (40.0%)	9 (40.9%)		

B

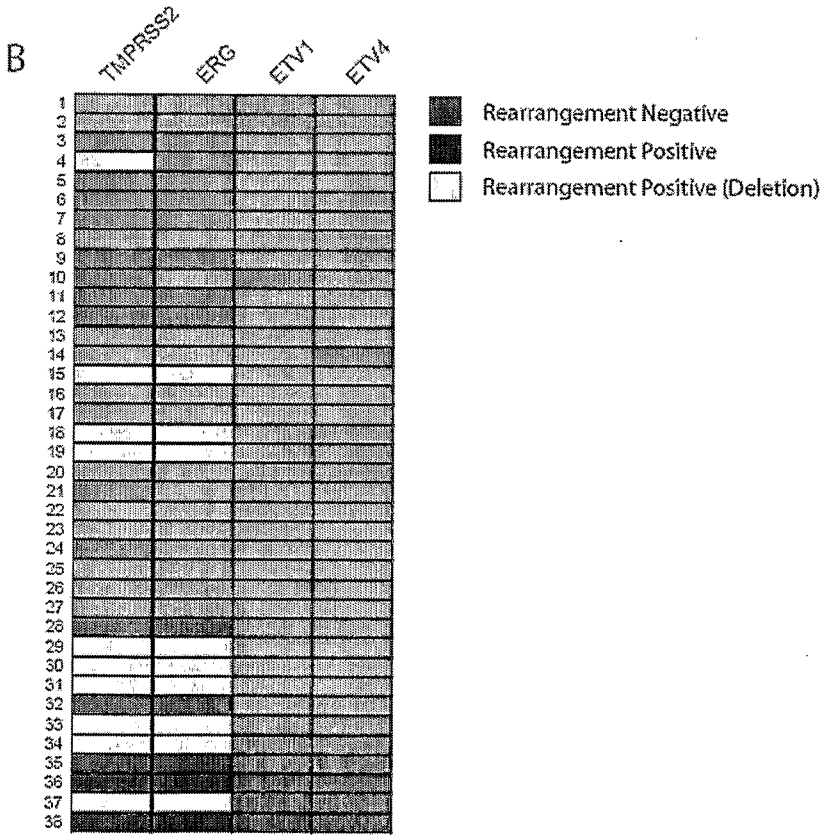


Figure 36

Gene	Exon	Sequence
TMRPSS2	1	cgcgagctaagcaggaggcggaggcggaggcggagggcgaggggcggggagcgccg cctggagcgcggcag
TMRPSS2	1,2	cgcgagctaagcaggaggcggaggcggaggcggagggcgaggggcggggagcgccg cctggagcgcggcaggtcatattgaacattccagatacctatcattactcgatgctgttgataac agcaagatggctttgaactca
TMRPSS2	1,2,3	cgcgagctaagcaggaggcggaggcggaggcggagggcgaggggcggggagcgccg cctggagcgcggcaggtcatattgaacattccagatacctatcattactcgatgctgttgataaca gcaagatggctttgaactcagggtcaccaccagctattggaccttactatgaaaaccatggatac caaccggaaaaccccctatcccgcacagcccactgtggtccccactgtctacgaggtgcatccg gctcagtactacccgtcccccgtgccccagtacgccccgagggtcctgacgcaggcttccaac cccgtcgtctgcacgcagcccaaatccccatccgggacagtgtgcacctcaa
TMRPSS2	1,2,3,4	cgcgagctaagcaggaggcggaggcggaggcggagggcgaggggcggggagcgccg cctggagcgcggcaggtcatattgaacattccagatacctatcattactcgatgctgttgataac agcaagatggctttgaactcagggtcaccaccagctattggaccttactatgaaaaccatggat accaaccggaaaaccccctatcccgcacagcccactgtggtccccactgtctacgaggtgcat ccggctcagtactacccgtcccccgtgccccagtacgccccgagggtcctgacgcaggctt ccaaccccgtcgtctgcacgcagcccaaatccccatccgggacagtgtgcacctcaaagac taagaaagcactgtgcatcaccttgaccctggggaccttcctcgtgggagctgcgctggccg ctggcctactctggaagttca
TMRPSS2	1,2,3,4,5	cgcgagctaagcaggaggcggaggcggaggcggagggcgaggggcggggagcgcc gcctggagcgcggcaggtcatattgaacattccagatacctatcattactcgatgctgttgata acagcaagatggctttgaactcagggtcaccaccagctattggaccttactatgaaaaccatg gataccaaccggaaaaccccctatcccgcacagcccactgtggtccccactgtctacgaggt gcatccggctcagtactacccgtcccccgtgccccagtacgccccgagggtcctgacgcag gcttccaaccccgtcgtctgcacgcagcccaaatccccatccgggacagtgtgcacctcaa agactaagaaagcactgtgcatcaccttgaccctggggaccttcctcgtgggagctgcgctg gccgctggcctactctggaagttcatgggcagcaagtgctccaactctgggatagagtgcga ctcctcaggtacctgcatcaacccctctaactggtgtgatggcgtgtcacactgccccggcgg ggaggacgagaatcggtgtg
TMRPSS2	upstream long	CTTTGATAAATAAGTTTGTAAGAGGAGCCTCAGCATCGTAAAGAGC TtTTCTCCCCGCTTCTCGCAG
TMRPSS2	upstream short	ATCGTAAAGAGCTtTTCTCCCCGCTTCTCGCAG
ERG	2	gttattccaggatctttggagacccgaggaaagccgtgttgaccaaaagcaagacaaatgactca cagagaaaaaagatggcagaaccaagggcaactaaag
ERG	3	ccgtcaggttctgaacagctggtagatgggctggcttactgaaggacatgattcagactgtcccgga cccagcagctcatatcaag
ERG	4	gaagccttatcagttgtgagtgaggaccagtcgttgtttgagtgtgcctacggaacgccacacctggctaagacaga gatgaccgcgtcctcctccagcgactatggacagacttccaagatgagcccacgcgtccctcagcaggattggctg tctcaacccccagccagggtcaccatcaaaatggaatgtaaccctagccaggtgaatggctcaag
ERG	5	gaactctcctgatgaatgcagtgtggccaaaggcgggaagatggtgggcagcccagacaccgttg ggatgaactacggcagctacatggaggagaagcacatgccacccccaaacatgaccacgaacg

		agcgcagagttatcgtgccagcag
ERG	6	atcctacgctatggagtacagaccatgtgcggcagtggctggagtgggcggtgaaagaatatggcc ttccagacgtcaacatcttgttattccagaacatcgatgggaaggaactgtgcaagatgaccaagga cgacttccagaggctcacccccagctacaacgccgacatccttctctcacatctccactacctcagag aga
ERG	7	ctcctcttccacatttgacttcagatgatgttgataaagccttacaaaactctccacggttaatgcatgct agaaacacag
ERG	7a	ggggtgcagcttttatttttcccaaatacttcagtatatcctgaagctacgcaaagaattacaactaggccag
ERG	8	atttaccatatgagccccccaggagatcagcctggaccggtcacggccaccccacgccccagtc gaaag
ERG	9	ctgctcaaccatctccttccacagtgcccaaaactgaagaccagcgtcctcagttag
ERG	10	atccttatcagattcttggaccaacaagtagccgccttgcaaatccag
ERG	11	gcagtggccagatccagctttggcagttcctcctggagctcctgtcggacagctccaactccagctgc atcacctgggaaggcaccaacggggagttcaagatgacggatcccgacgaggtggcccggcgct ggggagagcggaagagcaaacccaacatgaactacgataagctcagccgcgccctccgttacta ctatgacaagaacatcatgaccaaggtccatgggaagcgctacgcctacaagttcgacttccacgg gatcgcccaggccctccagccccacccccggagtcatctctgtacaagtaccctcagacctccc gtacatgggctcctatcacgcccacccacagaagatgaactttgtggcgccccaccctccagccctc cccgtgacatcttccagttttttgctgccccaaacccatactggaattcaccaactgggggtatatacc ccaacactaggctccccaccagccatatgccttctcatctgggcacttactactaa
ETV1	4	ctcaggtacctgacaatgatgagcagtttgtaccagactatcaggctgaaagtt
ETV1	5	tggcttttcatggcctgccactgaaaatcaagaaagaaccccacagtccatgttcagaaatcag ctctgcctgcagtcaagaacagccctttaaattcagctatggagaaaagtgcctgtacaatgtca g
ETV1	6	tgcctatgatcagaagccacaagtgggaatgaggccctccaacccccccacaccatccagca cgccagtgtccccactgcatcatgcatctccaaactcaactcatacaccgaaacctgaccgggc cttcccagctcacctccctccatcgcagtccataccagatagcagctaccccatggaccacag
ETV1	7	atttcgccgccagctttctgaaccctgtaactcctttcctcctttgccgacgatgccaagggaag gacgtcctatgtaccaacgccagatgtctgagccaaacatccccttcccaccacaaggctttaa gcaggagtaccacgacccagtgtatgaacacaacaccatggttggcagtgcggccagccaa agctttccccctcctctgatgattaaacaggaacccagagattttgcatatgactcag
ETV1	8	aagtgcctagctgccactccatttatatgaggcaagaaggcttcctggctcatcccagcaga acagaag
ETV1	9	gctgtatgtttgaaaagggccccaggcagttttatgatgacacctgtgttgtcccagaaaaattc gatg
ETV1	10	gagacatcaaacaagagccaggaatgtatcgggaaggacccacataccaacggcgaggat cacttcagctctggcagtttttggtagctcttctggatgacccttcaaattctcattttattgcctgga ctggtcgaggcatggaatttaaactgattgagcctgaagag
ETV1	11	gtggcccgacgttggggcattcagaaaaacaggccagctatgaactatgataaacttagccgt tcactccgctattactatgagaaaggaattatgcaaaag
ETV1	12	gtggctggagagagatatgtctacaagtttgtgtgtgatccagaagccctttttctccatggccttt ccagataatcagcgtccactgctgaagacagacatggaacgtcacatcaacgaggaggaca cagtgcctctttctcactttgatgagagcatggcctacatgccggaaggggggctgctgcaaccc ccacccctacaacgaaggctacgtgtattaa

ETV4	3	aaatcgcccggaaatgggagcttgcgcgaagcgctgatcggcccgctggggaagctcatgg acccgggctccctgccgccctcgactctgaag
ETV4	4	atctcttccaggatctaagtcacttccaggagacgtggctcgctgaag
ETV4	5	ctcaggtaccagacagtgatgagcagtttgttcctgatttccattcagaaaacc
ETV4	6	tagctttccacagccccaccaccaggatcaagaaggagccccagagtccccgcacagaccc ggccctgtcctgcagcaggaagccgccactcccctaccaccatggcgagcagtgcctttact ccag
ETV4	7	tgcctatgacccccccagacaaatcgccatcaagtcccctgcccctggtgcccttggacagtc gcccctacagccctttccccgggcagagcaacggaatttcctgagatcctctggcacctccca gccccaccctggccatgggtacctcggggaacatag
ETV4	8	ctccgtcttccagcagcccctggacatttgccactccttcacatctcagggaggggggccggga acccctcccagccccctaccaacaccagctgtcggagccctgcccaccctatccccagcaga gctttaagcaagaataccatgatcccctgtatgaacaggcgggccagccagccgtggaccag ggtggggtcaatgggcacaggtacccaggggcgggggtggtgatcaaacaggaacagacg gacttcgcctacgactcag
ETV4	9	gtgtcaccgggtgcgcatcaatgtacctccacacagagggcttctctgggccctctccaggtg acggggccatgg
ETV4	10	gctatggctatgagaaacctctgcgaccattcccagatgatgtctgcgttgtccctgagaaattt gaag
ETV4	11	gagacatcaagcaggaaggggtcggtgcatttcgagaggggccgccctaccagcgccggg gtgccctgcagctgtggcaatttctggtggccttgctggatgacccaacaaatgcccatttcatt gcctggacgggccggggaatggagttcaagctcattgagcctgaggag
ETV4	12	gtcgccaggctctggggcatccagaagaaccggccagccatgaattacgacaagctgagcc gctcgctccgatactattatgagaaaggcatcatgcagaag
ETV4	13	gtggctggtgagcgttacgtgtacaagtttgtgtgtgagcccgaggccctcttctctttggccttc ccggacaatcagcgtccagctctcaaggctgagtttgaccggcctgtcagtgaggaggacaca gtccctttgtcccacttggatgagagccccgcctacctcccagagctggctggccccgcccagc catttggccccaagggtggctactcttactag

Name	Reference	TMPRSS2	ETV1
	TMPRSS2:ETV1a	1	4-12
	TMPRSS2:ETV1b	1,2	4-12
		TMPRSS2 Exon	**ERG Exon**
TMPRSS2:ERG(1,2)	TMPRSS2:ERGb	1	2-11
TMPRSS2:ERG(1,3)	3	1	3-11
TMPRSS2:ERG(1,4)	TMPRSS2:ERGa	1	4-11
TMPRSS2:ERG(1,5)	2	1	5-11
TMPRSS2:ERG(2,2)	3	1,2	2-11
TMPRSS2:ERG(2,3)		1,2	3-11
TMPRSS2:ERG(2,4)	1	1,2	4-11
TMPRSS2:ERG(2,5)	2	1,2	5-11
TMPRSS2:ERG(3,4)	3	1-3	4-11
TMPRSS2:ERG(4,4)	1	1-4	4-11
TMPRSS2:ERG(4,5)	1	1-4	5-11
TMPRSS2:ERG(5,4)	1	1-5	4-11

		TMPRSS2	ETV4
	TMPRSS2:ETV4a	upstream long	Intron 2, exons 3-13
	TMPRSS2:ETV4b	upstream short	Intron 2, exons 3-13
Gene	**Accession number**		
TMPRSS2	NM_005656.2		
ERG	NM_004449.3		
ETV1	NM_004956.3		
ETV4	NM_001986.1		
TMPRSS2:ERGa	DQ204772		
TMPRSS2:ERGb	DQ204773.2		
TMPRSS2:ETV1a	DQ204770		
TMPRSS2:ETV1b	DQ204771		
TMPRSS2:ETV4a	DQ396625		
TMPRSS2:ETV4b	DQ396626		
References	1	PMID: 16575875	Genes Chromosomes Cancer. 2006 Jul;45(7):717-9
	2	PMID: 16820092	Neoplasia. 2006 Jun;8(6):465-9.
	3	PMID: 16951141	Cancer Res. 2006 Sep 1;66(17):8347-51

Figure 37

	Primer	SEQ ID NO
FLI1_exon1-f	GCTGCAGACTTGGCCAAATGGAC	202
FLI1_exon2-r	TCACCACCGACAGAGCCTCCTTA	203
FLI1_exon2/3-f	ACCACATGAATGGATCCAGGGAGTCT	204
FLI1_exon3-r	ACCAGCTTGCTGCATTTGCTAACG	205
FLI1_exon4-f	CTCCGCGCCACCACCCTCTA	206
FLI1_exon4/5-r	GGCCAGCAGTGAACTTTCCCTGAG	207
FLI1_exon3a-f	CTCCTCCCAACATGACCACCAAC	208
FLI1_exon3a-r	GTCTGCGGGGACGATGACTCTC	209
FLI1_exon4a-f	CATGTGAGGCAATGGCTGGAGTG	210
FLI1_exon4a-r	CCATGTTCTGGAAAAAGGATGTGTCG	211
FLI1_exon7-f	CCTTGGAGGGGCACAAACGAT	212
FLI1_exon8-r	GGTCGGGCCCAGGATCTGATAC	213
FLI1_exon9-f	CGCCAACGCCAGCTGTATCAC	214
FLI1_exon9-r	AGCGCCTGGCCACCTCATC	215
FLI1_exon10-f	ATGTTTTTATGACCAAAGCAGTTTCTTGTC	216
FLI1_exon10-r	ATGACGGGTTAAGTCCATGATTCTGTG	217

ERG		
forward-	CGAAAGCTGCTCAACCATCTC	218
reverse-	TAACTGAGGACGCTGGTCTTCA	219
FAM labeled MGB probe	CCACAGTGCCCAAAA	220
FLI1		221
forward-	CGGCAAAAGATATGCTTACAAATTT	222
reverse-	GACGACTCGGTCGGATGTG	223
FAM labeled MGB probe	CACGGCATTGCCCA	224
TMPRSS2:ERGa specific		
forward-	CGCGGCAGGAAGCCTTA	225
reverse-	TCCGTAGGCACACTCAAACAAC	226
FAM labeled MGB probe	CAGTTGTGAGTGAGGACC	227
ETV4		
forward-	GCTCGCTCCGATACTATTATGAGAA	228
reverse-	CACACACAAACTTGTACACGTAACG	229
FAM labeled MGB probe	ACCAGCCACCTTCTGC	230
ETV1		
forward-	GGTCGAGGCATGGAATTTAAACTGA	231
reverse-	GCTGGCCTGTTTTTCTGAATGC	232
FAM labeled MGB probe	TCGGGCCACCTCTTC	233