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(54) **METHODS FOR DIAGNOSING PROSTATE CANCER AND PREDICTING PROSTATE CANCER RELAPSE**

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(51) **Int. Cl.**

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C12Q 1/6886	(2018.01)
C12Q 1/6874	(2018.01)

(52) **U.S. Cl.**
CPC ***C12Q 1/6886*** (2013.01); ***C12Q 1/6874*** (2013.01); *C12Q 2600/112* (2013.01); *C12Q 2600/118* (2013.01); *C12Q 2600/156* (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to methods and compositions for diagnosing prostate cancer and/or determining whether a prostate cancer patient is at increased risk of suffering a relapse, or a rapid relapse, of his cancer. It is based, at least in part, on the results of a comprehensive genome analysis on 241 prostate cancer samples (104 prostate cancer, 85 matched bloods, 49 matched benign prostate tissues adjacent to cancer, and 3 cell lines) which indicate that (i) genome copy number variation (CNV) occurred in both cancer and non-cancer tissues, and (ii) CNV predicts prostate cancer progression.

2 Claims, 15 Drawing Sheets

Specification includes a Sequence Listing.

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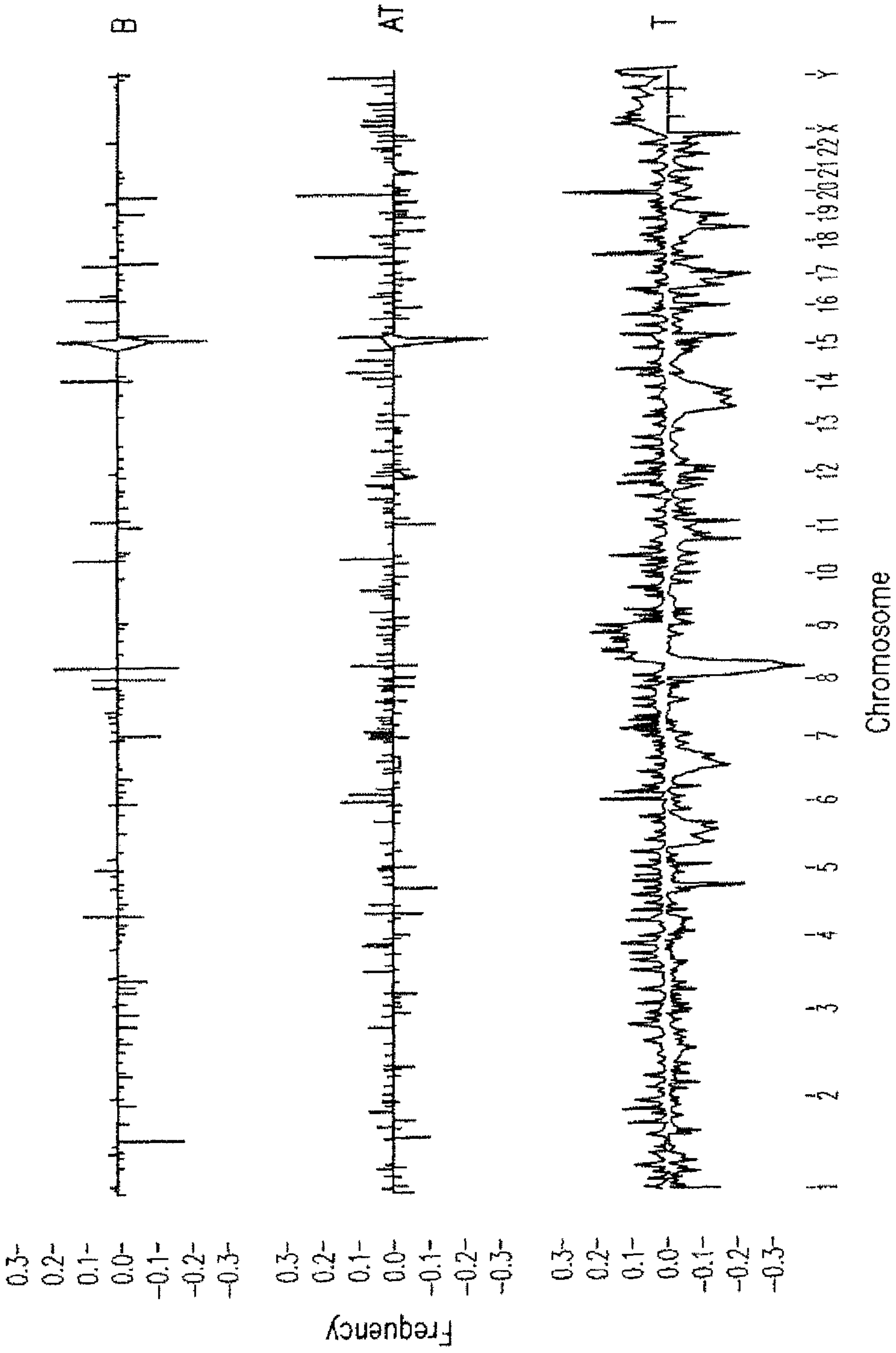
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Chromosome

FIG. 1A

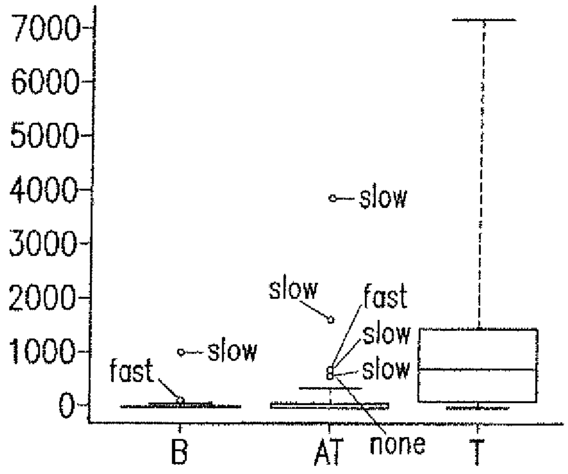


FIG. 1B

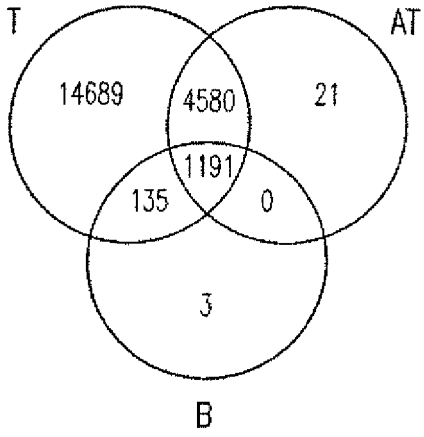
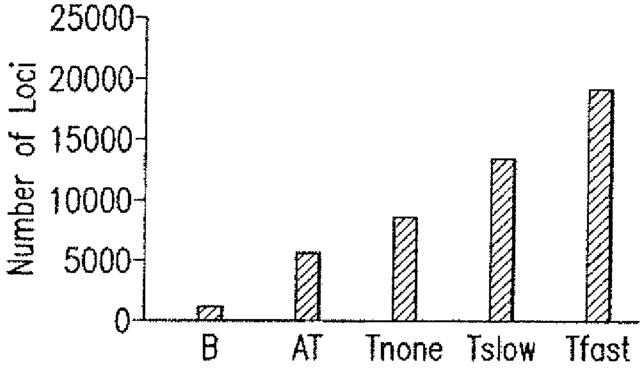


FIG. 1C



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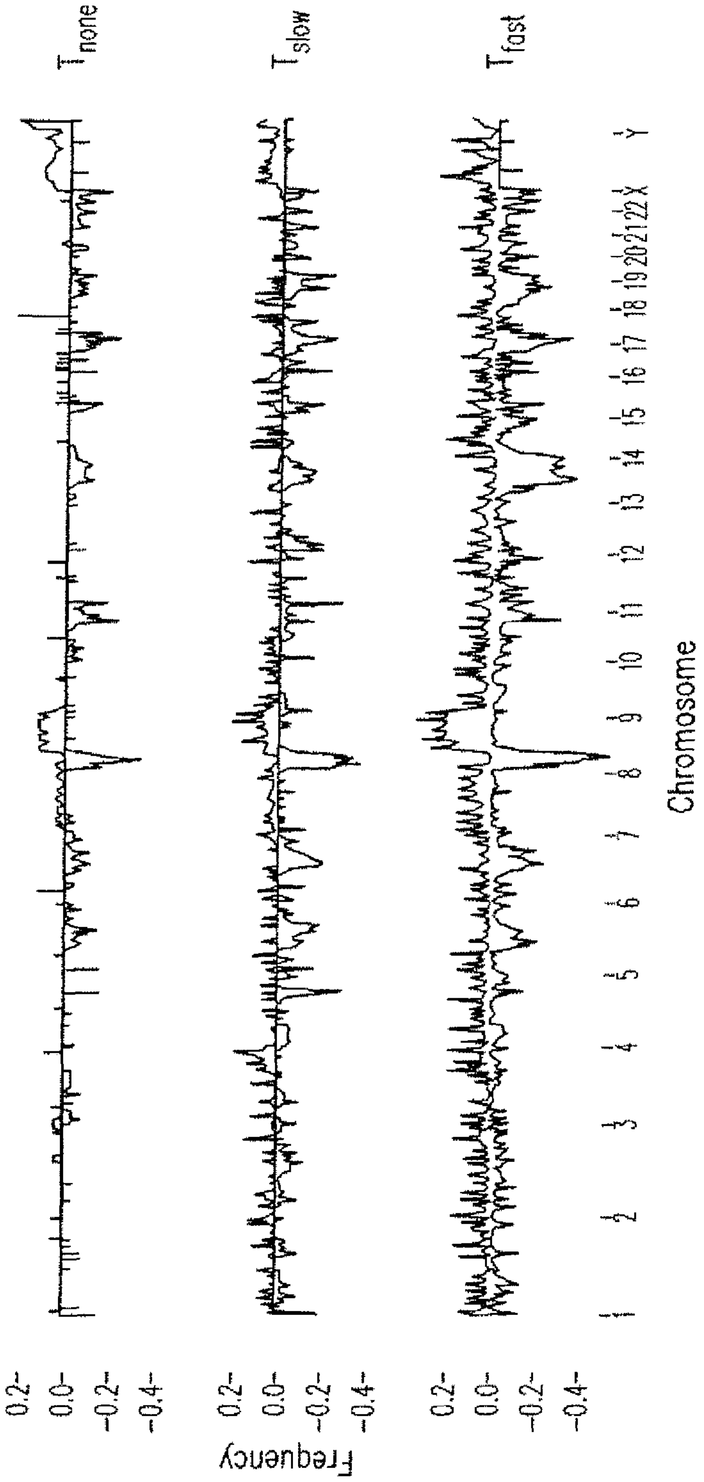
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13
14
15
16
17
18
19
20
21
22
X
Y
Chromosome

FIG. 2A

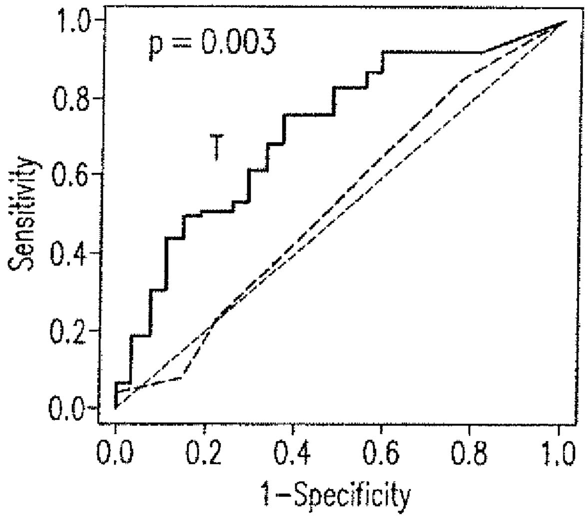
p = 0.003
T
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1−Specificity

FIG. 2B

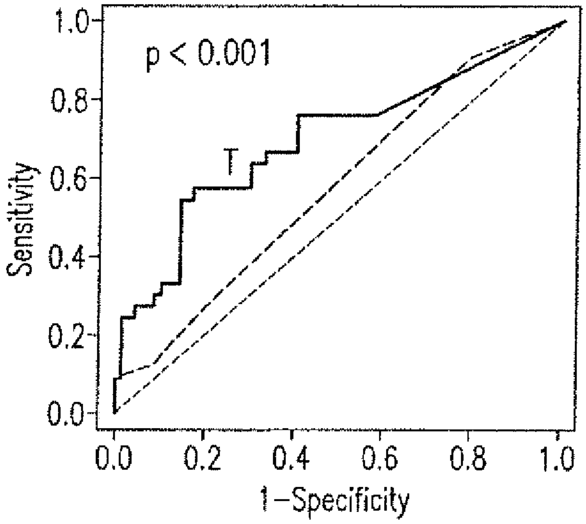
p < 0.001
T
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1−Specificity

FIG. 2C

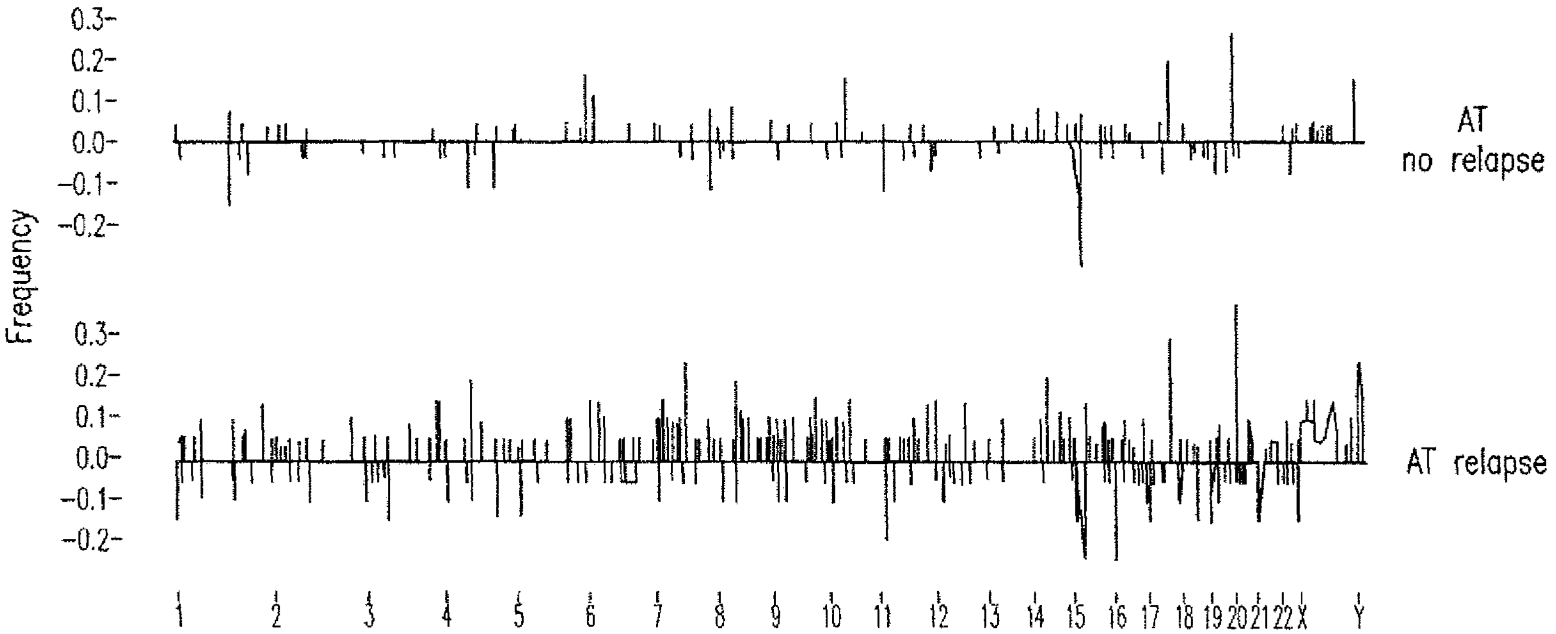
Frequency
0.3
0.2
0.1
0.0
-0.1
-0.2
AT
no relapse
0.3
0.2
0.1
0.0
-0.1
-0.2
AT relapse
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y

FIG. 3A

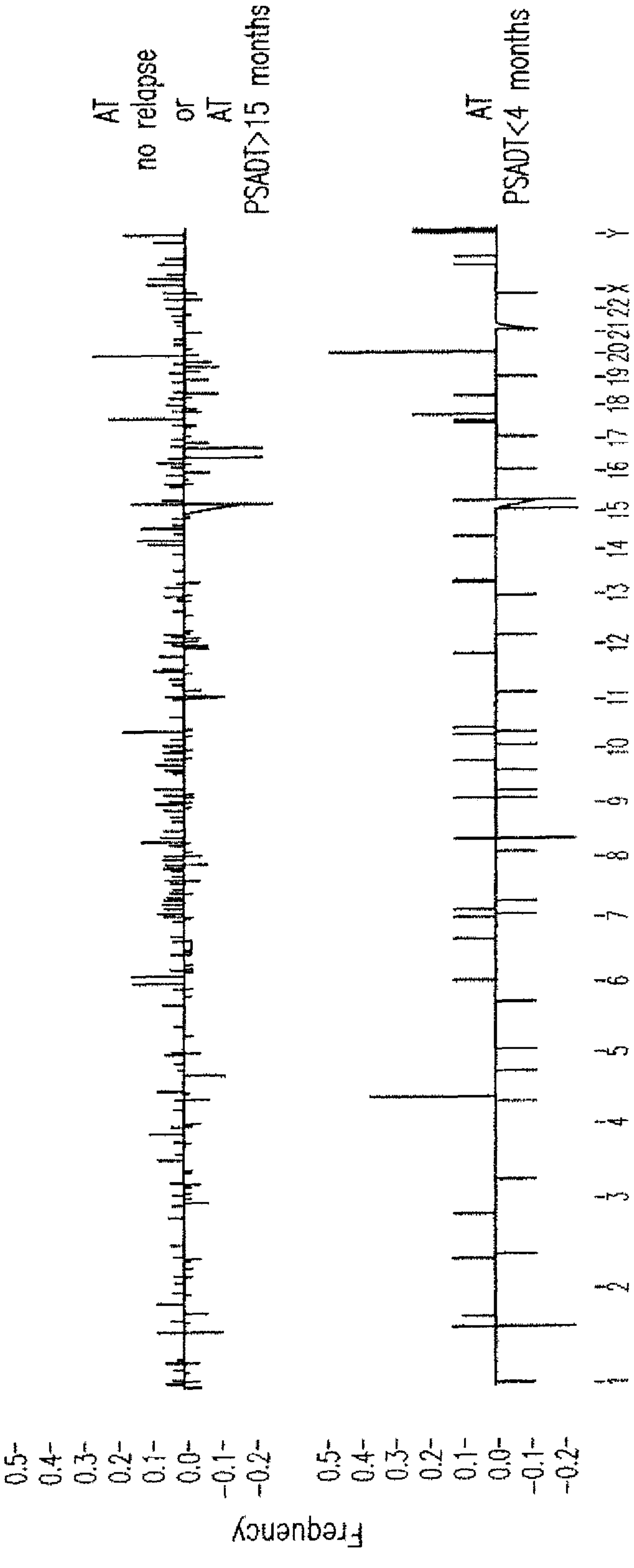
AT
no relapse
or
AT
PSADT>15 months
AT
PSADT<4 months
Frequency
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y

FIG. 3B

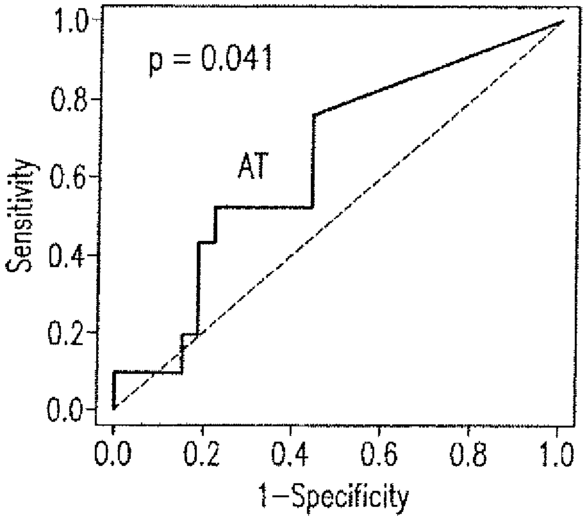
1.0
0.8
0.6
0.4
0.2
0.0
Sensitivity
p = 0.041
AT
0.0
0.2
0.4
0.6
0.8
1.0
1−Specificity

FIG. 3C

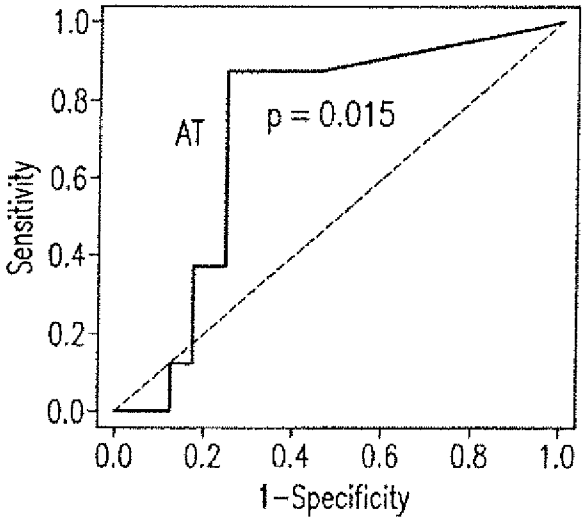
1.0
0.8
0.6
0.4
0.2
0.0
Sensitivity
AT
p = 0.015
0.0
0.2
0.4
0.6
0.8
1.0
1−Specificity

FIG. 3D

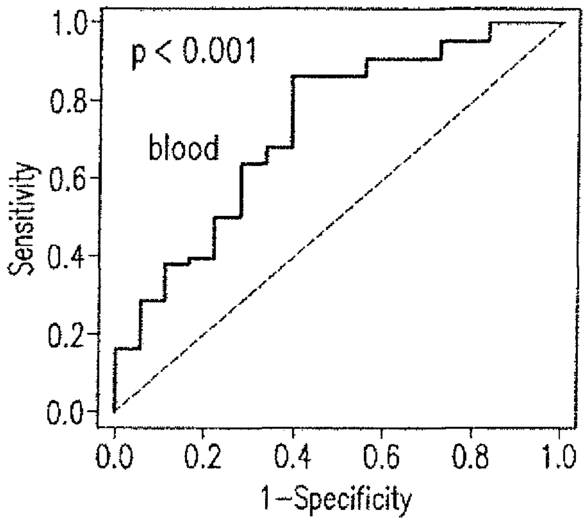

FIG. 4A

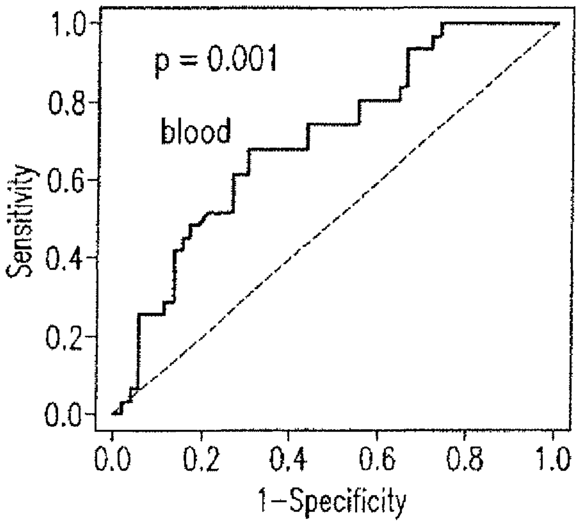

FIG. 4B

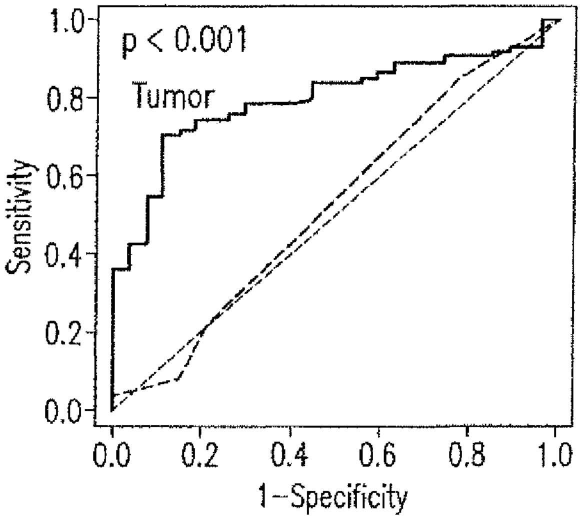

FIG. 4C

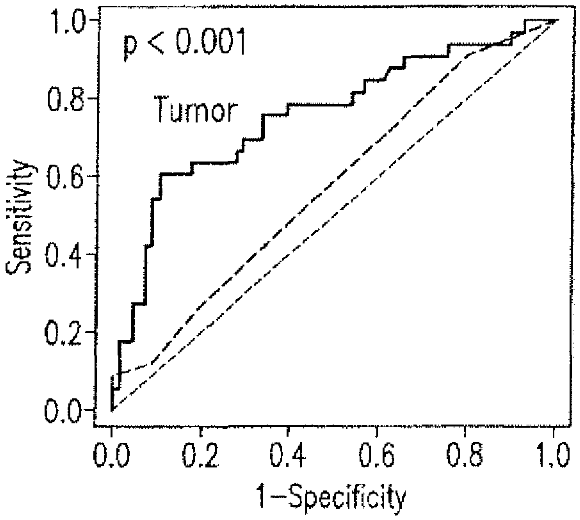

FIG. 4D

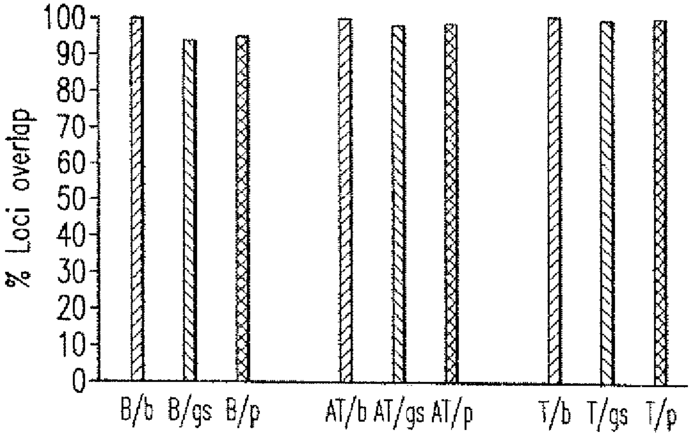

FIG. 5A

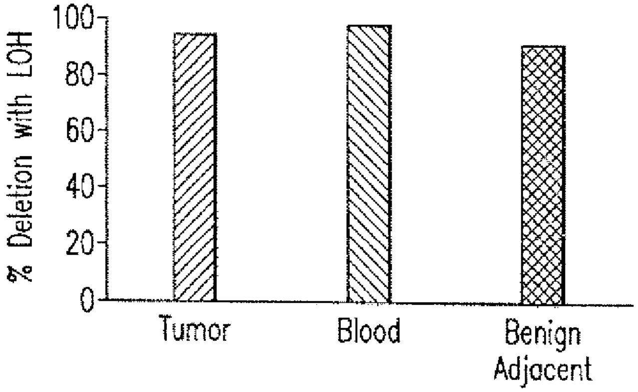

FIG. 5B

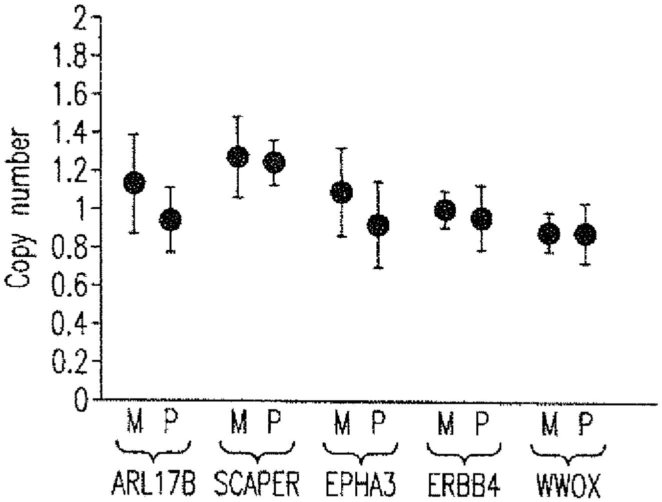

FIG. 5C

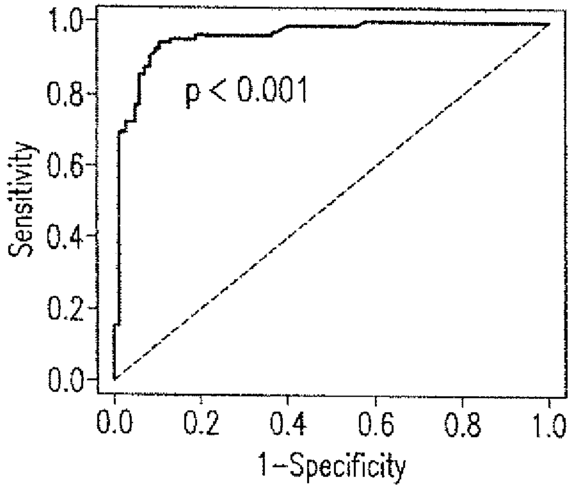

FIG. 5D

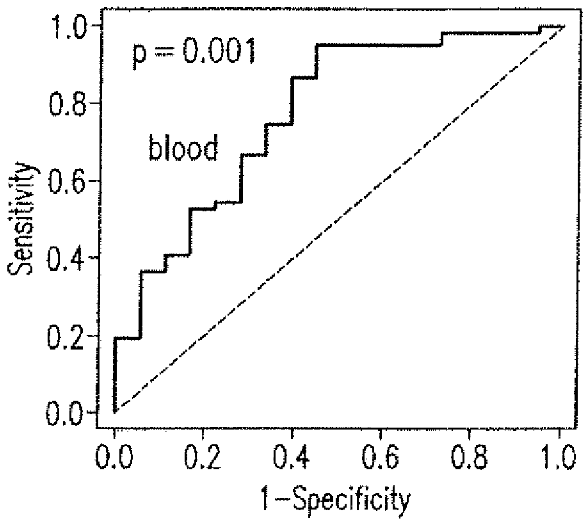

FIG. 6A

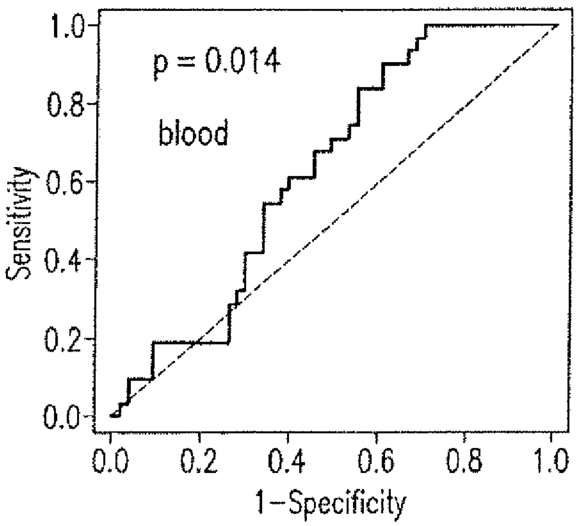

FIG. 6B

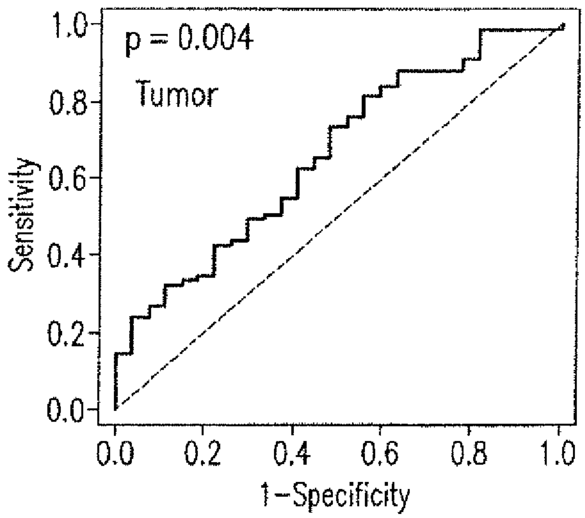

FIG. 6C

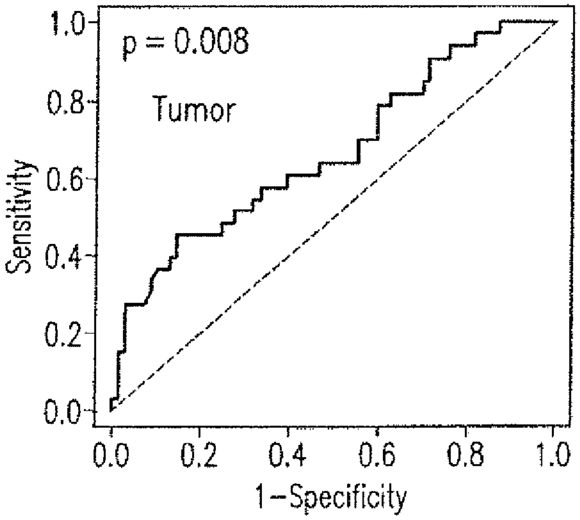

FIG. 6D

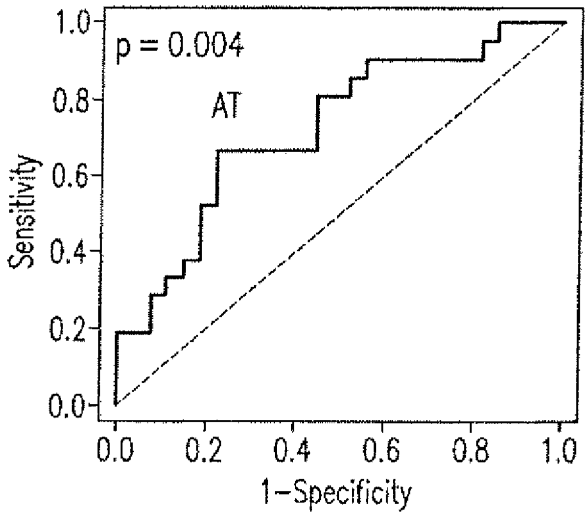
p = 0.004
AT
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1–Specificity

FIG. 7A

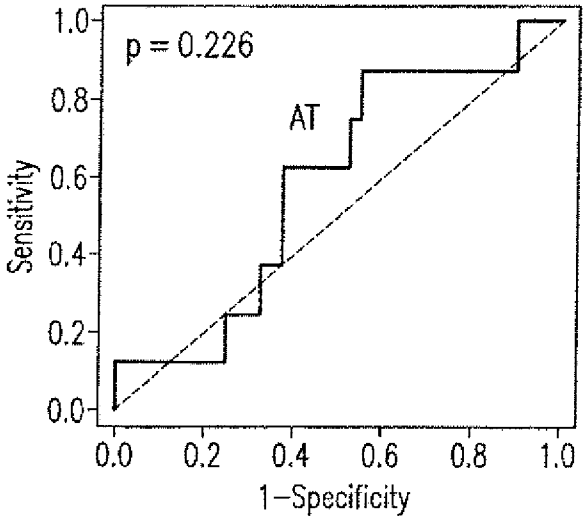
p = 0.226
AT
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1–Specificity

FIG. 7B

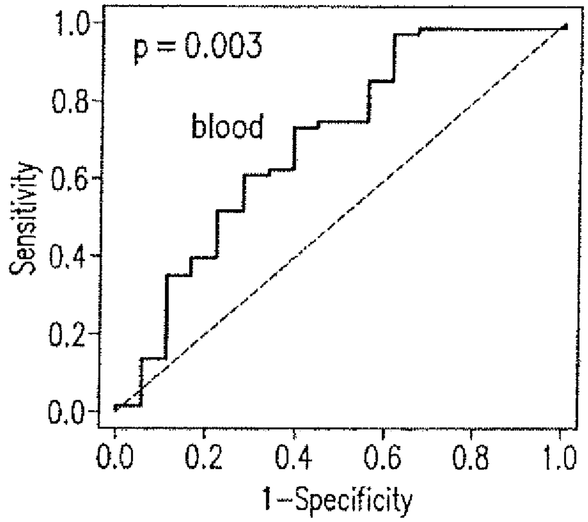

FIG. 8A

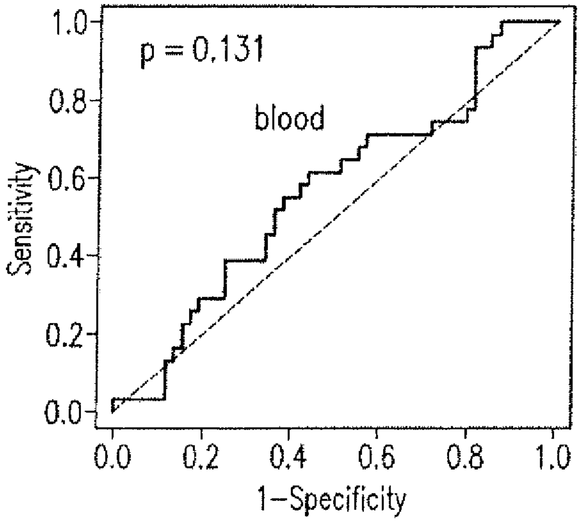

FIG. 8B

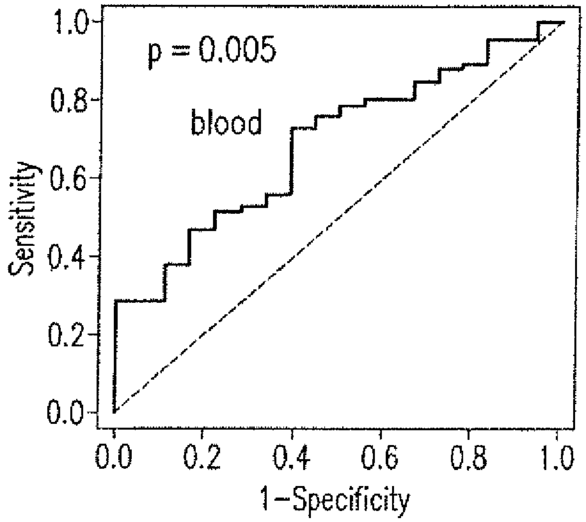

FIG. 8C

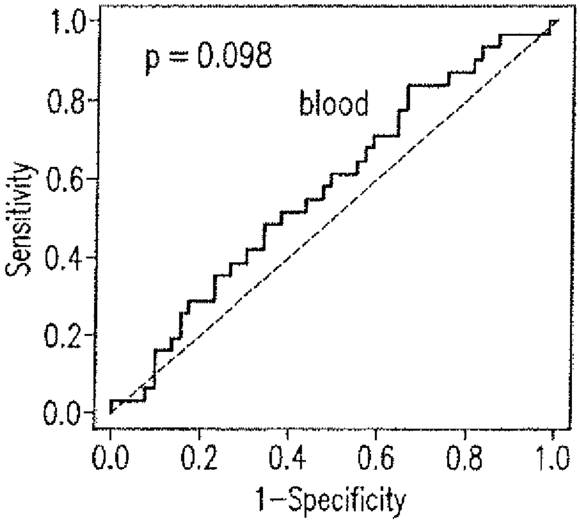

FIG. 8D

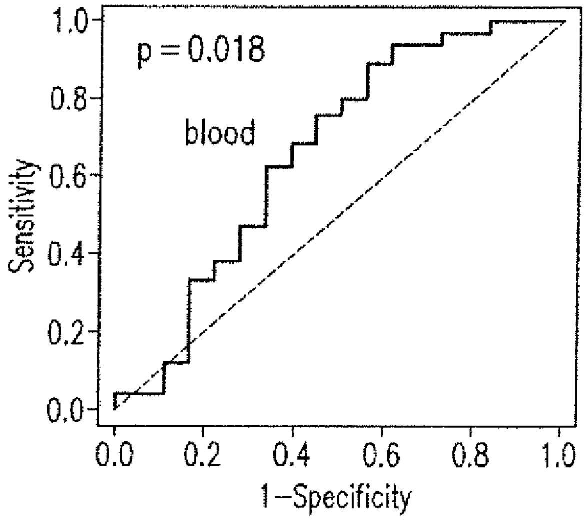

FIG. 9A

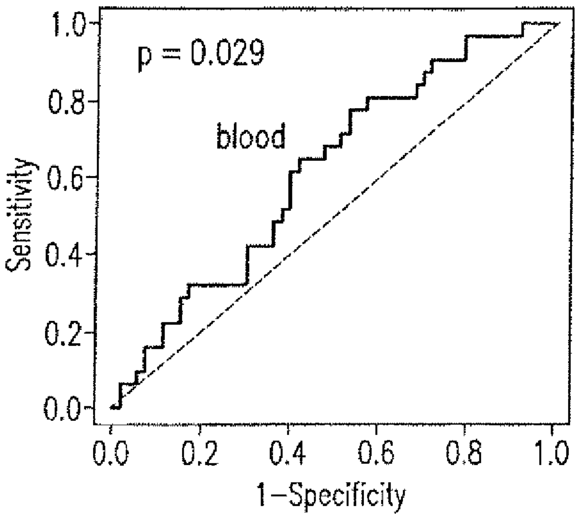

FIG. 9B

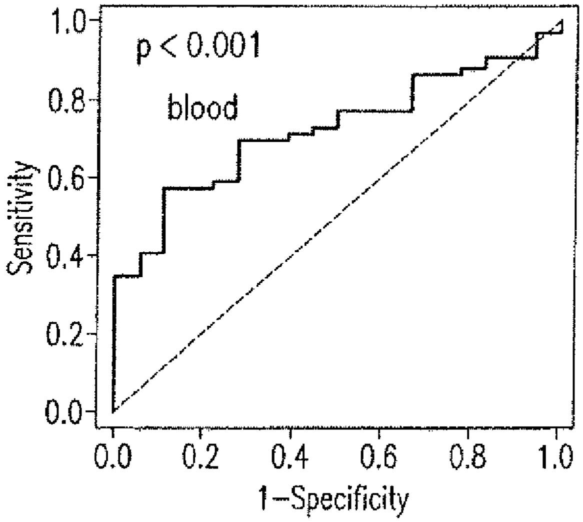

FIG. 9C

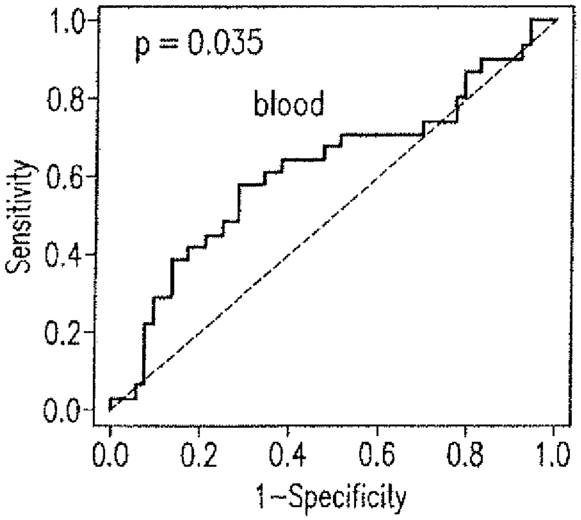

FIG. 9D

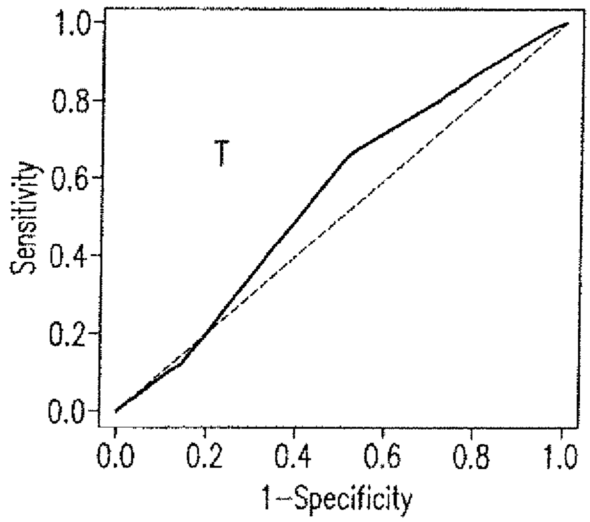

FIG. 10A

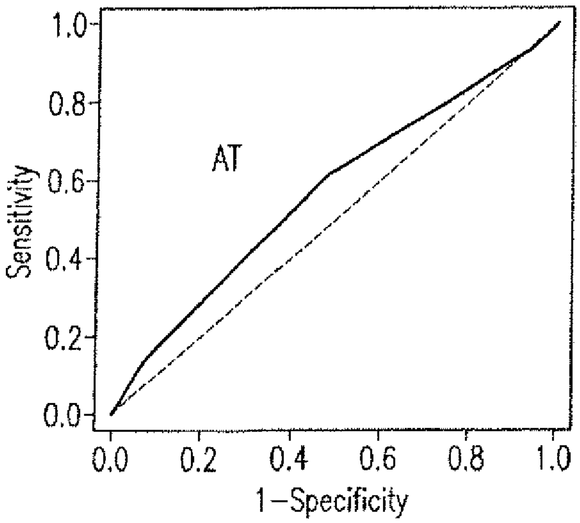

FIG. 10B

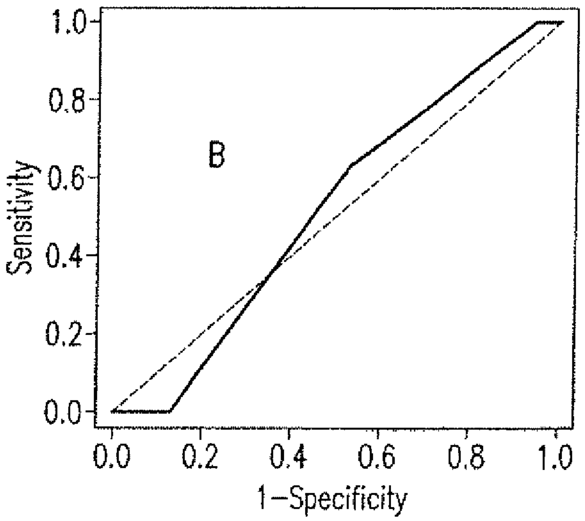

FIG. 10C

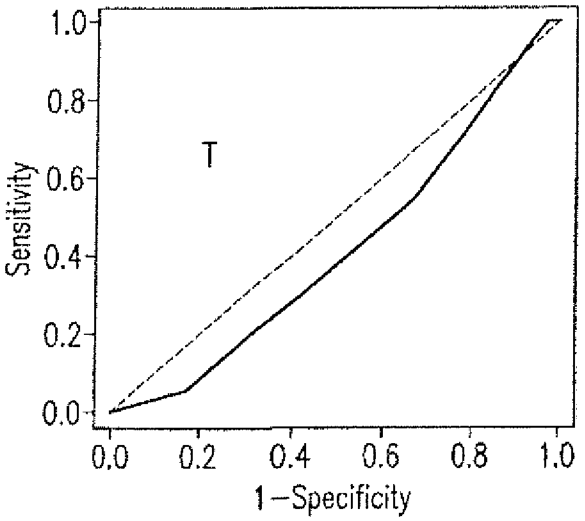

FIG. 10D

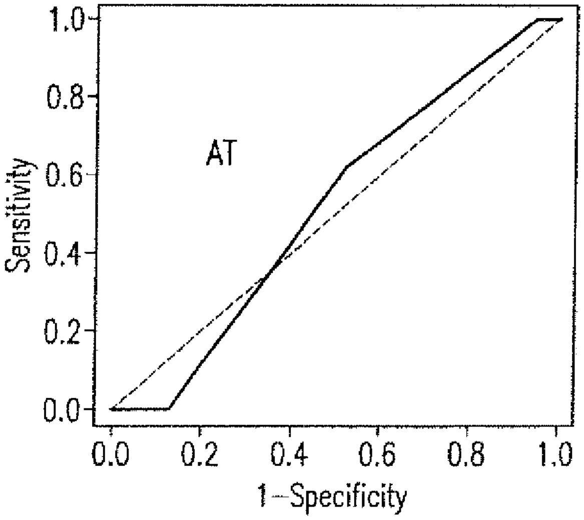

FIG. 10E

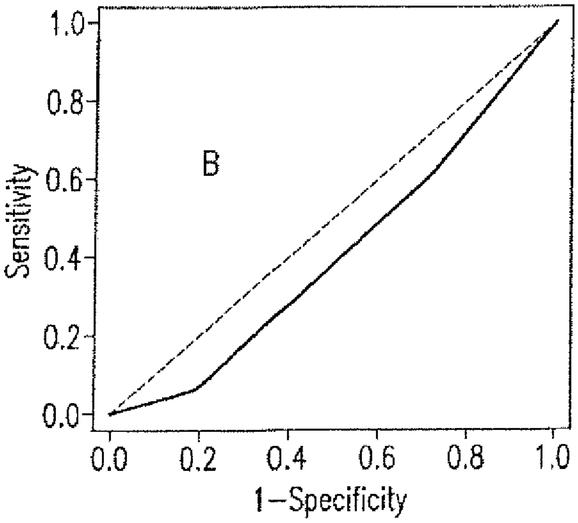

FIG. 10F

METHODS FOR DIAGNOSING PROSTATE CANCER AND PREDICTING PROSTATE CANCER RELAPSE

PRIORITY CLAIM

This application claims priority to U.S. Provisional Application No. 61/535,240, filed Sep. 15, 2011, the contents of which is hereby incorporated by reference in its entirety herein.

GRANT SUPPORT

This invention was made with government support under Grant No. CA098249 awarded by the National Institutes of Health. The government has certain rights in the invention.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Oct. 14, 2014, is named 072396.0574_SL.txt and is 6,786 bytes in size.

1. INTRODUCTION

The present invention relates to methods and compositions for diagnosing prostate cancer and/or determining whether a subject having prostate cancer is at increased risk for relapse or rapid relapse.

2. BACKGROUND OF THE INVENTION

Prostate cancer is one of the most common and lethal malignancies in men: The annual mortality rate reached 32,000 in the US in 2009 (1-3). Previous cytogenetic and other genome studies suggest a clear link between genome abnormalities and the prostate cancer (4-9). Currently, several treatment options are available for prostate cancer patients including watchful waiting, radiation, hormonal/chemo-therapy and radical prostatectomy. Gleason's grading alone or in combination with other clinical indicators such as serum prostate specific antigen levels and pathological or clinical staging has been the guiding tool in selecting these treatment options. Significant numbers of prostate cancer patients, however, experienced relapse after surgical resection of the prostate gland. There is clearly a need for better prediction of the behavior of prostate cancer.

3. SUMMARY OF THE INVENTION

The present invention relates to methods and compositions for diagnosing prostate cancer and/or determining whether a prostate cancer patient is at increased risk of suffering a relapse, or a rapid relapse, of his cancer. It is based, at least in part, on the results of a comprehensive genome analysis on 241 prostate cancer samples (104 prostate cancer, 85 matched bloods, 49 matched benign prostate tissues adjacent to cancer, and 3 cell lines) which indicate that (i) genome copy number variation (CNV) occurred in both cancer and non-cancer tissues, and (ii) CNV predicts prostate cancer progression.

Armed with the present invention, the health care practitioner is better able to advise a prostate cancer patient whether or not to undergo more aggressive forms of therapy or whether watchful waiting would be an appropriate recommendation, where in subjects at higher risk more aggressive forms of therapy may be recommended, including but not limited to prostate resection, antiandrogen therapy, radiotherapy and/or chemotherapy.

4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1A-D. Deletion and amplification of segments of genomes in blood, benign prostate tissues adjacent to cancer, and prostate cancer samples. (A) Histograms of genome deletion (blue) or amplification (red) of blood (B), benign prostate tissues adjacent to tumor (AT), and tumor (T) in 23 pairs of human chromosomes. (B) Box plot of number of genes overlapping with CNV per sample. Outliers in B and AT samples are indicated. (C) Venn diagram of deleted or amplified genes occurring in at least one sample overlapping between B, AT and T. (D) The spectrum of genes that are amplified or deleted in B, AT, tumors that did not relapse (Tnone), tumors that relapsed and had PSADT at or after 15th months of radical prostatectomy (Tslow), and tumors that relapsed and had PSADT within 4 months of radical prostatectomy (Tfast).

FIG. 2A-C. Genome copy variation in prostate cancer predicts relapse. (A) Histograms of genome deletion (blue) or amplification (red) of Tnone, Tslow and Tfast in 23 pairs of human chromosomes. (B) Receiver operating characteristic (ROC) curves of predicting prostate cancer relapse. The prostate cancer were separated into a group that relapsed within 5 years of prostatectomy (n=75) and a group that did not relapse (n=27). Prediction using gene deletions or amplifications unique to relapsing group generated through "leave-one-out" analysis was carried out to produce the ROC chart. The dotted line represents random prediction baseline. The broken line represents prediction generated from Gleason's grading. (C) ROC curves of predicting prostate cancer fast relapse. The prostate cancer were separated into a group that had PSADT within 4 months of prostatectomy (n=33) and a group that did not (n=69). Prediction using gene deletions or amplifications unique to fast relapsing group generated through "leave-one-out" analysis was carried out to produce the ROC chart. The dotted line represents random prediction baseline. The broken line represents prediction generated from Gleason's grading.

FIG. 3A-D. Genome copy variation in benign prostate tissues adjacent to cancer predicts prostate cancer relapse. (A) Histograms of genome deletion (blue) or amplification (red) of AT no relapse, AT relapse, AT not fast relapse, AT fast relapse in 23 pairs of human chromosomes. (B) ROC curves of AT predicting prostate cancer relapse. The AT samples were separated into a group that relapsed within 5 years of prostatectomy (n=21) and a group that did not relapse (n=28). Prediction using gene deletions or amplifications unique to relapsing group generated through "leave-one-out" analysis was carried out to produce the ROC chart. The dotted line represents random prediction baseline. (C) ROC curves of AT predicting prostate cancer fast relapse. The AT samples were separated into a group that had PSADT within 4 months of prostatectomy (n=8) and a group that did not (n=41). Prediction using gene deletions or amplifications unique to fast relapsing group generated through "leave-one-out" analysis was carried out to produce the ROC chart. The dotted line represents random prediction baseline.

FIG. 4A-D. Median size variation of CNV of blood and tumor samples predicts prostate cancer relapse and fast relapse. (A) ROC curves of CNV median size of B predicting prostate cancer relapse. The B samples were separated as described in (A). Prediction using various CNV median sizes was carried out to produce the ROC chart. The dotted line represents random prediction baseline. The optimal prediction rates for CNV median size of B model are 86% (57/66) sensitivity and 61% (11/18) specificity. (B) ROC curves of CNV median size of B predicting prostate cancer fast relapse. The B samples were separated into a group that had PSADT within 4 months of prostatectomy (n=31) and a group that did not (n=53). Prediction using various CNV median sizes was carried out to produce the ROC chart. The dotted line represents random prediction baseline. The optimal prediction rates for CNV median size of B model are 68% (21/31) sensitivity and 70% (37/53) specificity. (C) ROC curves of predicting prostate cancer relapse using median sizes of CNV from T samples. The prostate cancer were separated into a group that relapsed within 5 years of prostatectomy (n=75) and a group that did not relapse (n=27). Prediction using various CNV median sizes was carried out to produce the ROC chart. The dotted line represents random prediction baseline. The broken line represents prediction generated from Gleason's grading. The optimal prediction rates for CNV median size of T model are 71% (53/75) sensitivity and 89% (24/27) specificity. (D) ROC curves of predicting prostate cancer fast relapse using CNV median sizes from T samples. The prostate cancer were separated into a group that had PSADT within 4 months of prostatectomy (n=33) and a group that did not (n=69). Prediction using various CNV median sizes was carried out to produce the ROC chart. The dotted line represents random prediction baseline. The broken line represents prediction generated from Gleason's grading. The optimal prediction rates for CNV median size of T model are 61% (20/33) sensitivity and 90% (62/69) specificity.

FIG. **5**A-D. (A.) Percent overlap of genome segment abnormalities of B, AT, and T, comparing results of study for FIG. **1** and further experiments including additional samples. (B.) Percent deletions with loss of heterozygosity. (C.) Results of quantitative PCR analysis for genes ARL17B, SCAPER, EPHA3 and ERBB4. (D) Sensitivity versus specificity.

FIG. **6**A-D. (A,B) Sensitivity versus specificity in B samples. (C,D) Sensitivity versus specificity in T samples.

FIG. **7**A-B. Sensitivity versus specificity in AT samples (A) and (B).

FIG. **8**A-D. (A,B) Sensitivity versus specificity in B samples. (C,D) Sensitivity versus specificity in T samples.

FIGS. **9**A-D. (A), (B), (C) and (D) Sensitivity versus specificity in B samples.

FIG. **10**A-F. Sensitivity versus specificity in T samples (A,D), B samples (C,F), and AT samples (B,E).

5. DETAILED DESCRIPTION OF THE INVENTION

In certain non-limiting embodiments, the present invention provides for methods and compositions for diagnosing prostate cancer in a subject. In other non-limiting embodiments, the present invention provides for methods and compositions for determining whether a prostate cancer patient is at increased risk of suffering a relapse, or a rapid relapse, of his cancer. In other non-limiting embodiments, the present invention provides for methods and compositions for determining whether a prostate cancer patient is at decreased risk of suffering a relapse, or a rapid relapse, of his cancer (in other words, is at increased risk or has an increased likelihood of not suffering a relapse).

A "prostate cancer patient" is a subject having or who has had a carcinoma of the prostate. The use of the term "patient" does not suggest that the subject has received any treatment for the cancer, but rather that the subject has at some point come to the attention of the healthcare system. Said patient/subject, prior to or contemporaneous with the practicing of the invention, may be untreated for prostate cancer or may have received treatment, including but not limited to surgical, chemotherapeutic, antiandrogen, or radiologic treatment.

"Increased risk" means an increased likelihood that relapse will occur relative to other prostate cancer patients. In particular non-limiting embodiments, there is a statistically validated increase in the likelihood of relapse or rapid relapse relative to subjects without relapse or rapid relapse with a p value of 0.003 for relapse and <0.001 for fast relapse when using "gene specific" CNV of prostate cancer samples, 0.04 for relapse and 0.015 for fast relapse when using "gene specific" CNV of AT samples, <0.001 for relapse and 0.001 for fast relapse when using median sizes of CNV of blood samples from prostate cancer patients, <0.001 for both relapse and fast relapse when using "median sizes" CNV of prostate cancer samples, and 0.004 for relapse when using "mean sizes" of CNV of AT samples.

"Relapse," as that term is used herein, refers to a clinical course including one or more of the following: (i) where the cancer had been removed or put into remission, a recurrence of prostate cancer at the original site or occurrence at a new site, including metastatic spread; (ii) where the cancer had not been removed or put into remission, extension of the cancer and/or metastatic spread; (iii) whether or not the cancer had been treated, an advancement in the clinical grade, for example the Gleasons grade, of the cancer; and/or a prostate specific antigen ("PSA") doubling time of 15 months or longer.

By "rapid", or "relapse quickly", it is meant that relapse occurs within a period of 5 years. In certain embodiments, patients suffering a rapid relapse also manifest a PSA doubling time of 3 months or less or 4 months or less.

In particular, non-limiting embodiments, the method of the invention may be performed as follows. One or more sample may be obtained from a subject. For example, the sample may be a sample of malignant tumor (or presumptively malignant tumor, where a diagnosis has not yet been made) tissue (e.g., microdissection may be performed to achieve a tumor purity of at least about 70 percent or at least about 80 percent or greater than 80%). As another example, a sample may be tissue adjacent a malignant tumor tissue (e.g., prostate tissue that is not identified as tumor located in a prostate gland that contains tumor; in certain non-limiting embodiments the adjacent tissue is non-malignant prostate tissue located at least 3 mm from tumor tissue). As another example, a sample may be a tissue sample which is considered by a skilled artisan to appear abnormal (microscopically and/or macroscopically) and is to be tested to determine whether it is cancerous. As another example, a sample may be a blood sample that contains at least some nucleated cells (to serve as a source of DNA, e.g., whole blood or buffy coat). Multiple samples may be prepared for a single subject; for example, samples of tumor (meaning malignant) tissue, tissue adjacent tumor tissue, and blood may be prepared and the results of analysis of each may be compared.

For example, DNA may be extracted from a sample, for example using a Qiagen tissue kit or other method known in the art. Then genotyping may be performed to identify CNVs across the genome or a portion of the genome, for example, by fragmenting the DNA using restriction enzymes, ligated with adaptors, amplifying the fragments using primers that correspond to the adaptor sequences (for example, Genome wide human snp NSP/STY assay kit, Affymetrix, Calif.), optionally performing an additional fragmentation step, labeling the amplified (optionally further fragmented) DNA product, and then hybridizing the resulting labeled DNA with a plurality of test DNA molecules representative of the genome or a genome portion of interest, for example, but not limited to, as provided in an array such as Affymetrix Genome-Wide Human SNP Array 6.0, under appropriate conditions (for example as described by the array manufacturer). The results may then be interpreted to determine the number or approximate number of CNVs in the genome or portion thereof. For example, Partek Genome Suite 6.6™ or a Affymetrix Genotyping Console may be used.

In one set of non-limiting embodiments of the invention, the number of CNVs across the genome are determined. The present invention provides for a method of diagnosing a prostate cancer in a subject comprising determining the number and/or size of CNVs in a tumor sample, a sample of tissue adjacent a tumor, and/or in a blood sample, where if the number and/or size of CNVs exceeds a particular threshold, a diagnosis of prostate cancer is indicated. The present invention also provides for a method of determining that a prostate cancer patient is at increased risk for relapse or rapid relapse comprising determining the number and/or size of CNVs in a prostate tumor sample, tissue adjacent a prostate tumor, and/or blood, where if the number and/or size of CNVs exceeds a particular threshold, the subject is deemed at risk for relapse or rapid relapse.

In another set of non-limiting embodiments of the invention, CNV of one or more particular gene or chromosome or chromosome region is determined. In specific, non-limiting embodiments of the invention, genes for which CNVs may be determined may include one or more of the genes listed in Tables 2-5, where a CNV in one of the genes listed is indicative of increased risk of relapse (in Table 2 based on a prostate cancer tissue sample or in Table 4 based on tissue adjacent to prostate cancer tissue) or rapid relapse (in Table 3 based on a prostate cancer tissue sample or in Table 5 based on tissue adjacent to prostate cancer tissue). The present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse or rapid relapse comprising determining the number and/or size of CNVs of a specific gene as listed in Table 2, 3, 4 or 5 in a prostate tumor sample, tissue adjacent a prostate tumor, and/or blood, where if the number of CNVs for the gene exceeds a particular threshold, a diagnosis of prostate cancer is indicated and/or the subject is deemed at risk for relapse or rapid relapse.

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

(i) Diagnosis based on CNV number and size;
(ii) Assessment of risk based on CNV number and size;
(iii) Assessment of risk based on CNV of particular genes; and
(iv) Kits.

5.1 Diagnosis Based on CNV Number and Size

In non-limiting embodiments of the invention, the number of CNVs across the genome are determined. CNV may be detected using methodology known in the art, including the hybridization to gene arrays and the analysis of the results of hybridization using software that determines copy number variation, including, but not limited to, the method using Affymetrix products described above. In non-limiting embodiments of the invention, the entire genome or a portion thereof may be analyzed; for example, in a subset of non-limiting embodiments, the chromosome region for which CNVs is determined is one or more of 8p, 13p, 16p, 17p, and/or 8q.

In certain non-limiting embodiments, the present invention provides for a method of diagnosing a prostate cancer in a subject comprising determining the number and/or size of CNVs in DNA from a tumor sample, a sample of tissue adjacent a tumor, and/or in a blood sample, where if the number and/or size of CNVs exceeds a particular threshold, a diagnosis of prostate cancer is indicated.

In a tissue, CNV in at least about 90 loci, each locus being at least 10 kb in length, is consistent with a diagnosis of prostate cancer rather than benign tissue. Accordingly, the present invention provides for a method of diagnosing a prostate cancer in a subject comprising determining the number and size of CNVs in DNA from a tumor or prostate tissue sample, where if the number of CNVs exceeds 90 loci, each locus being at least 10 kb in length, a diagnosis of prostate cancer is indicated.

In a blood sample, CNV in at least 4 loci, each locus being at least 10 kb in length, is consistent with a diagnosis of prostate cancer rather than no malignancy. Accordingly, the present invention provides for a method of diagnosing a prostate cancer in a subject, where said subject is a male having one or more of the following clinical findings: increased serum prostate specific antigen, enlarged prostate on physical exam, difficulty urinating and/or urinary retention, comprising determining the number and/or size of CNVs in DNA from a blood sample from the subject, where if the number of CNVs exceeds 4 loci, each locus being at least 10 kb in length, a diagnosis of prostate cancer is indicated.

In a tissue or a blood sample, a deletion of at least 3 megabases in one or more of the following chromosome regions is consistent with a diagnosis of prostate cancer rather than benign tissue: 8p, 13p, 16q, and/or 17p. Deletions in these regions can be deduced from CNV information. Accordingly, the present invention provides for a method of diagnosing a prostate cancer in a subject comprising determining the presence of deletions in one or more of chromosome regions 8p, 13p, 16q, and/or 17p in DNA from a prostate tissue or a blood sample from the subject, where if there is a deletion of at least 3 megabases in one or more of these regions, a diagnosis of prostate cancer is indicated.

In a tissue or a blood sample, an amplification of a locus in chromosome region 8q and/or X is consistent with a diagnosis of prostate cancer rather than benign tissue. Amplification in these regions can be deduced using CNV information. Accordingly, the present invention provides for a method of diagnosing a prostate cancer in a subject comprising determining the presence of amplification in one or more of chromosome regions 8q and X in DNA from a prostate tissue or a blood sample from the subject, where if there is amplification of a locus in one or more of these regions, a diagnosis of prostate cancer is indicated.

If a diagnosis of prostate cancer is indicated, a healthcare provider may optionally take the further step of recommending and/or performing a further diagnostic test, such as a biopsy or prostate ultrasound, and/or recommending and/or performing a therapeutic procedure, for example but not limited to surgical excision, radiotherapy, and/or chemotherapy.

5.2 Assessment of Risk Based on CNV Size

In non-limiting embodiments of the invention, CNVs across the genome are determined. CNV may be detected using methodology known in the art, including the hybridization to gene arrays and the analysis of the results of hybridization using software that determines copy number variation, including, but not limited to, the method using Affymetrix products described above. In non-limiting embodiments of the invention, the entire genome or a portion thereof may be analyzed; for example, in a subset of non-limiting embodiments, the chromosome region for which CNVs is determined is one or more of 8p, 13p, 16p, 17p, and/or 8q.

In non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse or rapid relapse comprising determining the size of CNVs in a prostate tumor sample, tissue adjacent a prostate tumor, and/or blood, where if the size of CNVs is less than a particular threshold, the patient is deemed to be at decreased risk for relapse or rapid relapse.

In non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse or rapid relapse comprising determining the mean and/or median size of CNVs in a prostate tumor sample, tissue adjacent a prostate tumor, and/or blood, where if the mean or median size of CNVs is less than a particular threshold, the patient is deemed to be at decreased risk for relapse or rapid relapse.

In non-limiting embodiments, the present invention may utilize the average (mean) size of CNV to assess the likelihood that a prostate cancer will relapse. CNV size may be determined using the same genotyping analysis techniques as described above and as are known in the art. In particular non-limiting embodiments of the invention, using the Partek software described above, segments with copy number change may be obtained (including amplification and deletions), and those with the criteria $p<0.001$, length >2000 bp and >10 markers, may be selected and then the mean length of the CNVs thus identified may be determined.

In certain non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse comprising determining the size of CNVs in DNA from a blood sample from the patient, where if the average (i.e., mean) size of CNVs is 40 kb or less or 33 kb or less, the patient is deemed to be at decreased risk for relapse.

In certain non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse comprising determining the size of CNVs in DNA from a sample of tissue adjacent a prostate cancer from the patient, where if the mean size of CNVs is 95 kb or less or 81.1 kb or less, the patient is deemed to be at decreased risk for relapse.

In certain non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse comprising determining the size of CNVs in DNA from a sample of prostate cancer tissue from the patient, where if the mean size of CNVs is 385 kb or less or 105 kb or less, the patient is deemed to be at decreased risk for relapse.

In further non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse or rapid relapse comprising determining the mean or median size of CNVs in a prostate tumor sample, tissue adjacent a prostate tumor, and/or blood, where if the mean or median size of CNVs exceeds a particular threshold, the patient is deemed to be at increased risk for relapse or rapid relapse.

In one non-limiting embodiment, in a blood sample from a prostate cancer patient, an average (mean) CNV size of 70 kb or more, is consistent with a likelihood that the prostate cancer will relapse. Accordingly, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining the mean size of CNVs in DNA from a blood sample from the patient, where if the average (i.e., mean) size of CNVs is 70 kb or more, the patient is deemed to be at increased risk for relapse.

In other non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining the mean size of CNVs in DNA from a sample of tissue adjacent to prostate cancer from the patient, where if the mean size of CNVs is 246 kb or more, the patient is deemed to be at increased risk for relapse.

In other non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining the mean size of CNVs in DNA from a sample of prostate cancer tissue from the patient, where if the mean size of CNVs is 817 kb or more, the patient is deemed to be at increased risk for relapse.

In other non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for rapid relapse comprising determining the mean size of CNVs in DNA from a sample of prostate cancer tissue from the patient, where if the mean size of CNVs is 1060 kb or more, the patient is deemed to be at increased risk for rapid relapse.

In further non-limiting embodiments, the present invention may utilize the median size of CNV to assess the likelihood that a prostate cancer will relapse. CNV size may be determined using the same genotyping analysis techniques as described above and as are known in the art. In particular non-limiting embodiments of the invention, using the Partek software described above, segments with copy number change may be obtained (including amplification and deletions), and those with the criteria $p<0.001$, length >2000 bp and >10 markers, may be selected and then the median length of the CNVs thus identified may be determined.

In one non-limiting embodiment, in a blood sample from a prostate cancer patient, a median CNV size of about 17 kb or less is consistent with a likelihood that the prostate cancer will not relapse. Accordingly, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse comprising determining the median size of CNVs in a blood sample, where if the median size of CNVs is 17 kb or less, the subject is deemed to be at decreased risk for relapse.

In certain non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse comprising determining the median size of CNVs in DNA from a sample of tissue adjacent to a prostate cancer from the patient, where if the median size of CNVs is 16 kb or less, the patient is deemed to be at decreased risk for relapse.

In certain non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at decreased risk for relapse comprising determining the median size of CNVs in DNA from a sample of prostate cancer tissue from the patient, where if the median size of CNVs is 185 kb or less, the patient is deemed to be at decreased risk for relapse.

In certain other non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining the median size of CNVs in DNA from a blood sample from the patient, where if the median size of CNVs is 23 kb or more, the patient is deemed to be at increased risk for relapse.

In other non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining the median size of CNVs in DNA from a sample of tissue adjacent to prostate cancer from the patient, where if the median size of CNVs is 17384 or more or 18 kb or more, the patient is deemed to be at increased risk for relapse.

In other non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for rapid relapse comprising determining the median size of CNVs in DNA from a sample of tissue adjacent to prostate cancer from the patient, where if the median size of CNVs is 32651 bp or more, or 33 kb or more, the patient is deemed to be at increased risk for rapid relapse.

In other non-limiting embodiments, the present invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining the median size of CNVs in DNA from a sample of prostate cancer tissue from the patient, where if the median size of CNVs is 647 kb or more, the patient is deemed to be at increased risk for relapse.

If is determined that the patient is at increased risk for relapse or rapid relapse, a healthcare provider may optionally take the further step of recommending and/or performing frequent monitoring of the patient for recurrence (e.g., a PSA test or imaging (e.g. ultrasound, CT scan, MRI or PET scan)) and/or recommending and/or performing a therapeutic procedure, for example but not limited to surgical excision, radiotherapy, and/or chemotherapy.

5.3 Assessment of Risk by Cnv of Particular Genes

In non-limiting embodiments of the invention, the number of CNVs across the genome are determined. CNV may be detected using methodology known in the art, including the hybridization to gene arrays and the analysis of the results of hybridization using software that determines copy number variation, including, but not limited to, the method using Affymetrix products described above. In non-limiting embodiments of the invention, the entire genome or a portion thereof may be analyzed; for example, in a subset of non-limiting embodiments, the chromosome region for which CNVs is determined is one or more of 8p, 13p, 16p, 17p, and/or 8q. Further, the CNV of particular genes may be determined and utilized as set forth in this section.

In further non-limiting embodiments, a CNV in a gene in a prostate cancer tissue from a subject, where the gene is listed in Table 2, indicates that the subject is likely to relapse. In further non-limiting embodiments, a CNV in a gene in a prostate cancer tissue from a subject, where the gene is listed in Table 3, indicates that the subject is likely to experience rapid relapse.

In further non-limiting embodiments, a CNV in a gene in a tissue adjacent to prostate cancer tissue from a subject, where the gene is listed in Table 4, indicates that the subject is likely to relapse. In further non-limiting embodiments, a CNV in a gene in a tissue adjacent a prostate cancer tissue from a subject, where the gene is listed in Table 5, indicates that the subject is likely to experience rapid relapse.

In on set of non-limiting embodiments, the present invention provides for a gene-based prediction in any one or more of four scenarios: relapse or fast relapse prediction in tumor (T) or tissues adjacent to tumor (AT). According to this set of embodiments, the methods for these four scenarios are the same except for the gene lists used are different. In particular, for each scenario, two gene lists are utilized: one list for genes amplified (list "a") and one list for genes deleted (list 'b"). Using Partek, the copy number change status of each gene for each sample could be determined; the status could be amplified, deleted or unchanged.

For a given T sample, the number of genes in list "a" that are amplified and the number of genes in list "b" that are deleted are counted, and the number of amplified genes in list "a" may be designated "a" and the number of deleted genes in list "b" may be designated "b". Genes in list "a" for relapse include HECTD1, MIR1827, UBXN8, SMAP1, C6orf147, DDX43, SLC17A5, LRRIQ4, LRRC31, SAMD7, LOC100128164, SEC62, GPR160, and PHC3. Genes in list "b" for relapse include SLC7A5, CASA, BANP, ZFPM1, ZC3H18, IL17C, CYBA, MVD, MGC23284, SNAI3, RNF166, GALNS, TRAPPC2L, CBFA2T3, ACSF3, C16orf81, CDH15, ANKRD11, SPG7, RPL13, SNORD68, CDK10, SPATA2L, C16orf7, ZNF276, SYT16, GRIN2B, BCAT1, OVCH1, BEYLA, GPR125, and GBA3. If the number (a+b) is larger than a pre-set cutoff C (i.e. a+b>C), the corresponding sample is assigned the risk designation relapse or fast relapse, depending upon the list that is drawn from. In a particular non-limiting embodiment, in a+b>C, C=0 meaning that the threshold is 0 so that if a or b is a non-zero number, there is an increased risk of relapse.

In non-limiting embodiments, the invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining whether a gene is amplified or whether a gene is deleted in DNA from a sample of prostate cancer tissue from the patient, wherein (a) if one or more gene is amplified from the group consisting of HECTD1, MIR1827, UBXN8, SMAP1, C6orf147, DDX43, SLC17A5, LRRIQ4, LRRC31, SAMD7, LOC100128164, SEC62, GPR160, and PHC3 and/or (b) if one or more gene is deleted from the group consisting of SLC7A5, CASA, BANP, ZFPM1, ZC3H18, IL17C, CYBA, MVD, MGC23284, SNAI3, RNF166, GALNS, TRAPPC2L, CBFA2T3, ACSF3, C16orf81, CDH15, ANKRD11, SPG7, RPL13, SNORD68, CDK10, SPATA2L, C16orf7, ZNF276, SYT16, GRIN2B, BCAT1, OVCH1, BEYLA, GPR125, and GBA3, then the patient is deemed to be at increased risk for relapse.

In other non-limiting embodiments, genes in list "a" for rapid relapse include BRMS1L, KCNMB4, MIR548A1, ORC3L, SDAD1, CXCL9, ART3, CXCL10, CXCL11 Genes in list "b" for rapid relapse include GALNTL1, FLJ44817, KIAA0247, LOC100289511, SFRS5, SLC10A1, SLC8A3, SNORD56B, PABPC3, MTMR6, ATP8A2, NAV2, ZC3H12C, FDX1, ARHGAP20, C11orf88, LAYN, and CD28. In a particular non-limiting embodiment, in a+b>C, C=0, meaning that the threshold is 0 so that if a or b is a non-zero number, there is an increased risk of rapid relapse.

In non-limiting embodiments, the invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining whether a gene is amplified or whether a gene is deleted in DNA from a sample of prostate cancer tissue from the patient, wherein (a) if one or more gene is amplified from the group consisting of BRMS1L, KCNMB4, MIR548A1, ORC3L, SDAD1, CXCL9, ART3, CXCL10, and CXCL11 and/or (b) if one or more gene is deleted from the group consisting of GALNTL1, FLJ44817, KIAA0247, LOC100289511, SFRS5, SLC10A1, SLC8A3, SNORD56B, PABPC3, MTMR6, ATP8A2, NAV2, ZC3H12C, FDX1, ARHGAP20, C11orf88, LAYN, CD28, then the patient is deemed to be at increased risk for rapid relapse.

In related embodiments applied to AT, two gene lists are utilized: one list for genes amplified (list "c") and one list for genes deleted (list "d"). Using Partek, the copy number change status of each gene for each sample could be determined; the status could be amplified, deleted or unchanged. For a given T sample, the number of genes in list "c" that are amplified and the number of genes in list "d" that are deleted are counted, and the number of amplified genes in list "c" may be designated "c" and the number of deleted genes in list "d" may be designated "d". Genes in list "c" for relapse include DZIP1, ZHX2, DERL1, WDR67, COL22A1, BHLHE40 and, in a non-limiting embodiment, there is no gene in list "d". In a particular non-limiting embodiment, in a+b>C, C=0 meaning that the threshold is 0 so that if c or d is a non-zero number, there is a likelihood of relapse. In other non-limiting embodiments applied to AT, genes in list "c" for rapid relapse include MAGEL2, NDN, RSU1, ADCY2, UBE2E1 and genes in list "d" for rapid relapse based on AT include RPL23AP82, RABL2B, CA10, C13orf36, SMAD9, ALG5, RETNLB, TRAT1, GUCA1C, MORC1. In a particular non-limiting embodiment, in a+b>C, C=1 meaning that the threshold is I so that if the sum of c and d is greater than one, there is a likelihood of rapid relapse.

In non-limiting embodiments, the invention provides for a method of determining that a prostate cancer patient is at increased risk for relapse comprising determining whether a gene is amplified in DNA from a sample of tissue adjacent to prostate cancer tissue from the patient, wherein if one or more genes is amplified from the group consisting of DZIP1, ZHX2, DERL1, WDR67, COL22A1, BHLHE40 then the patient is deemed to be at increased risk for relapse.

In non-limiting embodiments, the invention provides for a method of determining that a prostate cancer patient is at increased risk for rapid relapse comprising determining whether a gene is amplified or whether a gene is deleted in DNA from a sample of tissue adjacent to prostate cancer tissue from the patient, wherein (a) if one or more genes is amplified from the group consisting of MAGEL2, NDN, RSU1, ADCY2, UBE2E1 and/or (b) one or more genes is deleted from the group consisting of RPL23AP82, RABL2B, CA10, C13orf36, SMAD9, ALG5, RETNLB, TRAT1, GUCA1C, MORC1, wherein the total number of genes amplified from the group listed in (a) and/or deleted from the group listed in (b) is greater than or equal to 2, then the patient is deemed to be at increased risk for rapid relapse.

If is determined that the patient is at increased risk for relapse or rapid relapse, a healthcare provider may optionally take the further step of recommending and/or performing frequent monitoring of the patient for recurrence (e.g., a PSA test or imaging (e.g. ultrasound, CT scan, MRI or PET scan), digital rectal exam) and/or recommending and/or performing a therapeutic procedure, for example but not limited to surgical excision, radiotherapy, and/or chemotherapy.

If is determined that the patient is at decreased risk for relapse, a healthcare provider may optionally take the further step of recommending that the patient not seek imminent further treatment and/or performing frequent monitoring of the patient for recurrence (e.g., a PSA test or imaging (e.g. ultrasound, CT scan, MRI or PET scan), digital rectal exam) ("watchful waiting").

5.4 Kits

In non-limiting embodiments, the present invention provides for kits that may be used to practice the invention. Such kits may include an array comprising nucleic acid representing at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 15, at least 20, at least 30, at least 40, or at least 50 of the following genes, where the genes listed below constitute up to 50 percent or up to 60 percent or up to 70 percent or up to 80 percent or up to 90 percent or up to 95 percent or up to 100 percent of the total set of genes represented in the array:

genes listed in Table 2;
genes listed in Table 3;
genes listed in Table 4;
genes listed in Table 5;
HECTD1, MIR1827, UBXN8, SMAP1, C6orf147, DDX43, SLC17A5, LRRIQ4, LRRC31, SAMD7, LOC100128164, SEC62, GPR160, PHC3, SLC7A5, CASA, BANP, ZFPM1, ZC3H18, IL17C, CYBA, MVD, MGC23284, SNAI3, RNF166, GALNS, TRAPPC2L, CBFA2T3, ACSF3, C16orf81, CDH15, ANKRD11, SPG7, RPL13, SNORD68, CDK10, SPATA2L, C16orf7, ZNF276, SYT16, GRIN2B, BCAT1, OVCH1, BEYLA, GPR125, GBA3, BRMS1L, KCNMB4, MIR548A1, ORC3L, SDAD1, CXCL9, ART3, CXCL10, CXCL11, GALNTL1, FLJ44817, KIAA0247, LOC100289511, SFRS5, SLC10A1, SLC8A3, SNORD56B, PABPC3, MTMR6, ATP8A2, NAV2, ZC3H12C, FDX1, ARHGAP20, C11orf88, LAYN, CD28 DZIP1, ZHX2, DERL1, WDR67, COL22A1, BHLHE40, MAGEL2, NDN, RSU1, ADCY2, UBE2E1, RPL23AP82, RABL2B, CA10, C13orf36, SMAD9, ALG5, RETNLB, TRAT1, GUCA1C, and MORC1.

For example, but not by way of limitation, an array may comprise sets of genes as listed above for lists "a", "b", "c" and/or "d".

Such kits may optionally comprise software, or internet access to software, in electronically readable form, that determines the number and size of CNVs in the genes represented in the array, and optionally software, or internet access to software, in electronically readable form, that determines whether CNVs in a DNA sample exceed or fall below a threshold set forth herein that indicates an increased risk of relapse or an increased risk of rapid relapse of prostate cancer.

6. EXAMPLE: GENOME ABNORMALITIES PRECEDE PROSTATE CANCER AND PREDICT CLINICAL RELAPSE

6.1 Materials and Methods

Tissue Processing, DNA Extraction, Amplicon Generation, Labeling, Hybridization, Washing and Scanning of SNP 6.0 Chips.

Prostate cancer samples were obtained from the University of Pittsburgh Medical Center Tissue Bank, Pittsburgh, Pa. These samples were collected from 1998 to 2009, To make the analysis balance, samples of short prostate specific antigen doubling time ("PSADT") (<4 months), long PSADT (>15 months), and no relapse (cancer free for >5 years after radical prostatectomy) each were made to constitute approximately one third of the total number. Whenever possible, nonrelapse samples were chosen to match pathological stages and Gleason grades of relapse samples.

A total of 214 samples were from whites, whereas 5 samples were from African Americans and 19 samples were from patients with an unknown race. The patients whom these samples were obtained from either experienced relapse or had no relapse for at least 5 years, based on chemical (serum PSA) and radiological evidence. Frozen tissues were used for blood, prostate cancer, and benign prostate tissue adjacent to cancer. Clinical follow-up was conducted by office examination record, blood PSA survey, and radiographical follow-up. These follow-up visits were performed for up to a 10-year period after the patient underwent a radical prostatectomy. The protocol was approved by the Institutional Review Board. For prostate cancer, microdissection was performed to achieve tumor purity >80%. For benign prostate tissues adjacent to cancer, benign tissues away from prostate cancer (at least 3 mm) were microdissected. Whenever available, whole blood or buffy coat from the same patients was used as a normal control. PC3, DU145, and LNCaP cells were obtained from American Type Culture Collection Inc, (Manassas, Va.) in 2000, 2001, and 2007, respectively. The genomes of these cell lines were tested for short tandem repeat DNA profiling on eight different loci (CSF1PO, D13S317, D16S539, D5S818, D7S820, THO1, TPDX, and vWA) of the genomes by PCR using the following sets of primers:

(SEQ ID NO: 1)
CSF1PO, 5'-AACCTGAGTCTGCCAAGGACTAGC-3'
and
(SEQ ID NO: 2)
5'-TTCCACACACCACTGGCCATCTTC-3';

(SEQ ID NO: 3)
D13S317, 5'-ACAGAAGTCTGGGATGTGGA-3'
and
(SEQ ID NO: 4)
5'-GCCCAAAAAGACAGACAGAA-3';

(SEQ ID NO: 5)
D16S539, 5'-GATCCCAAGCTCTTCCTCTT-3'
and
(SEQ ID NO: 6)
5-ACGTTTGTGTGTGCATCTGT-3';

(SEQ ID NO: 7)
D5S818, 5'-GGGTGATTTTCCTCTTTGGT-3'
and
(SEQ ID NO: 8)
5'-TGATTCCAATCATAGCCACA-3';

(SEQ ID NO: 9)
D7S820, 5'-TGTCATAGTTTAGAACGAACTAACG-3'
and
(SEQ ID NO: 10)
5'-CTGAGGTATCAAAAACTCAGAGG-3';

(SEQ ID NO: 11)
TH01, 5'-GTGGGCTGAAAAGCTCCCGATTAT-3'
and
(SEQ ID NO: 12)
5'-ATTCAAAGGGTATCTGGGCTCTGG-3';

(SEQ ID NO: 13)
TPOX, 5'-CTGGCACAGAACAGGCACTTAGG-3'
and
(SEQ ID NO: 14)
5'-GGAGGAACTGGGAACCACACAGGT-3';
and

(SEQ ID NO: 15)
vWA, 5'-CCCTAGTGGATGATAAGAATAATCAGTATG-3'
and
(SEQ ID N): 16)
5'-GGACAGATGATAAATACATAGGATGGATGG-3'.

These cell lines were authenticated because the short tandem repeat profiles of the cell lines have a perfect match with those published by American Type Culture Collection Inc. DNA was then extracted using a Qiagen tissue kit (Qiagen, Valencia, Calif.). Detailed case information is shown in Tables 1A-D. Genome DNA (500 ng), was digested with StyI and Nsp1 for 2 hours at 37° C. The digested DNA was purified and ligated with primer/adaptors at 16° C. for 12 to 16 hours. Amplicons were generated by performing PCR using primers provided by the manufacturer (Affymetrix, Santa Clara, Calif.) on the ligation products using the following program: 94° C. for 3 minutes and then 35 cycles of 94° C. for 30 seconds, 60° C. for 45 seconds, and 65° C. for 1 minute. This was followed by extension at 68° C. for 7 minutes. The PCR products were then purified and digested with DNaseI for 35 minutes at 37° C. to fragment the amplified DNA. The fragmented DNA was then labeled with biotinylated nucleotide through terminal deoxynucleotide transferase for 4 hours at 37° C. Fragmented DNA, 250 μg, was hybridized with a pre-equilibrated Affymetrix SNP 6.0 chip at 50° C. for 18 hours. Procedures of washing and scanning of SNP 6.0 chips followed the manuals provided by Affymetrix.

SYBR-Green Real Time Quantitation PCR:

LightCycler FastStart DNA Master SYBR-Green I kit was used for real time PCR amplification. The reaction was carried out in a MasterCycler Realplex™ (Eppendorf, Hauppauge, N.Y.). A quantitation standard curve of normal male DNA from 50,000 to 500,000 copies of genome was generated using known amounts of template copies. Twenty nanograms of genomic DNA were used for all of the experimental and control samples. Taq DNA polymerase was activated with a 2 min pre-incubation step at 94° C. Amplification of the following primers was performed:

ARL17B (ACTGTCATAGCAGTGCTGAGG(SEQ ID NO: 17)/
ACTTACCTACTGTAGGGACGG SEQ ID NO: 18),

SCAPER (AGGAAGGCCTATTCGTTCTCG SEQ ID NO: 19/
GAACAGTATGGGAGGAGTTCG(SEQ ID NO: 20),

WWOX (GCCAGTTGATGTGACAACTGC(SEQ ID NO: 21)/
CAGCTGAGAGTGGTTTCTTTGC(SEQ ID NO: 22)),

EPHA3 (ATCAGGACTTACCAGGTGTGC(SEQ ID NO: 23)/
ACCGTGTCTGGAAACATAGCC(SEQ ID NO: 24)),
and

ERBB4 (AGTGGCCTGTCCTTGCTTATC(SEQ ID NO: 25)/
CAGAGCAACAATTCTGACCGG(SEQ ID NO: 26))

with 35 cycles of the following program: 94° C. for 30 s, 62° C. for 30 s, and 68° C. for 3 min. Realplex™ data software was used to quantify and to fit the data with a standard curve. A separate β-actin (TCTTTGCACTTTCTGCATGTCCCC (SEQ ID NO: 27) /GTCCATCACGATGCCAGTGGTAC (SEQ ID NO:28)) DNA quantification was also performed as an internal control for each analysis.

Statistical Analysis:

Two hundred forty-one cell files were analyzed with the Genotyping console 4.0 from Affymetrix, Inc. for quality control analysis. Samples with QC call above 80% and QC contrast ratio above 0.4 were admitted into the analysis. To analyze CNV, cell files were imported into Partek GenomeSuite 6.6 to generate copy number from raw intensity. To plot the histograms, GC adjust was performed. Deletion or amplification of genomes were analyzed by first limiting to the regions with p-value less than 0.05/total number of regions detected, i.e. family-wise error rate (FWER) is controlled using Bonferroni's correction (10). The selected regions were subsequently filtered by limiting to the regions with at least 100 markers and 10 kb. The regions were then mapped to known genes. For a subset of the sample (i.e. tumor or relapse with rapid progression), the frequencies of amplification/deletion are calculated on the gene level. The frequencies were plotted to the genome corresponding to the gene locations.

Prediction Analysis and ROC Curve:

The following prediction analysis for the comparison of (1) non-relapse versus fast-relapse+slow-relapse); (2) non-relapse+slow-relapse versus fast-relapse was performed. A test sample was first left out from prediction model construction. The remaining samples were used as the training set. Loci with more than r % amplification or r % deletion in the case group but none locus aberration in the control group were selected as predictive loci. To predict the left-out test sample, the percentage of locus aberration (amplification or deletion) among the identified predictive loci was calculated. The test sample was predicted as a case if the percent of aberration is greater than p % threshold, and control otherwise. The "leave-one-out" cross-validation was repeated until each sample was left out and predicted. In this prediction scheme, r is a parameter that determines the number of predictive loci used in the model. For a given r, the threshold p % was varied to locus rate an ROC curve with sensitivity/specificity trade-off. We selected r that produced the best "area under curve" (AUC)(11). To report the best sensitivity and specificity trade-off and overall accuracy rate, we chose the threshold p % such that the Youden index (sensitivity+specificity−1) is maximized. This criterion gave equal importance to sensitivity and specificity. To further evaluate whether the prediction result is better than obtained by random, AUC was used as a test statistics, and permutation analysis was performed to assess the statistical significance. Specifically, class labels (case and control) were randomly shuffled and AUC calculation was performed. Such permutations were repeated for 1000 times to generate the null distribution. The p-value was calculated as the percentage that the 1000 null AUCs from permutation are greater than the observed AUC. The genes that are overlapped with the loci used in the test and the frequency of utilization are listed in Tables 2-5. For Gleason score prediction, the ROC curve was generated by varying Gleason score threshold. AUC and its associated p-value were similarly calculated. For CNV size prediction, CNV was limited to >2 kb, p<0.001 and >10 markers. The ROC curve was generated by varying sizes of CNV threshold. AUC and its associated p-value were similarly calculated.

Prediction Analysis for Blood Versus Tumor:

To predict blood versus tumor, the total number of aberrations in each sample was counted instead of the predictive locus selection described above. The ROC curve, AUC and the associated p-value were similarly generated.

6.2 Results

The SNP 6.0 chip hybridization results were analyzed through Partek Genome Suite 6.6™, using blood (B) samples as normal references. As shown in histograms of FIG. **1**A, abnormalities of genome in copy number can be found in all chromosomes in prostate cancer. An average of 91.6 loci (minimum of 10 kb) per sample involving 1092 genes were identified either amplified or deleted in prostate cancer genomes as determined by more than 100 markers, p<5.5x10-9 (Bonferroni correction, FIG. **1**B). Deletions of large segments of (>3 megabases) chromosome 8p, 13p, 16q and 17p occurred with high frequencies, while amplification of 8q and X chromosomes occurred in a subset of prostate cancer samples. Similar amplification and deletion of the same regions also occurred in benign prostate tissues adjacent to cancer, albeit with smaller sizes and lower frequency. Unexpectedly, the blood of prostate cancer patients contains significant abnormalities in genomes (1329 genes total, or 4.4 loci and 32.6 genes/sample). Most of these abnormalities are not unique and are overlapped with those of prostate cancer samples (FIG. **1**C). Prostate cancers were then subdivided based on clinical behavior: those with no relapse after prostatectomy (Tnone); those with relapse and slow increase in serum prostate specific antigen (FSA, doubling in more than 15 months) (Tslow); those with relapse and rapid increase in serum PSA (doubling in less than 4 months) (Tfast). The kinetics of PSA increase after prostatectomy is predictive of prostate-cancer specific death, with rapid increases highly associated with lethal prostate cancer(12). The spectrum of locus abnormalities increases from blood to prostate cancer in an incremental fashion: the least in blood to the most in rapidly progressive prostate cancer (Tfast) (FIG. **1**D).

To assess the reproducibility of these analyses, a large set of reference normal samples (n=800) available to public through Partek, Inc. was used. This re-analysis showed genome segment abnormalities of B, AT and T overlapped at least 93 percent between these two analyses (FIG. **5**A). In addition, a third analysis using a different set of normal samples (GeneSpring GX11, n=265) was performed, showing that 94% to 99% of the amplified or deleted genome segments from B, AT and T overlap with those obtained from Partek Genome Suite analyses using blood as baseline (FIG. **5**A). Affymetrix SNP6.0 contains separate probe sets for SNP and CNV detection. The majority of large genome deletions are accompanied with loss of heterozygosity (LOH). Profiles of LOH for B, AT and T samples were generated to validate the deletions detected by CNV analysis. Genome deletion frequently accompanied LOH (91% to 98%), with average matches for B, AT and T ranging from 93% to 96% (FIG. **5**B). This suggests that the analyses are reproducible and robust.

Five loci from chromosomes 16, 17, 3, 2 and 15 with deletions of at least 10 kb and overlapping with nearby genes were selected for quantitative-PCR analysis. As shown in FIG. **5**C, a deletion by Q-PCR was found in 4 of 5 samples predicted to have a deletion in the region overlapping with ARL17B, a gene homologous to ADP-ribosylation factor located at 17q2113. Similar confirmation was found in Q-PCR of SCAPER, the S-phase cyclin A-associated protein in the ER located at 15q2414 (5 of 5 samples), of WWOX, WW domain containing oxidoreductase located at 16q2315-17 (5 of 5 samples), of EPHA3 or ephrin receptor 3, a protein tyrosine receptor frequently mutated in a variety of human cancers 18-20 (4 of 5 samples), and of ERBB4 or v-erb-a erythroblastic leukemia viral oncogene homolog 421,22 (5 of 5 samples) in blood samples from prostate cancer patients. The concordance rate of Q-PCR and copy number analysis was 92%. Our analysis indicates that copy number variation is not limited to prostate cancer or benign prostate tissue adjacent to cancer, but is also found in blood from prostate cancer patients.

To investigate whether the CNV profiles of B, AT and T are distinctive from each other, classification analysis was performed to predict genomes of blood versus those of prostate cancer, by aggregating genome loci that have differential amplification or deletion proportion between blood and prostate cancer (see methods for more detail). The prediction accuracy under unbiased "leave-one-out" cross-validation(23) was 89% for blood (76/85) and 94% for prostate cancer (98/104). The overall accuracy was 92% (174/189, FIG. **5**D). To investigate whether AT is genetically more related to cancer or "normal" tissues, the CNV profiles of B and T samples were constructed into a logistic regression model as "normal" and "prostate cancer" training sets, respectively. This model was then utilized to classify each of the 49 AT samples as either "normal" or "prostate cancer". Such analysis predicts that 42 of 49 (86%) putatively benign prostate tissue is "cancer", while only 7 of the AT tissues were classified as "normal". All prostate cancer cell lines were classified as "cancer". These analyses clearly indicate that majority of AT samples have copy number profiles similar to prostate cancer's rather than to normal's, resembling a field effect similarly found for gene expression profiling(24).

The vast majority of prostate cancers are not lethal(25). Prediction analysis with "leave-one-out" cross-validation based on loci that have significant proportion of amplification or deletion in the group of relapse but none in the non-relapsed group was performed. The resulting Receiver Operating Characteristic curves (ROC) were generated by varying sensitivity-specificity trade-off (FIG. **2**A,B). The cutoff that generates the best Youden index (i.e. sensitivity+specificity-1) has an accuracy of 73% (74/102, ROC p=0.003, positive prediction=76% [57/75], negative prediction=63% [17/27]) for relapse prediction. Gleason's grading has been a strong predictor of recurrence but in this analysis it was statistically insignificant from baseline (ROC p=0.32) and much worse than CNV analysis.

Prostate cancers with rapid progression, as defined by rates of PSA rise, are lethal1(2,26). Those with PSA doubling time (PSADT)<4 months after relapse and those who died of prostate cancer were compared to those with PSADT >15 months or having no relapse. A similar prediction with "Leave-One-Out" cross-validation analysis was performed to examine the accuracy of CNV profiling (see the genes listed in TABLE 3) in predicting rapidly progressing prostate cancer. As shown in FIG. **2**C, the accuracy of predicting rapid progression was 75% (p<0.001) with positive and negative predictive value of 58% and 83%, respectively. In contrast, the histology of the cancer, as defined by Gleason grading, failed to achieve >50% predictive values simultaneously on positive and negative predictions (ROC p=0.074).

Since the genome alterations in AT are most similar to those of T, the CNV of AT to predict relapse was examined using cross-validation. As shown in FIGS. **3**A and **3**C, the CNV profile of AT is moderately predictive of prostate cancer relapse: a sensitivity of 76% and a specificity at 56% (ROC p=0.041) were observed. Surprisingly, the CNV profile of AT is more accurate in predicting fast relapse (88% sensitivity and 75% specificity, p=0.015, FIG. **3** B&D). Using the same approach, the CNV profiles from B failed to generate a ROC statistically different from baseline in predicting relapse or fast relapse. However, our analysis showed that the average and median sizes of CNV are significantly larger in blood samples (70 Kb and 23 kb, respectively) from patients with relapse than those without (40 kb and 17 kb). Based on the sizes of CNV, highly statistically significant ROCs were generated (FIG. **4**A-B), predicting 81% (p<0.001) relapse and 69% (p=0.001) fast relapse correctly through median CNV sizes. The CNV size correlation with relapse was also found in T (817 kb mean and 647 kb median for relapse vs. 385 kb and 185 kb for non-relapse) and AT samples (246 kb mean and 18 kb median for relapse vs. 95 kb and 16 kb for non-relapse), suggesting a larger CNV size a common feature for prostate cancer relapse regardless tissues. Both median and mean sizes of CNV from T and B, and mean size of CNV from AT predict prostate cancer relapse, while mean and median sizes of CNV from T and B predict fast relapse (FIGS. **4**A-D, **6**A-D and **7**A-B). Interestingly, similar relapse prediction results were also replicated using the sizes of either amplified or deleted loci of blood (FIGS. **8**A-D and **9**A-D).

To rule out aging being a factor in our analysis, correlation analyses between our gene-specific or size-based model and the patient age were performed, and revealed no significant correlation between age and our prediction methods. Age did not predict outcomes (FIG. **10**A-F).

To investigate the reproducibility of our prediction models, we collected an additional 25 samples, including 10 tumors, 10 benign tissues adjacent to tumors, and 5 blood samples from patients with prostate cancer. These experiments and analyses were performed in a separate time period and by different personnel. By using a genespecific model, we correctly predicted 7 of 10 relapse and 8 of 10 short PSADT from tumor samples, whereas we correctly predicted 7 of 10 for both relapse and short PSADT from AT samples. By using mean size of CNV from tumor, we correctly predicted 7 of 10 cases of both relapse and short PSADT, 7 of 10 for relapse from AT, and 4 of 5 for relapse and 4 of 5 for short PSADT from blood. By using median size of CNV from tumors, we correctly predicted 6 of 10 for relapse and 7 of 10 for short PSADT, whereas from blood, we correctly predicted 5 of 5 for relapse and 4 of 5 for short PSADT. Taken together, the gene-specific CNV model has an overall prediction rate of 72.5% in the replication data set, similar to those found in the first set of data. The mean CNV sizes of blood, tumor, and benign prostate tissues have an overall prediction rate of 72% for relapse, and the mean CNV sizes of blood and tumor samples have an overall prediction rate of 73% for short PSADT, whereas the median CNV sizes of blood and tumor have overall prediction rates of 73% for relapse and 80% for short PSADT. These results are also similar to those found in the original study, reflecting good consistency and reproducibility of our prediction models.

6.3 Discussion

Genome-wide analyses of prostate cancer using other methodologies were performed previously(27-30). However, there was no attempt to construct a model to predict the prognosis of prostate cancer. The genome abnormality found in blood from prostate cancer patients in this study is novel. Even though a tiny amount (<0.1% of blood cell population) of circulating tumor cells may exist in the blood sample(31, 32), the stringency of CNV analysis (>30% contamination to be detected) ruled out contamination of tumor cells in the blood as a contending interpretation. Analysis of some of the previously published matched normal samples of other malignancies (33,34) also reveals significant CNV. This suggests that CNV is widely present in tissues of patients carrying malignancies. However, it is unclear whether healthy individuals carry these abnormalities. The CNV of blood may be somatic and acquired through aging; this alteration would tend to be random and spontaneous. Alternatively, genome copy number abnormalities may occur at germ line level. To distinguish these two possibilities, longitudinal blood samples of the same aging individual could identify if CNV is accumulated. Independent of the mechanism, however, genome CNV correlates with the eventual behavior of prostate cancer: This is observed in the primary prostate cancer, in the histologically normal tissue from a prostate gland containing cancer and in the blood of prostate cancer patient. The field effect of genome alterations appears to extend beyond the organ to the entire host.

Conceivably, CNV analysis offers a better option than Gleason's grading in predicting the behavior of prostate cancer not only because of a better prediction rate on the tumor samples, but also its applicability to non-tumor tissues. There are several salient potentials for clinical application using the CNV tests: For a patient being diagnosed of prostate cancer, CNV analysis done on the blood or perhaps other normal tissues from the patient would eliminate the need for additional invasive procedure to decide a treatment mode. For a patient already having a radical prostatectomy, the CNV analysis on tumor or blood sample may help to decide whether additional treatment is warranted to prevent relapse. When morphology becomes in-determinate in a biopsy sample, the gene specific CNV field effect in benign prostate tissues may help to obtain a firmer diagnosis. The main limitation of the genome CNV analysis for clinical test is its requirement of high quality genome DNA. Formalin-fixed paraffin-embedded tissues may not be suitable. When gene specific CNV prediction is performed, a training set containing samples with known outcome is required for the prediction (while there is no need of training set when size of CNV analysis is performed). Despite these limitations, CNV analysis on the genome of blood, normal prostate or tumor tissues of the prostate cancer patients holds promise to become a more efficient and accurate way to predict the behavior of prostate cancer.

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Various publications are cited herein, the contents of which are hereby incorporated by reference in their entireties.

TABLE 1A

Case pathology grading, Clinical outcome and Age

Sample	Type	Relapse	Relapse Fast	Relapse Simple	Gleason's Grade	Age
LNCaP	C					
5772T	T	none	nf	n	7	60s
3806T	T					
Du145	C					
20968T	T	slow	nf	y	7	50s
15463T	T	none	nf	n	7	60s
8629T	T	none	nf	n	6	50s
PC3	C					
28685T	T	slow	nf	y	7	50s
11423T	T	slow	nf	y	7	70s
11462T	T	slow	nf	y	7	50s
25265T	T	none	nf	n	7	60s
25313T	T	none	nf	n	8	50s
2671T	T	slow	nf	y	7	60s
6647T	T	slow	nf	y	7	40s
9122T	T	none	nf	n	7	50s
678T	T	none	nf	n	9	70s
7270T	T	none	nf	n	9	70s
28925N	N					50s
1199T	T	slow	nf	y	8	50s
27086T	T	none	nf	n	6	50s
562T	T	none	nf	n	6	60s
34N	N	Nnone	Nnf	Nn		50s
36N	N	Nnone	Nnf	Nn		50s
9122N	N	Nnone	Nnf	Nn		50s
28278T	T	none	nf	n	7	50s
2691T	T	none	nf	n	7	50s
8629N	N	Nnone	Nnf	Nn		50s
8378T	T	none	nf	n	7	60s
8432T	T	none	nf	n	7	50s
6837T	T	slow	nf	y	6	70s
7943N	N	Nnone	Nnf	Nn		60s
8741T	T	none	nf	n	6	60s
34T	T	none	nf	n	7	50s
14878T	T	none	nf	n	8	60s
25313N	N	Nnone	Nnf	Nn		50s
678N	N	Nnone	Nnf	Nn		70s
GB195T	T	slow	nf	y	7	60s
HB591T	T	fast	f	y	7	60s
IB071T	T	fast	f	y	7	60s
JB426T	T	fast	f	y	7	60s
PR079T	T	slow	nf	y	7	60s
PR521T	T	slow	nf	y	7	50s
TP08-S00530T	T	fast	f	y	7	60s
TP09-S0006T	T	fast	f	y	8	50s
16464T	T	slow	nf	y	7	60s
16947T	T	slow	nf	y	8	70s
DB237T	T	slow	nf	y	6	70s
FB94T	T	slow	nf	y	7	60s
JB378T	T	slow	nf	y	6	60s
PR151T	T	slow	nf	y	7	60s

TABLE 1A-continued

Case pathology grading, Clinical outcome and Age

Sample	Type	Relapse	Relapse Fast	Relapse Simple	Gleason's Grade	Age
PR304T	T	slow	nf	y	8	60s
PR311T	T	slow	nf	y	8	60s
2644T	T	slow	nf	y	9	50s
19381T	T	none	nf	n	6	50s
7943T	T	none	nf	n	7	60s
TP09-S0420T	T	fast	f	y	7	50s
18176N	N	Nslow	Nnf	Ny		50s
19381N	N	Nnone	Nnf	Nn		50s
IB071N	N	Nfast	Nf	Ny		60s
JB426N	N	Nfast	Nf	Ny		60s
PR304N	N	Nslow	Nnf	Ny		60s
2644N	N	Nslow	Nnf	Ny		50s
15733N	N	Nnone	Nnf	Nn		50s
15875N	N	Nnone	Nnf	Nn		40s
PR310T	T	fast	f	y	7	60s
29671T	T	slow	nf	y	7	60s
15733T	T	none	nf	n	7	50s
18176T	T	slow	nf	y	6	50s
5772N	N	Nnone	Nnf	Nn		60s
7504T	T	none	nf	n	9	70s
28925T	T				7	50s
15875T	T	none	nf	n	7	40s
15922T	T	none	nf	n	7	60s
28278N	N	Nnone	Nnf	Nn		50s
4308T	T	none	nf	n	6	60s
7504N	N	Nnone	Nnf	Nn		70s
JB197T	T	fast	f	y	7	50s
TP08-S00268N	N	Nfast	Nf	Ny		60s
TP08-S00268T	T	fast	f	y	7	60s
TP09-S0420N	N	Nfast	Nf	Ny		50s
1199B	B	Bslow	Bnf	By		50s
9122B	B	Bnone	Bnf	Bn		50s
18176B	B	Bslow	Bnf	By		50s
25313B	B	Bnone	Bnf	Bn		50s
6634B	B	Bnone	Bnf	Bn		50s
678B	B	Bnone	Bnf	Bn		70s
7504B	B	Bnone	Bnf	Bn		70s
16464B	B	Bnone	Bnf	Bn		60s
4336B	B	Bslow	Bnf	By		60s
28685B	B	Bslow	Bnf	By		50s
4851B	B	Bnone	Bnf	Bn		60s
1942B	B	Bfast	Bf	By		60s
13563B	B	Bnone	Bnf	Bn		70s
TP09-S0420B	B	Bfast	Bf	By		50s
TP08-S00268B	B	Bfast	Bf	By		60s
DB237B	B	Bslow	Bnf	By		70s
PR151B	B	Bslow	Bnf	By		60s
13745B	B					60s
TP09-S0006B	B	Bfast	Bf	By		50s
PR331B	B	Bslow	Bnf	By		60s
28685B2	B	Bslow	Bnf	By		50s
IB071B	B	Bfast	Bf	By		60s
PR304B	B	Bslow	Bnf	By		60s
JB426B	B	Bfast	Bf	By		60s
7270B	B	Bnone	Bnf	Bn		70s
27086B	B	Bnone	Bnf	Bn		50s
TP09-S0420B2	B	Bfast	Bf	By		50s
DB237B2	B	Bslow	Bnf	By		70s
PR151B2	B	Bslow	Bnf	By		60s
PR310B	B	Bfast	Bf	By		60s
FB586B	B	Bslow	Bnf	By		50s
6634B2	B	Bnone	Bnf	Bn		50s
JB378B	B	Bslow	Bnf	By		60s
FB94B	B	Bslow	Bnf	By		60s
GB195B	B	Bslow	Bnf	By		60s
PR490B	B	Bslow	Bnf	By		60s
PR303B	B	Bslow	Bnf	By		70s
PR018B	B	Bslow	Bnf	By		60s
TP08-S00542B	B	Bfast	Bf	By		50s
GB400B	B	Bfast	Bf	By		60s
HB603B	B	Bfast	Bf	By		60s
DB237N	N	Nslow	Nnf	Ny		70s
11423N	N	Nslow	Nnf	Ny		70s
25265N	N	Nnone	Nnf	Nn		60s
8378N	N	Nnone	Nnf	Nn		60s

TABLE 1A-continued

Case pathology grading, Clinical outcome and Age

Sample	Type	Relapse	Relapse Fast	Relapse Simple	Gleason's Grade	Age
8432N	N	Nnone	Nnf	Nn		50s
15463N	N	Nnone	Nnf	Nn		60s
27086N	N	Nnone	Nnf	Nn		50s
4308N	N	Nnone	Nnf	Nn		60s
562N	N	Nnone	Nnf	Nn		60s
FB183T	T	slow	nf	y	7	60s
GB400T	T	fast	f	y	7	60s
HB021T	T	fast	f	y	6	50s
HB261T	T	none	nf	n	7	50s
HB312T	T	slow	nf	y	8	70s
HB526T	T	fast	f	y	6	60s
HB951T	T	fast	f	y	7	60s
IB134T	T	none	nf	n	9	70s
IB273T	T	fast	f	y	7	50s
IB298T	T	slow	nf	y	7	60s
20968N	N	Nslow	Nnf	Ny		50s
6647N	N	Nslow	Nnf	Ny		40s
15922N	N	Nnone	Nnf	Nn		60s
8741N	N	Nnone	Nnf	Nn		60s
FB183N	N	Nslow	Nnf	Ny		60s
HB526N	N	Nfast	Nf	Ny		60s
HB568T	T	fast	f	y	7	60s
PR236T	T	fast	f	y	10	60s
PR300T	T	fast	f	y	7	50s
PR303N	N	Nslow	Nnf	Ny		70s
PR434T	T	slow	nf	y	7	60s
TPG8-S00542N	N	Nfast	Nf	Ny		50s
FB120T	T	slow	nf	y	7	60s
FB174T	T	fast	f	y	7	60s
HB603T	T	slow	nf	y	7	60s
IB113T	T	slow	nf	y	7	70s
IB483T	T	fast	f	y	7	50s
IB684T	T	slow	nf	y	7	60s
KB170T	T	fast	f	y	7	70s
PR018T	T	slow	nf	y	7	60s
PR151N	N	Nslow	Nnf	Ny		60s
PR303T	T	slow	nf	y	6	70s
PR311N	N	Nslow	Nnf	Ny		60s
11462N	N	Nslow	Nnf	Ny		50s
29671N	N	Nslow	Nnf	Ny		60s
14878N	N	Nnone	Nnf	Nn		60s
16464N	N	Nnone	Nnf	Nn		60s
PR521B	B	Bslow	Bnf	By		50s
PR363B	B	Bslow	Bnf	By		60s
FB174B	B	Bfast	Bf	By		60s
FB421B	B	Bfast	Bf	By		60s
FB421T	T	fast	f	y	7	60s
HB033T	T	none	nf	n	7	50s
HB526N2	N	Nfast	Nf	Ny		60s
IB113B	B	Bslow	Bnf	By		70s
IB483T2	T	fast	f	y	7	50s
TP08-S00542T	T	fast	f	y	7	50s
TP09-S0006N	N	Nfast	Nf	Ny		50s
PR079B	B	Bslow	Bnf	By		60s
FB183B	B	Bslow	Bnf	By		60s
FB120B	B	Bslow	Bnf	By		60s
HB305B	B	Bfast	Bf	By		60s
HB305T	T	fast	f	y	6	60s
IB362T	T	slow	nf	y	7	50s
IB684B	B	Bslow	Bnf	By		60s
JB770B	B	Bfast	Bf	By		60s
JB770T	T	fast	f	y	8	60s
TP10-S093B	B	Bslow	Bnf	By		60s
TP10-S093T	T	slow	nf	y	7	60s
TP09-S0408B	B	Bfast	Bf	By		70s
TP09-S0408T	T	fast	f	y	8	70s
2691N	N	Nnone	Nnf	Nn		50s
28278N2	N	Nnone	Nnf	Nn		50s
4336T	T	slow	nf	y	6	60s
6634N	N	Nnone	Nnf	Nn		50s
6837T2	T	slow	nf	y	6	70s
7221T	T	fast	f	y	7	50s
4308B	B	Bnone	Bnf	Bn		60s
5396B	B	Bnone	Bnf	Bn		60s
9122B2	B	Bnone	Bnf	Bn		50s
TP08-S00530B	B	Bfast	Bf	By		60s
562B	B	Bnone	Bnf	Bn		60s
KB170B	B	Bfast	Bf	By		70s
IB298B	B	Bslow	Bnf	By		60s
HB591B	B	Bfast	Bf	By		60s
HB261B	B	Bnone	Bnf	Bn		50s
PR300B	B	Bfast	Bf	By		50s
PR236B	B	Bfast	Bf	By		60s
PR434B	B	Bslow	Bnf	By		60s
HB568B	B	Bfast	Bf	By		60s
IB134B	B	Bnone	Bnf	Bn		70s
IB483B	B	Bfast	Bf	By		50s
HB526B	B	Bfast	Bf	By		60s
HB021B	B	Bfast	Bf	By		50s
HB312B	B	Bslow	Bnf	By		70s
HB033B	B	Bnone	Bnf	Bn		50s
FB238T	T	slow	nf	y	7	60s
FB493T	T	slow	nf	y	6	50s
HB207T	T	fast	f	y	9	60s
HB235T	T	slow	nf	y	9	60s
HB504T	T	fast	f	y	8	50s
IB112T	T	slow	nf	y	7	60s
IB136T	T	fast	f	y	8	50s
PR306T	T	slow	nf	y	7	60s
TP10-S0638T	T	fast	f	y	10	50s
HB235B	B	Bslow	Bnf	By		60s
PR375B	B	Bfast	Bf	By		50s
FB238B	B	Bslow	Bnf	By		60s
IB136B	B	Bfast	Bf	By		50s
TP09-S0721B	B	Bfast	Bf	By		50s
HB504B	B	Bfast	Bf	By		50s
IB112B	B	Bslow	Bnf	By		60s
HB207B	B	Bfast	Bf	By		60s
PR306B	B	Bslow	Bnf	By		60s
TP09-S0638B	B	Bfast	Bf	By		50s
HB46B	B	Bslow	Bnf	By		60s
FB493B	B	Bslow	Bnf	By		50s
HB46T	T	slow	nf	y	8	60s
PR375T	T	fast	f	y	7	50s
TP09-S0721T	T	fast	f	y	10	50s

TABLE 1B

Clinical and Pathological Characteristics of Prostate Cancer Samples

	Relapse Status		
	None (n = 28)	Long PSADT (n = 42)	Short PSADT (n = 33)
Mean Age (P = 0.0783)	56.07	59.29	56.06
Cancer Stage (P = 0.0224)			
pT1	3 (2.9)	1 (1.0)	0 (0)
pT2	10 (9.7)	9 (8.7)	7 (6.8)
pT3a	7 (6.8)	18 (17.5)	6 (5.8)
pT3b	8 (7.8)	14 (13.6)	20 (19.4)
Gleason grade (P = 0.6569)			
6	6 (5.8)	8 (7.8)	3 (2.9)
7	16 (15.5)	26 (25.2)	21 (20.4)
8-10	6 (5.8)	8 (7.8)	9 (8.7)
Race (P = 0.2349)			
Black	1	2	0
Unknown	4	1	2
White	23	39	31

TABLE 1B-continued

Clinical and Pathological Characteristics of Prostate Cancer Samples

	Relapse Status		
	None (n = 28)	Long PSADT (n = 42)	Short PSADT (n = 33)
Median follow-up (months)	154	124.8	54.8
Median time to progression (months)	NA	47.355	1.87
Median PSADT (months)	NA	23.2	3.21
Mean preoperative PSA (P = 0.42)	8.61	12.31	10.79

Data are given as number (percentage) of the 103 samples unless otherwise indicated.
NA = not applicable

TABLE 1C

Clinical and Pathological Characteristics of Prostate Tissues Adjacent to Tumor

	Relapse Status		
	None (n = 28)	Long PSADT (n = 13)	Short PSADT (n = 8)
Mean Age (P = 0.554)	55	57.69	56.06
Cancer Stage (P = 0.541)			
pT1	3 (6.1)	0 (0)	0 (0)
pT2	11 (22.4)	4 (8.2)	3 (6.1)
pT3a	7 (14.3)	6 (12.2)	1 (2.0)
pT3b	7 (14.3)	3 (6.1)	4 (8.2)
Gleason grade (P = 0.9849)			
5	1 (2.0)	0 (0)	0 (0)
6	7 (14.3)	3 (6.1)	2 (4.1)
7	16 (32.7)	7 (14.3)	5 (10.2)
8-10	4 (8.2)	3 (6.1)	1 (2.0)
Race (P = 0.08387)			
Black	0	1	0
Unknown	6	0	0
White	22	12	8
Median follow up (months)	155	149	29.205
Median time to progression (months)	NA	54.6	3.09
Median (PSADT) months	NA	26.9	2.46
Mean preoperative PSA (P = 0.074)	8.23	12.98	6.3

Data are given as number (percentage) of the 49 samples unless otherwise indicated.
NA = not applicable

TABLE 1D

Clinical and Pathological Characteristics of Blood Samples from Patients with Prostate Cancer

	Relapse Status		
	None (n = 18)	Long PSADT (n = 35)	Short PSADT (n = 31)
Mean age (P = 0.268)	58.33	59.43	56.77
Cancer Stage (P = 0.003893)			
pT1	5 (6.0)	1 (1.2)	0 (0)
pT2	6 (7.1)	12 (14.3)	6 (7.1)
pT3a	1 (1.2)	10 (11.9)	5 (6.0)
pT3b	6 (7.1)	12 (14.3)	20 (23.8)
Gleason grade (P = 0.2248)			
6	5 (6.0)	8 (9.5)	3 (3.6)
7	7 (8.3)	21 (25.0)	18 (21.4)
8-10	6 (7.1)	6 (7.1)	10 (11.9)
Race (P = 0.08387)			
Black	0	1	0
Unknown	3	1	2
White	15	33	29
Median follow up (months)	152	109.14	54.8
Median time to progression (months)	NA	47.27	3.23
Median PSADT (months)	NA	26	3.21
Mean preoperative PSA (P = 0.868)	10.48	12.17	10.87

Data are given as number (percentage) of the 84 samples unless otherwise indicated.
NA = not applicable

TABLE 2

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
psiTPTE22	1	0.106667	0.133333	0.444444	0	psiTPTE22	22	22q11.1	15462801	15509721
XKR3	1	0.133333	0.133333	0.481481	0	XKR3	22	22q11.1	15644306	15682585
DNAL4	1	0.413333	0.133333	0.777778	0	DNAL4	22	22q13.1	37504459	37520108
BRD1	1	0.48	0.12	0.814815	0	BRD1	22	22q13.33	48552941	48604457
LOC90834	1	0.48	0.12	0.814815	0	LOC90834	22	22q13.33	48557542	48559963
ZBED4	1	0.48	0.12	0.814815	0	ZBED4	22	22q13.33	48633501	48669731
ALG12	1	0.48	0.12	0.814815	0	ALG12	22	22q13.33	48682857	48698111
CRELD2	1	0.48	0.12	0.814815	0	CRELD2	22	22q13.33	48698287	48707191
PIM3	1	0.48	0.12	0.814815	0	PIM3	22	22q13.33	48740147	48743724
IL17REL	1	0.48	0.12	0.814815	0	IL17REL	22	22q13.33	48775069	48793183

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
TTLL8	1	0.48	0.12	0.814815	0	TTLL8	22	22q13.33	48795679	48835183
PANX2	1	0.48	0.12	0.814815	0	PANX2	22	22q13.33	48951287	48960851
TRABD	1	0.48	0.12	0.814815	0	TRABD	22	22q13.33	48966487	48980155
SELO	1	0.48	0.12	0.814815	0	SELO	22	22q13.33	48981535	48998173
TUBGCP6	1	0.48	0.12	0.814815	0	TUBGCP6	22	22q13.33	48998245	49025528
KIF16B	1	0.106667	0.12	0.074074	0	KIF16B	20	20p12.1	16200749	16502079
PCSK2	1	0.146667	0.133333	0.222222	0	PCSK2	20	20p12.1	17155631	17413223
LGALS13	1	0.333333	0.145667	0.740741	0	LGALS13	19	19q13.2	44785009	44789955
LGALS14	1	0.346667	0.12	0.740741	0	LGALS14	19	19q13.2	44886786	44891929
CLC	1	0.346667	0.12	0.740741	0	CLC	19	19q13.2	44913735	44920509
RPH3AL	1	0.48	0.12	0.814815	0	RPH3AL	17	17p13.3	62294	202577
VPS53	1	0.48	0.12	0.777778	0	VPS53	17	17p13.3	361480	564847
GEMIN4	1	0.48	0.12	0.777778	0	GEMIN4	17	17p13.3	594411	602252
ELP2P	1	0.48	0.12	0.777778	0	ELP2P	17	17p13.3	602650	605327
NXN	1	0.466667	0.133333	0.777778	0	NXN	17	17p13.3	649335	829761
TIMM22	1	0.466667	0.133333	0.777778	0	TIMM22	17	17p13.3	847107	852141
ABR	1	0.466667	0.133333	0.777778	0	ABR	17	17p13.3	853509	959075
YWHAE	1	0.453333	0.133333	0.777778	0	YWHAE	17	17p13.3	1194586	1250307
CRK	1	0.453333	0.133333	0.777778	0	CRK	17	17p13.3	1272208	1306295
INPP5K	1	0.466667	0.133333	0.777778	0	INPP5K	17	17p13.3	1344622	1366933
LOC100306951	1	0.466667	0.133333	0.777778	0	LOC1003066951	17	17p13.3	1366963	1368139
PITPNA	1	0.466667	0.133333	0.777778	0	PITPNA	17	17p13.3	1368033	1412861
PRPF8	1	0.466667	0.133333	0.777778	0	PRPF8	17	17p13.3	1500673	1534927
WDR81	1	0.466667	0.133333	0.777778	0	WDR81	17	17p13.3	1566567	1588644
SERPINF2	1	0.466667	0.133333	0.777778	0	SERPINF2	17	17p13.3	1592880	1605310
SERPINF1	1	0.466667	0.133333	0.777778	0	SERPINF1	17	17p13.3	1612009	1527619
SMYD4	1	0.466667	0.133333	0.777778	0	SMYD4	17	17p13.3	1629579	1679926
RPA1	1	0.466667	0.133333	0.777778	0	RPA1	17	17p13.3	1680023	1749599
RTN4RL1	1	0.466667	0.133333	0.777778	0	RTN4RL1	17	17p13.3	1784721	1874929
SMG6	1	0.466667	0.133333	0.777778	0	SMG6	17	17p13.3	1909883	2153564
SRR	1	0.453333	0.133333	0.777778	0	SRR	17	17p13.3	2153998	2175304
METT10D	1	0.413333	0.133333	0.740741	0	METT10D	17	17p13.3	2266098	2361951
PAFAH1B1	1	0.413333	0.133333	0.740741	0	PAFAH1B1	17	17p13.3	2443673	2535660
KIAA0664	1	0.426667	0.133333	0.740741	0	KIAA0664	17	17p13.3	2539430	2561678
RAP1GAP2	1	0.426667	0.133333	0.740741	0	RAP1GAP2	17	17p13.3	2646482	2887786
OR3A2	1	0.28	0.146667	0.740741	0	OR3A2	17	17p13.3	3127934	3129019
TRPV3	1	0.413333	0.133333	0.740741	0	TRPV3	17	17p13.3	3363236	3408040
TRPV1	1	0.413333	0.133333	0.740741	0	TRPV1	17	17p13.3	3415490	3447086
SHPK	1	0.413333	0.133333	0.740741	0	SHPK	17	17p13.3	3458305	3486366
CTNS	1	0.413333	0.133333	0.740741	0	CTNS	17	17p13.3	3486511	3513147
TMEM93	1	0.413333	0.133333	0.740741	0	TMEM93	17	17p13.3	3518839	3519712
P2RX5	1	0.413333	0.133333	0.740741	0	P2RX5	17	17p13.3	3523271	3546333
ITGAE	1	0.413333	0.133333	0.740741	0	ITGAE	17	17p13.3	3564568	3651287
GSG2	1	0.413333	0.133333	0.740741	0	GSG2	17	17p13.3	3573946	3576742
C17orf85	1	0.4	0.133333	0.740741	0	C17orf85	17	17p13.2	3661209	3696290
CAMKK1	1	0.413333	0.146667	0.777778	0	CAMKK1	17	17p13.2	3710366	3743087
P2RX1	1	0.413333	0.133333	0.777778	0	P2RX1	17	17p13.2	3746634	3766710
CDRT15P	1	0.106667	0.146667	0.296296	0	CDRT15P	17	17p12	13868540	13869641
MIR1288	1	0.32	0.12	0.481481	0	MIR1288	17	17p11.2	16126053	16126128
TRPV2	1	0.346667	0.12	0.518519	0	TRPV2	17	17p11.2	16259613	16281043
NCRNA001	1	0.346667	0.12	0.518519	0	NCRNA001	17	17p11.2	16283026	16286064
SNORD49B	1	0.346667	0.12	0.518519	0	SNORD498	17	17p11.2	16283548	16283596
SNORD49A	1	0.346667	0.12	0.518519	0	SNORD49A	17	17p11.2	16284075	16284146
SNORD65	1	0.346667	0.12	0.518519	0	SNORD65	17	17p11.2	16285265	16285338
C17orf76	1	0.346667	0.12	0.518519	0	C17orf76	17	17p11.2	16286053	16336206
ZNF287	1	0.346667	0.12	0.518519	0	ZNF287	17	17p11.2	16394356	16413246
MPP3	1	0.466667	0.12	0.777778	0	MPP3	17	17q21.31	39233693	39266065
CD300LG	1	0.466667	0.12	0.777778	0	CD300LG	17	17q21.31	39280042	39291128
MPP2	1	0.466667	0.12	0.777778	0	MPP2	17	17q21.31	39308253	39340640
PPY	1	0.466667	0.133333	0.777778	0	PPY	17	17q21.31	39373698	39375360
PYY	1	0.466667	0.133333	0.777778	0	PYY	17	17q21.31	39385633	39437364
NAGS	1	0.466667	0.133333	0.777778	0	NAGS	17	17q21.31	39437558	39441963
TMEM101	1	0.466667	0.133333	0.777778	0	TMEM101	17	17q21.31	39444082	39447872
LSM12	1	0.466667	0.133333	0.777778	0	LSM12	17	17q21.31	39467530	39500514
G6PC3	1	0.466667	0.133333	0.777778	0	G6PC3	17	17q21.31	39503624	39509238
HDAC5	1	0.466667	0.133333	0.777778	0	HDAC5	17	17q21.31	39509647	39556541
C17orf53	1	0.466667	0.133333	0.777778	0	C17orf53	17	17q21.31	39574852	39595371
ASB16	1	0.466667	0.133333	0.777778	0	ASB16	17	17q21.31	39603600	39611978
C17orf65	1	0.466667	0.133333	0.777778	0	C17orf65	17	17q21.31	39608878	39619609
TMUB2	1	0.466667	0.133333	0.777778	0	TMUB2	17	17q21.31	39619880	39624626
ATXN7L3	1	0.466667	0.133333	0.777778	0	ATXN7L3	17	17q21.31	39624699	39631056
UBTF	1	0.466667	0.133333	0.777778	0	UBTF	17	17q21.31	39637927	39653777
SLC4A1	1	0.466667	0.133333	0.777778	0	SLC4A1	17	17q21.31	39681284	39701029
SLC25A39	1	0.466667	0.12	0.777778	0	SLC25A39	17	17q21.31	39752519	39757744

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
GRN	1	0.466667	0.12	0.777778	0	GRN	17	17q21.31	39778017	39785997
FAM171A2	1	0.466667	0.12	0.777778	0	FAM171A2	17	17q21.31	39786627	39796762
ITGA2B	1	0.466667	0.12	0.777778	0	ITGA2B	17	17q21.31	39805076	39822400
GPATCH8	1	0.466667	0.12	0.777778	0	GPATCH8	17	17q21.31	39828176	39936329
FZD2	1	0.426667	0.12	0.777778	0	FZD2	17	17q21.31	39990451	39992434
C17orf104	1	0.453333	0.12	0.777778	0	C17orf104	17	17q21.31	40089288	40108690
ADAM11	1	0.48	0.12	0.777778	0	ADAM11	17	17q21.31	40192094	40214741
HIGD1B	1	0.466667	0.12	0.777778	0	HIGD1B	17	17q21.31	40280805	40283375
EFTUD2	1	0.466667	0.12	0.777778	0	EFTUD2	17	17q21.31	40283181	40332520
KIF18B	1	0.48	0.12	0.777778	0	KIF18B	17	17q21.31	40358974	40380609
C1QL1	1	0.48	0.12	0.777778	0	C1QL1	17	17q21.31	40392587	40401171
DCAKD	1	0.48	0.12	0.777778	0	DCAKD	17	17q21.31	40456232	40484505
NMT1	1	0.48	0.12	0.777778	0	NMT1	17	17q21.31	40494206	40541909
PLCD3	1	0.48	0.12	0.777778	0	PLCD3	17	17q21.31	40544534	40565418
ACBD4	1	0.48	0.12	0.777778	0	ACBD4	17	17q21.31	40565493	40577325
HEXIM1	1	0.48	0.12	0.777778	0	HEXIM1	17	17q21.31	40580467	40585252
HEXIM2	1	0.48	0.12	0.777778	0	HEXIM2	17	17q21.31	40594047	40603190
FMNL1	1	0.48	0.12	0.777778	0	FMNL1	17	17q21.31	40655075	40680467
LOC100133991	1	0.48	0.12	0.777778	0	LOC100133991	17	17q21.31	40681086	40701780
C17orf46	1	0.48	0.12	0.777778	0	C17orf46	17	17q21.31	40687543	40695263
MAP3K14	1	0.48	0.12	0.777778	0	MAP3K14	17	17q21.31	40696271	40750198
ARHGAP27	1	0.48	0.12	0.777778	0	ARHGAP27	17	17q21.31	40827051	40839233
TNRC6A	1	0.32	0.12	0.666667	0	TNRC6A	16	16p12.1	24648550	24745049
FLI30679	1	0.413333	0.133333	0.666667	0	FLI30679	16	16q24.1	85146427	85148407
FOXC2	1	0.413333	0.133333	0.666667	0	FOXC2	16	16q24.1	85158358	85160037
FBXO31	1	0.426667	0.146667	0.665667	0	FBXO31	16	16q24.2	85920445	85974896
ZCCHC14	1	0.426667	0.146667	0.666667	0	ZCCHC14	16	16q24.2	85997353	86082962
JPH3	1	0.426667	0.173333	0.666667	0	JPH3	16	16q24.2	86194000	86289263
SLC7A5	1	0.426667	0.186667	0.666667	0	SLC7A5	16	16q24.2	86421130	86460602
CA5A	1	0.426667	0.186667	0.666667	0	CA5A	16	16q24.2	86479126	86527614
BANP	1	0.426667	0.186667	0.666667	0	BANP	16	16q24.2	86542539	86668426
ZFPM1	1	0.44	0.2	0.666667	0	ZFPM1	16	16q24.2	87047515	87129076
ZC3H18	1	0.44	0.2	0.666667	0	ZC3H18	16	16q24.2	87164290	87225873
IL17C	1	0.44	0.2	0.703704	0	IL17C	16	16q24.3	87232502	87234384
CYBA	1	0.44	0.2	0.703704	0	CYBA	16	16q24.3	87237198	87244959
MVD	1	0.44	0.2	0.703704	0	MVD	16	16q24.3	87245849	87256997
MGC23284	1	0.44	0.2	0.703704	0	MGC23284	16	16q24.3	87257282	87281054
SNAI3	1	0.44	0.2	0.703704	0	SNAI3	16	16q24.3	87271591	87280384
RNF166	1	0.44	0.2	0.703704	0	RNF166	16	16q24.3	87290410	87300302
GALNS	1	0.466667	0.2	0.703704	0	GALNS	16	16q24.3	87407643	87450876
TRAPPC2L	1	0.466667	0.2	0.703704	0	TRAPPC2L	16	16q24.3	87451007	87455022
CBFA2T3	1	0.466667	0.2	0.703704	0	CBFA2T3	16	16q24.3	87468768	87570903
ACSF3	1	0.466667	0.2	0.703704	0	ACSF3	16	16q24.3	87687755	87748499
C16orf81	1	0.466667	0.2	0.703704	0	C16orf81	16	16q24.3	87753129	87757585
CDH15	1	0.466667	0.2	0.703704	0	CDH15	16	16q24.3	87765664	87789402
ANKRD11	1	0.48	0.2	0.703704	0	ANKRD11	16	16q24.3	87861536	88084471
SPG7	1	0.48	0.186667	0.703704	0	SPG7	16	16q24.3	88102306	88151676
RPL13	1	0.48	0.186667	0.703704	0	RPL13	16	16q24.3	88154591	88157350
SNORD68	1	0.48	0.186667	0.703704	0	SNORD68	16	16q24.3	88155339	88155411
CDK10	1	0.48	0.186667	0.703704	0	CDK10	16	16q24.3	88280577	88290273
SPATA2L	1	0.48	0.186667	0.703704	0	SPATA2L	16	16q24.3	88290266	88295601
C16orf7	1	0.48	0.186667	0.703704	0	C16orf7	16	16q24.3	88301042	88314896
ZNF276	1	0.48	0.186667	0.703704	0	ZNF276	16	16q24.3	88314894	88334834
SPIRE2	1	0.48	0.173333	0.740741	0	SPIRE2	16	16q24.3	88422403	88465229
TUBB3	1	0.48	0.16	0.740741	0	TUBB3	16	16q24.3	88517246	88530007
DEF8	1	0.48	0.16	0.740741	0	DEF8	16	16q24.3	88542652	88553276
CENPBD1	1	0.48	0.16	0.740741	0	CENPBD1	16	16q24.3	88563702	88566444
OR11H4	1	0.08	0.12	0.111111	0	OR11H4	14	14q11.2	19780791	19781766
G2E3	1	0.026667	0.173333	0	0	G2E3	14	14q12	30098080	30158798
SCFD1	1	0.026667	0.133333	0	0	SCFD1	14	14q12	30161272	30274770
COCH	1	0.053333	0.133333	0	0	COCH	14	14q12	30413492	30429574
STRN3	1	0.16	0.053333	0	0	STRN3	14	14q12	30432756	30565359
AP4S1	1	0.173333	0.053333	0	0	AP4S1	14	14q12	30564434	30632390
HECTD1	1	0.186667	0.053333	0	0	HECTD1	14	14q12	30639075	30746441
AKAP6	1	0.04	0.146667	0	0	AKAP6	14	14q13.1	31868230	32372020
NPAS3	1	0.093333	0.133333	0	0	NPAS3	14	14q13.1	32478210	33343133
SAV1	1	0.12	0.013333	0	0.037037	SAV1	14	14q22.1	50170110	50204774
NIN	1	0.12	0	0	0.037037	NIN	14	14q22.1	50256231	50367590
BMP4	1	0.04	0.133333	0.037037	0	BMP4	14	14q22.2	53486205	53493305
SYT16	1	0.013333	0.2	0.037037	0	SYT16	14	14q23.2	61532294	61638181
GPHN	1	0.08	0.173333	0.185185	0	GPHN	14	14q23.3	66043878	66718279
ERH	1	0.186667	0.133333	0.333333	0	ERH	14	14q24.1	68916593	68934775
SMOC1	1	0.186667	0.12	0.333333	0	SMOC1	14	14q24.2	69415896	69568837
NRXN3	1	0.066667	0.173333	0.222222	0	NRXN3	14	14q24.3	77939846	79400514

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
LOC100101	1	0.106667	0.16	0.259259	0	LOC100101	13	13q12.11	18734941	18817114
TSC22D1	1	0.12	0.226667	0	0.111111	TSC22D1	13	13q14.11	43905655	44048702
RCBTB1	1	0.12	0.253333	0	0.148148	RCBTB1	13	13q14.3	49004083	49057721
ARL11	1	0.12	0.253333	0	0.148148	ARL11	13	13q14.3	49100625	49105733
EBPL	1	0.12	0.253333	0	0.148148	EBPL	13	13q14.3	49132811	49163625
KPNA3	1	0.12	0.253333	0	0.148148	KPNA3	13	13q14.3	49171445	49265057
LOC220429	1	0.12	0.253333	0	0.148148	LOC220429	13	13q14.3	49362546	49365518
C13orf1	1	0.12	0.253333	0	0.148148	C13orf1	13	13q14.3	49384843	49408627
NDUFA9	1	0.213333	0.133333	0.592593	0	NDUFA9	12	12p13.32	4628544	4666661
VWF	1	0.226667	0.133333	0.592593	0	VWF	12	12p13.31	5928301	6104098
GABARAPL	1	0.146667	0.133333	0.111111	0	GABARAPL	12	12p13.2	10256756	10266992
ETV6	1	0.066667	0.16	0.111111	0	ETV6	12	12p13.2	11694055	11939593
BCL2L14	1	0.173333	0.146667	0.148148	0	BCL2L14	12	12p13.2	12115145	12143895
LRP6	1	0.16	0.146667	0.148148	0	LRP6	12	12p13.2	12160228	12311079
MANSC1	1	0.16	0.146667	0.148148	0	MANSC1	12	12p13.2	12373485	12394437
LOH12CR2	1	0.16	0.146667	0.148148	0	LOH12CR2	12	12p13.2	12399611	12401269
LOH12CR1	1	0.16	0.146667	0.148148	0	LOH12CR1	12	12p13.2	12401287	12511106
DUSP16	1	0.133333	0.146667	0.111111	0	DUSP16	12	12p13.2	12520098	12606585
CREBL2	1	0.106667	0.16	0.074074	0	CREBL2	12	12p13.1	12656098	12689309
GPR19	1	0.106667	0.16	0.074074	0	GPR19	12	12p13.1	12705263	12740389
CDKN1B	1	0.106667	0.16	0.074074	0	CDKN1B	12	12p13.1	12761569	12766573
APOLD1	1	0.106667	0.16	0.074074	0	APOLD1	12	12p13.1	12770118	12835667
MIR613	1	0.106667	0.16	0.074074	0	MIR613	12	12p13.1	12808850	12808944
DDX47	1	0.133333	0.146667	0.074074	0	DDX47	12	12p13.1	12857547	12874183
RPL13AP20	1	0.133333	0.146667	0.074074	0	RPL13AP20	12	12p13.1	12919678	12920337
GPRC5A	1	0.133333	0.146667	0.074074	0	GPRC5A	12	12p13.1	12935223	12957868
MIR614	1	0.133333	0.146667	0.074074	0	MIR614	12	12p13.1	12960030	12960120
GPRC5D	1	0.133333	0.146667	0.074074	0	GPRC5D	12	12p13.1	12984976	12994586
HEBP1	1	0.133333	0.146667	0.074074	0	HEBP1	12	12p13.1	13019066	13044489
KIAA1467	1	0.12	0.146667	0.074074	0	KIAA1467	12	12p13.1	13088582	13127651
GRIN2B	1	0	0.186667	0.037037	0	GRIN2B	12	12p13.1	13605677	14024290
ST8SIA1	1	0.013333	0.16	0	0	ST8SIA1	12	12p12.1	22237592	22378916
KIAA0528	1	0.066667	0.146667	0.037037	0	KIAA0528	12	12p12.1	22492785	22588720
ETNK1	1	0.066667	0.146667	0.037037	0	ETNK1	12	12p12.1	22669343	22688617
BCAT1	1	0.013333	0.213333	0.037037	0	BCAT1	12	12p12.1	24855546	24993576
CASC1	1	0.066667	0.16	0	0	CASC1	12	12p12.1	25152490	25239362
IFLTD1	1	0.013333	0.12	0.037037	0	IFLTD1	12	12p12.1	25520283	25597446
OVCH1	1	0	0.213333	0	0	OVCH1	12	12p11.22	29471756	29541887
TMTC1	1	0.013333	0.12	0	0	TMTC1	12	12p11.22	29545024	29828960
FAM60A	1	0.186667	0.12	0.222222	0	FAM60A	12	12p11.21	31324794	31370389
SRGAP1	1	0.146667	0.04	0	0	SRGAP1	12	12q14.2	62524808	62827881
RASSF3	1	0.16	0.013333	0	0.037037	RASSF3	12	12q14.2	63290560	63375460
UHRF1BP1L	1	0.133333	0.093333	0	0	UHRF1BP1L	12	12q23.1	98954994	99060774
MIR1827	1	0.213333	0.026667	0	0	MIR1827	12	12q23.1	99107793	99107859
SCYL2	1	0.145667	0.026667	0	0	SCYL2	12	12q23.1	99185680	99258046
SLC17A8	1	0.133333	0.026667	0	0	SLC17A8	12	12q23.1	99274988	99339968
NR1H4	1	0.146667	0.026667	0	0	NR1H4	12	12q23.1	99391810	99481775
GAS2L3	1	0.146667	0.026667	0	0	GAS2L3	12	12q23.1	99491620	99542817
SLC5A8	1	0.106667	0.133333	0.111111	0	SLC5A8	12	12q23.2	1E+08	1E+08
PAH	1	0.093333	0.12	0.148148	0	PAH	12	12q23.2	1.02E+08	1.02E+08
C12orf42	1	0.106667	0.12	0.148148	0	C12orf42	12	12q23.2	1.02E+08	1.02E+08
BTBD10	1	0.093333	0.12	0.148148	0	BTBD10	11	11p15.2	13366132	13441415
OR5B12	1	0.08	0.133333	0.148148	0	OR5B12	11	11q12.1	57963256	57964201
LPXN	1	0.08	0.133333	0.148148	0	LPXN	11	11q12.1	58050922	58102216
RAB30	1	0.12	0.04	0	0	RAB30	11	11q14.1	82370126	82460533
CCDC90B	1	0.053333	0.12	0	0	CCDC90B	11	11q14.1	82650150	82675026
FAT3	1	0.04	0.173333	0	0	FAT3	11	11q14.3	91724910	92269284
BIRC3	1	0.133333	0.066667	0	0.074074	BIRC3	11	11q22.2	1.02E+08	1.02E+08
MMP7	1	0.12	0.066667	0	0.074074	MMP7	11	11q22.2	1.02E+08	1.02E+08
DDX10	1	0.066667	0.16	0.111111	0	DDX10	11	11q22.3	1.08E+08	1.08E+08
FRMPD2	1	0.226667	0.16	0.37037	0	FRMPD2	10	10q11.22	49034608	49152948
ERCC6	1	0.226667	0.173333	0.333333	0	ERCC6	10	10q11.23	50334497	50417154
PGBD3	1	0.226667	0.173333	0.333333	0	PGBD3	10	10q11.23	50393250	50402333
SGMS1	1	0.133333	0.133333	0.222222	0	SGMS1	10	10q11.23	51735351	52053744
FAM13C	1	0.12	0.133333	0	0.074074	FAM13C	10	10q21.1	60675896	60792359
ARID5B	1	0.146667	0.026667	0	0	ARID5B	10	10q21.2	63331449	63526710
ADO	1	0.146667	0.04	0	0	ADO	10	10q21.2	64234522	64238246
EGR2	1	0.146667	0.04	0	0	EGR2	10	10q21.2	64241766	64246133
JMJD1C	1	0.173333	0.026667	0	0	JMJD1C	10	10q21.2	64596994	64698989
REEP3	1	0.173333	0.04	0	0	REEP3	10	10q21.3	64951129	65051979
SLC24A2	1	0.026667	0.173333	0.037037	0	SLC24A2	9	9p22.1	19505978	19776927
MLLT3	1	0.026667	0.133333	0	0	MLLT3	9	9p21.3	20334968	20612515
IFNA13	1	0.04	0.146667	0	0	IFNA13	9	9p21.3	21357371	21358076
IFNA1	1	0.026667	0.16	0	0	IFNA1	9	9p21.3	21430440	21431316

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
LOC554202	1	0.026667	0.16	0	0	LOC554202	9	9p21.3	21444267	21549698
IFNE	1	0.026667	0.16	0	0	IFNE	9	9p21.3	21470841	21472313
1-Dec	1	0.12	0.133333	0.333333	0	1-Dec	9	9q33.1	1.17E+08	1.17E+08
PAPPA	1	0.093333	0.12	0.259259	0	PAPPA	9	9q33.1	1.18E+08	1.18E+08
TUBBP5	1	0.573333	0.12	0.851852	0	TUBBP5	9	9q34.3	1.4E+08	1.4E+08
TMEM66	1	0.12	0.36	0	0.185185	TMEM66	8	8p12	30040173	30060192
LEPROTL1	1	0.12	0.36	0	0.185185	LEPROTL1	8	8p12	30072464	30114755
MBOAT4	1	0.12	0.36	0	0.185185	MBOAT4	8	8p12	30108729	30121743
DCTN6	1	0.12	0.36	0	0.185185	DCTN6	8	8p12	30133355	30160603
RBPMS	1	0.133333	0.36	0	0.185185	RBPMS	8	8p12	30361486	30549277
UBXN8	1	0.186667	0.373333	0	0.185185	UBXN8	8	8p12	30721232	30744063
TEX15	1	0.133333	0.386667	0	0.222222	TEX15	8	8p12	30808602	30826076
BEYLA	1	0.173333	0.186667	0.185185	0	BEYLA	8	8q11.1	47871673	47886573
NKAIN3	1	0.106667	0.133333	0.111111	0	NKAIN3	8	8q12.3	63324055	64066183
STEAP1	1	0.146667	0.12	0	0.185185	STEAP1	7	7q21.13	89621625	89632078
GTPBP10	1	0.12	0.053333	0	0.074074	GTPBP10	7	7q21.13	89813926	89854587
CLDN12	1	0.12	0.053333	0	0.074074	CLDN12	7	7q21.13	89870732	89883205
ENPP5	1	0.04	0.133333	0.111111	0	ENPP5	6	6p12.3	46235721	46246677
CYP39A1	1	0.04	0.12	0.074074	0	CYP39A1	6	6p12.3	46525404	46728483
MEP1A	1	0.04	0.12	0.074074	0	MEP1A	6	6p12.3	46869053	46915479
SMAP1	1	0.186667	0.146667	0	0.185185	SMAP1	6	6q13	71434200	71628438
C6orf147	1	0.2	0.186667	0	0.111111	C6orf147	6	6q13	74040583	74076810
DDX43	1	0.186667	0.186667	0	0.111111	DDX43	6	6q13	74161006	74184004
MTO1	1	0.173333	0.2	0	0.111111	MTO1	6	6q13	74228175	74267901
SLC17A5	1	0.186667	0.186667	0	0.111111	SLC17A5	6	6q13	74359823	74420459
CD109	1	0.12	0.16	0	0.111111	CD109	6	6q13	74462229	74594761
MYO6	1	0.146667	0.173333	0	0.222222	MYO6	6	6q14.1	76515629	76685975
GABRR1	1	0.12	0.2	0	0.185185	GABRR1	6	6q15	89943942	89984216
GABRR2	1	0.133333	0.2	0	0.185185	GABRR2	6	6q15	90023958	90081687
RRAGD	1	0.133333	0.2	0	0.185185	RRAGD	6	6q15	90131056	90178715
ANKRD6	1	0.12	0.2	0	0.185185	ANKRD6	6	6q15	90199616	90400125
GJA1	1	0.133333	0.213333	0	0.296296	GJA1	6	6q22.31	1.22E+08	1.22E+08
ARHGAP18	1	0.013333	0.146667	0.037037	0	ARHGAP18	6	6q22.33	1.3E+08	1.3E+08
C6orf191	1	0.013333	0.133333	0	0	C6orf191	6	6q22.33	1.3E+08	1.3E+08
L3MBTL3	1	0.013333	0.133333	0	0	L3MBTL3	6	6q23.1	1.3E+08	1.31E+08
SAMD3	1	0.026667	0.12	0	0	SAMD3	6	6q23.1	1.31E+08	1.31E+08
RPS12	1	0.146667	0.026667	0	0	RPS12	6	6q23.2	1.33E+08	1.33E+08
SNORD101	1	0.146667	0.026667	0	0	SNORD101	6	6q23.2	1.33E+08	1.33E+08
SNORD100	1	0.133333	0.04	0	0	SNORD100	6	6q23.2	1.33E+08	1.33E+08
SNORA33	1	0.133333	0.04	0	0	SNORA33	6	6q23.2	1.33E+08	1.33E+08
EYA4	1	0	0.133333	0	0	EYA4	6	6q23.2	1.34E+08	1.34E+08
AHI1	1	0	0.146667	0	0	AHI1	6	6q23.3	1.36E+08	1.36E+08
ADAT2	1	0	0.133333	0	0	ADAT2	6	6q24.2	1.44E+08	1.44E+08
CKMT2	1	0.12	0.093333	0	0.037037	CKMT2	5	5q14.1	80564895	80597974
DMXL1	1	0.16	0.106667	0	0.111111	DMXL1	5	5q23.1	1.18E+08	1.19E+08
LARS	1	0.16	0	0	0.037037	LARS	5	5q32	1.45E+08	1.46E+08
RBM27	1	0.16	0	0	0.037037	RBM27	5	5q32	1.46E+08	1.46E+08
ZNF718	1	0.253333	0.133333	0.703704	0	ZNF718	4	4p16.3	43277	146491
MIR572	1	0.04	0.12	0.074074	0	MIR572	4	4p15.33	10979549	10979643
C1QTNF7	1	0.013333	0.133333	0	0	C1QTNF7	4	4p15.33	14950658	15056889
CD38	1	0.12	0.053333	0	0	CD38	4	4p15.32	15389029	15459805
FGFBP1	1	0.133333	0.053333	0	0	FGFBP1	4	4p15.32	15546290	15549070
PROM1	1	0.133333	0.053333	0	0	PROM1	4	4p15.32	15578947	15694693
TAPT1	1	0.026667	0.146667	0	0	TAPT1	4	4p15.32	15771226	15837260
FLJ39653	1	0.026667	0.146667	0	0	FLJ39653	4	4p15.32	15837384	15868909
LDB2	1	0.026667	0.133333	0	0	LDB2	4	4p15.32	16112262	16509523
QDPR	1	0.146667	0.04	0	0	QDPR	4	4p15.32	17097118	17122956
CLRN2	1	0.146667	0.04	0	0	CLRN2	4	4p15.32	17125886	17137826
LAP3	1	0.146667	0.04	0	0	LAP3	4	4p15.32	17188025	17218689
FAM184B	1	0.146667	0.04	0	0	FAM184B	4	4p15.32	17242809	17392234
DCAF16	1	0.146667	0.04	0	0	DCAF16	4	4p15.32	17411376	17421480
GPR125	1	0.026667	0.226667	0	0	GPR125	4	4p15.31	21998097	22126771
GBA3	1	0.026667	0.213333	0	0	GBA3	4	4p15.31	22303646	22430291
PARM1	1	0.04	0.146667	0	0	PARM1	4	4q13.3	76077322	76194348
FRAS1	1	0.026667	0.12	0	0	FRAS1	4	4q21.21	79197748	79586810
SLC10A6	1	0.12	0.026667	0	0	SLC10A6	4	4q21.3	87963645	87989441
AFF1	1	0.146667	0.013333	0	0	AFF1	4	4q21.3	88075178	88281230
KLHL8	1	0.12	0.013333	0	0	KLHL8	4	4q22.1	88301238	88360699
HSD17B13	1	0.12	0.013333	0	0	HSD17B13	4	4q22.1	88443965	88463081
HSD17B11	1	0.12	0.013333	0	0	HSD17B11	4	4q22.1	88476715	88531480
NUDT9	1	0.12	0.013333	0	0	NUDT9	4	4q22.1	88562759	88598524
SPARCL1	1	0.12	0.013333	0	0	SPARCL1	4	4q22.1	88613512	88669680
PHF17	1	0.133333	0.08	0	0.185185	PHF17	4	4q28.2	1.3E+08	1.3E+08
HHIP	1	0.04	0.12	0	0	HHIP	4	4q31.22	1.46E+08	1.46E+08

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
TBC1D5	1	0.053333	0.16	0.148148	0	TBC1D5	3	3p24.3	17173659	17759245
LOC285401	1	0.013333	0.146667	0.037037	0	LOC285401	3	3p14.2	63063404	63085776
SYNPR	1	0.026667	0.133333	0.037037	0	SYNPR	3	3p14.2	63238954	63577638
SNTN	1	0.013333	0.12	0.037037	0	SNTN	3	3p14.2	63613384	63625932
SUCLG2	1	0.013333	0.146667	0.037037	0	SUCLG2	3	3p14.1	67507833	67787729
FAM19A4	1	0	0.133333	0.037037	0	FAM19A4	3	3p14.1	68863607	69064402
MINA	1	0.173333	0.173333	0	0.259259	MINA	3	3q11.2	99143351	99173915
TM4SF4	1	0.173333	0	0	0.037037	TM4SF4	3	3q25.1	1.51E+08	1.51E+08
WWTR1	1	0.133333	0	0	0.037037	WWTR1	3	3q25.1	1.51E+08	1.51E+08
SERP1	1	0.12	0	0	0	SERP1	3	3q25.1	1.52E+08	1.52E+08
EIF2A	1	0.12	0	0	0	EIF2A	3	3q25.1	1.52E+08	1.52E+08
SELT	1	0.12	0	0	0	SELT	3	3q25.1	1.52E+08	1.52E+08
FAM194A	1	0.12	0	0	0	FAM194A	3	3q25.1	1.52E+08	1.52E+08
SIAH2	1	0.12	0	0	0	SIAH2	3	3q25.1	1.52E+08	1.52E+08
KPNA4	1	0.053333	0.146667	0.037037	0	KPNA4	3	3q26.1	1.62E+08	1.62E+08
LRRIQ4	1	0.226667	0.013333	0	0.037037	LRRIQ4	3	3q26.2	1.71E+08	1.71E+08
LRRC31	1	0.226667	0.013333	0	0.037037	LRRC31	3	3q26.2	1.71E+08	1.71E+08
SAMD7	1	0.226667	0.013333	0	0.037037	SAMD7	3	3q26.2	1.71E+08	1.71E+08
LOC100128164	1	0.226667	0.013333	0	0.037037	LOC100128164	3	3q26.2	1.71E+08	1.71E+08
SEC62	1	0.226667	0.013333	0	0.037037	SEC62	3	3q26.2	1.71E+08	1.71E+08
GPR160	1	0.24	0.013333	0	0.037037	GPR160	3	3q26.2	1.71E+08	1.71E+08
PHC3	1	0.226667	0.013333	0	0.037037	PHC3	3	3q26.2	1.71E+08	1.71E+08
KCNMB2	1	0.053333	0.133333	0.037037	0	KCNMB2	3	3q26.32	1.8E+08	1.8E+08
CCDC50	1	0.133333	0.12	0	0.074074	CCDC50	3	3q28	1.93E+08	1.93E+08
MIR217	1	0	0.133333	0	0	MIR217	2	2p16.1	56063606	56063716
MIR216A	1	0	0.133333	0	0	MIR216A	2	2p16.1	56069590	56069699
MIR216B	1	0	0.133333	0	0	MIR216B	2	2p16.1	56081354	56081435
CCDC85A	1	0	0.173333	0	0	CCDC85A	2	2p16.1	56264762	56466814
NCRNA001	1	0.026667	0.12	0.074074	0	NCRNA001	2	2q21.2	1.33E+08	1.33E+08
B3GALT1	1	0.013333	0.133333	0.037037	0	B3GALT1	2	2q24.3	1.68E+08	1.68E+08
ABCB11	1	0	0.16	0.074074	0	ABCB11	2	2q31.1	1.69E+08	1.7E+08
MTX2	1	0.013333	0.133333	0.074074	0	MTX2	2	2q31.1	1.77E+08	1.77E+08
ELAVL4	1	0.08	0.16	0.333333	0	ELAVL4	1	1p33	50286273	50440128
LOC729467	1	0.04	0.133333	0.148148	0	LOC729467	1	1p32.1	59370198	59385068
FGGY	1	0.053333	0.12	0.111111	0	FGGY	1	1p32.1	59535213	60000991
HOOK1	1	0.04	0.146667	0.111111	0	HOOK1	1	1p32.1	60053121	60114639
C1orf87	1	0.053333	0.146667	0.111111	0	C1orf87	1	1p32.1	60228654	60312015
RPE65	1	0.026667	0.133333	0.074074	0	RPE65	1	1p31.3	68667095	68688231
ANKRD13C	1	0.133333	0.08	0	0.074074	ANKRD13C	1	1p31.1	70497273	70593006
HHLA3	1	0.133333	0.08	0	0.074074	HHLA3	1	1p31.1	70593081	70606294
CTH	1	0.146667	0.066667	0	0.074074	CTH	1	1p31.1	70549543	70677842
DDAH1	1	0.013333	0.16	0.037037	0	DDAH1	1	1p22.3	85556757	85816635
COL24A1	1	0.013333	0.146667	0.037037	0	COL24A1	1	1p22.3	85967504	86394710
CLCA2	1	0.026667	0.173333	0	0	CLCA2	1	1p22.3	86662357	86694829
CLCA1	1	0.026667	0.173333	0	0	CLCA1	1	1p22.3	86707114	86738563
CLCA3P	1	0.013333	0.16	0	0	CLCA3P	1	1p22.3	86872547	86893647
SH3GLB1	1	0.013333	0.146667	0	0	SH3GLB1	1	1p22.3	86942845	86986456
GBP7	1	0.04	0.12	0.037037	0	GBP7	1	1p22.2	89370022	89414312
GBP4	1	0.04	0.12	0.037037	0	GBP4	1	1p22.2	89419419	89437222
LOC400759	1	0.026667	0.133333	0.037037	0	LOC400759	1	1p22.2	89645826	89663082
LRRC8B	1	0.013333	0.146667	0.037037	0	LRRC8B	1	1p22.2	89762985	89836007
LRRC8C	1	0.013333	0.12	0.111111	0	LRRC8C	1	1p22.2	89871232	89957682
LRRC8D	1	0.026667	0.12	0.074074	0	LRRC8D	1	1p22.2	90059161	90174576
EVI5	1	0.066667	0.12	0.111111	0	EVI5	1	1p22.1	92746841	93030550
C1orf114	1	0.013333	0.146667	0.037037	0	C1orf114	1	1q24.2	1.68E+08	1.68E+08
F5	1	0	0.12	0.037037	0	F5	1	1q24.2	1.68E+08	1.68E+08
SELP	1	0	0.133333	0.037037	0	SELP	1	1q24.2	1.68E+08	1.68E+08
SELL	1	0	0.133333	0.037037	0	SELL	1	1q24.2	1.68E+08	1.68E+08
SELE	1	0.026667	0.12	0.037037	0	SELE	1	1q24.2	1.68E+08	1.68E+08
C4BPA	1	0.146667	0.12	0.555556	0	C4BPA	1	1q32.2	2.05E+08	2.05E+08
MIR548F3	1	0.04	0.146667	0.074074	0	MIR548F3	1	1q41	2.13E+08	2.13E+08
CHRM3	1	0.026667	0.146667	0.037037	0	CHRM3	1	1q43	2.38E+08	2.38E+08
FMN2	1	0.026667	0.133333	0.074074	0	FMN2	1	1q43	2.38E+08	2.39E+08
GAB4	0.921569	0.333333	0.106667	0.518519	0	GAB4	22	22q11.1	15822827	15869113
CECR6	0.921569	0.453333	0.106667	0.740741	0	CECR6	22	22q11.1	15977189	15982258
CECR5	0.921569	0.453333	0.106667	0.740741	0	CECR5	22	22q11.1	15998410	16026178
CECR4	0.921569	0.453333	0.106667	0.740741	0	CECR4	22	22q11.1	16020279	16026335
CECR1	0.921569	0.453333	0.106667	0.740741	0	CECR1	22	22q11.1	16040192	16060546
LOC646851	0.921569	0.426667	0.106667	0.740741	0	LOC646851	22	22q13.1	37304071	37382581
ATF4	0.921569	0.453333	0.106667	0.814815	0	ATF4	22	22q13.1	38246515	38248638
RPS19BP1	0.921569	0.453333	0.106667	0.814815	0	RPS19BP1	22	22q13.1	38255044	38258807
PPARA	0.921569	0.48	0.106667	0.777778	0	PPARA	22	22q13.31	44925163	45018318
TTC38	0.921569	0.48	0.106667	0.777778	0	TTC38	22	22q13.31	45042525	45068570
CELSR1	0.921569	0.48	0.106667	0.777778	0	CELSR1	22	22q13.31	45135395	45311732

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
HDAC10	0.921569	0.48	0.106667	0.814815	0	HDAC10	22	22q13.33	49025742	49031962
SAPS2	0.921569	0.48	0.106667	0.814815	0	SAPS2	22	22q13.33	49128626	49230381
ADM2	0.921569	0.48	0.106667	0.814815	0	ADM2	22	22q13.33	49266878	49271733
MIOX	0.921569	0.48	0.106667	0.814815	0	MIOX	22	22q13.33	49272079	49275617
LMF2	0.921569	0.48	0.105667	0.814815	0	LMF2	22	22q13.33	49288242	49293002
NCAPH2	0.921569	0.48	0.106667	0.814815	0	NCAPH2	22	22q13.33	49293511	49305058
SCO2	0.921569	0.48	0.106667	0.814815	0	SCO2	22	22q13.33	49308863	49310901
DEFB115	0.921569	0.213333	0.106667	0.518519	0	DEFB115	20	20q11.21	29309128	29311097
UQCR	0.921569	0.506667	0.106667	0.851852	0	UQCR	19	19p13.3	1548154	1556484
TCF3	0.921569	0.506667	0.106667	0.851852	0	TCF3	19	19p13.3	1560293	1601287
COPE	0.921569	0.48	0.106667	0.777778	0	COPE	19	19p13.1	18871323	18891200
DDX49	0.921569	0.48	0.106667	0.777778	0	DDX49	19	19p13.11	18891494	18900437
HOMER3	0.921569	0.48	0.106667	0.777778	0	HOMER3	19	19p13.11	18901010	18912162
CEACAM7	0.921569	0.413333	0.106667	0.814815	0	CEACAM7	19	19q13.2	46869075	46883937
ANKRD30B	0.921569	0.04	0.106667	0.074074	0	ANKRD30B	18	18p11.21	14738239	14842738
CDRT4	0.921569	0.24	0.106667	0.407407	0	CDRT4	17	17p12	15280063	15311651
PIGL	0.921569	0.32	0.106667	0.481481	0	PIGL	17	17p11.2	16051234	16170299
TNFRSF13B	0.921569	0.453333	0.106667	0.740741	0	TNFRSF13B	17	17p11.2	16783123	16816128
MPRIP	0.921569	0.466667	0.106667	0.740741	0	MPRIP	17	17p11.2	16886832	17029598
PLD6	0.921569	0.466667	0.106667	0.740741	0	PLD6	17	17p11.2	17045036	17050372
FLCN	0.921569	0.466667	0.106667	0.740741	0	FLCN	17	17p11.2	17056252	17081228
COPS3	0.921569	0.466667	0.106667	0.740741	0	COPS3	17	17p11.2	17090864	17125317
NT5M	0.921569	0.466667	0.106667	0.740741	0	NT5M	17	17p11.2	17147405	17191703
MED9	0.921569	0.466667	0.106667	0.740741	0	MED9	17	17p11.2	17321025	17337260
RASD1	0.921569	0.466667	0.106667	0.740741	0	RASD1	17	17p11.2	17338478	17340433
PEMT	0.921569	0.466667	0.106667	0.740741	0	PEMT	17	17p11.2	17349602	17426471
RAI1	0.921569	0.48	0.106667	0.740741	0	RAI1	17	17p11.2	17525512	17555491
SREBF1	0.921569	0.466667	0.106667	0.740741	0	SREBF1	17	17p11.2	17655393	17681051
MIR33B	0.921569	0.466667	0.106667	0.740741	0	MIR33B	17	17p11.2	17657875	17557971
TOM1L2	0.921569	0.466667	0.106667	0.740741	0	TOM1L2	17	17p11.2	17687547	17816510
LRRC48	0.921569	0.466667	0.106667	0.740741	0	LRRC48	17	17p11.2	17816852	17860915
ATPAF2	0.921569	0.466667	0.106667	0.740741	0	ATPAF2	17	17p11.2	17862059	17883206
MYO15A	0.921569	0.48	0.106667	0.740741	0	MYO15A	17	17p11.2	17952745	18023842
ALKBH5	0.921569	0.466667	0.106667	0.740741	0	ALKBH5	17	17p11.2	18027592	18053993
SMCR8	0.921569	0.48	0.106667	0.740741	0	SMCR8	17	17p11.2	18159319	18172096
SHMT1	0.921569	0.48	0.106667	0.740741	0	SHMT1	17	17p11.2	18171912	18207582
EVPLL	0.921569	0.48	0.106667	0.740741	0	EVPLL	17	17p11.2	18221804	18233684
MEOX1	0.921569	0.466667	0.106667	0.777778	0	MEOX1	17	17q21.31	39073284	39094789
SOST	0.921569	0.466667	0.106667	0.777778	0	SOST	17	17q21.31	39186625	39191683
DUSP3	0.921569	0.466667	0.106667	0.777778	0	DUSP3	17	17q21.31	39199015	39211895
HS3ST2	0.921569	0.28	0.106667	0.666667	0	HS3ST2	16	16p12.1	22733361	22835161
PWRN1	0.921569	0.026667	0.106667	0.148148	0	PWRN1	15	15q11.2	22354397	22384018
AQP9	0.921569	0.04	0.106667	0.074074	0	AQP9	15	15q22.1	56217700	56265403
LOC91948	0.921569	0.04	0.106667	0.111111	0	LOC91948	15	15q26.2	96086850	96218664
ABHD12B	0.921569	0.106667	0	0	0.037037	ABHD12B	14	14q22.1	50408628	50441439
PYGL	0.921569	0.106667	0	0	0.037037	PYGL	14	14q22.1	50441686	50480999
PSPC1	0.921569	0.093333	0.106667	0.333333	0	PSPC1	13	13q12.11	19146896	19255084
DHRS12	0.921569	0.106667	0.226667	0	0.148148	DHRS12	13	13q14.3	51240132	51276295
FLI37307	0.921569	0.106667	0.226667	0	0.148148	FLI37307	13	13q14.3	51285484	51317288
ATP7B	0.921569	0.106667	0.226657	0	0.148148	ATP7B	13	13q14.3	51404806	51483632
ALG11	0.921569	0.106667	0.226667	0	0.148148	ALG11	13	13q14.3	51484551	51501782
UTP14C	0.921569	0.106667	0.226667	0	0.148148	UTP14C	13	13q14.3	51496828	51505736
NEK5	0.921569	0.106667	0.226667	0	0.148148	NEK5	13	13q14.3	51536901	51601216
NEK3	0.921569	0.106667	0.226667	0	0.148148	NEK3	13	13q14.3	51604780	51631998
THSD1	0.921569	0.106667	0.226667	0	0.148148	THSD1	13	13q14.3	51849305	51878631
HNRNPA1L2	0.921569	0.106667	0.226667	0	0.148148	HNRNPA1L2	13	13q14.3	52089606	52115921
LECT1	0.921569	0.106667	0.226667	0	0.148148	LECT1	13	13q14.3	52175400	52211949
ITPR2	0.921569	0.013333	0.106667	0.037037	0	ITPR2	12	12p11.23	26379552	26877399
CSRP2	0.921569	0.106667	0.106667	0	0.111111	CSRP2	12	12q21.2	75776627	75796931
PAWR	0.921569	0.106667	0.12	0	0.296296	PAWR	12	12q21.2	78509876	78608922
NEDD1	0.921569	0.066667	0.106667	0.074074	0	NEDD1	12	12q23.1	95825132	95871593
ANO4	0.921569	0.066667	0.106667	0	0	ANO4	12	12q23.1	99712505	1E+D8
GVIN1	0.921569	0.053333	0.106667	0.037037	0	GVIN1	11	11p15.4	6690954	6699687
APIP	0.921569	0.053333	0.106667	0.074074	0	APIP	11	11p13	34860419	34894516
FAM181B	0.921569	0.04	0.106667	0	0	FAM181B	11	11q14.1	82120694	82122555
HEPHL1	0.921569	0.04	0.106667	0.074074	0	HEPHL1	11	11q21	93394026	93487023
HTR3B	0.921569	0.213333	0.106657	0.37037	0	HTR3B	11	11q23.2	1.13E+08	1.13E+08
FLJ35024	0.921569	0.013333	0.106667	0.037037	0	FLJ35024	9	9p24.2	2525655	2612374
RFX3	0.921569	0.026667	0.106667	0.037037	0	RFX3	9	9p24.2	3214647	3515984
FREM1	0.921569	0.026667	0.106667	0	0	FREM1	9	9p22.3	14727151	14900235
BNC2	0.921569	0.04	0.106667	0.074074	0	BNC2	9	9p22.3	16399501	16860787
TLE4	0.921569	0.053333	0.106667	0.111111	0	TLE4	9	9q21.31	81376698	81531477
RASEF	0.921569	0.093333	0.106667	0.185185	0	RASEF	9	9q21.32	84787137	84867864
CCDC129	0.921569	0.053333	0.106667	0.037037	0	CCDC129	7	7p15.1	31523503	31659829

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
PDE1C	0.921569	0.053333	0.106667	0.037037	0	PDE1C	7	7p14.3	31795772	32077517
C7orf53	0.921569	0.106667	0.04	0	0.074074	C7orf53	7	7q31.1	1.12E+08	1.12E+08
CAV1	0.921569	0.106667	0.08	0	0.111111	CAV1	7	7q31.2	1.16E+08	1.16E+08
LOC100287718	0.921569	0.04	0.106667	0.074074	0	LOC100287718	6	6p12.3	46822658	46834901
IBTK	0.921569	0.106667	0.226667	0	0.333333	IBTK	6	6q14.1	82936675	83014168
PNRC1	0.921569	0.106667	0.2	0	0.185185	PNRC1	6	6q15	89847148	89851599
SFRS13B	0.921569	0.106667	0.2	0	0.185185	SFRS13B	6	6q15	89862397	89884520
CD180	0.921569	0.106667	0.146667	0	0.148148	CD180	5	5q13.1	66513860	66528374
ZCCHC9	0.921569	0.106667	0.106667	0	0.037037	ZCCHC9	5	5q14.1	80633158	80644720
ACOT12	0.921569	0.106667	0.106667	0	0.037037	ACOT12	5	5q14.1	80661703	80725745
PJA2	0.921569	0.106667	0.16	0	0.185185	PJA2	5	5q21.3	1.09E+08	1.09E+08
CDS1	0.921569	0.04	0.106667	0	0	CDS1	4	4q21.23	85723081	85791518
PTPN13	0.921569	0.106667	0.053333	0	0	PTPN13	4	4q21.3	87734492	87955353
OSTC	0.921569	0.106667	0	0	0.037037	OSTC	4	4q25	1.1E+08	1.1E+08
GAB1	0.921569	0.013333	0.106667	0	0	GAB1	4	4q31.21	1.44E+08	1.45E+08
SMARCA5	0.921569	0.013333	0.106667	0	0	SMARCA5	4	4q31.21	1.45E+08	1.45E+08
LOC441046	0.921569	0.013333	0.106667	0	0	LOC441046	4	4q31.21	1.45E+08	1.45E+08
FREM3	0.921569	0.013333	0.106667	0	0	FREM3	4	4q31.21	1.45E+08	1.45E+08
SCN10A	0.921569	0.106667	0.106667	0.259259	0	SCN10A	3	3p22.2	38713841	38810506
FHIT	0.921569	0.066667	0.106667	0.148148	0	FHIT	3	3p14.2	59710076	61212174
C3orf49	0.921569	0.026667	0.106667	0.037037	0	C3orf49	3	3p14.1	63780081	63809351
PROS1	0.921569	0.106667	0.173333	0	0.37037	PROS1	3	3q11.2	95074572	95175625
TMEM108	0.921569	0.066667	0.106667	0.074074	0	TMEM108	3	3q22.1	1.34E+08	1.35E+08
GYG1	0.921569	0.106667	0.026667	0	0.074074	GYG1	3	3q24	1.5E+08	1.5E+08
IQCJ	0.921569	0.053333	0.106667	0.037037	0	IQCJ	3	3q25.33	1.6E+08	1.6E+08
NMD3	0.921569	0.106667	0.04	0	0.074074	NMD3	3	3q26.1	1.62E+08	1.62E+08
TBL1XR1	0.921569	0.106667	0.013333	0	0	TBL1XR1	3	3q26.32	1.78E+08	1.78E+08
UTS2D	0.921569	0.106667	0.12	0	0.074074	UTS2D	3	3q28	1.92E+08	1.93E+08
LOC100271715	0.921569	0.013333	0.106667	0.074074	0	LOC100271715	2	2p22.1	39000093	39056093
SOS1	0.921569	0.013333	0.106667	0.074074	0	SOS1	2	2p22.1	39062194	39201109
GTF2A1L	0.921569	0.04	0.106667	0.222222	0	GTF2A1L	2	2p16.3	48698452	48813791
LHCGR	0.921569	0.04	0.106667	0.222222	0	LHCGR	2	2p16.3	48767417	48836385
ANTXR1	0.921569	0.093333	0.106667	0.222222	0	ANTXR1	2	2p14	69093780	69226999
LYPD1	0.921569	0.04	0.106667	0.074074	0	LYPD1	2	2q21.2	1.33E+08	1.33E+08
NCKAP5	0.921569	0.026667	0.106667	0.074074	0	NCKAP5	2	2q21.2	1.33E+08	1.34E+08
MGAT5	0.921569	0.093333	0.106667	0.148148	0	MGAT5	2	2q21.3	1.35E+08	1.35E+08
RAB3GAP1	0.921569	0.146667	0.106667	0.148148	0	RAB3GAP1	2	2q21.3	1.36E+08	1.36E+08
NEB	0.921569	0.04	0.106667	0.037037	0	NEB	2	2q23.3	1.52E+08	1.52E+08
BAZ2B	0.921569	0.066667	0.106667	0.148148	0	BAZ2B	2	2q24.2	1.6E+08	1.6E+08
LOC100130691	0.921569	0.013333	0.106667	0.037037	0	LOC100130691	2	2q31.2	1.78E+08	1.78E+08
SLC5A9	0.921569	0.146667	0.106667	0.518519	0	SLC5A9	1	1p33	48460944	48486904
BEND5	0.921569	0.146667	0.106667	0.37037	0	BEND5	1	1p33	48966127	49015135
ORC1L	0.921569	0.28	0.106667	0.481481	0	ORC1L	1	1p32.3	52611089	52642720
C8B	0.921569	0.08	0.106667	0.111111	0	C8B	1	1p32.2	57167471	57204277
DAB1	0.921569	0.08	0.106667	0.111111	0	DAB1	1	1p32.2	57236167	58488800
JUN	0.921569	0.04	0.106667	0.074074	0	JUN	1	1p32.1	59019051	59022374
EFCAB7	0.921569	0.093333	0.106667	0.074074	0	EFCAB7	1	1p31.3	63761601	63810952
CACHD1	0.921569	0.04	0.106667	0.074074	0	CACHD1	1	1p31.3	64709064	64931330
LEPR	0.921569	0.12	0.106667	0.074074	0	LEPR	1	1p31.3	65658836	65873699
LEPROT	0.921569	0.12	0.106667	0.074074	0	LEPROT	1	1p31.3	65658836	65674277
GNG5	0.921569	0.053333	0.106667	0.037037	0	GNG5	1	1p22.3	84736594	84744851
SPATA1	0.921569	0.053333	0.106667	0.037037	0	SPATA1	1	1p22.3	84744562	84804464
CTBS	0.921569	0.04	0.106667	0.037037	0	CTBS	1	1p22.3	84791394	84812752
C1orf180	0.921569	0.04	0.106667	0.037037	0	C1orf180	1	1p22.3	84866501	84873292
SSX2IP	0.921569	0.04	0.106667	0.037037	0	SSX2IP	1	1p22.3	84881978	84928829
LPAR3	0.921569	0.04	0.106667	0.037037	0	LPAR3	1	1p22.3	85051674	95131485
MCOLN2	0.921569	0.04	0.106667	0.037037	0	MCOLN2	1	1p22.3	85163854	85235385
MCOLN3	0.921569	0.026667	0.106667	0.037037	0	MCOLN3	1	1p22.3	85256353	85286758
WDR63	0.921569	0.026667	0.106667	0.037037	0	WDR63	1	1p22.3	85300581	85371409
HS2ST1	0.921569	0.04	0.106667	0	0	HS2ST1	1	1p22.3	87152923	87336713
RBMXL1	0.921569	0.066667	0.106667	0.037037	0	RBMXL1	1	1p22.2	89217728	89231232
TGFBR3	0.921569	0.04	0.106667	0.111111	0	TGPBR3	1	1p22.2	91918490	92124375
ARHGAP29	0.921569	0.066667	0.106667	0.148148	0	ARHGAP29	1	1p22.1	94407051	94475896
MGC4473	0.921569	0.013333	0.106667	0.037037	0	MGC4473	1	1q24.2	1.67E+08	1.67E+08
SLC19A2	0.921569	0.013333	0.106667	0.037037	0	SLC19A2	1	1q24.2	1.68E+08	1.68E+08
C1orf156	0.921569	0.04	0.106667	0.037037	0	C1orf156	1	1q24.2	1.68E+08	1.68E+08
C1orf112	0.921569	0.04	0.106667	0.037037	0	C1orf112	1	1q24.2	1.68E+08	1.68E+08
GORAB	0.921569	0	0.106667	0.037037	0	GORAB	1	1q24.2	1.69E+08	1.69E+08
RNF138P1	0.019608	0.12	0.146667	0.037037	0.037037	RNF138P1	5	5q11.2	54860427	54866128
MTX3	0.019608	0.12	0.133333	0.037037	0.037037	MTX3	5	5q14.1	79308297	73322845
USP33	0.019608	0.133333	0.106667	0.037037	0.037037	USP33	1	1p31.1	77934262	77998126
FAM73A	0.019608	0.133333	0.106667	0.037037	0.037037	FAM73A	1	1p31.1	78017897	78116670
TTTY12	0.009804	0.226667	0.12	0.259259	0.037037	TTTY12	Y	Yp11.2	7732965	7738724
CECR7	0.009804	0.32	0.133333	0.481481	0.037037	CECR7	22	22q11.1	15897460	15919683

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
EP300	0.009804	0.44	0.106667	0.740741	0.037037	EP300	22	22q13.2	39818560	39906028
MOV10L1	0.009804	0.48	0.12	0.777778	0.037037	MOV10L1	22	22q13.33	48870562	48942243
ABCC13	0.009804	0.04	0.146667	0.037037	0.037037	ABCC13	21	21q11.2	14567991	14595564
CYYR1	0.009804	0	0.146667	0	0.037037	CYYR1	21	21q21.3	26760399	26867453
HAO1	0.009804	0.053333	0.186667	0.143148	0.037037	HAO1	20	20p12.3	7811631	7869094
PLCB4	0.009804	0.066667	0.133333	0.074074	0.037037	PLCB4	20	20p12.2	9024932	9409463
PAK7	0.009804	0.106667	0.106667	0.074074	0.037037	PAK7	20	20p12.2	9466037	9767688
SNAP25	0.009804	0.08	0.12	0.074074	0.037037	SNAP25	20	20p12.2	10147477	10236066
BTBD3	0.009804	0.04	0.173333	0.074074	0.037037	BTBD3	20	20p12.2	11819477	11855244
ISM1	0.009804	0.066667	0.146667	0.111111	0.037037	ISM1	20	20p12.1	13150418	13229298
CRNKL1	0.009804	0.24	0.133333	0.481481	0.037037	CRNKL1	20	20p11.23	19963012	19984691
PSG1	0.009804	0.306667	0.133333	0.740741	0.037037	PSG1	19	19q13.31	48063198	48075712
ZNF180	0.009804	0.426667	0.106667	0.814815	0.037037	ZNF180	19	19q13.31	49671699	49696415
ZNF521	0.009804	0.026667	0.12	0.111111	0.037037	ZNF521	18	18q11.2	20895886	21186213
C18orf16	0.009804	0	0.133333	0	0.037037	C18orf16	18	18q11.2	22699270	22769909
CHST9	0.009804	0	0.133333	0	0.037037	CHST9	18	18q11.2	22749595	23019288
MOCOS	0.009804	0.106667	0.093333	0.037037	0.074074	MOCOS	18	18q12.2	32021478	32102684
FHOD3	0.009804	0.106667	0.093333	0.037037	0.037037	FHOD3	18	18q12.2	32131700	32614017
SLC14A2	0.009804	0.213333	0.106667	0.185185	0.037037	SLC14A2	18	18q12.3	41448764	41517059
SLC14A1	0.009804	0.226667	0.106667	0.185185	0.037037	SLC14A1	18	18q12.3	41558090	41586483
SIGLEC15	0.009804	0.226667	0.106667	0.185185	0.037037	SIGLEC15	18	18q12.3	41659543	41676520
KIAA1632	0.009804	0.226667	0.106667	0.185185	0.037037	KIAA1632	18	18q12.3	41681572	41801304
PSTPIP2	0.009804	0.226667	0.12	0.185185	0.037037	PSTPIP2	18	18q21.1	41817500	41906249
ATP5A1	0.009804	0.226667	0.12	0.185185	0.037037	ATP5A1	18	18q21.1	41918108	41938198
HAUS1	0.009804	0.226667	0.12	0.185185	0.037037	HAUS1	18	18q21.1	41938296	41962297
C18orf25	0.009804	0.226667	0.106667	0.222222	0.037037	C18orf25	18	18q21.1	42007986	42100954
RNF165	0.009804	0.253333	0.106667	0.222222	0.037037	RNF165	18	18q21.1	42168185	42294782
LOXHD1	0.009804	0.24	0.106667	0.222222	0.037037	LOXHD1	18	18q21.1	42310935	42393251
ST8SIA5	0.009804	0.24	0.106667	0.222222	0.037037	ST8SIA5	18	18q21.1	42513079	42591038
IER3IP1	0.009804	0.16	0.106667	0.222222	0.037037	IER3IP1	18	18q21.1	42935411	42956744
KIAA0427	0.009804	0.306667	0.106667	0.407407	0.037037	KIAA0427	18	18q21.1	44319425	44643577
SMAD7	0.009804	0.306667	0.106667	0.333333	0.037037	SMAD7	18	18q21.1	44700221	44731080
MYO5B	0.009804	0.24	0.106667	0.259259	0.037037	MYO5B	18	18q21.1	45603154	45975450
CCDC11	0.009804	0.213333	0.106667	0.259259	0.037037	CCDC11	18	18q21.1	46007562	46046864
SKA1	0.009804	0.2	0.12	0.259259	0.037037	SKA1	18	18q21.1	46155390	46174537
MAPK4	0.009804	0.16	0.16	0.259259	0.037037	MAPK4	18	18q21.1	46340482	46512195
MRO	0.009804	0.24	0.106667	0.259259	0.037037	MRO	18	18q21.2	46575488	46605753
ME2	0.009804	0.24	0.106667	0.259259	0.037037	ME2	18	18q21.2	46659430	46730159
ELAC1	0.009804	0.24	0.106667	0.259259	0.037037	ELAC1	18	18q21.2	46748385	46768489
ST8SIA3	0.009804	0.093333	0.133333	0.148148	0.037037	ST8SIA3	18	18q21.31	53170719	53187160
ONECUT2	0.009804	0.093333	0.133333	0.148148	0.037037	ONECUT2	18	18q21.31	53253915	53309529
ATP8B1	0.009804	0.186667	0.133333	0.185185	0.037037	ATP8B1	18	18q21.31	53464657	53550038
NEDD4L	0.009804	0.186667	0.133333	0.148148	0.037037	NEDD4L	18	18q21.31	53862617	54219753
ALPK2	0.009804	0.2	0.12	0.074074	0.037037	ALPK2	18	18q21.31	54299462	54447170
MALT1	0.009804	0.2	0.133333	0.074074	0.037037	MALT1	18	18q21.32	54489598	54568351
ZNF532	0.009804	0.213333	0.12	0.074074	0.037037	ZNF532	18	18q21.32	54681041	54804690
LOC390858	0.009804	0.186667	0.12	0.074074	0.037037	LOC390858	18	18q21.32	54853951	54871427
SEC11C	0.009804	0.146667	0.12	0.074074	0.037037	SEC11C	18	18q21.32	54958105	54977044
CPLX4	0.009804	0.146667	0.133333	0.074074	0.037037	CPLX4	18	18q21.32	55113618	55136862
LMAN1	0.009804	0.146667	0.133333	0.074074	0.037037	LMAN1	18	18q21.32	55146037	55177489
CCBE1	0.009804	0.146667	0.12	0.074074	0.037037	CCBE1	18	18q21.32	55252129	55515625
SOCS6	0.009804	0.106667	0.173333	0.037037	0.222222	SOCS6	18	18q22.2	66107117	66148415
ZNF516	0.009804	0.213333	0.106667	0.185185	0.037037	ZNF516	18	18q23	72200607	72304044
LOC284276	0.009804	0.24	0.106667	0.222222	0.037037	LOC284276	18	18q23	72369600	72400772
ZNF236	0.009804	0.253333	0.106667	0.222222	0.037037	ZNF236	18	18q23	72665104	72811671
C17orf97	0.009804	0.466667	0.12	0.740741	0.037037	C17orf97	17	17p13.3	260434	264802
OR1A2	0.009804	0.266667	0.16	0.703704	0.037037	OR1A2	17	17p13.3	3047563	3048493
ATP2A3	0.009804	0.413333	0.133333	0.740741	0.037037	ATP2A3	17	17p13.2	3773918	3814486
ZZEF1	0.009804	0.36	0.133333	0.740741	0.037037	ZZEF1	17	17p13.2	3854488	3993003
CYB5D2	0.009804	0.4	0.133333	0.740741	0.037037	CYB5D2	17	17p13.2	3993211	4007741
ANKFY1	0.009804	0.4	0.133333	0.740741	0.037037	ANKFY1	17	17p13.2	4013414	4114024
UBE2G1	0.009804	0.4	0.133333	0.740741	0.037037	UBE2G1	17	17p13.2	4119251	4216719
SPNS2	0.009804	0.413333	0.133333	0.740741	0.037037	SPNS2	17	17p13.2	4348878	4389978
SMTNL2	0.009804	0.413333	0.133333	0.740741	0.037037	SMTNL2	17	17p13.2	4434025	4458364
PELP1	0.009804	0.413333	0.133333	0.740741	0.037037	PELP1	17	17p13.2	4521428	4554382
ARRB2	0.009804	0.413333	0.133333	0.740741	0.037037	ARRB2	17	17p13.2	4560538	4571545
MED11	0.009804	0.413333	0.133333	0.740741	0.037037	MED11	17	17p13.2	4581472	4583646
CXCL16	0.009804	0.413333	0.133333	0.740741	0.037037	CXCL16	17	17p13.2	4583577	4589973
ZMYND15	0.009804	0.413333	0.133333	0.740741	0.037037	ZMYND15	17	17p13.2	4590068	4596160
TM4SF5	0.009804	0.413333	0.133333	0.740741	0.037037	TM4SF5	17	17p13.2	4621936	4633254
VMO1	0.009804	0.413333	0.133333	0.740741	0.037037	VMO1	17	17p13.2	4635321	4636470
GLTPD2	0.009804	0.413333	0.133333	0.740741	0.037037	GLTPD2	17	17p13.2	4638994	4640426
PSMB6	0.009804	0.413333	0.133333	0.740741	0.037037	PSMB6	17	17p13.2	4646415	4648749
PLD2	0.009804	0.413333	0.133333	0.740741	0.037037	PLD2	17	17p13.2	4657378	4673695

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
MINK1	0.009804	0.413333	0.133333	0.740741	0.037037	MINK1	17	17p13.2	4683303	4742135
RNF167	0.009804	0.413333	0.133333	0.740741	0.037037	RNF167	17	17p13.2	4784375	4789263
PFN1	0.009804	0.413333	0.133333	0.740741	0.037037	PFN1	17	17p13.2	4789692	4792571
ENO3	0.009804	0.413333	0.133333	0.740741	0.037037	ENO3	17	17p13.2	4795131	4801149
SPAG7	0.009804	0.413333	0.133333	0.740741	0.037037	SPAG7	17	17p13.2	4803244	4811857
CAMTA2	0.009804	0.413333	0.133333	0.740741	0.037037	CAMTA2	17	17p13.2	4812017	4831656
KIF1C	0.009804	0.413333	0.133333	0.740741	0.037037	KIF1C	17	17p13.2	4842000	4868721
GPR172B	0.009804	0.413333	0.133333	0.740741	0.037037	GPR172B	17	17p13.2	4876621	4879452
ZNF594	0.009804	0.373333	0.133333	0.740741	0.037037	ZNF594	17	17p13.2	5023555	5035903
C17orf87	0.009804	0.373333	0.133333	0.740741	0.037037	C17orf87	17	17p13.2	5054625	5078808
RABEP1	0.009804	0.373333	0.146667	0.740741	0.037037	RABEP1	17	17p13.2	5126282	5229857
C1Q8P	0.009804	0.373333	0.133333	0.740741	0.037037	C1QBP	17	17p13.2	5276823	5283196
DHX33	0.009804	0.373333	0.133333	0.740741	0.037037	DHX33	17	17p13.2	5286315	5312906
DERL2	0.009804	0.36	0.133333	0.740741	0.037037	DERL2	17	17p13.2	5318337	5330219
MIS12	0.009804	0.36	0.133333	0.740741	0.037037	MIS12	17	17p13.2	5330971	5334855
NLRP1	0.009804	0.36	0.133333	0.740741	0.037037	NLRP1	17	17p13.2	5345443	5428557
WSCD1	0.009804	0.386667	0.133333	0.740741	0.037037	WSCD1	17	17p13.2	5914658	5968472
PITPNM3	0.009804	0.4	0.133333	0.740741	0.037037	PITPNM3	17	17p13.2	6295307	6400602
KIAA0753	0.009804	0.36	0.186667	0.740741	0.037037	KIAA0753	17	17p13.2	6422369	6484972
SLC13A5	0.009804	0.4	0.146667	0.740741	0.037037	SLC13A5	17	17p13.2	5528765	6557465
XAF1	0.009804	0.386667	0.146667	0.740741	0.037037	XAF1	17	17p13.2	6599880	6619689
FBXO39	0.009804	0.386667	0.146667	0.740741	0.037037	FBXO39	17	17p13.2	6620276	6631689
TEKT1	0.009804	0.386667	0.146667	0.740741	0.037037	TEKT1	17	17p13.2	6644024	6675785
ALOX12P2	0.009804	0.386667	0.146667	0.740741	0.037037	ALOX12P2	17	17p13.2	6697619	6744393
ALOX12	0.009804	0.413333	0.146667	0.740741	0.037037	ALOX12	17	17p13.1	6840108	6854780
RNASEK	0.009804	0.413333	0.146667	0.740741	0.037037	RNASEK	17	17p13.1	6856522	6858576
C17orf49	0.009804	0.413333	0.146667	0.740741	0.037037	C17orf49	17	17p13.1	6858797	6861563
MIR195	0.009804	0.413333	0.146667	0.740741	0.037037	MIR195	17	17p13.1	6861658	6861745
MIR497	0.009804	0.413333	0.146667	0.740741	0.037037	MIR497	17	17p13.1	6861954	6862066
BCL6B	0.009804	0.413333	0.146667	0.740741	0.037037	BCL6B	17	17p13.1	6867093	6873686
SLC16A13	0.009804	0.413333	0.146667	0.740741	0.037037	SLC16A13	17	17p13.1	6880118	6884164
SLC16A11	0.009804	0.413333	0.146667	0.740741	0.037037	SLC16A11	17	17p13.1	6885673	6887967
ASGR2	0.009804	0.413333	0.146667	0.703704	0.037037	ASGR2	17	17p13.1	6945365	6958853
ASGR1	0.009804	0.413333	0.146667	0.703704	0.037037	ASGR1	17	17p13.1	7017475	7023608
DLG4	0.009804	0.413333	0.145667	0.703704	0.037037	DLG4	17	17p13.1	7033934	7061653
ACADVL	0.009804	0.413333	0.146667	0.703704	0.037037	ACADVL	17	17p13.1	7063877	7069310
MIR324	0.009804	0.413333	0.146667	0.703704	0.037037	MIR324	17	17p13.1	7067340	7067423
DVL2	0.009804	0.413333	0.146667	0.703704	0.037037	DVL2	17	17p13.1	7069385	7078588
PHF23	0.009804	0.413333	0.146667	0.703704	0.037037	PHF23	17	17p13.1	7079071	7083550
GABARAP	0.009804	0.413333	0.146667	0.703704	0.037037	GABARAP	17	17p13.1	7084462	7086478
DULLARD	0.009804	0.413333	0.146667	0.703704	0.037037	DULLARD	17	17p13.1	7087630	7095720
C17orf81	0.009804	0.413333	0.146667	0.703704	0.037037	C17orf81	17	17p13.1	7096096	7103984
CLDN7	0.009804	0.413333	0.146667	0.703704	0.037037	CLDN7	17	17p13.1	7103946	7106520
SLC2A4	0.009804	0.413333	0.146667	0.703704	0.037037	SLC2A4	17	17p13.1	7125778	7132092
YBX2	0.009804	0.413333	0.146667	0.703704	0.037037	YBX2	17	17p13.1	7132295	7138601
WRAP53	0.009804	0.4	0.16	0.703704	0.037037	WRAP53	17	17p13.1	7530114	7547545
EFNB3	0.009804	0.4	0.16	0.703704	0.037037	EFNB3	17	17p13.1	7549245	7555419
DNAH2	0.009804	0.4	0.16	0.703704	0.037037	DNAH2	17	17p13.1	7563764	7677784
KDM6B	0.009804	0.4	0.16	0.703704	0.037037	KDM6B	17	17p13.1	7683960	7698844
TMEM88	0.009804	0.4	0.16	0.703704	0.037037	TMEM88	17	17p13.1	7699109	7700143
LSMD1	0.009804	0.4	0.16	0.703704	0.037037	LSMD1	17	17p13.1	7700728	7701898
CYB5D1	0.009804	0.4	0.16	0.703704	0.037037	CYB5D1	17	17p13.1	7701789	7706326
CHD3	0.009804	0.4	0.16	0.703704	0.037037	CHD3	17	17p13.1	7728848	7756801
SCARNA21	0.009804	0.4	0.16	0.703704	0.037037	SCARNA21	17	17p13.1	7750166	7750304
LOC284023	0.009804	0.4	0.16	0.703704	0.037037	LOC284023	17	17p13.1	7757366	7759991
KCNAB3	0.009804	0.4	0.16	0.703704	0.037037	KCNAB3	17	17p13.1	7766752	7773479
TRAPPC1	0.009804	0.4	0.16	0.703704	0.037037	TRAPPC1	17	17p13.1	7774388	7776043
CNTROB	0.009804	0.4	0.16	0.703704	0.037037	CNTROB	17	17p13.1	7776198	7793622
GUCY2D	0.009804	0.4	0.16	0.703704	0.037037	GUCY2D	17	17p13.1	7846713	7864384
ALOX12B	0.009804	0.4	0.146667	0.703704	0.037037	ALOX12B	17	17p13.1	7916679	7931747
ALOXE3	0.009804	0.4	0.146667	0.703704	0.037037	ALOXE3	17	17p13.1	7939943	7962586
HES7	0.009804	0.4	0.146667	0.703704	0.037037	HES7	17	17p13.1	7964633	7968136
PER1	0.009804	0.4	0.146667	0.703704	0.037037	PER1	17	17p13.1	7984513	7996479
VAMP2	0.009804	0.4	0.146667	0.703704	0.037037	VAMP2	17	17p13.1	8003190	8007019
TMEM107	0.009804	0.4	0.146667	0.703704	0.037037	TMEM107	17	17p13.1	8017021	8020440
C17orf59	0.009804	0.4	0.146667	0.703704	0.037037	C17orf59	17	17p13.1	8032376	8034290
AURKB	0.009804	0.4	0.146667	0.703704	0.037037	AURKB	17	17p13.1	8048774	8054609
C17orf44	0.009804	0.4	0.146667	0.703704	0.037037	C17orf44	17	17p13.1	8064673	8068087
C17orf68	0.009804	0.4	0.146667	0.703704	0.037037	C17orf68	17	17p13.1	8068864	8092139
PFAS	0.009804	0.4	0.146667	0.703704	0.037037	PFAS	17	17p13.1	8093321	8114534
SLC25A35	0.009804	0.4	0.146667	0.703704	0.037037	SLC25A35	17	17p13.1	8131807	8138896
RANGRF	0.009804	0.4	0.146667	0.703704	0.037037	RANGRF	17	17p13.1	8132714	8134131
ARHGEF15	0.009804	0.4	0.146667	0.703704	0.037037	ARHGEF15	17	17p13.1	8154315	8166555
LOC100128288	0.009804	0.4	0.133333	0.703704	0.037037	LOC100128288	17	17p13.1	8202456	8204585

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
KRBA2	0.009804	0.4	0.133333	0.703704	0.037037	KRBA2	17	17p13.1	8212698	8215584
RPL26	0.009804	0.4	0.133333	0.703704	0.037037	RPL26	17	17p13.1	8221559	8227291
RNF222	0.009804	0.4	0.133333	0.703704	0.037037	RNF222	17	17p13.1	8234750	8241870
NDEL1	0.009804	0.4	0.133333	0.703704	0.037037	NDEL1	17	17p13.1	8279904	8312207
MYH10	0.009804	0.4	0.133333	0.703704	0.037037	MYH10	17	17p13.1	8318255	8474762
CCDC42	0.009804	0.4	0.12	0.703704	0.037037	CCDC42	17	17p13.1	8573972	8588880
SPDYE4	0.009804	0.4	0.12	0.703704	0.037037	SPDYE4	17	17p13.1	8597149	8602603
MFSD6L	0.009804	0.373333	0.146667	0.703704	0.037037	MFSD6L	17	17p13.1	8641153	8643393
PIK3R6	0.009804	0.373333	0.146667	0.703704	0.037037	PIK3R6	17	17p13.1	8646780	8711720
PIK3R5	0.009804	0.4	0.12	0.666667	0.037037	PIK3R5	17	17p13.1	8722959	8809750
NTN1	0.009804	0.386667	0.12	0.666667	0.037037	NTN1	17	17p13.1	8865584	9088043
STX8	0.009804	0.386667	0.12	0.666667	0.037037	STX8	17	17p13.1	9094513	9420001
WDR16	0.009804	0.386667	0.12	0.592593	0.037037	WDR16	17	17p13.1	9420669	9487502
USP43	0.009804	0.386667	0.12	0.592593	0.037037	USP43	17	17p13.1	5489675	9573729
GLP2R	0.009804	0.373333	0.106667	0.555556	0.037037	GLP2R	17	17p13.1	9670106	9733748
GAS7	0.009804	0.386667	0.106667	0.555556	0.037037	GAS7	17	17p13.1	9754651	9870349
MYH13	0.009804	0.36	0.106667	0.555556	0.037037	MYH13	17	17p13.1	10144908	10217048
C17orf39	0.009804	0.466667	0.106667	0.703704	0.037037	C17orf39	17	17p11.2	17883336	17912444
ACLY	0.009804	0.466667	0.106667	0.703704	0.037037	ACLY	17	17q21.2	37276705	37328799
KCNJ16	0.009804	0.106667	0.146667	0.296296	0.037037	KCNJ16	17	17q24.3	65583021	65643342
IRF8	0.009804	0.36	0.133333	0.62963	0.037037	IRF8	16	16q24.1	84490275	84513713
MAP1LC3B	0.009804	0.426667	0.146667	0.62963	0.037037	MAP1LC3B	16	16q24.2	85983302	85995881
KLHDC4	0.009804	0.426667	0.186667	0.62963	0.037037	KLHDC4	16	16q24.2	86298919	86357044
FANCA	0.009804	0.48	0.186667	0.703704	0.037037	FANCA	16	16q24.3	88331460	88410567
MEIS2	0.009804	0.013333	0.133333	0.037037	0.037037	MEIS2	15	15q14	34970524	35180793
SPRED1	0.009804	0.026667	0.146667	0.037037	0.037037	SPRED1	15	15q14	36332344	36436743
SHC4	0.009804	0.013333	0.106667	0.037037	0.037037	SHC4	15	15q21.1	46903227	47042934
ATP8B4	0.009804	0.013333	0.133333	0.074074	0.037037	ATP8B4	15	15q21.2	47937727	48198712
PIGB	0.009804	0.12	0.026667	0.037037	0	PIGB	15	15q21.3	53398425	53435139
CCPG1	0.009804	0.12	0.026667	0.037037	0	CCPG1	15	15q21.3	53434730	53487835
MIR628	0.009804	0.12	0.026667	0.037037	0	MIR628	15	15q21.3	53452430	53452525
DYX1C1	0.009804	0.12	0.026667	0.037037	0	DYX1C1	15	15q21.3	53497246	53587725
PYGO1	0.009804	0.12	0.026667	0.037037	0	PYGO1	15	15q21.3	53625513	53668343
PRTG	0.009804	0.12	0.026667	0.037037	0	PRTG	15	15q21.3	53691042	53822470
AGBL1	0.009804	0.106667	0.146667	0.296296	0.037037	AGBL1	15	15q25.3	84486246	85373288
MCTP2	0.009804	0.12	0	0.037037	0	MCTP2	15	15q26.2	92642434	92828185
STXBP6	0.009804	0.04	0.16	0.037037	0.037037	STXBP6	14	14q12	24351144	24588936
PRKD1	0.009804	0.04	0.2	0	0.037037	PRKD1	14	14q12	29115438	29466651
TRIM9	0.009804	0.106667	0	0.037037	0.037037	TRIM9	14	14q22.1	50511731	50632173
C14orf37	0.009804	0.013333	0.12	0	0.037037	C14orf37	14	14q23.1	57540561	57688601
ACTR10	0.009804	0.106667	0.013333	0.037037	0	ACTR10	14	14q23.1	57736586	57772107
PSMA3	0.009804	0.106667	0.04	0.037037	0	PSMA3	14	14q23.1	57781346	57808480
FLJ31306	0.009804	0.106667	0.04	0.037037	0	FLJ31306	14	14q23.1	57801837	57834609
FLJ43390	0.009804	0.013333	0.213333	0.037037	0.037037	FLJ43390	14	14q23.2	61653828	61664886
KCNH5	0.009804	0.013333	0.2	0.037037	0.037037	KCNH5	14	14q23.2	62243698	62581709
FUT8	0.009804	0.093333	0.106667	0.222222	0.037037	FUT8	14	14q23.3	64947593	65279716
DIO2	0.009804	0.013333	0.186667	0.037037	0.037037	DIO2	14	14q31.1	79733622	79748279
C14orf145	0.009804	0.013333	0.16	0.037037	0.037037	C14orf145	14	14q31.1	80032574	80475638
TSHR	0.009804	0.026667	0.16	0	0.037037	TSHR	14	14q31.1	80491622	80682400
POLR1D	0.009804	0.16	0.12	0.333333	0.037037	POLR1D	13	13q12.2	27094003	27139549
KL	0.009804	0.106667	0.106667	0.037037	0.074074	KL	13	13q13.1	32488571	32538282
STARD13	0.009804	0.106667	0.12	0.037037	0.074074	STARD13	13	13q13.1	32575273	32678188
MIR548F5	0.009804	0.12	0.186667	0.037037	0.111111	MIR548F5	13	13q13.3	34946406	35413383
SMAD9	0.009804	0.146667	0.186667	0.037037	0.111111	SMAD9	13	13q13.3	36320207	36392410
ALG5	0.009804	0.16	0.213333	0.037037	0.111111	ALG5	13	13q13.3	36421310	36471505
LOC646982	0.009804	0.066667	0.24	0.074074	0.037037	LOC646982	13	13q14.11	39819273	39953144
FOXO1	0.009804	0.12	0.226667	0.074074	0.037037	FOXO1	13	13q14.11	40027801	40138735
MIR320D1	0.009804	0.12	0.24	0.074074	0.037037	MIR320D1	13	13q14.11	40199964	40200012
MRPS31	0.009804	0.12	0.24	0.074074	0.037037	MRPS31	13	13q14.11	40201432	40243348
SLC25A15	0.009804	0.12	0.213333	0.074074	0.037037	SLC25A15	13	13q14.11	40261547	40284596
SUGT1L1	0.009804	0.106667	0.213333	0.074074	0.037037	SUGT1L1	13	13q14.11	40269127	40393887
MIR621	0.009804	0.106667	0.213333	0.074074	0.037037	MIR621	13	13q14.11	40282902	40282998
ELF1	0.009804	0.106667	0.213333	0.074074	0.037037	ELF1	13	13q14.11	40404056	40454419
WBP4	0.009804	0.12	0.213333	0.074074	0.037037	WBP4	13	13q14.11	40533697	40556140
KBTBD6	0.009804	0.106667	0.226667	0.074074	0.037037	KBTBD6	13	13q14.11	40599709	40604937
MTRF1	0.009804	0.08	0.226667	0.037037	0.037037	MTRF1	13	13q14.11	40688516	40735714
NARG1L	0.009804	0.08	0.226667	0.037037	0.037037	NARG1L	13	13q14.11	40783341	40830855
KIAA0564	0.009804	0.04	0.266667	0.037037	0.037037	KIAA0564	13	13q14.11	41038961	41433222
DGKH	0.009804	0.013335	0.293333	0.037037	0.037037	DGKH	13	13q14.11	41520889	41701889
NUFIP1	0.009804	0.12	0.24	0.037037	0.111111	NUFIP1	13	13q14.12	44411384	44461614
KIAA1704	0.009804	0.12	0.24	0.037037	0.111111	KIAA1704	13	13q14.12	44461687	44500405
GTF2F2	0.009804	0.12	0.24	0.037037	0.111111	GTF2F2	13	13q14.12	44592631	44756240
KCTD4	0.009804	0.12	0.24	0.037037	0.111111	KCTD4	13	13q14.12	44664988	44673176
TPT1	0.009804	0.12	0.253333	0.037037	0.111111	TPT1	13	13q14.12	44809304	44813298

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
SNORA31	0.009804	0.12	0.253333	0.037037	0.111111	SNORA31	13	13q14.12	44809615	44809745
LOC100190939	0.009804	0.12	0.253333	0.037037	0.111111	LOC100190939	13	13q14.12	44813480	44863617
COG3	0.009804	0.12	0.253333	0.037037	0.111111	COG3	13	13q14.12	44937072	45008762
ABCC4	0.009804	0.133333	0.16	0.037037	0.222222	ABCC4	13	13q32.1	94470084	94751689
UBAC2	0.009804	0.2	0.12	0.037037	0.074074	UBAC2	13	13q32.3	98650680	98836753
MIR623	0.009804	0.226667	0.12	0.037037	0.074074	MIR623	13	13q32.3	98806386	98806484
TM9SF2	0.009804	0.146667	0.173333	0.037037	0.074074	TM9SF2	13	13q32.3	98951729	99013278
CLYBL	0.009804	0.186667	0.12	0.037037	0.074074	CLYBL	13	13q32.3	99056920	99347389
PCCA	0.009804	0.16	0.12	0.037037	0.074074	PCCA	13	13q32.3	99539338	99980690
TMTC4	0.009804	0.146667	0.12	0.037037	0.074074	TMTC4	13	13q32.3	1E+08	1E+08
ANKRD10	0.009804	0.293333	0.12	0.444444	0.037037	ANKRD10	13	13q34	1.1E+08	1.1E+08
C13orf28	0.009804	0.4	0.106667	0.62963	0.037037	C13orf28	13	13q34	1.12E+08	1.12E+08
TUBGCP3	0.009804	0.413333	0.12	0.592593	0.037037	TUBGCP3	13	13q34	1.12E+08	1.12E+08
C13orf35	0.009804	0.44	0.12	0.62963	0.037037	C13orf35	13	13q34	1.12E+08	1.12E+08
ATP11A	0.009804	0.44	0.133333	0.666667	0.037037	ATP11A	13	13q34	1.12E+08	1.13E+08
MCF2L	0.009804	0.44	0.133333	0.666667	0.037037	MCF2L	13	13q34	1.13E+08	1.13E+08
F7	0.009804	0.44	0.133333	0.666667	0.037037	F7	13	13q34	1.13E+08	1.13E+08
F10	0.009804	0.44	0.133333	0.666667	0.037037	F10	13	13q34	1.13E+08	1.13E+08
PROZ	0.009804	0.44	0.133333	0.666667	0.037037	PROZ	13	13q34	1.13E+08	1.13E+08
PCID2	0.009804	0.44	0.133333	0.666667	0.037037	PCID2	13	13q34	1.13E+08	1.13E+08
CUL4A	0.009804	0.44	0.133333	0.666667	0.037037	CUL4A	13	13q34	1.13E+08	1.13E+08
LAMP1	0.009804	0.44	0.133333	0.666667	0.037037	LAMP1	13	13q34	1.13E+08	1.13E+08
GRTP1	0.009804	0.44	0.133333	0.666667	0.037037	GRTP1	13	13q34	1.13E+08	1.13E+08
TMCO3	0.009804	0.466667	0.133333	0.62963	0.037037	TMCO3	13	13q34	1.13E+08	1.13E+08
TFDP1	0.009804	0.466667	0.12	0.666667	0.037037	TFDP1	13	13q34	1.13E+08	1.13E+08
GRK1	0.009804	0.466667	0.12	0.666667	0.037037	GRK1	13	13q34	1.13E+08	1.13E+08
FLJ44054	0.009804	0.466667	0.12	0.666667	0.037037	FLJ44054	13	13q34	1.13E+08	1.14E+08
GAS6	0.009804	0.466667	0.12	0.666667	0.037037	GAS6	13	13q34	1.14E+08	1.14E+08
FAM70B	0.009804	0.466667	0.12	0.666667	0.037037	FAM70B	13	13q34	1.14E+08	1.14E+08
RASA3	0.009804	0.466667	0.12	0.666667	0.037037	RASA3	13	13q34	1.14E+08	1.14E+08
CDC16	0.009804	0.466667	0.12	0.666667	0.037037	CDC16	13	13q34	1.14E+08	1.14E+08
ZNF828	0.009804	0.466667	0.12	0.666667	0.037037	ZNF828	13	13q34	1.14E+08	1.14E+08
ACSM4	0.009804	0.146667	0.146667	0.37037	0.037037	ACSM4	12	12p13.31	7348195	7372237
LOC374443	0.009804	0.013333	0.2	0.074074	0.037037	LOC374443	12	12p13.31	9691910	9702276
CLECL1	0.009804	0.013333	0.2	0.037037	0.037037	CLECL1	12	12p13.31	9766358	9777128
CD69	0.009804	0.013333	0.2	0.037037	0.037037	CD69	12	12p13.31	9796351	9804755
CLEC2A	0.009804	0.026667	0.186667	0.037037	0.037037	CLEC2A	12	12p13.31	9957093	9976248
CLEC12A	0.009804	0.013333	0.213333	0.037037	0.037037	CLEC12A	12	12p13.2	10015275	10029462
CLEC1B	0.009804	0.04	0.186667	0.037037	0.037037	CLEC1B	12	12p13.2	10036929	10043167
CLEC12B	0.009804	0.026667	0.213333	0.037037	0.037037	CLEC12B	12	12p13.2	10054498	10062667
CLEC9A	0.009804	0.013333	0.213333	0.037037	0.037037	CLEC9A	12	12p13.2	10074543	10109833
CLEC1A	0.009804	0.013333	0.213333	0.037037	0.037037	CLEC1A	12	12p13.2	10114347	10142873
KLRC1	0.009804	0.013333	0.2	0.037037	0.037037	KLRC1	12	12p13.2	10489904	10497247
STYK1	0.009804	0.013333	0.16	0.037037	0.037037	STYK1	12	12p13.2	10662805	10718159
CSDA	0.009804	0.013333	0.16	0.037037	0.037037	CSDA	12	12p13.2	10742945	10767221
PLBD1	0.009804	0.106667	0.146667	0.074074	0.037037	PLBD1	12	12p13.1	14547864	14612059
GUCY2C	0.009804	0.08	0.146667	0.074074	0.037037	GUCY2C	12	12p13.1	14656836	14740787
PLEKHA5	0.009804	0.053333	0.12	0.037037	0.037037	PLEKHA5	12	12p12.3	19173915	19420599
SOX5	0.009804	0	0.253333	0	0.037037	SOX5	12	12p12.1	23576498	23993905
C12orf67	0.009804	0	0.24	0	0.037037	C12orf67	12	12p12.1	24611165	24628370
CCDC91	0.009804	0.013333	0.253333	0	0.037037	CCDC91	12	12p11.22	28301400	28594367
YAF2	0.009804	0.12	0.04	0.037037	0	YAF2	12	12q12	40837174	40918318
ADAMTS20	0.009804	0.026667	0.16	0.074074	0.037037	ADAMTS20	12	12q12	42034279	42231992
TWF1	0.009804	0.053333	0.106667	0.074074	0.037037	TWF1	12	12q12	42473793	42486446
TMEM117	0.009804	0.053333	0.106667	0.074074	0.037037	TMEM117	12	12q12	42516229	43069809
DBX2	0.009804	0.026667	0.12	0.074074	0.037037	DBX2	12	12q12	43694806	43731150
MON2	0.009804	0.16	0.013333	0.037037	0.037037	MON2	12	12q14.1	61146864	61277631
PPM1H	0.009804	0.173333	0.013333	0.037037	0.037037	PPM1H	12	12q14.1	61324031	61614933
C12orf66	0.009804	0.12	0.026667	0.037037	0	C12orf66	12	12q14.2	62872686	62902344
C12orf56	0.009804	0.12	0.026667	0.037037	0	C12orf56	12	12q14.2	62947032	63070613
TBK1	0.009804	0.146667	0.026667	0.037037	0	TBK1	12	12q14.2	63132204	63182159
GNS	0.009804	0.146667	0.026667	0.037037	0	GNS	12	12q14.2 -1	63393489	63439494
CPM	0.009804	0.106667	0.04	0.037037	0	CPM	12	12q15	67531225	67613247
CPSF6	0.009804	0.16	0.013333	0.037037	0	CPSF6	12	12q15	67919584	67954406
MIR1279	0.009804	0.16	0.013333	0.037037	0	MIR1279	12	12q15	67953204	67953265
FRS2	0.009804	0.146667	0.013333	0.037037	0	FRS2	12	12q15	68150396	68259830
CCT2	0.009804	0.146667	0.013333	0.037037	0	CCT2	12	12q15	68265475	68281625
BEST3	0.009804	0.146667	0.013333	0.037037	0	BEST3	12	12q15	68333656	68379464
ZDHHC17	0.009804	0.106667	0.066667	0.037037	0.111111	ZDHHC17	12	12q21.2	75681935	75771606
WDR51B	0.009804	0.106667	0.066667	0.037037	0.185185	WDR51B	12	12q21.33	88337634	88443909
EEA1	0.009804	0.106667	0.013333	0.037037	0	EEA1	12	12q22	91690416	91847239
NUDT4	0.009804	0.186667	0.013333	0.037037	0	NUDT4	12	12q22	92295832	92321156
NUDT4P1	0.009804	0.186667	0.013333	0.037037	0	NUDT4P1	12	12q22	92295877	92320183
SOCS2	0.009804	0.133333	0.013333	0.037037	0	SOCS2	12	12q22	92487729	92494110

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
CRADD	0.009804	0.133333	0.013333	0.037037	0	CRADD	12	12q22	92595282	92768663
ANKS1B	0.009804	0.12	0.066667	0.037037	0	ANKS1B	12	12q23.1	97653202	98072604
OR51A7	0.009804	0.053333	0.12	0.037037	0.037037	OR51A7	11	11p15.4	4885175	4886115
OR52A1	0.009804	0.013333	0.133333	0	0.037037	OR52A1	11	11p15.4	5129237	5130176
OR51V1	0.009804	0.013333	0.146667	0	0.037037	OR51V1	11	11p15.4	5177541	5178507
OR51B4	0.009804	0.013333	0.12	0	0.037037	OR51B4	11	11p15.4	5278820	5279753
OR51B5	0.009804	0.013333	0.133333	0	0.037037	OR51B5	11	11p15.4	5320392	5321331
OR51B6	0.009804	0.013333	0.133333	0	0.037037	OR51B6	11	11p15.4	5329314	5330253
UBQLN3	0.009804	0.013333	0.133333	0	0.037037	UBQLN3	11	11p15.4	5485106	5487730
UBQLNL	0.009804	0.013333	0.133333	0	0.037037	UBQLNL	11	11p15.4	5492199	5494533
TRIM6	0.009804	0.173333	0.013333	0.037037	0.037037	TRIM6	11	11p15.4	5573923	5590765
TRIM6-TRIM34	0.009804	0.173333	0.013333	0.037037	0.037037	TRIM6-TRIM34	11	11p15.4	5574460	5622200
TRIM34	0.009804	0.173333	0.013333	0.037037	0.037037	TRIM34	11	11p15.4	5597750	5622202
FAM160A2	0.009804	0.12	0.013333	0.037037	0	FAM160A2	11	11p15.4	6189140	6212518
CNGA4	0.009804	0.12	0.013333	0.037037	0	CNGA4	11	11p15.4	6216906	6222284
CCKBR	0.009804	0.12	0.013333	0.037037	0	CCKBR	11	11p15.4	6237542	6249933
PRKCDBP	0.009804	0.133333	0.013333	0.037037	0	PRKCDBP	11	11p15.4	6296752	6298317
SMPD1	0.009804	0.133333	0.013333	0.037037	0	SMPD1	11	11p15.4	6368231	6372803
APBB1	0.009804	0.133333	0.013333	0.037037	0	APBB1	11	11p15.4	6372931	6396877
HPX	0.009804	0.133333	0.013333	0.037037	0	HPX	11	11p15.4	6408844	6418831
TRIM3	0.009804	0.133333	0.013333	0.037037	0	TRIM3	11	11p15.4	6426419	6451782
ARFIP2	0.009804	0.133333	0.013333	0.037037	0	ARFIP2	11	11p15.4	6453502	6459172
FXC1	0.009804	0.133333	0.013333	0.037037	0	FXC1	11	11p15.4	6459253	6462488
DNHD1	0.009804	0.133333	0.013333	0.037037	0	DNHD1	11	11p15.4	6475102	6549829
RRP8	0.009804	0.2	0.013333	0.037037	0.037037	RRP8	11	11p15.4	6577728	6581388
ILK	0.009804	0.2	0.013333	0.037037	0.037037	ILK	11	11p15.4	6581540	6588676
TAF10	0.009804	0.2	0.013333	0.037037	0	TAF10	11	11p15.4	6588649	6590022
TPP1	0.009804	0.2	0.013333	0.037037	0	TPP1	11	11p15.4	6590573	6597269
RBMXL2	0.009804	0.013333	0.146667	0.037037	0.037037	RBMXL2	11	11p15.4	7066741	7068956
SYT9	0.009804	0.013333	0.12	0.037037	0.037037	SYT9	11	11p15.4	7229757	7446847
PDE3B	0.009804	0.04	0.106667	0.074074	0.037037	PDE3B	11	11p15.2	14621845	14850179
FSHB	0.009804	0.013333	0.186667	0.037037	0.037037	FSHB	11	11p14.1	30209139	30213401
MPPED2	0.009804	0.026667	0.173333	0	0.037037	MPPED2	11	11p14.1	30362616	30564507
CSTF3	0.009804	0.16	0.12	0.185185	0.037037	CSTF3	11	11p13	33062706	33139614
OR4C16	0.009804	0.026667	0.2	0.037037	0.037037	OR4C16	11	11q11	55096180	55097113
SPRYD5	0.009804	0.053333	0.186667	0.074074	0.037037	SPRYD5	11	11q11	55407349	55415859
ZFP91	0.009804	0.08	0.133333	0.148148	0.037037	ZFP91	11	11q12.1	58103163	58145092
ZFP91-CNT	0.009804	0.08	0.133333	0.148148	0.037037	ZFP91-CNT	11	11q12.1	58103163	58149780
CNTF	0.009804	0.08	0.133333	0.148148	0.037037	CNTF	11	11q12.1	58146722	58149780
C11orf73	0.009804	0.106667	0.026667	0.037037	0	C11orf73	11	11q14.2	85690901	85734633
ME3	0.009804	0.12	0.026667	0.037037	0	ME3	11	11q14.2	85829798	86060889
GRM5	0.009804	0.04	0.173333	0	0.037037	GRM5	11	11q14.2	87877393	88436465
MTMR2	0.009804	0.026667	0.133333	0.037037	0.037037	MTMR2	11	11q21	95205694	95297020
MAML2	0.009804	0.04	0.12	0.037037	0.037037	MAML2	11	11q21	95351088	95715993
CWF19L2	0.009804	0.053333	0.146667	0.074074	0.037037	CWF19L2	11	11q22.3	1.07E+08	1.07E+08
NCAM1	0.009804	0.106667	0.146667	0.333333	0.037037	NCAM1	11	11q23.1	1.12E+08	1.13E+08
C11orf71	0.009804	0.106667	0.12	0.333333	0.037037	C11orf71	11	11q23.2	1.14E+08	1.14E+08
RBM7	0.009804	0.106667	0.12	0.333333	0.037037	RBM7	11	11q23.2	1.14E+08	1.14E+08
FAM55A	0.009804	0.093333	0.146667	0.296296	0.037037	FAM55A	11	11q23.2	1.14E+08	1.14E+08
FAM55B	0.009804	0.093333	0.146667	0.333333	0.037037	FAM55B	11	11q23.2	1.14E+08	1.14E+08
LOC399959	0.009804	0.093333	0.133333	0.37037	0.037037	LOC399959	11	11q24.1	1.21E+08	1.22E+08
TMEM225	0.009804	0.053333	0.16	0.148148	0.037037	TMEM225	11	11q24.1	1.23E+08	1.23E+08
OR8G2	0.009804	0.053333	0.12	0.074074	0.037037	OR8G2	11	11q24.2	1.24E+08	1.24E+08
OR8D1	0.009804	0.04	0.16	0.111111	0.037037	OR8D1	11	11q24.2	1.24E+08	1.24E+08
OR8D2	0.009804	0.04	0.16	0.111111	0.037037	OR8D2	11	11q24.2	1.24E+08	1.24E+08
OR8B4	0.009804	0.04	0.12	0.111111	0.037037	OR8B4	11	11q24.2	1.24E+08	1.24E+08
OR8A1	0.009804	0.04	0.106667	0.111111	0.037037	OR8A1	11	11q24.2	1.24E+08	1.24E+08
DNAJC1	0.009804	0.106667	0.026667	0.037037	0.074074	DNAJC1	10	10p12.31	22085483	22332657
RTKN2	0.009804	0.066667	0.12	0	0.037037	RTKN2	10	10q21.2	63622959	63698473
ZNF365	0.009804	0.066667	0.12	0	0.037037	ZNF365	10	10q21.2	63803922	63832224
NRG3	0.009804	0.106667	0.106667	0.037037	0.074074	NRG3	10	10q23.1	83625050	84736916
RBM20	0.009804	0.12	0.08	0.037037	0.111111	RBM20	10	10q25.2	1.12E+08	1.13E+08
GLIS3	0.009804	0.013333	0.173333	0.037037	0.037037	GLIS3	9	9p24.2	3814128	4290036
C9orf70	0.009804	0.013333	0.173333	0.037037	0.037037	C9orf70	9	9p24.2	3888646	3891248
NFIB	0.009804	0.026667	0.106667	0	0.037037	NFIB	9	9p22.3	14071847	14303946
ADAMTSL1	0.009804	0.026667	0.16	0.037037	0.037037	ADAMTSL1	9	9p22.2	18464104	18900948
KIAA1797	0.009804	0.026667	0.12	0	0.037037	KIAA1797	9	9p21.3	20648309	20985955
PTPLAD2	0.009804	0.026667	0.146667	0.037037	0.037037	PTPLAD2	9	9p21.3	20996365	21021636
IFNW1	0.009804	0.04	0.146667	0	0.037037	IFNW1	9	9p21.3	21130631	21132145
IFNA21	0.009804	0.04	0.146667	0	0.037037	IFNA21	9	9p21.3	21155636	21156660
MOBKL2B	0.009804	0.133333	0.04	0.037037	0.037037	MOBKL2B	9	9p21.2	27315207	27519851
KIF9	0.009804	0.106667	0	0.037037	0	KIF9	9	9q21.11	72189333	72219394
RORB	0.009804	0.013333	0.146667	0.074074	0.037037	RORB	9	9q21.13	76302072	76491938
LPPR1	0.009804	0.026667	0.133333	0.148148	0.037037	LPPR1	9	9q31.1	1.03E+08	1.03E+08

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
MRPL50	0.009804	0.04	0.106667	0.111111	0.037037	MRPL50	9	9q31.1	1.03E+08	1.03E+08
ZNF189	0.009804	0.04	0.106667	0.111111	0.037037	ZNF189	9	9q31.1	1.03E+08	1.03E+08
ALDOB	0.009804	0.04	0.12	0.111111	0.037037	ALDOB	9	9q31.1	1.03E+08	1.03E+08
RNF20	0.009804	0.04	0.146667	0.111111	0.037037	RNF20	9	9q31.1	1.03E+08	1.03E+08
GRIN3A	0.009804	0.026667	0.146667	0.111111	0.037037	GRIN3A	9	9q31.1	1.03E+08	1.04E+08
ZNF462	0.009804	0.04	0.146667	0.074074	0.037037	ZNF462	9	9q31.2	1.09E+08	1.09E+08
DBC1	0.009804	0.12	0.106667	0.148148	0.037037	DBC1	9	9q33.1	1.21E+08	1.21E+08
ERICH1	0.009804	0.333333	0.186667	0.518519	0.037037	ERICH1	8	8p23.3	604200	671227
ASAH1	0.009804	0.106667	0.386667	0.037037	0.222222	ASAH1	8	8p22	17958205	17986788
DPYSL2	0.009804	0.106667	0.36	0.037037	0.185185	DPYSL2	8	8p21.2	26491338	26571611
STMN4	0.009804	0.133333	0.346667	0.037037	0.185185	STMN4	8	8p21.2	27149731	27171821
TRIM35	0.009804	0.133333	0.346667	0.037037	0.185185	TRIM35	8	8p21.2	27198321	27224752
PTK2B	0.009804	0.146667	0.346667	0.037037	0.185185	PTK2B	8	8p21.2	27224916	27372821
EPHX2	0.009804	0.146667	0.346667	0.037037	0.185185	EPHX2	8	8p21.1	27404562	27458404
CLU	0.009804	0.146667	0.346667	0.037037	0.185135	CLU	8	8p21.1	27510368	27528245
SCARA3	0.009804	0.12	0.373333	0.037037	0.185185	SCARA3	8	8p21.1	27547496	27586457
CCDC25	0.009804	0.106667	0.346667	0.037037	0.185185	CCDC25	8	8p21.1	27646752	27686090
ESCO2	0.009804	0.106667	0.346667	0.037037	0.185185	ESCO2	8	8p21.1	27687977	27718344
PBK	0.009804	0.146667	0.346667	0.037037	0.185185	PBK	8	8p21.1	27723057	27751269
SCARA5	0.009804	0.173333	0.346667	0.037037	0.185185	SCARA5	8	8p21.1	27783669	27906118
C8orf80	0.009804	0.16	0.346667	0.037037	0.185185	C8orf80	8	8p21.1	27935400	27997308
ELP3	0.009804	0.16	0.346667	0.037037	0.185185	ELP3	8	8p21.1	28006503	28104589
PNOC	0.009804	0.16	0.346667	0.037037	0.185185	PNOC	8	8p21.1	28230568	28256788
FBXO16	0.009804	0.106667	0.346667	0.037037	0.185185	FBXO16	8	8p21.1	28341848	28403704
EXTL3	0.009804	0.106667	0.346667	0.037037	0.185185	EXTL3	8	8p21.1	28615072	28667122
INTS9	0.009804	0.106667	0.346667	0.037037	0.185185	INTS9	8	8p21.1	28681099	28803618
KIF13B	0.009804	0.12	0.36	0.037037	0.185185	KIF13B	8	8p21.1	28980714	29176530
DUSP4	0.009804	0.106667	0.346667	0.037037	0.185185	DUSP4	8	8p21.1	29249537	29262242
FUT10	0.009804	0.16	0.36	0.037037	0.296296	FUT10	8	8p12	33347886	33450207
SNTG1	0.009804	0.12	0.16	0.111111	0.037037	SNTG1	8	8q11.22	50987150	51867981
ST18	0.009804	0.12	0.133333	0.111111	0.037037	ST18	8	8q11.23	53185945	53484993
MIR124-2	0.009804	0.106667	0.133333	0.111111	0.037037	MIR124-2	8	8q12.3	65454260	65454367
C8orf34	0.009804	0.133333	0.146667	0.111111	0.037037	C8orf34	8	8q13.2	69512702	69893812
KCNB2	0.009804	0.133333	0.106667	0.111111	0.037037	KCNB2	8	8q13.3	73612180	74013139
PGCP	0.009804	0.16	0.106667	0.148148	0.037037	PGCP	8	8q22.1	97726675	98224899
C1GALT1	0.009804	0.133333	0.106667	0.111111	0.037037	C1GALT1	7	7p21.3	7188771	7250507
EEPD1	0.009804	0.146667	0.013333	0.037037	0	EEPD1	7	7p14.2	36159361	36307678
ANLN	0.009804	0.16	0	0.037037	0	ANLN	7	7p14.2	36395957	36459926
AOAH	0.009804	0.12	0	0.037037	0	AOAH	7	7p14.2	36519133	36730679
RALA	0.009804	0.133333	0	0.037037	0	RALA	7	7p14.1	39629687	39714243
LOC349114	0.009804	0.146667	0	0.037037	0	LOC349114	7	7p14.1	39739692	39800747
CDK13	0.009804	0.186667	0	0.037037	0	CDK13	7	7p14.1	39956484	40103257
C7orf10	0.009804	0.2	0	0.037037	0	C7orf10	7	7p14.1	40141100	40866883
PION	0.009804	0.133333	0	0.037037	0.074074	PION	7	7q11.23	76778004	76883654
PTPN12	0.009804	0.146667	0.013333	0.037037	0.074074	PTPN12	7	7q11.23	77004709	77107325
TMEM60	0.009804	0.186667	0.013333	0.037037	0.074074	TMEM60	7	7q11.23	77260982	77265684
PHTF2	0.009804	0.186667	0.013333	0.037037	0.074074	PHTF2	7	7q11.23	77266045	77424758
MAGI2	0.009804	0.186667	0	0.037037	0.074074	MAGI2	7	7q21.11	77484310	78920827
SEMA3C	0.009804	0.146667	0.146667	0.037037	0.148148	SEMA3C	7	7q21.11	80209790	80386604
CACNA2D1	0.009804	0.16	0.133333	0.037037	0.296296	CACNA2D1	7	7q21.11	81417354	81910968
SEMA3A	0.009804	0.12	0.16	0.037037	0.333333	SEMA3A	7	7q21.11	83425595	83662154
MTERF	0.009804	0.186667	0.026667	0.037037	0	MTERF	7	7q21.2	91339957	91347953
AKAP9	0.009804	0.213333	0	0.037037	0	AKAP9	7	7q21.2	91408125	91577923
CYP51A1	0.009804	0.173333	0	0.037037	0	CYP51A1	7	7q21.2	91579399	91601777
LOC401387	0.009804	0.173333	0	0.037037	0	LOC401387	7	7q21.2	91612134	91632527
KRIT1	0.009804	0.173333	0.013333	0.037037	0	KRIT1	7	7q21.2	91666219	91713165
CCDC132	0.009804	0.08	0.146667	0.037037	0.037037	CCDC132	7	7q21.3	92699589	92826275
GNGT1	0.009804	0.08	0.16	0.074074	0.037037	GNGT1	7	7q21.3	93373756	93378422
NRCAM	0.009804	0.133333	0.08	0.037037	0.037037	NRCAM	7	7q31.1	1.08E+08	1.08E+08
IFRD1	0.009804	0.12	0.04	0.037037	0.074074	IFRD1	7	7q31.1	1.12E+08	1.12E+08
MET	0.009804	0.066667	0.106667	0.074074	0.037037	MET	7	7q31.2	1.16E+08	1.16E+08
ST7	0.009804	0.106667	0.066667	0.037037	0.111111	ST7	7	7q31.2	1.16E+08	1.17E+08
ST7OT3	0.009804	0.106667	0.066667	0.037037	0.111111	ST7OT3	7	7q31.2	1.17E+08	1.17E+08
MBOAT1	0.009804	0.106667	0.013333	0.037037	0	MBOAT1	6	6p22.3	20208914	20320650
E2F3	0.009804	0.12	0.013333	0.037037	0	E2F3	6	6p22.3	20510116	20601925
CDKAL1	0.009804	0.146667	0.013333	0.037037	0	CDKAL1	6	6p22.3	20642667	21339744
SOX4	0.009804	0.173333	0.013333	0.037037	0	SOX4	6	6p22.3	21701951	21706829
FLJ22536	0.009804	0.16	0.013333	0.037037	0	FLJ22536	6	6p22.3	21774654	22302594
ZNRD1	0.009804	0.266667	0.106667	0.444444	0.037037	ZNRD1	6	6p21.33	30137015	30140666
DNAH8	0.009804	0.186667	0.133333	0.555556	0.037037	DNAH8	6	6p21.2	38798530	39106546
MIR206	0.009804	0.013333	0.106667	0.037037	0.037037	MIR206	6	6p12.2	52117106	52117192
MIR133B	0.009804	0.013333	0.106667	0.037037	0.037037	MIR133B	6	6p12.2	52121680	52121798
PAQR8	0.009804	0.12	0.013333	0.037037	0.037037	PAQR8	6	6p12.2	52334885	52380535
BACH2	0.009804	0.16	0.2	0.037037	0.185185	BACH2	6	6q15	90692969	91063349

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
SOBP	0.009804	0.12	0.16	0.037037	0.074074	SOBP	6	6q21	1.08E+08	1.08E+08
SCML4	0.009804	0.146667	0.146667	0.037037	0.074074	SCML4	6	6q21	1.08E+08	1.08E+08
SEC63	0.009804	0.146667	0.146667	0.037037	0.074074	SEC63	6	6q21	1.08E+08	1.08E+08
OSTM1	0.009804	0.146667	0.146667	0.037037	0.074074	OSTM1	6	6q21	1.08E+08	1.09E+08
NR2E1	0.009804	0.146667	0.146667	0.037037	0.074074	NR2E1	6	6q21	1.09E+08	1.09E+08
SNX3	0.009804	0.146667	0.146667	0.037037	0.074074	SNX3	6	6q21	1.09E+08	1.09E+08
LACE1	0.009804	0.146667	0.146667	0.037037	0.074074	LACE1	6	6q21	1.09E+08	1.09E+08
FOXO3	0.009804	0.146667	0.146667	0.037037	0.074074	FOXO3	6	6q21	1.09E+08	1.09E+08
ARMC2	0.009804	0.146667	0.146667	0.037037	0.074074	ARMC2	6	6q21	1.09E+08	1.09E+08
SESN1	0.009804	0.133333	0.146667	0.037037	0.074074	SESN1	6	6q21	1.09E+08	1.1E+08
PPIL6	0.009804	0.146667	0.146667	0.037037	0.074074	PPIL6	6	6q21	1.1E+08	1.1E+08
SLC22A16	0.009804	0.133333	0.133333	0.037037	0.111111	SLC22A16	6	6q21	1.11E+08	1.11E+08
CDK19	0.009804	0.146667	0.133333	0.037037	0.111111	CDK19	6	6q21	1.11E+08	1.11E+08
SLC16A10	0.009804	0.133333	0.133333	0.037037	0.111111	SLC16A10	6	6q21	1.12E+08	1.12E+08
KIAA1919	0.009804	0.146667	0.133333	0.037037	0.111111	KIAA1919	6	6q21	1.12E+08	1.12E+08
REV3L	0.009804	0.133333	0.146667	0.037037	0.111111	REV3L	6	6q21	1.12E+08	1.12E+08
TRAF3IP2	0.009804	0.146667	0.145667	0.037037	0.111111	TRAF3IP2	6	6q21	1.12E+08	1.12E+08
FYN	0.009804	0.133333	0.133333	0.037037	0.148148	FYN	6	6q21	1.12E+08	1.12E+08
SGK1	0.009804	0.133333	0.026667	0.037037	0	SGK1	6	6q23.2	1.35E+08	1.35E+08
ALDH8A1	0.009804	0.12	0.026667	0.037037	0	ALDH8A1	6	6q23.3	1.35E+08	1.35E+08
C6orf217	0.009804	0	0.16	0	0.037037	C6orf217	6	6q23.3	1.36E+08	1.36E+08
PDE7B	0.009804	0	0.173333	0	0.037037	PDE7B	6	6q23.3	1.36E+08	1.37E+08
NHSL1	0.009804	0.146667	0.04	0.037037	0	NHSL1	6	6q23.3	1.39E+08	1.39E+08
CCDC28A	0.009804	0.146667	0.04	0.037037	0	CCDC28A	6	6q24.1	1.39E+08	1.39E+08
ECT2L	0.009804	0.146667	0.04	0.037037	0	ECT2L	6	6q24.1	1.39E+08	1.39E+08
C6orf115	0.009804	0.146667	0.04	0.037037	0	C6orf115	6	6q24.1	1.39E+08	1.39E+08
HECA	0.009804	0.146667	0.04	0.037037	0	HECA	6	6q24.1	1.39E+08	1.4E+08
TXLNB	0.009804	0.146667	0.04	0.037037	0	TXLNB	6	6q24.1	1.4E+08	1.4E+08
LOC153910	0.009804	0	0.146667	0.037037	0.037037	LOC153910	6	6q24.1 - 6c24.2	1.43E+08	1.43E+08
MLLT4	0.009804	0.186667	0.106667	0.37037	0.037037	MLLT4	6	6q27	1.68E+08	1.68E+08
BASP1	0.009804	0.146667	0.013333	0.037037	0.037037	BASP1	5	5p15.1	17270750	17329944
TTC33	0.009804	0.173333	0	0.037037	0	TTC33	5	5p13.1	40747435	40791830
PRKAA1	0.009804	0.173333	0	0.037037	0	PRKAA1	5	5p13.1	40795238	40834055
RPL37	0.009804	0.173333	0	0.037037	0	RPL37	5	5p13.1	40867187	40871145
SNORD72	0.009804	0.173333	0	0.037037	0	SNORD72	5	5p13.1	40868515	40868595
CARD6	0.009804	0.173333	0	0.037037	0	CARD6	5	5p13.1	40877167	40891214
C7	0.009804	0.04	0.12	0	0.037037	C7	5	5p13.1	40945356	41018799
HEATR7B2	0.009804	0.013333	0.12	0	0.037037	HEATR7B2	5	5p13.1	41033879	41107202
C6	0.009804	0.013333	0.133333	0	0.037037	C6	5	5p13.1	41178093	41249425
PLCXD3	0.009804	0.013333	0.133333	0	0.037037	PLCXD3	5	5p13.1	41342805	41546488
OXCT1	0.009804	0.013333	0.12	0	0.037037	OXCT1	5	5p13.1	41765924	41906549
C5orf51	0.009804	0.013333	0.12	0	0.037037	C5orf51	5	5p13.1	41940227	41957496
FBXO4	0.009804	0.013333	0.12	0	0.037037	FBXO4	5	5p13.1	41961113	41977430
GHR	0.009804	0.013333	0.133333	0	0.037037	GHR	5	5p12	42459783	42757684
SEPP1	0.009804	0.04	0.12	0	0.037037	SEPP1	5	5p12	42835739	42847782
MGC42105	0.009804	0.146667	0	0.037037	0	MGC42105	5	5p12	43228084	43316710
HMGCS1	0.009804	0.146667	0	0.037037	0	HMGCS1	5	5p12	43325250	43349353
C5orf28	0.009804	0.16	0.013333	0.037037	0	C5orf28	5	5p12	43480111	43519750
PAIP1	0.009804	0.133333	0.04	0.037037	0	PAIP1	5	5p12	43562127	43592953
ARL15	0.009804	0.04	0.16	0	0.037037	ARL15	5	5q11.2	53216371	53642161
HSPB3	0.009804	0.026667	0.146667	0	0.037037	HSPB3	5	5q11.2	53787202	53787965
GZMA	0.009804	0.04	0.16	0.037037	0.057037	GZMA	5	5q11.2	54434231	54441838
CDC20B	0.009804	0.04	0.16	0.037037	0.037037	CDC20B	5	5q11.2	54444556	54504763
CCNO	0.009804	0.08	0.133333	0.037037	0.037037	CCNO	5	5q11.2	54562738	54565266
DHX29	0.009804	0.08	0.133333	0.037037	0.037037	DHX29	5	5q11.2	54587830	54639279
SKIV2L2	0.009804	0.08	0.133333	0.037037	0.037037	SKIV2L2	5	5q11.2	54639333	54757167
PPAP2A	0.009804	0.08	0.146667	0.037037	0.037037	PPAP2A	5	5q11.2	54756440	54866631
SLC38A9	0.009804	0.093333	0.146667	0.037037	0.037037	SLC38A9	5	5q11.2	54957433	55043921
BDP1	0.009804	0.146667	0.12	0.037037	0.074074	BDP1	5	5q13.2	70787198	70899406
MCCC2	0.009804	0.133333	0.12	0.037037	0.074074	MCCC2	5	5q13.2	70918871	70990287
TMEM174	0.009804	0.08	0.12	0.037037	0.037037	TMEM174	5	5q13.2	72504779	72506725
FOXD1	0.009804	0.066667	0.106667	0.037037	0.037037	FOXD1	5	5q13.2	72777841	72780109
SV2C	0.009804	0.013333	0.16	0.037037	0.037037	SV2C	5	5q13.3	75415061	75657173
F2R	0.009804	0.146667	0.08	0.037037	0.037037	F2R	5	5q13.3	76047624	76067352
F2R11	0.009804	0.133333	0.08	0.037037	0.037037	F2RL1	5	5q13.3	76150589	76166896
S100Z	0.009804	0.133333	0.08	0.037037	0.037037	S100Z	5	5q13.3	76181882	76252813
LHFPL2	0.009804	0.106667	0.08	0.037037	0.037037	LHFPL2	5	5q14.1	77816794	77980405
DMGDH	0.009804	0.08	0.133333	0.037037	0.037037	DMGDH	5	5q14.1	78329185	78401206
BHMT2	0.009804	0.133333	0.08	0.037037	0.037037	BHMT2	5	5q14.1	78401339	78421032
BHMT	0.009804	0.133333	0.08	0.037037	0.037037	BHMT	5	5q14.1	78443360	78463870
JMY	0.009804	0.133333	0.08	0.037037	0.037037	JMY	5	5q14.1	78567710	78658793
HOMER1	0.009804	0.133333	0.08	0.037037	0.037037	HOMER1	5	5q14.1	78705542	78845457
CMYA5	0.009804	0.12	0.08	0.037037	0.037037	CMYA5	5	5q14.1	79021415	79131806
THBS4	0.009804	0.146667	0.08	0.037037	0.037037	THBS4	5	5q14.1	79366747	79414864

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
SERINC5	0.009804	0.146667	0.08	0.037037	0.037037	SERINC5	5	5q14.1	79443230	79587627
FAM151B	0.009804	0.146667	0.093333	0.037037	0.037037	FAM151B	5	5q14.1	79819556	79873963
MSH3	0.009804	0.08	0.12	0.037037	0.037037	MSH3	5	5q14.1	79986050	80208391
3-Mar	0.009804	0.106667	0.08	0.037037	0.074074	3-Mar	5	5q23.2	1.26E+08	1.26E+08
STK32A	0.009804	0.013333	0.133333	0	0.037037	STK32A	5	5q32	1.47E+08	1.47E+08
TTC1	0.009804	0.133333	0.026667	0.037037	0.074074	TTC1	5	5q33.3	1.59E+08	1.59E+08
HSP90AB2P	0.009804	0.013333	0.146667	0	0.037037	HSP90AB2P	4	4p15.33	12944135	12949024
RAB28	0.009804	0.013333	0.16	0	0.037037	RAB28	4	4p15.33	12978445	13095088
KCNIP4	0.009804	0.026667	0.213333	0	0.037037	KCNIP4	4	4p15.31	20339337	21308417
PPARGC1A	0.009804	0.026667	0.226667	0	0.037037	PPARGC1A	4	4p15.2	23402742	23500799
LGI2	0.009804	0.106667	0.053333	0.037037	0	LGI2	4	4p15.2	24609569	24641513
SEPSECS	0.009804	0.12	0.066667	0.037037	0	SEPSECS	4	4p15.2	24730726	24771303
PI4K2B	0.009804	0.12	0.053333	0.037037	0	PI4K2B	4	4p15.2	24844751	24889930
ZCCHC4	0.009804	0.12	0.053333	0.037037	0	ZCCHC4	4	4p15.2	24923494	24981104
TLR10	0.009804	0.053333	0.186667	0.037037	0.037037	TLR10	4	4p14	38450647	38460985
UCHL1	0.009804	0.106667	0.053333	0.037037	0	UCHL1	4	4p13	40953655	40965203
LIMCH1	0.009804	0.106667	0.053333	0.037037	0	LIMCH1	4	4p13	41057561	41396819
PHOX2B	0.009804	0.133333	0.066667	0.037037	0	PHOX2B	4	4p13	41440856	41445745
TMEM33	0.009804	0.146667	0.053333	0.037037	0	TMEM33	4	4p13	41631894	41657582
SLC30A9	0.009804	0.16	0.053333	0.037037	0.037037	SLC30A9	4	4p13	41687280	41784309
BEND4	0.009804	0.16	0.053333	0.037037	0.037037	BEND4	4	4p13	41807629	41849653
RASL11B	0.009804	0.12	0	0.037037	0	RASL11B	4	4q12	53423252	53427760
SCFD2	0.009804	0.12	0	0.037037	0	SCFD2	4	4q12	53433908	53927000
PDGFRA	0.009804	0.106667	0.013333	0.037037	0	PDGFRA	4	4q12	54790021	54859170
AFP	0.009804	0.04	0.133333	0	0.037037	AFP	4	4q13.3	74520797	74540357
AFM	0.009804	0.04	0.133333	0	0.037037	AFM	4	4q13.3	74566326	74588583
RASSF6	0.009804	0.04	0.12	0	0.037037	RASSF6	4	4q13.3	74657726	74704999
CXCL6	0.009804	0.04	0.146667	0	0.037037	CXCL6	4	4q13.3	74921137	74923342
PPBPL1	0.009804	0.04	0.146667	0	0.037037	PPBPL1	4	4q13.3	74932447	74933418
PF4	0.009804	0.04	0.146667	0	0.037037	PF4	4	4q13.3	75065660	75066580
PPBP	0.009804	0.04	0.146667	0	0.037037	PPBP	4	4q13.3	75071620	75072765
CXCL3	0.009804	0.04	0.146667	0	0.037037	CXCL3	4	4q13.3	75121176	75123355
CXCL2	0.009804	0.04	0.146667	0	0.037037	CXCL2	4	4q13.3	75181618	75183862
MTHFD2L	0.009804	0.04	0.16	0	0.037037	MTHFD2L	4	4q13.3	75242693	75387677
AREG	0.009804	0.04	0.146667	0	0.037037	AREG	4	4q13.3	75699653	75709510
BTC	0.009804	0.066667	0.133333	0	0.037037	BTC	4	4q13.3	75890472	75938907
C4orf26	0.009804	0.133333	0.013333	0.037037	0	C4orf26	4	4q21.1	76700232	76708952
CDKL2	0.009804	0.106667	0.026667	0.037037	0	CDKL2	4	4q21.1	76720728	76774746
G3BP2	0.009804	0.12	0.013333	0.037037	0	G3BP2	4	4q21.1	76786977	76817368
ARD1B	0.009804	0.026667	0.226667	0	0.037037	ARD1B	4	4q21.21	80457296	80466196
GDEP	0.009804	0.026667	0.213333	0	0.037037	GDEP	4	4q21.21	80967649	81003424
PRDM8	0.009804	0.04	0.16	0	0.037037	PRDM8	4	4q21.21	81325448	81344507
C4orf22	0.009804	0.026667	0.16	0	0.037037	C4orf22	4	4q21.21	81475898	82103927
BMP3	0.009804	0.026667	0.186667	0	0.037037	BMP3	4	4q21.21	82171143	82197710
PRKG2	0.009804	0.026667	0.173333	0	0.037037	PRKG2	4	4q21.21	82228861	82345240
RASGEF1B	0.009804	0.053333	0.12	0	0.037037	RASGEF1B	4	4q21.21	82567243	82612086
TMEM150C	0.009804	0.173333	0.04	0.037037	0	TMEM150C	4	4q21.22	83624628	83702151
SCD5	0.009804	0.173333	0.04	0.037037	0	SCD5	4	4q21.22	83769714	83939035
SEC31A	0.009804	0.173333	0.04	0.037037	0	SEC31A	4	4q21.22	83958838	84031425
COPS4	0.009804	0.173333	0.04	0.037037	0	COPS4	4	4q21.22	84175263	84215996
PLAC8	0.009804	0.173333	0.04	0.037037	0	PLAC8	4	4q21.22	84230235	84250037
COQ2	0.009804	0.173333	0.04	0.037037	0	COQ2	4	4q21.23	84404002	84425092
HPSE	0.009804	0.173333	0.04	0.037037	0	HPSE	4	4q21.23	84435492	84475059
HELQ	0.009804	0.173333	0.04	0.037037	0	HELQ	4	4q21.23	84547523	84596050
MRPS18C	0.009804	0.173333	0.04	0.037037	0	MRPS18C	4	4q21.23	84596142	84601954
FAM175A	0.009804	0.173333	0.04	0.037037	0	FAM175A	4	4q21.23	84601120	84625315
AGPAT9	0.009804	0.173333	0.04	0.037037	0	AGPAT9	4	4q21.23	84676677	84746051
C4orf12	0.009804	0.026667	0.133333	0	0.037037	C4orf12	4	4q21.23	86106995	86147193
MAPK10	0.009804	0.026667	0.146667	0	0.037037	MAPK10	4	4q21.3	87155300	87593308
PKD2	0.009804	0.12	0.013333	0.037037	0	PKD2	4	4q22.1	89147844	89217954
ABCG2	0.009804	0.12	0.013333	0.037037	0	ABCG2	4	4q22.1	89230440	89299036
PPM1K	0.009804	0.133333	0.013333	0.037037	0	PPM1K	4	4q22.1	89400556	89424913
HERC6	0.009804	0.12	0.013333	0.037037	0	HERC6	4	4q22.1	89518915	89583272
HERC5	0.009804	0.12	0.013333	0.037037	0	HERC5	4	4q22.1	89597291	89646338
PIGY	0.009804	0.12	0.013333	0.037037	0	PIGY	4	4q22.1	89661158	89663979
ANK2	0.009804	0.16	0.053333	0.037037	0.074074	ANK2	4	4q25	1.14E+08	1.15E+08
CEP170L	0.009804	0.12	0.16	0.037037	0.185185	CEP170L	4	4q26	1.2E+08	1.2E+08
MFSD8	0.009804	0.146667	0.08	0.037037	0.111111	MFSD8	4	4q28.1 - 4c	1.29E+08	1.29E+08
C4orf29	0.009804	0.146667	0.08	0.037037	0.111111	C4orf29	4	4q28-2	1.29E+08	1.29E+08
LARP1B	0.009804	0.146667	0.066667	0.037037	0.111111	LARP1B	4	4q28.2	1.29E+08	1.29E+08
USP38	0.009804	0.013333	0.186667	0	0.037037	USP38	4	4q31.21	1.44E+08	1.44E+08
GYPA	0.009804	0.013333	0.16	0	0.037037	GYPA	4	4q31.22	1.45E+08	1.45E+08
TMEM184C	0.009804	0.12	0	0.037037	0	TMEM184C	4	4q31.23	1.49E+08	1.49E+08
PRMT10	0.009804	0.12	0	0.037037	0	PRMT10	4	4q31.23	1.49E+08	1.49E+08

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
ARHGAP10	0.009804	0.133333	0	0.037037	0	ARHGAP10	4	4q31.23	1.49E+08	1.49E+08
NR3C2	0.009804	0.106667	0	0.037037	0	NR3C2	4	4q31.23	1.49E+08	1.5E+08
DCLK2	0.009804	0.12	0.026667	0.037037	0.037037	DCLK2	4	4q31.3	1.51E+08	1.51E+08
LRBA	0.009804	0.013333	0.133333	0.037037	0.037037	LRBA	4	4q31.3	1.51E+08	1.52E+08
ANXA2P1	0.009804	0.186667	0.013333	0.037037	0.037037	ANXA2P1	4	4q31.3	1.54E+08	1.54E+08
MND1	0.009804	0.186667	0.013333	0.037037	0.037037	MND1	4	4q31.3	1.54E+08	1.55E+08
KIAA0922	0.009804	0.186667	0.013333	0.037037	0.037037	KIAA0922	4	4q31.3	1.55E+08	1.55E+08
DCHS2	0.009804	0.026667	0.12	0	0.037037	DCHS2	4	4q32.1	1.55E+08	1.56E+08
FGB	0.009804	0.026667	0.12	0	0.037037	FGB	4	4q32.1	1.56E+08	1.56E+08
FGA	0.009804	0.026667	0.12	0	0.037037	FGA	4	4q32.1	1.56E+08	1.56E+08
FGG	0.009804	0.026667	0.12	0	0.037037	FGG	4	4q32.1	1.56E+08	1.56E+08
RBM46	0.009804	0.026667	0.12	0	0.037037	RBM46	4	4q32.1	1.56E+08	1.56E+08
RXFP1	0.009804	0.08	0.106667	0	0.037037	RXFP1	4	4q32.1	1.6E+08	1.6E+08
SH3RF1	0.009804	0.12	0.026667	0.037037	0.037037	SH3RF1	4	4q32.3	1.7E+08	1.7E+08
NEK1	0.009804	0.12	0.026667	0.037037	0.037037	NEK1	4	4q33	1.71E+08	1.71E+08
CLCN3	0.009804	0.12	0.04	0.037037	0.037037	CLCN3	4	4q33	1.71E+08	1.71E+08
C4orf27	0.009804	0.12	0.04	0.037037	0.037037	C4orf27	4	4q33	1.71E+08	1.71E+08
MFAP3L	0.009804	0.12	0.04	0.037037	0.037037	MFAP3L	4	4q33	1.71E+08	1.71E+08
AADAT	0.009804	0.106667	0.053333	0.037037	0.037037	AADAT	4	4q33	1.71E+08	1.71E+08
IL5RA	0.009804	0.106667	0.026667	0.037037	0.037037	IL5RA	3	3p26.3	3086401	3127059
TRNT1	0.009804	0.106667	0.026667	0.037037	0.037037	TRNT1	3	3p26.3	3143600	3155707
GRM7	0.009804	0.013333	0.146667	0.037037	0.037037	GRM7	3	3p26.1	6877802	7758219
DVWA	0.009804	0.093333	0.133333	0.296296	0.037037	DVWA	3	3p24.3	15181875	15222471
RAB5A	0.009804	0.186667	0.026667	0.037037	0.037037	RAB5A	3	3p24.3	19963576	20001663
C3orf48	0.009804	0.186667	0.026667	0.037037	0.037037	C3orf48	3	3p24.3	19996458	20028770
KAT2B	0.009804	0.173333	0.04	0.037037	0.037037	KAT2B	3	3p24.3	20056528	20170901
THRB	0.009804	0.026667	0.146667	0.037037	0.037037	THRB	3	3p24.2	24133649	24511318
FAM19A1	0.009804	0.013333	0.133333	0	0.037037	FAM19A1	3	3p14.1	68136144	68677462
ARL13B	0.009804	0.106667	0.173333	0.037037	0.333333	ARL13B	3	3q11.2	95181672	95256814
STX19	0.009804	0.106667	0.173333	0.037037	0.333333	STX19	3	3q11.2	95215905	95230145
DHFRL1	0.009804	0.106667	0.173333	0.037037	0.333333	DHFRL1	3	3q11.2	95259456	95264351
RG9MTD1	0.009804	0.186667	0	0.037037	0.148148	RG9MTD1	3	3q12.3	1.03E+08	1.03E+08
PCNP	0.009804	0.186667	0	0.037037	0.148148	PCNP	3	3q12.3	1.03E+08	1.03E+08
ZBTB11	0.009804	0.186667	0	0.037037	0.148148	ZBTB11	3	3q12.3	1.03E+08	1.03E+08
LOC100009676	0.009804	0.186667	0	0.037037	0.148148	LOC100009676	3	3q12.3	1.03E+08	1.03E+08
RPL24	0.009804	0.186667	0	0.037037	0.148148	RPL24	3	3q12.3	1.03E+08	1.03E+08
CEP97	0.009804	0.173333	0	0.037037	0.148148	CEP97	3	3q12.3	1.03E+08	1.03E+08
FAM55C	0.009804	0.173333	0	0.037037	0.148148	FAM55C	3	3q12.3	1.03E+08	1.03E+08
NFKBIZ	0.009804	0.16	0	0.037037	0.148148	NFKBIZ	3	3q12.3	1.03E+08	1.03E+08
LOC152225	0.009804	0.16	0	0.037037	0.148148	LOC152225	3	3q12.3	1.03E+08	1.03E+08
BOC	0.009804	0.146667	0	0.037037	0.074074	BOC	3	3q13.2	1.14E+08	1.14E+08
NAT13	0.009804	0.173333	0	0.037037	0.074074	NAT13	3	3q13.2	1.15E+08	1.15E+08
GRAMD1C	0.009804	0.186667	0	0.037037	0.074074	GRAMD1C	3	3q13.31	1.15E+08	1.15E+08
KIAA1407	0.009804	0.106667	0.08	0.037037	0.074074	KIAA1407	3	3q13.31	1.15E+08	1.15E+08
QTRTD1	0.009804	0.106667	0.08	0.037037	0.074074	QTRTD1	3	3q13.31	1.15E+08	1.15E+08
DRD3	0.009804	0.133333	0.053333	0.037037	0.074074	DRD3	3	3q13.31	1.15E+08	1.15E+08
ZNF80	0.009804	0.12	0.053333	0.037037	0.074074	ZNF80	3	3q13.31	1.15E+08	1.15E+08
COL6A6	0.009804	0.093333	0.12	0.074074	0.037037	COL6A6	3	3q22.1	1.32E+08	1.32E+08
ATP2C1	0.009804	0.093333	0.12	0.074074	0.037037	ATP2C1	3	3q22.1	1.32E+08	1.32E+08
ASTE1	0.009804	0.106667	0.106667	0.074074	0.037037	ASTE1	3	3q22.1	1.32E+08	1.32E+08
NEK11	0.009804	0.106667	0.106667	0.074074	0.037037	NEK11	3	3q22.1	1.32E+08	1.33E+08
MRPL3	0.009804	0.093333	0.12	0.074074	0.037037	MRPL3	3	3q22.1	1.33E+08	1.33E+08
CPNE4	0.009804	0.093333	0.133333	0.074074	0.037037	CPNE4	3	3q22.1	1.33E+08	1.33E+08
AADACL2	0.009804	0.04	0.106667	0	0.037037	AADACL2	3	3q25.1	1.53E+08	1.53E+08
LOC401093	0.009804	0.04	0.106667	0	0.037037	LOC401093	3	3q25.1	1.53E+08	1.53E+08
MBNL1	0.009804	0.04	0.106667	0	0.037037	MBNL1	3	3q25.1	1.53E+08	1.54E+08
P2RY1	0.009804	0.04	0.12	0	0.037037	P2RY1	3	3q25.2	1.54E+08	1.54E+08
C3orf79	0.009804	0.04	0.106667	0.037037	0.037037	C3orf79	3	3q25.2	1.55E+08	1.55E+08
SGEF	0.009804	0.04	0.12	0.037037	0.037037	SGEF	3	3q25.2	1.55E+08	1.55E+08
DHX36	0.009804	0.04	0.106667	0.037037	0.037037	DHX36	3	3q25.2	1.55E+08	1.56E+08
MME	0.009804	0.04	0.106667	0.037037	0.037037	MME	3	3q25.31	1.56E+08	1.56E+08
SLC33A1	0.009804	0.186667	0	0.037037	0	SLC33A1	3	3q25.31	1.57E+08	1.57E+08
GMPS	0.009804	0.186667	0	0.037037	0	GMPS	3	3q25.31	1.57E+08	1.57E+08
CCNL1	0.009804	0.12	0.04	0.037037	0	CCNL1	3	3q25.32	1.58E+08	1.58E+08
GFM1	0.009804	0.106667	0.04	0.037037	0	GFM1	3	3q25.32	1.6E+08	1.6E+08
LXN	0.009804	0.106667	0.04	0.037037	0	LXN	3	3q25.32	1.6E+08	1.6E+08
SKIL	0.009804	0.226667	0	0.037037	0.037037	SKIL	3	3q26.2	1.72E+08	1.72E+08
CLDN11	0.009804	0.226667	0	0.037037	0.037037	CLDN11	3	3q26.2	1.72E+08	1.72E+08
SLC7A14	0.009804	0.226667	0	0.037037	0.037037	SLC7A14	3	3q26.2	1.72E+08	1.72E+08
TMEM212	0.009804	0.146667	0	0.037037	0	TMEM212	3	3q26.31	1.73E+08	1.73E+08
FNDC3B	0.009804	0.133333	0.013333	0.037037	0	FNDC3B	3	3q26.31	1.73E+08	1.74E+08
GHSR	0.009804	0.16	0.013333	0.037037	0	GHSR	3	3q26.31	1.74E+08	1.74E+08
TNFSF10	0.009804	0.2	0	0.037037	0	TNFSF10	3	3q26.31	1.74E+08	1.74E+08
ECT2	0.009804	0.04	0.12	0.037037	0.037037	ECT2	3	3q26.31	1.74E+08	1.74E+08

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
ZMAT3	0.009804	0.2	0.026667	0.037037	0.037037	ZMAT3	3	3q26.32	1.8E4+08	1.8E+08
PEX5L	0.009804	0.04	0.12	0.074074	0.037037	PEX5L	3	3q26.33	1.81E+08	1.81E+08
CCDC39	0.009804	0.04	0.133333	0.074074	0.037037	CCDC39	3	3q26.33	1.82E+08	1.82E+08
TPRG1	0.009804	0.066667	0.12	0	0.037037	TPRG1	3	3q28	1.9E+08	1.91E+08
IL1RAP	0.009804	0.053333	0.173333	0	0.037037	IL1RAP	3	3q28	1.92E+08	1.92E+08
FAM157A	0.009804	0.48	0.106667	0.62963	0.037037	FAM157A	3	3q29	1.99E+08	1.99E+08
VSNL1	0.009804	0.026667	0.133333	0.111111	0.037037	VSNL1	2	2p24.2	17585288	17701188
LCLAT1	0.009804	0.093333	0.12	0.333333	0.037037	LCLAT1	2	2p23.1	30523627	30720596
HNRPLL	0.009804	0.013333	0.146667	0.074074	0.037037	HNRPLL	2	2p22.1	38643832	38683683
MTIF2	0.009804	0.12	0.013333	0.037037	0	MTIF2	2	2p16.1	55317260	55349820
CCDC88A	0.009804	0.12	0.053333	0.037037	0	CCDC88A	2	2p16.1	55368484	55500562
VRK2	0.009804	0.013333	0.213333	0	0.037037	VRK2	2	2p16.1	58127233	58240560
C2orf86	0.009804	0.106667	0.026667	0.037037	0.037037	C2orf86	2	2p15	63202039	63518591
SLC5A7	0.009804	0.053333	0.173333	0.185185	0.037037	SLC5A7	2	2q12.3	1.08E+08	1.08E+08
EPB41L5	0.009804	0.16	0.106667	0.259259	0.037037	EPB41L5	2	2q14.2	1.2E+08	1.21E+08
NXPH2	0.009804	0.04	0.266667	0.037037	0.037037	NXPH2	2	2q22.1	1.39E+08	1.39E+08
LYPD6B	0.009804	0.08	0.133333	0.111111	0.037037	LYPD6B	2	2q23.2	1.5E+08	1.5E+08
LYPD6	0.009804	0.026667	0.186667	0.037037	0.037037	LYPD6	2	2q23.2	1.5E+08	1.5E+08
RND3	0.009804	0.025667	0.173333	0.037037	0.037037	RND3	2	2q23.3	1.51E+08	1.51E+08
FMNL2	0.009804	0.04	0.12	0.037037	0.037037	FMNL2	2	2q23.3	1.53E+08	1.53E+08
PRPF40A	0.009804	0.026667	0.12	0.037037	0.037037	PRPF40A	2	2q23.3	1.53E+08	1.53E+08
ACVR1	0.009804	0.066667	0.133333	0.074074	0.037037	ACVR1	2	2q24.1	1.58E+08	1.58E+08
UPP2	0.009804	0.053333	0.133333	0.074074	0.037037	UPP2	2	2q24.1	1.59E+08	1.59E+08
RBMS1	0.009804	0.013333	0.106667	0.074074	0.037037	RBMS1	2	2q24.2	1.61E+08	1.61E+08
SF3B1	0.009804	0.16	0.013333	0.037037	0.037037	SF3B1	2	2q33.1	1.98E+08	1.98E+08
COQ10B	0.009804	0.16	0.013333	0.037037	0.037037	COQ10B	2	2q33.1	1.98E+08	1.98E+08
HSPD1	0.009804	0.16	0.013333	0.037037	0.037037	HSPD1	2	2q33.1	1.98E+08	1.98E+08
PIKFYVE	0.009804	0.173333	0.053333	0.037037	0.037037	PIKFYVE	2	2q33.3	2.09E+08	2.09E+08
PTH2R	0.009804	0.12	0.093333	0.037037	0	PTH2R	2	2q33.3	2.09E+08	2.09E+08
KIAA1486	0.009804	0.013333	0.146567	0.074074	0.037037	KIAA1486	2	2q36.3	2.26E+08	2.26E+08
PRKAA2	0.009804	0.106667	0.106667	0.222222	0.037037	PRKAA2	1	1p32.2	56883578	56953597
PGM1	0.009804	0.106667	0.066667	0.037037	0	PGM1	1	1p31.3	63831535	63898506
PDE4B	0.009804	0	0.186667	0	0.037037	PDE4B	1	1p31.3	66030781	66612851
SGIP1	0.009804	0	0.2	0	0.037037	SGIP1	1	1p31.3	66772413	66983357
TCTEX1D1	0.009804	0	0.2	0	0.037037	TCTEX1D1	1	1p31.3	66990728	67017318
SLC35D1	0.009804	0	0.12	0	0.037037	SLC35D1	1	1p31.3	67237604	67292669
IL12RB2	0.009804	0.106667	0.053333	0.037037	0	IL12RB2	1	1p31.3	67545635	67635172
SERBP1	0.009804	0.12	0.053333	0.037037	0	SERBP1	1	1p31.3	67646081	67668712
DEPDC1	0.009804	0.013333	0.24	0	0.037037	DEPDC1	1	1p31.2	68712423	68735388
PTGER3	0.009804	0.013333	0.186667	0	0.037037	PTGER3	1	1p31.1	71090624	71286080
MSH4	0.009804	0.026667	0.146667	0	0.037037	MSH4	1	1p31.1	76035218	76151512
ASB17	0.009804	0.026667	0.146667	0	0.037037	ASB17	1	1p31.1	76157148	76170705
ST6GALNAC3	0.009804	0.013333	0.173333	0	0.037037	ST6GALNAC3	1	1p31.1	76312977	75815479
GIPC2	0.009804	0.013333	0.2	0	0.037037	GIPC2	1	1p31.1	78284177	78375701
MGC27382	0.009804	0.013333	0.24	0	0.037037	MGC27382	1	1p31.1	78467871	78607734
TTLL7	0.009804	0.013333	0.226667	0	0.037037	TTLL7	1	1p31.1	84107645	84237422
PRKACB	0.009804	0.013333	0.2	0	0.037037	PRKACB	1	1p31.1	84316333	84476770
SAMD13	0.009804	0.013333	0.186667	0.037037	0.037037	SAMD13	1	1p31.1	84536637	84589069
UOX	0.009804	0.013333	0.186667	0.037037	0.037037	UOX	1	1p31.1	84603229	84636165
DNASE2B	0.009804	0.026667	0.173333	0.037037	0.037037	DNASE2B	1	1p31.1	84636803	84653280
LOC339524	0.009804	0.16	0.08	0.037037	0	LOC339524	1	1p22.3	87368036	87407473
PKN2	0.009804	0.04	0.173333	0	0.037037	PKN2	1	1p22.2	88922510	89074527
GTF2B	0.009804	0.16	0.093333	0.037037	0	GTF2B	1	1p22.2	89090909	89129890
ABCD3	0.009804	0.04	0.146667	0.111111	0.037037	ABCD3	1	1p21.3	94656521	94716849
AGL	0.009804	0.12	0.08	0.037037	0.074074	AGL	1	1p21.2	1E+08	1E+08
SPRR2F	0.009804	0.133333	0.146667	0.481481	0.037037	SPRR2F	1	1q21.3	1.51E+08	1.51E+08
SPRR2C	0.009804	0.16	0.106667	0.481481	0.037037	SPRR2C	1	1q21.3	1.51E+08	1.51E+08
SPRR2G	0.009804	0.16	0.106667	0.481481	0.037037	SPRR2G	1	1q21.3	1.51E+08	1.51E+08
PYHIN1	0.009804	0.04	0.106667	0.037037	0.037037	PYHIN1	1	1q23.1	1.57E+08	1.57E+08
IFI16	0.009804	0.04	0.106667	0.074074	0.037037	IFI16	1	1q23.1	1.57E+08	1.57E+08
AIM2	0.009804	0.04	0.106667	0.074074	0.037037	AIM2	1	1q23.1 - 1c	1.57E+08	1.57E+08
CD84	0.009804	0.093333	0.12	0.185185	0.037037	CD84	1	1q23.2 - 1c	1.59E+08	1.59E+08
SLAMF1	0.009804	0.093333	0.12	0.185185	0.037037	SLAMF1	1	1q23.3	1.59E+08	1.59E+08
SLAMF7	0.009804	0.133333	0.106667	0.185185	0.037037	SLAMF7	1	1q23.3	1.59E+08	1.59E+08
C1orf111	0.009804	0.2	0.026667	0.037037	0	C1orf111	1	1q23.3	1.61E+08	1.61E+08
UHMK1	0.009804	0.146667	0.026667	0.037037	0	UHMK1	1	1q23.3	1.61E+08	1.61E+08
RGS5	0.009804	0.013333	0.133333	0	0.037037	RGS5	1	1q23.3	1.61E+08	1.61E+08
SFT2D2	0.009804	0.12	0.04	0.037037	0	SFT2D2	1	1q24.2	1.66E+08	1.66E+08
ANKRD36B	0.009804	0.12	0.04	0.037037	0	ANKRD36B	1	1q24.2	1.66E+08	1.66E+08
TBX19	0.009804	0.12	0.04	0.037037	0	TBX19	1	1q24.2	1.67E+08	1.67E+08
KIFAP3	0.009804	0	0.186667	0.037037	0.037037	KIFAP3	1	1q24.2	1.68E+08	1.68E+08
METTL11B	0.009804	0	0.16	0.037037	0.037037	METTL11B	1	1q24.2	1.68E+08	1.68E+08
FMO3	0.009804	0	0.2	0.037037	0.037037	FMO3	1	1q24.3	1.69E+08	1.69E+08
MIR1295	0.009804	0	0.2	0.037037	0.037037	MIR1295	1	1q24.3	1.69E+08	1.69E+08

TABLE 2-continued

Gene list for predicting prostate cancer relapse using prostate cancer tissue

Symbol	freq. use	freq. amp. case	freq. del. case	freq. control	freq. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
FMO2	0.009804	0	0.186667	0.037037	0.037037	FMO2	1	1q24.3	1.69E+08	1.69E+08
DNM3	0.009804	0.025667	0.106667	0.037037	0.037037	DNM3	1	1q24.3	1.7E+08	1.71E+08
C1orf105	0.009804	0	0.133333	0.037037	0.037037	C1orf105	1	1q24.3	1.71E+08	1.71E+08
RC3H1	0.009804	0.133333	0.013333	0.037037	0	RC3H1	1	1q25.1	1.72E+08	1.72E+08
RABGAP1L	0.009804	0.12	0.013333	0.037037	0.037037	RABGAP1L	1	1q25.1	1.72E+08	1.73E+08
NMNAT2	0.009804	0.146667	0	0.037037	0.074074	NMNAT2	1	1q25.3	1.81E+08	1.82E+08
NCF2	0.009804	0.106667	0.013333	0.037037	0.074074	NCF2	1	1q25.3	1.82E+08	1.82E+08
KCNK2	0.009804	0.066667	0.16	0.074074	0.037037	KCNK2	1	1q41	2.13E+08	2.13E+08
GPATCH2	0.009804	0.026667	0.12	0.037037	0.037037	GPATCH2	1	1q41	2.16E+08	2.16E+08
LOC400804	0.009804	0.053333	0.146667	0.074074	0.037037	LOC400804	1	1q41	2.2E+08	2.2E+08
RYR2	0.009804	0.146667	0.053333	0.037037	0	RYR2	1	1q43	2.35E+08	2.36E+08
AKT3	0.009804	0.026667	0.146667	0.074074	0.037037	AKT3	1	1q44	2.42E+08	2.42E+08
LOC148324	0.009804	0.106667	0.106667	0.222222	0.037037	LOC148824	1	1q44	2.46E+08	2.46E+08
OR2C3	0.009804	0.106667	0.106667	0.222222	0.037037	OR2C3	1	1q44	2.46E+08	2.46E+08
OR2L13	0.009804	0.066667	0.186667	0.185185	0.037037	OR2L13	1	1q44	2.46E+08	2.46E+08
OR2M5	0.009804	0.066667	0.2	0.185185	0.037037	OR2M5	1	1q44	2.46E+08	2.46E+08

TABLE 3

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
VAPA	1	0.242424	0.121212	0.26087	0	VAPA	18	18p11.22	9903955	9950019
C18orf19	1	0.181818	0.121212	0.217391	0	C18orf19	18	18p11.21	13653346	13716592
RNMT	1	0.181818	0.121212	0.217391	0	RNMT	18	18p11.21	13716704	13754555
ZNF267	1	0.181818	0.121212	0.434783	0	ZNF267	16	16p11.2	31792580	31836129
COCH	1	0.121212	0.060606	0	0.115942	COCH	14	14q12	30413492	30429574
BRMS1L	1	0.151515	0.060606	0	0.057971	BRMS1L	14	14q13.2	35365348	35410921
OTX2OS1	1	0.121212	0.060606	0	0.014493	OTX2OS1	14	14q23.1	56349654	56467302
TMEM30B	1	0.090909	0.121212	0.086957	0	TMEM30B	14	14q23.1	60813842	60818284
PRKCH	1	0.090909	0.121212	0.086957	0	PRKCH	14	14q23.1	60858268	61087452
HIF1A	1	0.090909	0.121212	0.072464	0	HIF1A	14	14q23.2	61231872	61284731
FAM71D	1	0.181818	0.121212	0.188406	0	FAM71D	14	14q23.3	66725899	66765021
MPP5	1	0.181818	0.121212	0.188406	0	MPP5	14	14q23.3	66777774	66872290
VTI1B	1	0.212121	0.121212	0.217391	0	VTI1B	14	14q24.1	67187619	67211356
RDH11	1	0.212121	0.121212	0.217391	0	RDH11	14	14q24.1	67213271	67232264
RDH12	1	0.212121	0.121212	0.217391	0	RDH12	14	14q24.1	67238356	67270922
ZFYVE26	1	0.212121	0.121212	0.217391	0	ZFYVE26	14	14q24.1	67282990	67353060
ACTN1	1	0.30303	0.121212	0.289855	0	ACTN1	14	14q24.1	68410593	68515837
GALNTL1	1	0.242424	0.151515	0.289855	0	GALNTL1	14	14q24.1	68796434	68890944
FLJ44817	1	0.242424	0.151515	0.289855	0	FLJ44817	14	14q24.1	69021224	69064969
KIAA0247	1	0.212121	0.151515	0.289855	0	KIAA0247	14	14q24.1	69148063	69251613
LOC100289511	1	0.212121	0.151515	0.289855	0	LOC100289511	14	14q24.1-14q24.2	69302753	69304184
SFRS5	1	0.212121	0.151515	0.289855	0	SFRS5	14	14q24.1-14q24.2	69303582	69308476
SLC10A1	1	0.212121	0.151515	0.289855	0	SLC10A1	14	14q24.2	69312305	69333760
SLC8A3	1	0.151515	0.151515	0.26087	0	SLC8A3	14	14q24.2	69580687	69616677
SYNJ2BP	1	0.121212	0.121212	0.246377	0	SYNJ2BP	14	14q24.2	69902966	69953561
MED6	1	0.151515	0.121212	0.275362	0	MED6	14	14q24.2	70120710	70137138
TTC9	1	0.151515	0.121212	0.289855	0	TTC9	14	14q24.2	70178257	70211831
MAP3K9	1	0.151515	0.121212	0.289855	0	MAP3K9	14	14q24.2	70264607	70345642
PCNX	1	0.151515	0.121212	0.289855	0	PCNX	14	14q24.2	70443875	70651853
SNORD56B	1	0.212121	0.151515	0.289855	0	SNORD56B	14	14q24.2	70934807	70934878
LOC145474	1	0.212121	0.121212	0.289855	0	LOC145474	14	14q24.2	71024331	71026172
SIPA1L1	1	0.212121	0.121212	0.289855	0	SIPA1L1	14	14q24.2	71065795	71275874
RGS6	1	0.181818	0.121212	0.289855	0	RGS6	14	14q24.2	71469539	72102992
DPF3	1	0.333333	0.121212	0.376812	0	DPF3	14	14q24.2	72206413	72430563
DCAF4	1	0.333333	0.121212	0.391304	0	DCAF4	14	14q24.2	72462793	72496110
ZFYVE1	1	0.333333	0.121212	0.391304	0	ZFYVE1	14	14q24.2	72505912	72563593
ENTPD5	1	0.333333	0.121212	0.449275	0	ENTPD5	14	14q24.3	73502936	73555780
C14orf45	1	0.333333	0.121212	0.449275	0	C14orf45	14	14q24.3	73555812	73602549
ALDH6A1	1	0.333333	0.121212	0.449275	0	ALDH6A1	14	14q24.3	73596625	73620950
ABCD4	1	0.363636	0.121212	0.376812	0	ABCD4	14	14q24.3	73821733	73839521
TMEM90A	1	0.363636	0.121212	0.376812	0	TMEM90A	14	14q24.3	73942349	73962559
BCYRN1	1	0.30303	0.121212	0.347826	0	BCYRN1	14	14q24.3	75406358	75658554
TGFB3	1	0.30303	0.121212	0.347826	0	TGFB3	14	14q24.3	75494195	75517846
C14orf179	1	0.30303	0.121212	0.347826	0	C14orf179	14	14q24.3	75521849	75619846
ESRRB	1	0.363636	0.121212	0.376812	0	ESRRB	14	14q24.3	75907443	76037932
VASH1	1	0.363636	0.121212	0.376812	0	VASH1	14	14q24.3	76297988	76319117

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
ANGEL1	1	0.363636	0.121212	0.376812	0	ANGEL1	14	14q24.3	76323339	76349037
C14orf166B	1	0.363636	0.121212	0.376812	0	C14orf166B	14	14q24.3	76362478	76406399
C14orf4	1	0.333333	0.121212	0.347826	0	C14orf4	14	14q24.3	76560639	76564788
KIAA1737	1	0.333333	0.121212	0.347826	0	KIAA1737	14	14q24.3	76634331	76653384
ZDHHC22	1	0.333333	0.121212	0.347826	0	ZDHHC22	14	14q24.3	76667366	76677888
TMEM63C	1	0.333333	0.121212	0.347826	0	TMEM63C	14	14q24.3	76717855	76795592
NGB	1	0.333333	0.121212	0.347826	0	NGB	14	14q24.3	76801587	76807409
MIR1260	1	0.333333	0.121212	0.347826	0	MIR1260	14	14q24.3	76802314	76802385
POMT2	1	0.333333	0.121212	0.347826	0	POMT2	14	14q24.3	76811054	76856979
GSTZ1	1	0.333333	0.121212	0.347826	0	GSTZ1	14	14q24.3	76856983	76867694
TMED8	1	0.333333	0.121212	0.347826	0	TMED8	14	14q24.3	76877867	76913150
C14orf174	1	0.333333	0.121212	0.347826	0	C14orf174	14	14q24.3	76913515	76927341
C14orf148	1	0.333333	0.121212	0.347826	0	C14orf148	14	14q24.3	76930177	76959133
C14orf133	1	0.30303	0.121212	0.347826	0	C14orf133	14	14q24.3	76962771	76993658
AHSA1	1	0.30303	0.121212	0.347826	0	AHSA1	14	14q24.3	76994126	77005561
ISM2	1	0.30303	0.121212	0.347826	0	ISM2	14	14q24.3	77010493	77034964
SPTLC2	1	0.272727	0.121212	0.333333	0	SPTLC2	14	14q24.3	77043023	77152864
C14orf156	1	0.272727	0.121212	0.318841	0	C14orf156	14	14q24.3	77244178	77253697
SNW1	1	0.272727	0.121212	0.318841	0	SNW1	14	14q24.3	77253597	77297251
C14orf178	1	0.272727	0.121212	0.318841	0	C14orf178	14	14q24.3	77296646	77305839
ADCK1	1	0.272727	0.121212	0.318841	0	ADCK1	14	14q24.3	77336179	77470050
KCNK10	1	0.090909	0.121212	0.318841	0	KCNK10	14	14q31.3	87716207	87863010
PTPN21	1	0.121212	0.121212	0.333333	0	PTPN21	14	14q31.3	88001875	88090877
ZC3H14	1	0.121212	0.121212	0.333333	0	ZC3H14	14	14q31.3	88099006	88149606
EML5	1	0.121212	0.121212	0.333333	0	EML5	14	14q31.3	88150956	88328911
TTC8	1	0.121212	0.121212	0.333333	0	TTC8	14	14q31.3	88360731	88414089
LOC284232	1	0.060606	0.121212	0.173913	0	LOC284232	13	13q11	18306543	18344110
EFHA1	1	0.181818	0.121212	0.173913	0	EFHA1	13	13q12.11	20964839	21076308
FGF9	1	0.181818	0.121212	0.15942	0	FGF9	13	13q12.11	21143215	21176641
SGCG	1	0.181818	0.121212	0.173913	0	SGCG	13	13q12.12	22653060	22797305
SACS	1	0.181818	0.121212	0.188406	0	SACS	13	13q12.12	22800965	22905842
TNFRSF19	1	0.212121	0.121212	0.173913	0	TNFRSF19	13	13q12.12	23042723	23148233
MIPEP	1	0.121212	0.121212	0.173913	0	MIPEP	13	13q12.12	23202328	23361560
SPATA13	1	0.181818	0.121212	0.202899	0	SPATA13	13	13q12.12	23632861	23779213
MIR2276	1	0.181818	0.121212	0.202899	0	MIR2276	13	13q12.12	23634555	23634644
C1QTNF9	1	0.212121	0.121212	0.202899	0	C1QTNF9	13	13q12.12	23781716	23794670
PARP4	1	0.181818	0.121212	0.217391	0	PARP4	13	13q12.12	23893069	23984949
RNF17	1	0.151515	0.121212	0.318841	0	RNF17	13	13q12.12	24236301	24352059
CENPJ	1	0.151515	0.121212	0.318841	0	CENPJ	13	13q12.12	24354412	24395086
PABPC3	1	0.151515	0.151515	0.318841	0	PABPC3	13	13q12.13	24568276	24570705
MTMR6	1	0.151515	0.151515	0.318841	0	MTMR6	13	13q12.13	24718341	24759705
ATP8A2	1	0.121212	0.151515	0.318841	0	ATP8A2	13	13q12.13	24844209	25493421
SHISA2	1	0.090909	0.121212	0.26087	0	SHISA2	13	13q12.13	25516735	25523199
RNF6	1	0.090909	0.121212	0.26087	0	RNF6	13	13q12.13	25684905	25694509
WASF3	1	0.121212	0.121212	0.333333	0	WASF3	13	13q12.13	26029840	26161081
USP12	1	0.151515	0.121212	0.333333	0	USP12	13	13q12.13	26540438	26644030
PAN3	1	0.060606	0.121212	0.231884	0	PAN3	13	13q12.2	27610643	27767476
MTUS2	1	0.090909	0.121212	0.246377	0	MTUS2	13	13q12.3	28496748	28978085
KCNMB4	1	0.151515	0.030303	0	0.028986	KCNMB4	12	12q15	69046329	69111246
PTPRR	1	0.121212	0.060606	0	0.043478	PTPRR	12	12q15	69318129	69600852
TPH2	1	0.121212	0.181818	0	0.202899	TPH2	12	12q21.1	70618893	70712489
TRHDE	1	0.121212	0.212121	0	0.231884	TRHDE	12	12q21.1	70952796	71345689
C12orf12	1	0.121212	0.212121	0	0.217391	C12orf12	12	12q21.33	89870123	89873085
EPYC	1	0.121212	0.212121	0	0.217391	EPYC	12	12q21.33	89881589	89922935
NAV2	1	0.030303	0.151515	0.130435	0	NAV2	11	11p15.1	19328847	20099724
FLJ32810	1	0.121212	0.181818	0	0.101449	FLJ32810	11	11q22.1	1E+08	1E+08
MMP20	1	0.121212	0.181818	0	0.101449	MMP20	11	11q22.2	1.02E+08	1.02E+08
SLC35F2	1	0.242424	0.121212	0.246377	0	SLC35F2	11	11q22.3	1.07E+08	1.07E+08
RAB39	1	0.242424	0.121212	0.246377	0	RAB39	11	11q22.3	1.07E+08	1.07E+08
CUL5	1	0.212121	0.121212	0.246377	0	CUL5	11	11q22.3	1.07E+08	1.07E+08
C11orf65	1	0.181818	0.121212	0.188406	0	C11orf65	11	11q22.3	1.08E+08	1.08E+08
KDELC2	1	0.181818	0.121212	0.188406	0	KDELC2	11	11q22.3	1.08E+08	1.08E+08
EXPH5	1	0.181818	0.121212	0.188406	0	EXPH5	11	11q22.3	1.08E+08	1.08E+08
ZC3H12C	1	0.151515	0.151515	0.144928	0	ZC3H12C	11	11q22.3	1.09E+08	1.1E+08
FDX1	1	0.181818	0.151515	0.130435	0	FDX1	11	11q22.3	1.1E+08	1.1E+08
ARHGAP20	1	0.181818	0.151515	0.130435	0	ARHGAP20	11	11q22.3	1.1E+08	1.1E+08
POU2AF1	1	0.212121	0.121212	0.217391	0	POU2AF1	11	11q23.1	1.11E+08	1.11E+08
C11orf88	1	0.121212	0.151515	0.217391	0	C11orf88	11	11q23.1	1.11E+08	1.11E+08
LAYN	1	0.121212	0.151515	0.217391	0	LAYN	11	11q23.1	1.11E+08	1.11E+08
SIK2	1	0.212121	0.121212	0.217391	0	SIK2	11	11q23.1	1.11E+08	1.11E+08
PPP2R1B	1	0.212121	0.121212	0.217391	0	PPP2R1B	11	11q23.1	1.11E+08	1.11E+08
ALG9	1	0.181818	0.121212	0.217391	0	ALG9	11	11q23.1	1.11E+08	1.11E+08
IL18	1	0.181818	0.121212	0.217391	0	IL18	11	11q23.1	1.12E+08	1.12E+08
BCO2	1	0.151515	0.121212	0.217391	0	BCO2	11	11q23.1	1.12E+08	1.12E+08
PTS	1	0.121212	0.121212	0.202899	0	PTS	11	11q23.1	1.12E+08	1.12E+08
C11orf34	1	0.121212	0.121212	0.202899	0	C11orf34	11	11q23.1	1.12E+08	1.12E+08

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
TTC12	1	0.212121	0.121212	0.289855	0	TTC12	11	11q23.1	1.13E+08	1.13E+08
DRD2	1	0.212121	0.121212	0.304348	0	DRD2	11	11q23.1	1.13E+08	1.13E+08
TMPRSS5	1	0.212121	0.121212	0.304348	0	TMPRSS5	11	11q23.2	1.13E+08	1.13E+08
CLDN25	1	0.212121	0.121212	0.289855	0	CLDN25	11	11q23.2	1.13E+08	1.13E+08
USP28	1	0.212121	0.121212	0.289855	0	USP28	11	11q23.2	1.13E+08	1.13E+08
BUD13	1	0.242424	0.121212	0.449275	0	BUD13	11	11q23.3	1.16E+08	1.16E+08
ZNF259	1	0.242424	0.121212	0.449275	0	ZNF259	11	11q23.3	1.16E+08	1.16E+08
APOA5	1	0.242424	0.121212	0.449275	0	APOA5	11	11q23.3	1.16E+08	1.16E+08
SIK3	1	0.272727	0.121212	0.449275	0	SIK3	11	11q23.3	1.16E+08	1.16E+08
PAFAH1B2	1	0.242424	0.121212	0.449275	0	PAFAH1B2	11	11q23.3	1.17E+08	1.17E+08
TAGLN	1	0.30303	0.121212	0.449275	0	TAGLN	11	11q23.3	1.17E+08	1.17E+08
PCSK7	1	0.30303	0.121212	0.449275	0	PCSK7	11	11q23.3	1.17E+08	1.17E+08
RNF214	1	0.30303	0.121212	0.449275	0	RNF214	11	11q23.3	1.17E+08	1.17E+08
BACE1	1	0.30303	0.121212	0.449275	0	BACE1	11	11q23.3	1.17E+08	1.17E+08
HYOU1	1	0.393939	0.121212	0.507246	0	HYOU1	11	11q23.3	1.18E+08	1.18E+08
VPS11	1	0.393939	0.121212	0.507246	0	VPS11	11	11q23.3	1.18E+08	1.18E+08
HMBS	1	0.393939	0.121212	0.507246	0	HMBS	11	11q23.3	1.18E+08	1.18E+08
H2AFX	1	0.393939	0.121212	0.507246	0	H2AFX	11	11q23.3	1.18E+08	1.18E+08
DPAGT1	1	0.393939	0.121212	0.507246	0	DPAGT1	11	11q23.3	1.18E+08	1.18E+08
TRPM3	1	0.060606	0.121212	0.014493	0	TRPM3	9	9q21.11	72339786	72926335
MIR548A1	1	0.151515	0.090909	0	0.028986	MIR548A1	6	6p22.3	18679994	18680091
ORC3L	1	0.151515	0.242424	0	0.202899	ORC3L	6	6q15	88356562	88433888
C5orf33	1	0.121212	0.060606	0	0.028986	C5orf33	5	5p13.2	36228451	36277658
RANBP3L	1	0.121212	0.060606	0	0.028986	RANBP3L	5	5p13.2	36284862	36337769
EGFLAM	1	0.121212	0	0	0	EGFLAM	5	5p13.2	38294290	38500408
LIFR	1	0.121212	0	0	0	LIFR	5	5p13.1	38510822	38592506
OSMR	1	0.121212	0	0	0	OSMR	5	5p13.1	38881717	38922516
RICTOR	1	0.121212	0	0	0	RICTOR	5	5p13.1	38973780	39110259
DAB2	1	0.121212	0.030303	0	0.072464	DAB2	5	5p13.1	39407537	39461093
SDAD1	1	0.181818	0.030303	0	0.014493	SDAD1	4	4q21.1	77090092	77131138
CXCL9	1	0.181818	0.030303	0	0.014493	CXCL9	4	4q21.1	77141647	77147666
ART3	1	0.181818	0.030303	0	0.014493	ART3	4	4q21.1	77151361	77252980
CXCL10	1	0.181818	0.030303	0	0.014493	CXCL10	4	4q21.1	77161295	77163675
CXCL11	1	0.181818	0.030303	0	0.014493	CXCL11	4	4q21.1	77173864	77176258
CCNG2	1	0.121212	0.030303	0	0.043478	CCNG2	4	4q21.1	78297381	78310238
RASGEF1B	1	0.121212	0.060606	0	0.115942	RASGEF1B	4	4q21.21	82567243	82612086
SMAD1	1	0.121212	0.030303	0	0	SMAD1	4	4q31.22	1.47E+08	1.47E+08
MMAA	1	0.121212	0	0	0	MMAA	4	4q31.22	1.47E+08	1.47E+08
C4orf51	1	0.121212	0	0	0	C4orf51	4	4q31.22	1.47E+08	1.47E+08
ZNF827	1	0.121212	0	0	0	ZNF827	4	4q31.22	1.47E+08	1.47E+08
MPP4	1	0.060606	0.121212	0.15942	0	MPP4	2	2q33.1	2.02E+08	2.02E+08
ALS2	1	0.060606	0.121212	0.15942	0	ALS2	2	2q33.1	2.02E+08	2.02E+08
CD28	1	0.060606	0.151515	0.086957	0	CD28	2	2q33.2	2.04E+08	2.04E+08
ERO1LB	1	0.181818	0.121212	0.202899	0	ERO1LB	1	1q42.3	2.34E+08	2.35E+08
PLD5	1	0.090909	0.121212	0.086957	0	PLD5	1	1q43	2.4E+08	2.41E+08
LOC100101116	0.970588	0.212121	0.090909	0.231884	0	LOC100101116	Y	Yp11.2	6318442	6339606
TTTY1	0.970588	0.212121	0.090909	0.231884	0	TTTY1	Y	Yp11.2	6318472	6339606
LOC100101117	0.970588	0.212121	0.090909	0.231884	0	LOC100101117	Y	Yp11.2	6334285	6356486
TTTY2	0.970588	0.212121	0.090909	0.231884	0	TTTY2	Y	Yp11.2	6334285	6356486
LOC100192426	0.970588	0.090909	0.090909	0.217391	0	LOC100192426	18	18p11.23	8350818	8357033
RAB12	0.970588	0.242424	0.090909	0.246377	0	RAB12	18	18p11.22	8599443	8629381
KIAA0802	0.970588	0.242424	0.090909	0.246377	0	KIAA0802	18	18p11.22	8707369	8822776
RALBP1	0.970588	0.272727	0.090909	0.26087	0	RALBP1	18	18p11.22	9465530	9528107
APCDD1	0.970588	0.242424	0.090909	0.246377	0	APCDD1	18	18p11.22	10444625	10478699
NAPG	0.970588	0.242424	0.090909	0.246377	0	NAPG	18	18p11.22	10515873	10542763
FAM38B	0.970588	0.272727	0.090909	0.231884	0	FAM38B	18	18p11.22	10660244	11138762
GNAL	0.970588	0.272727	0.090909	0.217391	0	GNAL	18	18p11.21	11679136	11873145
CHMP1B	0.970588	0.333333	0.090909	0.217391	0	CHMP1B	18	18p11.21	11841389	11844449
IMPA2	0.970588	0.30303	0.090909	0.289855	0	IMPA2	18	18p11.21	11971455	12020877
CIDEA	0.970588	0.272727	0.090909	0.231884	0	CIDEA	18	18p11.21	12244318	12267595
AFG3L2	0.970588	0.272727	0.090909	0.231884	0	AFG3L2	18	18p11.21	12319108	12367195
SLMO1	0.970588	0.272727	0.090909	0.231884	0	SLMO1	18	18p11.21	12397895	12422235
SPIRE1	0.970588	0.212121	0.090909	0.202899	0	SPIRE1	18	18p11.21	12436511	12647913
PTPN2	0.970588	0.212121	0.090909	0.217391	0	PTPN2	18	18p11.21	12775480	12874335
SEH1L	0.970588	0.181818	0.090909	0.217391	0	SEH1L	18	18p11.21	12937983	12977537
CEP192	0.970588	0.181818	0.090909	0.217391	0	CEP192	18	18p11.21	12981361	13115050
C18orf1	0.970588	0.272727	0.090909	0.231884	0	C18orf1	18	18p11.21	13208786	13642754
MC2R	0.970588	0.212121	0.090909	0.231884	0	MC2R	18	18p11.21	13872043	13905536
ZNF519	0.970588	0.090909	0.090909	0.101449	0	ZNF519	18	18p11.21	14094724	14122430
GP2	0.970588	0.242424	0.090909	0.492754	0	GP2	16	16p12.3	20229312	20246337
GSG1L	0.970588	0.424242	0.090909	0.565217	0	GSG1L	16	16p11.2	27706351	27982332
NOVA1	0.970588	0.090909	0.181818	0	0.217391	NOVA1	14	14q12	25984929	26136801
PRKD1	0.970588	0.090909	0.121212	0	0.173913	PRKD1	14	14q12	29115438	29466651
ARHGAP5	0.970588	0.090909	0	0	0.043478	ARHGAP5	14	14q12	31615246	31698686
AKAP6	0.970588	0.090909	0.121212	0	0.101449	AKAP6	14	14q13.1	31868230	32372020
RALGAPA1	0.970588	0.090909	0.030303	0	0.115942	RALGAPA1	14	14q13.2	35077309	35348184

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
PTGDR	0.970588	0.030303	0.090909	0.028986	0	PTGDR	14	14q22.1	51804181	51813193
KIAA0586	0.970588	0.121212	0.090909	0.014493	0	KIAA0586	14	14q23.1	57964463	58085303
DACT1	0.970588	0.121212	0.090909	0.014493	0	DACT1	14	14q23.1	58174510	58184792
SGPP1	0.970588	0.242424	0.090909	0.217391	0	SGPP1	14	14q23.2	63220688	63264510
SYNE2	0.970588	0.242424	0.090909	0.217391	0	SYNE2	14	14q23.2	63389436	63762923
ATP6V1D	0.970588	0.242424	0.090909	0.217391	0	ATP6V1D	14	14q23.3	66874342	66896345
EIF2S1	0.970588	0.242424	0.090909	0.217391	0	EIF2S1	14	14q23.3	66896787	66922987
PLEK2	0.970588	0.242424	0.090909	0.217391	0	PLEK2	14	14q23.3	66923453	66948582
PLEKHH1	0.970588	0.242424	0.090909	0.217391	0	PLEKHH1	14	14q24.1	67069761	67126009
PIGH	0.970588	0.212121	0.090909	0.217391	0	PIGH	14	14q24.1	67125776	67136771
ARG2	0.970588	0.212121	0.090909	0.217391	0	ARG2	14	14q24.1	67156332	67188190
LTBP2	0.970588	0.333333	0.090909	0.376812	0	LTBP2	14	14q24.3	74034639	74148788
KIAA0317	0.970588	0.333333	0.090909	0.376812	0	KIAA0317	14	14q24.3	74197708	74249561
FCF1	0.970588	0.333333	0.090909	0.362319	0	FCF1	14	14q24.3	74249603	74273144
YLPM1	0.970588	0.333333	0.090909	0.362319	0	YLPM1	14	14q24.3	74299822	74373767
PROX2	0.970588	0.333333	0.090909	0.362319	0	PROX2	14	14q24.3	74391588	74400291
DLST	0.970588	0.333333	0.090909	0.362319	0	DLST	14	14q24.3	74418347	74440204
RPS6KL1	0.970588	0.363636	0.090909	0.362319	0	RPS6KL1	14	14q24.3	74442099	74458899
PGF	0.970588	0.363636	0.090909	0.362319	0	PGF	14	14q24.3	74478291	74492045
EIF2B2	0.970588	0.333333	0.090909	0.362319	0	EIF2B2	14	14q24.3	74539365	74546047
MLH3	0.970588	0.333333	0.090909	0.362319	0	MLH3	14	14q24.3	74550220	74587989
ACYP1	0.970588	0.333333	0.090909	0.362319	0	ACYP1	14	14q24.3	74589681	74600490
FAM164C	0.970588	0.333333	0.090909	0.362319	0	FAM164C	14	14q24.3	74606052	74614553
NEK9	0.970588	0.333333	0.090909	0.362319	0	NEK9	14	14q24.3	74618572	74663532
TMED10	0.970588	0.333333	0.090909	0.362319	0	TMED10	14	14q24.3	74667924	74713103
JDP2	0.970588	0.333333	0.090909	0.362319	0	JDP2	14	14q24.3	74964262	75009156
BATF	0.970588	0.30303	0.090909	0.362319	0	BATF	14	14q24.3	75058537	75083081
FLVCR2	0.970588	0.30303	0.090909	0.318841	0	FLVCR2	14	14q24.3	75114693	75184266
FOXN3	0.970588	0.151515	0.090909	0.333333	0	FOXN3	14	14q31.3	88692269	89155248
C14orf143	0.970588	0.212121	0.090909	0.376812	0	C14orf143	14	14q32.11	89333222	89490843
C14orf64	0.970588	0.060606	0.090909	0.26087	0	C14orf64	14	14q32.2	97461700	97514215
GPR12	0.970588	0.181818	0.090909	0.333333	0	GPR12	13	13q12.13	26227341	26232923
RPL21	0.970588	0.181818	0.090909	0.333333	0	RPL21	13	13q12.2	26723692	26728703
RPL21P28	0.970588	0.181818	0.090909	0.333333	0	RPL21P28	13	13q12.2	26723693	26728699
SNORD102	0.970588	0.181818	0.090909	0.333333	0	SNORD102	13	13q12.2	26727201	26727273
SNORA27	0.970588	0.181818	0.090909	0.333333	0	SNORA27	13	13q12.2	26727538	26727664
RASL11A	0.970588	0.181818	0.090909	0.333333	0	RASL11A	13	13q12.2	26742464	26745828
GTF3A	0.970588	0.151515	0.090909	0.333333	0	GTF3A	13	13q12.2	26896681	26907847
MTIF3	0.970588	0.151515	0.090909	0.333333	0	MTIF3	13	13q12.2	26907776	26922335
GSX1	0.970588	0.121212	0.090909	0.347826	0	GSX1	13	13q12.2	27264780	27266090
PDX1	0.970588	0.121212	0.090909	0.333333	0	PDX1	13	13q12.2	27392168	27398452
ATP5EP2	0.970588	0.121212	0.090909	0.333333	0	ATP5EP2	13	13q12.2	27417343	27417711
CDX2	0.970588	0.121212	0.090909	0.333333	0	CDX2	13	13q12.2	27434278	27441318
PRHOXNB	0.970588	0.121212	0.090909	0.333333	0	PRHOXNB	13	13q12.2	27450243	27460775
FLT3	0.970588	0.121212	0.090909	0.333333	0	FLT3	13	13q12.2	27475411	27572730
FLT1	0.970588	0.090909	0.090909	0.231884	0	FLT1	13	13q12.2	27772483	27967266
POMP	0.970588	0.121212	0.090909	0.231884	0	POMP	13	13q12.3	28131241	28151092
SLC46A3	0.970588	0.121212	0.090909	0.231884	0	SLC46A3	13	13q12.3	28172220	28191151
SLC7A1	0.970588	0.151515	0.090909	0.26087	0	SLC7A1	13	13q12.3	28981552	29067826
KATNAL1	0.970588	0.151515	0.090909	0.246377	0	KATNAL1	13	13q12.3	29674767	29779164
LOC10018949	0.970588	0.151515	0.090909	0.246377	0	LOC10018949	13	13q12.3	29812409	29846037
HMGB1	0.970588	0.181818	0.090909	0.246377	0	HMGB1	13	13q12.3	29930879	29938082
ALOX5AP	0.970588	0.181818	0.090909	0.275362	0	ALOX5AP	13	13q12.3	30207669	30236557
KRT3	0.970588	0.212121	0.090909	0.478261	0	KRT3	12	12q13.13	51469736	51476160
TSPAN8	0.970588	0.090909	0.090909	0	0.15942	TSPAN8	12	12q21.1	69805144	69838047
LGR5	0.970588	0.090909	0.121212	0	0.15942	LGR5	12	12q21.1	70120080	70264889
KITLG	0.970588	0.090909	0.181818	0	0.246377	KITLG	12	12q21.32	87410698	87498370
VEZT	0.970588	0.181818	0.090909	0.188406	0	VEZT	12	12q22	94135653	94220698
TMEM132C	0.970588	0.060606	0.090909	0.275362	0	TMEM132C	12	12q24.32	1.27E+08	1.28E+08
EIF3F	0.970588	0.121212	0.090909	0.15942	0	EIF3F	11	11p15.4	7965443	7974295
SBF2	0.970588	0.181818	0.090909	0.188406	0	SBF2	11	11p15.4	9756790	10272331
MICALCL	0.970588	0.121212	0.090909	0.231884	0	MICALCL	11	11p15.3	12265023	12337268
LDLRAD3	0.970588	0.121212	0.090909	0.130435	0	LDLRAD3	11	11p13	35922188	35209418
COMMD9	0.970588	0.151515	0.090909	0.130435	0	COMMD9	11	11p13	36250418	36267576
PRR5L	0.970588	0.151515	0.090909	0.130435	0	PRR5L	11	11p13	36274301	36443330
FAM181B	0.970588	0.090909	0.121212	0	0.057971	FAM181B	11	11q14.1	82120694	82122555
DLG2	0.970588	0.090909	0.181818	0	0.115942	DLG2	11	11q14.1	82843706	85015963
RAB38	0.970588	0.090909	0.181818	0	0.101449	RAB38	11	11q14.2	87486079	87548248
CTSC	0.970388	0.090909	0.151515	0	0.130435	CTSC	11	11q14.2	87666408	87710590
GRM5	0.970588	0.090909	0.181818	0	0.115942	GRM5	11	11q14.2	87877393	88436465
TRPC6	0.970588	0.090909	0.272727	0	0.188406	TRPC6	11	11q22.1	1.01E+08	1.01E+08
KIAA1377	0.970588	0.090909	0.212121	0	0.173913	KIAA1377	11	11q22.1	1.01E+08	1.01E+08
YAP1	0.970588	0.090909	0.181818	0	0.130435	YAP1	11	11q22.1	1.01E+08	1.02E+08
MMP27	0.970588	0.090909	0.151515	0	0.057971	MMP27	11	11q22.2	1.02E+08	1.02E+08
MMP8	0.970588	0.090909	0.151515	0	0.057971	MMP8	11	11q22.2	1.02E+08	1.02E+08
MMP10	0.970588	0.090909	0.151515	0	0.043478	MMP10	11	11q22.2	1.02E+08	1.02E+08

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
MMP1	0.970588	0.090909	0.151515	0	0.043478	MMP1	11	11q22.2	1.02E+08	1.02E+08
PDGFD	0.970588	0.090909	0.212121	0	0.144928	PDGFD	11	11q22.3	1.03E+08	1.04E+08
CASP4	0.970588	0.090909	0.272727	0	0.188406	CASP4	11	11q22.3	1.04E+08	1.04E+08
CASP5	0.970588	0.090909	0.272727	0	0.188406	CASP5	11	11q22.3	1.04E+08	1.04E+08
CARD16	0.970588	0.090909	0.272727	0	0.188406	CARD16	11	11q22.3	1.04E+08	1.04E+08
GRIA4	0.970588	0.090909	0.242424	0	0.15942	GRIA4	11	11q22.3	1.05E+08	1.05E+08
SLN	0.970588	0.242424	0.090909	0.217391	0	SLN	11	11q22.3	1.07E+08	1.07E+08
ACAT1	0.970588	0.212121	0.090909	0.246377	0	ACAT1	11	11q22.3	1.07E+08	1.08E+08
NPAT	0.970588	0.212121	0.090909	0.246377	0	NPAT	11	11q22.3	1.08E+08	1.08E+08
ATM	0.970588	0.212121	0.090909	0.231884	0	ATM	11	11q22.3	1.08E+08	1.08E+08
FDXACB1	0.970588	0.212121	0.090909	0.217391	0	FDXACB1	11	11q23.1	1.11E+08	1.11E+08
C11orf1	0.970588	0.212121	0.090909	0.217391	0	C11orf1	11	11q23.1	1.11E+08	1.11E+08
CRYAB	0.970588	0.212121	0.090909	0.217391	0	CRYAB	11	11q23.1	1.11E+08	1.11E+08
HSPB2	0.970588	0.212121	0.090909	0.217391	0	HSPB2	11	11q23.1	1.11E+08	1.11E+08
C11orf52	0.970588	0.212121	0.090909	0.217391	0	C11orf52	11	11q23.1	1.11E+08	1.11E+08
DIXDC1	0.970588	0.212121	0.090909	0.217391	0	DIXDC1	11	11q23.1	1.11E+08	1.11E+08
PIH1D2	0.970588	0.212121	0.090909	0.217391	0	PIH1D2	11	11q23.1	1.11E+08	1.11E+08
C11orf57	0.970588	0.212121	0.090909	0.217391	0	C11orf57	11	11q23.1	1.11E+08	1.11E+08
TIMM8B	0.970588	0.212121	0.090909	0.217391	0	TIMM8B	11	11q23.1	1.11E+08	1.11E+08
SDHD	0.970588	0.212121	0.090909	0.217391	0	SDHD	11	11q23.1	1.11E+08	1.11E+08
CEP164	0.970588	0.30303	0.090909	0.449275	0	CEP164	11	11q23.3	1.17E+08	1.17E+08
DSCAML1	0.970588	0.30303	0.090909	0.463768	0	DSCAML1	11	11q23.3	1.17E+08	1.17E+08
FXYD6	0.970588	0.30303	0.090909	0.478261	0	FXYD6	11	11q23.3	1.17E+08	1.17E+08
TMPRSS13	0.970588	0.30303	0.090909	0.478261	0	TMPRSS13	11	11q23.3	1.17E+08	1.17E+08
IL10RA	0.970588	0.30303	0.090909	0.478261	0	IL10RA	11	11q23.3	1.17E+08	1.17E+08
TMPRSS4	0.970588	0.30303	0.090909	0.478261	0	TMPRSS4	11	11q23.3	1.17E+08	1.17E+08
SCN4B	0.970588	0.30303	0.090909	0.478261	0	SCN4B	11	11q23.3	1.18E+08	1.18E+08
MPZL2	0.970588	0.30303	0.090909	0.478261	0	MPZL2	11	11q23.3	1.18E+08	1.18E+08
MLL	0.970588	0.333333	0.090909	0.478261	0	MLL	11	11q23.3	1.18E+08	1.18E+08
TMEM25	0.970588	0.393939	0.090909	0.507246	0	TMEM25	11	11q23.3	1.18E+08	1.18E+08
C11orf60	0.970588	0.393939	0.090909	0.507246	0	C11orf60	11	11q23.3	1.18E+08	1.18E+08
ARCN1	0.970588	0.393939	0.090909	0.507246	0	ARCN1	11	11q23.3	1.18E+08	1.18E+08
PHLDB1	0.970588	0.393939	0.090909	0.507246	0	PHLDB1	11	11q23.3	1.18E+08	1.18E+08
TREH	0.970588	0.393939	0.090909	0.507246	0	TREH	11	11q23.3	1.18E+08	1.18E+08
CXCR5	0.970588	0.393939	0.090909	0.507246	0	CXCR5	11	11q23.3	1.18E+08	1.18E+08
BCL9L	0.970588	0.393939	0.090909	0.507246	0	BCL9L	11	11q23.3	1.18E+08	1.18E+08
THY1	0.970588	0.393939	0.090909	0.507246	0	THY1	11	11q23.3	1.19E+08	1.19E+08
PVRL1	0.970588	0.363636	0.090909	0.507246	0	PVRL1	11	11q23.3	1.19E+08	1.19E+08
GRIK4	0.970588	0.30303	0.090909	0.463768	0	GRIK4	11	11q23.3	1.2E+08	1.2E+08
OPCML	0.970588	0.090909	0.090909	0.173913	0	OPCML	11	11q25	1.32E+08	1.33E+08
ZNF33A	0.970588	0.090909	0.090909	0.15942	0	ZNF33A	10	10p11.21	38339584	38389002
LOC728640	0.970588	0.090909	0.242424	0	0.202899	LOC728640	10	10q21.1	60244781	60147298
LOC389705	0.970588	0.090909	0.030303	0	0.014493	LOC389705	9	9p22.3	14983325	15009723
CNTLN	0.970588	0.090909	0.121212	0	0.057971	CNTLN	9	9p22.2	17125038	17292050
SH3GL2	0.970588	0.090909	0.090909	0	0.043478	SH3GL2	9	9p22.2	17568953	17787121
IFNW1	0.970588	0.090909	0.121212	0	0.115942	IFNW1	9	9p21.3	21130631	21332145
IFNA21	0.970588	0.090909	0.121212	0	0.115942	IFNA21	9	9p21.3	21155636	21156660
IFNA13	0.970588	0.090909	0.090909	0	0.115942	IFNA13	9	9p21.3	21357371	21358076
C9orf135	0.970588	0.060606	0.090909	0.014493	0	C9orf135	9	9q21.11	71625551	71710969
MAMDC2	0.970588	0.090909	0.090909	0.014493	0	MAMDC2	9	9921.11	71848317	72031709
RHEB	0.970588	0.30303	0.090909	0.434783	0	RHEB	7	7q36.1	1.51E+08	1.51E+08
RHACTR1	0.970588	0.060606	0.090909	0.072464	0	PHACTR1	6	6p24.1	12825819	13395508
SNHG5	0.970588	0.090909	0.30303	0	0.333333	SNHG5	6	6q14.3	86443444	86445171
SNORD50A	0.970588	0.090909	0.30303	0	0.333333	SNORD50A	6	6q14.3	86443731	86443806
SNORD50B	0.970588	0.090909	0.30303	0	0.333333	SNORD50B	6	6q14.3	86444026	86444097
GJB7	0.970588	0.090909	0.242424	0	0.202899	GJB7	6	6q15	88049416	88095716
C6orf162	0.970588	0.090909	0.242424	0	0.202899	C6orf162	6	6q15	88089025	88108763
C6orf163	0.970588	0.090909	0.242424	0	0.202899	C6orf163	6	6q15	88111290	88131900
C6orf164	0.970588	0.090909	0.242424	0	0.202899	C6orf164	6	6q15	88163561	88166179
C6orf165	0.970588	0.090909	0.242424	0	0.202899	C6orf165	6	6q15	88174409	88230911
SLC35A1	0.970588	0.090909	0.242424	0	0.202899	SLC35A1	6	6q15	88239362	88278771
RARS2	0.970588	0.090909	0.242424	0	0.202899	RARS2	6	6q15	88280816	88356455
TAAR8	0.970588	0.090909	0.060606	0	0.043478	TAAR8	6	6q23.2	1.33E+08	1.33E+08
FYB	0.970588	0.090909	0	0	0.014493	FYB	5	5p13.1	39141114	39255425
UGT2B10	0.970588	0.090909	0.272727	0	0.289855	UGT2B10	4	4q13.2	69716302	69732329
UGT2A3	0.970588	0.090909	0.272727	0	0.289855	UGT2A3	4	4q13.2	69828766	69852099
MUC7	0.970588	0.090909	0.181818	0	0.202899	MUC7	4	4q13.3	71330798	71383303
ADAMTS3	0.970588	0.090909	0.181818	0	0.289855	ADAMTS3	4	4q13.3	73365551	73653381
AFP	0.970588	0.090909	0.121212	0	0.101449	AFP	4	4q13.3	74520797	74540357
AFM	0.970588	0.090909	0.121212	0	0.101449	AFM	4	4q13.3	74566326	74588583
RASSF6	0.970588	0.090909	0.121212	0	0.086957	RASSF6	4	4q13.3	74657726	74704999
CXCL6	0.970588	0.090909	0.151515	0	0.101449	CXCL6	4	4q13.3	74921137	74923342
PPBPL1	0.970588	0.090909	0.151515	0	0.101449	PPBPL1	4	4q13.3	74932447	74933418
PF4	0.970588	0.090909	0.151515	0	0.101449	PF4	4	4q13.3	75065660	75066580
PPBP	0.970588	0.090909	0.151515	0	0.101449	PPBP	4	4q13.3	75071620	75072765
CXCL3	0.970588	0.090909	0.151515	0	0.101449	CXCL3	4	4q13.3	75121176	75123355

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
CXCL2	0.970588	0.090909	0.151515	0	0.101449	CXCL2	4	4q13.3	75181618	75183862
MTHFD2L	0.970588	0.090909	0.151515	0	0.115942	MTHFD2L	4	4q13.3	75242693	75387677
AREG	0.970588	0.090909	0.121212	0	0.115942	AREG	4	4q13.3	75699653	75709510
PARM1	0.970588	0.090909	0.151515	0	0.086957	PARM1	4	4q13.3	76077322	76194348
FAM47E	0.970588	0.090909	0.030303	0	0.014493	FAM47E	4	4q21.1	77391877	77423948
ANKRD56	0.970588	0.090909	0.060606	0	0.014493	ANKRD56	4	4q21.1	78035106	78038027
11-Sep	0.970588	0.090909	0.030303	0	0.014493	11-Sep	4	4q21.1	78089919	78178793
ANXA3	0.970588	0.090909	0.060606	0	0.028986	ANXA3	4	4q21.21	79691766	79750630
BMP2K	0.970588	0.090909	0.090909	0	0.028986	BMP2K	4	4q21.21	79916556	80019619
PRDM8	0.970588	0.090909	0.121212	0	0.130435	PRDM8	4	4q21.21	81325448	81344507
CDS1	0.970588	0.090909	0.151515	0	0.043478	CDS1	4	4q21.23	85723081	85791518
WDFY3	0.970588	0.090909	0.121212	0	0.043478	WDFY3	4	4q21.23	85809723	86106569
MANBA	0.970588	0.090909	0.030303	0	0.101449	MANBA	4	4q24	1.04E+08	1.04E+08
TET2	0.970588	0.090909	0.151515	0	0.231884	TET2	4	4q24	1.06E+08	1.06E+08
HHIP	0.970588	0.090909	0.090909	0	0.086957	HHIP	4	4q31.22	1.46E+08	1.46E+08
CLSTN2	0.970588	0.090909	0.090909	0.26087	0	CLSTN2	3	3q23	1.41E+08	1.42E+08
CDC42EP3	0.970588	0	0.090909	0.072464	0	CDC42EP3	2	2p22.2	37724247	37752831
C2orf89	0.970588	0.151515	0.090909	0.318841	0	C2orf89	2	2p11.2	84902307	84961764
IL1RL2	0.970588	0.151515	0.090909	0.202899	0	IL1RL2	2	2q12.1	1.02E+08	1.02E+08
PKN2	0.970588	0.090909	0.212121	0	0.101449	PKN2	1	1p22.2	88922510	89074527
PHGDH	0.970588	0.060606	0.090909	0.086957	0	PHGDH	1	1p12	1.2E+08	1.2E+08
REG4	0.970588	0.030303	0.090909	0.086957	0	REG4	1	1p12	1.2E+08	1.2E+08
NBPF7	0.970588	0.030303	0.090909	0.086957	0	NBPF7	1	1p12	1.2E+08	1.2E+08
ADAM30	0.970588	0.030303	0.090909	0.086957	0	ADAM30	1	1p12	1.2E+08	1.2E+08
NOTCH2	0.970588	0.030303	0.090909	0.086957	0	NOTCH2	1	1p12	1.2E+08	1.2E+08
NENF	0.970588	0.121212	0.090909	0.246377	0	NENF	1	1q32.3	2.11E+08	2.11E+08
CNIH4	0.970588	0.181818	0.090909	0.304348	0	CNIH4	1	1q42.11	2.23E+08	2.23E+08
SNAP47	0.970588	0.272727	0.090909	0.42029	0	SNAP47	1	1q42.13	2.26E+08	2.26E+08
SIPA1L2	0.970588	0.212121	0.090909	0.275362	0	SIPA1L2	1	1q42.2	2.31E+08	2.31E+08
KIAA1383	0.970588	0.151515	0.090909	0.246377	0	KIAA1383	1	1q42.2	2.31E+08	2.31E+08
C1orf57	0.970588	0.151515	0.090909	0.231884	0	C1orf57	1	1q42.2	2.31E+08	2.31E+08
PCNXL2	0.970588	0.151515	0.090909	0.231884	0	PCNXL2	1	1q42.2	2.31E+08	2.31E+08
KIAA1804	0.970588	0.151515	0.090909	0.231884	0	KIAA1804	1	1q42.2	2.32E+08	2.32E+08
KCNK1	0.970588	0.121212	0.090909	0.217391	0	KCNK1	1	1q42.2	2.32E+08	2.32E+08
SLC35F3	0.970588	0.121212	0.090909	0.217391	0	SLC35F3	1	1q42.2	2.32E+08	2.33E+08
TARBP1	0.970588	0.242424	0.090909	0.246377	0	TARBP1	1	1q42.2	2.33E+08	2.33E+08
B3GALNT2	0.970588	0.242424	0.090909	0.275362	0	B3GALNT2	1	1q42.3	2.34E+08	2.34E+08
GNG4	0.970588	0.242424	0.090909	0.275362	0	GNG4	1	1q42.3	2.34E+08	2.34E+08
LYST	0.970588	0.212121	0.090909	0.275362	0	LYST	1	1q42.3	2.34E+08	2.34E+08
NID1	0.970588	0.242424	0.090909	0.26087	0	NID1	1	1q42.3	2.34E+08	2.34E+08
GPR137B	0.970588	0.272727	0.090909	0.26087	0	GPR137B	1	1q42.3	2.34E+08	2.34E+08
EDARADD	0.970588	0.272727	0.090909	0.246377	0	EDARADD	1	1q43	2.35E+08	2.35E+08
HEATR1	0.970588	0.242424	0.090909	0.188406	0	HEATR1	1	1q43	2.35E+08	2.35E+08
SMC5	0.019608	0.090909	0.090909	0.014493	0.014493	SMC5	9	9q21.11	72063698	72159610
TTTY8	0.009804	0.212121	0.121212	0.202899	0.014493	TTTY8	Y	Yp11.2	10138709	10141309
TTTY8B	0.009804	0.212121	0.121212	0.202899	0.014493	TTTY8B	Y	Yp11.2	10138709	10141309
TTTY7	0.009804	0.212121	0.121212	0.202899	0.014493	TTTY7	Y	Yp11.2	10154433	10162872
TTTY7B	0.009804	0.212121	0.121212	0.202899	0.014493	TTTY7B	Y	Yp11.2	10154433	10162872
LOC100101115	0.009804	0.212121	0.121212	0.202899	0.014493	LOC100101115	Y	Yp11.2	10165262	10168906
TTTY21	0.009804	0.212121	0.121212	0.202899	0.014493	TTTY21	Y	Yp11.2	10165262	10168906
TTTY22	0.009804	0.212121	0.121212	0.202899	0.014493	TTTY22	Y	Yp11.2	10248762	10260855
C22orf25	0.009804	0.424242	0.121212	0.681159	0.014493	C22orf25	22	22q11.21	18388631	18433448
MIR185	0.009804	0.424242	0.121212	0.681159	0.014493	MIR185	22	22q11.21	18400662	18400743
DGCR8	0.009804	0.424242	0.090909	0.681159	0.014493	DGCR8	22	22q11.21	18447834	18479401
ZNF74	0.009804	0.393939	0.090909	0.666667	0.014493	ZNF74	22	22q11.21	19078480	19092753
SCARF2	0.009804	0.393939	0.090909	0.666667	0.014493	SCARF2	22	22q11.21	19108875	19122147
KLHL22	0.009804	0.393939	0.090909	0.666667	0.014493	KLHL22	22	22q11.21	19125806	19180123
MED15	0.009804	0.393939	0.090909	0.666667	0.014493	MED15	22	22q11.21	19191886	19271920
POM121L4P	0.009804	0.393939	0.090909	0.666667	0.014493	POM121L4P	22	22q11.21	19373843	19376010
TMEM191A	0.009804	0.393939	0.090909	0.666667	0.014493	TMEM191A	22	22q11.21	19385402	19388892
PI4KA	0.009804	0.393939	0.090909	0.666667	0.014493	PI4KA	22	22q11.21	19391979	19418956
SERPIND1	0.009804	0.363636	0.090909	0.637681	0.014493	SERPIND1	22	22q11.21	19458383	19472009
SNAP29	0.009804	0.333333	0.090909	0.623188	0.014493	SNAP29	22	22q11.21	19543292	19575500
CRKL	0.009804	0.333333	0.090909	0.623188	0.014493	CRKL	22	22q11.21	19601714	19638039
FLJ39582	0.009804	0.363636	0.090909	0.623188	0.014493	FLJ39582	22	22q11.21	19686211	19694663
MGC16703	0.009804	0.363636	0.090909	0.623188	0.014493	MGC16703	22	22q11.21	19692496	19698577
P2RX6	0.009804	0.363636	0.090909	0.623188	0.014493	P2RX6	22	22q11.21	19699442	19712303
SLC7A4	0.009804	0.363636	0.090909	0.623188	0.014493	SLC7A4	22	22q11.21	19713007	19716848
PRAME	0.009804	0.30303	0.090909	0.623188	0.014493	PRAME	22	22q11.22	21220123	21231697
LOC648691	0.009804	0.30303	0.090909	0.623188	0.014493	LOC648691	22	22q11.22	21231756	21239007
RTDR1	0.009804	0.333333	0.090909	0.652174	0.014493	RTDR1	22	22q11.22	21731593	21814242
GNAZ	0.009804	0.333333	0.090909	0.652174	0.014493	GNAZ	22	22q11.22	21742669	21797222
RAB36	0.009804	0.333333	0.090909	0.652174	0.014493	RAB36	22	22q11.23	21817513	21836532
BCR	0.009804	0.333333	0.090909	0.652174	0.014493	BCR	22	22q11.23	21852552	21990225
ZDHHC8P	0.009804	0.333333	0.090909	0.652174	0.014493	ZDHHC8P	22	22q11.23	22062792	22074800
IGLL1	0.009804	0.363636	0.090909	0.637681	0.014493	IGLL1	22	22q11.23	22245313	22252496

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
LOC91316	0.009804	0.30303	0.121212	0.623188	0.014493	LOC91316	22	22q11.23	22310676	22389611
ZNF70	0.009804	0.363636	0.090909	0.637681	0.014493	ZNF70	22	22q11.23	22413772	22423280
MMP11	0.009804	0.363636	0.090909	0.637681	0.014493	MMP11	22	22q11.23	22445036	22456504
SMARCB1	0.009804	0.363636	0.090909	0.637681	0.014493	SMARCB1	22	22q11.23	22459150	22506706
CABIN1	0.009804	0.363636	0.121212	0.637681	0.014493	CABIN1	22	22q11.23	22737765	22904597
GGT5	0.009804	0.30303	0.121212	0.637681	0.014493	GGT5	22	22q11.23	22945622	22971111
UPB1	0.009804	0.272727	0.121212	0.623188	0.014493	UPB1	22	22q11.23	23221251	23252554
C22orf13	0.009804	0.272727	0.121212	0.623188	0.014493	C22orf13	22	22q11.23	23266408	23281276
SNRPD3	0.009804	0.272727	0.121212	0.623188	0.014493	SNRPD3	22	22q11.23	23281618	23298510
GGT1	0.009804	0.272727	0.121212	0.623188	0.014493	GGT1	22	22q11.23	23309718	23354973
C22orf36	0.009804	0.30303	0.121212	0.623188	0.014493	C22orf36	22	22q11.23	23311591	23319036
LOC644165	0.009804	0.30303	0.121212	0.623188	0.014493	LOC644165	22	22q11.23	23358882	23379327
SGSM1	0.009804	0.333333	0.121212	0.652174	0.014493	SGSM1	22	22q11.23	23532136	23652814
KIAA1671	0.009804	0.333333	0.121212	0.652174	0.014493	KIAA1671	22	22q11.23	23753941	23923414
CRYBB2	0.009804	0.333333	0.121212	0.652174	0.014493	CRYBB2	22	22q11.23	23945612	23957837
ADRBK2	0.009804	0.30303	0.090909	0.623188	0.014493	ADRBK2	22	22q11.23	24290861	24455259
MYO18B	0.009804	0.30303	0.090909	0.623188	0.014493	MYO188	22	22q12.1	24468120	24757008
MIR1302-1	0.009804	0.212121	0.121212	0.57971	0.014493	MIR1302-1	22	22q12.1	24513501	25125580
HPS4	0.009804	0.30303	0.090909	0.608696	0.014493	HPS4	22	22q12.1	25177446	25209821
SRRD	0.009804	0.30303	0.090909	0.608696	0.014493	SRRD	22	22q12.1	25209850	25217905
TFIP11	0.009804	0.30303	0.090909	0.608696	0.014493	TFIP11	22	22q12.1	25217895	25238438
TPST2	0.009804	0.30303	0.090909	0.57971	0.014493	TPST2	22	22q12.1	25251714	25291371
MIR548J	0.009804	0.30303	0.090909	0.57971	0.014493	MIR548J	22	22q12.1	25281178	25281290
CRYBA4	0.009804	0.30303	0.090909	0.565217	0.014493	CRYBA4	22	22q12.1	25347928	25356637
MIAT	0.009804	0.272727	0.090909	0.550725	0.014493	MIAT	22	22q12.1	25383484	25402439
RFPL3	0.009804	0.242424	0.090909	0.608696	0.014493	RFPL3	22	22q12.3	31080872	31087149
RFP135	0.009804	0.242424	0.090909	0.608696	0.014493	RFPL3S	22	22q12.3	31085893	31097064
C22orf28	0.009804	0.242424	0.090909	0.608696	0.014493	C22orf28	22	22q12.3	31113562	31138275
SYN3	0.009804	0.242424	0.090909	0.608696	0.014493	SYN3	22	22q12.3	31238540	31784378
TIMP3	0.009804	0.242424	0.090909	0.608696	0.014493	TIMP3	22	22q12.3	31526802	31589029
LARGE	0.009804	0.242424	0.090909	0.594203	0.014493	LARGE	22	22q12.3	31999062	32646417
ISX	0.009804	0.151515	0.090909	0.57971	0.014493	ISX	22	22q12.3	33792130	33813381
TOM1	0.009804	0.30303	0.090909	0.608696	0.014493	TOM1	22	22q12.3	34025268	34073986
HMOX1	0.009804	0.333333	0.090909	0.623188	0.014493	HMOX1	22	22q12.3	34107087	34120195
MCM5	0.009804	0.333333	0.090909	0.623188	0.014493	MCM5	22	22q12.3	34126116	34150496
RASD2	0.009804	0.333333	0.090909	0.623188	0.014493	RASD2	22	22q12.3	34267298	34279992
MB	0.009804	0.30303	0.090909	0.637681	0.014493	MB	22	22q12.3	34332757	34343331
ABCC13	0.009804	0.090909	0.121212	0.014493	0.115942	ABCC13	21	21q11.2	14567991	14595564
KRTAP11-1	0.009804	0.121212	0.090909	0.101449	0.014493	KRTAP11-1	21	21q22.11	31174835	31175746
KRTAP19-8	0.009804	0.151515	0.090909	0.144928	0.014493	KRTAP19-8	21	21q22.11	31332349	31332667
CLDN14	0.009804	0.30303	0.090909	0.463768	0.014493	CLDN14	21	21q22.13	36754790	36760596
SMCHD1	0.009804	0.090909	0.090909	0.173913	0.014493	SMCHD1	18	18p11.32	2645886	2795016
EMILIN2	0.009804	0.151515	0.090909	0.202899	0.014493	EMILIN2	18	18p11.32	2837028	2904091
LPIN2	0.009804	0.212121	0.090909	0.188406	0.014493	LPIN2	18	18p11.32	2906992	3001946
LOC727896	0.009804	0.060606	0.090909	0.15942	0.014493	LOC727896	18	18p11.31	2933215	2936622
TGIF1	0.009804	0.181818	0.090909	0.188406	0.014493	TGIF1	18	18p11.31	3402072	3448407
DLGAP1	0.009804	0.151515	0.090909	0.188406	0.014493	DLGAP1	18	18p11.31	3488837	3835297
FLJ35776	0.009804	0.151515	0.090909	0.188406	0.014493	FLJ35776	18	18p11.31	3584112	3587377
EPB41L3	0.009804	0.060606	0.121212	0.086957	0.014493	EPB41L3	18	18p11.31	5382388	5533987
L3MBTL4	0.009804	0.030303	0.121212	0.072464	0.014493	L3MBTL4	18	18p11.31	5944705	6404911
ARHGAP28	0.009804	0.090909	0.090909	0.144928	0.014493	ARHGAP28	18	18p11.31	6824484	6905713
LAMA1	0.009804	0.121212	0.090909	0.173913	0.014493	LAMA1	18	18p11.31	6931886	7107814
LRRC30	0.009804	0.121212	0.090909	0.173913	0.014493	LRRC30	18	18p11.23	7221137	7222043
ANKRD12	0.009804	0.242424	0.090909	0.246377	0.014493	ANKRD12	18	18p11.22	9126758	9275207
RAB31	0.009804	0.272727	0.090909	0.26087	0.014493	RAB31	18	18p11.22	9698228	9852554
ROCK1	0.009804	0.151515	0.121212	0.130435	0.014493	ROCK1	18	18q11.1	16783701	16945811
GREB1L	0.009804	0.151515	0.121212	0.173913	0.014493	GREB1L	18	18q11.1	17076201	17356788
ESCO1	0.009804	0.151515	0.121212	0.173913	0.014493	ESCO1	18	18q11.2	17363260	17434692
SNRPD1	0.009804	0.151515	0.121212	0.173913	0.014493	SNRPD1	18	18q11.2	17446258	17464207
ABHD3	0.009804	0.151515	0.121212	0.173913	0.014493	ABHD3	18	18q11.2	17484856	17538765
MIR320C1	0.009804	0.151515	0.121212	0.173913	0.014493	MIR320C1	18	18q11.2	17517469	17517557
MIB1	0.009804	0.151515	0.121212	0.173913	0.014493	MIB1	18	18q11.2	17575543	17704911
CTAGE1	0.009804	0.030303	0.121212	0.130435	0.014493	CTAGE1	18	18q11.2	18247562	18251877
EPN2	0.009804	0.393939	0.090909	0.594203	0.014493	EPN2	17	17p11.2	19081283	19180622
B9D1	0.009804	0.393939	0.090909	0.594203	0.014493	B9D1	17	17p11.2	19187076	19206640
MIR1180	0.009804	0.393939	0.090909	0.594203	0.014493	MIR1180	17	17p11.2	19188412	19188481
MAPK7	0.009804	0.393939	0.090909	0.594203	0.014493	MAPK7	17	17p11.2	19221627	19227450
MFAP4	0.009804	0.393939	0.090909	0.594203	0.014493	MFAP4	17	17p11.2	19227348	19231087
RNF112	0.009804	0.393939	0.090909	0.594203	0.014493	RNF112	17	17p11.2	19255084	19261180
PCTP	0.009804	0.030303	0.090909	0.217391	0.014493	PCTP	17	17q22	51183355	51209748
EIF3CL	0.009804	0.424242	0.090909	0.565217	0.014493	EIF3CL	16	16p11.2	28298401	28322664
EIF3C	0.009804	0.424242	0.090909	0.565217	0.014493	EIF3C	16	16p11.2	28298404	28322667
CLN3	0.009804	0.424242	0.090909	0.565217	0.014493	CLN3	16	16p11.2	28396101	28410905
APOB48R	0.009804	0.424242	0.090909	0.565217	0.014493	APOB48R	16	16p11.2	28413494	28417784
IL27	0.009804	0.424242	0.090909	0.565217	0.014493	IL27	16	16p11.2	28418184	28425657
NUPR1	0.009804	0.424242	0.090909	0.565217	0.014493	NUPR1	16	16p11.2	28456163	28457997

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
CCDC101	0.009804	0.424242	0.090909	0.565217	0.014493	CCDC101	16	16q11.2	28472750	28510612
ATXN2L	0.009804	0.424242	0.090909	0.565217	0.014493	ATXN2L	16	16p11.2	28741915	28756060
SH2B1	0.009804	0.424242	0.090909	0.565217	0.014493	SH2B1	16	16p11.2	28782579	28793035
ATP2A1	0.009804	0.424242	0.090909	0.565217	0.014493	ATP2A1	16	16p11.2	28797310	28823332
SPNS1	0.009804	0.424242	0.090909	0.565217	0.014493	SPNS1	16	16p11.2	28893597	28903370
LAT	0.009804	0.424242	0.090909	0.565217	0.014493	LAT	16	16p11.2	28903648	28909606
RUNDC2C	0.009804	0.424242	0.090909	0.565217	0.014493	RUNDC2C	16	16p11.2	29210042	29293099
SLC7A5P1	0.009804	0.424242	0.090909	0.565217	0.014493	SLC7A5P1	16	16p11.2	29531925	29532540
SPN	0.009804	0.424242	0.090909	0.565217	0.014493	SPN	16	16p11.2	29581801	29589325
QPRT	0.009804	0.424242	0.090909	0.565217	0.014493	QPRT	16	16p11.2	29597942	29616816
C16orf54	0.009804	0.424242	0.090909	0.565217	0.014493	C16orf54	16	16p11.2	29661287	29664842
MAZ	0.009804	0.424242	0.090909	0.565217	0.014493	MAZ	16	16p11.2	29725356	29730006
PRRT2	0.009804	0.424242	0.090909	0.565217	0.014493	PRRT2	16	16p11.2	29730910	29734704
C16orf53	0.009804	0.424242	0.090909	0.565217	0.014493	C16orf53	16	16p11.2	29735029	29741318
MVP	0.009804	0.424242	0.090909	0.565217	0.014493	MVP	16	16p11.2	29739288	29766843
CDIPT	0.009804	0.424242	0.090909	0.565217	0.014493	CDIPT	16	16p11.2	29777179	29782080
LOC440356	0.009804	0.424242	0.090909	0.565217	0.014493	LOC440356	16	16p11.2	29782505	29786876
SEZ6L2	0.009804	0.424242	0.090909	0.565217	0.014493	SEZ6L2	16	16p11.2	29789981	29818082
ASPHD1	0.009804	0.424242	0.090909	0.565217	0.014493	ASPHD1	16	16p11.2	29819648	29824879
KCTD13	0.009804	0.424242	0.090909	0.565217	0.014493	KCTD13	16	16p11.2	29825162	29845047
TMEM219	0.009804	0.424242	0.090909	0.565217	0.014493	TMEM219	16	16p11.2	29880852	29891875
TAOK2	0.009804	0.424242	0.090909	0.565217	0.014493	TAOK2	16	16p11.2	29892723	29911083
C16orf92	0.009804	0.424242	0.090909	0.565217	0.014493	C16orf92	16	16p11.2	29942156	29943525
FAM57B	0.009804	0.424242	0.090909	0.565217	0.014493	FAM57B	16	16p11.2	29943249	29949688
ALDOA	0.009804	0.424242	0.090909	0.565217	0.014493	ALDOA	16	16p11.2	29971992	29989237
ITGAM	0.009804	0.393939	0.090909	0.565217	0.014493	ITGAM	16	16p11.2	31178789	31251715
RASGRP1	0.009804	0	0.121212	0.057971	0.014493	RASGRP1	15	15q14	36567594	36644300
C15orf53	0.009804	0	0.121212	0.057971	0.014493	C15orf53	15	15q14	36776091	36779532
THBS1	0.009804	0.030303	0.121212	0.086957	0.014493	THBS1	15	15q14	37660572	37676961
SCG3	0.009804	0	0.090909	0.115942	0.014493	SCG3	15	15q21.2	49760842	49800515
TMOD3	0.009804	0.030303	0.090909	0.130435	0.014493	TMOD3	15	15q21.2	49909181	49989139
RAB27A	0.009804	0.030303	0.121212	0.057971	0.014493	RAB27A	15	15q21.3	53283092	53349878
STXBP6	0.009804	0.090909	0.121212	0.014493	0.130435	STXBP6	14	14q12	24351144	24588936
HEATR5A	0.009804	0.121212	0	0.014493	0.043478	HEATR5A	14	14q12	30830745	30927933
C14orf126	0.009804	0.121212	0	0.014493	0.043478	C14orf126	14	14q12	30984994	30996432
NUBPL	0.009804	0.121212	0	0.014493	0.043478	NUBPL	14	14q12	31100342	31400181
NPAS3	0.009804	0.181818	0.090909	0.014493	0.101449	NPAS3	14	14q13.1	32478210	33343133
SSTR1	0.009804	0.090909	0.151515	0.014493	0.130435	SSTR1	14	14q21.1	37746955	37752020
MAP4K5	0.009804	0.181818	0	0.014493	0.028986	MAP4K5	14	14q22.1	49954993	50069127
ATL1	0.009804	0.181818	0	0.014493	0.028986	ATL1	14	14q22.1	50069550	50169535
FRMD6	0.009804	0.030303	0.090909	0	0.014493	FRMD6	14	14q22.1	51025605	51267195
DDHD1	0.009804	0.090909	0.030303	0.014493	0	DDHD1	14	14q22.2	52573210	52689797
PELI2	0.009804	0.030303	0.090909	0	0.014493	PELI2	14	14q22.3	55654846	55837785
DAAM1	0.009804	0.060606	0.151515	0.014493	0.014493	DAAM1	14	14q23.1	58725152	58906225
JKAMP	0.009804	0.060606	0.151515	0.028986	0.014493	JKAMP	14	14q23.1	59020914	59041835
C14orf38	0.009804	0.060606	0.151515	0.028986	0.014493	C14orf38	14	14q23.1	59041539	59113303
RHOJ	0.009804	0.121212	0.121212	0.101449	0.014493	RHOJ	14	14q23.2	62740898	62828313
GPHB5	0.009804	0.121212	0.121212	0.101449	0.014493	GPHB5	14	14q23.2	62849395	62854317
PPP2R5E	0.009804	0.151515	0.090909	0.101449	0.014493	PPP2R5E	14	14q23.2	62911108	63079833
SMOC1	0.009804	0.121212	0.242424	0.275362	0.014493	SMOC1	14	14q24.2	69415896	69568837
COX16	0.009804	0.121212	0.151515	0.231884	0.014493	COX16	14	14q24.2	69861552	69896198
HEATR4	0.009804	0.363636	0.121212	0.42029	0.014493	HEATR4	14	14q24.3	73014945	73095405
DNAL1	0.009804	0.363636	0.121212	0.434783	0.014493	DNAL1	14	14q24.3	73181331	73238403
PNMA1	0.009804	0.363636	0.121212	0.434783	0.014493	PNMA1	14	14q24.3	73248239	73250882
C14orf43	0.009804	0.363636	0.121212	0.434783	0.014493	C14orf43	14	14q24.3	73251578	73323650
PTGR2	0.009804	0.333333	0.121212	0.434783	0.014493	PTGR2	14	14q24.3	73388287	73421920
ZNF410	0.009804	0.333333	0.121212	0.434783	0.014493	ZNF410	14	14q24.3	73423339	73468557
LIN52	0.009804	0.333333	0.121212	0.376812	0.014493	LIN52	14	14q24.3	73621409	73736871
TTLL5	0.009804	0.272727	0.121212	0.304348	0.014493	TTLL5	14	14q24.3	75197374	75491176
STON2	0.009804	0.121212	0.121212	0.043478	0.014493	STON2	14	14q31.1	80806662	80934681
GJA3	0.009804	0.272727	0.121212	0.304348	0.014493	GJA3	13	13q12.11	19610395	19633184
GJB2	0.009804	0.272727	0.121212	0.304348	0.014493	GJB2	13	13q12.11	19659606	19665115
GJB6	0.009804	0.272727	0.121212	0.304348	0.014493	GJB6	13	13q12.11	19694101	19704535
CRYL1	0.009804	0.272727	0.121212	0.304348	0.014493	CRYL1	13	13q12.11	19875806	19998013
IFT88	0.009804	0.242424	0.121212	0.289855	0.014493	IFT88	13	13q12.11	20039208	20163577
IL17D	0.009804	0.272727	0.121212	0.289855	0.014493	IL17D	13	13q12.11	20175482	20195238
N6AMT2	0.009804	0.272727	0.121212	0.289855	0.014493	N6AMT2	13	13q12.11	20201073	20246058
LATS2	0.009804	0.212121	0.121212	0.246377	0.014493	LATS2	13	13q12.11	20445176	20533723
SAP18	0.009804	0.212121	0.121212	0.217391	0.014493	SAP18	13	13q12.11	20612653	20621224
SKA3	0.009804	0.212121	0.121212	0.217391	0.014493	SKA3	13	13q12.11	20625735	20648742
ZDHHC20	0.009804	0.181818	0.121212	0.173913	0.014493	ZDHHC20	13	13q12.11	20848508	20931424
NUPL1	0.009804	0.121212	0.181818	0.304348	0.014493	NUPL1	13	13q12.13	24773666	24814562
B3GALTL	0.009804	0.121212	0.090909	0.217391	0.014493	B3GALTL	13	13q12.3	30672112	30804412
TPP2	0.009804	0.090909	0.333333	0.014493	0.086957	TPP2	13	13q33.1	1.02E+08	1.02E+08
COL4A1	0.009804	0.272727	0.181818	0.347826	0.014493	COL4A1	13	13q34	1.1E+08	1.1E+08
COL4A2	0.009804	0.272727	0.181818	0.347826	0.014493	COL4A2	13	13q34	1.1E+08	1.1E+08

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
RAB20	0.009804	0.333333	0.181818	0.376812	0.014493	RAB20	13	13q34	1.1E+08	1.1E+08
CARKD	0.009804	0.333333	0.181818	0.405797	0.014493	CARKD	13	13q34	1.1E+08	1.1E+08
CARS2	0.009804	0.333333	0.181818	0.405797	0.014493	CARS2	13	13q34	1.1E+08	1.1E+08
C13orf29	0.009804	0.30303	0.181818	0.391304	0.014493	C13orf29	13	13q34	1.1E+08	1.1E+08
ARHGEF7	0.009804	0.333333	0.181818	0.453768	0.014493	ARHGEF7	13	13q34	1.11E+08	1.11E+08
LEMD3	0.009804	0.030303	0.121212	0.014493	0.014493	LEMD3	12	12q14.3	63849618	63928407
PTPRB	0.009804	0.090909	0.060606	0.014493	0.028986	PTPRB	12	12q15	69196899	69317487
ZFC3H1	0.009804	0.090909	0.121212	0.014493	0.144928	ZFC3H1	12	12q21.1	70289649	70344017
KCNC2	0.009804	0.121212	0.242424	0.014493	0.289855	KCNC2	12	12q21.1	73720163	73889779
CAPS2	0.009804	0.121212	0.242424	0.014493	0.246377	CAPS2	12	12q21.1	73956026	74010104
GLIPR1L2	0.009804	0.121212	0.242424	0.014493	0.246377	GLIPR1L2	12	12q21.1	74071156	74104088
NAP1L1	0.009804	0.151515	0.060606	0.014493	0.101449	NAP1L1	12	12q21.2	74724939	74765006
NAV3	0.009804	0.090909	0.212121	0.014493	0.318841	NAV3	12	12q21.2	76749200	77130922
SYT1	0.009804	0.090909	0.212121	0.014493	0.304348	SYT1	12	12q21.2	77781904	78369919
LiN7A	0.009804	0.090909	0.212121	0.014493	0.289855	LIN7A	12	12q21.31	79715302	79855826
MIR618	0.009804	0.090909	0.181818	0.014493	0.289855	MIR618	12	12q21.31	79853647	79853744
PPFIA2	0.009804	0.090909	0.242424	0.014493	0.318841	PPFIA2	12	12q21.31	80177487	80677241
RASSF9	0.009804	0.090909	0.181818	0.014493	0.333333	RASSF9	12	12q21.31	84722462	84754450
LUM	0.009804	0.121212	0.212121	0.014493	0.231884	LUM	12	12q21.33	90021363	90029674
BTG1	0.009804	0.121212	0.090909	0.014493	0.028986	BTG1	12	12q21.33	91058187	91063805
PLEKHG7	0.009804	0.121212	0.090909	0.014493	0.028986	PLEKHG7	12	12q22	91654396	91690000
PLXNC1	0.009804	0.151515	0.090909	0.115942	0.014493	PLXNC1	12	12q22	93066630	93223357
SRRM4	0.009804	0.121212	0.090909	0.42029	0.014493	SRRM4	12	12q24.23	1.18E+08	1.18E+08
OR52B4	0.009804	0.030303	0.090909	0.144928	0.014493	OR52B4	11	11p15.4	4345157	4346102
OR52K2	0.009804	0	0.090909	0.130435	0.014493	OR52K2	11	11p15.4	4427146	4428091
OR52N2	0.009804	0.060606	0.090909	0.072464	0.014493	OR52N2	11	11p15.4	5798142	5799108
OR2AG2	0.009804	0.030303	0.121212	0.057971	0.014493	OR2AG2	11	11p15.4	6745814	6746765
PDHX	0.009804	0.030303	0.151515	0.057971	0.014493	PDHX	11	11p13	34894253	34974251
SLC1A2	0.009804	0.090909	0.090909	0.043478	0.014493	SLC1A2	11	11p13	35229328	35397682
PAMR1	0.009804	0.030303	0.151515	0.028986	0.014493	PAMR1	11	11p13	35409952	35503753
FJX1	0.009804	0.030303	0.181818	0.028986	0.014493	FJX1	11	11p13	35596311	35598996
TRIM44	0.009804	0.030303	0.181818	0.028986	0.014493	TRIM44	11	11p13	35640929	35787507
TRAF6	0.009804	0.121212	0.090909	0.101449	0.014493	TRAF6	11	11p12	36467299	36488399
PRCP	0.009804	0.121212	0.090909	0.028986	0.014493	PRCP	11	11q14.1	82213057	82289206
C11orf82	0.009804	0.121212	0.090909	0.028986	0.014493	C11orf82	11	11q14.1	82290385	82323348
CCDC90B	0.009804	0.090909	0.151515	0.014493	0.057971	CCDC90B	11	11q14.1	82650150	82675026
C11orf75	0.009804	0.090909	0.121212	0.130435	0.014493	C11orf75	11	11q21	92851287	92916195
PANX1	0.009804	0.090909	0.151515	0.043478	0.014493	PANX1	11	11q21	93501742	93554786
GPR83	0.009804	0.121212	0.090909	0.043478	0.014493	GPR83	11	11q21	93750125	93774234
MAML2	0.009804	0.090909	0.121212	0.014493	0.086957	MAML2	11	11q21	95351088	95715993
DYNC2H1	0.009804	0.090909	0.151515	0.014493	0.188406	DYNC2H1	11	11q22.3	1.02E+08	1.03E+08
DDI1	0.009804	0.151515	0.151515	0.014493	0.144928	DDI1	11	11q22.3	1.03E+08	1.03E+08
ZW10	0.009804	0.212121	0.121212	0.275362	0.014493	ZW10	11	11q23.2	1.13E+08	1.13E+08
AMICA1	0.009804	0.242424	0.151515	0.449275	0.014493	AMICA1	11	11q23.3	1.18E+08	1.18E+08
CD3G	0.009804	0.333333	0.090909	0.478261	0.014493	CD3G	11	11q23.3	1.18E+08	1.18E+08
UBE4A	0.009804	0.333333	0.090909	0.478261	0.014493	UBE4A	11	11q23.3	1.18E+08	1.18E+08
DDX6	0.009804	0.393939	0.090909	0.492754	0.014493	DDX6	11	11q23.3	1.18E+08	1.18E+08
LOC100216001	0.009804	0.030303	0.090909	0.15942	0.014493	LOC100216001	10	10p15.1	4682378	4710263
LOC338588	0.009804	0.030303	0.090909	0.15942	0.014493	LOC338588	10	10p15.1	4688348	4694605
tAKR	0.009804	0	0.090909	0.188406	0.014493	tAKR	10	10p15.1	4903861	4948466
C10orf18	0.009804	0.151515	0.090909	0.304348	0.014493	C10orf18	10	10p15.1	5766807	5846950
GDI2	0.009804	0.242424	0.090909	0.318841	0.014493	GDI2	10	10p15.1	5847192	5895519
ARHGAP12	0.009804	0.090909	0.090909	0.086957	0.014493	ARHGAP12	10	10p11.22	32135231	32257777
LOC100129055	0.009804	0	0.151515	0.115942	0.014493	LOC100129055	10	10p11.21	38504605	38543279
HSD17B7P2	0.009804	0	0.151515	0.115942	0.014493	HSD17B7P2	10	10p11.21	38685314	38707440
TFAM	0.009804	0.090909	0.181818	0.014493	0.231884	TFAM	10	10q21.1	59815182	59825904
BICC1	0.009804	0.090909	0.242424	0.014493	0.231884	BICC1	10	10q21.1	59942910	60258852
PGM5	0.009804	0.060606	0.121212	0.057971	0.014493	PGM5	9	9q13	70161635	70335798
LOC440173	0.009804	0.121212	0.090909	0.318841	0.014493	LOC440173	9	9q21.33	88813187	88846862
SLC7A2	0.009804	0.090909	0.393939	0.014493	0.333333	SLC7A2	8	8p22	17398975	17472349
MTUS1	0.009804	0.090909	0.393939	0.014493	0.318841	MTUS1	8	8p22	17545584	17702707
FGL1	0.009804	0.121212	0.393939	0.014493	0.333333	FGL1	8	8p22	17766180	17797328
TMEM106B	0.009804	0.090909	0.151515	0.014493	0.173913	TMEM106B	7	7p21.3	12217373	12243415
MEOX2	0.009804	0.121212	0.030303	0.014493	0.231884	MEOX2	7	7p21.1	15617362	15692834
AGR3	0.009804	0.121212	0.030303	0.014493	0.101449	AGR3	7	7p21.1	16865555	16888139
SNX13	0.009804	0.121212	0.030303	0.014493	0.15942	SNX13	7	7p21.1	17796911	17946657
PRPS1L1	0.009804	0.090909	0.060606	0.014493	0.15942	PRPS1L1	7	7p21.1	18032925	18034012
HDAC9	0.009804	0.090909	0.121212	0.014493	0.173913	HDAC9	7	7p21.1	18501894	18674991
CHN2	0.009804	0.030303	0.090909	0.072464	0.014493	CHN2	7	7p15.1	29200646	29520470
POU6F2	0.009804	0.030303	0.121212	0.057971	0.014493	POU6F2	7	7p14.1	38984134	39470916
GLI3	0.009804	0.030303	0.151515	0.043478	0.014493	GLI3	7	7p14.1	41967075	42243144
CDK6	0.009804	0.151515	0.121212	0.014493	0.130435	CDK6	7	7q21.2	92072173	92303878
CALD1	0.009804	0.121212	0.090909	0.115942	0.014493	CALD1	7	7q33	1.34E+08	1.34E+08
LY86	0.009804	0.181818	0.121212	0.289855	0.014493	LY86	6	6p25.1	6533933	6600216
BMP6	0.009804	0.181818	0.090909	0.304348	0.014493	BMP6	6	6p24.3	7672010	7826961
RNF144B	0.009804	0.090909	0.151515	0.014493	0.043478	RNF144B	6	6p22.3	18495573	18576830

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
GPR116	0.009804	0	0.090909	0.072464	0.014493	GPR116	6	6p12.3	46928204	46997674
GPR110	0.009804	0	0.090909	0.072464	0.014493	GPR110	6	6p12.3	47075772	47118042
COL9A1	0.009804	0.090909	0.212121	0.014493	0.26087	COL9A1	6	6q13	70982464	71069508
SNX14	0.009804	0.121212	0.272727	0.014493	0.289855	SNX14	6	6q14.3	86271934	86360349
SYNCRIP	0.009804	0.121212	0.272727	0.014493	0.289855	SYNCRIP	6	6q14.3	86374222	86409360
ZNF292	0.009804	0.090909	0.242424	0.014493	0.217391	ZNF292	6	6q15	87921988	88030126
RSPH4A	0.009804	0.090909	0.333333	0.014493	0.26087	RSPH4A	6	6q22.1	1.17E+08	1.17E+08
SLC22A3	0.009804	0.151515	0.030303	0.014493	0.014493	SLC22A3	6	6q25.3	1.61E+08	1.61E+08
LPA	0.009804	0.030303	0.090909	0.014493	0.014493	LPA	6	6q25.3	1.61E+08	1.61E+08
DNAH5	0.009804	0.151515	0.030303	0.014493	0.014493	DNAH5	5	5p15.2	13743437	13997590
PRLR	0.009804	0.090909	0.060606	0.014493	0.072464	PRLR	5	5p13.2	35091559	35266552
ERBB2IP	0.009804	0.090909	0.151515	0.014493	0.130435	ERBB2IP	5	5q12.3	65258140	65412607
LOC100303749	0.009804	0.090909	0.151515	0.014493	0.130435	LOC100303749	5	5q12.3	65276391	65277158
ENC1	0.009804	0.090909	0.121212	0.014493	0.057971	ENC1	5	5q13.3	73958990	73973006
HEXB	0.009804	0.090909	0.121212	0.014493	0.057971	HEXB	5	5q13.3	74016725	74052870
ZNF608	0.009804	0.090909	0.090909	0.014493	0.130435	ZNF608	5	5q23.2	1.24E+08	1.24E+08
YIPF7	0.009804	0.090909	0.212121	0.014493	0.289855	YIPF7	4	4p13	44319111	44348416
ATP10D	0.009804	0.121212	0.121212	0.014493	0.188406	ATP10D	4	4p12	47182167	47290261
LRRC66	0.009804	0.060506	0.121212	0.028986	0.014493	LRRC66	4	4q12	52554623	52578544
SPATA18	0.009804	0.060606	0.151515	0.028986	0.014493	SPATA18	4	4q12	52612350	52658216
USP46	0.009804	0.090909	0.090909	0.072464	0.014493	USP46	4	4q12	53151886	53217517
ANKRD17	0.009804	0.181818	0.060606	0.014493	0.072464	ANKRD17	4	4q13.3	74159366	74343367
BTC	0.009804	0.121212	0.121212	0.014493	0.101449	BTC	4	4q13.3	75890472	75938907
PPEF2	0.009804	0.181818	0.030303	0.014493	0	PPEF2	4	4q21.1	77000050	77042706
NAAA	0.009804	0.181818	0.030303	0.014493	0	NAAA	4	4q21.1	77050832	77081191
SCARB2	0.009804	0.090909	0.030303	0.014493	0.014493	SCARB2	4	4q21.1	77298918	77354060
CCNI	0.009804	0.121212	0.030303	0.014493	0.014493	CCNI	4	4q21.1	78188199	78216150
MRPL1	0.009804	0.121212	0.090909	0.014493	0.043478	MRPL1	4	4q21.1	79002829	79092969
PTPN13	0.009804	0.121212	0.090909	0.057971	0.014493	PTPN13	4	4q21.3	87734492	87955353
UBE2D3	0.009804	0.090909	0.030303	0.014493	0.086957	UBE2D3	4	4q24	1.04E+08	1.04E+08
CISD2	0.009804	0.090909	0.030303	0.014493	0.086957	CISD2	4	4q24	1.04E+08	1.04E+08
NHEDC1	0.009804	0.090909	0.030303	0.014493	0.086957	NHEDC1	4	4q24	1.04E+08	1.04E+08
HADH	0.009804	0.090909	0.030303	0.014493	0.028986	HADH	4	4q25	1.09E+08	1.09E+08
LEF1	0.009804	0.090909	0.030303	0.014493	0.028986	LEF1	4	4q25	1.09E+08	1.09E+08
CCDC109B	0.009804	0.121212	0.030303	0.014493	0.014493	CCDC109B	4	4q25	1.11E+08	1.11E+08
CFI	0.009804	0.121212	0.030303	0.014493	0.014493	CFI	4	4q25	1.11E+08	1.11E+08
LOC285501	0.009804	0.090909	0.030303	0.014493	0.202899	LOC285501	4	4q34.3	1.79E+08	1.79E+08
ADAMTS9	0.009804	0	0.090909	0.101449	0.014493	ADAMTS9	3	3p14.1	64476371	64648406
ROBO2	0.009804	0.090909	0.212121	0.014493	0.333333	ROBO2	3	3p12.3	77171984	77779354
GABRR3	0.009804	0.090909	0.272727	0.014493	0.26087	GABRR3	3	3q11.2	99188217	99236522
GUCA1C	0.009804	0.090909	0.030303	0.014493	0.057971	GUCA1C	3	3q13.13	1.1E+08	1.1E+08
MORC1	0.009804	0.090909	0.030303	0.014493	0.057971	MORC1	3	3q13.13	1.1E+08	1.1E+08
TNIK	0.009804	0.060606	0.090909	0.072464	0.014493	TNIK	3	3q26.2	1.72E+08	1.73E+08
ETV5	0.009804	0.151515	0.090909	0.333333	0.014493	ETV5	3	3q27.2	1.87E+08	1.87E+08
HRG	0.009804	0.181818	0.090909	0.362319	0.014493	HRG	3	3q27.3	1.88E+08	1.88E+08
MASP1	0.009804	0.121212	0.090909	0.246377	0.014493	MASP1	3	3q27.3	1.88E+08	1.88E+08
SST	0.009804	0.090909	0.121212	0.246377	0.014493	SST	3	3q27.3	1.89E+08	1.89E+08
CRIM1	0.009804	0.060606	0.090909	0.086957	0.014493	CRIM1	2	2p22.2	36436901	36631783
TACR1	0.009804	0.090909	0.090909	0.144928	0.014493	TACR1	2	2p13.1	75127098	75280154
UNC50	0.009804	0.121212	0.090909	0.246377	0.014493	UNC50	2	2q11.2	98591474	98601410
MGAT4A	0.009804	0.121212	0.090909	0.246377	0.014493	MGAT4A	2	2q11.2	98602001	98714022
PLA2R1	0.009804	0.030303	0.090909	0.043478	0.014493	PLA2R1	2	2q24.2	1.61E+08	1.61E+08
STK39	0.009804	0.090909	0.060606	0.014493	0.043478	STK39	2	2q24.3	1.69E+08	1.69E+08
C2orf77	0.009804	0.151515	0.121212	0.086957	0.014493	C2orf77	2	2q31.1	1.7E+08	1.7E+08
PHOSPHO2	0.009804	0.151515	0.090909	0.086957	0.014493	PHOSPHO2	2	2q31.1	1.7E+08	1.7E+08
KLHL23	0.009804	0.151515	0.090909	0.086957	0.014493	KLHL23	2	2q31.1	1.7E+08	1.7E+08
SSB	0.009804	0.151515	0.090909	0.115942	0.014493	SSB	2	2q31.1	1.7E+08	1.7E+08
METTL5	0.009804	0.151515	0.090909	0.115942	0.014493	METTL5	2	2q31.1	1.7E+08	1.7E+08
UBR3	0.009804	0.151515	0.090909	0.115942	0.014493	UBR3	2	2q31.1	1.7E+08	1.71E+08
ZAK	0.009804	0.090909	0.090909	0.115942	0.014493	ZAK	2	2q31.1	1.74E+08	1.74E+08
COL5A2	0.009804	0.090909	0.121212	0.014493	0.130435	COL5A2	2	2q32.2	1.9E+08	1.9E+08
SLC40A1	0.009804	0.090909	0.090909	0.014493	0.130435	SLC40A1	2	2q32.2	1.9E+08	1.9E+08
ASNSD1	0.009804	0.121212	0.090909	0.014493	0.130435	ASNSD1	2	2q32.2	1.9E+08	1.9E+08
ANKAR	0.009804	0.090909	0.090909	0.014493	0.101449	ANKAR	2	2q32.2	1.9E+08	1.9E+08
OSGEPL1	0.009804	0.090909	0.090909	0.0144193	0.101449	OSGEPL1	2	2q32.2	1.9E+08	1.9E+08
ORMDL1	0.009804	0.090909	0.090909	0.014493	0.101449	ORMDL1	2	2q32.2	1.9E+08	1.9E+08
PMS1	0.009804	0.090909	0.090909	0.014493	0.101449	PMS1	2	2q32.2	1.9E+08	1.9E+08
STAT1	0.009804	0.090909	0.030303	0.014493	0.043478	STAT1	2	2q32.2	1.92E+08	1.92E+08
MYO1B	0.009804	0.090909	0.090909	0.014493	0.043478	MYO1B	2	2q32.3	1.92E+08	1.92E+08
TMEFF2	0.009804	0.090909	0.151515	0.014493	0.144928	TMEFF2	2	2q32.3	1.93E+08	1.93E+08
ANKRD44	0.009804	0.090909	0.060606	0.014493	0.028986	ANKRD44	2	2q33.1	1.98E+08	1.98E+08
MAP2	0.009804	0.090909	0.212121	0.014493	0.144928	MAP2	2	2q34	2.1E+08	2.1E+08
UNC80	0.009804	0.090909	0.181818	0.014493	0.15942	UNC80	2	2q34	2.1E+08	2.11E+08
ACADL	0.009804	0.090909	0.090909	0.014493	0.130435	ACADL	2	2q34	2.11E+08	2.11E+08
MYL1	0.009804	0.151515	0.090909	0.014493	0.130435	MYL1	2	2q34	2.11E+08	2.11E+08
LANCL1	0.009804	0.090909	0.181818	0.014493	0.130435	LANCL1	2	2q34	2.11E+08	2.11E+08

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
CPS1	0.009804	0.090909	0.212121	0.014493	0.217391	CPS1	2	2q34	2.11E+08	2.11E+08
ERBB4	0.009804	0.090909	0.212121	0.014493	0.246377	ERBB4	2	2q34	2.12E+08	2.13E+08
LOC728323	0.009804	0.363636	0.121212	0.608696	0.014493	LOC728323	2	2q37.3	2.43E+08	2.43E+08
PPAP2B	0.009804	0.090909	0.121212	0.217391	0.014493	PPAP2B	1	1p32.2	56733021	56817846
TACSTD2	0.009804	0.060606	0.181818	0.188406	0.014493	TACSTD2	1	1p32.1	58813683	58815755
NFIA	0.009804	0.060606	0.121212	0.115942	0.014493	NFIA	1	1p31.3	61315534	61701048
TM2D1	0.009804	0.121212	0.121212	0.173913	0.014493	TM2D1	1	1p31.3	61919307	61963684
INADL	0.009804	0.090909	0.121212	0.173913	0.014493	INADL	1	1p31.3	61980737	62402180
KANK4	0.009804	0.121212	0.121212	0.15942	0.014493	KANK4	1	1p31.3	62474425	62557672
USP1	0.009804	0.121212	0.121212	0.115942	0.014493	USP1	1	1p31.3	62674563	62690064
DOCK7	0.009804	0.121212	0.121212	0.115942	0.014493	DOCK7	1	1p31.3	62692985	62926558
ALG6	0.009804	0.060606	0.151515	0.115942	0.014493	ALG6	1	1p31.3	63605849	63676821
PGM1	0.009804	0.090909	0.121212	0.086957	0.014493	PGM1	1	1p31.3	63831535	63898506
ROR1	0.009804	0.090909	0.181818	0.086957	0.014493	ROR1	1	1p31.3	64012278	64381641
JAK1	0.009804	0.151515	0.090909	0.173913	0.014493	JAK1	1	1p31.3	65071494	65204776
MIR101-1	0.009804	0.121212	0.090909	0.130435	0.014493	MIR101-1	1	1p31.3	65296705	65296780
AK3L1	0.009804	0.121212	0.090909	0.130435	0.014493	AK3L1	1	1p31.3	65385820	65465764
LOC339524	0.009804	0.151515	0.151515	0.115942	0.014493	LOC339524	1	1p22.3	87368036	87407473
GTF2B	0.009804	0.151515	0.181818	0.115942	0.014493	GTF2B	1	1p22.2	89090909	89129890
CCBL2	0.009804	0.121212	0.181818	0.043478	0.014493	CCBL2	1	1p22.2	89174044	89231232
GBP7	0.009804	0.090909	0.151515	0.014493	0.057971	GBP7	1	1p22.2	89370022	89414312
GBP4	0.009804	0.090909	0.151515	0.014493	0.057971	GBP4	1	1p22.2	89419419	89437222
ZNF644	0.009804	0.090909	0.121212	0.072464	0.014493	ZNF644	1	1p22.2	91153445	91259619
HFM1	0.009804	0.030303	0.151515	0.057971	0.014493	HFM1	1	1p22.2	91498911	91643015
HSP90B3P	0.009804	0.121212	0.151515	0.072464	0.014493	HSP90B3P	1	1p22.2	91873156	91881923
TGFBR3	0.009804	0.060606	0.212121	0.057971	0.014493	TGFBR3	1	1p22.2	91918490	92124376
BRDT	0.009804	0.181818	0.121212	0.115942	0.014493	BRDT	1	1p22.1	92187516	92252574
EPHX4	0.009804	0.181818	0.121212	0.115942	0.014493	EPHX4	1	1p22.1	92268121	92301682
BTBD8	0.009804	0.181818	0.121212	0.115942	0.014493	BTBD8	1	1p22.1	92318450	92385984
KIAA1107	0.009804	0.181818	0.121212	0.115942	0.014493	KIAA1107	1	1p22.1	92405197	92422868
GFI1	0.009804	0.181818	0.121212	0.130435	0.014493	GFI1	1	1p22.1	92712906	92721945
RPL5	0.009804	0.121212	0.151515	0.101449	0.014493	RPL5	1	1p22.1	93070182	93080070
SNORD21	0.009804	0.121212	0.151515	0.101449	0.014493	SNORD21	1	1p22.1	93075434	93075529
FAM69A	0.009804	0.121212	0.121212	0.101449	0.014493	FAM69A	1	1p22.1	93080309	93199668
MTF2	0.009804	0.121212	0.121212	0.101449	0.014493	MTF2	1	1p22.1	93317380	93377225
DR1	0.009804	0.151515	0.181818	0.101449	0.014493	DR1	1	1p22.1	93584066	93600737
FNBP1L	0.009804	0.151515	0.151515	0.101449	0.014493	FNBP1L	1	1p22.1	93686427	93792807
BCAR3	0.009804	0.181818	0.151515	0.144928	0.014493	BCAR3	1	1p22.1	93799937	93919974
DNTTIP2	0.009804	0.181818	0.121212	0.15942	0.014493	DNTTIP2	1	1p22.1	94107924	94117331
GCLM	0.009804	0.181818	0.121212	0.15942	0.014493	GCLM	1	1p22.1	94125178	94147601
ABCA4	0.009804	0.181818	0.121212	0.173913	0.014493	ABCA4	1	1p22.1	94230982	94359294
TMEM56	0.009804	0.090909	0.151515	0.115942	0.014493	TMEM56	1	1p21.3	95355482	95435748
FAM102B	0.009804	0.030303	0.121212	0.086957	0.014493	FAM102B	1	1p13.3	1.09E+08	1.09E+08
C1orf59	0.009804	0.090909	0.090909	0.115942	0.014493	C1orf59	1	1p13.3	1.09E+08	1.09E+08
PRPF38B	0.009804	0.090909	0.090909	0.115942	0.014493	PRPF38B	1	1p13.3	1.09E+08	1.09E+08
FNDC7	0.009804	0.060606	0.090909	0.115942	0.014493	FNDC7	1	1p13.3	1.09E+08	1.09E+08
STXBP3	0.009804	0.060606	0.090909	0.115942	0.014493	STXBP3	1	1p13.3	1.09E+08	1.09E+08
AKNAD1	0.009804	0.060606	0.090909	0.130435	0.014493	AKNAD1	1	1p13.3	1.09E+08	1.09E+08
GPSM2	0.009804	0.090909	0.090909	0.173913	0.014493	GPSM2	1	1p13.3	1.09E+08	1.09E+08
CLCC1	0.009804	0.090909	0.090909	0.173913	0.014493	CLCC1	1	1p13.3	1.09E+08	1.09E+08
WDR47	0.009804	0.090909	0.090909	0.188406	0.014493	WDR47	1	1p13.3	1.09E+08	1.09E+08
MYBPHL	0.009804	0.151515	0.090909	0.202899	0.014493	MYBPHL	1	1p13.3	1.1E+08	1.1E+08
SORT1	0.009804	0.121212	0.090909	0.202899	0.014493	SORT1	1	1p13.3	1.1E+08	1.1E+08
ATXN7L2	0.009804	0.121212	0.090909	0.231884	0.014493	ATXN7L2	1	1p13.3	1.1E+08	1.1E+08
CYB561D1	0.009804	0.121212	0.090909	0.231884	0.014493	CYB561D1	1	1p13.3	1.1E+08	1.1E+08
AMIGO1	0.009804	0.121212	0.090909	0.231884	0.014493	AMIGO1	1	1p13.3	1.1E+08	1.1E+08
CD53	0.009804	0	0.090909	0.144928	0.014493	CD53	1	1p13.3	1.11E+08	1.11E+08
C1orf103	0.009804	0	0.121212	0.15942	0.014493	C1orf103	1	1p13.3	1.11E+08	1.11E+08
FAM46C	0.009804	0.121212	0.090909	0.173913	0.014493	FAM46C	1	1p12	1.18E+08	1.18E+08
WARS2	0.009804	0.090909	0.090909	0.072464	0.014493	WARS2	1	1p12	1.19E+08	1.19E+08
HAO2	0.009804	0	0.121212	0.057971	0.014493	HAO2	1	1p12	1.2E+08	1.2E+08
HSD3B2	0.009804	0	0.121212	0.057971	0.014493	HSD3B2	1	1p12	1.2E+08	1.2E+08
HSD3B1	0.009804	0.060606	0.121212	0.072464	0.014493	HSD3B1	1	1p12	1.2E+08	1.2E+08
ZNF697	0.009804	0.030303	0.121212	0.057971	0.014493	ZNF697	1	1p12	1.2E+08	1.2E+08
CHD1L	0.009804	0.060606	0.121212	0.188406	0.014493	CHD1L	1	1q21.1	1.45E+08	1.45E+08
NOS1AP	0.009804	0.030303	0.121212	0.086957	0.014493	NOS1AP	1	1q23.3	1.6E+08	1.61E+08
C1orf156	0.009804	0.090909	0.060606	0.014493	0.086957	C1orf156	1	1q24.2	1.68E+08	1.68E+08
C1orf112	0.009804	0.090909	0.060606	0.014493	0.086957	C1orf112	1	1q24.2	1.68E+08	1.68E+08
RGL1	0.009804	0.090909	0.030303	0.014493	0.043478	RGL1	1	1q25.3	1.82E+08	1.82E+08
APOBEC4	0.009804	0.090909	0.030303	0.014493	0.043478	APOBEC4	1	1q25.3	1.82E+08	1.82E+08
C1orf21	0.009804	0.121212	0.030303	0.014493	0.057971	C1orf21	1	1q25.3	1.83E+08	1.83E+08
TPR	0.009804	0.090909	0.060606	0.014493	0.115942	TPR	1	1q31.1	1.85E+08	1.85E+08
C1orf27	0.009804	0.090909	0.060606	0.014493	0.115942	C1or127	1	1q31.1	1.85E+08	1.85E+08
PDC	0.009804	0.090909	0.060606	0.014493	0.115942	PDC	1	1q31.1	1.85E+08	1.85E+08
CRB1	0.009804	0.121212	0.151515	0.014493	0.275362	CRB1	1	1q31.3	1.96E+08	1.96E+08
C4BPB	0.009804	0.181818	0.090909	0.362319	0.014493	C4BPB	1	1q32.2	2.05E+08	2.05E+08

TABLE 3-continued

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Transcript. start	Transcript. end
DUSP10	0.009804	0.060606	0.181818	0.057971	0.014493	DUSP10	1	1q41	2.2E+08	2.2E+08
NVL	0.009804	0.181818	0.090909	0.304348	0.014493	NVL	1	1q42.11	2.22E+08	2.23E+08
H3F3A	0.009804	0.30303	0.090909	0.405797	0.014493	H3F3A	1	1q42.12	2.24E+08	2.24E+08
LOC440926	0.009804	0.30303	0.090909	0.405797	0.014493	LOC440926	1	1q42.12	2.24E+08	2.24E+08
GGPS1	0.009804	0.242424	0.090909	0.289855	0.014493	GGPS1	1	1q42.3	2.34E+08	2.34E+08
TBCE	0.009804	0.242424	0.090909	0.289855	0.014493	TBCE	1	1q42.3	2.34E+08	2.34E+08
ACTN2	0.009804	0.242424	0.090909	0.130435	0.014493	ACTN2	1	1q43	2.35E+08	2.35E+08
MTR	0.009804	0.242424	0.090909	0.15942	0.014493	MTR	1	1q43	2.35E+08	2.35E+08
RYR2	0.009804	0.121212	0.090909	0.115942	0.014493	RYR2	1	1q43	2.35E+08	2.36E+08
LOC100130331	0.009804	0.060606	0.090909	0.014493	0.014493	LOC100130331	1	1q43	2.36E+08	2.36E+08
ZP4	0.009804	0.060606	0.090909	0.014493	0.014493	ZP4	1	1q43	2.36E+08	2.36E+08

TABLE 4

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
RNF160	1	0.142857	0.047619	0	0.037037	RNF160	21	21q21.3	29222337	29287149
BTBD3	1	0	0.142857	0	0	BTBD3	20	20p12.2	11819477	11855244
SPTLC3	1	0	0.142857	0	0	SPTLC3	20	20p12.1	12937627	13095412
ISM1	1	0	0.142857	0	0	ISM1	20	20p12.1	13150418	13229298
TASP1	1	0	0.142857	0	0	TASP1	20	20p12.1	13318036	13567584
MACROD2	1	0	0.142857	0	0	MACROD2	20	20p12.1	13924146	15981842
PSGl	1	0.333333	0.142857	0.481481	0	PSGl	19	19q13.31	48063198	48075712
ST8SIA3	1	0.238095	0	0	0	ST8SIA3	18	18q21.31	53170719	53187160
ONECUT2	1	0.238095	0	0	0	ONECUT2	18	18q21.31	53253915	53309529
TNFRSF11A	1	0.190476	0	0	0	TNFRSF11A	18	18q21.33	58143528	58204485
ZCCHC2	1	0.238095	0	0	0	ZCCHC2	18	18q21.33	58341638	58396799
ZNF407	1	0.190476	0	0	0	ZNF407	18	18q22.3	70471907	70762000
TSHZ1	1	0.190476	0	0	0	TSHZ1	18	18q22.3	71051719	71130890
RBL2	1	0.190476	0	0	0.037037	R8L2	16	16q12.2	52025852	52083062
CDH11	1	0.142857	0.095238	0	0.037037	CDH11	16	16q21	63538184	63713421
LOC283867	1	0.142857	0.047619	0	0	LOC283867	16	16q21	63875903	64167705
MAGEL2	1	0.142857	0	0	0	MAGEL2	15	15q11.2	21439791	21444087
NDN	1	0.142857	0	0	0	NDN	15	15q11.2	21481647	21483544
MIR548A3	1	0.047619	0.190476	0	0	MIR548A3	15	15q21.1	44584617	45037888
NEDD4	1	0.142857	0	0	0	NEDD4	15	15q21.3	53906414	54073128
CGNL1	1	0.190476	0	0	0	CGNL1	15	15q21.3	55455997	55630214
OR11G2	1	0.238095	0	0	0.074074	OR11G2	14	14q11.2	19735335	19736373
OR11H4	1	0.238095	0	0	0.074074	OR11H4	14	14q11.2	19780791	19781766
AP4S1	1	0.238095	0	0	0	AP451	14	14q12	30564434	30632390
HECTD1	1	0.238095	0	0	0	HECTD1	14	14q12	30639075	30746441
SSTR1	1	0	0.142857	0	0	SSTR1	14	14q21.1	37746955	37752020
PPIL5	1	0.142857	0	0	0	PPIL5	14	14q22.1	49135165	49151141
RPL36AL	1	0.142857	0	0	0	RPL36AL	14	14q22.1	49155157	49157100
MGAT2	1	0.142857	0	0	0	MGAT2	14	14q22.1	49157239	49159950
C14orf104	1	0.142857	0	0	0	C14orf104	14	14q22.1	49161642	49171699
POLE2	1	0.142857	0	0	0	POLE2	14	14q22.1	49180029	49224686
KLHDC1	1	0.142857	0	0	0	KLHDC1	14	14q22.1	49229635	49289615
ARF6	1	0.142857	0	0	0	ARF6	14	14q22.1	49429486	49433523
C14orf182	1	0.142857	0	0	0	C14orf182	14	14q22.1	49518180	49543989
CGRRF1	1	0.142857	0	0	0	CGRRF1	14	14q22.2	54046337	54075085
SAMD4A	1	0.142857	0	0	0	SAMD4A	14	14q22.2	54104387	54329784
TMEM30B	1	0.142857	0	0	0	TMEM30B	14	14q23.1	60813842	60818284
PRKCH	1	0.142857	0	0	0	PRKCH	14	14q23.1	60858268	61087452
ZDHHC20	1	0.142857	0	0	0	ZDHHC20	13	13q12.11	20848508	20931424
EFHA1	1	0.142857	0	0	0	EFHA1	13	13q12.11	20964839	21076308
FGF9	1	0.142857	0	0	0	FGF9	13	13q12.11	21143215	21176641
FAM48A	1	0	0.190476	0	0	FAM48A	13	13q13.3	36481451	36531851
FREM2	1	0	0.142857	0	0	FREM2	13	13q13.3	38159173	38359268
C13orf23	1	0	0.142857	0	0	C13orf23	13	13q13.3	38482002	38510253
DHRS12	1	0.142857	0	0	0	DHRS12	13	13q14.3	51240132	51276295
FU37307	1	0.142857	0	0	0	FU37307	13	13q14.3	51285484	51317288
ATP7B	1	0.142857	0	0	0	ATP7B	13	13q14.3	51404806	51483632
ALG11	1	0.142857	0	0	0	ALG11	13	13q14.3	51484551	51501782
UTP14C	1	0.142857	0	0	0	UTP14C	13	13q14.3	51496828	51505736
NEKS	1	0.142857	0	0	0	NEKS	13	13q14.3	51536901	51601216
NEK3	1	0.142857	0	0	0	NEK3	13	13q14.3	51604780	51631998
THSD1	1	0.142857	0	0	0	THSD1	13	13q14.3	51849305	51878631
LOC647288	1	0	0.142857	0	0	LOC647288	13	13q22.2	74709890	74712519

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
ABCC4	1	0.190476	0	0	0	ABCC4	13	13q32.1	94470084	94751689
DZIP1	1	0.380952	0	0	0	DZIP1	13	13q32.1	95028457	95094959
DNAJC3	1	0.190476	0	0	0	DNAJC3	13	13q32.1	95127403	95245243
TM9SF2	1	0.190476	0	0	0	TM9SF2	13	13q32.3	98951729	99013278
PCCA	1	0.190476	0	0	0	PCCA	13	13q32.3	99539338	99980690
ITGBL1	1	0	0.142857	0	0	ITGBL1	13	13q33.1	1.01E+08	1.01E+08
FGF14	1	0	0.142857	0	0	FGF14	13	13q33.1	1.01E+08	1.01E+08
IRS2	1	0.190476	0	0	0	IRS2	13	13q34	1.09E+08	1.09E+08
KLRC1	1	0	0.142857	0.037037	0	KLRC1	12	12p13.2	10489904	10497247
PRR4	1	0	0.142857	0.037037	0	PRR4	12	12p13.2	10889715	11215481
PRH1	1	0	0.142857	0.037037	0	PRH1	12	12p13.2	10924827	11215478
TAS2R30	1	0	0.142857	0.037037	0	TAS2R30	12	12p13.2	11177151	11178111
PRB3	1	0	0.142857	0.037037	0	PRB3	12	12p13.2	11310124	11313909
FAR2	1	0	0.142857	0	0	FAR2	12	12p11.22	29267865	29378274
OVCH1	1	0	0.142857	0	0	OVCH1	12	12p11.22	29471756	29541887
PRICKLE1	1	0.142857	0	0	0	PRICKLE1	12	12q12	41138408	41269840
NEUROD4	1	0.047619	0.190476	0.259259	0	NEUROD4	12	12q13.2	53699996	53710069
CDK17	1	0.142857	0	0	0	CDK17	12	12q23.1	95196173	95318437
ANKS1B	1	0.190476	0	0	0	ANKS1B	12	12q23.1	97653202	98072604
UBQLN3	1	0	0.142857	0	0	UBQLN3	11	11P15.4	5485106	5487730
UBQLNL	1	0	0.142857	0	0	UBQLNL	11	11p15.4	5492199	5494533
TRIM6	1	0.142857	0	0	0	TRIM6	11	11p15.4	5573923	5590765
TRIM6-T1m34	1	0.142857	0	0	0	TRIM6-T1M34	11	11p15.4	5574460	5622200
TRIM34	1	0.142857	0	0	0	TRIM34	11	11p15.4	5597750	5622202
SERGEF	1	0.142857	0	0	0	SERGEF	11	11p15.1	17766172	17991214
TPH1	1	0.142857	0	0	0	TPH1	11	11p15.1	17998660	18018912
MRGPRX3	1	0.142857	0	0	0	MRGPRX3	11	11p15.1	18099078	18116602
MRGPRX4	1	0.142857	0	0	0	MRGPRX4	11	11p15.1	18150960	18152404
ELP4	1	0.190476	0.047619	0	0.037037	ELP4	11	11p13	31487873	31761906
PAX6	1	0.190476	0.047619	0	0.037037	PAX6	11	11p13	31762916	31789456
LOC441601	1	0	0.238095	0.037037	0	LOC441601	11	11p11.12	50195575	50214200
PRCP	1	0.142857	0	0	0.074074	PRCP	11	11q14.1	82213057	82289206
C11orf82	1	0.142857	0	0	0.074074	C11orf82	11	11q14.1	82290385	82323348
RAB30	1	0.142857	0	0	0.037037	RAB30	11	11q14.1	82370126	82460533
CCDC82	1	0	0.142857	0	0	CCDC82	11	11q21	95725577	95762732
JRKL	1	0	0.142857	0	0	JRKL	11	11q21	95762806	95766376
LOC254312	1	0.190476	0	0	0	LOC254312	10	10p14	11016910	11034133
CUGBP2	1	0.190476	0	0	0	CUGBP2	10	10p14	11087265	11418679
PTER	1	0.142857	0	0	0	PTER	10	10p13	16518973	16595743
MLLT10	1	0.142857	0	0	0	MLLT10	10	10p12.31	21863108	22072561
DNAJC1	1	0.142857	0	0	0	DNAJC1	10	10p12.31	22085483	22332657
PRINS	1	0.142857	0	0	0	PRINS	10	10p12.1	24576060	24584982
MIR603	1	0.142857	0	0	0	MIR603	10	10p12.1	24604620	24604717
ARHGAP21	1	0.142857	0	0	0	ARHGAP21	10	10p12.1	24912544	25052604
PRTFDC1	1	0.142857	0	0	0	PRTFDC1	10	10p12.1	25177560	25281540
GPR158	1	0	0.190476	0	0	GPR158	10	10p12.1	25504296	25931164
ZEB1	1	0	0.142857	0.037037	0	ZEB1	10	10p11.22	31647430	31858134
FAM13C	1	0	0.142857	0	0	FAM13C	10	10q21.1	60675896	60792359
RNLS	1	0	0.142857	0	0	RNLS	10	10q23.31	90023601	90333063
UPN	1	0	0.142857	0	0	UPN	10	10q23.31	90511143	90527980
KDM4C	1	0.238095	0	0	0	KDM4C	9	9p24.1	6710863	7067265
PGM5	1	0.142857	0.047619	0	0	PGM5	9	9q13	70161635	70335798
C9orf71	1	0.142857	0	0	0	C9orf71	9	9q13	70341318	70345604
PIP5K1B	1	0.142857	0	0	0	P5P5K1B	9	9q21.11	70510436	70813912
FAM108B1	1	0.142857	0	0	0	FAM108B1	9	9q21.13	73667188	73715969
PAPPA	1	0.047619	0.142857	0	0	PAPPA	9	9q33.1	1.18E+08	1.18E+08
ZDHHC2	1	0.142857	0	0	0	ZDHHC2	8	8p22	17058207	17124612
CSGALNAC	1	0.142857	0	0	0	CSGALNAC	8	8p21.3	19305952	19504337
INTS10	1	0.142857	0	0	0	INTS10	8	8p21.3	19719198	19753867
LPL	1	0.142857	0	0	0	LPL	8	8p21.3	19840862	19869051
FUT10	1	0.190476	0.047619	0	0.037037	FUT10	8	8p12	33347886	33450207
FAM150A	1	0.142857	0	0	0	FAM150A	8	8q11.23	53609151	53640575
OPRK1	1	0.142857	0	0	0	OPRK1	8	8q11.23	54300829	54326748
ATP6V1H	1	0.142857	0	0	0	ATP6V1H	8	8q11.23	54790668	54918404
RGS20	1	0.142857	0	0	0	RGS20	8	8q11.23	54926921	55034415
TGS1	1	0.142857	0	0	0	TGS1	8	8q12.1	56848345	56900560
LYN	1	0.142857	0	0	0	LYN	8	8q12.1	56954940	57086495
RPS20	1	0.142857	0	0	0	RPS20	8	8q12.1	57143293	57149695
SNORD54	1	0.142857	0	0	0	SNORD54	8	8q12.1	57148952	57149015
MOS	1	0.142857	0	0	0	MOS	8	8q12.1	57188055	57189096
PLAG1	1	0.142857	0	0	0	PLAG1	8	8q12.1	57236022	57286414
CHCHD7	1	0.142857	0	0	0	CHCHD7	8	8q12.1	57286869	57293731
CSPP1	1	0.190476	0	0	0	CSPP1	8	8q13.2	68139157	68271051
ARFGEF1	1	0.142857	0	0	0	ARFGEF1	8	8q13.2	68272451	68418467

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
CPA6	1	0.142857	0	0	0	CPA6	8	8q13.2	68496959	68821175
TERF1	1	0.142857	0.047619	0	0	TERF1	8	8q21.11	74083651	74122542
MRPS28	1	0.142857	0.047619	0	0.111111	MRPS28	8	8q21.13	80993650	81105062
TPD52	1	0.142857	0.047619	0	0.111111	TPD52	8	8q21.13	81109660	81155566
ZNF704	1	0.190476	0	0	0.111111	ZNF704	8	8q21.13	81713324	81949572
PAG1	1	0.142857	0	0	0.111111	PAG1	8	8q21.13	82042601	82186859
PDP1	1	0.190476	0	0	0	PDP1	8	8q22.1	94998259	95007471
PTDSS1	1	0.190476	0	0	0	PTDSS1	8	8q22.1	97343343	97415951
SDC2	1	0.190476	0	0	0	SDC2	8	8q22.1	97575058	97693214
PGCP	1	0.142857	0.047619	0	0	PGCP	8	8q22.1	97726675	98224899
LAPTM4B	1	0.190476	0	0	0	LAPTM4B	8	8q22.1	98856985	98934007
MATN2	1	0.190476	0	0	0	MATN2	8	8q22.1	98950487	99118123
C8orf47	1	0.190476	0	0	0	C8orf47	8	8q22.2	99145926	99175015
NIPAL2	1	0.142857	0.047619	0	0	NIPAL2	8	8q22.2	99273563	99375798
STK3	1	0.142857	0.047619	0	0	STK3	8	8q22.2	99536037	99907086
VPS13B	1	0.142857	0.047619	0	0	VPS13B	8	8q22.2	1E+08	1E+08
HAS2	1	0.142857	0	0	0	HAS2	8	3q24.13	1.23E+08	1.23E+08
ZHX2	1	0.285714	0	0	0	ZHX2	8	8q24.13	1.24E+08	1.24E+08
DERL1	1	0.285714	0	0	0	DERL1	8	8q24.13	1.24E+08	1.24E+08
WDR67	1	0.285714	0	0	0	WDR67	8	8q24.13	1.24E+08	1.24E+08
ASAP1	1	0.142857	0	0	0	ASAP1	8	8q24.21	1.31E+08	1.31E+08
ADCY8	1	0.142857	0	0	0	ADCY8	8	8q24.22	1.32E+08	1.32E+08
ZFAT	1	0.190476	0	0	0	ZFAT	8	8q24.22	1.36E+08	1.36E+08
ZFATAS	1	0.190476	0	0	0	ZFATAS	8	8q24.22	1.36E+08	1.36E+08
KHDRBS3	1	0.142857	0	0	0	KHDRBS3	8	8q24.23	1.37E+08	1.37E+08
FAM135B	1	0.142857	0.047619	0	0	FAM135B	8	8q24.23	1.39E+08	1.4E+08
COL22A1	1	0.333333	0	0	0	COL22A1	8	8q24.23	1.4E+08	1.4E+08
GPNMB	1	0.142857	0	0	0	GPNMB	7	7p15.3	23252841	23281255
RPS2P32	1	0.190476	0	0	0	RPS2P32	7	7p153	23496532	23497555
C7orf46	1	0.190476	0	0	0	C7orf46	7	7p15.3	23686274	23708795
HOXA3	1	0.190476	0	0	0	HOXA3	7	7p15.2	27112334	27125740
HOXA4	1	0.190476	0	0	0	HOXA4	7	7p15.2	27134651	27136925
EVX1	1	0.190476	0	0	0	EVX1	7	7p15.2	27248689	27252718
HIBADH	1	0.190476	0	0	0	HIBADH	7	7p15.2	27531586	27669128
C7orf25	1	0.190476	0	0	0	C7orf25	7	7p14.1	42915397	42918215
PSMA2	1	0.190476	0	0	0	PSMA2	7	7p14.1	42922987	42938331
HECW1	1	0.190476	0	0	0	HECW1	7	7p14.1	43118723	43569464
C7orf44	1	0.190476	0	0	0	C7orf44	7	7p13	43645384	43735609
BLVRA	1	0.190476	0	0	0	BLVRA	7	7p13	43754797	43813467
PEX1	1	0.190476	0	0	0	PEX1	7	7q21.2	91954273	91995782
C7orf64	1	0.190476	0	0	0	C7orf64	7	7q21.2	91996023	92004760
MGC16142	1	0.190476	0	0	0	MGC16142	7	7q21.2	92005725	92007014
FAM133B	1	0.190476	0	0	0	FAM133B	7	7q21.2	92028008	92057643
SLC26A5	1	0.142857	0	0	0	SLC26A5	7	7q22.1	1.03E+08	1.03E+08
RELN	1	0.142857	0	0	0	RELN	7	7q22.1	1.03E+08	1.03E+08
ORC5L	1	0.142857	0	0	0	ORC5L	7	7q22.1	1.04E+08	1.046E+08
LHFPL3	1	0.142857	0	0	0	LHFPL3	7	7q22.1	1.04E+08	1.04E+08
STRA8	1	0.142857	0	0	0	STRA8	7	7q33	1.35E+08	1.35E+08
CNOT4	1	0.142857	0	0	0	CNOT4	7	7q33	1.35E+08	1.35E+08
MRPS33	1	0.142857	0	0	0	MRPS33	7	7q34	1.4E+08	1.4E+08
HIVEP1	1	0.142857	0	0	0	HIVEP1	6	6p24.1	12120710	12273219
MRS2	1	0.142857	0	0	0	MRS2	6	6p22.2	24511132	24533796
GPLD1	1	0.142857	0	0	0	GPLD1	6	6p22.2	24536384	24597830
ALDH5A1	1	0.142857	0	0	0	ALDH5A1	6	6p22.2	24603176	24645415
SUPT3H	1	0	0.190476	0.074074	0	SUPT3H	6	6p21.1	44904448	45453649
AHI1	1	0	0.142857	0	0	AHI1	6	6q23.3	1.36E+08	1.36E+08
C6orf217	1	0	0.142857	0	0	C6orf217	6	6q23.3	1.36E+08	1.36E+08
PDE7B	1	0	0.142857	0	0	PDE7B	6	6q23.3	1.36E+08	1.37E+08
UTRN	1	0.142857	0	0	0	UTRN	6	6q24.2	1.45E+08	1.45E+08
GRM1	1	0	0.142857	0	0	GRM1	6	6q24.3	1.46E+08	1.47E+08
OPRM1	1	0	0.190476	0	0	OPRM1	6	6q25.2	1.54E+08	1.54E+08
CNKSR3	1	0.190476	0	0	0	CNKSR3	6	6q25.2	1.55E+08	1.55E+08
RBM16	1	0.190476	0	0	0	RBM16	6	6q25.2	1.55E+08	1.55E+08
TIAM2	1	0.190476	0	0	0	TIAM2	6	6q25.2	1.55E+08	1.56E+08
TFB1M	1	0.190476	0	0	0	TFB1M	6	6q25.3	1.56E+08	1.56E+08
CLDN20	1	0.190476	0	0	0	CLDN20	6	6q25.3	1.56E+08	1.56E+08
ARID1B	1	0.190476	0	0	0	ARID1B	6	6q25.3	1.57E+08	1.58E+08
ZDHHC14	1	0.190476	0	0	0	ZDHHC14	6	6q25.3	1.58E+08	1.58E+08
SLC22A2	1	0.142857	0	0	0	SLC22A2	6	6q25.3	1.61E+08	1.61E+08
PLG	1	0.142857	0	0	0	PLG	6	6q26	1.61E+08	1.61E+08
BASP1	1	0.142857	0	0	0.037037	BASP1	5	5p15.1	17270750	17329944
C5orf22	1	0.190476	0	0	0	C5orf22	5	5p13.3	31568130	31590923
ZFR	1	0.190476	0	0	0	ZFR	5	5p13.3	32390213	32480602
CSorf42	1	0.142857	0	0	0	CSorf42	5	5p13.2	37142087	37285288

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
WDR70	1	0.190476	0	0	0	WDR70	5	5p13.2	37415169	37788532
F2RL2	1	0	0.142857	0.037037	0	F2RL2	5	5q13.3	75947063	75954997
TRIM36	1	0.047619	0.142857	0	0	TRIM36	5	5q22.3	1.14E+08	1.15E+08
DMXL1	1	0.190476	0.047619	0	0	DMXL1	5	5q23.1	1.18E+08	1.19E+08
SGCD	1	0	0.190476	0	0	SGCD	5	5q33.3	1.56E+08	1.56E+08
HTRA3	1	0.47619	0.142857	0.703704	0	HTRA3	4	4p16.1	8322392	8359735
NCAPG	1	0	0.238095	0	0	NCAPG	4	4p15.32	17421623	17455586
LCORL	1	0	0.238095	0	0	LCORL	4	4p15.32	17453938	17532582
TLR1	1	0.190476	0	0	0	TLR1	4	4p14	38474271	38482808
TLR6	1	0.190476	0	0	0	TLR6	4	4p14	38501728	38534833
FAM114A1	1	0.190476	0	0	0	FAM114A1	4	4p14	38545832	38621822
MIR574	1	0.190476	0	0	0	MIR574	4	4p14	38546048	38546144
TMEM156	1	0.190476	0	0	0	TMEM156	4	4p14	38644836	38710437
KLHLS	1	0.190476	0	0	0	KLHLS	4	4p14	38723054	38800225
WDR19	1	0.190476	0	0	0	WDR19	4	4p14	38860419	38963826
RFC1	1	0.190476	0	0	0	RFC1	4	4p14	38965471	39044391
KLB	1	0.238095	0	0	0	KLB	4	4p14	39084868	39129547
RPL9	1	0.238095	0	0	0	RPL9	4	4p14	39132140	39136964
LIAS	1	0.238095	0	0	0	LIAS	4	4p14	39137060	39155667
LOC401127	1	0.238095	0	0	0	LOC401127	4	4p14	39158270	39159917
UGDH	1	0.238095	0	0	0	UGDH	4	4p14	39176770	39205607
C4orf34	1	0.238095	0	0	0	C4orf34	4	4p14	39228941	39316877
EPGN	1	0	0.142857	0	0	EPGN	4	4q13.3	75393068	75398172
AREG	1	0	0.142857	0	0	AREG	4	4q13.3	75699653	75709510
BTC	1	0	0.142857	0	0	BTC	4	4q13.3	75890472	75938907
BMP3	1	0	0.142857	0	0	BMP3	4	4q21.21	82171143	82197710
PRKG2	1	0	0.142857	0	0	PRKG2	4	4q21.21	82228861	82345240
RASGEF1B	1	0	0.142857	0	0	RASGEF1B	4	4q21.21	82567243	82612086
TBC1D9	1	0	0.142857	0	0	TBC1D9	4	4q31.21	1.42E+08	1.42E+08
RNF150	1	0	0.142857	0	0	RNF150	4	4q31.21	1.42E+08	1.42E+08
IL15	1	0	0.142857	0	0	IL15	4	4q31.21	1.43E+08	1.43E+08
INPP4B	1	0	0.142857	0	0	INPP4B	4	4q31.21	1.43E+08	1.44E+08
RPS3A	1	0.142857	0	0	0	RPS3A	4	4q31.3	1.52E+08	1.52E+08
SNORD73A	1	0.142857	0	0	0	SNORD73A	4	4q31.3	1.52E+08	1.52E+08
SH3D19	1	0.142857	0	0	0	SH3D19	4	4q31.3	1.52E+08	1.52E+08
SUMF1	1	0	0.142857	0	0	SUMF1	3	3p25.2	4377829	4483967
EGOT	1	0.190476	0	0	0	EGOT	3	3p26.2	4765878	4768275
BHLHE40	1	0.333333	0	0	0	BHLHE40	3	3p26.2	4996097	5001864
TPRXL	1	0.190476	0.142857	0.259259	0	TPRXL	3	3p25.1	13953808	14082481
TBC1D5	1	0	0.142857	0	0	TBC1D5	3	3p24.3	17173659	17759245
RAB5A	1	0.142857	0.095238	0	0.037037	RAB5A	3	3p24.3	19963576	20001663
C3orf48	1	0.142857	0.095238	0	0.037037	C3orf48	3	3p24.3	19996458	20028770
KAT2B	1	0.142857	0.095238	0	0.037037	KAT2B	3	3p24.3	20056528	20170901
NGLY1	1	0.047619	0.142857	0	0	NGLY1	3	3p24.2	25735440	25799994
OSBPL10	1	0.190476	0.095238	0	0.037037	OSBPL10	3	3p23	31677321	31998243
MITF	1	0	0.142857	0	0	MITF	3	3p14.1	69871323	70100178
MIR1284	1	0.142857	0.047619	0	0	MIR1284	3	3p14.1	71673811	71673931
CEP97	1	0.142857	0.047619	0	0.074074	CEP97	3	3q12.3	1.03E+08	1.03E+08
FAM55C	1	0.142857	0.047619	0	0.074074	FAM55C	3	3q12.3	1.03E+08	1.03E+08
LOC151658	1	0	0.142857	0	0	LOC151658	3	3q13.12	1.09E+08	1.09E+08
LOC285205	1	0	0.142857	0	0	LOC285205	3	3q13.12	1.09E+08	1.09E+08
HHLA2	1	0	0.142857	0	0	HHLA2	3	3q13.13	1.1E+08	1.1E+08
MYH15	1	0	0.142857	0	0	MYH15	3	3q13.13	1.1E+08	1.1E+08
KIAA1524	1	0	0.142857	0	0	KIAA1524	3	3q13.13	1.1E+08	1.1E+08
DZIP3	1	0	0.142857	0	0	DZIP3	3	3q13.13	1.1E+08	1.1E+08
STXBP5L	1	0	0.142857	0	0	STXBP5L	3	3q13.33	1.22E+08	1.23E+08
SPSB4	1	0.142857	0	0	0	SPSB4	3	3q23	1.42E+08	1.42E+08
ACPL2	1	0.142857	0	0	0	ACPL2	3	3q23	1.42E+08	1.42E+08
ZBTB38	1	0.142857	0	0	0	ZBTB38	3	3q23	1.43E+08	1.43E+08
RNF7	1	0.238095	0	0	0	RNF7	3	3q23	1.43E+08	1.43E+08
GRK7	1	0.238095	0	0	0	GRK7	3	3q23	1.43E+08	1.43E+08
ATP1B3	1	0.238095	0	0	0	ATP1B3	3	3q23	1.43E+08	1.43E+08
TFDP2	1	0.238095	0	0	0	TFDP2	3	3q23	1.43E+08	1.43E+08
GK5	1	0.238095	0	0	0	GK5	3	3q23	1.43E+08	1.43E+08
XRN1	1	0.238095	0	0	0	XRN1	3	3q23	1.44E+08	1.44E+08
ATR	1	0.238095	0	0	0	ATR	3	3q23	1.44E+08	1.44E+08
PLS1	1	0.190476	0	0	0	PLS1	3	3q23	1.44E+08	1.44E+08
PCOLCE2	1	0.190476	0	0	0	PCOLCE2	3	3q23	1.44E+08	1.44E+08
LOC201651	1	0	0.142857	0	0	LOC201651	3	3q25.1	1.53E+08	1.53E+08
AADAC	1	0	0.142857	0	0	AADAC	3	3q25.1	1.53E+08	1.53E+08
LOC401093	1	0	0.142857	0	0	LOC401093	3	3q25.1	1.53E+08	1.53E+08
MBNL1	1	0	0.142857	0	0	MBNL1	3	3q25.1	1.53E+08	1.54E+08
P2RY1	1	0	0.142857	0	0	P2RY1	3	3q25.2	1.54E+08	1.54E+08
LEKR1	1	0	0.142857	0	0	LEKR1	3	3q25.31	1.58E+08	1.58E+08

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
GFM1	1	0	0.142857	0	0	GFM1	3	3q25.32	1.6E+08	1.6E+08
LXN	1	0	0.142857	0	0	LXN	3	3q25.32	1.6E+08	1.6E+08
KPNA4	1	0	0.190476	0	0	KPNA4	3	3q26.1	1.62E+08	1.62E+08
PPM1L	1	0	0.142857	0	0	PPM1L	3	3q26.1	1.62E+08	1.62E+08
KCNMB2	1	0	0.190476	0	0	KCNMB2	3	3q26.32	1.8E+08	1.8E+08
ZMAT3	1	0	0.190476	0	0	ZMAT3	3	3q26.32	1.8E+08	1.8E+08
PIK3CA	1	0	0.190476	0	0	PIK3CA	3	3q26.32	1.8E+08	1.8E+08
PEX5L	1	0	0.142857	0	0	PEX5L	3	3q26.33	1.81E+08	1.81E+08
CCDC39	1	0.047619	0.142857	0	0	CCDC39	3	3q26.33	1.82E+08	1.82E+08
FXR1	1	0.142857	0.047619	0	0	FXR1	3	3q26.33	1.82E+08	1.82E+08
ATP11B	1	0.142857	0	0	0	ATP11B	3	3q26.33	1.84E+08	1.84E+08
UTS2D	1	0	0.142857	0	0	UTS2D	3	3q28	1.92E+08	1.93E+08
PYDC2	1	0	0.142857	0	0	PYDC2	3	3q28	1.93E+08	1.93E+08
VSNL1	1	0.047619	0.142857	0	0	VSNL1	2	2p24.2	17585288	17701188
KLHL29	1	0.190476	0	0	0	KLHL29	2	2p24.1	23461803	23784986
MTIF2	1	0.190476	0	0	0	MTIF2	2	2p16.1	55317260	55349820
CCDC88A	1	0.190476	0	0	0	CCDC88A	2	2p16.1	55368484	55500562
MIR217	1	0	0.142857	0	0	MIR217	2	2p16.1	56063606	56063716
MIR216A	1	0	0.142857	0	0	MIR216A	2	2p16.1	56069590	56069699
MIR216B	1	0	0.142857	0	0	MIR216B	2	2p16.1	56081354	56081435
CCDC85A	1	0	0.142857	0	0	CCDC85A	2	2p16.1	56264762	56466814
BCL11A	1	0.238095	0	0	0	BCL11A	2	2p16.1	60531806	60634138
FAM161A	1	0.142857	0	0	0	FAM161A	2	2p15	61905487	61934783
CCT4	1	0.142857	0	0	0	CCT4	2	2p15	61948766	61969296
COMMD1	1	0.142857	0	0	0	COMMD1	2	2p15	61986307	62216710
B3GNT2	1	0.142857	0	0	0	B3GNT2	2	2p15	62276766	62305371
IL18RAP	1	0.142857	0	0	0	IL18RAP	2	2q12.1	1.02E+08	1.02E+08
SLC9A4	1	0.142857	0	0	0	SLC9A4	2	2q12.1	1.02E+08	1.03E+08
TNFA1P6	1	0.190475	0	0	0	TNFA1P6	2	2q23.3	1.52E+08	1.52E+08
STAM2	1	0	0.142857	0	0	STAM2	2	2q23.3	1.53E+08	1.53E+08
EVX2	1	0.142857	0	0	0	EVX2	2	2q31.1	1.77E+08	1.77E+08
HOXD13	1	0.142857	0	0	0	HOXD13	2	2q31.1	1.77E+08	1.77E+08
HOXD12	1	0.142857	0	0	0	HOXD12	2	2q31.1	1.77E+08	1.77E+08
HOXD11	1	0.142857	0	0	0	HOXD11	2	2q31.1	1.77E+08	1.77E+08
HOXD10	1	0.142857	0	0	0	HOXD10	2	2q31.1	1.77E+08	1.77E+08
HOXD9	1	0.142857	0	0	0	HOXD9	2	2q31.1	1.77E+08	1.77E+08
HOXD8	1	0.142857	0	0	0	HOXD8	2	2q31.1	1.77E+08	1.77E+08
CD28	1	0.142857	0	0	0	CD28	2	2q33.2	2.04E+08	2.04E+08
CTLA4	1	0.142857	0	0	0	CTLA4	2	2q33.2	2.04E+08	2.04E+08
ICOS	1	0.142857	0	0	0	ICOS	2	2q33.2	2.05E+08	2.05E+08
PLEKHM3	1	0.142857	0	0	0.037037	PLEKHM3	2	2q33.3	2.08E+08	2.09E+08
CRYGD	1	0.142857	0	0	0	CRYGD	2	2q33.3	2.09E+08	2.09E+08
CRYGC	1	0.142857	0	0	0	CRYGC	2	2q33.3	2.09E+08	2.09E+08
PIKFYVE	1	0.142857	0	0	0	PIKFYVE	2	2q33.3	2.09E+08	2.09E+08
KIAA1486	1	0	0.142857	0	0	KIAA1486	2	2q36.3	2.26E+08	2.26E+08
PDE48	1	0	0.142857	0	0	PDE48	1	1p31.3	66030781	66612851
IL23R	1	0.142857	0	0	0	IL23R	1	1p31.3	67404757	67498239
IL12RB2	1	0.142857	0	0	0	IL12RB2	1	1p31.3	67545635	67635172
CCBL2	1	0.142857	0	0	0	CCBL2	1	1p22.2	89174044	89231232
RPL5	1	0.142857	0	0	0	RPL5	1	1p22.1	93070182	93080070
SNORD21	1	0.142857	0	0	0	SNORD21	1	1p22.1	93075434	93075529
FAM69A	1	0.142857	0	0	0	FAM69A	1	1p22.1	93080309	93199668
MTF2	1	0.142857	0	0	0	MTF2	1	1p22.1	93317380	93377225
DR1	1	0.142857	0	0	0	DR1	1	1p22.1	93584066	93600737
FNBP1L	1	0.142857	0	0	0	FNBP1L	1	1p22.1	93686427	93792807
RC3H1	1	0.142857	0	0	0	RC3H1	1	1q25.1	1.72E+08	1.72E+08
GPR52	1	0	0.142857	0	0	GPR52	1	1q25.1	1.73E+08	1.73E+08
C1orf49	1	0.142857	0	0	0	C1orf49	1	1q25.2	1.77E+08	1.77E+08
Clorf220	1	0.142857	0	0	0	Clorf220	1	1q25.2	1.77E+08	1.77E+08
FAM20B	1	0.238095	0	0	0	FAM20B	1	1q25.2	1.77E+08	1.77E+08
ABL2	1	0.238095	0	0	0	ABL2	1	1q25.2	1.77E+08	1.77E+08
SOAT1	1	0.190476	0	0	0	SOAT1	1	1q25.2	1.78E+08	1.78E+08
C1orf125	1	0.190476	0	0	0	C1orf125	1	1425.2	1.78E+08	1.78E+08
NPHS2	1	0.190476	0	0	0	NPHS2	1	1q25.2	1.78E+08	1.78E+08
TDRD5	1	0.142857	0.047619	0	0	TDRD5	1	1q25.2	1.78E+08	1.78E+08
FAM163A	1	0.190476	0	0	0	FAM163A	1	1q25.2	1.78E+08	1.78E+08
TOR1AIP2	1	0.190476	0	0	0	TOR1AIP2	1	1q25.2	1.78E+08	1.78E+08
CEP350	1	0.142857	0.047619	0	0	CEP350	1	1q25.2	1.78E+08	1.78E+08
STX6	1	0.142857	0	0	0	STX6	1	1q25.3	1.79E+08	1.79E+08
MR1	1	0.142857	0	0	0	MR1	1	1q25.3	1.79E+08	1.79E+08
OR2M5	1	0.095238	0.190476	0.111111	0	OR2M5	1	1q44	2.46E+08	2.46E+08
OR2M2	1	0.095238	0.190476	0.111111	0	OR2M2	1	1q44	2.46E+08	2.46E+08
OR2T6	1	0.095238	0.190476	0.111111	0	OR2T6	1	1q44	2.47E+08	2.47E+08
RFX7	0.4375	0.095238	0.095238	0	0	RFX7	15	15q21.3	54170023	54322776

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
ZNF462	0.4375	0.095238	0.095238	0	0	ZNF462	9	9q31.2	1.09E+08	1.09E+08
IPCEF1	0.4375	0.095238	0.095238	0	0	IPCEF1	6	6q25.2	1.55E+08	1.55E+08
TLR10	0.4375	0.095238	0.095238	0	0	TLR10	4	4p14	38450647	38460985
PDZRN3	0.4375	0.095238	0.095238	0	0	PDZRN3	3	3p13	73514342	73756763
SR140	0.4375	0.095238	0.095238	0	0	SR140	3	3q23	1.44E+08	1.44E+08
CCDC50	0.4375	0.095238	0.095238	0	0	CCDC50	3	3q28	1.93E+08	1.93E+08
FCRLB	0.4375	0.095238	0.095238	0	0	FCRLB	1	1q23.3	1.6E+08	1.6E+08
ALG5	0.416667	0.142857	0.095238	0.037037	0	ALG5	13	13q13.3	36421910	36471505
NEDD9	0.416667	0.190476	0.095233	0.037037	0	NEDD9	6	6p24.1	11291518	11490568
SGOL1	0.416667	0.095238	0.142857	0	0.037037	SGOL1	3	3p24.3	20177089	20202688
RASA2	0.416667	0.095238	0.142857	0	0.037037	RASA2	3	3q23	1.43E+08	1.43E+08
VAMP7	0.395833	0.285714	0.095238	0.333333	0	VAMP7	X	Xq28	1.55E+08	1.55E+08
IL9R	0.395833	0.285714	0.095238	0.333333	0	IL9R	X	Xq28	1.55E+08	1.55E+08
RPL23AP82	0.395833	0.809524	0.095238	0.777778	0	RPL23AP82	22	22q13.33	49542380	49584931
RABL2B	0.395833	0.809524	0.095238	0.777778	0	RABL2B	22	22q13.33	49552786	49568954
C21orf7	0.395833	0.095238	0.047619	0	0	C21orf7	21	21q21.3	29374744	29470074
CLDN17	0.395833	0.047619	0.095238	0	0	CLDN17	21	21q21.3	30460132	30460807
KRTAP19-3	0.395833	0.047619	0.095238	0	0	KRTAP19-3	21	21q22.11	30785653	30786147
KRTAP19-4	0.395833	0.047619	0.095238	0	0	KRTAP19-4	21	21q22.11	30791045	30791300
KRTAP19-5	0.395833	0.047619	0.095238	0	0	KRTAP19-5	21	21q22.11	30796061	30796280
KRTAP19-7	0.395833	0.047619	0.095238	0	0	KRTAP19-7	21	21q22.11	30855288	30855480
KRTAP20-2	0.395833	0.047619	0.095238	0.037037	0	KRTAP20-2	21	21q22.11	30929454	30929652
KRTAP20-3	0.395833	0.047619	0.095238	0.037037	0	KRTAP20-3	21	21q22.11	30937054	30937327
HAO1	0.395833	0	0.095238	0	0	HAO1	20	20p12.3	7811631	7869094
TMX4	0.395833	0	0.095238	0	0	TMX4	20	20p12.3	7909716	7948394
PLCB1	0.395833	0	0.095238	0	0	PLCB1	20	20p12.3	8061296	8813548
PLCB4	0.395833	0	0.095238	0	0	PLCB4	20	20p12.2	9024932	9409463
PAK7	0.395833	0	0.095238	0	0	PAK7	20	20p12.2	9466037	9767688
SNAP25	0.395833	0	0.095238	0	0	SNAP25	20	20p12.2	10147477	10236066
C20orf94	0.395833	0	0.095238	0	0	C20orf94	20	20p12.2	10363951	10552028
JAG1	0.395833	0	0.095238	0	0	JAG1	20	20p12.2	10566332	10602695
ESF1	0.395833	0.095238	0.047619	0	0	ESF1	20	20p12.1	13642969	13713533
C20orf7	0.395833	0.095238	0.047619	0	0	C20orf7	20	20p12.1	13713672	13747066
KIF16B	0.395833	0	0.095238	0	0	KIF16B	20	20p12.1	16200749	16502079
DOK5	0.395833	0.095238	0.095238	0.148148	0	DOK5	20	20q13.2	52525673	52701118
CETN1	0.395833	0.095238	0	0	0	CETN1	18	18p11.32	570369	571525
CLUL1	0.395833	0.095238	0	0	0	CLUL1	18	18p11.32	586998	640294
TYMS	0.395333	0.095238	0	0	0	TYMS	18	18p11.32	647604	663500
ENOSF1	0.395833	0.095233	0	0	0	ENOSF1	18	18p11.32	662544	702663
YES1	0.395833	0.095238	0	0	0	YES1	18	18p11.32	711592	802328
LOC642597	0.395833	0	0.095238	0	0	LOC642597	18	18p11.31	5133672	5187256
ZNF519	0.395833	0.095238	0.095238	0.074074	0	ZNF519	18	18p11.21	14094724	14122430
ANKRD30B	0.395833	0.095238	0.095238	0.074074	0	ANKRD30B	18	13p11.21	14738239	14842738
SERPINB13	0.395833	0.095238	0	0	0.037037	SERPINB13	18	18q21.33	59405514	59417413
SERPINB8	0.395833	0.095238	0	0	0.037037	SERPINB8	18	18q21.33	59788243	59804868
SOCS6	0.395833	0.095238	0	0	0.037037	SOCS6	18	18q22.2	66107117	66148415
KRT25	0.395833	0.190476	0.095238	0.259259	0	KRT25	17	17q21.2	36157800	36165111
KRT26	0.395833	0.190476	0.095238	0.259259	0	KRT26	17	17q21.2	36176018	36181938
CA10	0.395833	0.142857	0.095238	0.185185	0	CA10	17	17q21.33	47062673	47592161
TANC2	0.395833	0.238095	0.095238	0.333333	0	TANC2	17	17q23.3	58440630	58858800
KCNJ16	0.395833	0.047613	0.095238	0.222222	0	KCNJ16	17	17q24.3	65583021	65643342
TOX3	0.395833	0.047619	0.095238	0	0	TOX3	16	16q12.1	51029419	51138308
CNTNAP4	0.395833	0.095238	0.047619	0	0	CNTNAP4	16	16q23.1	74868677	75150637
SCG5	0.395833	0.095238	0	0	0	SCG5	15	15q13.3	30721162	30776591
AVEN	0.395833	0.095238	0	0	0	AVEN	15	15q14	31945720	32118596
CHRM5	0.395833	0.095238	0	0	0	CHRM5	15	15q14	32048381	32144580
PGBD4	0.395833	0.095238	0	0	0	PGBD4	15	15q14	32181566	32183884
C15orf29	0.395833	0.095238	0	0	0	C15orf29	15	15q14	32220167	32289590
TMEM85	0.395833	0.095238	0	0	0	TMEM85	15	15q14	32304537	32309645
SLC12A6	0.395833	0.095238	0	0	0	SLC12A6	15	15q14	32309489	32417254
NOP10	0.395833	0.095238	0	0	0	NOP10	15	15q14	32421209	32422655
C15orf55	0.395833	0.095238	0	0	0	C15orf55	15	15q14	32425358	32437224
MEIS2	0.395833	0.047619	0.095238	0	0	MEIS2	15	15q14	34970524	35180793
SPRED1	0.395833	0.047619	0.095238	0.037037	0	SPRED1	15	15q14	36332344	36436743
DMXL2	0.395833	0.095238	0.095238	0.037037	0	DMXL2	15	15q21.2	49527231	49702260
ONECUT1	0.395833	0.095238	0	0	0.037037	ONECUT1	15	15q21.2	50836645	50869502
RAB27A	0.395833	0.095238	0	0	0	RAB27A	15	15q21.3	53283092	53349878
PIGB	0.395833	0.095238	0	0	0	PIGB	15	15q21.3	53398425	53435139
CCPG1	0.395833	0.095238	0	0	0	CCPG1	15	15q21.3	53434730	53487835
MIR628	0.395833	0.095238	0	0	0	MIR628	15	15q21.3	53452430	53452525
DYX1C1	0.395833	0.095238	0	0	0	DYX1C1	15	15q21.3	53497246	53587725
PYGO1	0.395833	0.095238	0	0	0	PYGO1	15	15q21.3	53625513	53668343
PRTG	0.395833	0.095238	0	0	0	PRTG	15	15q21.3	53691042	53822470
TEX9	0.395833	0.095238	0.095238	0	0.037037	TEX9	15	15q21.3	54444935	54525365

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
ZNF280D	0.395833	0.095238	0	0	0	ZNF280D	15	15q21.3	54709666	54813080
TCF12	0.395833	0.095238	0.047619	0	0	TCF12	15	15q21.3	54998125	55368007
NEO1	0.395833	0.190476	0.095238	0.333333	0	NEO1	15	15q24.1	71131928	71384599
LOC91948	0.395833	0.047619	0.095238	0.074074	0	LOC91948	15	15q26.2	96086850	96218664
C15orf51	0.395833	0.190476	0.095238	0.185185	0	C15orf51	15	15q26.3	98147884	98164656
COCH	0.395833	0.095238	0	0	0.037037	COCH	14	14q12	30413492	30429574
EGLN3	0.395833	0.095238	0	0	0	EGLN3	14	14q13.1	33463172	33490036
MIPOL1	0.395833	0	0.095238	0	0	MIPOL1	14	14q21.1	36736869	37086619
RPS29	0.395833	0.095238	0	0	0	RPS29	14	14q22.1	49113792	49122845
C14orf183	0.395833	0.095238	0	0	0	C14orf183	14	14q22.1	49620119	49629112
SOS2	0.395833	0.095238	0	0	0	SOS2	14	14q22.1	49653596	49767850
L2HGDH	0.395833	0.095238	0	0	0	L2HGDH	14	14q22.1	49778902	49848698
ATP5S	0.395833	0.095238	0	0	0	ATP5S	14	14q22.1	49848797	49862419
CDKL1	0.395833	0.095238	0	0	0	CDKL1	14	14q22.1	49866470	49932368
MAP4K5	0.395833	0.095238	0	0	0	MAP4K5	14	14q22.1	49954993	50069127
ATL1	0.395833	0.095238	0	0	0	ATL1	14	14q22.1	50069550	50169535
SAV1	0.395833	0.095238	0	0	0	SAV1	14	14q22.1	50170110	50204774
NIN	0.395833	0.095238	0	0	0	NIN	14	14q22.1	50256231	50367590
ABHD12B	0.395833	0.095238	0	0	0	ABHD12B	14	14q22.1	50408628	50441439
PYGL	0.395833	0.095238	0	0	0	PYGL	14	14q22.1	50441686	50480999
TRIM9	0.395833	0.095238	0	0	0	TRIM9	14	14q22.1	50511731	50632173
FRMD6	0.395833	0.095238	0	0	0	FRMD6	14	14q22.1	51025605	51267195
CDKN3	0.395833	0.095238	0	0	0	CDKN3	14	14q22.2	53933423	53956683
ACTR10	0.395833	0.095238	0	0	0	ACTR10	14	14q23.1	57736586	57772107
PSMA3	0.395833	0.095238	0	0	0.037037	PSMA3	14	14q23.1	57781346	57808480
FL131306	0.395833	0.095238	0	0	0.037037	FL131306	14	14q23.1	57801837	57834609
ARID4A	0.395833	0.095238	0	0	0	ARID4A	14	14q23.1	57834975	57910205
NRXN3	0.395833	0.047619	0.095238	0.074074	0	NRXN3	14	14q24.3	77939846	79400514
ZMYM2	0.395833	0.190476	0.095238	0.111111	0	ZMYM2	13	13q12.11	19430810	19558940
KL	0.395833	0.095238	0	0	0	KL	13	13q13.1	32488571	32538282
STARD13	0.395833	0.095238	0	0	0	STARD13	13	13q13.1	32575273	32678188
NBEA	0.395833	0	0.095238	0	0	NBEA	13	13q13.2	34414456	35144874
C13orf36	0.395833	0.047619	0.095238	0	0	C13orf36	13	13q13.3	36146049	36169976
SMAD9	0.395833	0.095238	0.095238	0.037037	0	SMAD9	13	13q13.3	36320207	36392410
TSC22D1	0.395833	0.095238	0	0	0	TSC22D1	13	13q14.11	43905655	44048702
NUFIP1	0.395833	0.095238	0	0	0	NUFIP1	13	13q14.12	44411384	44461614
KIAA1704	0.395833	0.095238	0	0	0	KIAA1704	13	13q14.12	44461687	44500405
GTF2F2	0.395833	0.095238	0	0	0	GTF2F2	13	13q14.12	44592631	44756240
KCTD4	0.395833	0.095238	0	0	0	KCTD4	13	13q14.12	44664988	44673176
TPT1	0.395833	0.095238	0	0	0	TPT1	13	13q14.12	44809304	44813298
SNORA31	0.395833	0.095238	0	0	0	SNORA31	13	13q14.12	44809615	44809745
LOC1001939	0.395833	0.095238	0	0	0	LOC1001939	13	13q14.12	44813480	44853617
COG3	0.395833	0.095238	0	0	0	COG3	13	13q14.12	44937072	45008762
FAM194B	0.395833	0.095238	0	0	0	FAM194B	13	13q14.12	45013433	45087876
esd	0.395833	0	0.095238	0	0	esd	13	13q14.2	46243392	46269369
HTR2A	0.395833	0	0.095238	0	0	HTR2A	13	13q14.2	46305514	46369171
SUCLA2	0.395833	0.095238	0	0	0	SUCLA2	13	13q14.2	47414792	47473464
NUDT15	0.395833	0.095238	0	0	0	NUDT15	13	13q14.2	47509704	47519284
MED4	0.395833	0.095238	0	0	0	MED4	13	13q14.2	47548093	47567242
ITM2B	0.395833	0.095238	0	0	0	ITM2B	13	13q14.2	47705275	47734234
RNASEH2B	0.395833	0.095238	0	0	0	RNASEH2B	13	13q14.3	50381893	50442596
GUCY1B2	0.395833	0.095238	0	0	0	GUCY1B2	13	13q14.3	50466649	50538295
FAM124A	0.395833	0.095238	0	0	0	FAM124A	13	13q14.3	50694508	50753618
SERPINE3	0.395833	0.095238	0	0	0	SERPINE3	13	13q14.3	50813169	50834241
INTS6	0.395833	0.095238	0	0	0	INTS6	13	13q14.3	50833702	50925277
WDFY2	0.395833	0.095238	0	0	0	WDFY2	13	13q14.3	51056485	51234173
HNRNPA1L	0.395833	0.095238	0	0	0	HNRNPA1L	13	13q14.3	52089606	52115921
KLF12	0.395833	0	0.095238	0	0	KLF12	13	13q22.1	73158150	73606068
TBC1D4	0.395833	0	0.095238	0	0	TBC1D4	13	13q22.2	74756810	74954252
COMMD6	0.395833	0	0.095238	0	0	COMMD6	13	13q22.2	74997351	75009993
LM07	0.395833	0	0.095238	0	0	LM07	13	13q22.2	75092571	75332006
DCT	0.395833	0.095238	0.095238	0	0.111111	DCT	13	13q32.1	93889842	93929938
TMTC4	0.395833	0.095238	0	0	0	TMTC4	13	13q32.3	1E+08	1E+08
LOC374443	0.395833	0	0.095238	0.037037	0	LOC374443	12	12p13.31	9691910	9702276
CLECL1	0.395833	0	0.095238	0.037037	0	CLECL1	12	12p13.31	9766358	9777128
CD69	0.395833	0	0.095238	0.037037	0	CD69	12	12p13.31	9796351	9804765
CLEC2A	0.395833	0	0.095238	0.037037	0	CLEC2A	12	12p13.31	9957093	9976248
CLEC12A	0.395833	0	0.095238	0.037037	0	CLEC12A	12	12p13.2	10015275	10029462
CLEC1B	0.395833	0	0.095238	0.037037	0	CLEC1B	12	12p13.2	10036929	10043167
CLEC12B	0.395833	0	0.095238	0.037037	0	CLEC12B	12	12p13.2	10054498	10062667
CLEC9A	0.395833	0	0.095238	0.037037	0	CLEC9A	12	12p13.2	10074543	10109833
CLEC1A	0.395833	0	0.095238	0.037037	0	CLEC1A	12	12p13.2	10114347	10142873
STYK1	0.395833	0	0.095238	0.037037	0	STYK1	12	12p13.2	10662805	10718159
CSDA	0.395833	0	0.095238	0.037037	0	CSDA	12	12p13.2	10742945	10767221

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
KIAAD528	0.395833	0	0.095238	0	0	KIAAD528	12	12P12.1	22492785	22588720
ETNK1	0.395833	0	0.095238	0	0	ETNK1	12	12p12.1	22669343	22688617
TMTC1	0.395833	0	0.095238	0	0	TMTC1	12	12p11.22	29545024	29828960
GXYLT1	0.395833	0	0.095238	0	0	GXYLT1	12	12q12	40761915	40824941
ZCRB1	0.395833	0.095238	0	0	0	ZCRB1	12	12q12	40992155	41006200
PPHLN1	0.395833	0.095238	0	0	0	PPHLN1	12	12q12	41006214	41128690
ADAMTS20	0.395833	0	0.095238	0	0	ADAMTS20	12	12q12	42034279	42231992
NELL2	0.395833	0.047619	0.095238	0	0	NELL2	12	12q12	43188325	43556901
DBX2	0.395833	0.047619	0.095238	0	0	DBX2	12	12q12	43694806	43731150
KIAA0748	0.395833	0.095238	0.095238	0.259259	0	KIAA0748	12	12q13.2	53630132	53664724
MON2	0.395833	0.095238	0	0	0.037037	MON2	12	12q14.1	61146864	61277631
SRGAP1	0.395833	0.095238	0	0	0	SRGAP1	12	12q14.2	62524808	62827881
C12orf66	0.395833	0.095238	0	0	0	C12orf66	12	12q14.2	62872686	62902344
C12orf56	0.395833	0.095238	0	0	0	C12orf56	12	12q14.2	62947032	63070613
TBK1	0.395833	0.095238	0	0	0	TBK1	12	12q14.2	63132204	63182159
GNS	0.395833	0.095238	0	0	0	GNS	12	12q14.2-12q14.3	63393489	63439494
TBC1D15	0.395833	0.095238	0.095238	0	0.037037	TBC1D15	12	12q21.1	70519754	70606895
MRS2P2	0.395833	0.095238	0.095238	0	0.037037	MRS2P2	12	12q21.1	70528343	70531031
METAP2	0.395833	0.095238	0	0	0	METAP2	12	12q22	94391953	94433745
USP44	0.395833	0.095238	0	0	0	USP44	12	12q22	94435018	94466752
NTN4	0.395833	0.095238	0	0	0	NTN4	12	12q22	94575714	94708668
CCDC38	0.395833	0.095238	0	0	0	CCDC38	12	12q23.1	94784958	94860560
AMDHD1	0.395833	0.095238	0	0	0	AMDHD1	12	12q23.1	94861202	94886501
HAL	0.395833	0.095238	0	0	0	HAL	12	12q23.1	94891273	94914203
C12orf42	0.395833	0	0.095238	0.111111	0	C12orf42	12	12q23.2	1.02E+08	1.02 E+08
OR51F1	0.395833	0	0.095238	0	0	OR51F1	11	11p15.4	4746785	4747724
OR51S1	0.395833	0	0.095238	0	0	OR51S1	11	11p15.4	4826043	4827015
OR51A7	0.395833	0	0.095238	0	0	OR51A7	11	11p15.4	4885176	4886115
OR51G2	0.395833	0	0.095238	0	0	OR51G2	11	11p15.4	4892525	4893470
OR51L1	0.395833	0	0.095238	0	0	OR51L1	11	11p15.4	4976789	4977737
OR52J3	0.395833	0	0.095238	0	0	OR52J3	11	11p15.4	5024332	5025268
OR52E2	0.395833	0	0.095238	0	0	OR52E2	11	11p15.4	5036456	5037434
OR52A1	0.395833	0	0.095238	0	0	OR52A1	11	11p15.4	5129237	5130176
OR51V1	0.395833	0	0.095238	0	0	OR51V1	11	11p15.4	5177541	5178507
OR51B4	0.395833	0	0.095238	0	0	OR51B4	11	11p15.4	5278820	5279753
OR51B5	0.395833	0	0.095238	0	0	OR51B5	11	11p15.4	5320392	5321331
OR51B6	0.395833	0	0.095238	0	0	OR51B6	11	11P15.4	5329314	5330253
OR5P3	0.395833	0	0.095238	0.074074	0	OR5P3	11	11p15.4	7803160	7804096
PSMA1	0.395833	0	0.095238	0	0	PSMA1	11	11p15.2	14482999	14621757
PDE3B	0.395833	0	0.095238	0	0	PDE3B	11	11p15.2	14621845	14850179
INSC	0.395833	0.095238	0	0	0	INSC	11	11p15.2	15090546	15225331
LDLRAD3	0.395833	0.095238	0	0	0	LDLRAD3	11	11p13	35922188	36209418
COMMDS	0.395833	0.095238	0	0	0	COMMDS	11	11p13	36250418	36267576
PRR5L	0.395833	0.095238	0	0	0	PRR5L	11	11p13	36274301	36443330
PCF11	0.395833	0.095238	0.047619	0	0.074074	PCF11	11	11q14.1	82545785	82574484
ANKRD42	0.395833	0.095238	0.047619	0	0.074074	ANKRD42	11	11q14.1	82582939	82637662
MMP7	0.395833	0.095238	0	0	0.037037	MMP7	11	11q22.2	1.02E+08	1.02E+08
FAM55A	0.395833	0.190476	0.095238	0.148148	0	FAM55A	11	11q23.2	1.14E+08	1.14E+08
FAM55B	0.395833	0.190476	0.095238	0.148148	0	FAM55B	11	11q23.2	1.14E+08	1.14E+08
RSU1	0.395833	0.095238	0	0	0	RSU1	10	10p13	16672623	16899460
ST8SIA6	0.395833	0.095238	0	0	0	ST8SIA6	10	10p12.33	17402682	17536261
PTPLA	0.395833	0.095238	0	0	0	PTPLA	10	10p12.33	17671964	17699380
STAM	0.395833	0.095238	0	0	0	STAM	10	10p12.33	17726130	17797914
SLC39A12	0.395833	0.095238	0	0	0	SLC39A12	10	10p12.33	18280774	18372228
CACNB2	0.395833	0.095238	0	0	0	CACNB2	10	10p12.33	18469612	18870695
NSUN6	0.395833	0.095238	0	0	0	NSUN6	10	10p12.33	18874270	18980557
ARL5B	0.395833	0.095238	0	0	0	ARL5B	10	10p12.33	18988319	19006947
GAD2	0.395833	0.095238	0	0	0	GAD2	10	10p12.1	26545242	26633498
APB1IP	0.395833	0.095238	0	0	0	APB1IP	10	10p12.1	26767272	26896739
C10orf50	0.395833	0.095238	0	0	0	C10orf50	10	10p12.1	26918800	26923256
LOC731789	0.395833	0.095238	0	0	0	LOC731789	10	10p12.1	26972043	26982389
PDSS1	0.395833	0.095238	0	0	0	PDSS1	10	10p12.1	27026601	27075733
ABI1	0.395833	0.095238	0	0	0	ABI1	10	10p12.1	27075531	27189966
KIF5B	0.395833	0.095238	0	0	0	KIF5B	10	10p11.22	32337944	32385378
EPC1	0.395833	0.095238	0	0	0	EPC1	10	10p11.22	32597865	32676120
CCDC7	0.395833	0.047619	0.095238	0	0	CCDC7	10	10p11.22	32775047	32903499
LOC100129055	0.395833	0	0.095238	0	0	LOC100129055	10	10p11.21	38504605	38543279
HSD17B7P2	0.395833	0	0.095238	0	0	HSD17B7P2	10	10p11.21	38685314	38707440
LRIT2	0.395833	0.095238	0	0	0	LRIT2	10	10q23.1	85970229	85975265
LRIT1	0.395833	0.095238	0	0	0	LRIT1	10	10q23.1	85981256	85991198
RGR	0.395833	0.095238	0	0	0	RGR	10	10q23.1	85994789	86008925
PTEN	0.395833	0	0.095238	0	0	PTEN	10	10q23.31	89613175	89718513
LIPK	0.395833	0.047619	0.095238	0.037037	0	LIPK	10	10q23.31	90474281	90502494

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
STAMBPL1	0.395833	0	0.095238	0	0	STAMBPL1	10	10q23.31	90630006	90673225
ACTA2	0.395833	0	0.095238	0	0	ACTA2	10	10q23.31	90684813	90741128
LIPA	0.395833	0	0.095238	0	0	LIPA	10	10q23.31	90963306	91001641
IFIT3	0.395833	0	0.095238	0	0	IFIT3	10	10q23.31	91077582	91090705
IFIT5	0.395333	0	0.095238	0	0	IFIT5	10	10q23.31	91164305	91170739
SLC16A12	0.395833	0	0.095238	0	0	SLC16A12	10	10q23.31	91180036	91285294
PANK1	0.395833	0	0.095238	0	0	PANK1	10	10q23.31	91332729	91393628
MIR107	0.395833	0	0.095238	0	0	MIR107	10	10q23.31	91342485	91342565
TM9SF3	0.395833	0.285714	0.095238	0.259259	0	TM9SF3	10	10q24.1	98267857	98336800
PIK3AP1	0.395833	0.285714	0.095238	0.259259	0	PIK3AP1	10	10q24.1	98343059	98470270
CCDC147	0.395833	0.095238	0.095238	0.037037	0	CCDC147	10	10q25.1	1.06E+08	1.06E+08
SLC1A1	0.395833	0.095238	0	0	0	SLC1A1	9	9p24.2	4480444	4577470
UHRF2	0.395833	0.095238	0	0	0	UHRF2	9	9p24.1	6403151	6497052
PTPLAD2	0.395833	0	0.095238	0	0	PTPLAD2	9	9p21.3	20996365	21021636
IFNW1	0.395833	0	0.095238	0	0	IFNW1	9	9p21.3	21130631	21132145
IFNA21	0.395833	0	0.095238	0	0	IFNA21	9	9p21.3	21155636	21156660
MOBKL2B	0.395833	0.095238	0.047619	0	0.111111	MOBKL2B	9	9p21.2	27315207	27519851
KLF9	0.395833	0.095238	0	0	0	KLF9	9	9q21.11	72189333	72219394
TRPM3	0.395833	0.095238	0	0	0	TRPM3	9	9q21.11	72339786	72926335
TMEM2	0.395833	0.095238	0	0	0	TMEM2	9	9q21.13	73488102	73573621
GDA	0.395833	0.095238	0	0	0	GDA	9	9q21.13	73954113	74056961
ZFAND5	0.395833	0.095238	0	0	0	ZFAND5	9	9q21.13	74156161	74169984
TMC1	0.395833	0.095238	0	0	0	TMC1	9	9q21.13	74326537	74641088
ALDH1A1	0.395833	0	0.095238	0	0	ALDH1A1	9	9q21.13	74705407	74757790
PRUNE2	0.395833	0.095238	0	0	0	PRUNE2	9	9q21.13	78416112	78710824
GAS1	0.395833	0.142857	0.095238	0.222222	0	GAS1	9	9q21.33	88749097	88751925
CKS2	0.395833	0.333333	0.095238	0.296296	0	CKS2	9	9q22.2	91115933	91121439
5ECISBP2	0.395833	0.333333	0.095238	0.296296	0	5ECISBP2	9	9q22.2	91123232	91164382
LPPR1	0.395833	0	0.095238	0.037037	0	LPPR1	9	9q31.1	1.03E+08	1.03E+08
MRPL50	0.395833	0.047619	0.095238	0.037037	0	MRPL50	9	9q31.1	1.03E+08	1.03E+08
ZNF189	0.395833	0.047619	0.095238	0.037037	0	ZNF189	9	9q31.1	1.03E+08	1.03E+08
ALDOB	0.395833	0.047619	0.095238	0.037037	0	ALDOB	9	9q31.1	1.03E+08	1.03E+08
RNF20	0.395833	0.047619	0.095238	0.037037	0	RNF20	9	9q31.1	1.03E+08	1.03E+08
GRIN3A	0.395833	0.047619	0.095238	0.037037	0	GRIN3A	9	9q31.1	1.03E+08	1.04E+08
NIPSNAP3A	0.395833	0.095238	0.047619	0	0.037037	NIPSNAP3A	9	9q31.1	1.07E+08	1.07E+08
FSD1L	0.395833	0.047619	0.095238	0	0	FSD1L	9	9q31.2	1.07E+08	1.07E+08
FKTN	0.395833	0.047619	0.095238	0	0	FKTN	9	9q31.2	1.07E+08	1.07E+08
TAL2	0.395833	0.095238	0.047619	0	0	TAL2	9	9q31.2	1.07E+08	1.07E+08
IKBKAP	0.395833	0.095238	0	0	0	IKBKAP	9	9q31.3	1.11E+08	1.11E+08
CTNNAL1	0.395833	0.095238	0	0	0	CTNNAL1	9	9q31.3	1.11E+08	1.11E+08
C9orf5	0.395833	0.095238	0	0	0	C9orf5	9	9q31.3	1.11E+08	1.11E+08
TNFSF15	0.395833	0.095238	0.095238	0.037037	0	TNFSF15	9	9q32	1.17E+08	1.17E+08
TNFSF8	0.395833	0.095238	0.095238	0.037037	0	TNFSF8	9	9q33.1	1.17E+08	1.17E+08
TNC	0.395833	0.095238	0.095238	0.037037	0	TNC	9	9q33.1	1.17E+08	1.17E+08
ASTN2	0.395833	0.095238	0.047619	0	0	ASTN2	9	9q33.1	1.18E+08	1.19E+08
DBC1	0.395833	0.047619	0.095238	0	0	DBC1	9	9q33.1	1.21E+08	1.21E+08
SH2D4A	0.395833	0.095238	0	0	0	SH2D4A	8	8p21.3	19215487	19297597
ADAM7	0.395833	0	0.095238	0.037037	0	ADAM7	8	8p21.2	24354454	24422166
ADAM9	0.395833	0	0.095238	0.037037	0	ADAM9	8	8p11.23	38973662	39081937
ADAM32	0.395833	0	0.095238	0.037037	0	ADAM32	8	8p11.23	39084207	39261594
POTEA	0.395833	0.047619	0.095238	0.148148	0	POTEA	8	8p11.1	43266742	43337486
SNTG1	0.395833	0.095238	0.047619	0	0.037037	SNTG1	8	8q11.22	50987150	51867981
PXDNL	0.395833	0.095238	0	0	0	PXDNL	8	8q11.22	52394690	52884559
ST18	0.395833	0.047619	0.095238	0	0	ST18	8	8q11.23	53185945	53484993
RB1CC1	0.395833	0.095238	0	0	0	RB1CC1	8	8q11.23	53697571	53789580
XKR4	0.395833	0.095238	0	0	0	XKR4	8	8q12.1	56177571	56601265
SDR16C6	0.395833	0.095238	0	0	0	SDR16C6	8	8q12.1	57448181	57470479
FAM110B	0.395833	0.095238	0	0	0	FAM110B	8	8q12.1	59069667	59224832
UBXN2B	0.395833	0.095238	0.047619	0	0	UBXN2B	8	8q12.1	59486377	59526615
NSMAF	0.395833	0.095238	0.047619	0	0	NSMAF	8	8q12.1	59658620	59734521
TOX	0.395833	0.095238	0.047619	0	0	TOX	8	8q12.1	59880531	60194322
CA8	0.395833	0.095238	0	0	0	CA8	8	8q12.1	61263977	61356509
RAB2A	0.395833	0.095238	0	0	0	RAB2A	8	8q12.1	61592113	61696184
CHD7	0.395833	0.095238	0	0	0	CHD7	8	8q12.2	61753893	61942022
CLVS1	0.395833	0.095238	0	0	0	CLVS1	8	8q12.2	62363079	62576757
ASPH	0.395833	0.095238	0	0	0	ASPH	8	8q12.3	62575670	62764963
NKAIN3	0.395833	0.095238	0.047619	0	0.037037	NKAIN3	8	8q12.3	63324055	64066183
ARMC1	0.395833	0.095238	0	0	0	ARMC1	8	8q13.1	66677628	66708987
MTFR1	0.395833	0.095238	0	0	0	MTFR1	8	8q13.1	66719442	66783127
PDE7A	0.395833	0.095238	0	0	0	PDE7A	8	8q13.1	66792460	66863876
DNAJC5B	0.395833	0.095238	0	0	0	DNAJC5B	8	8q13.1	67096345	67175310
TRIM55	0.395833	0.095238	0	0	0	TRIM55	8	8q13.1	67201832	67250273
STAU2	0.395833	0.095238	0.095238	0	0.037037	STAU2	8	8q21.11	74495160	74821717
TMEM70	0.395833	0.095238	0.095238	0	0.037037	TMEM70	8	8q21.11	75050984	75057568

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
FABP5	0.395833	0.095238	0.095238	0	0.148148	FABP5	8	8q21.13	82355340	82359564
RGS22	0.395833	0.095238	0	0	0	RGS22	8	8q22.2	1.01E+08	1.01E+08
FBXO43	0.395833	0.095238	0	0	0	FBXO43	8	8q22.2	1.01E+08	1.01E+08
POLR2K	0.395833	0.095238	0	0	0	POLR2K	8	8q22.2	1.01E+08	1.01E+08
SPAG1	0.395833	0.095238	0	0	0	SPAG1	8	8q22.2	1.01E+08	1.01E+08
DPYS	0.395833	0.095238	0	0	0.148148	DPYS	8	8q22.3	1.05E+08	1.06E+08
COL14A1	0.395833	0.095238	0.047619	0	0	COL14A1	8	8q24.12	1.21E+08	1.21E+08
MRPL13	0.395833	0	0.095238	0	0	MRPL13	8	8q24.12	1.21E+08	1.22E+08
MTBP	0.395833	0	0.095238	0	0	MTBP	8	8q24.12	1.22E+08	1.22E+08
LOC727677	0.395833	0.095238	0.047619	0	0	LOC727677	8	8q24.21	1.29E+08	1.29E+08
GSDMC	0.395833	0.095238	0	0	0.037037	GSDMC	8	8q24.21	1.31E+08	1.31E+08
FAM49B	0.395833	0.095238	0	0	0.037037	FAM49B	8	8q24.21	1.31E+08	1.31E+08
OC90	0.395333	0.095238	0	0	0	OC90	8	8q24.22	1.33E+08	1.33E+08
HHLA1	0.395833	0.095238	0	0	0	HHLA1	8	8q24.22	1.33E+08	1.33E+08
KCNQ3	0.395833	0.095238	0	0	0	KCNQ3	8	8q24.22	1.33E+08	1.34E+08
HPYR1	0.395833	0.095238	0	0	0	HPYR1	8	8q24.22	1.34E+08	1.34E+08
TMEM71	0.395833	0.095238	0	0	0	TMEM71	8	8q24.22	1.34E+08	1.34E+08
COL28A1	0.395833	0.095238	0.047619	0	0.111111	COL28A1	7	7p21.3	7364769	7541986
RPA3	0.395833	0.095238	0.047619	0	0.074074	RPA3	7	7p21.3	7643100	7724764
GLCCI1	0.395833	0.095238	0.047619	0	0.074074	GLCCI1	7	7p21.3	7974948	8095235
TOMM7	0.395833	0.095238	0	0	0	TOMM7	7	7p15.3	22818777	22828947
KLHL7	0.395833	0.095238	0	0	0	KLHL7	7	7p15.3	23111878	23181564
NUPL2	0.395833	0.095238	0	0	0	NUPL2	7	7p15.3	23187971	23207155
C7orf30	0.395833	0.095238	0.047619	0	0	C7orf30	7	7p15.3	23305465	23315706
IGF2BP3	0.395833	0.095238	0.047619	0	0	IGF2BP3	7	7p15.3	23316353	23476521
STK31	0.395833	0.095238	0	0	0	STK31	7	7p15.3	23716363	23838653
CPVL	0.395833	0.095238	0	0	0	CPVL	7	7p15.1	29001772	29152679
CHN2	0.395833	0.095238	0	0	0	CHN2	7	7p15.1	29200646	29520470
NEUROD6	0.395833	0.095238	0	0	0	NEUROD6	7	7p15.1	31343605	31347064
AVL9	0.395833	0.095238	0	0	0	AVL9	7	7p14.3	32501701	32590305
KBTBD2	0.395833	0.095238	0	0	0	KBTBD2	7	7p14.3	32874303	32897994
NT5C3	0.395833	0.095238	0	0	0	NT5C3	7	7p14.3	33020267	33068935
RP9	0.395833	0.095238	0	0	0	RP9	7	7p14.3	33100935	33115528
BMPER	0.395833	0.095238	0	0	0	BMPER	7	7p14.3	33911637	34160637
EEPD1	0.395833	0.095238	0	0	0	EEPD1	7	7p14.2	36159361	36307678
ANLN	0.395833	0.095238	0	0	0	ANLN	7	7p14.2	36395957	36459926
AOAH	0.395833	0.095238	0	0	0	AOAH	7	7p14.2	36519133	36730679
ABCA13	0.395833	0.095238	0.047619	0	0.037037	ABCA13	7	7p12.3	48208389	48657638
MTERF	0.395833	0.095238	0	0	0	MTERF	7	7q21.2	91339957	91347953
AKAP9	0.395833	0.095238	0	0	0	AKAP9	7	7q21.2	91408125	91577923
CYP51A1	0.395833	0.095238	0	0	0	CYP51A1	7	7q21.2	91579399	91601777
LOC401387	0.395833	0.095238	0	0	0	LOC401387	7	7q21.2	91612134	91632527
KRIT1	0.395833	0.095238	0	0	0	KRIT1	7	7q21.2	91566219	91713165
LMTK2	0.395833	0.333333	0.095238	0.296296	0	LMTK2	7	7q21.3	97574133	97676879
LAMB1	0.395833	0.095238	0	0	0	LAMB1	7	7q31.1	1.07E+08	1.07E+08
AKR1B1	0.395833	0.095238	0	0	0	AKR1B1	7	7q33	1.34E+08	1.34E+08
AKR1B10	0.395833	0.095238	0	0	0	AKR1B10	7	7q33	1.34E+08	1.34E+08
C6orf105	0.395833	0.095238	0	0	0	C6orf105	6	6p24.1	11821876	11887267
RNF144B	0.395833	0.095238	0	0	0.037037	RNF144B	6	6p22.3	18495573	18576830
SOX4	0.395833	0.095238	0	0	0	SOX4	6	6p22.3	21701951	21706829
FLJ22536	0.395833	0.095238	0	0	0	FLJ22536	6	6p22.3	21774654	22302594
DCDC2	0.395833	0.095238	0.047619	0	0	DCDC2	6	6p22.2	24279962	24466260
KIAA0319	0.395833	0.095238	0	0	0	KIAA0319	6	6p22.2	24652311	24754363
ACOT13	0.395833	0.095238	0	0	0	ACOT13	6	6p22.2	24775242	24813273
C6orf62	0.395833	0.095238	0	0	0	C6orf62	6	6p22.2	24813070	24827383
FAM65B	0.395833	0.095238	0	0	0	FAM65B	6	6p22.2	24912492	25019175
SCGN	0.395833	0.047619	0.095238	0.037037	0	SCGN	6	6p22.2	25760408	25809988
SLC17A1	0.395833	0.047619	0.095238	0.037037	0	SLC17A1	6	6p22.2	25891105	25940267
NCRNA00171	0.395833	0.285714	0.095238	0.259259	0	NCRNA00171	6	6p21.33	30076768	30135941
ZNRD1	0.395833	0.285714	0.095238	0.259259	0	ZNRD1	6	6p21.33	30137015	30140666
C6orf141	0.395833	0.095238	0.190476	0	0.074074	C6orf141	6	6p12.3	49626072	49627766
GCM1	0.395833	0.095238	0	0	0	GCM1	6	6p12.1	53099721	53121584
SMAP1	0.395833	0.095238	0.095238	0	0.148148	SMAP1	6	6q13	71434200	71628438
MYO6	0.395833	0.095238	0.095238	0	0.111111	MYO6	6	6q14.1	76515629	76685975
HTR1E	0.395833	0	0.095238	0	0	HTR1E	6	6q15	87703743	87783110
GJA1	0.395833	0.095238	0.095238	0	0.111111	GJA1	6	6q22.31	1.22E+08	1.22E+08
EPM2A	0.395833	0	0.095238	0	0	EPM2A	6	6q24.3	1.46E+08	1.46E+08
NOX3	0.395833	0.095238	0	0	0	NOX3	6	6q25.3	1.56E+08	1.56E+08
SLC22A3	0.395833	0.095238	0	0	0	SLC22A3	6	6q25.3	1.61E+08	1.61E+08
LPA	0.395833	0.095238	0	0	0	LPA	6	6q25.3	1.61E+08	1.61E+08
ADCY2	0.395833	0.095238	0	0	0	ADCY2	5	5p15.31	7449343	7883195
NPR3	0.395833	0.095238	0	0	0	NPR3	5	5p13.3	32747422	32823012
DAB2	0.395833	0	0.095238	0	0	DAB2	5	5p13.1	39407537	39461093
TTC33	0.395833	0.095238	0	0	0	TTC33	5	5p13.1	40747435	40791830

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromosome	cytoband	Transcript. start	Transcript. end
PRKAA1	0.395833	0.095238	0	0	0	PRKAA1	5	5p13.1	40795238	40834055
RPL37	0.395833	0.095238	0	0	0	RPL37	5	5p13.1	40867187	40871145
SNORD72	0.395833	0.095238	0	0	0	SNORD72	5	5p13.1	40868515	40868595
CARD6	0.395833	0.095238	0	0	0	CARD6	5	5p13.1	40877167	40891214
C7	0.395833	0	0.095238	0.037037	0	C7	5	5p13.1	40945356	41018799
ACTBL2	0.395833	0.095238	0.047619	0	0	ACTBL2	5	5q11.2	56811600	56814394
IPO11	0.395833	0.095238	0	0	0.037037	IPO11	5	5q12.1	61744330	61960172
LHFPL2	0.395833	0.095238	0	0	0	LHFPL2	5	5q14.1	77816794	77980405
ARSB	0.395833	0.095238	0	0	0	ARSB	5	5q14.1	78108793	78318114
RASGRF2	0.395833	0.095238	0	0	0.037037	RASGRF2	5	5q14.1	80292314	80557710
CKMT2	0.395833	0.095238	0	0	0.037037	CKMT2	5	5q14.1	80564895	80597974
ZCCHC9	0.395833	0.095238	0	0	0.037037	ZCCHC9	5	5q14.1	80633158	80644720
ACOT12	0.395833	0.095238	0	0	0.037037	ACOT12	5	5q14.1	80661703	80725745
MEF2C	0.395833	0.095238	0.238095	0	0.185185	MEF2C	5	5q14.3	88049815	88235626
RHOBTB3	0.395833	0.095238	0.047619	0	0.148148	RHOBTB3	5	5q15	95092606	95157828
GLRX	0.395833	0.095238	0.047619	0	0.148148	GLRX	5	5q15	95175309	95184334
C5orf27	0.395833	0.095238	0.047619	0	0.148148	C5orf27	5	5q15	95213592	95221591
TSSK1B	0.395833	0	0.095238	0	0	TSSK1B	5	5q22.2	1.13E+08	1.13E+08
3-Mar	0.395833	0.095238	0.047619	0	0.037037	3-Mar	5	5q23.2	1.26E+08	1.26E+08
CDC42SE2	0.395833	0.095238	0	0	0	CDC42SE2	5	5q31.1	1.31E+08	1.31E+08
RAPGEF6	0.395833	0.095238	0	0	0	RAPGEF6	5	5q31.1	1.31E+08	1.31E+08
FNIP1	0.395833	0.095238	0	0	0	FNIP1	5	5q31.1	1.31E+08	1.31E+08
GRIA1	0.395833	0	0.095238	0	0	GRIA1	5	5q33.2	1.53E+08	1.53E+08
GEMIN5	0.395833	0.047619	0.095238	0.148148	0	GEMIN5	5	5q33.2	1.54E+08	1.54E+08
KIF4B	0.395833	0	0.095238	0.111111	0	KIF4B	5	5q33.2	1.54E+08	1.54E+08
EBF1	0.395833	0	0.095238	0	0	EBF1	5	5q33.3	1.58E+08	1.58E+08
TTC1	0.395833	0.095238	0	0	0	TTC1	5	5q33.3	1.59E+08	1.59E+08
C5orf54	0.395833	0.095238	0.095238	0.037037	0	C5orf54	5	5q33.3	1.6E+08	1.6E+08
QDPR	0.395833	0.095238	0	0	0	QDPR	4	4p15.32	17097118	17122956
CLRN2	0.395833	0.095238	0	0	0	CLRN2	4	4p15.32	17125886	17137826
LAP3	0.395833	0.095238	0	0	0	LAP3	4	4p15.32	17188025	17218689
FAM184B	0.395833	0.095238	0	0	0	FAM184B	4	4p15.32	17242809	17392234
DCAF16	0.395833	0.095238	0	0	0	DCAF16	4	4p15.32	17411376	17421480
C4orf19	0.395833	0.095238	0	0	0.037037	C4orf19	4	4p14	37131947	37271528
RELL1	0.395833	0.095238	0	0	0	RELL1	4	4p14	37268817	37364395
PGM2	0.395833	0.095238	0	0	0	PGM2	4	4p14	37504677	37540955
T8C1D1	0.395833	0.095238	0	0	0	T8C1D1	4	4p14	37569115	37817190
FLI13197	0.395833	0.095238	0	0	0	FLI13197	4	4p14	38290717	38342645
ANKRD17	0.395833	0	0.095238	0	0	ANKRD17	4	4q13.3	74159366	74343367
AFP	0.395833	0	0.095238	0	0	AFP	4	4q13.3	74520797	74540357
AFM	0.395833	0	0.095238	0	0	AFM	4	4q13.3	74566326	74588583
RA5SF6	0.395833	0	0.095238	0	0	RA5SF6	4	4q13.3	74657726	74704999
DCLK2	0.395833	0.047619	0.095238	0	0	DCLK2	4	4q31.3	1.51E+08	1.51E+08
FAM160A1	0.395833	0.095238	0	0	0	FAM160A1	4	4q31.3	1.53E+08	1.53E+08
ITPR1	0.395833	0.095238	0.047819	0	0	ITPR1	3	3p26.2	4510032	4864523
DVWA	0.395833	0.238095	0.095238	0.185185	0	DVWA	3	3p24.3	15181875	15222471
PLCL2	0.395833	0	0.095238	0	0	PLCL2	3	3p24.3	16901456	17107102
UBE2E2	0.395833	0	0.095238	0	0	UBE2E2	3	3p24.3	23219788	23607301
UBE2E1	0.395833	0.095238	0.047619	0	0	UBE2E1	3	3p24.2	23822443	23907812
PDCD6IP	0.395833	0.095238	0.047619	0	0.037037	PDCD6IP	3	3p22.3	33815070	33886199
FOXPI	0.395833	0.095238	0.047619	0	0	FOXPI	3	3p14.1	71087426	71715831
GXYLT2	0.395833	0.095238	0.047619	0	0	GXYLT2	3	3p13	73020075	73107213
PPP4R2	0.395833	0.095238	0.047619	0	0	PPP4R2	3	3p13	73128809	73197702
RETNLB	0.395833	0	0.095238	0	0	RETNLB	3	3q13.13	1.1E+08	1.1E+08
TRAT1	0.395833	0	0.095238	0	0	TRAT1	3	3q13.13	1.1E+08	1.1E+08
GUCA1C	0.395833	0	0.095238	0	0	GUCA1C	3	3q13.13	1.1E+08	1.1E+08
MORC1	0.395833	0	0.095238	0	0	MORC1	3	3q13.13	1.1E+08	1.1E+08
BOC	0.395833	0.095238	0.047619	0	0.037037	BOC	3	3q13.2	1.14E+08	1.14E+08
NAT13	0.395833	0.095238	0.047619	0	0	NAT13	3	3q13.2	1.15E+08	1.15E+08
POLQ	0.395833	0.095238	0.047619	0	0	POLQ	3	3q13.33	1.23E+08	1.23E+08
ARGFX	0.395833	0.095238	0.047619	0	0	ARGFX	3	3q13.33	1.23E+08	1.23E+08
FBXO40	0.395833	0.095238	0.047619	0	0	FBXO40	3	3q13.33	1.23E+08	1.23E+08
GOLGB1	0.395833	0.047619	0.095238	0	0	GOLGB1	3	3q13.33	1.23E+08	1.23E+08
ACAD11	0.395833	0	0.095238	0	0	ACAD11	3	3q22.1	1.34E+08	1.34E+08
CCRL1	0.395833	0	0.095238	0	0	CCRL1	3	3q22.1	1.34E+08	1.34E+08
UBA5	0.395833	0	0.095238	0	0	UBA5	3	3q22.1	1.34E+08	1.34E+08
NCRNA001	0.395833	0	0.095238	0	0	NCRNA001	3	3q22.1	1.34E+08	1.34E+08
TMEM108	0.395833	0	0.095238	0	0	TMEM108	3	3q22.1	1.34E+08	1.35E+08
C3orf79	0.395833	0	0.095238	0	0	C3orf79	3	3q25.2	1.55E+08	1.55E+08
PLCH1	0.395833	0	0.095238	0	0	PLCH1	3	3q25.31	1.57E+08	1.57E+08
SHOX2	0.395833	0	0.095238	0	0	SHOX2	3	3q25.32	1.59E+08	1.59E+08
RSRC1	0.395833	0	0.095238	0	0	RSRC1	3	3q25.32	1.59E+08	1.6E+08
MFSD1	0.395833	0	0.095238	0	0	MFSD1	3	3q25.33	1.6E+08	1.6E+08
IQCI	0.395833	0	0.095238	0	0	IQCI	3	3q25.33	1.6E+08	1.6E+08

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
SCHIP1	0.395833	0	0.095238	0	0	SCHIP1	3	3q25.33	1.6E+08	1.61E+08
C3orf57	0.395833	0	0.095238	0	0	C3orf57	3	3q26.1	1.63E+08	1.63E+08
TBL1XR1	0.395833	0.095238	0	0	0	TBL1XR1	3	3q26.32	1.78E+08	1.78E+08
ZNF639	0.395833	0.095238	0	0	0	ZNF639	3	3q26.32	1.81E+08	1.81E+08
GN84	0.395833	0.095238	0	0	0	GN84	3	3q26.33	1.81E+08	1.81E+08
ACTL6A	0.395833	0.095238	0	0	0	ACTL6A	3	3q26.33	1.81E+08	1.81E+08
MRPL47	0.395833	0.095238	0.047619	0	0	MRPL47	3	3q26.33	1.81E+08	1.81E+08
USP13	0.395833	0.095238	0	0	0	USP13	3	3q26.33	1.81E+08	1.81E+08
SOX2OT	0.395833	0.095238	0.095238	0	0.037037	SOX2OT	3	3q26.33	1.83E+08	1.83E+08
TPRG1	0.395833	0	0.095238	0.037037	0	TPRG1	3	3q28	1.9E+08	1.91E+08
TP63	0.395833	0	0.095238	0.037037	0	TP63	3	3q28	1.91E+08	1.91E+08
LEPREL1	0.395833	0	0.095233	0	0	LEPREL1	3	3q28	1.91E+08	1.91E+08
CLDN1	0.395833	0	0.095238	0	0	CLDN1	3	3q28	1.92E+08	1.92E+08
IL1RAP	0.395833	0	0.095238	0	0	IL1RAP	3	3q28	1.92E+08	1.92E+08
LOC647309	0.395833	0	0.095238	0	0	LOC647309	3	3q28	1.92E+08	1.92E+08
SNAR-I	0.395833	0	0.095238	0	0	SNAR-I	3	3q28	1.92E+08	1.92E+08
HRASLS	0.395833	0.047619	0.095238	0	0	HRASLS	3	3q29	1.94E+08	1.94E+08
ATP13A5	0.395833	0.047619	0.095238	0	0	ATP13A5	3	3q29	1.94E+08	1.95E+08
ROCK2	0.395833	0.333333	0.095238	0.259259	0	ROCK2	2	2p25.1	11239229	11402163
C2orf43	0.395833	0.047619	0.095238	0	0	C2orf43	2	2p24.1	20748299	20886309
CRIM1	0.395833	0.095238	0	0	0	CRIM1	2	2p22.2	36436901	36631783
CDKL4	0.395833	0.095238	0	0	0	CDKL4	2	2p22.1	39259192	39310178
MAP4K3	0.395833	0.095238	0	0	0	MAP4K3	2	2p22.1	39329926	39517724
SLC9A2	0.395833	0.095238	0.047619	0	0	SLC9A2	2	2q12.1	1.03E+08	1.03E+08
SLC5A7	0.395833	0.047619	0.095238	0.074074	0	SLC5A7	2	2q12.3	1.08E+08	1.08E+08
DDX18	0.395833	0.095238	0	0	0.037037	DDX18	2	2q14.1	1.18E+08	1.18E+08
CCDC93	0.395833	0.095238	0	0	0.037037	CCDC93	2	2q14.1	1.18E+08	1.18E+08
MGAT5	0.395833	0.095238	0	0	0	MGAT5	2	2q21.3	1.35E+08	1.35E+08
KIFSC	0.395833	0.095238	0.047619	0	0.037037	KIFSC	2	2q23.1	1.49E+08	1.5E+08
MIR1978	0.395833	0.095238	0.047619	0	0.037037	MIR1978	2	2q23.1	1.49E+08	1.49E+08
RND3	0.395833	0	0.095238	0	0	RND3	2	2q23.3	1.51E+08	1.51E+08
DPP4	0.395833	0.095238	0	0	0.111111	DPP4	2	2q24.2	1.63E+08	1.63E+08
DYNC1I2	0.395833	0.047619	0.095238	0.074074	0	DYNC1I2	2	2q31.1	1.72E+08	1.72E+08
OLA1	0.395833	0.095238	0.047619	0	0	OLA1	2	2q31.1	1.75E+08	1.75E+08
GPR155	0.395833	0.095238	0	0	0	GPR155	2	2q31.1	1.75E+08	1.75E+08
WIPF1	0.395833	0.095238	0	0	0	WIPF1	2	2q31.1	1.75E+08	1.75E+08
CHRNA1	0.395833	0.095238	0	0	0	CHRNA1	2	2q31.1	1.75E+08	1.75E+08
KCTD18	0.395833	0.095238	0	0	0	KCTD18	2	2q33.1	2.01E+08	2.01E+08
SGOL2	0.395833	0.095238	0	0	0	SGOL2	2	2q33.1	2.01E+08	2.01E+08
AOX1	0.395833	0.095238	0	0	0	AOX1	2	2q33.1	2.01E+08	2.01E+08
PARD3B	0.395833	0	0.095238	0	0	PARD3B	2	2q33.2	2.05E+08	2.06E+08
TMEM57	0.395833	0.47619	0.095238	0.592593	0	TMEM57	1	1p36.11	25629975	25699284
LDLRAP1	0.395833	0.47619	0.095238	0.592593	0	LDLRAP1	1	1p36.11	25742663	25767965
SKINTL	0.395833	0.047619	0.095238	0.222222	0	SKINTL	1	1p33	48339974	48420688
DNAJC6	0.395833	0.095238	0	0	0	DNAJC6	1	1p31.3	65503018	65654141
LEPR	0.395833	0.095238	0	0	0	LEPR	1	1p31.3	65558836	65873699
LEPROT	0.395833	0.095238	0	0	0	LEPROT	1	1p31.3	65658836	65674277
TCTEX1D1	0.395833	0	0.095238	0	0	TCTEX1D1	1	1p31.3	66990728	67017318
WDR78	0.395833	0	0.095238	0	0	WDR78	1	1p31.3	67051161	67163159
SLC35D1	0.395833	0	0.095238	0	0	SLC35D1	1	1p31.3	67237604	67292669
SERBP1	0.395833	0.095238	0	0	0	SERBP1	1	1p31.3	67646081	67668712
HFM1	0.395833	0.095238	0	0	0	HFM1	1	1p22.2	91498911	91643015
CDC7	0.395833	0.095238	0	0	0	CDC7	1	1p22.2	91738992	91763909
HSP90B3P	0.395833	0.095238	0	0	0	HSP90B3P	1	1p22.2	91873156	91881923
TGFBR3	0.395833	0.095238	0	0	0	TGFBR3	1	1p22.2	91918490	92124376
BRDT	0.395833	0.095238	0	0	0	BRDT	1	1p22.1	92187516	92252574
EPHX4	0.395833	0.095238	0	0	0	EPHX4	1	1p22.1	92268121	92301682
BTBD8	0.395833	0.095238	0	0	0	BTBD8	1	1p22.1	92318450	92385984
KIAA1107	0.395833	0.095238	0	0	0	KIAA1107	1	1p22.1	92405197	92422868
GFI1	0.395833	0.095238	0	0	0	GFI1	1	1p22.1	92712906	92721945
EV15	0.395833	0.095238	0	0	0	EV15	1	1p22.1	92746841	93030550
ABCD3	0.395833	0.095238	0.047619	0	0	ABCD3	1	1p21.3	94656521	94716849
SLC44A3	0.395833	0.095238	0	0	0	SLC44A3	1	1p21.3	95058489	35133391
CNN3	0.395833	0.095238	0	0	0	CNN3	1	1p21.3	95135095	95165324
ALG14	0.395833	0.095238	0	0	0	ALG14	1	1p21.3	95220867	95311096
TMEM56	0.395833	0.095238	0.047619	0	0.037037	TMEM56	1	1p21.3	95355482	95435748
GDAP2	0.395833	0	0.095238	0.037037	0	GDAP2	1	1p12	1.18E+08	1.18E+08
SPAG17	0.395833	0	0.095238	0.037037	0	SPAG17	1	1p12	1.18E+08	1.19E+08
TBX15	0.395833	0	0.095238	0	0	TBX15	1	1p12	1.19E+08	1.19E+08
SPRR2F	0.395833	0.095238	0.095238	0.185185	0	SPRR2F	1	1q21.3	1.51E+08	1.51E+08
SPRR2C	0.395833	0.095238	0.095238	0.185185	0	SPRR2C	1	1q21.3	1.51E+08	1.51E+08
SPRR2G	0.395833	0.095238	0.095238	0.185185	0	SPRR2G	1	1q21.3	1.51E+08	1.51E+08
CD1D	0.395833	0.047619	0.095238	0.074074	0	CD1D	1	1q23.1	1.56E+08	1.56E+08
CD1A	0.395833	0.047619	0.095238	0.074074	0	CD1A	1	1q23.1	1.56E+08	1.56E+08

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
SPTA1	0.395833	0.047619	0.095238	0.074074	0	SPTA1	1	1q23.1	1.57E+08	1.57E+08
OR6K6	0.395833	0.047619	0.095238	0.074074	0	OR6K6	1	1q23.1	1.57E+08	1.57E+08
PYHIN1	0.395833	0.047619	0.095238	0.074074	0	PYHIN1	1	1q23.1	1.57E+08	1.57E+08
IFI16	0.395833	0.047519	0.095238	0.074074	0	IFI16	1	1q23.1	1.57E+08	1.57E+08
AIM2	0.395833	0.047619	0.095238	0.074074	0	AIM2	1	1q23.1-1q23.2	1.57E+08	1.57E+08
DUSP12	0.395833	0.047619	0.095238	0	0	DUSP12	1	1q23.3	1.6E+08	1.6E+08
ATF6	0.395833	0.047619	0.095238	0	0	ATF6	1	1q23.3	1.6E+08	1.6E+08
M1R556	0.395833	0.095233	0	0	0	M1R556	1	1q23.3	1.61E+08	1.61E+08
UHMK1	0.395833	0.095238	0	0	0	UHMK1	1	1q23.3	1.61E+08	1.61E+08
FAM78B	0.395833	0.095238	0	0	0	FAM78B	1	1q24.1	1.64E+08	1.64E+08
GPA33	0.395833	0.095238	0	0	0	GPA33	1	1q24.1	1.65E+08	1.65E+08
DUSP27	0.395833	0.095238	0	0	0	DUSP27	1	1q24.1	1.65E+08	1.65E+08
POU2F1	0.395833	0.095238	0	0	0	POU2F1	1	1q24.2	1.65E+08	1.66E+08
CD247	0.395833	0.095238	0	0	0	CD247	1	1q24.2	1.66E+08	1.66E+08
CREG1	0.395833	0.095238	0	0	0	CREG1	1	1q24.2	1.66E+08	1.06E+08
RCSD1	0.395833	0.095238	0	0	0	RCSD1	1	1q24.2	1.66E+08	1.66E+08
MPZL1	0.395833	0.095238	0	0	0	MPZL1	1	1q24.2	1.66E+08	1.66E+08
ADCY10	0.395833	0.095238	0	0	0	ADCY10	1	1q24.2	1.66E+08	1.66E+08
BRP44	0.395833	0.095238	0	0	0	BRP44	1	1q24.2	1.66E+08	1.66E+08
DCAF6	0.395833	0.095238	0	0	0	DCAF6	1	1q24.2	1.66E+08	1.66E+08
GPR161	0.395833	0.095238	0	0	0	GPR161	1	1q24.2	1.66E+08	1.66E+08
ANKRD36B	0.395833	0.095238	0	0	0	ANKRD36B	1	1q24.2	1.66E+08	1.66E+08
MIR557	0.395833	0.095238	0	0	0	MIR557	1	1q24.2	1.67E+08	1.67E+08
KIFAP3	0.395833	0	0.095238	0	0	KIFAP3	1	1q24.2	1.68E+08	1.68E+08
METTL11B	0.395833	0	0.095238	0	0	METTL11B	1	1q24.2	1.68E+08	1.68E+08
FMO3	0.395833	0	0.095238	0	0	FMO3	1	1q24.3	1.69E+08	1.69E+08
MIR1295	0.395833	0	0.095238	0	0	MIR1295	1	1q24.3	1.69E+08	1.69E+08
FMO2	0.395833	0	0.095238	0	0	FMO2	1	1q24.3	1.69E+08	1.69E+08
FMO1	0.395833	0	0.095238	0	0	FMO1	1	1q24.3	1.69E+08	1.7E+08
FMO4	0.395833	0.095238	0	0	0	FMO4	1	1q24.3	1.7E+08	1.7E+08
TOP1P1	0.395833	0.095238	0	0	0	TOP1P1	1	1q24.3	1.7E+08	1.7E+08
BAT2L2	0.395833	0.095238	0	0	0	BAT2L2	1	1q24.3	1.7E+08	1.7E+08
MYOC	0.395833	0.095238	0	0	0	MYOC	1	1q24.3	1.7E+08	1.7E+08
C1orf105	0.395833	0	0.095238	0	0	C1orf105	1	1q24.3	1.71E+08	1.71E+08
C1orf9	0.395833	0	0.095238	0	0	C1orf9	1	1q24.3	1.71E+08	1.71E+08
RABGAP1L	0.395833	0.095238	0.047619	0	0	RABGAP1L	1	1q25.1	1.72E+08	1.73E+08
XPR1	0.395833	0.095238	0	0	0	XPR1	1	1q25.3	1.79E+08	1.79E+08
CACNA1E	0.395833	0.095238	0	0	0	CACNA1E	1	1q25.3	1.8E+08	1.8E+08
LAMC1	0.395833	0.095238	0	0	0	LAMC1	1	1q25.3	1.81E+08	1.81E+08
LAMC2	0.395833	0.095238	0	0	0	LAMC2	1	1q25.3	1.81E+08	1.81E+08
C4BPA	0.395833	0.095238	0.095238	0.259259	0	C4BPA	1	1q32.2	2.05E+08	2.05E+08
SYT14	0.395833	0.095238	0.095238	0.111111	0	SYT14	1	1q32.2	2.08E+08	2.08E+08
LOC400804	0.395833	0	0.095238	0	0	LOC400804	1	1q41	2.2E+08	2.2E+08
AKT3	0.395833	0	0.095238	0	0	AKT3	1	1q44	2.42E+08	2.42E+08
OR2L13	0.395833	0.095238	0.095238	0.111111	0	OR2L13	1	1q44	2.46E+08	2.46E+08
C21orf34	0.020833	0	0.142857	0	0.037037	C21orf34	21	21q21.1	16364713	16903966
SMCHD1	0.020833	0.190476	0	0.037037	0	SMCHD1	18	18p11.3	2645886	2795016
LOC727896	0.020833	0.238095	0	0.037037	0	LOC727896	18	18p11.3	2933215	2936622
ARHGAP28	0.020833	0.190475	0	0.037037	0	ARHGAP28	18	18p11.31	6824484	6905713
PTPRM	0.020833	0.190476	0	0.037037	0	PTPRM	18	18p11.23	7557314	8396860
CTAGE1	0.020833	0.190476	0	0.037037	0	CTAGE1	18	18q11.2	18247562	18251877
RBBP8	0.020833	0.285714	0	0.037037	0.111111	RBBP8	18	18q11.2	18767293	18860448
MAPRE2	0.020833	0	0.142857	0	0.037037	MAPRE2	18	18q12.1	30810890	30976376
FHOD3	0.020833	0.142857	0	0.037037	0	FHOD3	18	18q12.2	32131700	32614017
KIAA1328	0.020833	0	0.142857	0.037037	0.037037	KIAA1328	18	18q12.2	32663078	33059287
DYM	0.020833	0.047619	0.142857	0.148148	0.037037	DYM	18	18q21.1	44824170	45241078
ALPK2	0.020833	0.238095	0	0.037037	0	ALPK2	18	18q21.31	54299462	54447170
MALT1	0.020833	0.238095	0	0.037037	0	MALT1	18	18q21.32	54489598	54568351
ZNF532	0.020833	0.238095	0	0.037037	0	ZNF532	18	18q21.32	54681041	54804690
LOC390858	0.020833	0.238095	0	0.037037	0	LOC390858	18	18q21.32	54853951	54871427
SEC11C	0.020833	0.238095	0	0.037037	0	SEC11C	18	18q21.32	54958105	54977044
CPLX4	0.020833	0.238095	0	0.037037	0	CPLX4	18	18q21.32	55113618	55136862
LMAN1	0.020833	0.238095	0	0.037037	0	LMAN1	18	18q21.32	55146037	55177489
CCBE1	0.020833	0.238095	0	0.037037	0	CCBE1	18	18q21.32	55252129	55515625
PHLPP1	0.020833	0.190476	0	0.037037	0	PHLPP1	18	18q21.33	58533714	58798647
SERPINB3	0.020833	0	0.190476	0	0.037037	SERPINB3	18	18q21.33	59473411	59480178
CYB5A	0.020833	0.238095	0	0.037037	0	CYB5A	18	18q22.3	70071507	70110202
FAM69C	0.020833	0.238095	0	0.037037	0	FAM69C	18	18q22.3	70253943	70275484
CNDP2	0.020833	0.238095	0	0.037037	0	CNDP2	18	18q22.3	70314480	70341668
CHD9	0.020833	0.190476	0	0.037037	0	CHD9	16	16q12.2	51646446	51918916
AKTIP	0.020833	0.142857	0	0.037037	0	AKTIP	16	16q12.2	52082693	52094672
IRX3	0.020833	0.142857	0	0.037037	0	IRX3	16	16q12.2	52574713	52877880
WWOX	0.020833	0.142857	0.047619	0.037037	0	WWOX	16	16q23.1	76691052	77804066

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
SNRPN	0.020833	0.190476	0	0.037037	0	SNRPN	15	15q11.2	22619887	22774823
ATPBD4	0.020833	0.047619	0.142857	0.037037	0.037037	ATPBD4	15	15q14	33450462	33625697
C15orf41	0.020833	0.047619	0.142857	0	0.037037	C15orf41	15	15q14	34659104	34889742
CSNK1A1P	0.020833	0.047619	0.142857	0	0.037037	CSNK1A1P	15	15q14	34878594	34898000
LOC145845	0.020833	0.047619	0.142857	0	0.037037	LOC145845	15	15q14	34943936	34966027
GLDN	0.020833	0.190476	0	0.037037	0	GLDN	15	15q21.2	49421005	49487502
GCOM1	0.020833	0.190476	0	0.037037	0	GCOM1	15	15q21.3	55671406	55797046
GRINL1A	0.020833	0.190476	0	0.037037	0	GRINL1A	15	15q21.3	55786193	55797046
AQP9	0.020833	0.142857	0.047619	0.037037	0	AQP9	15	15q22.1	56217700	56265403
SCAPER	0.020833	0.238095	0.142857	0.481481	0.037037	SCAPER	15	15q24.3	74427584	74941341
TTC5	0.020833	0.238095	0	0.037037	0.037037	TTC5	14	14q11.2	19827141	19843994
CCNB1IP1	0.020833	0.238095	0	0.037037	0.037037	CCNB1IP1	14	14q11.2	19849369	19871298
SNORD126	0.020833	0.238095	0	0.037037	0.037037	SNORD126	14	14q11.2	19864440	19864539
MIR1201	0.020833	0.238095	0	0.037037	0.037037	MIR1201	14	14q11.2	19864449	19864531
RPPH1	0.020833	0.238095	0	0.037037	0.037037	RPPH1	14	14q11.2	19881070	19881411
PARP2	0.020833	0.238095	0	0.037037	0.037037	PARP2	14	14q11.2	19881613	19895904
METT11D1	0.020833	0.285724	0	0.037037	0	METT11D1	14	14q11.2	20527805	20535035
S1C39A2	0.020833	0.285714	0	0.037037	0	S1C39A2	14	14q11.2	20537259	20539871
NDRG2	0.020833	0.285714	0	0.037037	0	NDRG2	14	14q11.2	20554762	20563776
TPPP2	0.020833	0.285714	0	0.037037	0	TPPP2	14	14q11.2	20568185	20570171
RNASE13	0.020833	0.285714	0	0.037037	0	RNASE13	14	14q11.2	20570819	20572785
RNASE7	0.020833	0.285714	0	0.037037	0	RNASE7	14	14q11.2	20580225	20582233
RNASE8	0.020833	0.285714	0	0.037037	0	RNASE8	14	14q11.2	20595892	20596357
FLI10357	0.020833	0.285714	0	0.037037	0	FLI10357	14	14q11.2	20608367	20627877
ZNF219	0.020833	0.285714	0	0.037037	0	ZNF219	14	14q11.2	20628045	20637014
C14orf176	0.020833	0.285714	0	0.037037	0	C14orf176	14	14q11.2	20636936	20641723
OR5AU1	0.020833	0.285714	0	0.037037	0	OR5AU1	14	14q11.2	20692936	20694025
HNRNPC	0.020833	0.285714	0	0.037037	0	HNRNPC	14	14q11.2	20747136	20807473
RPGRIP1	0.020833	0.285714	0	0.037037	0	RPGRIP1	14	14q11.2	20825976	20889301
SUPT16H	0.020833	0.285714	0	0.037037	0	SUPT16H	14	14q11.2	20889472	20922266
RAB2B	0.020833	0.285714	0	0.037037	0	RAB2B	14	14q11.2	20997020	21014673
TOX4	0.020833	0.285714	0	0.037037	0	TOX4	14	14q11.2	21015175	21037160
METTL3	0.020833	0.285714	0	0.037037	0	METTL3	14	14q11.2	21036122	21049298
SALL2	0.020833	0.285714	0	0.037037	0	SALL2	14	14q11.2	21059072	21075178
OR10G3	0.020833	0.285714	0	0.037037	0	OR10G3	14	14q11.2	21107774	21108716
STRN3	0.020833	0.285714	0	0.037037	0	STRN3	14	14q12	30432756	30565359
MIA2	0.020833	0.142857	0.047619	0.037037	0.074074	MIA2	14	14q21.1	38772876	38792327
CTAGE5	0.020833	0.142857	0.047619	0.037037	0.074074	CTAGE5	14	14q21.1	38804227	38890149
GCH1	0.020833	0.190476	0	0.037037	0	GCH1	14	14q22.2	54378474	54439293
WDHD1	0.020833	0.190476	0	0.037037	0	WDHD1	14	14q22.3	54476692	54563558
MAPK1IP1L	0.020833	0.190476	0	0.037037	0	MAPK1IP1L	14	14q22.3	54588115	54606666
DLGAP5	0.020833	0.190476	0	0.037037	0	DLGAP5	14	14q22.3	54684589	54728150
FBXO34	0.020833	0.190476	0	0.037037	0	FBXO34	14	14q22.3	54807774	54890081
KIAA0831	0.020833	0.190476	0	0.037037	0	KIAA0831	14	14q22.3	54902863	54948330
TBPL2	0.020833	0.190476	0	0.037037	0	TBPL2	14	14q22.3	54950683	54977017
HIF1A	0.020833	0.142857	0	0.037037	0	HIF1A	14	14q23.2	61231872	61284731
DIO2	0.020833	0	0.142857	0	0.037037	DIO2	14	14q31.1	79733622	79748279
LOC284232	0.020833	0.142857	0	0.037037	0.074074	LOC284232	13	13q11	18306543	18344110
SGCG	0.020833	0.238095	0	0.037037	0	SGCG	13	13q12.12	22653060	22797305
MIPEP	0.020833	0.238095	0	0.037037	0	MIPEP	13	13q12.12	23202328	23361560
TRPC4	0.020833	0	0.190476	0	0.037037	TRPC4	13	13q13.3	37108775	37341940
CLDN10	0.020833	0.380952	0	0.037037	0	CLDN10	13	13q32.1	94883854	95030012
UBAC2	0.020833	0.238095	0	0.037037	0	UBAC2	13	13q32.3	98650680	98836753
MIR623	0.020833	0.190476	0	0.037037	0	MIR623	13	13q32.3	98806386	98806484
CLYBL	0.020833	0.190476	0	0.037037	0	CLYBL	13	13q32.3	99056920	99347389
A2LD1	0.020833	0.142857	0	0.037037	0	A2LD1	13	13q32.3	99981811	99983999
CCDC91	0.020833	0	0.190476	0	0.037037	CCDC91	12	12p11.22	28301400	28594367
LRIG3	0.020833	0	0.190476	0	0.037037	LRIG3	12	12q14.1	57552204	57600530
TPH2	0.020833	0	0.190476	0	0.037037	TPH2	12	12q21.1	70618893	70712489
LOC100128191	0.020833	0.333333	0	0.037037	0	LOC100128191	12	12q23.1	97430884	97434136
TMPO	0.020833	0.333333	0	0.037037	0	TMPO	12	12q23.1	97433540	97466867
SLC25A3	0.020833	0.333333	0	0.037037	0	SLC25A3	12	12q23.1	97511534	97519909
APAF1	0.020833	0.285714	0	0.037037	0	APAF1	12	12q23.1	97563209	97653343
SOX6	0.020833	0.047619	0.190476	0	0.037037	SOX6	11	11p15.2-11p15.1	15944572	16387007
ABCC8	0.020833	0.285714	0	0.037037	0	ABCC8	11	11p15.1	17371008	17455026
USH1C	0.020833	0.285714	0	0.037037	0	USH1C	11	11p15.1	17472019	17522540
LOC494141	0.020833	0.142857	0	0.037037	0	LOC494141	11	11p15.1	18187261	18189631
SAA4	0.020833	0.142857	0	0.037037	0	SAA4	11	11p15.1	18209480	18214932
SAA2	0.020833	0.142857	0	0.037037	0	SAA2	11	11p15.1	18217164	18226759
SAA1	0.020833	0.142857	0	0.037037	0	SAA1	11	11p15.1	18244348	18248103
HPS5	0.020833	0.142857	0	0.037037	0	HPS5	11	11p15.1	18256793	18300298
GTF2H1	0.020833	0.142857	0	0.037037	0	GTF2H1	11	11p15.1	18300392	18345167
CCDC73	0.020833	0.285714	0	0.037037	0	CCDC73	11	11p13	32580202	32772764

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
QSER1	0.020833	0.285714	0	0.037037	0	QSER1	11	11p13	32871368	32958391
DEPDC7	0.020833	0.285714	0	0.037037	0.037037	DEPDC7	11	11p13	32993986	33011705
TCP11L1	0.020833	0.285714	0	0.037037	0.037037	TCP11L1	11	11p13	33017539	33051685
LOC283267	0.020833	0.285714	0	0.037037	0	LOC283267	11	11p13	33054272	33057576
CSTF3	0.020833	0.238095	0.047619	0.037037	0	CSTF3	11	11p13	33062706	33139614
ABTB2	0.020833	0.238095	0	0.037037	0	ABTB2	11	11p13	34129111	34335379
CAT	0.020833	0.238095	0	0.037037	0	CAT	11	11p13	34417048	34450183
ZDHHC5	0.020833	0.285714	0	0.037037	0	ZDHHC5	11	11q12.1	57192050	57225236
MED19	0.020833	0.285714	0	0.037037	0	MED19	11	11q12.1	57227763	57236250
TMX2	0.020833	0.285714	0	0.037037	0	TMX2	11	11q12.1	57236618	57265021
C11orf31	0.020833	0.285714	0	0.037037	0	C11orf31	11	11q12.1	57265298	57267460
BTBD18	0.020833	0.285714	0	0.037037	0	BTBD18	11	11q12.1	57267563	57275830
CTNND1	0.020833	0.285714	0	0.037037	0	CTNND1	11	11q12.1	57285810	57343229
OR9Q1	0.020833	0.190476	0	0.037037	0	OR9Q1	11	11q12.1	57547929	57705615
OR6Q1	0.020833	0.190476	0	0.037037	0	OR6Q1	11	11q12.1	57555001	57555955
KIAA1377	0.020833	0	0.190476	0	0.037037	KIAA1377	11	11q22.1	1.01E+08	1.01E+08
CADM1	0.020833	0.142857	0.190476	0.185185	0.037037	CADM1	11	11q23.2	1.15E+08	1.15E+08
LOC399959	0.020833	0.047619	0.142857	0.111111	0.037037	LOC399959	11	11q24.1	1.21E+08	1.22E+08
MKX	0.020833	0.190476	0	0.037037	0	MKX	10	10p12.1	28001809	28074785
ARMC4	0.020833	0.190476	0	0.037037	0	ARMC4	10	10p12.1	28141103	28327984
MPP7	0.020833	0.190476	0	0.037037	0	MPP7	10	10p11.23	28379929	28611074
CREM	0.020833	0.238095	0	0.037037	0	CREM	10	10p11.21	35455507	35508782
CCNY	0.020833	0.238095	0	0.037037	0	CCNY	10	10p11.21	35575959	35900854
LOC728640	0.020833	0	0.238095	0	0.037037	LOC728640	10	10q21.1	60144781	60147298
C10orf107	0.020333	0	0.142857	0	0.037037	C10orf107	10	10q21.2	63092725	63196096
ANXA2P3	0.020833	0	0.190476	0	0.037037	ANXA2P3	10	10q21.3	66255291	66256641
LIPF	0.020833	0	0.142857	0	0.037037	LIPF	10	10q23.31	90414074	90428553
TCF7L2	0.020833	0.190476	0	0.037037	0	TCF7L2	10	10q25.2	1.15E+08	1.15E+08
HABP2	0.020833	0.142857	0.047619	0.037037	0	HABP2	10	10q25.3	1.15E+08	1.15E+08
NRAP	0.020833	0.190476	0.047619	0.037037	0	NRAP	10	10q25.3	1.15E+08	1.15E+08
CASP7	0.020833	0.190476	0	0.037037	0	CASP7	10	10q25.3	1.15E+08	1.15E+08
C10orf81	0.020833	0.190476	0	0.037037	0	C10orf81	10	10q25.3	1.16E+08	1.16E+08
NHLRC2	0.020833	0.190476	0	0.037037	0	NHLRC2	10	10q25.3	1.16E+08	1.16E+08
ADRB1	0.020833	0.190476	0	0.037037	0	ADRB1	10	10q25.3	1.16E+08	1.16E+08
C10orf118	0.020833	0.238095	0	0.037037	0	C10orf118	10	10q25.3	1.16E+08	1.16E+08
MIR2110	0.020833	0.238095	0	0.037037	0	MIR2110	10	10q25.3	1.16E+08	1.16E+08
TDRD1	0.020833	0.238095	0	0.037037	0	TDRD1	10	10q25.3	1.16E+08	1.16E+08
ATRNL1	0.020833	0.047619	0.238095	0.074074	0.037037	ATRNL1	10	10q25.3	1.17E+08	1.18E+08
DOCK8	0.020833	0.285714	0	0.037037	0	DOCK8	9	9p24.3	204865	455250
KANK1	0.020833	0.333333	0	0.037037	0	KANK1	9	9p24.3	494703	736104
SNAPC3	0.020833	0.142857	0	0.037037	0	SNAPC3	9	9p22.3	15412782	15451628
C9orf93	0.020833	0.142857	0	0.037037	0	C9orf93	9	9p22.3	15543097	15961898
IFNA14	0.020833	0	0.142857	0	0.037037	IFNA14	9	9p21.3	21229201	21229979
C9orf82	0.020833	0.142857	0.047619	0.037037	0.074074	C9orf82	9	9p21.2	26830684	26882827
IFT74	0.020833	0.142857	0.047619	0.037037	0.037037	IFT74	9	9p21.2	26937037	27052932
FXN	0.020833	0.238095	0	0.037037	0	FXN	9	9q21.11	70840299	70883814
TJP2	0.020833	0.238095	0	0.037037	0	TJP2	9	9q21.11	70926044	71059945
FAM189A2	0.020833	0.142857	0	0.037037	0	FAM189A2	9	9q21.11	71129308	71197191
APBA1	0.020833	0.238095	0	0.037037	0	APBA1	9	9q21.11	71232269	71477096
RASEF	0.020833	0	0.142857	0.037037	0.037037	RASEF	9	9q21.32	84787137	84867864
SLC44A1	0.020833	0.238095	0	0.037037	0	SLC44A1	9	9q31.1	1.07E+08	1.07E+08
KLF4	0.020833	0.190476	0	0.037037	0	KLF4	9	9q31.2	1.09E+08	1.09E+08
EPB4114B	0.020833	0.190476	0	0.037037	0	EPB4114B	9	9q31.3	1.11E+08	1.11E+08
PALM2	0.020833	0.142857	0	0.037037	0	PALM2	9	9q31.3	1.11E+08	1.12E+08
PALM2-AKAP2	0.020833	0.142857	0	0.037037	0	PALM2-AKAP2	9	9q31.3	1.12E+08	1.12E+08
AKAP2	0.020833	0.142857	0	0.037037	0	AKAP2	9	9q31.3	1.12E+08	1.12E+08
C9orf152	0.020833	0.142857	0	0.037037	0	C9orf152	9	9q31.3	1.12E+08	1.12E+08
FGF20	0.020833	0	0.142857	0	0.037037	FGF20	8	8p22	16894705	16904046
MAK16	0.020833	0.238035	0	0.037037	0.037037	MAK16	8	8p12	33462227	33478320
TCEA1	0.020833	0.142857	0	0.037037	0	TCEA1	8	8q11.23	55041669	55097562
RRS1	0.020833	0.190476	0	0.037037	0	RRS1	8	8q13.1	67503817	67505523
ADHFE1	0.020833	0.190476	0	0.037037	0	ADHFE1	8	8q13.1	67507272	67543599
C8orf46	0.020833	0.190476	0	0.037037	0	C8orf46	8	8q13.1	67568045	67593312
VCPIP1	0.020833	0.238095	0	0.037037	0	VCPIP1	8	8q13.1	67705042	67742007
C8orf44	0.020833	0.238095	0	0.037037	0	C8orf44	8	8q13.1	67751008	67755790
SGK3	0.020833	0.190476	0	0.037037	0	SGK3	8	8q13.1	67787445	67936812
NCOA2	0.020833	0.190476	0	0.037037	0	NCOA2	8	8q13.3	71186821	71478575
KCNB2	0.020833	0.047619	0.142857	0	0.037037	KCNB2	8	8q13.3	73612180	74013139
C8orf84	0.020833	0.142857	0.047619	0.037037	0	C8orf84	8	8q21.11	74139334	74168062
RDH10	0.020833	0.142857	0.047619	0.037037	0	RDH10	8	8q21.11	74369819	74400069
UBE2W	0.020833	0.190476	0.047619	0.037037	0	UBE2W	8	8q21.11	74865394	74953665
TCEB1	0.020833	0.190476	0.047619	0.037037	0	TCEB1	8	8q21.11	75021188	75046901
HEY1	0.020833	0.142857	0.047619	0.037037	0.111111	HEY1	8	8q21.13	80838800	80842654

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
RUNX1T1	0.020833	0.047619	0.142857	0	0.037037	RUNX1T1	8	8q21.3	93040328	93144368
C8orf83	0.020833	0	0.333333	0	0.037037	C8orf83	8	8q22.1	93965039	94047516
CDH17	0.020833	0.238095	0	0.037037	0	CDH17	8	8q22.1	95208570	95298708
GEM	0.020833	0.238095	0	0.037037	0	GEM	8	8q22.1	95330663	95343724
TSPYL5	0.020833	0.190476	0	0.037037	0	TSPYL5	8	8q22.1	98354890	98359353
MTDH	0.020833	0.190476	0	0.037037	0	MTDH	8	8q22.1	98725583	98811664
ANKRD46	0.020833	0.238095	0	0.037037	0	ANKRD46	8	8q22.2-8q22.3	1.02E+08	1.02E+08
SNX31	0.020833	0.238095	0	0.037037	0	SNX31	8	8q22.3	1.02E+08	1.02E+08
NACAP1	0.020833	0.190476	0	0.037037	0	NACAP1	8	8q22.3	1.02E+08	1.02E+08
GRHL2	0.020833	0.190476	0	0.037037	0	GRHL2	8	8q22.3	1.03E+08	1.03E+08
ATAD2	0.020833	0.285714	0	0.037037	0	ATAD2	8	8q24.13	1.24E+08	1.24E+08
WDYHV1	0.020833	0.285714	0	0.037037	0	WDYHV1	8	8q24.13	1.24E+08	1.25E+08
FBXO32	0.020833	0.285714	0	0.037037	0	FBXO32	8	8q24.13	1.25E+08	1.25E+08
ANXA13	0.020833	0.285714	0	0.037037	0	ANXA13	8	8q24.13	1.25E+08	1.25E+08
FAM91A1	0.020833	0.285714	0	0.037037	0	FAM91A1	8	8q24.13	1.25E+08	1.25E+08
FER1L6	0.020833	0.238095	0	0.037037	0	FER1L6	8	8q24.13	1.25E+08	1.25E+08
TRMT12	0.020833	0.285714	0	0.037037	0	TRMT12	8	8q24.13	1.26E+08	1.26E+08
RNF139	0.020833	0.285714	0	0.037037	0	RNF139	8	8q24.13	1.26E+08	1.26E+08
TATDN1	0.020833	0.285714	0	0.037037	0	TATDN1	8	8q24.13	1.26E+08	1.26E+08
NDUFB9	0.020833	0.285714	0	0.037037	0	NDUFB9	8	8q24.13	1.26E+08	1.26E+08
MTSS1	0.020833	0.285714	0	0.037037	0	MTSS1	8	8q24.13	1.26E+08	1.26E+08
LOC157381	0.020833	0.285714	0	0.037037	0	LOC157381	8	8q24.13	1.26E+08	1.26E+08
ZNF572	0.020833	0.285714	0	0.037037	0	ZNF572	8	8q24.13	1.26E+08	1.26E+08
SQLE	0.020833	0.285714	0	0.037037	0	SQLE	8	8q24.13	1.26E+08	1.26E+08
KIAA0196	0.020833	0.285714	0	0.037037	0	KIAA0196	8	8q24.13	1.26E+08	1.26E+08
NSMCE2	0.020833	0.285714	0	0.037037	0	NSMCE2	8	8q24.13	1.26E+08	1.25E+08
ASAP1IT1	0.020833	0.142857	0	0.037037	0	ASAP1IT1	8	8q24.21	1.31E+08	1.31E+08
TG	0.020833	0.238095	0	0.037037	0	TG	8	8q24.22	1.34E+08	1.34E+08
SLA	0.020833	0.285714	0	0.037037	0	SLA	8	8q24.22	1.34E+08	1.34E+08
CLK2P	0.020833	0.190476	0	0.037037	0	CLK2P	7	7p15.3	23590860	23592672
CCDC126	0.020833	0.190476	0	0.037037	0	CCDC126	7	7p15.3	23603523	23650853
WIPF3	0.020833	0.142857	0	0.037037	0	WIPF3	7	7p15.1	29840866	29912317
SCRN1	0.020833	0.142857	0	0.037037	0	SCRN1	7	7p15.1	29326245	29996260
C7orf41	0.020833	0.342857	0	0.037037	0	C7orf41	7	7p15.1	30141077	30168907
NOD1	0.020833	0.142857	0	0.037037	0	NOD1	7	7p15.1	30430668	30484919
CRHR2	0.020833	0.190476	0	0.037037	0	CRHR2	7	7p15.1	30659388	30588666
INMT	0.020833	0.190476	0	0.037037	0	INMT	7	7p15.1	30758276	30763744
FAM188B	0.020833	0.190476	0	0.037037	0	FAM188B	7	7p15.1	30777558	30898528
AQP1	0.020833	0.190476	0	0.037037	0	AQP1	7	7p15.1	30917993	30931657
GHRHR	0.020833	0.190476	0	0.037037	0	GHRHR	7	7p15.1	30970161	30985669
ADCYAP1R	0.020833	0.190476	0	0.037037	0	ADCYAP1R	7	7p15.1	31058667	31112837
CDK13	0.020833	0.142857	0	0.037037	0	CDK13	7	7p14.1	39956484	40103257
C7orf10	0.020833	0.238095	0	0.037037	0	C7orf10	7	7p14.1	40141100	40866883
HUS1	0.020833	0.285714	0	0.037037	0	HUS1	7	7p12.3	47970308	47985772
UPP1	0.020833	0.238095	0	0.037037	0	UPP1	7	7p12.3	48094880	48114856
RSBN1L	0.020833	0.190476	0	0.037037	0.074074	RSBN1L	7	7q11.23	77163679	77247057
CCDC132	0.020833	0	0.190476	0	0.037037	CCDC132	7	7q21.3	92699589	92826275
GNGT1	0.020833	0	0.190476	0	0.037037	GNGT1	7	7q21.3	93373756	93378422
COL1A2	0.020833	0	0.190476	0	0.037037	COL1A2	7	7q21.3	93861809	93898481
CASD1	0.020833	0	0.142857	0	0.037037	CASD1	7	7q21.3	93977106	94024265
SGCE	0.020333	0	0.142857	0	0.037037	SGCE	7	7q21.3	94052472	94123458
FAM185A	0.020833	0.142857	0	0.037037	0	FAM185A	7	7q22.1	1.02E+08	1.02E+08
FBXL13	0.020833	0.142857	0	0.037037	0	FBXL13	7	7q22.1	1.02E+08	1.03E+08
WDR91	0.020833	0.142857	0	0.037037	0	WDR91	7	7q33	1.35E+08	1.35E+08
NUP205	0.020833	0.190476	0	0.037037	0	NUP205	7	7q33	1.35E+08	1.35E+08
PL-5283	0.020833	0.190476	0	0.037037	0	PL-5283	7	7q33	1.35E+08	1.35E+08
SLC13A4	0.020833	0.190476	0	0.037037	0	SLC13A4	7	7q33	1.35E+08	1.35E+08
TRPV5	0.020833	0.142857	0	0.037037	0	TRPV5	7	7q34	1.42E+08	1.42E+08
C7orf34	0.020833	0.142857	0	0.037037	0	C7orf34	7	7q34	1.42E+08	1.42E+08
KEL	0.020833	0.142857	0	0.037037	0	KEL	7	7q34	1.42E+08	1.42E+08
TAS2R39	0.020833	0.142857	0	0.037037	0.037037	TAS2R39	7	7q34	1.43E+08	1.43E+08
TAS2R40	0.020833	0.142857	0	0.037037	0	TAS2R40	7	7q34	1.43E+08	1.43E+08
TMEM139	0.020833	0.142857	0	0.037037	0	TMEM139	7	7q34	1.43E+08	1.43E+08
CASP2	0.020833	0.142857	0	0.037037	0	CASP2	7	7q34	1.43E+08	1.43E+08
CLCN1	0.020833	0.142857	0	0.037037	0	CLCN1	7	7q34	1.43E+08	1.43E+08
FAM131B	0.020833	0.142857	0	0.037037	0	FAM131B	7	7q34	1.43E+08	1.43E+08
TFAP2A	0.020833	0.238095	0	0.037037	0	TFAP2A	6	6p24.3	10504902	10520594
C6orf218	0.020833	0.238095	0	0.037037	0	C6orf218	6	6p24.3	10536004	10543042
SLC17A2	0.020833	0.190476	0	0.037037	0	SLC17A2	6	6p22.2	26020963	26038819
TRIM38	0.020333	0.190476	0	0.037037	0	TRIM38	6	6p22.2	26071050	26093332
HIST1H4C	0.020833	0.190476	0	0.037037	0	HIST1H4C	6	6p22.1	26212155	26212545
HIST1H1T	0.020833	0.190476	0	0.037037	0	HIST1H1T	6	6p22.1	26215619	26216344
HIST1H2BC	0.020833	0.238095	0	0.037037	0	HIST1H2BC	6	6p22.1	26231674	26232112

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
HIST1H2AC	0.020833	0.238095	0	0.037037	0	HIST1H2AC	6	6p22.1	26232352	26232898
HIST1H1E	0.020833	0.238095	0	0.037037	0.037037	HIST1H1E	6	6p22.1	26264538	26265323
HIST1H2BD	0.020833	0.238095	0	0.037037	0.037037	HIST1H2BD	6	6p22.1	26266328	26266851
HIST1H1D	0.020833	0.190476	0	0.037037	0.037037	HIST1H1D	6	6p22.1	26342419	26343196
HIST1H4F	0.020833	0.190476	0	0.037037	0.037037	HIST1H4F	6	6p22.1	26348633	26349001
BTN3A2	0.020833	0.190476	0	0.037037	0	BTN3A2	6	6p22.1	26473377	26486528
BTN3A1	0.020833	0.190476	0	0.037037	0	BTN3A1	6	6p22.1	26510444	26523422
BTN2A3	0.020833	0.190476	0	0.037037	0	BTN2A3	6	6p22.1	26529598	26538796
BTN3A3	0.020833	0.190476	0	0.037037	0	BTN3A3	6	6p22.1	26548679	26561622
BTN2A1	0.020833	0.190476	0	0.037037	0	BTN2A1	6	6p22.1	26566168	26577845
BTN1A1	0.020833	0.190476	0	0.037037	0	BTN1A1	6	6p22.1	26509474	26618632
HCG11	0.020833	0.190476	0	0.037037	0	HCG11	6	6p22.1	26629913	26635590
HMGN4	0.020833	0.190476	0	0.037037	0	HMGN4	6	6p22.1	26646551	26655144
ABT1	0.020833	0.190476	0	0.037037	0	ABT1	6	6p22.1	26705159	26708257
ZNF322A	0.020833	0.190476	0	0.037037	0	ZNF322A	6	6p22.1	26742590	26767943
PRSS16	0.020833	0.238035	0	0.037037	0	PRSS16	6	6p22.1	27323481	27332378
POM121L2	0.020833	0.238095	0	0.037037	0	POM121L2	6	6p22.1	27384821	27387991
FKSG83	0.020833	0.238095	0	0.037037	0	FKSG83	6	6p22.1	27400557	27401721
ZNF204P	0.020833	0.238095	0	0.037037	0	ZNF204P	6	6p22.1	27433582	27447284
ZNF391	0.020833	0.285714	0	0.037037	0	ZNF391	6	6p22.1	27464503	27477207
GPR111	0.020833	0	0.190476	0	0.037037	GPR111	6	6p12.3	47732285	47773491
GPR115	0.020833	0	0.190476	0	0.037037	GPR115	6	6p12.3	47774248	47797717
OPN5	0.020833	0	0.190476	0	0.037037	OPN5	6	6p12.3	47857757	47902076
C6orf138	0.020833	0	0.190476	0	0.037037	C6orf138	6	6p12.3	47953723	48144385
PKHD1	0.020833	0	0.190476	0	0.037037	PKHD1	6	6p12.2	51588104	52050383
C6orf142	0.020833	0	0.190476	0	0.037037	C6orf142	6	6p12.1	53991673	54239038
GTF3C6	0.020833	0.190476	0	0.037037	0	GTF3C6	6	6q21	1.11E+08	1.11E+08
RPF2	0.020833	0.190476	0	0.037037	0	RPF2	6	6q21	1.11E+08	1.11E+08
RFX6	0.020833	0	0.238095	0	0.037037	RFX6	6	6q22.2	1.17E+08	1.17E+08
ROS1	0.020833	0	0.238095	0	0.037037	ROS1	6	6q22.2	1.18E+08	1.18E+08
DCBLD1	0.020833	0	0.238095	0	0.037037	DCBLD1	6	6q22.2	1.18E+08	1.18E+08
NUS1	0.020833	0	0.142857	0	0.037037	NUS1	6	6q22.2	1.18E+08	1.18E+08
LAMA2	0.020833	0	0.142857	0	0.037037	LAMA2	6	6q22.33	1.29E+08	1.3E+08
GPR126	0.020833	0	0.142857	0	0.037037	GPR126	6	6q24.1	1.43E+08	1.43E+08
UST	0.020833	0.142857	0	0.037037	0	UST	6	6q25.1	1.49E+08	1.49E+08
MAP3K7IP2	0.020833	0.142857	0	0.037037	0	MAP3K7IP2	6	6q25.1	1.5E+08	1.5E+08
SUMO4	0.020833	0.142857	0	0.037037	0	SUMO4	6	6q25.1	1.5E+08	1.5E+08
SNX9	0.020833	0.238095	0	0.037037	0	SNX9	6	6q25.3	1.58E+08	1.58E+08
GTF2H5	0.020833	0.238095	0	0.037037	0	GTF2H5	6	6q25.3	1.59E+08	1.59E+08
TAGAP	0.020833	0.238095	0	0.037037	0	TAGAP	6	6q25.3	1.59E+08	1.59E+08
FNDC1	0.020833	0.238095	0	0.037037	0	FNDC1	6	6q25.3	1.6E+08	1.6E+08
WTAP	0.020833	0.238095	0	0.037037	0	WTAP	6	6q25.3	1.6E+08	1.6E+08
ACAT2	0.020833	0.238095	0	0.037037	0	ACAT2	6	6q25.3	1.6E+08	1.6E+08
IGF2R	0.020833	0.238095	0	0.037037	0	IGF2R	6	6q25.3	1.6E+08	1.6E+08
LOC729603	0.020833	0.238095	0	0.037037	0	LOC729603	6	6q25.3	1.6E+08	1.6E+08
SLC22A1	0.020833	0.238095	0	0.037037	0	SLC22A1	6	6q25.3	1.6E+08	1.6E+08
MAP3K4	0.020833	0.190476	0	0.037037	0	MAP3K4	6	6q26	1.61E+08	1.61E+08
PARK2	0.020833	0.190476	0	0.037037	0	PARK2	6	6q26	1.62E+08	1.63E+08
LOC285796	0.020833	0.190476	0	0.037037	0	LOC285796	6	6q26	1.64E+08	1.64E+08
ADAMTS16	0.020833	0.142857	0	0.037037	0	ADAMTS16	5	5p15.32	5193443	5373413
FU33360	0.020833	0.285714	0	0.037037	0	FU33360	5	5p15.31	6363554	6390406
MED10	0.020833	0.285714	0	0.037037	0	MED10	5	5p15.31	6425039	6431640
UBE2QL1	0.020833	0.285714	0	0.037037	0	UBE2QL1	5	5p15.31	6501736	6545706
LOC255167	0.020833	0.285714	0	0.037037	0	LOC255167	5	5p15.31	6635287	6641613
NSUN2	0.020833	0.285714	0	0.037037	0	NSUN2	5	5p15.31	6652352	6686158
SRD5A1	0.020833	0.285714	0	0.037037	0	SRD5A1	5	5p15.31	6686500	6722676
POLS	0.020833	0.285714	0	0.037037	0	POLS	5	5p15.31	6767718	6810162
FBXL7	0.020833	0	0.190475	0	0.037037	FBXL7	5	5p15.1	15553305	15992901
11-Mar	0.020833	0	0.142857	0	0.037037	11-Mar	5	5p15.1	16120474	16232898
LOC285696	0.020833	0.238095	0	0.037037	0.037037	LOC285696	5	5p15.1	17183137	17270532
PDZD2	0.020833	0.238095	0	0.037037	0	PDZD2	5	5p13.3	31834788	32146796
MTMR12	0.020833	0.238095	0	0.037037	0	MTMR12	5	5p13.3	32262868	32348872
PLCXD3	0.020833	0	0.142857	0	0.037037	PLCXD3	5	5p13.1	41342805	41546488
OXCT1	0.020833	0	0.142857	0	0.037037	OXCT1	5	5p13.1	41765924	41906549
C5orf51	0.020833	0	0.142857	0	0.037037	C5orf51	5	5p13.1	41940227	41957496
FBXO4	0.020833	0	0.142857	0	0.037037	FBXO4	5	5p13.1	41961113	41977430
GHR	0.020833	0	0.142857	0	0.037037	GHR	5	5p12	42459783	42757684
SEPP1	0.020833	0	0.142857	0	0.037037	SEPP1	5	5p12	42835739	42847782
GAPT	0.020833	0	0.190476	0	0.037037	GAPT	5	5q11.2	57823087	57827943
RAB3C	0.020833	0	0.190476	0	0.037037	RAB3C	5	5q11.2	57914696	58183164
PDE4D	0.020833	0	0.142857	0	0.037037	PDE4D	5	5q11.2	58300623	59225379
S1C30A5	0.020833	0.190476	0	0.037037	0	S1C30A5	5	5q13.2	68425574	68436324
CCNB1	0.020833	0.190476	0	0.037037	0	CCNB1	5	5q13.2	58498669	68509827
CENPH	0.020833	0.190476	0	0.037037	0	CENPH	5	5q13.2	68521131	68541941

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
MRPS36	0.020833	0.190476	0	0.037037	0	MRPS36	5	5q13.2	68549329	68561742
CDK7	0.020833	0.190476	0	0.037037	0	CDK7	5	5q13.2	68566378	68609014
CCDC125	0.020833	0.190476	0	0.037037	0	CCDC125	5	5q13.2	68612275	68652167
TAF9	0.020833	0.190476	0	0.037037	0	TAF9	5	5q13.2	68683309	68701597
RAD17	0.020833	0.190476	0	0.037037	0	RAD17	5	5q13.2	68700880	68746388
LOC653391	0.020833	0.190476	0	0.037037	0	LOC653391	5	5q13.2	68713443	69917304
MARVELD2	0.020833	0.190476	0	0.037037	0	MARVELD2	5	5q13.2	68746699	68775593
OCLN	0.020833	0.190476	0	0.037037	0	OCLN	5	5q13.2	68823875	68885890
BDP1	0.020833	0.142857	0	0.037037	0	BDP1	5	5q13.2	70787198	70899406
MCCC2	0.020833	0.142857	0	0.037037	0	MCCC2	5	5q13.2	70918871	70990287
FBXL17	0.020833	0	0.142857	0	0.037037	FBXL17	5	5q21.3	1.07E+08	1.08E+08
C5orf13	0.020833	0	0.190476	0	0.037037	C5orf13	5	5q22.1	1.11E+08	1.11E+08
EPB41L4A	0.020833	0	0.142857	0	0.037037	EPB41L4A	5	5q22.2	1.12E+08	1.12E+08
KCNN2	0.020833	0	0.238095	0	0.037037	KCNN2	5	5q22.3	1.14E+08	1.14E+08
DTWD2	0.020833	0	0.285714	0	0.037037	DTWD2	5	5q23.1	1.18E+08	1.18E+08
SNCAIP	0.020833	0	0.142857	0	0.037037	SNCAIP	5	5q23.2	1.22E+08	1.22E+08
PRDM6	0.020833	0	0.142857	0	0.037037	PRDM6	5	5q23.2	1.22E+08	1.23E+08
CEP120	0.020833	0	0.285714	0	0.037037	CEP120	5	5q23.2	1.23E+08	1.23E+08
CSNK1G3	0.020833	0	0.285714	0	0.037037	CSNK1G3	5	5q23.2	1.23E+08	1.23E+08
ZNF608	0.020833	0	0.190476	0	0.037037	ZNF608	5	5q23.2	1.24E+08	1.24E+08
SLC27A6	0.020833	0	0.142857	0	0.037037	SLC27A6	5	5q23.3	1.28E+08	1.28E+08
ISOC1	0.020833	0	0.142857	0	0.037037	ISOC1	5	5q23.3	1.28E+08	1.28E+08
ADAMTS19	0.020833	0	0.190476	0	0.037037	ADAMTS19	5	5q23.3	1.29E+08	1.29E+08
CHSY3	0.020833	0	0.190476	0	0.037037	CHSY3	5	5q23.3	1.29E+08	1.3E+08
KCTD16	0.020833	0	0.142857	0	0.037037	KCTD16	5	5q32	1.44E+08	1.44E+08
TIMD4	0.020833	0.190476	0	0.037037	0	TIMD4	5	5q33.3	1.56E+08	1.56E+08
MIR146A	0.020833	0.047619	0.142857	0	0.037037	MIR146A	5	5q33.3	1.6E+08	1.6E+08
ATP10B	0.020833	0	0.190476	0	0.037037	ATP10B	5	5q34	2.6E+08	1.6E+08
HSP90AB2P	0.020833	0	0.142857	0	0.037037	HSP90AB2P	4	4p15.33	12944135	12949024
RAB28	0.020833	0	0.190476	0	0.037037	RAB28	4	4p15.33	12978445	13095088
ARAP2	0.020833	0.190476	0.190476	0.037037	0.111111	ARAP2	4	4p14	35744017	35922375
SPINK2	0.020833	0.142857	0	0.037037	0	SPINK2	4	4q12	57370791	57382651
REST	0.020833	0.142857	0	0.037037	0	REST	4	4q12	57468799	57493098
CSN1S2A	0.020833	0	0.285714	0	0.037037	CSN1S2A	4	4q13.3	70967692	70985578
CSN1S2B	0.020833	0	0.285714	0	0.037037	CSN1S2B	4	4q13.3	71033910	71047011
C4orf40	0.020833	0	0.285714	0	0.037037	C4orf40	4	4q13.3	71054493	71066916
ODAM	0.020833	0	0.285714	0	0.037037	ODAM	4	4q13.3	71096833	71104883
SMR3A	0.020833	0	0.285714	0	0.037037	SMR3A	4	4q13.3	71261082	71267413
MUC7	0.020833	0	0.238095	0	0.037037	MUC7	4	4q13.3	71330798	71383303
RUFY3	0.020833	0.190476	0.095238	0.037037	0.037037	RUFY3	4	4q13.3	71783518	71874478
MOBKL1A	0.020833	0.190476	0.095238	0.037037	0.037037	MOBKL1A	4	4q13.3	71986928	72072756
DCK	0.020833	0.190476	0.095238	0.037037	0.037037	DCK	4	4q13.3	72078129	72115494
CXCL6	0.020833	0	0.142857	0	0.037037	CXCL6	4	4q13.3	74921137	74923342
PPBPL1	0.020833	0	0.142857	0	0.037037	PPBPL1	4	4q13.3	74932447	74933418
PF4	0.020833	0	0.142857	0	0.037037	PF4	4	4q13.3	75065660	75066580
PPBP	0.020833	0	0.142857	0	0.037037	PPBP	4	4q13.3	75071620	75072765
CXCL3	0.020833	0	0.142857	0	0.037037	CXCL3	4	4q13.3	75121176	75123355
CXCL2	0.020833	0	0.142857	0	0.037037	CXCL2	4	4q13.3	75181618	75183862
MTHFD2L	0.020833	0	0.142857	0	0.037037	MTHFD2L	4	4q13.3	75242693	75387677
ARD1B	0.020833	0	0.142857	0	0.037037	ARD1B	4	4q21.21	80457296	80466196
GDEP	0.020833	0	0.190476	0	0.037037	GDEP	4	4q21.21	80967649	81003424
PRDM8	0.020833	0	0.190476	0	0.037037	PRDM8	4	4q21.21	81325448	81344507
C4orf22	0.020833	0	0.190476	0	0.037037	C4orf22	4	4q21.21	81475898	82103927
MANBA	0.020833	0.095238	0.142857	0.037037	0.037037	MANBA	4	4q24	1.04E+08	1.04E+08
SCOC	0.020833	0.142857	0	0.037037	0	SCOC	4	4q31.1	1.41E+08	1.42E+08
USP38	0.020833	0	0.142857	0	0.037037	USP38	4	4q31.21	1.44E+08	1.44E+08
TMEM154	0.020833	0.142857	0	0.037037	0	TMEM154	4	4q31.3	1.54E+08	1.54E+08
FHDC1	0.020833	0.142857	0	0.037037	0	FHDC1	4	4q31.3	1.54E+08	1.54E+08
TRIM2	0.020833	0.142857	0	0.037037	0	TRIM2	4	4q31.3	1.54E+08	1.54E+08
ANXA2P1	0.020833	0.142857	0	0.037037	0	ANXA2P1	4	4q31.3	1.54E+08	1.54E+08
MND1	0.020833	0.142857	0	0.037037	0	MND1	4	4q31.3	1.54E+08	1.55E+08
KIAA0922	0.020833	0.142857	0	0.037037	0	KIAA0922	4	4q31.3	1.55E+08	1.55E+08
RBM46	0.020333	0	0.142857	0	0.037037	RBM46	4	4q32.1	1.56E+08	1.56E+08
NPY2R	0.020833	0	0.190476	0	0.037037	NPY2R	4	4q32.1	1.56E+08	1.56E+08
MAP9	0.020833	0	0.190476	0	0.037037	MAP9	4	4q32.1	1.56E+08	1.57E+08
GUCY1A3	0.020833	0	0.190476	0	0.037037	GUCY1A3	4	4q32.1	1.57E+08	1.57E+08
GUCY1B3	0.020833	0	0.190476	0	0.037037	GUCY1B3	4	4q32.1	1.57E+08	1.57E+08
TD02	0.020833	0	0.190476	0	0.037037	TD02	4	4q32.1	1.57E+08	1.57E+08
CTSO	0.020833	0	0.190475	0	0.037037	CTSO	4	4q32.1	1.57E+08	1.57E+08
ZFP42	0.020833	0.238095	0	0.037037	0	ZFP42	4	4q35.2	1.89E+08	1.89E+08
TRIML2	0.020833	0.238095	0	0.037037	0	TRIML2	4	4q35.2	1.89E+08	1.89E+08
TRIML1	0.020833	0.285714	0	0.037037	0	TRIML1	4	4q35.2	1.89E+08	1.89E+08
CNTN4	0.020833	0	0.142857	0	0.037037	CNTN4	3	3p26.3	2117247	3074646
SATB1	0.020833	0	0.238095	0	0.037037	SATB1	3	3p24.3	18364270	18455257

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
KCNH8	0.020833	0	0.238095	0	0.037037	KCNH8	3	3p24.3	19165021	19552140
CMC1	0.020833	0.047619	0.190476	0	0.037037	CMC1	3	3p24.1	28258128	28336268
TGFBR2	0.020833	0.047619	0.238095	0	0.037037	TGFBR2	3	3p24.1	30622998	30710638
GADL1	0.020833	0.047619	0.238095	0	0.037037	GADL1	3	3p24.1-3p	30742696	30911158
CLASP2	0.020833	0.238095	0	0.037037	0	CLASP2	3	3p22.3	33512742	33734853
CCDC66	0.020833	0.333333	0	0.037037	0	CCDC66	3	3p14.3	56566224	56630887
C3orf63	0.020833	0.333333	0	0.037037	0	C3orf63	3	3p14.3	56629200	56692176
ARHGEF3	0.020833	0.333333	0	0.037037	0	ARHGEF3	3	3p14.3	56736486	57088377
SPATA12	0.020833	0.380952	0	0.037037	0	SPATA12	3	3p14.3	57069509	57084501
IL17RD	0.020833	0.380952	0	0.037037	0	IL17RD	3	3p14.3	57099050	57174444
DNAH12	0.020833	0.333333	0	0.037037	0.037037	DNAH12	3	3p14.3	57302767	57505112
EIF4E3	0.020833	0.142857	0.047619	0.037037	0	EIF4E3	3	3p13	71811132	71886223
GPR27	0.020833	0.142857	0.047619	0.037037	0	GPR27	3	3p13	71885891	71887019
PROK2	0.020833	0.142857	0.047619	0.037037	0	PROK2	3	3p13	71903496	71917048
RG9MTD1	0.020833	0.238095	0	0.037037	0.037037	RG9MTD1	3	3q12.3	1.03E+08	1.03E+08
PCNP	0.020833	0.238095	0	0.037037	0.037037	PCNP	3	3q12.3	1.03E+08	1.03E+08
ZBTB11	0.020833	0.285714	0	0.037037	0.037037	ZBTB11	3	3q12.3	1.03E+08	1.03E+08
LOC100009676	0.020833	0.285714	0	0.037037	0.037037	LOC100009676	3	3q12.3	1.03E+08	1.03E+08
RPL24	0.020833	0.285714	0	0.037037	0.037037	RPL24	3	3q12.3	1.03E+08	1.03E+08
LOC100302640	0.020833	0	0.190476	0	0.037037	LOC100302640	3	3q13.12	1.08E+08	1.08E+08
LOC344595	0.020833	0	0.190476	0	0.037037	LOC344595	3	3q13.12	1.08E+08	1.08E+08
CCDC54	0.020833	0	0.142857	0	0.037037	CCDC54	3	3q13.12	1.09E+08	1.09E+08
BBX	0.020833	0	0.142857	0	0.037037	BBX	3	3q13.12	1.09E+08	1.09E+08
FLI25363	0.020833	0.238095	0	0.037037	0.037037	FLI25363	3	3q13.13	1.11E+08	1.11E+08
TMPRSS7	0.020833	0	0.142857	0	0.037037	TMPRSS7	3	3q13.2	1.13E+08	1.13E+08
SLC9A10	0.020833	0	0.142857	0	0.037037	SLC9A10	3	3q13.2	1.13E+08	1.13E+08
CD200	0.020833	0	0.142857	0	0.037037	CD200	3	3q13.2	1.14E+08	1.14E+08
BTLA	0.020833	0	0.142857	0	0.037037	BTLA	3	3q13.2	1.14E+08	1.14E+08
SLC35A5	0.020833	0	0.142857	0	0.037037	SLC35A5	3	3q13.2	1.14E+08	1.14E+08
CCDC80	0.020833	0	0.142857	0	0.037037	CCDC80	3	3q13.2	1.14E+08	1.14E+08
CD200R1L	0.020833	0	0.142857	0	0.037037	CD200R1L	3	3q13.2	1.14E+08	1.14E+08
ZBTB20	0.020833	0	0.142857	0	0.037037	ZBTB20	3	3q13.31	1.16E+08	1.16E+08
COL29A1	0.020833	0	0.142857	0.074074	0.037037	COL29A1	3	3q22.1	1.32E+08	1.32E+08
COL6A6	0.020833	0	0.142857	0	0.037037	COL6A6	3	3q22.1	1.32E+08	1.32E+08
PIK3R4	0.020833	0	0.190476	0	0.037037	PIK3R4	3	3q22.1	1.32E+08	1.32E+08
ATP2C1	0.020833	0	0.190476	0	0.037037	ATP2C1	3	3q22.1	1.32E+08	1.32E+08
ASTE1	0.020833	0	0.190476	0	0.037037	ASTE1	3	3q22.1	1.32E+08	1.32E+08
NEK11	0.020833	0	0.190476	0	0.037037	NEK11	3	3q22.1	1.32E+08	1.33E+08
NUDT16	0.020833	0	0.142857	0	0.037037	NUDT16	3	3q22.1	1.33E+08	1.33E+08
MRPL3	0.020833	0	0.142857	0	0.037037	MRPL3	3	3q22.1	1.33E+08	1.33E+08
CPNE4	0.020833	0	0.142857	0	0.037037	CPNE4	3	3q22.1	1.33E+08	1.33E+08
BFSP2	0.020833	0.142857	0	0.037037	0	BFSP2	3	3q22.1	1.35E+08	1.35E+08
CDV3	0.020833	0.190476	0	0.037037	0	CDV3	3	3q22.1	1.35E+08	1.35E+08
TOPBP1	0.020833	0.190476	0	0.037037	0	TOPBP1	3	3q22.1	1.35E+08	1.35E+08
TF	0.020833	0.190476	0	0.037037	0	TF	3	3q22.1	1.35E+08	1.35E+08
DZIP1L	0.020833	0.190476	0	0.037037	0	DZIP1L	3	3q22.3	1.39E+08	1.39E+08
DBR1	0.020833	0.190476	0	0.037037	0	DBR1	3	3q22.3	1.39E+08	1.39E+08
ARMC8	0.020833	0.190476	0	0.037037	0	ARMC8	3	3q22.3	1.39E+08	1.39E+08
TXNDC6	0.020833	0.238095	0	0.037037	0	TXNDC6	3	3q22.3	1.39E+08	1.4E+08
MRAS	0.020833	0.238095	0	0.037037	0	MRAS	3	3q22.3	1.4E+08	1.4E+08
ESYT3	0.020833	0.238095	0	0.037037	0	ESYT3	3	3q22.3	1.4E+08	1.4E+08
CEP70	0.020833	0.190475	0	0.037037	0	CEP70	3	3q22.3	1.4E+08	1.4E+08
FAIM	0.020833	0.190476	0	0.037037	0	FAIM	3	3q22.3	1.4E+08	1.4E+08
PIK3CB	0.020833	0.190476	0	0.037037	0	PIK3CB	3	3q22.3	1.4E+08	1.4E+08
FOXL2	0.020833	0.190476	0	0.037037	0	FOXL2	3	3q22.3	1.4E+08	1.4E+08
C3orf72	0.020833	0.190476	0	0.037037	0	C3orf72	3	3q22.3	1.4E+08	1.4E+08
BPESC1	0.020833	0.190476	0	0.037037	0	BPESC1	3	3q22.3	1.4E+08	1.4E+08
AADACL2	0.020833	0	0.142857	0	0.037037	AADACL2	3	3q25.1	1.53E+08	1.53E+08
SLC33A1	0.020833	0.285714	0	0.037037	0	SLC33A1	3	3q25.31	1.57E+08	1.57E+08
GMPS	0.020833	0.285714	0	0.037037	0	GMPS	3	3q25.31	1.57E+08	1.57E+08
LRRIQ4	0.020833	0.238095	0	0.037037	0	LRRIQ4	3	3q26.2	1.71E+08	1.71E+08
LRRC31	0.020833	0.238095	0	0.037037	0	LRRC31	3	3q26.2	1.71E+08	1.71E+08
SAMD7	0.020833	0.238095	0	0.037037	0	SAMD7	3	3q26.2	1.71E+08	1.71E+08
LOC100128164	0.020833	0.238095	0	0.037037	0	LOC100128164	3	3q26.2	1.71E+08	1.71E+08
SEC62	0.020833	0.238095	0	0.037037	0	SEC62	3	3q26.2	1.71E+08	1.71E+08
MCCC1	0.020833	0.333333	0	0.037037	0	MCCC1	3	3q27.1	1.84E+08	1.84E+08
FGF12	0.020833	0	0.142857	0	0.037037	FGF12	3	3q28	1.93E+08	1.94E+08
DLG1	0.020833	0.238095	0.142857	0.407407	0.037037	DLG1	3	3q29	1.98E+08	1.99E+08
KIDINS220	0.020833	0.190476	0.142857	0.185185	0.037037	KIDINS220	2	2p25.1	8786438	8895207
KCNS3	0.020833	0.142857	0	0.037037	0	KCNS3	2	2p24.2	17923426	17977707
GALM	0.020833	0.142857	0	0.037037	0	GALM	2	2p22.1	38746556	38815413
GEMIN6	0.020833	0.142857	0	0.037037	0	GEMIN6	2	2p22.1	38858831	38862611
DHX57	0.020833	0.142857	0	0.037037	0	DHX57	2	2p22.1	38878379	38956525
MORN2	0.020833	0.142857	0	0.037037	0	MORN2	2	2p22.1	38956607	38963353

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
SLC8A1	0.020833	0	0.142857	0	0.037037	SLC8A1	2	2p22.1	40192790	40510949
MSH6	0.020833	0.142857	0	0.037037	0.074074	MSH6	2	2p16.3	47863725	47887597
FBXO11	0.020833	0.142857	0	0.037037	0.074074	FBXO11	2	2p16.3	47887563	47986319
VRK2	0.020833	0	0.142857	0	0.037037	VRK2	2	2p16.1	58127233	58240560
FANCL	0.020833	0	0.142857	0	0.037037	FANCL	2	2p16.1	58239882	58322020
PAPOLG	0.020833	0.238095	0	0.037037	0	PAPOLG	2	2p16.1	60836887	60879603
REL	0.020833	0.238095	0	0.037037	0	REL	2	2p16.1	60962256	61003683
PUS10	0.020833	0.238095	0	0.037037	0	PUS10	2	2p16.1	61021054	61098870
KIAA1841	0.020833	0.238095	0	0.037037	0	KIAA1841	2	2p15	61146510	61204918
C2orf74	0.020833	0.238095	0	0.037037	0	C2orf74	2	2p15	61225747	61245469
USP34	0.020833	0.238095	0	0.037037	0	USP34	2	2p15	61268094	61551354
XPO1	0.020833	0.285714	0	0.037037	0	XPO1	2	2p15	61558573	61618923
RAB1A	0.020833	0.142857	0	0.037037	0	RAB1A	2	2p14	65167493	65210940
MAP4K4	0.020833	0.190476	0	0.037037	0	MAP4K4	2	2q11.2	1.02E+08	1.02E+08
IL1R2	0.020833	0.190476	0	0.037037	0	IL1R2	2	2q11.2	1.02E+08	1.02E+08
IL1R1	0.020833	0.142857	0	0.037037	0	IL1R1	2	2q12.1	1.02E+08	1.02E+08
IL1RL2	0.020833	0.142857	0	0.037037	0	IL1RL2	2	2q12.1	1.02E+08	1.02E+08
IL1RL1	0.020833	0.142857	0	0.037037	0	IL1RL1	2	2q12.1	1.02E+08	1.02E+08
IL18R1	0.020833	0.142857	0	0.037037	0	IL18R1	2	2q12.1	1.02E+08	1.02E+08
MFSD9	0.020833	0	0.142857	0	0.037037	MFSD9	2	2q12.1	1.03E+08	1.03E+08
TMEM182	0.020833	0	0.142857	0	0.037037	TMEM182	2	2q12.1	1.03E+08	1.03E+08
MRPS9	0.020833	0.142857	0	0.037037	0	MRPS9	2	2q12.1	1.05E+08	1.05E+08
PLGLA	0.020833	0.190476	0	0.037037	0	PLGLA	2	2q12.2	1.06E+08	1.06E+08
RGPD3	0.020833	0.190476	0	0.037037	0	RGPD3	2	2q12.2	1.06E+08	1.06E+08
ACVR2A	0.020833	0	0.190476	0	0.037037	ACVR2A	2	2q22.3	1.48E+08	1.48E+08
MBD5	0.020833	0	0.142857	0	0.037037	MBD5	2	2q23.1	1.49E+08	1.49E+08
EPC2	0.020833	0	0.238095	0	0.037037	EPC2	2	2q23.1	1.49E+08	1.49E+08
DAPL1	0.020833	0.142857	0	0.037037	0	DAPL1	2	2q24.1	1.59E+08	1.59E+08
TANC1	0.020833	0.142857	0	0.037037	0	TANC1	2	2q24.1	1.6E+08	1.6E+08
TTN	0.020833	0	0.142857	0	0.037037	TTN	2	2q31.2	1.79E+08	1.79E+08
CCDC141	0.020833	0	0.142857	0	0.037037	CCDC141	2	2q31.2	1.79E+08	1.79E+08
SESTD1	0.020833	0	0.142857	0	0.037037	SESTD1	2	2q31.2	1.8E+08	1.8E+08
ZNF385B	0.020833	0	0.190475	0	0.037037	ZNF385B	2	2q31.2	1.8E+08	1.8E+08
MIR1258	0.020833	0	0.190476	0	0.037037	MIR1258	2	2q31.3	1.8E+08	1.8E+08
SF3B1	0.020833	0.238095	0	0.037037	0	SF3B1	2	2q33.1	1.98E+08	1.98E+08
COQ10B	0.020833	0.238095	0	0.037037	0	COQ10B	2	2q33.1	1.98E+08	1.98E+08
HSPD1	0.020833	0.238095	0	0.037037	0	HSPD1	2	2q33.1	1.98E+08	1.98E+08
RFTN2	0.020833	0	0.142857	0	0.037037	RFTN2	2	2q33.1	1.98E+08	1.98E+08
PLCL1	0.020833	0	0.142857	0	0.037037	PLCL1	2	2q33.1	1.98E+08	1.99E+08
BZW1	0.020833	0.142857	0	0.037037	0	BZW1	2	2q33.1	2.01E+08	2.01E+08
BZW1L1	0.020833	0.142857	0	0.037037	0	BZW1L1	2	2q33.1	2.01E+08	2.01E+08
PPIL3	0.020833	0.142857	0	0.037037	0	PPIL3	2	2q33.1	2.01E+08	2.01E+08
N1F3L1	0.020833	0.142857	0	0.037037	0	N1F3L1	2	2q33.1	2.01E+08	2.01E+08
ORC2L	0.020833	0.142857	0	0.037037	0	ORC2L	2	2q33.1	2.01E+08	2.02E+08
FAM126B	0.020833	0.190476	0	0.037037	0	FAM126B	2	2q33.1	2.02E+08	2.02E+08
NDUFB3	0.020833	0.190476	0	0.037037	0	NDUFB3	2	2q33.1	2.02E+08	2.02E+08
CFLAR	0.020833	0.190476	0	0.037037	0	CFLAR	2	2q33.1	2.02E+08	2.02E+08
CASP10	0.020833	0.142857	0	0.037037	0	CASP10	2	2q33.1	2.02E+08	2.02E+08
CASP8	0.020833	0.142857	0	0.037037	0	CASP8	2	2q33.1	2.02E+08	2.02E+08
ALS2CR12	0.020833	0.142857	0	0.037037	0	ALS2CR12	2	2q33.1	2.02E+08	2.02E+08
TRAK2	0.020833	0.142857	0.047619	0.037037	0	TRAK2	2	2q33.1	2.02E+08	2.02E+08
STRAD8	0.020833	0.142857	0.047619	0.037037	0	STRAD8	2	2q33.1	2.02E+08	2.02E+08
MPP4	0.020833	0.190476	0	0.037037	0	MPP4	2	2q33.1	2.02E+08	2.02E+08
ALS2	0.020833	0.190476	0	0.037037	0	ALS2	2	2q33.1	2.02E+08	2.02E+08
CDK15	0.020833	0.190476	0	0.037037	0	CDK15	2	2q33.1	2.02E+08	2.02E+08
FAM117B	0.020833	0.238095	0	0.037037	0	FAM117B	2	2q33.1	2.03E+08	2.03E+08
ALS2CR8	0.020833	0.190476	0	0.037037	0	ALS2CR8	2	2q33.2	2.03E+08	2.04E+08
NBEAL1	0.020833	0.190476	0	0.037037	0	NBEAL1	2	2q33.2	2.04E+08	2.04E+08
CYP20A1	0.020833	0.190476	0	0.037037	0	CYP20A1	2	2q33.2	2.04E+08	2.04E+08
ABI2	0.020833	0.190476	0	0.037037	0	ABI2	2	2q33.2	2.04E+08	2.04E+08
RAPH1	0.020833	0.190476	0	0.037037	0	RAPH1	2	2q33.2	2.04E+08	2.04E+08
INO80D	0.020833	0.142857	0	0.037037	0	INO80D	2	2q33.3	2.07E+08	2.07E+08
NDUFS1	0.020833	0.142857	0	0.037037	0	NDUFS1	2	2q33.3	2.07E+08	2.07E+08
EEF1B2	0.020833	0.142857	0	0.037037	0	EEF1B2	2	2q33.3	2.07E+08	2.07E+08
SNORD51	0.020833	0.142857	0	0.037037	0	SNORD51	2	2q33.3	2.07E+08	2.07E+08
SNORA41	0.020833	0.142857	0	0.037037	0	SNORA41	2	2q33.3	2.07E+08	2.07E+08
GPR1	0.020833	0.142857	0	0.037037	0	GPR1	2	2q33.3	2.07E+08	2.07E+08
CCNYL1	0.020833	0.142857	0	0.037037	0	CCNYL1	2	2q33.3	2.08E+08	2.08E+08
PECR	0.020833	0.142857	0	0.037037	0	PECR	2	2q35	2.17E+08	2.17E+08
4-Mar	0.020833	0.142857	0	0.037037	0	4-Mar	2	2q35	2.17E+08	2.17E+08
DEPDC1	0.020833	0	0.190476	0	0.037037	DEPDC1	1	1p31.2	68712423	68735388
LRRC7	0.020833	0	0.190476	0	0.037037	LRRC7	1	1p31.1	69998446	70361760
PIN1L	0.020833	0	0.190476	0	0.037037	PIN1L	1	1p31.1	70157593	70158589
ANKRD13C	0.020833	0	0.142857	0	0.037037	ANKRD13C	1	1p31.1	70497273	70593006

TABLE 4-continued

Gene list for predicting prostate cancer relapse using AT

Symbol	freq. use	freq. amp. case	freq. del. case	freq. amp. control	freq. del. control	Gene. Symbol	chromo-some	cytoband	Tran-script. start	Tran-script. end
HHLA3	0.020833	0	0.142857	0	0.037037	HHLA3	1	1p31.1	70593081	70606294
CTH	0.020833	0	0.142857	0	0.037037	CTH	1	1p31.1	70649543	70677842
USP33	0.020833	0.142857	0	0.037037	0.074074	USP33	1	1p31.1	77934262	77998126
FAM73A	0.020833	0.190476	0	0.037037	0.074074	FAM73A	1	1p31.1	78017897	78116670
TTLL7	0.020833	0	0.142857	0	0.037037	TTLL7	1	1p31.1	84107645	84237422
PRKACB	0.020833	0	0.142857	0	0.037037	PRKACB	1	1p31.1	84316333	84476770
SAMD13	0.020833	0	0.142857	0	0.037037	SAMD13	1	1p31.1	84536637	84589069
UOX	0.020833	0	0.142857	0	0.037037	UOX	1	1p31.1	84603229	84636165
PKN2	0.020833	0	0.142857	0	0.037037	PKN2	1	1p22.2	88922510	89074527
GTF2B	0.020833	0.142857	0	0.037037	0	GTF2B	1	1p22.2	89090909	89129890
BCAR3	0.020833	0.142857	0	0.037037	0	BCAR3	1	1p22.1	93799937	93919974
TRIM33	0.020833	0.142857	0	0.037037	0	TRIM33	1	1p13.2	1.15E+08	1.15E+08
DENND2C	0.020833	0.142857	0	0.037037	0	DENND2C	1	1p13.2	1.15E+08	1.15E+08
AMPD1	0.020833	0.142857	0	0.037037	0	AMPD1	1	1p13.2	1.15E+08	1.15E+08
NRAS	0.020833	0.142857	0	0.037037	0	NRAS	1	1p13.2	1.15E+08	1.15E+08
CSDE1	0.020833	0.142857	0	0.037037	0	CSDE1	1	1p13.2	1.15E+08	1.15E+08
SIKE1	0.020833	0.142857	0	0.037037	0	SIKE1	1	1p13.2	1.15E+08	1.15E+08
FAM46C	0.020833	0.190476	0	0.037037	0	FAM46C	1	1p12	1.18E+08	1.18E+08
HFE2	0.020833	0.285714	0	0.037037	0	HFE2	1	1q11.1	1.44E+08	1.44E+08
PQLR3GL	0.020833	0.238095	0	0.037037	0	PQLR3GL	1	1q21.1	1.44E+08	1.44E+08
LIX1L	0.020833	0.238095	0	0.037037	0	LIX1L	1	1q21.1	1.44E+08	1.44E+08
RBM8A	0.020833	0.238095	0	0.037037	0	RBM8A	1	1q21.1	1.44E+08	1.44E+08
GNRHR2	0.020833	0.238095	0	0.037037	0	GNRHR2	1	1q21.1	1.44E+08	1.44E+08
PEX11B	0.020833	0.238095	0	0.037037	0	PEX11B	1	1q21.1	1.44E+08	1.44E+08
ITGA10	0.020833	0.238095	0	0.037037	0	ITGA10	1	1q21.1	1.44E+08	1.44E+08
ANKRD35	0.020833	0.238095	0	0.037037	0	ANKRD35	1	1q21.1	1.44E+08	1.44E+08
RNF115	0.020833	0.238095	0	0.037037	0	RNF115	1	1q21.1	1.44E+08	1.44E+08
SLAMF6	0.020833	0.190476	0	0.037037	0	SLAMF6	1	1q23.2	1.59E+08	1.59E+08
CD84	0.020833	0.190476	0	0.037037	0	CD84	1	1q23.2-1c	1.59E+08	1.59E+08
SLAMF7	0.020833	0.142857	0	0.037037	0	SLAMF7	1	1q23.3	1.59E+08	1.59E+08
CD244	0.020833	0.190476	0	0.037037	0	CD244	1	1q23.3	1.59E+08	1.59E+08
UFC1	0.020833	0.238095	0	0.037037	0.037037	UFC1	1	1q23.3	1.59E+08	1.59E+08
USP21	0.020833	0.238095	0	0.037037	0.037037	USP21	1	1q23.3	1.59E+08	1.59E+08
PPOX	0.020833	0.238095	0	0.037037	0.037037	PPOX	1	1q23.3	1.59E+08	1.59E+08
B4GALT3	0.020833	0.238095	0	0.037037	0.037037	B4GALT3	1	1q23.3	1.59E+08	1.59E+08
NR1I3	0.020833	0.238095	0	0.037037	0	NR1I3	1	1q23.3	1.59E+08	1.59E+08
PCP4L1	0.020833	0.238095	0	0.037037	0	PCP4L1	1	1q23.3	1.59E+08	1.6E+08
MPZ	0.020833	0.238095	0	0.037037	0	MPZ	1	1q23.3	1.6E+08	1.6E+08
SDHC	0.020833	0.238095	0	0.037037	0	SDHC	1	1q23.3	1.6E+08	1.6E+08
LOC642502	0.020833	0.238095	0	0.037037	0	LOC64250	1	1q23.3	1.6E+08	1.6E+08
C1orf192	0.020833	0.238095	0	0.037037	0	C1orf192	1	1q23.3	1.6E+08	1.6E+08
OLFML2B	0.020833	0.190476	0	0.037037	0	OLFML2B	1	1q23.3	1.6E+08	1.6E+08
NOS1AP	0.020833	0.142857	0	0.037037	0	NOS1AP	1	1q23.3	1.6E+08	1.61E+08
C1orf111	0.020833	0.190476	0	0.037037	0	C1orf111	1	1q23.3	1.61E+08	1.61E+08
RGS5	0.020833	0	0.142857	0	0.037037	RGS5	1	1q23.3	1.61E+08	1.61E+08
KIAA1614	0.020833	0.238095	0	0.037037	0	KIAA1614	1	1q25.3	1.79E+08	1.79E+08
HEATR1	0.020833	0.190476	0	0.037037	0	HEATR1	1	1q43	2.35E+08	2.35E+08
ACTN2	0.020833	0.190476	0	0.037037	0	ACTN2	1	1q43	2.35E+08	2.35E+08
RYR2	0.020833	0.142857	0	0.037037	0	RYR2	1	1q43	2.35E+08	2.36E+08
ZNF238	0.020833	0.238095	0	0.037037	0	ZNF238	1	1q44	2.42E+08	2.42E+08
C1orf100	0.020833	0.238095	0	0.037037	0	C1orf100	1	1q44	2.43E+08	2.43E+08
ADSS	0.020833	0.238095	0	0.037037	0	ADSS	1	1q44	2.43E+08	2.43E+08
C1orf101	0.020833	0.238095	0	0.037037	0	C1orf101	1	1q44	2.43E+08	2.43E+08
PPPDE1	0.020833	0.190476	0.047619	0.037037	0	PPPDE1	1	1q44	2.43E+08	2.43E+08
FAM36A	0.020833	0.238095	0	0.037037	0	FAM36A	1	1q44	2.43E+08	2.43E+08
EFCAB2	0.020833	0.238095	0	0.037037	0	EFCAB2	1	1q44	2.43E+08	2.43E+08
KIF26B	0.020833	0.238095	0	0.037037	0	KIF26B	1	1q44	2.43E+08	2.44E+08

TABLE 5

Gene list for predicting prostate cancer fast relapse using AT

Symbol	freq.use	freq.amp. case	freq.del. case	freq.amp. control	freq.del. control	Gene.Symbol	chromosome	cytoband	Transcript. start	Transcript. end
RPL23AP82	1	0.75	0.25	0.8	0	RPL23AP82	22	22q13.33	49542380	49584931
RABL2B	1	0.75	0.25	0.8	0	RABL2B	22	22q13.33	49552786	49568954
CA10	1	0.25	0.25	0.15	0	CA10	17	17q21.33	47062673	47592161
MAGEL2	1	0.375	0	0	0	MAGEL2	15	15q11.2	21439791	21444087
NDN	1	0.375	0	0	0	NDN	15	15q11.2	21481647	21483544
C13orf36	1	0	0.25	0.025	0	C13orf36	13	13q13.3	36146049	36169976

TABLE 5-continued

Gene list for predicting prostate cancer fast relapse using AT

Symbol	freq.use	freq.amp. case	freq.del. case	freq.amp. control	freq.del. control	Gene.Symbol	chromosome	cytoband	Transcript. start	Transcript. end
SMAD9	1	0	0.25	0.075	0	SMAD9	13	13q13.3	36320207	36392410
ALG5	1	0.125	0.25	0.075	0	ALG5	13	13q13.3	36421910	36471505
RSU1	1	0.25	0	0	0	RSU1	10	10p13	16672623	16899460
ADCY2	1	0.25	0	0	0	ADCY2	5	5p15.31	7449343	7883195
UBE2E1	1	0.25	0	0	0.025	UBE2E1	3	3p24.2	23822443	23907812
RETNLB	1	0	0.25	0	0	RETNLB	3	3q13.13	1.1E+08	1.1E+08
TRAT1	1	0	0.25	0	0	TRAT1	3	3q13.13	1.1E+08	1.1E+08
GUCA1C	1	0	0.25	0	0	GUCA1C	3	3q13.13	1.1E+08	1.1E+08
MORC1	1	0	0.25	0	0	MORC1	3	3q13.13	1.1E+08	1.1E+08
TTTY8	0.979167	0.125	0.125	0.275	0	TTTY8	Y	Yp11.2	10138709	10141309
TTTY8B	0.979167	0.125	0.125	0.275	0	TTTY8B	Y	Yp11.2	10138709	10141309
TTTY7	0.979167	0.125	0.125	0.275	0	TTTY7	Y	Yp11.2	10154433	10162872
TTTY7B	0.979167	0.125	0.125	0.275	0	TTTY7B	Y	Yp11.2	10154433	10162872
LOC100101115	0.979167	0.125	0.125	0.275	0	LOC100101115	Y	Yp11.2	10165262	10168906
TTTY21	0.979167	0.125	0.125	0.275	0	TTTY21	Y	Yp11.2	10165262	10168906
YIPF6	0.979167	0.125	0.125	0.275	0	YIPF6	X	Xq12	67635611	67669027
LOC96610	0.979167	0.625	0.125	0.575	0	L0C96610	22	22q11.22	20982463	21007325
STX16	0.979167	0.5	0.125	0.45	0	STX 16	20	20q13.32	56659734	56687989
ZNF440	0.979167	0.875	0.125	0.625	0	ZNF440	19	19p13.2	11786107	11807017
FKBP8	0.979167	0.75	0.125	0.575	0	FKBP8	19	19p13.11	18503568	18515384
ZNF30	0.979167	0.875	0.125	0.5	0	ZNF30	19	19q13.11	40109647	40127917
PSMC4	0.979167	0.875	0.125	0.55	0	PSMC4	19	19q13.2	45168913	45179194
MAMSTR	0.979167	0.75	0.125	0.575	0	MAMSTR	19	19q13.33	53908067	53914789
RASIP1	0.979167	0.75	0.125	0.575	0	RASIP1	19	19q13.33	53915654	53935783
IZUMO1	0.979167	0.75	0.125	0.575	0	IZUMO1	19	19q13.33	53935957	53941979
DSG2	0.979167	0.125	0	0	0.05	DSG2	18	18q12.1	27332025	27382813
ZNF287	0.979167	0.375	0.125	0.325	0	ZNF287	17	17p11.2	16394356	16413246
SLC4A1	0.979167	0.5	0.125	0.5	0	SLC4A1	17	17q21.31	39681284	39701029
SPAG9	0.979167	0.5	0.125	0.225	0	SPAG9	17	17q21.33	46394535	46553226
NME1	0.979167	0.5	0.125	0.275	0	NME1	17	17q21.33	46585919	46594450
NME1-NME2	0.979167	0.5	0.125	0.275	0	NME1-NME2	17	17q21.33	46585919	46604105
NME2	0.979167	0.5	0.125	0.275	0	NME2	17	17q21.33	46597890	46604105
MBTD1	0.979167	0.375	0.125	0.2	0	MBTD1	17	17q21.33	46609785	46692427
UTP18	0.979167	0.375	0.125	0.2	0	UTP18	17	17q21.33	46692896	46730292
TOM1L1	0.979167	0	0.125	0.1	0	TOM1L1	17	17q22	50333051	50394328
COX11	0.979167	0	0.125	0.1	0	COX11	17	17q22	50384258	50401064
STXBP4	0.979167	0	0.125	0.1	0	STXBP4	17	17q22	50401125	50596449
RSL1D1	0.979167	0.5	0.125	0.425	0	RSL1D1	16	16q13.13	11835556	11852944
VPS4A	0.979167	0.625	0.125	0.375	0	VPS4A	16	16q22.1	67902788	67916448
COG8	0.979167	0.625	0.125	0.375	0	COG8	16	16q22.1	67920025	67931028
PDF	0.979167	0.625	0.125	0.375	0	PDF	16	16q22.1	67920025	67922000
NIP7	0.979167	0.625	0.125	0.375	0	NIP7	16	16q22.1	67931047	67934511
TMED6	0.979167	0.625	0.125	0.375	0	TMED6	16	16q22.1	67934650	67943214
PAR1	0.979167	0.125	0	0	0.075	PAR1	15	15q11.2	22931882	22934294
FSIP1	0.979167	0	0.125	0.125	0	FSIP1	15	15q14	37679524	37862332
NRG4	0.979167	0.5	0.125	0.45	0	NRG4	15	15q24.2	74022899	74091841
NTRK3	0.979167	0.375	0.125	0.25	0	NTRK3	15	15q25.3	86220992	86600666
FBXO33	0.979167	0.125	0.125	0	0.1	FBXO33	14	14q21.1	38936628	38971456
DDHD1	0.979167	0.125	0	0	0	DDHD1	14	14q22.2	52573210	52689797
FUT8	0.979167	0	0.125	0.175	0	FUT8	14	14q23.3	64947593	65279716
CYP46A1	0.979167	0.5	0.125	0.475	0	CYP46A1	14	14q32.2	99220508	99263392
RFC3	0.979167	0	0.125	0	0	RFC3	13	13q13.2	33290206	33438696
MIR548F5	0.979167	0	0.125	0.05	0	MIR548F5	13	13q13.3	34946406	35413383
DCLK1	0.979167	0	0.125	0	0	DCLK1	13	13q13.3	35241123	35603465
SOHLH2	0.979167	0	0.125	0	0	SOHLH2	13	13q13.3	35640347	35686753
CCNA1	0.979167	0	0.125	0	0	CCNA1	13	13q13.3	35903967	35915020
MYO16	0.979167	0.125	0	0	0.025	MYO16	13	13q33.3	1.08E+08	1.09E+08
YAF2	0.979167	0	0.125	0.025	0	YAF2	12	12q12	40837174	40918318
WDR51B	0.979167	0.125	0.25	0	0.05	WDR51B	12	12q21.33	88337634	88443909
OR51E1	0.979167	0.125	0	0	0	OR51E1	11	11p15.4	4621732	4633291
OR51E2	0.979167	0.125	0	0	0	OR51E2	11	11p15.4	4657977	4675653
FLJ46111	0.979167	0.125	0.125	0.25	0	FLJ46111	11	11p15.4	9072486	9074314
DNAJC24	0.979167	0.125	0	0	0.075	DNAJC24	11	11p13	31347953	31410959
ASRGL1	0.979167	0.5	0.125	0.45	0	ASRGL1	11	11q12.3	61861350	61917464
SCGB1A1	0.979167	0.5	0.125	0.45	0	SCGB1A1	11	11q12.3	61943099	61947244
PAK1	0.979167	0.125	0.125	0.2	0	PAKI	11	11q14.1	76710708	76862757
AKR1C1	0.979167	0	0.125	0.1	0	AKR1C1	10	10p15.1	4995454	5010159
AKR1C2	0.979167	0	0.125	0.1	0	AKR1C2	10	10p15.1	5021965	5050208
CUBN	0.979167	0.125	0	0	0	CUBN	10	10p13	16905971	17211823
MYO3A	0.979167	0.125	0	0	0	MYO3A	10	10p12.1	26263008	26541472
CCDC6	0.979167	0.125	0	0	0	CCDC6	10	10q21.2	61218527	61336825
KCNMA1	0.979167	0.25	0.125	0.175	0	KCNMA1	10	10q22.3	78299365	79067584
PDCD4	0.979167	0	0.125	0.05	0	PDCD4	10	10q25.2	1.13E+08	1.13E+08
RLN1	0.979167	0	0.125	0	0	RLN1	9	9p24.1	5324969	5329874
SLC24A2	0.979167	0.125	0	0	0.025	SLC24A2	9	9p22.1	19505978	19776927

TABLE 5-continued

Gene list for predicting prostate cancer fast relapse using AT

Symbol	freq.use	freq.amp. case	freq.del. case	freq.amp. control	freq.del. control	Gene.Symbol	chromosome	cytoband	Transcript. start	Transcript. end
LOC440173	0.979167	0.25	0.125	0.175	0	LOC440173	9	9q21.33	88813187	88846862
ASTN2	0.979167	0	0.125	0.05	0	ASTN2	9	9q33.1	1.18E+08	1.19E+08
LHX3	0.979167	0.875	0.125	0.725	0	LHX3	9	9q34.3	1.38E+08	1.38E+08
QSOX2	0.979167	0.875	0.125	0.725	0	QSOX2	9	9q34.3	1.38E+08	1.38E+08
TNFRSF10C	0.979167	0.25	0.125	0.175	0	TNFRSF10C	8	8p21.3	23016379	23030896
TERF1	0.979167	0	0.125	0.075	0	TERF1	8	8q21.11	74083651	74122542
C8orf84	0.979167	0	0.125	0.1	0	C8orf84	8	8q21.11	74139334	74168062
RDH10	0.979167	0	0.125	0.1	0	RDH10	8	8q21.11	74369819	74400069
UBE2W	0.979167	0.125	0.125	0.1	0	UBE2W	8	8q21.11	74865394	74953665
TCEB1	0.979167	0.125	0.125	0.1	0	TCEB1	8	8q21.11	75021188	75046901
C7orf30	0.979167	0	0.125	0.05	0	C7orf30	7	7p15.3	23305465	23315706
IGF2BP3	0.979167	0	0.125	0.05	0	IGF2BP3	7	7p15.3	23316353	23476521
CALU	0.979167	0.25	0.125	0.3	0	CALU	7	7q32.1	1.28E+08	1.28E+08
MIR548A1	0.979167	0.125	0	0	0.025	MIR548A1	6	6p22.3	18679994	18680091
HMGA1	0.979167	0.625	0.125	0.425	0	HMGA1	6	6p21.31	34312555	34321986
TCP11	0.979167	0.5	0.125	0.325	0	TCP11	6	6p21.31	35193827	35217166
KLEHL31	0.979167	0	0.125	0	0	KLHL31	6	6p12.1	53620658	53638466
LRRC1	0.979167	0	0.125	0	0	LRRC1	6	6p12.1	53767737	53896879
SLC22A16	0.979167	0.125	0	0	0	SLC22A16	6	6q21	1.11E+08	1.11E+08
RICTOR	0.979167	0	0.125	0	0	RICTOR	5	5p13.1	38973780	39110259
FYB	0.979167	0	0.125	0	0	FYB	5	5p13.1	39141114	39255425
FAM169A	0.979167	0	0.125	0	0	FAM169A	5	5q13.3	74109155	74198372
SEMA6A	0.979167	0	0.125	0	0	SEMA6A	5	5q23.1	1.16E+08	1.16E+08
DMXL1	0.979167	0.125	0.125	0.075	0	DMXL1	5	5q23.1	1.18E+08	1.19E+08
TNFAIP8	0.979167	0	0.125	0.025	0	TNFAIP8	5	5q23.1	1.19E+08	1.19E+08
SAR1B	0.979167	0.375	0.125	0.35	0	SAR1B	5	5q31.1	1.34E+08	1.34E+08
RNF130	0.979167	0.5	0.125	0.525	0	RNF130	5	5q35.3	1.79E+08	1.79E+08
MIR340	0.979167	0.5	0.125	0.525	0	MIR340	5	5q35.3	1.79E+08	1.79E+08
SLC30A9	0.979167	0.125	0.125	0	0.05	SLC30A9	4	4p13	41687280	41784309
BEND4	0.979167	0.125	0.125	0	0.05	BEND4	4	4p13	41807629	41849653
POLR2B	0.979167	0	0.125	0	0	POLR2B	4	4q12	57539866	57592092
IGFBP7	0.979167	0	0.125	0	0	IGFBP7	4	4q12	57592001	57671297
HELQ	0.979167	0.125	0.125	0.125	0	HELQ	4	4q21.23	84547523	84596050
MRPS18C	0.979167	0.125	0.125	0.125	0	MRPS18C	4	4q21.23	84596142	84601954
FAM175A	0.979167	0.125	0.125	0.125	0	FAM175A	4	4q21.23	84601120	84625315
DCLK2	0.979167	0.125	0.125	0	0.025	DCLK2	4	4q31.3	1.51E+08	1.51E+08
TRIM61	0.979167	0.125	0.125	0	0.05	TRIM61	4	4q32.3	1.66E+08	1.66E+08
C4orf39	0.979167	0.125	0.125	0	0.05	C4orf39	4	4q32.3	1.66E+08	1.66E+08
NKTR	0.979167	0.25	0.125	0.275	0	NKTR	3	3p22. 1	42617151	42665238
DOCK3	0.979167	0.375	0.125	0.275	0	DOCK3	3	3p21.31	50687676	51396670
LRIG1	0.979167	0.125	0	0	0	LRIG1	3	3p14.1	66511911	66633536
GXYLT2	0.979167	0	0.125	0.05	0	GXYLT2	3	3p13	73020075	73107213
PPP4R2	0.979167	0	0.125	0.05	0	PPP4R2	3	3p13	73128809	73197702
WDR52	0.979167	0	0.125	0.025	0	WDR52	3	3q13.2	1.14E+08	1.15E+08
SIDT1	0.979167	0	0.125	0.025	0	SIDT1	3	3q13.2	1.15E+08	1.15E+08
NAT13	0.979167	0	0.125	0.05	0	NAT13	3	3q13.2	1.15E+08	1.15E+08
POLQ	0.979167	0	0.125	0.05	0	POLQ	3	3q13.33	1.23E+08	1.23E+08
ARGFX	0.979167	0	0.125	0.05	0	ARGFX	3	3q13.33	1.23E+08	1.23E+08
FBXO40	0.979167	0	0.125	0.05	0	FBXO40	3	3q13.33	1.23E+08	1.23E+08
PLSCR1	0.979167	0.125	0.375	0	0.175	PLSCR1	3	3q24	1.48E+08	1.48E+08
TM4SF4	0.979167	0.125	0	0	0.025	TM4SF4	3	3q25.1	1.51E+08	1.51E+08
WWTR1	0.979167	0.125	0	0	0.025	WWTR1	3	3q25.1	1.51E+08	1.51E+08
NMD3	0.979167	0	0.125	0.025	0	NMD3	3	3q26.1	1.62E+08	1.62E+08
MRPL47	0.979167	0.125	0.125	0.025	0	MRPL47	3	3q26.33	1.81E+08	1.81E+08
TMEM17	0.979167	0.125	0	0	0	TMEM17	2	2p15	62580860	62587109
EHBP1	0.979167	0	0.125	0	0	EHBP1	2	2p15	62754517	63127124
C2orf86	0.979167	0	0.125	0.025	0	C2orf86	2	2p15	63202039	63518591
MDH1	0.979167	0	0.125	0.025	0	MDH1	2	2p15	63669626	63687833
RPL31	0.979167	0.25	0.125	0.175	0	RPL31	2	2q11.2	1.01E+08	1.01E+08
SLC9A2	0.979167	0	0.125	0.05	0	SLC9A2	2	2q12.1	1.03E+08	1.03E+08
GCG	0.979167	0.125	0	0	0.125	GCG	2	2q24.2	1.63E+08	1.63E+08
FAP	0.979167	0.125	0	0	0.125	FAP	2	2q24.2	1.63E+08	1.63E+08
C2orf77	0.979167	0.125	0	0	0	C2orf77	2	2q311	1.7E+08	1.7E+08
PHOSPHO2	0.979167	0.125	0	0	0	PHOSPHO2	2	2q31.1	1.7E+08	1.7E+08
KLHL23	0.979167	0.125	0	0	0	KLHL23	2	2q31.1	1.7E+08	1.7E+08
SSB	0.979167	0.125	0	0	0	SSB	2	2q31.1	1.7E+08	1.7E+08
METTL5	0.979167	0.125	0	0	0	METTL5	2	2q31.1	1.7E+08	1.7E+08
UBR3	0.979167	0.125	0	0	0	UBR3	2	2q31.1	1.7E+08	1.71E+08
C1orf64	0.979167	0.625	0.125	0.575	0	C1orf64	1	1p36.13	16203318	16205772
CYP4A22	0.979167	0.375	0.125	0.325	0	CYP4A22	1	1p33	47375694	47387114
C1orf141	0.979167	0	0.125	0.025	0	C1orf141	1	1p31.3	67330447	67366809
ABCD3	0.979167	0.125	0.125	0.025	0	ABCD3	1	1p21.3	94656521	94716849
RABGAP1L	0.979167	0	0.125	0.05	0	RABGAP1L	1	1q25.1	1.72E+08	1.73E+08
RBBP5	0.979167	0.375	0.125	0.35	0	RBBP5	1	1q32.1	2.03E+08	2.03E+08
RFX7	0.041667	0.125	0.125	0.025	0.025	RFX7	15	15q21.3	54170023	54322776

TABLE 5-continued

Gene list for predicting prostate cancer fast relapse using AT

Symbol	freq.use	freq.amp. case	freq.del. case	freq.amp. control	freq.del. control	Gene.Symbol	chromosome	cytoband	Transcript. start	Transcript. end
IPCEF1	0.041667	0.125	0.125	0.025	0.025	IPCEF1	6	6q25.2	1.55E+08	1.55E+08
TLR10	0.041667	0.125	0.125	0.025	0.025	TLR10	4	4p14	38450647	38460985
PHOX2B	0.041667	0.125	0.125	0.025	0.025	PHOX2B	4	4p13	41440856	41445745
PDCD6IP	0.041667	0.125	0.125	0.025	0.025	PDCD6IP	3	3p22.3	33815070	33886199
SR140	0.041667	0.125	0.125	0.025	0.025	SR140	3	3q23	1.44E+08	1.44E+08
KIF5C	0.041667	0.125	0.125	0.025	0.025	KIF5C	2	2q23.1	1.49E+08	1.5E+08
MIR1978	0.041667	0.125	0.125	0.025	0.025	MIR1978	2	2q23.1	1.49E+08	1.49E+08
VAMP7	0.020833	0.375	0.125	0.3	0.025	VAMP7	X	Xq28	1.55E+08	1.55E+08
IL9R	0.020833	0.375	0.125	0.3	0.025	IL9R	X	Xq28	1.55E+08	1.55E+08
ATXN10	0.020833	0.625	0.125	0.575	0.025	ATXN10	22	22q13.31	44446342	44619851
RNF160	0.020833	0.125	0.125	0.05	0.025	RNF160	21	21q21.3	29222337	29287149
C21orf7	0.020833	0.125	0	0.025	0.025	C21orf7	21	21q21.3	29374744	29470074
CLDN17	0.020833	0	0.125	0.025	0.025	CLDN17	21	21q21.3	30460132	30460807
KRTAP19-3	0.020833	0	0.125	0.025	0.025	KRTAP19-3	21	21q22.11	30785653	30786147
KRTAPI9-4	0.020833	0	0.125	0.025	0.025	KRTAP19-4	21	21q22.11	30791045	30791300
KRTAP19-5	0.020833	0	0.125	0.025	0.025	KRTAP19-5	21	21q22.11	30796061	30796280
KRTAP19-7	0.020833	0	0.125	0.025	0.025	KRTAP19-7	21	21q22.11	30855288	30855480
KRTAP20-2	0.020833	0	0.125	0.05	0.025	KRTAP20-2	21	21q22.11	30929454	30929652
KRTAP20-3	0.020833	0	0.125	0.05	0.025	KRTAP20-3	21	21q22.11	30937054	30937327
PSG1	0.020833	0.5	0.25	0.4	0.025	PSG1	19	19q13.31	48063198	48075712
ZNF519	0.020833	0.125	0.125	0.075	0.025	ZNF519	18	18p11.21	14094724	14122430
ANKRD30B	0.020833	0.125	0.125	0.075	0.025	ANKRD30B	18	18p11.21	14738239	14842738
TTR	0.020833	0.125	0	0.025	0.025	TTR	18	18q12.1	27425728	27432983
B4GALT6	0.020833	0.125	0	0.025	0.025	B4GALT6	18	18q12.1	27456207	27518685
MCART2	0.020833	0.125	0	0.025	0.025	MCART2	18	18q12.1	27593657	27594842
KIAA1012	0.020833	0.125	0	0.025	0.025	KIAA1012	18	18q12.1	27663134	27777090
SERPINB13	0.020833	0.125	0	0.025	0.025	SERPINB13	18	18q21.33	59405514	59417413
TANC2	0.020833	0.375	0.125	0.275	0.025	TANC2	17	17q23.3	58440630	58858800
CDH11	0.020833	0.25	0	0.025	0.075	CDH11	16	16q21	63538184	63713421
LOC283867	0.020833	0.25	0	0.025	0.025	LOC283867	16	16q21	63875903	64167705
CNTNAP4	0.020833	0.125	0	0.025	0.025	CNTNAP4	16	16q23.1	74868677	75150637
SCG5	0.020833	0.125	0	0.025	0	SCG5	15	15q13.3	30721162	30776591
MEIS2	0.020833	0	0.125	0.025	0.025	MEIS2	15	15q14	34970524	35180793
DMXL2	0.020833	0.125	0.125	0.05	0.025	DMXL2	15	15q21.2	49527231	49702260
RAB27A	0.020833	0.125	0	0.025	0	RAB27A	15	15q21.3	53283092	53349878
PIGB	0.020833	0.125	0	0.025	0	PIGB	15	15q21.3	53398425	53435139
CCPG1	0.020833	0.125	0	0.025	0	CCPG1	15	15q21.3	53434730	53487835
MIR628	0.020833	0.125	0	0.025	0	MIR628	15	15q21.3	53452430	53452525
DYX1C1	0.020833	0.125	0	0.025	0	DYX1C1	15	15q21.3	53497246	53587725
PYGO1	0.020833	0.125	0	0.025	0	PYGO1	15	15q21.3	53625513	53668343
PRTG	0.020833	0.125	0	0.025	0	PRTG	15	15q21.3	53691042	53822470
NEDD4	0.020833	0.25	0	0.025	0	NEDD4	15	15q21.3	53906414	54073128
TEX9	0.020833	0.125	0.125	0.025	0.05	TEX9	15	15q21.3	54444936	54525365
ZNF280D	0.020833	0.125	0	0.025	0	ZNF280D	15	15q21.3	54709666	54813080
TCF12	0.020833	0.125	0	0.025	0.025	TCF12	15	15q21.3	54998125	55368007
NEO1	0.020833	0.25	0.125	0.275	0.025	NEO1	15	15q24.1	71131928	71384599
MIPOL1	0.020833	0	0.125	0	0.025	MIPOL1	14	14q21.1	36736869	37086619
CDKN3	0.020833	0.125	0	0.025	0	CDKN3	14	14q22.2	53933423	53956683
C14orf145	0.020833	0	0.25	0	0.025	C14orf145	14	14q31.1	80032574	80475638
TSHR	0.020833	0	0.25	0	0.025	TSHR	14	14q31.1	80491622	80682400
STON2	0.020833	0	0.25	0.025	0.025	STON2	14	14q31.1	80806662	80934681
SEL1L	0.020833	0	0.25	0.025	0.025	SEL1L	14	14q31.1	81008994	81069959
ZMYM2	0.020833	0.125	0.125	0.15	0.025	ZMYM2	13	13q12.11	19430810	19558940
NBEA	0.020833	0	0.125	0	0.025	NBEA	13	13q13.2	34414456	35144874
SPG20	0.020833	0	0.125	0	0.025	SPG20	13	13q13.3	35773777	35842318
COG6	0.020833	0	0.125	0	0.025	COG6	13	13q13.3	39127764	39263803
RNASEH2B	0.020833	0.125	0	0.025	0	RNASEH2B	13	13q14.3	50381893	50442596
GUCY1B2	0.020833	0.125	0	0.025	0	GUCY1B2	13	13q14.3	50466649	50538295
FAM124A	0.020833	0.125	0	0.025	0	FAM124A	13	13q14.3	50694508	50753618
SERPINE3	0.020833	0.125	0	0.025	0	SERPINE3	13	13q14.3	50813169	50834241
INTS6	0.020833	0.125	0	0.025	0	INTS6	13	13q14.3	50833702	50925277
DCT	0.020833	0.125	0.125	0.025	0.1	DCT	13	13q32.1	93889842	93929938
DNAJC3	0.020833	0.375	0	0.025	0	DNAJC3	13	13q32.1	95127403	95245243
TMTC4	0.020833	0.125	0	0.025	0	TMTC4	13	13q32.3	1E+08	1E+08
AEBP2	0.020833	0.125	0	0.025	0.075	AEBP2	12	12p12.3	19483875	19566441
GXYLT1	0.020833	0	0.125	0	0.025	GXYLT1	12	12q12	40761915	40824941
SRGAP1	0.020833	0.125	0	0.025	0	SRGAP1	12	12q14.2	62524808	62827881
C12orf66	0.020833	0.125	0	0.025	0	C12orf66	12	12q14.2	62872686	62902344
C12orf56	0.020833	0.125	0	0.025	0	C12orf56	12	12q14.2	62947032	63070613
TBK1	0.020833	0.125	0	0.025	0	TBK1	12	12q14.2	63132204	63182159
GNS	0.020833	0.125	0	0.025	0	GNS	12	12q14.2-12q14.3	63393489	63439494
ZFC3H1	0.020833	0	0.25	0	0.025	ZFC3H1	12	12q21.1	70289649	70344017
TBC1D15	0.020833	0	0.25	0.05	0.025	TBC1D15	12	12q21.1	70519754	70606895
MRS2P2	0.020833	0	0.25	0.05	0.025	MRS2P2	12	12q21.1	70528343	70531031

TABLE 5-continued

Gene list for predicting prostate cancer fast relapse using AT

Symbol	freq.use	freq.amp. case	freq.del. case	freq.amp. control	freq.del. control	Gene.Symbol	chromosome	cytoband	Transcript. start	Transcript. end
METAP2	0.020833	0.125	0	0.025	0	METAP2	12	12q22	94391953	94433745
USP44	0.020833	0.125	0	0.025	0	USP44	12	12q22	94435018	94466752
NTN4	0.020833	0.125	0	0.025	0	NTN4	12	12q22	94575714	94708668
CCDC38	0.020833	0.125	0	0.025	0	CCDC38	12	12q23.1	94784958	94860560
AMDHD1	0.020833	0.125	0	0.025	0	AMDHD1	12	12q23.1	94861202	94886501
HAL	0.020833	0.125	0	0.025	0	HAL	12	12q23.1	94891273	94914203
OR52K2	0.020833	0.125	0	0.025	0.025	OR52K2	11	11p15.4	4427146	4428091
C11orf40	0.020833	0.125	0	0.025	0.025	C11orf40	11	11p15.4	4549229	4555627
API5	0.020833	0.25	0	0.025	0	API5	11	11p12	43290081	43322659
TTC17	0.020833	0.25	0	0.025	0	TTC17	11	11p12	43337067	43472072
MIR670	0.020833	0.25	0	0.025	0	MIR670	11	11p11.2	43537782	43537880
CCDC82	0.020833	0	0.25	0	0.025	CCDC82	11	11q21	95725577	95762732
JRKL	0.020833	0	0.25	0	0.025	JRKL	11	11q21	95762806	95766376
OR8D1	0.020833	0.125	0	0.025	0.025	OR8D1	11	11q24.2	1.24E+08	1.24E+08
OR8D2	0.020833	0.125	0	0.025	0.025	OR8D2	11	11q24.2	1.24E+08	1.24E+08
C10orf18	0.020833	0.375	0.125	0.225	0.025	C10orf18	10	10p15.1	5766807	5846950
LOC254312	0.020833	0.375	0	0.025	0	LOC254312	10	10p14	11016910	11034133
CUGBP2	0.020833	0.375	0	0.025	0	CUGBP2	10	10p14	11087265	11418679
PTER	0.020833	0.25	0	0.025	0	PTER	10	10p13	16518973	16595743
GAD2	0.020833	0.125	0	0.025	0	GAD2	10	10p12.1	26545242	26633498
APBB1IP	0.020833	0.125	0	0.025	0	APBB1IP	10	10p12.1	26767272	26896739
C10orf50	0.020833	0.125	0	0.025	0	C10orf50	10	10p12.1	26918800	26923256
LOC731789	0.020833	0.125	0	0.025	0	LOC731789	10	10p12.1	26972043	26982389
PDSS1	0.020833	0.125	0	0.025	0	PDSS1	10	10p12.1	27026601	27075733
ABI1	0.020833	0.125	0	0.025	0	ABI1	10	10p12.1	27075531	27189966
CCDC7	0.020833	0	0.125	0.025	0.025	CCDC7	10	10p11.22	32775047	32903499
FAM13C	0.020833	0	0.25	0	0.025	FAM13C	10	10q21.1	60675896	60792359
TM9SF3	0.020833	0.25	0.125	0.275	0.025	TM9SF3	10	10q24.1	98267857	98336800
PIK3AP1	0.020833	0.25	0.125	0.275	0.025	PIK3AP1	10	10q24.1	98343059	98470270
PLAA	0.020833	0.125	0.125	0.1	0.025	PLAA	9	9p21.2	26893369	26937469
IFT74	0.020833	0.125	0.125	0.075	0.025	IFT74	9	9p21.2	26937037	27052932
ALDH1A1	0.020833	0	0.125	0	0.025	ALDH1A1	9	9q21.13	74705407	74757790
GAS1	0.020833	0.25	0.125	0.175	0.025	GAS1	9	9q21.33	88749097	88751925
LPPR1	0.020833	0	0.125	0.025	0.025	LPPR1	9	9q31.1	1.03E+08	1.03E+08
MRPL50	0.020833	0	0.125	0.05	0.025	MRPL50	9	9q31.1	1.03E+08	1.03E+08
ZNF189	0.020833	0	0.125	0.05	0.025	ZNF189	9	9q31.1	1.03E+08	1.03E+08
ALDOB	0.020833	0	0.125	0.05	0.025	ALDOB	9	9q31.1	1.03E+08	1.03E+08
RNF20	0.020833	0	0.125	0.05	0.025	RNF20	9	9q31.1	1.03E+08	1.03E+08
GRIN3A	0.020833	0	0.125	0.05	0.025	GRIN3A	9	9q31.1	1.03E+08	1.04E+08
TNFSF15	0.020833	0	0.125	0.075	0.025	TNFSF15	9	9q32	1.17E+08	1.17E+08
TNFSF8	0.020833	0	0.125	0.075	0.025	TNFSF8	9	9q33.1	1.17E+08	1.17E+08
TNC	0.020833	0	0.125	0.075	0.025	TNC	9	9q33.1	1.17E+08	1.17E+08
PAPPA	0.020833	0	0.25	0.025	0.025	PAPPA	9	9q33.1	1.18E+08	1.18E+08
DBC1	0.020833	0	0.125	0.025	0.025	DBC1	9	9q33.1	1.21E+08	1.21E+08
ADAM9	0.020833	0	0.125	0.025	0.025	ADAM9	8	8p11.23	38973662	39081937
ADAM32	0.020833	0	0.125	0.025	0.025	ADAM32	8	8p11.23	39084207	39261594
ADAM18	0.020833	0	0.125	0.025	0.025	ADAM18	8	8p11.22	39561299	39706645
ADAM2	0.020833	0	0.125	0.025	0.025	ADAM2	8	8p11.22	39720412	39814937
POTEA	0.020833	0	0.125	0.125	0.025	POTEA	8	8p11.1	43266742	43337486
ST18	0.020833	0	0.125	0.025	0.025	ST18	8	8q11.23	53185945	53484993
ARMC1	0.020833	0.125	0	0.025	0	ARMC1	8	8q13.1	66677628	66708987
MTFR1	0.020833	0.125	0	0.025	0	MTFR1	8	8q13.1	66719442	66783127
PDE7A	0.020833	0.125	0	0.025	0	PDE7A	8	8q13.1	66792460	66863876
DNAJC5B	0.020833	0.125	0	0.025	0	DNAJC5B	8	8q13.1	67096345	67175310
TRIM55	0.020833	0.125	0	0.025	0	TRIM55	8	8q13.1	67201832	67250273
TMEM70	0.020833	0	0.25	0.05	0.025	TMEM70	8	8q21.11	75050984	75057568
JPH1	0.020833	0	0.25	0.025	0.025	JPH1	8	8q21.11	75309493	75396118
COL14A1	0.020833	0.125	0	0.025	0.025	COL14A1	8	8q24.12	1.21E+08	1.21E+08
MRPL13	0.020833	0	0.125	0	0.025	MRPL13	8	8q24.12	1.21E+08	1.22E+08
MTBP	0.020833	0	0.125	0	0.025	MTBP	8	8q24.12	1.22E+08	1.22E+08
C1GALT1	0.020833	0.125	0.125	0.075	0.025	C1GALT1	7	7p21.3	7188771	7250507
COL28A1	0.020833	0.125	0.125	0.025	0.075	COL28A1	7	7p21.3	7364769	7541986
RPA3	0.020833	0.125	0.125	0.025	0.05	RPA3	7	7p21.3	7643100	7724764
GLCCI1	0.020833	0.125	0.125	0.025	0.05	GLCCI1	7	7p21.3	7974948	8095235
ABCA13	0.020833	0.125	0	0.025	0.05	ABCA13	7	7p12.3	48208389	48657638
PION	0.020833	0.125	0	0.025	0.075	PION	7	7q11.23	76778004	76883654
CDK6	0.020833	0	0.125	0.075	0.025	CDK6	7	7q21.2	92072173	92303878
LAMB1	0.020833	0.125	0	0.025	0	LAMB1	7	7q31.1	1.07E+08	1.07E+08
AKR1B1	0.020833	0.125	0	0.025	0	AKR1B1	7	7q33	1.34E+08	1.34E+08
AKR1B10	0.020833	0.125	0	0.025	0	AKRIB10	7	7q33	1.34E+08	1.34E+08
RNF144B	0.020833	0.125	0	0.025	0.025	RNF144B	6	6p22.3	18495573	18576830
SOX4	0.020833	0.125	0	0.025	0	SOX4	6	6p22.3	21701951	21706829
FLJ22536	0.020833	0.125	0	0.025	0	FLJ22536	6	6p22.3	21774654	22302594
LOC100287718	0.020833	0	0.125	0	0.025	LOC100287718	6	6p12.3	46822658	46834901
MEP1A	0.020833	0	0.125	0	0.025	MEP1A	6	6p12.3	46869053	46915479

TABLE 5-continued

Gene list for predicting prostate cancer fast relapse using AT

Symbol	freq.use	freq.amp. case	freq.del. case	freq.amp. control	freq.del. control	Gene.Symbol	chromosome	cytoband	Transcript. start	Transcript. end
GPR116	0.020833	0	0.125	0	0.025	GPR116	6	6p12.3	46928204	46997674
GPR110	0.020833	0	0.125	0	0.025	GPR110	6	6p12.3	47075772	47118042
TNFRSF21	0.020833	0	0.125	0	0.025	TNFRSF21	6	6p12.3	47307227	47385640
CD2AP	0.020833	0	0.25	0	0.025	CD2AP	6	6p12.3	47553484	47702956
SMAP1	0.020833	0.125	0.125	0.025	0.125	SMAP1	6	6q13	71434200	71628438
CDK19	0.020833	0.125	0	0.025	0	CDK19	6	6q21	1.11E+08	1.11E+08
SLC22A3	0.020833	0.125	0	0.025	0	SLC22A3	6	6q25.3	1.61E+08	1.61E+08
LPA	0.020833	0.125	0	0.025	0	LPA	6	6q25.3	1.61E+08	1.61E+08
DAB2	0.020833	0	0.125	0	0.025	DAB2	5	5p13.1	39407537	39461093
TTC33	0.020833	0.125	0	0.025	0	TTC33	5	5p13.1	40747435	40791830
PRKAA1	0.020833	0.125	0	0.025	0	PRKAA1	5	5p13.1	40795238	40834055
RPL37	0.020833	0.125	0	0.025	0	RPL37	5	5p13.1	40867187	40871145
SNORD72	0.020833	0.125	0	0.025	0	SNORD72	5	5p13.1	40868515	40868595
CARD6	0.020833	0.125	0	0.025	0	CARD6	5	5p13.1	40877167	40891214
C7	0.020833	0	0.125	0.025	0.025	C7	5	5p13.1	40945356	41018799
IPO11	0.020833	0.125	0	0.025	0.025	IPO11	5	5q12.1	61744330	61960172
RHOBTB3	0.020833	0.125	0.125	0.025	0.1	RHOBTB3	5	5q15	95092606	95157828
GLRX	0.020833	0.125	0.125	0.025	0.1	GLRX	5	5q15	95175309	95184334
C5orf27	0.020833	0.125	0.125	0.025	0.1	C5orf27	5	5q15	95213692	95221591
TSSK1B	0.020833	0	0.125	0	0.025	TSSK1B	5	5q22.2	1.13E+08	1.13E+08
SNX2	0.020833	0	0.25	0	0.025	SNX2	5	5q23.2	1.22E+08	1.22E+08
SNX24	0.020833	0	0.25	0	0.025	SNX24	5	5q23.2	1.22E+08	1.22E+08
PPIC	0.020833	0	0.25	0	0.025	PPIC	5	5q23.2	1.22E+08	1.22E+08
3-Mar	0.020833	0	0.125	0.05	0.025	3-Mar	5	5q23.2	1.26E+08	1.26E+08
CDC42SE2	0.020833	0.125	0	0.025	0	CDC42SE2	5	5q31.1	1.31E+08	1.31E+08
RAPGEF6	0.020833	0.125	0	0.025	0	RAPGEF6	5	5q31.1	1.31E+08	1.31E+08
FNIP1	0.020833	0.125	0	0.025	0	FNIP1	5	5q31.1	1.31E+08	1.31E+08
GEMIN5	0.020833	0	0.125	0.125	0.025	GEMIN5	5	5q33.2	1.54E+08	1.54E+08
KIF4B	0.020833	0	0.125	0.075	0.025	KIF4B	5	5q33.2	1.54E+08	1.54E+08
EBF1	0.020833	0	0.125	0	0.025	EBF1	5	5q33.3	1.58E+08	1.58E+08
C5orf54	0.020833	0	0.125	0.075	0.025	C5orf54	5	5q33.3	1.6E+08	1.6E+08
ZNF718	0.020833	0.375	0.125	0.5	0.025	ZNF718	4	4p16.3	43277	146491
ZNF876P	0.020833	0.375	0.125	0.5	0.025	ZNF876P	4	4p16.3	196389	239772
HTRA3	0.020833	0.5	0.25	0.625	0.025	HTRA3	4	4p16.1	8322392	8359735
QDPR	0.020833	0.125	0	0.025	0	QDPR	4	4p15.32	17097118	17122956
CLRN2	0.020833	0.125	0	0.025	0	CLRN2	4	4p15.32	17125886	17137826
LAP3	0.020833	0.125	0	0.025	0	LAP3	4	4p15.32	17188025	17218689
FAM184B	0.020833	0.125	0	0.025	0	FAM184B	4	4p15.32	17242809	17392234
DCAF16	0.020833	0.125	0	0.025	0	DCAF16	4	4p15.32	17411376	17421480
TMEM33	0.020833	0.25	0	0.025	0.025	TMEM33	4	4p13	41631894	41657582
CNGA1	0.020833	0	0.25	0.025	0.025	CNGA1	4	4p12	47632751	47709719
NIPAL1	0.020833	0	0.25	0	0.025	NIPAL1	4	4p12	47713548	47733838
TXK	0.020833	0	0.25	0	0.025	TXK	4	4p12	47763167	47831031
TEC	0.020833	0	0.25	0	0.025	TEC	4	4p12	47832557	47966572
RUFY3	0.020833	0.375	0.25	0.05	0.025	RUFY3	4	4q13.3	71789518	71874478
MOBKL1A	0.020833	0.375	0.25	0.05	0.025	MOBKL1A	4	4q13.3	71986928	72072756
DCK	0.020833	0.375	0.25	0.05	0.025	DCK	4	4q13.3	72078129	72115494
EIF4E	0.020833	0.125	0	0.025	0.05	EIF4E	4	4q23	1E+08	1E+08
SGMS2	0.020833	0	0.125	0.025	0.025	SGMS2	4	4q25	1.09E+08	1.09E+08
CYP2U1	0.020833	0	0.125	0	0.025	CYP2U1	4	4q25	1.09E+08	1.09E+08
GAB1	0.020833	0	0.125	0	0.025	GAB1	4	4q31.21	1.44E+08	1.45E+08
SMARCA5	0.020833	0	0.125	0	0.025	SMARCA5	4	4q31.21	1.45E+08	1.45E+08
LOC441046	0.020833	0	0.125	0	0.025	LOC441046	4	4q31.21	1.45E+08	1.45E+08
FREM3	0.020833	0	0.125	0	0.025	FREM3	4	4q31.21	1.45E+08	1.45E+08
GYPA	0.020833	0	0.125	0	0.025	GYPA	4	4q31.22	1.45E+08	1.45E+08
FAM160A1	0.020833	0.125	0	0.025	0	FAM160A1	4	4q31.3	1.53E+08	1.53E+08
PLCL2	0.020833	0	0.125	0	0.025	PLCL2	3	3p24.3	16901456	17107102
RAB5A	0.020833	0.125	0.25	0.05	0.025	RAB5A	3	3p24.3	19963576	20001663
C3orf48	0.020833	0.125	0.25	0.05	0.025	C3orf48	3	3p24.3	19996458	20028770
KAT2B	0.020833	0.125	0.25	0.05	0.025	KAT2B	3	3p24.3	20056528	20170901
SGOL1	0.020833	0.125	0.25	0.025	0.05	SGOL1	3	3p24.3	20177089	20202688
UBE2E2	0.020833	0	0.125	0	0.025	UBE2E2	3	3p24.3	23219788	23607301
C3orf67	0.020833	0.25	0	0.025	0.025	C3orf67	3	3p14.2	58702777	59010756
PDZRN3	0.020833	0	0.125	0.05	0.025	PDZRN3	3	3p13	73514342	73756763
LOC151658	0.020833	0	0.25	0	0.025	LOC151658	3	3q13.12	1.09E+08	1.09E+08
LOC285205	0.020833	0	0.25	0	0.025	LOC285205	3	3q13.12	1.09E+08	1.09E+08
HHLA2	0.020833	0	0.25	0	0.025	HHLA2	3	3q13.13	1.1E+08	1.1E+08
MYH15	0.020833	0	0.25	0	0.025	MYH15	3	3q13.13	1.1E+08	1.1E+08
KIAA1524	0.020833	0	0.25	0	0.025	KIAA1524	3	3q13.13	1.1E+08	1.1E+08
DZIP3	0.020833	0	0.25	0	0.025	DZIP3	3	3q13.13	1.1E+08	1.1E+08
C3orf66	0.020833	0	0.125	0	0.025	C3orf66	3	3q13.13	1.1E+08	1.1E+08
BOC	0.020833	0	0.125	0.05	0.025	BOC	3	3q13.2	1.14E+08	1.14E+08
GOLGB1	0.020833	0	0.125	0.025	0.025	GOLGB1	3	3q13.33	1.23E+08	1.23E+08
ACAD11	0.020833	0	0.125	0	0.025	ACAD11	3	3q22.1	1.34E+08	1.34E+08
CCRL1	0.020833	0	0.125	0	0.025	CCRL1	3	3q22.1	1.34E+08	1.34E+08

TABLE 5-continued

Gene list for predicting prostate cancer fast relapse using AT

Symbol	freq.use	freq.amp. case	freq.del. case	freq.amp. control	freq.del. control	Gene.Symbol	chromosome	cytoband	Transcript. start	Transcript. end
UBA5	0.020833	0	0.125	0	0.025	UBA5	3	3q22.1	1.34E+08	1.34E+08
NCRNA00119	0.020833	0	0.125	0	0.025	NCRNA00119	3	3q22.1	1.34E+08	1.34E+08
TMEM108	0.020833	0	0.125	0	0.025	TMEM108	3	3q22.1	1.34E+08	1.35E+08
RNF13	0.020833	0	0.125	0	0.025	RNF13	3	3q25.1	1.51E+08	1.51E+08
C3orf57	0.020833	0	0.125	0	0.025	C3orf57	3	3q26.1	1.63E+08	1.63E+08
ZNF639	0.020833	o	0.125	0.025	0	ZNF639	3	3q26.32	1.81E+08	1.81E+08
GNB4	0.020833	0.125	0	0.025	0	GNB4	3	3q26.33	1.81E+08	1.81E+08
ACTL6A	0.020833	0.125	0	0.025	0	ACTL6A	3	3q26.33	1.81E+08	1.81E+08
USP13	0.020833	0.125	0	0.025	0	USP13	3	3q26.33	1.81E+08	1.81E+08
CCDC50	0.020833	0	0.125	0.05	0.025	CCDC50	3	3q28	1.93E+08	1.93E+08
ROCK2	0.020833	0.375	0.125	0.275	0.025	ROCK2	2	2p25.1	11239229	11402163
GTF2A1L	0.020833	0.125	0	0.025	0.1	GTF2A1L	2	2p16.3	48698452	48813791
LHCGR	0.020833	0.125	0	0.025	0.1	LHCGR	2	2p16.3	48767417	48836385
DDX18	0.020833	0.125	0	0.025	0.025	DDX18	2	2q14.1	1.18E+08	1.18E+08
CCDC93	0.020833	0.125	0	0.025	0.025	CCDC93	2	2q14.1	1.18E+08	1.18E+08
LYPD6B	0.020833	0	0.125	0	0.025	LYPD6B	2	2q23.2	1.5E+08	1.5E+08
LYPD6	0.020833	0	0.125	0	0.025	LYPD6	2	2q23.2	1.5E+08	1.5E+08
DPP4	0.020833	0.125	0	0.025	0.075	DPP4	2	2q24.2	1.63E+08	1.63E+08
OLA1	0.020833	0.125	0	0.025	0.025	OLA1	2	2q31.1	1.75E+08	1.75E+08
KCTD18	0.020833	0.125	0	0.025	0	KCTD18	2	2q33.1	2.01E+08	2.01E+08
SGOL2	0.020833	0.125	0	0.025	0	SGOL2	2	2q33.1	2.01E+08	2.01E+08
AOX1	0.020833	0.125	0	0.025	0	AOX1	2	2q33.1	2.01E+08	2.01E+08
ZCCHC17	0.020833	0.625	0.125	0.475	0.025	ZCCHC17	1	1p35.2	31542429	31610368
TCTEX1D1	0.020833	0	0.125	0	0.025	TCTEX1D1	1	1p31.3	66990728	67017318
WDR78	0.020833	0	0.125	0	0.025	WDR78	1	1p31.3	67051161	67163159
SLC35D1	0.020833	0	0.125	0	0.025	SLC35D1	1	1p31.3	67237604	67292669
HFM1	0.020833	0.125	0	0.025	0	HFM1	1	1p22.2	91498911	91643015
CDC7	0.020833	0.125	0	0.025	0	CDC7	1	1p22.2	91738992	91763909
HSP90B3P	0.020833	0.125	0	0.025	0	HSP90B3P	1	1p22.2	91873156	91881923
TGFBR3	0.020833	0.125	0	0.025	0	TGFBR3	1	1p22.2	91918490	92124376
BRDT	0.020833	0.125	0	0.025	0	BRDT	1	1p22.1	92187516	92252574
EPHX4	0.020833	0.125	0	0.025	0	EPHX4	1	1p22.1	92268121	92301682
BTBD8	0.020833	0.125	0	0.025	0	BTBD8	1	1p22.1	92318450	92385984
KIAA1107	0.020833	0.125	0	0.025	0	KIAA1107	1	1p22.1	92405197	92422868
GFI1	0.020833	0.125	0	0.025	0	GFI1	1	1p22.1	92712906	92721945
EVI5	0.020833	0.125	0	0.025	0	EVI5	1	1p22.1	92746841	93030550
RPL5	0.020833	0.25	0	0.025	0	RPL5	1	1p22.1	93070182	93080070
SNORD21	0.020833	0.25	0	0.025	0	SNORD21	1	1p22.1	93075434	93075529
FAM69A	0.020833	0.25	0	0.025	0	FAM69A	1	1p22.1	93080309	93199668
MTF2	0.020833	0.25	0	0.025	0	MTF2	1	1p22.1	93317380	93377225
ARHGAP29	0.020833	0.125	0	0.025	0.025	ARHGAP29	1	1p22.1	94407051	94475896
FCRLB	0.020833	0.125	0	0.025	0.05	FCRLB	1	1q23.3	1.6E+08	1.6E+08
FAM78B	0.020833	0.125	0	0.025	0	FAM78B	1	1q24.1	1.64E+08	1.64E+08
XPR1	0.020833	0.125	0	0.025	0	XPR1	1	1q25.3	1.79E+08	1.79E+08
CACNA1E	0.020833	0.125	0	0.025	0	CACNA1E	1	1q25.3	1.8E+08	1.8E+08
AKT3	0.020833	0	0.125	0	0.025	AKT3	1	1q44	2.42E+08	2.42E+08

SEQUENCE LISTING

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What is claimed is:

1. A method of treating prostate cancer in a human patient in need thereof comprising:

a) obtaining a sample from a patient;

b) determining whether gene the SDA1 Domain Containing 1 (SDAD1) gene is amplified in DNA obtained from the sample;

c) determining that the patient is at increased risk of rapid relapse of prostate cancer when the SDAD1 gene is amplified; and

d) upon determination that the patient is at increased risk of rapid relapse of prostate cancer then treating the patient that is at increased risk of rapid relapse of prostate cancer by performing frequent monitoring for recurrence by prostate specific antigen test, ultrasound imaging, CT imaging, MRI imaging, PET scan or digital rectal exam or performing a surgical excision, a radiotherapy and/or a chemotherapy.

2. The method of claim **1**, wherein the sample is selected from the group consisting of a prostate tissue sample and a blood sample.

* * * * *