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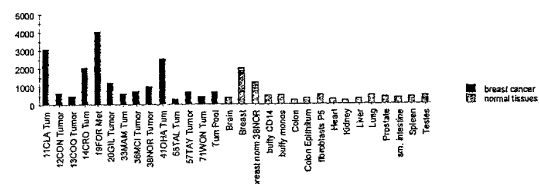
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(54) 【発明の名称】 乳癌の診断及び治療の新規方法、組成物及び乳癌調節剤用の選別方法

(57) 【要約】

本明細書では乳癌の診断及び予後判定に用いることができる方法が記述される。本明細書では、また、乳癌をモデル化することに関して候補生物活性物質をスクリーニングするのに利用できる方法が記述される。さらに、乳癌及びその他の癌に治療的に介入するための方法及び分子標的（遺伝子とその産物）が記述される。



【特許請求の範囲】

【請求項 1】

薬剤候補をスクリーニングする方法であって：

- a) B C H 1, B C A 2, B C J 7, B C N 1, B C N 5, B C O 2, B C Q 5, B C R 2, B C X 2 及び B C Y 3 又はその断片から成る群から選択されるタンパク質をコードする発現プロフィール遺伝子を発現する細胞を供するステップ；
- b) 前記細胞に薬剤候補を加えるステップ；及び
- c) 前記薬剤候補が前記発現プロフィール遺伝子の発現に及ぼす効果を決定するステップとを含む方法。

【請求項 2】

前記決定するステップは前記薬剤候補が存在しないときの発現レベルと前記薬剤候補が存在するときの発現レベルとを比較するステップを含み、前記薬剤候補が存在するときその濃度を変えることができ、前記比較は薬剤候補の添加又は除去の後に行うことができることを特徴とする請求項 1 に記載の方法。

【請求項 3】

前記プロフィール遺伝子の発現が該薬剤候補の導入の結果減少することを特徴とする請求項 1 に記載の方法。

【請求項 4】

乳癌モジュレーター・タンパク質 (B C M P) に結合できる生物活性物質をスクリーニングする方法であって、前記 B C M P が B C H 1 又はその断片であり、前記方法は：前記 B C M P と候補生物活性物質とを組み合わせるステップと；前記候補作用物質の前記 B C M P との結合を決定するステップとを含むことを特徴とする方法。

【請求項 5】

乳癌モジュレーター・タンパク質 (B C M P) の活性を変調できる生物活性物質をスクリーニングする方法であって、前記 B C M P が B C H 1 又はその断片であり、前記方法は：前記 B C M P と候補生物活性物質とを組み合わせるステップと；前記候補作用物質が前記 B C M P の生物活性に及ぼす影響を決定するステップとを含むことを特徴とする方法。

【請求項 6】

乳癌薬剤候補の効果を評価する方法であって：

- a) 前記薬剤を患者に投与するステップ；
- b) 前記患者から細胞サンプルを取り出すステップ；及び
- c) 前記細胞の発現プロフィールを決定するステップ；

を含む方法。

【請求項 7】

さらに、前記発現プロフィールを健康な人の発現プロフィールと比較するステップを含む請求項 6 に記載の方法。

【請求項 8】

B C H 1 又はその断片をコードする核酸セグメントを含むバイオチップであって、前記バイオチップが 1 0 0 0 未満の核酸プローブを含むことを特徴とするバイオチップ。

【請求項 9】

乳癌を診断する方法であって：

- a) 第一の個体の第一の組織タイプにおいて B C H 1 又はその断片をコードする遺伝子の発現を決定するステップ；及び
 - b) 前記第一の個体からの第二の正常組織タイプ又は第二の影響されない個体からの前記遺伝子からの前記発現を比較するステップ；
- を含み、前記発現の差が第一の個体が乳癌であることを示すことを特徴とする方法。

【請求項 10】

B C H 1、又はその断片、に特異的に結合する抗体。

【請求項 11】

前記断片が B C H 1 p 1 又は B C H 1 p 2 であることを特徴とする請求項 10 に記載の抗

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体。

【請求項 1 2】

前記抗体がモノクローナル抗体であることを特徴とする請求項 1 0 に記載の抗体。

【請求項 1 3】

前記抗体がヒト化抗体であることを特徴とする請求項 1 0 に記載の抗体。

【請求項 1 4】

前記抗体が抗体フラグメントであることを特徴とする請求項 1 0 に記載の抗体。

【請求項 1 5】

乳癌モジュレーター・タンパク質（BCMP）又はその断片と前記 BCMP 又はその断片と結合する抗体の結合を妨害できる生物活性物質をスクリーニングする方法であって、前記方法が：

a) BCMP 又はその断片、候補生物活性物質、及び前記 BCMP 又はその断片と結合する抗体を組み合わせるステップ；及び

b) 前記 BCMP 又はその断片と前記抗体の結合を決定するステップ；

を含む方法。

【請求項 1 6】

乳癌を阻害する方法であって、前記方法が BCH 1 又はその断片に対する抗体を含む組成物を細胞に投与するステップを含む方法。

【請求項 1 7】

前記細胞がある個体の細胞である請求項 1 6 に記載の方法。

【請求項 1 8】

前記個体が癌に罹患していることを特徴とする請求項 1 7 に記載の方法。

【請求項 1 9】

前記断片が BCH 1 p 1 又は BCH 1 p 2 から成る群から選択されることを特徴とする請求項 1 6 に記載の方法。

【請求項 2 0】

前記抗体がヒト化抗体であることを特徴とする請求項 1 6 に記載の方法。

【請求項 2 1】

前記抗体が抗体断片であることを特徴とする請求項 1 6 に記載の方法。

【請求項 2 2】

細胞における乳癌を阻害する方法であって、前記方法が BCH 1 に対するアンチセンス分子を含む組成物を細胞に投与するステップを含むことを特徴とする方法。

【請求項 2 3】

本質的に BCH 1 p 1 から成るペプチド。

【請求項 2 4】

請求項 2 3 のペプチドを含む組成物。

【請求項 2 5】

本質的に BCH 1 p 2 から成るペプチド。

【請求項 2 6】

請求項 2 5 のペプチドを含む組成物。

【請求項 2 7】

ある個体に免疫応答を誘発する方法であって、前記方法が BCH 1 又はその断片を含む組成物を前記個体に投与するステップを含む方法。

【請求項 2 8】

ある個体に免疫応答を誘発する方法であって、前記方法が BCH 1 又はその断片をコードする配列を含む核酸を含む組成物を前記個体に投与するステップを含む方法。

【請求項 2 9】

ある個体に免疫応答を誘発することができる組成物であって、前記組成物が BCH 1 又はその断片及び医薬として許容されるキャリアを含む組成物。

【請求項 3 0】

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ある個体に免疫応答を誘発することができる組成物であって、前記組成物が B C H 1 又はその断片をコードする配列を含む核酸及び医薬として許容されるキャリアを含む組成物。

【請求項 3 1】

ある個体の乳癌を治療する方法であって、前記個体に B C H 1 の阻害物質を投与するステップを含む方法。

【請求項 3 2】

前記阻害物質が抗体であることを特徴とする請求項 3 1 に記載の方法。

【請求項 3 3】

前記個体が抗エストロゲンに不応答であり、エストロゲン受容体にポジティブであることを特徴とする請求項 3 1 に記載の方法。

【請求項 3 4】

前記方法がさらに抗エストロゲンを投与するステップを含むことを特徴とする請求項 3 3 に記載の方法。

【請求項 3 5】

乳癌に罹患した個体の予後を判定する方法であって、あるサンプルにおける B C H 1 のレベルを決定するステップを含み、高いレベルの B C H 1 が予後の悪さを示すことを特徴とする方法。

【請求項 3 6】

乳癌に罹患した個体が抗エストロゲン治療に不応答であるかどうかを決定する方法であって、B C H 1 のレベルを決定するステップを含み、高いレベルの B C H 1 がある個体が不応答であることを示すことを特徴とする方法。

【請求項 3 7】

B C H 1、又はその断片、の効果を中和する方法であって、前記タンパク質に特異的な作用物質を前記タンパク質に中和を達成するに十分な量で接触させるステップを含む方法。

【発明の詳細な説明】

発明の分野

本発明は、乳癌に関する発現プロファイル及び核酸の同定に関し、そのような発現プロファイル及び核酸の乳癌診断、予後及び治療での使用に関する。本発明は更に、乳癌を調節する候補薬剤及び／又は標的の同定方法及び使用方法に関する。

発明の背景

乳癌は、欧米の人々では顕著に見られる癌である。これは正常乳房上皮組織が浸潤性癌へ病的形質転換する結果生じる。乳癌に関連した最近特徴づけられた遺伝的変化が数多くあった。しかしながら、乳癌の発生に関わる遺伝的変化を全て同定する必要がある。

診断における乳癌の撮像には問題が多く、限界があった。加えて、移動局所性リンパ節への腫瘍細胞の拡がり（転移）は重要な予後因子で、リンパ節転移がない患者の 5 年生存率が 80 % であるのにリンパ節転移がある患者では 45 ~ 50 % に低下する。最近の報告では、微小転移性は癌胎児性抗体に対する m R N A の存在に基づく逆転写酵素-PCR 法を用いてリンパ節から検出できることが示された。L i e f e r s e t a l . , N e w E n g l a n d J . o f M e d . 3 3 9 (4) : 2 2 3 (1 9 9 8) 。

このように、乳癌の診断及び予後に使える方法であればなお望まれている。学会や産業界では、新規配列を確認する努力をしてきたが新規配列の機能の確認には同じ程度の努力が行なわれていなかった。例えば、データベースは登録番号 W 7 2 8 3 8 の配列を示すが当該配列の機能、まして病気の状態に関するデータはない。従って、本発明で提供するものは乳癌の診断及び予後に使用できる方法である。更に、乳癌を調節する能力を有する生物活性剤候補を選別する方法を提供する。加えて本明細書には乳癌及び他の癌における治療に介在する分子標的を提供する。

発明の要旨

本発明は、乳癌を調節する組成物を選別する方法を提供する。また本明細書では細胞、好ましくは乳癌細胞の増殖を阻止する方法を提供する。また本明細書では癌の治療方法と共に組成物も提供する。

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一つの側面では、薬物候補の選別法は発現プロフィール遺伝子又はその断片を発現する細胞の提供を含んでいる。発現プロフィール遺伝子の好ましい態様は、癌細胞、好ましくは乳癌細胞で他の細胞と比較して異なる発現をする遺伝子である。本明細書の方法における好ましい発現プロフィール遺伝子の態様にはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2からなる群が含まれるが、これに限らない；当該群のタンパク質の断片も好ましい。他の態様では、核酸は図1、2、3、4、5、6、7、8、9、10、11及び12から選択する。好ましい核酸は図10、より好ましくは図11及び最も好ましくは図12のものである。当該方法は薬物候補の細胞への添加及び発現プロフィール遺伝子の発現への薬物候補の効果の測定を更に含んでなる。

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一つの態様では、薬物候補の選別法には薬物候補が存在する場合の発現程度と存在しない場合の発現程度の比較が含まれるが、存在する場合の薬物候補濃度は変化させることができ、比較は薬物候補の添加又は除去した後に行なわれる。好ましい態様では、当該細胞は少なくとも2種の発現プロフィール遺伝子を発現する。当該プロフィール遺伝子は増加も示せば減少も示す。

また、本明細書中では乳癌調節因子タンパク質（BCMP）に結合できる生物活性剤の選別法を提供し、当該方法にはBCMPと生物活性剤候補の結合及び候補薬剤とBCMPとの結合の測定を含む。好ましくは、BCMPはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2からなる群より選択したタンパク質又はその断片である。他の一つの態様では、当該タンパク質は図1、2、3、4、5、6、7、8、9、10、11及び12から選択した核酸にコード化されている。好ましい核酸は図10で、より好ましくは図11で、最も好ましくは図12のものである。

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更に本明細書中にはBCMPの活性を調節することができる生物活性剤の選別する方法を提供する。一つの態様では、BCMPと生物活性候補の結合、BCMPの生物活性に対する候補薬剤の効果の測定を含む。好ましくは、BCMPはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2からなる群より選択したタンパク質又は断片である。他の態様では、当該タンパク質は図1、2、3、4、5、6、7、8、9、10、11及び12から選択した核酸にコード化されている。好ましい核酸は図10で、より好ましくは図11で、最も好ましくは図12のものである。

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また、本明細書中ではBCMPを発現又は過剰発現するトランスジェニック動物或いは例えば遺伝子ノックアウトの結果の如きBCMP欠損動物への投与を含む乳癌治療薬候補の効果の評価する方法を提供する。

加えて、本明細書では当該薬物を患者に投与すること及び当該患者から細胞試料を除去することを含んだ乳癌治療薬候補の効果評価法を提供する。そして当該細胞の表現プロフィールを測定する。本方法は更に当該プロフィールと正常者の発現プロフィールとの比較を含んでなる。

更に、本明細書では好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片からなる群から選択した乳癌タンパク質をコードしている核酸切片を含むバイオチップを提供し、そこにおけるバイオチップは1000より少ない核酸のプロンプを含んでなる。好ましくは少なくとも2つの核酸切片が含まれている。他の態様では、核酸は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択されたものである。好ましい核酸は図10、より好ましくは図11及び最も好ましくは図12のものである。

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更に、乳癌に関連した障害を診断する方法を提供する。当該方法は、一番目の個人の一番目の組織タイプにある乳癌タンパク質、好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片からなる群から選択した乳癌タンパク質をコ

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ード化した遺伝子の発現の測定、そして最初の個人或いは二番目の個人から得た二番目の正常組織タイプの遺伝子発現への分布の比較を含んでなる。他の態様では、図1、2、3、4、5、6、7、8、9、10、11及又は12から選択した核酸が当該タンパク質をコードしている。好ましい核酸は図10、更に好ましくは図11及び最も好ましくは図12の中のものである。発現での差異は、最初の個人が乳癌に関係した障害を有していることを示す。

他の側面では本発明は、好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片からなる群から選択した乳癌タンパク質に特異的に結合する抗体を提供する。他の態様では、当該タンパク質は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択した核酸によりコード化されたタンパク質である。好ましい核酸は図10、より好ましくは図11そして最も好ましくは図12にあるものである。好ましい態様では、BCH1の断片はBCH1 p1及びBCH1 p2から選択したものである。乳癌タンパク質として他の好ましい断片は図の中に示した。好ましくは、抗体はモノクローナル抗体である。抗体は本明細書に記載した一重鎖抗体のような抗体の断片や他の分子との抱合体でありうる。他の態様では、当該抗体はヒト化抗体である。

他の態様では、乳癌タンパク質(BCMP)又はその断片との結合を阻害することができる生物活性剤及び前記BCMP又はその断片と結合する抗体を選択する方法を提供する。好ましい態様では、当該方法はBCMP又はその断片、生物活性剤候補及び前記BCMP又はその断片に結合する抗体の組合せを含んでなる。当該方法は更に前記BCMP又はその断片と前記抗体の結合の測定を含む。結合に変化がある場合、薬剤は阻害剤と確認される。阻害剤は作動薬であるか拮抗薬でありうる。好ましくは、抗体は当該薬と共に乳癌を阻害する。

更なる側面では、乳癌を阻害する方法を提供する。一つの態様では、当該方法では好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片からなる群から選択した乳癌調整タンパク質に抗体を含んだ組成物の細胞への投与を含んでなる。他の一つの態様では、当該タンパク質は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択した核酸にコード化されている。好ましい核酸は図10、より好ましくは図11、そして最も好ましくは図12にある。

当該方法は*in vitro*又は*in vivo*で実施できるが、個体への*in vivo*が好ましい。好ましい態様では、当該乳癌阻害の方法は乳癌の個体に提供される。本明細書に記載の如く、乳癌阻害の方法はアンチセンス分子や好ましくは小分子を含む乳癌タンパク質活性の阻害剤を投与して実施できる。

同時に、本明細書では個体の中の免疫応答を引き出す方法を提供する。一つの態様では、本明細書で提供する方法は個体に、好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片から構成された群から選択した乳癌調節タンパク質を含む組成物の投与を含んでなる。他の態様では、当該タンパク質は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択した核酸にコード化されている。好ましい核酸は、図10、好ましくは図11、最も好ましくは図12のものである。他の側面では前記組成物は、好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片から構成された群から選択した乳癌調節タンパク質をコード化した配列を含む核酸を含有する。他の態様では、核酸は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択する。好ましい核酸は、図10、より好ましくは図11及び最も好ましくは図12にあるものである。

更に本明細書では個体の免疫応答を誘起する能力のある組成物を提供する。一つの態様では、本明細書で提供した組成物には、好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX

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3、BCA2及びBCR2或いはその断片から構成された群から選択した乳癌調節タンパク質及び薬剤許容担体を含んでなる。他の態様では、当該タンパク質は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択した核酸によりコード化されている。好ましい核酸は、図10、より好ましくは図11及び最も好ましくは図12にあるものである。他の態様では前記組成物は、好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片から構成された群から選択した乳癌調節タンパク質をコードしている配列を含む核酸及び薬剤許容担体を含む。他の態様では、核酸は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択する。好ましくは、核酸は、図10、より好ましくは図11及び最も好ましくは図12にあるものである。 10

好ましくはBCR3、BCQ8、BCQ5、BCH1、BCN1、BCN2、BCN5、BCO2、BCX2、BCJ7、BCY3、BCX3、BCA2及びBCR2或いはその断片から構成された群から選択した乳癌調節タンパク質の効果を中和する方法も提供する。好ましくは、該当方法は前記タンパク質と前記タンパク質に特異的薬剤を、中和するのに十分な量での接触を含んでなる。他の態様では、当該タンパク質は図1、2、3、4、5、6、7、8、9、10、11及又は12から選択した核酸によりコードされている。好ましい核酸は図10、より好ましくは図11及び最も好ましくは図12にあるものである。

本発明の他の側面では、個体の乳癌の治療法を提供する。一つの態様では、当該方法は前記個体へのBCH1の阻害剤投与を含んでなる。他の態様では、当該個体は抗エストロゲン薬に対して応答無しで、エストロゲン受容体について陽性である。場合により、当該方法は更に抗エストロゲン薬の前記個体への投与を含んでなる。 20

また、本明細書は乳癌の個体の予後を試料中に存在するBCH1、BCH1のレベルが高いと予後が良くないことを示す、のレベルの測定を提供する。その上、本発明の他の側面では、乳癌である個体が抗エストロゲン薬治療に無応答かどうかを、高レベルであれば個体は無応答であるBCH1のレベル測定を含んだ方法を提供する。好ましくは、本明細書の方法はタモキシフェン抵抗であるヒトを確認する際に使用される。

本明細書には新規の配列も提供される。本発明の他の側面については、以下の発明の記述で当事者であれば明らかである。 30

本発明の詳細な記載

本発明は、乳癌の診断及び予後評価の際の新規方法と共に乳癌を調節する組成物を選別する方法を提供する。一つの側面では、診断又は予後情報のどちらか必要な異なる患者の試料につき遺伝子の発現レベルを測定し、発現プロファイルを提供する。ある試料の発現プロファイルは当該試料の状態の“指紋”である；二つの状態で、同様な発現をするなにか特別な遺伝子を持つかもしれないが、多くの遺伝子を同時に評価すると細胞の状態に特有な遺伝子発現プロファイルの発生を起こす。これで、正常組織と乳癌組織とは区別されるだろうし、乳癌組織内では異なる予後状態（例えば、長期間生存見通しが有るか乏しいか）が測定できる。既知の異なる状態にある乳癌組織の発現プロファイルを比較すれば、それらの各状態では何れの遺伝子が重要であるか（遺伝子の上昇制御及び下降制御を含めて）の情報が得られる。乳癌と正常組織で異なって発現する配列と共に異なる予後結果を生じる異なる発現を確認すれば、数多くの方法でその情報が使用できる。例えば、ある治療方式の評価を評価できる：ある患者の長期予後を改善する際に化学療法薬物が効果あるか。同様に、既知の発現プロファイルにより患者の試料と比較して診断ができ又は確認できる。更に、これらの遺伝子発現プロファイル（各個の遺伝子につき）はある発現プロファイルを模倣又は変化させることを目的として薬物候補を選別できる。：例えば、乳癌発現プロファイルを抑制するか又は悪い予後プロファイルを良い予後プロファイルへ変換する薬物の選別。これは重要な乳癌遺伝子の1群を含み、これらの選別に用いることができるバイオチップを作成することで行なわれる。これらの方法はタンパク質を基礎にしてもでき、即ち乳癌タンパク質の表現レベルを評価して診断及び予後目的に又は候補薬剤の選 40 50

別もできる。加えて、アンチセンス核酸の投与或いは治療薬として乳癌タンパク質（抗体及び他のその調節剤を含む）の投与を含み、遺伝治療目的で乳癌核酸配列の投与ができる。

かくして、本発明は乳癌の中で異なって発現する核酸及びタンパク質配列で、本明細書では“乳癌配列”と名付けたものを提供する。以下に概説したように、乳癌配列には、乳癌中で上昇制御（即ち、高レベルで発現）するものと共に乳癌中で下降制御（即ち、低レベルで発現）されたものを含む。好ましい態様では、乳癌配列はヒトから由来のものである：しかし当技術分野の者であれば理解するように、他の生物からの乳癌配列は病気の動物モデル及び薬物評価で有用である：そこで、げっ歯類（ラット、マウス、ハムスター、モルモット、その他）、霊長類、家畜（羊、ヤギ、ブタ、乳牛、馬、その他）などの哺乳類を含んだ脊椎動物からの他の乳癌配列も提供する。他の生物からの乳癌配列は以下に概要を述べる技術を用いて得られる。

乳癌配列は核酸配列及びアミノ酸配列の両方を含むことができる。好ましい態様では、乳癌配列は組換え核酸である。本明細書での“組換え核酸”という単語は、もともと一般的にポリメラーゼ及びエンドヌクレアーゼでの処理で *in vitro* で生成した核酸を意味し、自然界では見出されるものではない。こうして単離した直線の核酸又は自然では結合しないDNA分子を *in vitro* で結合して作成した発現ベクターは両方とも本発明の目的において組換え体と考える。一旦組換え核酸ができ、宿主細胞又は宿主生物に再導入されると、それは非組換え的に複製をする、即ち *in vitro* 作用というより宿主細胞の *in vivo* 細胞機械を用いて；しかし一旦組換え的に生成したそのような核酸は、引き続いて非組換え的に複製するが本発明の目的では依然組換え体と考える。

同様に、“組換えタンパク質”は組換え技術を用いて、即ち上記の組換え核酸の発現により作成する。組換えタンパク質は天然由来のタンパク質と比べ少なくとも一つ又はそれより多い特徴で区別される。例えば、当該タンパク質は幾つかの又は全てのタンパク質及び野生株型宿主では通常会合している化合物からは単離又は精製されていて、実質的には純粋である。例えば、単離されたタンパク質は自然状態では通常会合している物質の少なくとも幾つかとは随伴することがなく、所与試料の全タンパク質の重量に対して少なくとも約0.5%程度、より好ましくは5%を構成する。実質的に純粋なタンパク質は、少なくとも全タンパク質の75重量%、好ましくは少なくとも約80%、特に好ましくは少なくとも約90%を構成する。当該定義では異なる生物又は宿主細胞中の一つの生物由来である乳癌タンパク質の生産物を含む。代わりとして、当該タンパク質は誘導プロモーター又は高発現プロモーターの使用により通常見られる以上の顕著な高濃度で作られるので、当該タンパク質は亢進した濃度レベルで製造される。代わりとして、当該タンパク質は、下記のようにエピトープタグ添加又はアミノ酸置換、挿入及び欠失などがあり、天然で見られない形である。

好ましい態様として、乳癌配列は核酸である。当分野の者であれば分かるように又下記に概説するように、乳癌配列は診断での応用を含めて種々な応用面に有用で、天然生成核酸を検出すると共に選別にも応用される；例えば乳癌配列に対する核酸プローブを含むバイオチップが生成できる。最も広い意味では、本明細書の“核酸”又は“オリゴヌクレオチド”又は文字通りの当量は、共有結合で結合した少なくとも二つのヌクレオチドを意味する。本発明の核酸は一般的にホスホジエステル結合を有するが、幾つかの場合は以下に概略するように代わりの骨格である核酸類似体を含む。例えばホスホルアミド (Beaucage et al., Tetrahedron 49 (10) : 1925 (1993)) 及びその参考文献；Letsinger, J. Org. Chem. 35 : 3800 (1970)；Sprinzl et al. Eur. J. Biochem. 81 : 579 (1977)；Letsinger et al., Nucl Acids Res. 14 : 3487 (1986)；Sawai et al., Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110 : 4470 (1988) 及び Pauweis et al., Chemica Scripta 26 : 1419 (1985))、ホスホロチオエート (Mag et al., Nuc

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leic Acids Res. 19:1437 (1991); 及び米国特許番号 5, 644, 048、ホスホロジチオエート (Briu et al., J. Am. Chem. Soc. 111:2321 (1989)、O-メチルホスホロアミダイト結合 (参照 Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press)、及びペプチド核酸骨格及び結合 (Eghoim, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem Int. Ed. Engl, 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carisson et al., Nature 380:207 (1996)、全て参照により援用されている)。他の核酸類似体には陽荷電骨格 (Denpcy et al., Pro. Natl. Acad. Sci. USA 92:6097 (1995); 非イオン性骨格 (米国特許番号 5, 386, 023, 5, 637, 684, 5, 602, 240, 5, 216, 141 及び 4, 469, 863; Kiedowskiet al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modification in Antisense Research", Ed. Y. S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medical Chem Lett. 4:395 (1994); Jeff et al., J. Biomolecular NM R 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) 及び非リボース骨格で、米国特許番号 5, 235, 033 と 5, 034, 506 及び第 6 章と第 7 章、ACS Symposium Series 580, "Carbohydrate Modifications in Antisense Research, Ed. Y. S. Sanghui and P. Dan Cook に記述されているものを含む。一つ又はそれより大きな炭素環糖を含む核酸も又核酸の一つの定義内に含まれる (参照 Jenkins et al., Chem. Soc. Rev. (1995) pp 169~176)。数種の核酸類似体は Rawls, C & E news June 2, 1997 p 35 に記載されている。これらの参考文献は本明細書に特に参照により本明細書に援用されている。リボースリン酸骨格の修飾は種々の理由で行なわれるが、例えば生理的環境におけるその分子の安定性及び半減期を長くしたり、バイオチップでのプローブとするためである。

当技術分野の当事者であれば分かるように、これらの核酸類似体は本発明で利用できる。加えて、天然由来核酸と類似体の混合物は作成可能である; 代わりとして異なる核酸類似体の混合物及び天然由来核酸と類似体の混合物も作成できる。

特に好ましくはペプチド核酸類似体を含むペプチド核酸 (PNA) である。これらの骨格は実質的に中性条件では非イオン性で、天然由来の核酸のホスホジエステル骨格が高荷電しているのと対比的である。これは二つの利点となる。一つには PNA 骨格はハイブリダイゼーション速度で改良を示す。PNA s は、不一致対完全一致塩基対についての融点 (T_m) に大きな変化をもたらす。DNA 及び RNA は典型的には内部的ミスマッチでは T_m に 2~4 °C の低下を示す。非イオン性 PNA 骨格ではこの低下が 7~9 °C 近くまでになる。同様に、その非イオン性性質によりこれらの骨格に付着している塩基のハイブリダイゼーションは塩濃度に比較的感受性が低い。加えて、PNA s は細胞性酵素では分解しないのでより安定である。

当該核酸は、述べたように一重鎖又は二重鎖或いは二重鎖又は一重鎖配列両方の部分を含む。当技術分野の当事者であれば明らかなように、一重鎖 ("Watson") の表現は他の鎖の配列を規定する ("Click")。: そこで本明細書で提供した配列は配列の相補体も含んでいる。当該核酸はゲノムや cDNA である DNA, RNA かハイブリ

ッド、当該核酸はデオキシリボ及びリボースヌクレオチドのいずれの組合せ及びウラシル、アデニン、チミン、シトシン、グアニン、イノシン、キサンチンヒポキサンチン、イソシトシン、イソグアニンその他を含む塩基のいずれかの組合せを含有する。本明細書で用いたように“ヌクレオチド”の用語はヌクレオチド、ヌクレオシド、ヌクレオチド類似体及びアミノ酸修飾ヌクレオチドのような修飾ヌクレオシドを含む。加えて、“ヌクレオシド”は非天然由来類似体構造を含む。こうして例えばペプチド核酸の個々の単位、各々塩基を含んでいるのは本明細書ではヌクレオシドと呼ぶ。

乳癌配列は、当初本明細書で概要を述べた乳癌配列と実質的に核酸及びアミノ酸配列によれば相同であることが確認できる。そのような相同性は全核酸又はアミノ酸配列に基づいていて、以下に概要を述べるように相同プログラム又はハイブリダイゼーション条件を用いて決定する。 10

本発明の乳癌配列は次のように同定できる。正常及び腫瘍の組織は核酸プローブを含むバイオチップへ適用される。試料は応用する場合、最初細かく裁断し、mRNAの調製における当技術分野で知られている如く処理される。適したバイオチップは市販で入手でき、例としてはAffmetrixからの試料がある。本明細書で記述したように遺伝子発現プロファイルを発生させ、データを分析する。

好ましい態様では、正常と病気状態における発現での変化を示す当該遺伝子を他の正常な組織で肺、心臓、肝臓、乳房、腎臓、筋肉、前立腺、小腸、大腸、脾臓、骨及び胎盤などだが、これに限らない組織の発現した遺伝子と比較する。好ましい態様では、乳癌選別において確認された遺伝子でも他の組織で顕著な量を発現したものはプロファイルから除去するが、ある態様ではこれは必要ない。これは、薬物の選別において標的は病気特異的であるのが好ましく、可能な副作用を最小にするためである。 20

好ましい態様では、乳癌配列は乳癌で上昇制御されたもので、それはこれらの遺伝子の発現が正常乳房組織と比較して乳癌では高いことである：本明細書で用いる“上昇制御”は少なくとも約2倍変化、好ましくは少なくとも3倍変化で、少なくとも約5倍高いのが望ましい。本明細書の全ての登録番号はGenBank配列データベースのものであり、登録番号の配列は参照により本明細書に援用する。GenBankは当技術分野では知られている、参照、例えばBenson, D A, et al., Nucleic Acids Research 26:1~7 (1998) 及びhttp://www.ncbi.nlm.nih.gov/である。加えて、これらの遺伝子は心臓、脳、肺、腎臓、前立腺、小腸、睾丸、線維芽細胞及び脾臓では限られた相対量又は全然発現されないことが判明した。 30

好ましい態様では、乳癌配列は乳癌では下降制御されているもので、即ちこれらの遺伝子の発現は乳癌では正常乳房組織と比較して低い。本明細書で用いる“下降制御”は少なくとも2倍変化、好ましくは少なくとも約3倍変化で、少なくとも5倍かそれ以上が好ましい。

本発明の乳癌タンパク質は分泌タンパク質、膜貫通タンパク質又は細胞内タンパク質に分類される。好ましい態様では、乳癌タンパク質は細胞内タンパク質である。細胞内タンパク質は、細胞機能及び複製（例えばシグナル経路を含む）の全ての面に関係する；そのようなタンパク質の異常な発現は細胞過程が上昇制御又は無制御となる。例えば、多くの細胞内タンパク質はタンパク質キナーゼ活性、タンパク質ホスファターゼ活性、プロテアーゼ活性、ヌクレオチドサイ클ラーゼ活性、ポリメラーゼ活性やその他の類似な酵素的活性を有する。細胞内タンパク質はまた、タンパク質の形成化複合体に関係するシグナル認識粒子受容体又は種々な細胞下局在化へのターゲッティングタンパク質として働き、オルガネラの構造状態を維持するのに関係している。 40

細胞内タンパク質の特徴付において評価が高まっている概念は、明確な機能がそれに起因する一つ以上のモチーフのタンパク質が存在することである。タンパク質の酵素ドメインで見出される保存配列に加えて、タンパク質-タンパク質相互作用に関係するタンパク質の中に高度な保存タンパク質が確認されている。例えば、Src-相同-2 (SH2) ドメインはリン酸化チロシン標的を配列依存の遣り方で結合する。SH2ドメインとは別個 50

の P T B ドメインもまたリン酸化チロシン標的を結合する。S H 3 ドメインはプロリンに富んだ標的を結合する。加えて、P H ドメイン、テトラトリコペプチド反復及び W D ドメインなど数少ないが、タンパク質-タンパク質相互作用を仲介する。これらの幾つかはリン脂質又は他の二次メッセンジャーと結合する際にも関与する。当技術分野の当事者には理解される如く、これらのモチーフは一次配列に基づいて確認できる：そこでタンパク質の配列分析は、分子の酵素的可能性及び／又はタンパク質が会合するだろう分子についての洞察を与える。

好ましい態様では、乳癌配列は膜貫通タンパク質である。

膜貫通タンパク質は細胞のリン脂質二重層に架かる分子である。それは分子内ドメイン、分子外ドメイン又は両方を有している。そのようなタンパク質の分子内ドメインは、既に分子内タンパク質につき記述したのと同じ多くの機能を有している。例えば、分子内ドメインは酵素的活性を有し更に／又は追加タンパク質への結合部位として働く。しばしば膜貫通タンパク質の分子内ドメインは両方の役割を果たす。例えば、あるチロシンキナーゼ受容体はタンパク質キナーゼ活性及び S H 2 ドメインの両方を有する。加えて、受容体自身におけるチロシンの自己リン酸化は、タンパク質を含有する追加 S H 2 ドメインにつき結合部位を作り出す。

膜貫通タンパク質は一つから数多くの膜貫通ドメインを含有する。例えば、チロシンキナーゼ受容体、あるサイトカイン受容体、グアニリルシクラーゼ及びセリン／トレオニンタンパク質キナーゼ受容体は単一膜貫通ドメインを含有する。しかし、チャンネル及びアデニルシクラーゼを含む種々な他のタンパク質は数多くの膜貫通ドメインを含有する。多くの重要な細胞表面受容体は 7 個の膜通過領域を含有するので“7 回膜貫通ドメイン”に分類される。重要な膜貫通タンパク質受容体にはインスリン受容体、インスリン様成長因子受容体、ヒト成長ホルモン受容体、グルコース輸送体、トランスフェリン受容体、上皮成長因子受容体、低密度リポタンパク質受容体、上皮成長因子受容体、レプチン受容体、I L - 1 受容体や I L - 2 受容体などのインターロイキン受容体であるが、これに限らない。

膜貫通ドメインの特徴は、約 20 の連続した疎水性アミノ酸で、荷電したアミノ酸がそれに続いている。それで、ある種のタンパク質のアミノ酸配列分析に基づきタンパク質内の膜貫通ドメインの局在及び数は予測できる。

しかしながら膜貫通タンパク質の細胞外ドメインは異なっている；保存モチーフが繰り返し種々の細胞外ドメインの中に見出される。保存構造及び／又は機能は異なった細胞外モチーフによるものとみなされる。例えば、サイトカイン受容体はシステインのクラスター及び W S X W S (W = トリプトファン、S = セリン、X = アミノ酸) モチーフにより特徴付けられる。免疫グロブリン様ドメインは高度に保存されている。ムチン様ドメインは細胞接着に関係しているようであり、ロイシンに富む反復はタンパク質-タンパク質相互作用に加わっている。膜貫通ドメインは、本明細書の可溶性タンパク質を作り出す際には除去される。

多くの細胞外ドメインは他の分子を結合する際に関係する。一つの側面では、細胞外ドメインは受容体である。受容体ドメインを結合する因子は、ペプチド、タンパク質又はアデノシンや同種のもののような小分子である環状配位子を含む。例えば、E G F、F G F 及び P D G F のような成長因子は循環性成長因子で、それらの同族受容体と結合して種々な細胞応答を開始する。他の因子にはサイトカイン、マイトジェン因子、神経栄養因子及び同種のもが含まれる。細胞外ドメインは同じように細胞会合分子と結合する。この点で、それらは細胞-細胞相互作用を仲介する。細胞会合した配位子は当該細胞に、例えばグリコシルホスファチジルイノシトール (G P I) アンカーを通して繋ぎ止めることができ、それ自身は膜貫通タンパク質である。細胞外ドメインは同様に細胞外マトリックスと会合し、細胞構造の維持に寄与する。

膜貫通している乳癌タンパク質は、本明細書に記述した免疫療法の良好な標的であるので本発明では特に好ましい。加えて、以下に概要を述べたように膜貫通タンパク質は想像形式として有効になりえる。

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好ましい態様では、乳癌タンパク質は分泌タンパク質である；その分泌は構成性又は調節性のどちらかである。これらのタンパク質は分泌経路へ分子を標的とさせるシグナルペプチド又はシグナル配列を有する。分泌したタンパク質は数多くの生理的現象に関連する；それらの循環性性質により種々な他の細胞タイプへの信号伝達に役立っている。当該分泌タンパク質は自己分泌方式（因子を分泌した細胞に作用）、パラ分泌方式（因子を分泌した細胞の近接細胞に作用）又は内分泌方式（遠方の細胞に作用）で機能する。分泌された分子は生理の多くの面における調節又は変更に応用される。分泌タンパク質である乳癌タンパク質は診断標識として、例えば血液試験における良好な標的として役立つので本特許では特に好ましい。

乳癌配列は、当初本明細書で概要を述べた乳癌配列に相同な実際の核酸及び／又はアミノ酸配列により同定される。そのような相同性は全体の核酸又はアミノ酸配列に基づいており、以下に述べるように相同性プログラム又はハイブリダイゼーション条件を用いて一般的に決定されている。

本明細書で用いたように、核酸配列が図のアミノ酸配列をコードしている核酸配列との全相同性で好ましくは約75%より大、より好ましくは約80%より大、それより好ましくは約85%より大そして最も好ましくは90%より大であれば、核酸は“乳癌核酸”である。幾つかの態様では、相同性は高々約93~95又は98%程度である。本文での相同性とは配列類似性又は同一性を意味し、中でも同一性が好ましい。相同性の目的での好ましい対比は正しい配列に対する配列エラーを含む配列を比較することである。当該相同性は当技術分野で知られている標準手法、Smith & Waterman, Adv. Appl. Math. 2:482 (1981)の局部相同性アルゴリズム、Needleman & Wunsch, J. Mol. Biol. 48:443 (1970)の相同性整列アルゴリズム、Pearson & Lipman, PNAS USA 85:2444 (1988)の類似点の検索法、これらのアルゴリズムのコンピュータによる実行（GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI）、好ましくはデフォルト設定を用いたDevereux et al., Nucleic Acid Res. 12:387-395 (1984)が記述したBest Fit配列プログラム、又は精査を含んだ既知標準手法を用いて決定されるが、これらに限らない。

好ましい態様では、配列の同一性又は類似性を決定した配列は図で述べた配列から選択する。一つの態様では、本明細書で利用した配列は、図の中に述べたものである。他の態様では、当該配列は図で述べた天然由来の対立遺伝子変種である。他の態様では、当該配列はこれから本明細書に記述するような配列変種である。

有用なアルゴリズムの一例はPILEUPである。PILEUPは関連配列の群から段階的、対による整列法を用いて多数の配列整列を作り出す。これは整列を作り出すのに用いたクラスター化関係を示す樹木のプロットもできる。PILEUPは、Feng & Doolittle, J. Mol. Evol. 35:351 (1987)の段階的整列法の簡易化法を用いた；本方法はHiggins & Sharp CABIOS 5:151-153 (1989)が記述した方法と類似している。有用なPILEUPパラメータには、デフォルトギャップ重み3.00、デフォルトギャップ長さ0.10及び重み付け末端ギャップを含む。

他の有用なアルゴリズムの例はBLASTアルゴリズムで、Altschul et al., J. Mol. Biol. 215, 403-410 (1990)及びKarlin et al., PNAS USA 90:5873-5787 (1993)に記載されている。特に有用なBLASTプログラムは、Altschul et al., Methods in Enzymology, 266:460-480 (1996)；<http://blast.wustl.edu/blast/README.html>から得たWU-BLAST-2プログラムである。WU-BLAST-2プログラムは数種の検索パラ

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メータを用いるが、その多くはデフォルト値が設定されている。調整できるパラメータは次の値で設定する：オーバーラップスパン＝1、オーバーラップフラクション＝0.125、ワード閾値（T）＝11。HSP S及びHSP S2パラメータは動的値であり、個々の配列の組成及び目的の配列を検索している個々のデータベースの組成に依存してプログラム自体により確立される；しかしながら、値は感度を上げるために調整される。A%アミノ酸配列同一性値は、整列領域における“より長い”配列の残基全数で合致した同一残基数を割った数で決定する。“より長い”配列は、整列領域において最も実際の残基を有するものである（整列スコアを最大にするためにWU-Blast-2で導入したギャップは無視する）。

こうして、“パーセント（%）核酸配列同一性”は候補配列の中にある配列のヌクレオチド残基と同一であるヌクレオチド残基のパーセントとして定義される。好ましい方法ではデフォルトパラメータに、オーバーラップスパン及びオーバーラップフラクションをそれぞれ1と0.125に設定したWU-BLAST-2のBLASTNモジュールを利用する。

当該整列は整列させる配列中へのギャップの導入を含む。加えて、図のそれより多い或いは少ないヌクレオチドを含有する配列については、相同性のパーセントはヌクレオチドの全数に関し相同なヌクレオチドの数に基づいて決定されると理解される。そこで、例えば、本明細書で確認して以下で検討する配列より短い配列の相同性は、当該短い配列におけるヌクレオチドの数を用いて決定する。

一つの態様では、核酸の相同性はハイブリダイゼーション研究で決定する。そこで、例えば、図において確認したタンパク質をコードしている核酸配列又はそれらの片方に対して高い厳密性のもとでハイブリッド形成する核酸は乳癌配列と考えられる。高い厳密性条件は当技術分野では既知であるが、Maniatis et al. *Molecular Cloning: A Laboratory Manual*, 2d Edition, 1989, and *Short Protocols in Molecular Biology*, ed. Ausbel, et al., の例を参照。両方とも参照により本明細書中に援用されている。高い厳密性は配列依存性であり、異なる環境においては違うものである。より長い配列であればより高い温度で特異的にハイブリッド形成する。核酸のハイブリダイゼーションへの広範囲のガイドはTijssen, *Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, “Overview of principles of hybridization and the strategy of nucleic acid assays” (1993)に見出せる。一般的に、厳密な条件では、限定したイオン強度pHにおいて特定の配列については熱融点（Tm）より約5～10℃低い温度を選択する。Tmは、標的に対して相補的なプローブの50%が平衡状態で（目標配列が過剰に存在するので、Tmではプローブの50%が平衡で占められる）、標的配列にハイブリッドする温度（限定したイオン強度、pH及び核酸濃度）である。厳密な条件とは、塩濃度が約1.0Mナトリウムイオンより低く、典型的には約0.01～1.0Mナトリウムイオン濃度（又は他の塩類）でpH7.0～8.3及び温度は短いプローブ（例えば、10～50ヌクレオチド）に対しては少なくとも約30℃で、長いプローブ（例えば、50ヌクレオチドより大）では少なくとも約60℃である。厳密条件はまたホルムアミドのような不安定化剤の添加で達成する。

他の態様では、厳密程度が低いハイブリダイゼーション条件を使用する；例えば当技術分野では既知の中程度又は低厳密条件が使われる；上記Maniatis and Ausubel, 及び上記Tijssenを参照。

加えて、本発明の乳癌核酸配列はより長い遺伝子の断片で、即ちそれらは核酸切片である。この状況で“遺伝子”にはコード領域、非コード領域及びコードと非コード領域の混合がふくまれる。従って、当技術分野の当事者では知られているが、本明細書で提供した配列を用い、より長い又は完全長配列のクローニングにつき当技術分野では良く知られた技

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術を利用して乳癌遺伝子の追加配列を得ることができる；参照、上記のManiatis et al. , 及びAusubel et al. , 参照により本明細書中に援用する。

一旦乳癌核酸が確認されると、クローンされ、必要あればその構成要素は再び結合されて全乳癌核酸が形成される。一旦その天然源、例えばプラスミド又は他のベクター或いはそれから切取ったもの内に直線的核酸切片として含有されているものから単離すると、組換え乳癌核酸は更に他の乳癌核酸を同定し単離するプローブとして使用することができる。また修飾又は変種乳癌核酸及びタンパク質を作成する“前駆体”核酸として使用できる。本発明の乳癌核酸は数種の分野で使用される。最初の態様では、乳癌核酸への核酸プローブを作成し、以下に概要を述べる選別及び診断法に使用したり、例えば遺伝子治療及び／又はアンチセンス応用のためのバイオチップに付着する。その代わりとしては、乳癌タンパク質のコード領域を含む乳癌核酸を乳癌タンパク質の発現するための発現ベクターに挿入して、更に選別目的又は患者への投与用とする。

好ましい態様では、乳癌核酸への核酸プローブ（図に概要を記述したペプチドをコードした核酸及び／又はその相補）を作成する。バイオチップに付着した当該核酸プローブは乳癌核酸に対し実質的に相補、即ち標的配列（試料の標的配列又は例えばサンドウィッチアッセイにおける他のプローブ配列）になるように設計するので本発明の標的配列及びプローブのハイブリダイゼーションが起こる。以下に概要を述べたように、この相補性は完全である必要はない；標的配列と本発明の一重鎖核酸との間のハイブリダイゼーションを妨害する塩基対のミスマッチの数はいくつかあるかもしれない。しかし、変異の数が相当多くなるとハイブリダイゼーション条件が最も少ない厳密性であってもハイブリダイゼーションは起こらず、当該配列は相補的標的配列ではない。こうして、本明細書における“実質的相補”は、概要を記したようにプローブが通常の反応条件、特に高厳密性条件のもとでハイブリッド形成を行なうのに十分な標的配列への相補性がある。

核酸プローブは一般的に一重鎖であるが部分的に一重で部分的に二重鎖でも有り得る。プローブの撚り具合は標的配列の構造、組成及び性質で決定される。一般的に、核酸プローブは約8～100塩基長の範囲で、10～約80塩基が好ましく、特に好ましくは30～50塩基である。このことは、通常遺伝子全体は使用されない。幾つかの態様では、より大層長い核酸が使用することができ最大、数百塩基である。

好ましい態様では、配列当たり一より多いプローブを、重なり合うプローブ或いは用いる標的の異なる部分へのプローブと共に使用する。これは、二つ、三つ、四つ又はそれ以上のプローブ、好ましくは三つをある標的に対して過剰に用いて作る。当該プローブは重なり合うか（例えば、少し共通の配列をもつ）又は別々のものである。

当技術分野の当事者であれば知っている通り、核酸は様々な広い方法で固体担体に付着又は固定化できる。本明細書の“固定化”及び文字上の相当物により、核酸プローブと固体担体の間の会合又は結合は以下に概要を述べるような結合、洗浄、分析及び除去などの条件下でも充分安定であることを意味する。結合は共有又は非共有でありうる。本明細書での“非共有結合”及び文字上での相当物により、静電氣的、疎水性及び親水性相互作用の一つ又はそれ以上を意味する。非共有結合に含まれるものにはストレプトアビジンの担体への如き分子の共有付着及びストレプトアビジンへのビオチニル化プローブの非共有結合が含まれる。本明細書の“共有結合”及び文字上での相当物により、固体担体及びプローブの二つの部分がシグマ結合、パイ結合及び配位結合を含む少なくとも一つの結合で付着することを意味する。共有結合はプローブと固体担体の間で直接形成できるか、橋架け剤又は固体かプローブか両方の上に特定の反応性基を含有させて形成できる。固定化にはまた共有及び非共有相互作用の組合せが含まれる。

一般的に、当技術分野の当事者であれば知っている種々な方法でバイオチップにプローブを付着する。本明細書に記述するように、核酸を先ず合成し、次いでバイオチップに付着するか、或いは直接的にバイオチップの上に合成する。

当該バイオチップは適切な固体担体を含む。本明細書の“基体”又は“固体担体”又は他の文字上での相当物により、核酸プローブの付着又は会合に際し適切に別個で個々の部位

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を含有するように修飾でき、少なくとも一つの検出法で検出できるいずれの材料も意味する。当技術分野の当事者であれば知っている如く、可能性のある基体の数は多数で、ガラスと修飾や機能化したガラス、プラスチック（アクリル、ポリスチレン及びスチレンと他の材料の共重合体、ポリプロピレン、ポリエチレン、ポリブチレン、ポリウレタン、テフロンJ、その他を含む）、多糖類、ナイロン又はニトロセルロース、樹脂、シリカ又は修飾シリコーンを含むシリカ母体材料、炭素、金属、無機ガラス、プラスチックなどを含む。一般的には、基体は光学的検出できるが感知できる蛍光は示さない。好ましい基体は、その全体を参照により本明細書に援用した共出願中の標題A Reusable Low Fluorescent Plastic Biochip, 米国出願番号09/270,214, 受付1999年3月15に記述してある。

一般的には、基材は平面であるが、当技術分野の当事者であれば分かるが、基材の他の形状も同様に使用される。例えば、フロースルー試料分析で試料量を最小で済ませるのにプローブは管の内部壁に配置する。同様に、基材は柔軟で、特別なプラスチックで作った閉鎖細胞泡を含める柔軟性泡のようなものでもよい。

好ましい態様では、バイオチップやプローブの表面は当該二つの次に示す付着用の化学官能基で誘導化されている。かくして、例えばバイオチップはアミノ基がより好ましいが、アミノ基、カルボキシ基、オキソ基及びチオール基などを含んだ化学官能基で修飾されるが、これに限らない。これらの官能基を用い、当該プローブはプローブ上の官能基を用いて付着できる。例えば、アミノ基を含有する核酸は例えば当技術分野では知られているリンカー、例えばよく知られているホモ又はヘテロ二官能リンカー（参照1994年度Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200、参照により本明細書で参照）を用いてアミノ基を含む表面に付着可能である。加えて、幾つかの例では、アルキル基などの追加リンカー（置換及びヘテロアルキル基を含む）が使用される。

本態様では、当該オリゴヌクレオチドは当技術分野で知られているように合成され、固体担体の表面に付着させる。当技術分野の当事者であれば知っているように、5'又は3'末端は固体担体に付着されるが、付着は内部ヌクレオチドを介する。

追加の態様では、固体担体への固定化は非共有であるが非常に強い。例えば、ジオチニル化オリゴヌクレオチドを作成し、それをストレプトアビジンを共有結合で被覆した表面に結合すると付着が生じる。

それに代わるものとして、当技術分野で知られているようにオリゴヌクレオチドは表面に合成する。たとえば、光重合化合物と技術を用いて光活性化技術を用いる。好ましい態様では、核酸は、WO 95/25116、WO 95/35505：米国特許番号5,700,637及び5,445,934及びその中の参考文献などに記述され、全て参照により本最初明細書に援用されるが、これらの良く知られた写真石板法を用いてin situで合成できる：付属様式のこれらの方法はAffimetrix Gene Chip（商標）技術の基礎を形成している。

好ましい態様では、乳癌タンパク質をコードしている乳癌核酸は、以下に記述した如く選別用アッセイに用いることができる乳癌タンパク質を発現する種々の発現ベクターを作成するのに用いられる。発現ベクターは自己複製染色体外ベクター又は宿主ゲノムに合体するベクターである。一般的にこれらの発現ベクターは、乳がんタンパク質をコードした核酸に作用できるように連結した転写調節及び翻訳調節核酸を含む。用語“調節配列”はある宿主生物中で作用できるように連結したコード化配列の発現に際し必要なDNA配列を称する。原核生物に適した調節配列は例えば、プロモーター、場合によりオペレーター配列及びリボソーム結合部位を含む。原核細胞はプロモーター、ポリアデニル化シグナル及びエンハンサーを利用することで知られている。

核酸が他の核酸配列と機能関連で配置されたとき、核酸は“作用できるように連結する”である。例えば、ポリペプチドの分泌に加わるプレタンパク質として発現されれば、プレ配列又は分泌リーダー用のDNAはポリペプチド用のDNAと作用できるように連結して

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いる：プロモーター又はエンハンサーが配列の転写に影響するとすればコード化配列と作用できるように連結している；又は翻訳を促進するように配置していれば、リボソーム結合部位はコード化配列に作用できるように連結している。一般的に、“作用できるように連結する”は、結合したDNA配列では隣接しているが、分泌リーダーの場合は隣接し、リーディングフェーズである。しかしながら、エンハンサーでは隣接している必要はない。連結は都合の良い制限部位での連結反応で達成される。そのような部位が存在しなければ、従来の慣行に従って合成オリゴヌクレオチドアダプター又はリンカーを用いる。転写及び翻訳調節核酸は一般的に乳癌タンパク質を発現するのに用いられる宿主細胞に適している。；例えば、Bacillus菌からの転写及び翻訳調節核酸配列は、Bacillus菌中の乳癌タンパク質を発現するのに好都合に使える。適切な発現ベクターの数多くの型及び適した調節配列は当技術分野では種々の宿主細胞において知られている。一般に、転写および翻訳調節配列には、プロモーター配列、リボソーム結合部位、転写開始および転写中止配列、翻訳開始および翻訳中止配列、およびエンハンサー配列およびアクチベーター配列が挙げられ得るが、限定されるものではない。好ましい実施形態において、調節配列はプロモーター配列および転写開始および転写中止配列が挙げられる。

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プロモーター配列は構成プロモーター類または誘導プロモーター類のいずれかをコード化する。プロモーター類は自然発生のプロモーター類またはハイブリッドプロモーター類のいずれであってもよい。1個以上のプロモーター要素を組み合わせるハイブリッドプロモーター類もまた当業界に知られており、本発明において有用である。

また、発現ベクターは追加の要素を含んで成り得る。例えば、発現ベクターは2つの複製系を有し得るので、2つの生物、例えば、発現にかかる哺乳動物または昆虫細胞において、またクローン化並びに増幅にかかる原核性宿主において維持されるのを可能にする。さらに、組込み発現ベクターでは、発現ベクターが宿主細胞ゲノムに相同性の少なくとも1配列、好ましくは発現構築を配置する2つの相同性配列を含有する。組込みベクターは、ベクターに封入するために適当な相同性配列を選択することにより、宿主細胞の特異的な遺伝子座に方向づけることができる。組込みベクター類の構築体は当業界によく知られている。

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また、好ましい実施形態において、発現ベクターは選択性のマーカー遺伝子を含有し、形質転換される宿主細胞の選択を可能にする。選択遺伝子は当業界によく知られており、使用する宿主細胞により異なってくる。

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本発明の乳癌蛋白は、乳癌蛋白をコード化する核酸を含む発現ベクターにより形質変換された宿主細胞を乳癌蛋白の発現を誘導または引き起こす妥当な条件下で培養することにより産生する。乳癌蛋白発現にとって妥当な条件は、発現ベクターおよび宿主細胞の選択により異なり、慣例的な実験を介して当業者により容易に確かめられる。例えば、発現ベクターにおける構成プロモーターの使用には、宿主細胞の生育と増殖の最適化が必要となるが、誘導プロモーターの使用には、誘導のために適当な増殖条件を必要とする。さらに幾つかの実施形態において、採取時機が重要となる。例えば、昆虫細胞発現に用いられるバキュロウイルス系は溶菌性ウィルスであり、したがって採取時期の選択は、生産収量によってきわめて重要なものとなり得る。

適当な宿主細胞としては、酵母、細菌、始原菌、カビ類、および昆虫細胞や動物細胞が挙げられる。ドロソフィラメラングスター (Drosophila melanogaster) 細胞、サッカロミセスセレビジエ (Saccharomyces cerevisiae) および他の酵母類、大腸菌、枯草菌、Sf9細胞、C129細胞、293細胞、アカパンカビ、BHK、CHO、COS、ヒーラ細胞、THP1細胞株 (マクロファージ細胞株) およびヒト細胞並びに細胞系が特に興味深い。

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好ましい実施形態において、乳癌蛋白は哺乳動物細胞に発現する。哺乳動物の発現系はまた当業界に知られており、レトロウイルス系を含む。ここに引用文献として特別に組み入れているPCIT/US97/01019およびPCIT/US97/01048に一般に記載されているように、好ましい発現ベクター系は、レトロウィルスベクター系である。ウィルス遺伝子が高度に発現することが多く、広い宿主範囲を有することから、哺乳動物プ

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ロモーターとして特に使用されるのは、哺乳動物のウィルス遺伝子からのプロモーター類である。例として、SV40初期プロモーター、マウス乳房腫瘍ウイルスLTRプロモーター、アデノウイルス主要後期プロモーター、単純ヘルペスウィルスプロモーターおよびCMVプロモーターが挙げられる。典型的には、哺乳動物細胞によって認識される転写終結配列およびポリアデニル化配列は、転写中止コドンに対し3'位に位置する調節領域であるので、プロモーター要素と共にコード化配列を配置する。転写終結およびポリアデニル化シグナルの例としては、SV40から誘導されるものが挙げられる。

外因性の核酸を他の宿主と同様に、哺乳動物宿主に導入する方法は、当業界によく知られており、使用される宿主細胞により異なるものとなる。この技術としては、デキストラン介在トランスフェクション、リン酸カルシウム沈殿、ポリブレン介在トランスフェクション、プロトプラスト融合、電気泳動、ウィルス感染、ポリヌクレオチド（類）のリポソーム中へのカプセル化、およびDNAの核内への直接マイクロ注入が挙げられる。

好ましい実施形態において、乳癌蛋白は細菌系に発現する。細菌発現系は当業界によく知られている。バクテリオファージからのプロモーターもまた使用することができ、当業界に知られている。さらに、合成プロモーターおよびハイブリッドプロモーターも有用であり、例えばtacプロモーターはtrpおよびlacプロモーター配列のハイブリッドである。さらに、細菌プロモーターとしては、細菌RNAポリメラーゼを結合し、転写を開始する能力を有する非細菌源の自然発生のプロモーター類を挙げることができる。機能性プロモーター配列に加えて、効率的なリボソーム結合部位が望ましい。発現ベクターにはまた、細菌中の乳癌蛋白分泌のために提供するシグナルペプチド配列を含んでもよい。蛋白は、増殖媒質（グラム陽性細菌）中、または細胞（グラム陰性細菌）の内膜と外膜との間に位置するペリプラスム間隙のいずれかに分泌される。細菌発現ベクターはまた、形質転換された細菌株の選択を可能にする選択マーカー遺伝子を含んでもよい。好適な選択遺伝子としては、アンピシリン、クロラムフェニコール、エリスロマイシン、カナマイシン、ネオマイシンおよびテトラサイクリンなどの薬剤に対して、抵抗性のある細菌を提供する遺伝子が挙げられる。選択マーカー類にはまた、ヒスチジン、トリプトファンおよびロイシンの生合成経路における遺伝子などの生合成遺伝子が挙げられる。これらの構成要素が発現ベクター内へ組込まれる細菌用の発現ベクターは当業界によく知られており、細菌の中では枯草菌、大腸菌、ストレプトコッカス・クレモリス、ストレプトコッカス・リビダンス（*Streptococcus lividans*）用のベクター類が挙げられる。細菌発現ベクター類は、塩化カルシウム処理、電気泳動などの当業界によく知られた技術を用いて細菌宿主細胞に形質転換される。

1実施形態において、乳癌蛋白は昆虫細胞に産生する。昆虫細胞の形質転換用の発現ベクター、特にバキュロウイルス由来の発現ベクター類は当業界によく知られている。

好ましい実施形態において、乳癌蛋白は酵母細胞に産生する。酵母発現系は当業界によく知られており、サッカロミセス・セレビジエ（*Saccharomyces cerevisiae*）、カンジダアルビカンスおよびC. マルトーサ（*C. maltosa*）、ハンセンラーポリモルファ（*Hansenula polymorpha*）、クルイベロミセス・フラギリス（*Kluyveromyces fragilis*）およびK. ラクチス（*K. lactis*）、ピチア・ギレリモンジー（*Pichia guilliermondii*）およびP. パストリス（*P. pastoris*）、分裂酵母ポンベ（*Schizosaccharomyces pombe*）およびヤロウィア・リポリチカ（*Yarrowia lipolytica*）のための発現ベクターが挙げられる。

乳癌蛋白はまた、当業界によく知られた技術を用いて融合蛋白として作製してもよい。したがって、例えば、モノクローナル抗体の創製に関して、所望のエピトープが小さい場合、乳癌蛋白は免疫原を形成するために担体蛋白に融合してもよい。他に、乳癌蛋白は発現を増加させるために、または他の理由のために融合蛋白として作製されてもよい。例えば、乳癌蛋白が乳癌ペプチドである場合、該ペプチドをコード化する核酸は、発現目的のために他の核酸に結合してもよい。

実施形態の1つにおいて、本発明の乳癌の核酸、蛋白および抗体を標識化する。ここでの

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「標識化」とは、化合物が、該化合物の検出を可能にするために付加された少なくとも1つの要素、同位元素または化学化合物を有することを意味する。一般に、標識は以下の3つに分類される：a) 放射活性または重同位元素であり得る同位元素標識；b) 抗体または抗原であり得る免疫標識；およびc) 着色または蛍光染色。該標識は、乳癌の核酸、蛋白および抗体に任意の位置で組み込むことができる。例えば、該標識は、直接または間接的に検出性シグナルを生成することができる必要がある。検出可能な部分は、³H、¹⁴C、³²P、³⁵Sまたは¹²⁵Iなどの放射性同位元素、蛍光イソシアネート、ローダミンまたはルシフェリンなどの蛍光または化学発光化合物、またはアルカリホスファターゼ、ペクターガラクトシダーゼまたはわさび大根ペルオキシダーゼなどの酵素であってもよい。抗体を標識に結合するために当業界に知られた方法としては、Hunterら，Nature，144：945（1962）；Davidら，Biochemistry，13：1014（1974）；Painら，J. Immunol. Meth.，（1981）；およびNygren，J. Histochem. およびCytochem.，30：407（1982）により記載されたこれらの任意の方法を用いることができる。10

したがって、本発明はまた、乳癌蛋白配列を提供する。本発明の乳癌蛋白は幾つかの方法で確認できる。ここでの「蛋白」とは、タンパク質類、ポリペプチド類およびペプチド類を含む。当業者により認識されるように、本発明の核酸配列は、蛋白配列を生成するのに用いることができる。これを実施するには、多様な方法があり、全遺伝子をクローン化し、その読み枠およびアミノ酸配列を証明すること、または乳癌蛋白が、使用されるデータベース中の或る蛋白に相同性であることを想定して相同性を探索するために知られた配列と比較することにより読み枠を提供することなどが挙げられる。一般に核酸配列は、3つの全ての構成物を相同性に関して探索するプログラムに入力する。これは、以下のNCBI進展BLASTパラメータを用いて好ましい実施形態で成される。該プログラムはblastxまたはblastnである。該データベースはnrである。該入力データは「Sequence in FASTA format」としてである。生物リストは「none」である。「expect」は10であり；フィルターはデフォルトである。「descriptions」は500であり、「alignments」は500であり、「alignment view」はペアワイズである。「Query Genetic Codes」は標準（1）である。マトリクスはBLOSUM62であり；ギャップ存在コストは11であり、残基当たりのギャップコストは1であり；およびラムダ比はB5デフォルトである。この結果、推定蛋白配列が出来上がる。20

ここに決定されるように、自然発生の配列のアミノ酸変異体もまた乳癌蛋白の実施形態の1つに含まれる。好ましくは、該変異体が野生型配列に対し約75%以上相同性であるのが好ましく、80%以上がさらに好ましく、約85%以上がさらに好ましく、90%以上が最も好ましい。幾つかの実施形態において、相同性は約93%から95%または98%と同じ高さにもなる。核酸に関して、これに関連する相同性とは配列の類似性または同一性を意味するが、同一性であることが好ましい。該相同性は、核酸の相同性に関して上記のような当業者に知られた標準的な技術を用いて決定される。30

本発明の乳癌蛋白は、野生型のアミノ酸配列よりも短くても、または長くてもよい。したがって、好ましい実施形態では、乳癌蛋白の定義内で、ここでは野生型配列の部分またはフラグメントが含まれる。さらに上述のように、本発明の乳癌核酸は、当業者に知られている技術を用いて追加のコード領域、すなわち追加の蛋白配列を獲得するために使用してもよい。40

好ましい実施形態において、乳癌蛋白は野生型配列に比べて誘導または変異乳癌蛋白である。すなわち、以下に詳述するように、誘導乳癌ペプチドは少なくとも1個のアミノ酸の置換、欠失、挿入を含み、特にアミノ酸置換が好ましい。アミノ酸置換、挿入、欠失は乳癌ペプチド内のいずれの残基に生じててもよい。

アミノ酸配列変異体は、本発明の乳癌蛋白の実施形態の1つにまた含まれる。これらの変異体は、3分類、すなわち置換変異体、挿入変異体、欠失変異体の1つ以上に分類される。これらの変異体は通常、カセットまたはPCR変異誘発またはその他当業界でよく知ら50

れている技術を用いて、乳癌蛋白をコード化するDNA内ヌクレオチドの部位特異的変異誘発により調製し、この変異体をコード化するDNAを産生し、その後、上述したように組換え細胞培養中でDNAを発現させる。しかし、約100～150残基までを有する変異乳癌蛋白フラグメントは、確立された技術を用いてイン・ビトロ合成により調製してもよい。アミノ酸配列配列変異体は予め決定されている変異の特質、すなわち乳癌蛋白アミノ酸配列の自然発生の対立遺伝子変異または種間変異から区別される特性により特徴づけられる。以下に詳述するように該変異体は、特性を修飾して選別することもできるが、一般には自然発生の類縁体と同一の定性的な生物学的活性を示す。

アミノ酸配列変異を導入する部位または領域は予め決定されるが、変異それ自体は予め決定される必要はない。例えば、与えられた部位の変異性能を最適化するために、標的コドンまたは標的領域において、無作為の誘発変異を行なって発現した乳癌変異体を、所望の活性を有する最適な組合せでスクリーニングすることができる。既知の配列を有するDNA内の予め決められた部位に置換変異体を作製する技術はよく知られており、例えばM13プライマー変異誘発およびPCR変異誘発がある。変異体のスクリーニングは乳癌蛋白活性のアッセイを用いて行なわれる。

アミノ酸の置換は、一般に1個の残基であり、挿入はかなり多くの挿入が可能であるが、通常約1～20個のアミノ酸の範囲である。欠失は、約1～20残基の範囲であるが、時にははるかに多い欠失も可能である。

最終的誘導体に到達するために、置換、欠失、挿入またはそれらの任意の組合せを用いることができる。一般にこれらの変化は、分子の変化を最小化するために、2, 3個のアミノ酸において成される。しかし、一定の状況においては、より大きな変化が許容される。乳がん蛋白特性における変化の少ないことが望まれる場合は、一般に以下のチャートに従って置換が行われる。

チャート 1

原残基	置換例
A l a	S e r
A r g	L y s
A s n	G l n、H i s
A s p	G l u
C y s	S e r
G l a	A s n
G l u	A s p
G l y	P r o
H i s	A s n、G l n
I l e	L e u、V a l
L e u	I l e、V a l
L y s	A r g、G l n、G l u
M e t	L e u、I l e
P h e	M e t、L e u、T y r
S e r	T h r
T h r	S e r
T r p	T y r
T y r	T r p、P h e
V a l	I l e、L e u

機能または免疫学的特性における大きな変化は、表1で示したものより保守性の低い置換基を選択することにより成される。例えば、アルファ螺旋構造またはベータシート構造などの変更領域におけるポリペプチド骨格構造；標的部位における分子の電荷または疎水性；または側鎖の嵩高さに対しより大きな影響を与える置換を行なうことができる。ポリペプチドの特性に大きな変化を生じさせると一般に考えられる置換は、(a) 親水性残基、例えばセリル、トレオニルと、疎水性残基、例えばロイシル、イソロイシル、フェニルア

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ラニル、バリル、アラニルなどの疎水性残基との交互の置換；（b）システインまたはプロリンと、その他の残基との交互の置換；（c）正電荷の側鎖を有する残基、例えばリジル、アルギニル、ヒスチジルと、負電荷の側鎖、例えばグルタミル、アスパルチルとの交互の置換；または（d）嵩高い側鎖、例えばフェニルアラニンを有する残基と、側鎖を持たない残基、例えばグリシンとの交互の置換である。

変異体は、必要に応じて乳癌蛋白の特性を変化させるために選択されることもあるが、一般には、自然発生の類縁体と同一の定性的生物学的活性を示し、同一の免疫反応を誘導する。他に、変異体は乳癌蛋白の生物学的活性を変化させるために設計してもよい。例えばグリコシル化部位を変化させるか、または除いてもよい。

乳癌ポリペプチドの共有結合修飾も本発明の範囲に含まれる。共有結合修飾の1つに、乳癌ポリペプチドの標的アミノ酸残基を、乳癌ポリペプチドの選択された側鎖またはNまたはC末端残基と反応することのできる有機誘導化剤と反応させることが挙げられる。二元機能剤による誘導化は、例えば以下に詳述するように、抗乳癌抗体の精製、またはスクリーニングアッセイのための方法に使用するため、乳癌を水に不溶性の支持マトリクスまたは支持面に架橋させるために有用である。通常使用される架橋剤として、例えば、1, 1-ビス（ジアゾアセチル）-2-フェニルエタン、グルタルアルデヒド、N-ヒドロキシスクシンイミドエステル類、例えば4-アジドサリチル酸とのエステル、3, 3'-ジチオビス（プロピオン酸スクシンイミジル）などのジスクシンイミジルエステルを含むホモ二元機能イミドエステル、ビス-N-マレイイミド-1, 8-オクタンなどの二元機能マレイミド類およびメチル-3-〔（p-アジドフェニル）ジチオ〕プロピオイミデートなどの試薬が挙げられる。

その他の修飾としては、グルタミニル残基およびアスパラギニル残基の各々相当するグルタミル残基、アスパルチル残基への脱アミド化、プロリンおよびリジンのヒドロキシル化、セリル、トレオニル、チロシル残基のヒドロキシル基のリン酸化、リジン、アルギニンおよびヒスチジンの側鎖の α -アミノ基のメチル化〔T. E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco, pp. 79-86 (1983)〕、N-末端アミンのアセチル化および任意のC-末端カルベキシル基のアミド化が挙げられる。

本発明の範囲に含まれる乳癌ポリペプチドの共有結合修飾のその他の種類は、ポリペプチドの本来のグリコシル化パターンの変更を含む。「本来のグリコシル化パターンの変更」は、ここでは本来の配列の乳癌ポリペプチドに見られる1つ以上の炭水化物の欠失および／または、本来の配列乳癌ポリペプチドには存在しないグリコシル化部位の1つ以上の付加を意味する目的のために意図されている。

グリコシル化部位の乳癌ポリペプチドへの付加は、そのアミノ酸配列を変更することにより達成できる。この変更は、例えば1つ以上のセリンまたはトレオニン残基を、本来の配列乳癌ポリペプチドへ付加または置換（O-結合グリコシル化部位に関して）することにより行なうことができる。乳癌アミノ酸配列は、DNAレベルでの変化により、特に予め選択された塩基における乳癌ポリペプチドをコード化するDNAを、所望のアミノ酸へ翻訳するようなコドンを生じるように変異させることにより、任意に変更させることができる。

乳癌ポリペプチド上の糖質部分数を増加させる他の手段は、グリコシル類をポリペプチドに化学結合または酵素結合するものである。このような方法は、当業界、例えば1987年9月11日に公表されたWO第87/05330号およびAppl inおよびWristonの乳癌、*Crit. Rev. Biochem.*, pp. 259-306 (1981)に記載されている。

乳癌ポリペプチド上に存在する糖質部分の除去は、化学的または酵素的またはグリコシル化の標的として働くアミノ酸残基に対してコード化するコドンの変異置換により成就できる。化学的脱グリコシル法は、当業界に知られており、例えばHakimuddinらの*Arch. Biochem. Biophys.*, 259: 52 (1987)およびEdg

eらのAnal. Biochem., 118:131(1981)により記載されている。ポリペプチド上の糖質部分の酵素的切断は、ThotakuraらのMeth. Enzymol., 138:350(1987)により記載されるように多種のエンドーおよびエキソグリコシダーゼ類の使用により達成できる。

乳癌の共有結合修飾の他のタイプは、米国特許第4,640,835号;米国特許第4,496,689号;米国特許第4,301,144号;米国特許第4,670,417号;米国特許第4,791,192号または米国特許第4,179,337号に記載された方法で、乳癌ポリペプチドを多種の非蛋白ポリマー類の1つ、例えばポリエチレングリコール、ポリプロピレングリコールまたはポリオキシアルキレン類に結合することを含んで成る。

本発明の乳癌ポリペプチドはまた、他の非相同性ポリペプチドまたはアミノ酸配列に融合された乳癌ポリペプチドを含むキメラ分子を形成する方法で修飾してもよい。実施形態の1つにおいて、このようなキメラ分子は、抗タグ抗体が選択的に結合できるエピトープを提供するタグポリペプチドを有する乳癌ポリペプチドの融合を含んで成る。該エピトープタグは一般に、乳癌ポリペプチドのアミノーまたはカルボキシルー末端に位置する。乳癌ポリペプチドのこのようなエピトープタグ体の存在は、タグポリペプチドに対する抗体を用いて検出できる。また、エピトープタグの提供により、乳癌ポリペプチドを、エピトープタグに結合する抗タグ抗体または他のタイプのアフィニティーマトリクスを用いてアフィニティ精製により容易に精製できる。他の実施形態において、キメラ分子は、乳癌ポリペプチドと免疫グロブリンまたは免疫グロブリンの特別領域との融合を含んで成る。キメラ分子の二価形体ではこのような融合は、IgG分子のFc領域にされ得るであろう。

さまざまなタグポリペプチドおよびそれぞれの抗体は本技術分野でよく公知である。例としては、ポリーヒスチジン(ポリーヒス)またはポリーヒスチジン-グリシン(ポリーヒス-グリ)タグ、インフルエンザHAタグポリペプチドおよびその抗体12CA5(Field et al., Mol. Cell. Biol., 8:2159-2165(1988))、c-mycタグおよびそれに対する8F9、3C7、6E10、G4、B7および9E10抗体(Evan et al., Molecular and Cellular Biology, 5:3610-3616(1985))、および単純ヘルペス糖タンパク質D(gD)タグとその抗体(Paborsky et al., Protein Engineering, 3(6):547-553(1990))が含まれる。他のタグポリペプチドには、Flag-ペプチド(Hopp et al., Biotechnology, 6:1204-1210(1988))、KT3エピトープペプチド(Martin et al., Science, 255:192-194(1992))、チューブリンエピトープペプチド(Skinner et al., J. Biol. Chem., 266:15163-15166(1991))、およびT7遺伝子10タンパク質ペプチドタグ(Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397(1990))が含まれる。

また、1つの実施形態における乳癌タンパク質の決定に際し、乳癌ファミリーの他の乳癌タンパク質および他の生物からの乳癌タンパク質が含まれ、それらは以下で概略したようにクローン化し、発現させる。したがって、プローブまたは変性ポリメラーゼ連鎖反応(PCR)プライマー配列を、ヒトまたは他の生物から他の関連乳癌タンパク質を発見するのに使用してよい。当業者に明らかであろうように、とりわけ有用なプローブおよび/またはPCRプライマー配列には、乳癌核酸配列の固有の領域が含まれる。本技術分野で一般的に公知であるように、好ましいPCRプライマーは長さにして約15~約35ヌクレオチドであり、好ましくは約20~約30であり、必要ならばイノシンを含んでよい。PCR反応の条件は本技術分野でよく公知である。

さらに、本明細書で概略するように、乳癌タンパク質は、たとえば付加的な配列の解明、エピトープまたは精製タグの添加、他の融合配列の添加などによって、図で記載したもの

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よりも長く作製できる。

乳癌タンパク質はまた、乳癌核酸によってコードされているものとして同定してよい。したがって、乳癌タンパク質は、本明細書で概略したような、配列表の配列、またはその相補的な配列にハイブリッド形成する可能性のある核酸によってコードされる。

好ましい実施様態において、たとえば免疫治療のために、乳癌タンパク質を抗体を作製するために使用する場合、乳癌タンパク質は、全長タンパク質で少なくとも1つのエピトープまたは決定基を共有しなければならない。本明細書において、「エピトープ (e p i t o p e)」または「決定基 (d e t e r m i n a n t)」は、抗体またはMHCに関連したT細胞受容体を作製および／または結合する可能性のあるタンパク質の一部分を意味する。したがって、ほとんどの場合、より小さな乳癌タンパク質に対して作製された抗体は、全長タンパク質に結合できる可能性がある。好ましい実施様態において、エピトープは固有であり、したがって、固有のエピトープに対して作製された抗体は、ほとんどまたは全く交差反応性は示さない。好ましい実施様態において、エピトープはBCH1 p 1、BCH1 p 2、BCR3 p 1、BCR3 p 2、BCQ8 p 1、BCQ8 p 2、BCQ5 p 1、BCQ5 p 2、BCN1 p 1、BCN1 p 2より選択し、BCH1 p 1およびBCH1 p 2が好ましい。1つの実施様態において、エピトープまたはBCH1 p 1の断片はKLHまたはBSAに共役させる。

1つの実施様態において、語句「抗体 (a n t i b o d y)」には、抗体全体の改変によって産出されるか、組換え体DNA技術を用いてde novoにて合成された、Fab、Fab₂、単鎖抗体 (たとえばFv)、キメラ抗体などを含む、本技術分野で公知であるような抗体断片が含まれる。

ポリクローナル抗体を調製する方法は当業者に公知である。ポリクローナル抗体は、たとえば免疫薬剤、もし望むのならばアジュバントの1つまたはそれ以上の注入によって哺乳動物内で作製することができる。典型的には、免疫薬剤および／またはアジュバントは、多重皮下または腹腔内注射にて哺乳動物に注射する。免疫薬剤は、BCH1またはその断片またはその融合タンパク質を含んでよい。免疫薬剤を、免役されている哺乳動物において免疫原性であることが知られているタンパク質に共役させることが有用であり得る。そのような免疫原性タンパク質の例には、キーホールリンペットヘモシアニン、血清アルブミン、ウシチログロブリンおよびダイズチロシン阻害剤が限定はしないが含まれる。使用してよいアジュバントの例には、フロイト完全アジュバントおよびMPL-TDMアジュバント (モノホスホリル脂質A、合成トレハロースジコリノミコレート) が含まれる。免疫プロトコールは、過度に実験を行わずに当業者によって選択されてよい。

あるいは、抗体はモノクローナル抗体であってよい。モノクローナル抗体は、Kohler and Milstein, Nature, 256: 495 (1976) によって記述されたもののようなハイブリドーマ方法を用いて調製してよい。ハイブリドーマ方法において、マウス、ハムスターまたは他の適切な宿主動物を、典型的には免疫薬剤で免役し、免疫剤に特異的に結合する可能性のある抗体を産出するか、産出することが可能であるリンパ球を誘発させる。あるいは、リンパ球をin vitroにて免役してよい。免疫薬剤は典型的には、BCH1ポリペプチドまたはその断片またはその融合タンパク質を含む可能性がある。一般的に、ヒト由来の細胞が望ましい場合、末梢血液リンパ球 (「PB L s」) を使用し、非ヒト哺乳動物供給源が望ましい場合脾臓細胞またはリンパ管細胞を使用する。次いでリンパ球を、ポリエチレングリコールのような好適な融合剤を用いて不滅化した細胞株と融合させ、ハイブリドーマ細胞を形成させる (Goding, Monoclonal Antibodies. Principle and Practice, Academic Press, (1986) pp. 59-103)。不滅化した細胞株は通常、形質転換した哺乳動物細胞、とりわけ齧歯類、ウシおよびヒト由来の骨髓腫細胞である。通常ラットまたはマウス骨髓腫細胞株を使用する。ハイブリドーマ細胞は、好ましくは1つまたはそれ以上の、融合していない不滅化細胞の増殖または生存を阻害する基質を含む好適な培養培地中で培養してよい。たとえば、親細胞が酵素ヒポキサンチングアニンホスホリボシル転移酵素 (HGPRTまたはHPR T) を欠損している場合、ハイ

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ブリドーマのための培養培地は典型的にはヒポキサンチン、アミノプテリンおよびチミジンを含む可能性があり（「HAT培地」）、基質はHGPRT-欠損細胞の増殖を防止する。

1つの実施様態において、抗体は二重特異性抗体である。二重特異性抗体は、少なくとも2つの異なる抗原に対して特異性を持っている、モノクローナル、好ましくはヒトまたはヒト化された抗体である。本発明の場合において、1つの結合特異性は乳癌タンパク質またはその断片に関してであり、他は任意の他の抗原に対してであり、好ましくは細胞表面タンパク質またはレセプターまたはレセプターサブユニットであり、好ましくは1つは腫瘍特異的である。

好ましい実施様態において、乳癌に対する抗体は、以下で記述するように乳癌の生物学的機能を減ずるかまたは除去することが可能である。したがって、（ポリクローナル、または好ましくはモノクローナルどちらかの）抗乳癌抗体の乳癌（または乳癌を含む細胞）への添加が、乳癌活性を減少させるかまたは除去しうる。一般的に、少なくとも25%の活性の減少が好ましく、少なくとも約50%がとりわけ好ましく、約95～100%の減少が特に好ましい。

好ましい実施様態において、乳癌タンパク質に対する抗体はヒト化した抗体である。非ヒト（たとえば齧歯類）抗体のヒト化形態は、非ヒト免疫グロブリンから由来した最小配列を含む免疫グロブリン、免疫グロブリン鎖または（Fv、Fab、Fab₂または抗体の他の抗原結合配列のような）その断片のキメラ分子である。ヒト化抗体には、レシピエントの相補性決定領域（CDR）が、望ましい特異性、親和性および能力を持っているマウス、ラットまたはウサギのような非ヒト種のCDR（ドナー抗体）からの残基で置換された、ヒト免疫グロブリン（レシピエント抗体）が含まれる。いくつかの場合、ヒト免疫グロブリンのFv骨格残基を、相当する非ヒト残基にて置換する。ヒト化抗体はまた、レシピエント抗体または導入したCDRまたは骨格配列どちらにも発見できない残基を含んでもよい。一般的に、ヒト化抗体は本質的に少なくとも1つ、典型的には2つの可変領域のすべてを含む可能性があり、その中で、すべてまたは本質的にすべてのCDR領域が非ヒト免疫グロブリンのCDR領域相当し、すべてまたは本質的にすべてのFR領域がヒト免疫グロブリン共通配列のそれである。ヒト化抗体は、任意にまた、免疫グロブリン定常領域（Fc）の少なくとも1部分、典型的にはヒト免疫グロブリンの定常領域を含む（Jones et al., Nature, 321: 552-525 (1986)、Riechmann et al., Nature, 332: 323-329 (1988)、Presta, Curr. Opin. Struct. Biol., 2: 593-596 (1992)）。

非ヒト抗体のヒト化のための方法は本技術分野で公知である。一般的に、ヒト化抗体は1つまたはそれ以上の、非ヒトである供給源よりその中に導入された核酸残基を持つ。これらの非ヒトアミノ酸残基はしばしば導入残基と呼び、典型的には導入可変領域よりとられる。ヒト化は、齧歯類CDRsまたはCDR配列をヒト抗体の相当する配列に置換することで、本質的にWinterとその共同研究者らの方法にしたがって実施する（Jones et al., Nature, 321: 522-525 (1986)、Riechmann et al., Nature, 332: 323-327 (1988)、Verthoeven et al., Science, 239: 1534-1536 (1986)）。よって、そのようなヒト化抗体はキメラ抗体であり（米国特許第4,818,587号）、そこで本質的にほとんど、野生型のヒト可変領域は、非ヒト種からの相当する配列によって置換される。実際に、ヒト化抗体は典型的には、いくつかのCDR残基と可能性のあるいくつかのFR残基が、齧歯類抗体の相同性部位からの残基で置換されたヒト抗体である。

ヒト抗体はまた、ファージディスプレイライブラリー（Hoogenboom and Winter, J. Mol. Biol., 227: 381 (1991)、Marks et al., J. Mol. Biol., 222: 581 (1991)）を含む、本技術分野で公知のさまざまな技術を使用して産出できる。Cole et al. およびBoe

mer et al. の技術もまた、ヒトモノクローナル抗体の調製のために使用可能である (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R Liss, p. 77 (1985) および Bormer et al., J. Immunol., 147 (1): 86-95 (1991))。同様に、ヒト抗体は、ヒト免疫グロブリン座をトランスジェニック動物、たとえば内生免疫グロブリン遺伝子を部分的にまたは完全に不活性化したマウス内に導入することで作製することができる。誘発に際して、ヒト抗体産出が観察され、遺伝子再編成、組立、および抗体の能力の範囲を含むすべての観点でヒトで見られるものにとっても似ている。このアプローチはたとえば、米国特許第 5, 545, 807 号、第 5, 545, 806 号、第 5, 569, 825 号、第 5, 625, 126 号、第 5, 633, 425 号、第 5, 661, 016 号で、および以下の科学的発行物、Marks et al., Bio/Technology 10, 779-783 (1992)、Lonberg et al., Nature 368: 856-859 (1994)、Morrison, Nature 368: 812-13 (1994)、Fishwild et al., Nature Biotechnology 14, 845-51 (1996)、Neuberger, Nature Biotechnology 14, 826 (1996)、Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995) で記述されている。

免疫療法は、乳癌タンパク質に対して作製された抗体での乳癌の処置を意味する。本明細書で使用したように、免疫治療は受動的または能動的であってよい。本明細書で定義したような受動的免疫療法は、レシピエント（患者）への抗体の受動的な伝送である。能動的免疫化は、レシピエント（患者）での抗体および／または T-細胞応答の誘導である。免疫応答の誘導は、それに対して抗体ができる抗原をレシピエントに提供することの結果である。当業者によって理解されるように、抗原は、それに対して抗体がレシピエント内に作製されることが望ましいようなポリペプチドを注入すること、またはレシピエントを抗体を発現可能な核酸と、抗原の発現のための条件下で接触させることによって産出してよい。

好ましい実施様態において、それに対して抗体が産出される乳癌タンパク質は上述のように分泌タンパク質である。理論に結びつけることなしに、治療のために使用した抗体は、分泌タンパク質に結合し、そのレセプターへの結合より分泌タンパク質を防ぎ、これによって分泌乳癌タンパク質を不活性化する。

他の好ましい実施様態において、それに対して抗体が作製される乳癌タンパク質は膜貫通タンパク質である。理論によって結びつけることなしに、治療のために使用した抗体は乳癌タンパク質の細胞外領域に結合し、循環リガンドまたは細胞関連分子のような他のタンパク質への結合を防止する。抗体は膜貫通乳癌タンパク質のダウンレギュレーションを引き起こす可能性がある。当業者に理解されるであろうように、抗体は競合、非競合または競合しない、乳癌タンパク質の細胞外領域に結合しているタンパク質の阻害剤であってよい。抗体はまた、乳癌タンパク質のアнтаゴニストである。さらに抗体は膜貫通乳癌タンパク質の活性化を防止する。1つの観点において、抗体が乳癌タンパク質への他の分子の結合を防止した場合、抗体は細胞の増殖を防止する。抗体はまた細胞を、TNF- α 、TNF- β 、IL-1、INF- γ および IL-2 を限定はしないが含む細胞傷害性剤、または 5FU、ビンブラスチン、アクチノマイシン D、シスプラチン、メトトレキサートのようなものを含む化学治療剤へ感作する。いくつかの場合、抗体は膜貫通タンパク質と複合体形成した場合に血清補体を活性化するサブタイプに属し、これによって細胞傷害性を仲介している。したがって、乳癌は、患者に対して膜貫通乳癌タンパク質に対する抗体を投与することで治療する。

他の好ましい実施様態において、抗体は治療部分に共役させる。1つの観点において、治療部分は乳癌タンパク質の活性を調節する小分子である。他の観点において、治療部分は、乳癌細胞に関連した、またはきわめて近い分子の活性を調節する。化学部位は、乳癌に関連したタンパク質分解酵素またはタンパク質リン酸化酵素のような酵素的活性を阻害す

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る可能性がある。

好ましい実施様態において、治療的部位はまた細胞傷害性薬剤であってよい。この方法において、細胞傷害性薬剤を癌組織または細胞に対して標的化することは、結果として乳癌細胞の数の減少となり、これにより乳癌に関連した症状が減少する。細胞傷害性薬剤は数多く、変化し、細胞毒性薬品または毒素またはそのような毒素の活性断片が含まれるが、限定はしない。好適な毒素およびその相当する断片には、ジフテリアA鎖、エキソトキシンA鎖、リシンA鎖、アブリンA鎖、クルシン、クロチン、フェノマイシン、エノマイシンなどが含まれる。細胞毒医薬剤にはまた、放射性同位体を乳癌タンパク質に対して作製された抗体に共役すること、または放射性核種を抗体に共有結合したキレート剤と結合することで作製された放射化学品も含まれる。治療部分を膜貫通乳癌タンパク質に対して標的化することは、乳癌を患っている領域での治療部分の局所濃度を増加させるのに役に立つだけでなく、治療部分に関連する可能性がある有害な副作用を減少させるのに役に立つ。本発明の乳癌抗体は乳癌タンパク質に特異的に結合する。本明細書において「特異的に結合する (specifically bind)」は、抗体が、少なくとも $10^{-4} \sim 10^{-5} \text{ M}^{-1}$ の範囲、好ましくは $10^{-7} \sim 10^{-9} \text{ M}^{-1}$ の範囲での結合定数でタンパク質に結合することを意味する。

好ましい実施様態において、乳癌タンパク質は発現の後に精製し、または単離する。乳癌タンパク質は、どのような他の成分が試料中に存在するかに依存して当業者に公知の様々な方法にて単離し、または精製してよい。標準の精製方法には、電気泳動的、分子的、免疫学的小およびイオン交換、疎水性、アフィニティーおよび逆相HPLCクロマトグラフィーを含むクロマトグラフィー技術、およびクロマトフォーカシングが含まれる。たとえば、乳癌タンパク質は標準の抗乳癌抗体カラムを用いて精製してよい。タンパク質濃縮と関連して限界濾過およびダイアフィルトレーション技術もまた有用である。好適な精製技術での一般的なガイドラインに関しては、Scopes, R., Protein Purification, Springer-Verlag, NY (1982)を参照のこと。精製の必要性の程度は、乳癌タンパク質の使用に依存して変化する可能性がある。いくつかの場合、精製は必要ない可能性がある。

いったん発現し、必要な場合精製したならば、乳癌タンパク質および核酸は多くの適用において有用である。

1つの観点において、遺伝子の発現レベルは、乳癌表現型における異なる細胞状態に関して決定され、すなわち通常の乳組織および乳癌組織における遺伝子の発現レベルを(いくつかの場合以下で概略したように、予後に関連した乳癌のひどさを変更するために)、発現プロファイルを提供するように評価する。特定の細胞状態または発達点の発現プロファイルは、本質的に状態の「識別特徴 (finger print)」であり、2つの状態が任意の特定の遺伝子を同様に発現している可能性がある一方で、多くの遺伝子の評価が同時に、細胞の状態に固有である遺伝子発現プロファイルの生成を可能にする。異なる状態の細胞の発現プロファイルを比較することによって、それらの状態それぞれにおいて、どの遺伝子が重要であるか(遺伝子のアップーおよびダウンレギュレーション両方を含めて)に関連した情報が得られる。よって、正常または乳癌組織の遺伝子発現プロファイルを持つ特定の患者からの組織で診断を行ってよく、または確認してよい。

本明細書で使用するところの「識別的発現(差動的発現) (differential expression)」または文法的同義語は、細胞内および細胞間での遺伝子の時間的なおよび/または細胞発現パターンにおける定性的および定量的両方の違いを意味する。したがって識別的に発現した遺伝子は、たとえば正常組織対乳癌組織において、活性化または不活性化を含めて定性的にその発現を変化させることができる。したがって遺伝子は他の状態と比較して、特定の状態で作り出されるか、または作り出されない可能性がある。当業者に理解されるように、2つまたはそれ以上の状態の比較を行うことができる。そのような定性的に制御された遺伝子は、1つのそのような状態または細胞型で標準技術によって検出可能であるが、両方で検出はできない状態または細胞型での発現パターンを示す可能性がある。あるいは、決定は、発現が増加または減少する定量的なものであり、

すなわち遺伝子の発現はアップレギュレートされ、結果として転写物の量が増加するか、ダウンレギュレートされ、結果として転写物の量が減少するかどちらかである。発現が異なる程度は、参考文献として本明細書に組み込んだ、Affymetrix GeneChipTM 発現アレイ、Lockhart, Nature Biotechnology, 14:1675-1680 (1996) の使用によるような、以下で概略したような標準の特性化技術を介して定量するのに十分大きいことのみが必要とされる。他の技術には、定量的逆転写PCR、ノザン解析およびPNaseプロテクションが含まれるが、限定はされない。以上で概略したように、好ましくは発現の変化（すなわちアップレギュレートまたはダウンレギュレート）は少なくとも約50%、より好ましくは少なくとも約100%、より好ましくは少なくとも約150%、より好ましくは少なくとも約200%、300~少なくとも1000%がとりわけ好ましい。 10

当業者によって理解されるであろうように、これは遺伝子転写物またはタンパク質レベルのどちらかで評価されてよく、すなわち遺伝子発現量は、遺伝子転写物のDNAまたはRNA同等物に対する核酸プローブを用いてモニタしてよく、遺伝子発現レベルの定量、または最終遺伝子産物そのもの（タンパク質）は、たとえば乳癌タンパク質に対する抗体と標準免疫アッセイ（ELISA等）または、質量分析アッセイ、2Dゲル電気泳動アッセイなどを含む他の技術を使用することでモニタできる。したがって、乳癌遺伝子に関するタンパク質、すなわち乳癌表現型で重要であるとして同定されたものは、乳癌診断試験で評価することができる。

好ましい実施様態において、多重タンパク質発現モニタリングを同様に実施できるけれども、遺伝子発現モニタリングを行い、多くの遺伝子、すなわち発現プロファイルを同時にモニタする。同様に、これらのアッセイは同じように個々の基準において実施してよい。本実施様態において、乳癌核酸プローブは、特定の細胞での乳癌配列の検出と定量のために本明細書にて概略したようにバイオチップに結合させる。 20

好ましい実施様態において、乳癌タンパク質をコードしている核酸を検出する。乳癌タンパク質をコードしているDNAまたはRNAを検出してよく、とりわけ興味のあるものは、乳癌タンパク質をコードしているmRNAを検出する方法である。試料中のmRNAの存在は、乳癌遺伝子がmRNAを形成するために転写されたことの示唆であり、タンパク質が発現されていることを示している。mRNAを検出するためのプローブは、mRNAと相補的であり、塩基対である任意のヌクレオチド/デオキシヌクレオチドプローブでありえ、オリゴヌクレオチド、cDNAまたはRNAを限定しないが含む。プローブはまた、本明細書で定義したような、検出可能な標識を持つべきである。1つの方法において、mRNAは、ナイロン膜のような固体支持体上で試験するために核酸を固定化し、試料にプローブをハイブリッド形成した後に検出する。非特異的に結合したプローブを取り除くための洗浄に続き、標識を検出する。他の方法では、mRNAの検出は*in situ*で実施する。この方法において、透過した細胞または組織試料を、プローブが標的mRNAとハイブリッド形成するのに十分な時間で、検出可能な標識化核酸プローブと接触させる。非特異的に結合したプローブを除くための洗浄の後に、標識を検出する。たとえば乳癌タンパク質をコードしているmRNAに相補的であるジゴキシゲニン標識化リボプローブ（RNAプローブ）を、抗ジゴキシゲニン二次抗体をジゴキシゲニンに結合させることで 30 40

検出し、ニトロブルーテトラゾリウムおよび5-ブロモ-4-クロロ-3-インドリルリン酸で現像する。

好ましい実施様態において、本明細書で記述したような3種類のタンパク質（分泌、膜貫通または細胞内タンパク質）をいくつかは診断アッセイで使用する。乳癌タンパク質、抗体、核酸、改変タンパク質および乳癌配列を含んでいる細胞を診断アッセイで使用する。これは、個々の遺伝子または相当するポリペプチドレベル上で行いうる。好ましい実施様態において、好ましくはハイスループットスクリーニング技術と関連して発現プロファイルを使用し、遺伝子および/または相当するポリペプチドの発現に関するモニタリングを可能にする。

本明細書で記述し、概略したように、細胞内、膜貫通または分泌タンパク質を含む乳癌タ 50

ンパク質が乳癌のマーカーとして使用できることが見いだせる。推定される乳癌組織または患者でのこれらのタンパク質の検出によって、乳癌の決定または診断が可能である。当業者に公知の多くの方法が乳癌の検出で使用できることがわかる。1つの実施様態において、抗体を乳癌タンパク質を検出するのに使用する。好ましい方法は、ゲル上の電気泳動（典型的には変性および還元タンパク質ゲルであるが、等電点焦点ゲルのようなものを含む任意の他の型のゲルでもよい）によって試料または患者よりタンパク質を分離する。タンパク質の分離に続き、乳癌タンパク質を、乳癌タンパク質に対して作製した抗体での免疫ブロッティングによって検出する。免疫ブロッティングの方法は当業者に良く公知である。

他の好ましい方法において、乳癌タンパク質に対する抗体は、*in situ* イメージング技術で使用できることがみいだせる。この方法において、細胞を、乳癌タンパク質（類）に対する1つ〜多くの抗体と接触させる。非特異的抗体結合を取り除くための洗浄に続き、抗体または抗体類の存在を検出する。1つの実施様態において、抗体は検出可能な標識を含む二次抗体とインキュベートすることによって検出する。他の方法では、乳癌タンパク質（類）に対する一次抗体が検出可能な標識を含む。他の好ましい実施様態において、それぞれ1つの多重一次抗体が異なる検出可能な標識を持つ。この方法で、多数の乳癌タンパク質に対する同時スクリーニングでの特別な使用がみいだせる。当業者に理解されるであろうように、多くの他の組織学的イメージング技術が本発明で有用である。

好ましい実施様態において、標識は異なる波長の放射を検出および区別することができる分光計で検出する。さらに、蛍光活性化細胞ソーター（FACS）も本方法で使用する。

他の好ましい実施様態において、抗体は、血液試料からの乳癌の診断において使用できることが見いだせる。すでに記載したように、ある乳癌タンパク質は分泌／循環分子である。したがって、血液試料は、分泌乳癌タンパク質に関してプローブし、試験するための試料として有用である。抗体は、当業者によって理解されるであろうように、ELISA、免疫ブロッティング（ウェスタンブロッティング）、免疫沈降、BIACORE技術などの任意のすでに記載した免疫アッセイ技術によって乳癌を検出するのに使用できる。

好ましい実施様態において、組織アレイに対する標識化乳癌核酸プローブの*in situ* ハイブリッド形成を行う。たとえば、乳癌組織および／または正常組織を含む組織試料のアレイを使用する。そして本技術分野で公知のような*in situ* ハイブリッド形成を行う。

個々そして標準間の識別特徴を比較した場合に、当業者が診断および予後を行うことが可能であることが理解される。さらに、診断を示す遺伝子が、予後を示唆するものと異なっておりことが理解される。

好ましい実施様態において、乳癌タンパク質、抗体、核酸、改変タンパク質および乳癌配列を含んでいる細胞を予後アッセイに使用する。上記のように、長期予後に関して遺伝子発現プロファイルは、乳癌のひどさに相関して生成されうる。さらに、このことは、タンパク質または遺伝子レベルのどちらかで行ってよく、遺伝子の使用が好ましい。上記のように、乳癌プローブを組織または患者における乳癌配列の決定および定量的ためにバイオチップに結合させる。アッセイは診断に関して概略したように実施する。

好ましい実施様態において、本明細書で記述したような任意の3種類のタンパク質を薬品スクリーニングアッセイで使用する。乳癌タンパク質、抗体、核酸、改変タンパク質および乳癌配列を含んでいる細胞を、薬品スクリーニングアッセイで使用する、または薬品候補物の「遺伝子発現プロファイル」またはポリペプチドの発現プロファイルにおける効果を評価することで使用する。好ましい実施様態において、好ましくはハイスループットスクリーニング技術と関連して発現プロファイルを使用し、候補薬品で処置した後の遺伝子の発現プロファイルについてモニタリングすることを可能にする。Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 # 69。

好ましい実施様態において、乳癌タンパク質、抗体、核酸、改変タンパク質および天然の

または改変した乳癌タンパク質を含んでいる細胞をスクリーニングアッセイで使用する。したがって、本発明は、乳癌表現型を調節する組成物に関するスクリーニングのための新規方法を提供する。上述のように、このことは個々の遺伝子レベル上で、または薬品候補の「遺伝子発現プロファイル」における効果を評価することによって行うことができる。好ましい実施形態において、発現プロファイルを、好ましくはハイスループットスクリーニング技術と関連させて使用し、候補薬剤で処置した後の遺伝子の発現プロファイルに関してモニタリングすることを可能にする。上記 Z l o k a r n i k を参照のこと。

ここで差動的に発現される遺伝子が同定されたので、いろいろな分析を実行することができる。ある好ましい実施形態では、分析は個々の遺伝子又はタンパク質レベルについて行われる。すなわち、ある特定遺伝子が乳癌でアップレギュレートされると同定されたら、この遺伝子の応答を変調する仕方で、好ましくはこの遺伝子をダウンレギュレートするように、しかし場合によってはこの遺伝子をアップレギュレートするように候補生物活性物質がスクリーニングされる。“変調”とは、このように遺伝子発現の増加も減少も含む。好ましい変調の量は、正常組織と腫瘍組織を比較したときの元の遺伝子発現の差に依存し、差は少なくとも10%、好ましくは50%、さらに好ましくは100-300%、実施形態によっては300-1000%以上、になる。すなわち、ある遺伝子が正常組織に比べて腫瘍組織で4倍の増加を示す場合、約4分の1の減少が望ましく、正常組織に比べて腫瘍組織での発現が10分の1の減少を示す場合、候補物質での発現は10倍の増加が望ましいということになる。

当業者には理解できるように、これは遺伝子レベルで評価して行うこともタンパク質レベルで評価して行うこともできる。すなわち、核酸プローブを用い遺伝子発現レベルを定量化することによって遺伝子発現の量をモニターすることも、あるいは遺伝子産物そのものを、例えば乳癌タンパク質の抗体を用い標準的な免疫分析によって、モニターすることもできる。

ある好ましい実施形態では、遺伝子発現のモニタリングを行っていくつかの遺伝子すなわち、発現プロファイル、が同時にモニターされるが、複数のタンパク質発現のモニタリングも行うことができる。

この実施形態では、ある特定細胞における乳癌シーケンスの検出と定量化のために乳癌核酸プローブがここで述べたバイオチップに装着される。この分析については以下でさらに詳しく述べる。

一般に、好ましい実施形態では、候補の生物活性物質が分析の前に細胞に加えられる。さらに、スクリーニングを行って、乳癌を変調する、乳癌タンパク質を変調する、乳癌タンパク質と結合する、あるいは乳癌タンパク質と抗体の結合を妨害する生物活性物質候補が同定される。

本明細書において用いられる“生物活性物質候補”又は“薬剤候補”という用語、又は文法的に同等なもの、は、何らかの分子、例えばタンパク質、オリゴペプチド、小さな有機分子、多糖類、ポリヌクレオチド、等であって、直接又は間接に乳癌表現型又は乳癌シーケンス（核酸シーケンスもタンパク質シーケンスも含む）の発現を変化させることができる生物活性物質かどうかテストされるもの、を指す。好ましい実施形態では、生物活性物質は、発現プロファイル、又は本明細書で述べる発現プロファイル核酸又はタンパク質、を変調する。特に好ましい実施形態では、候補物質は乳癌表現型を抑制する、例えば正常な乳組織と同じフィンガープリントにまで、抑制するものである。同様に、候補物質は好ましくは重症な乳癌表現型を抑制する。一般に、いろいろな濃度に対する応答の差を明らかにするために、異なる物質濃度で複数の分析ミックスが平行して行われる。普通、それらの濃度の一つはネガティブ対照として、すなわち、ゼロ濃度又は検出不可能なレベルで、用いられる。

候補物質には多くの化学的な部類が含まれるが、普通は有機分子、好ましくは分子量が100ダルトンより大きく約2500ダルトン未満の小さな有機化合物、である。好ましい小分子は2000D未満、又は1500D未満、又は1000D未満、又は500D未満、である。候補物質はタンパク質との構造的な相互作用、特に水素結合、に必要な機能グ

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ループを含み、普通少なくともアミン、カルボニル、ヒドロキシル又はカルボキシル基を含み、好ましくは少なくとも二つの機能的な化学基を含む。候補物質は、しばしば、環式炭素又は複素環式構造及び／又は芳香族又はポリ芳香族構造を一つ以上の上記機能グループで置換したものを含む。候補物質は、また、ペプチド、糖類、脂肪酸、ステロイド、プリン、ピリミジン、それらの誘導体、構造類似物又は組み合わせ、などの生体分子の間にも見られる。特に好ましいものはペプチドである。

候補物質は、合成又は天然の化合物のライブラリーなど、多種多様な源から得られる。例えば、いろいろな有機化合物及び生体分子のランダム及び有向合成の手段は、ランダムなオリゴヌクレオチドの発現を含めて多数ある。あるいはまた、バクテリア、菌類、植物及び動物からの抽出物という形の天然化合物のライブラリーが利用できる又は容易に作成できる。さらに、天然又は合成物質のライブラリー及び化合物は、通常の化学的、物理的、及び生化学的な手段によって容易に修飾される。既知の薬剤物質に対して、アシル化、アルキル化、エステル化、アミド化など、有向又はランダムな化学的修飾を行って構造的な類似体を生成することができる。

ある好ましい実施形態では、候補生物活性物質はタンパク質である。本明細書では、“タンパク質”という用語で、共有結合で付着した少なくとも二つのアミノ酸を意味し、タンパク質、ポリペプチド、オリゴペプチド、及びペプチドを含む。タンパク質は、天然に見られるアミノ酸及びペプチド結合で構成されることも、合成のペプチド類似構造で構成されることもある。本明細書で用いられる“アミノ酸”又は“ペプチド残基”という用語は、天然に見られるアミノ酸と合成のアミノ酸の両方を意味する。例えば、本発明の目的には、ホモフェニルアラニン、シトルリン、ポラロイシンはアミノ酸と見なされる。“アミノ酸”は、また、プロリンやヒドロキシプロリンなど、イミノ酸残基も含む。側鎖は（R）配置でも（S）配置でも良い。好ましい実施形態では、アミノ酸は（S）又はL-配置である。天然には見られない側鎖が用いられる場合、例えば生体での分解を防ぐ又は遅らせるために非アミノ酸置換基を用いることがある。

ある好ましい実施形態では、候補生物活性物質は天然に見られるタンパク質又は天然に見られるタンパク質の断片である。従って、例えば、タンパク質を含む細胞抽出物、又はタンパク質様の細胞抽出物のランダム又は有向消化物、が用いられる。このようにして、原核細胞及び真核細胞のタンパク質のライブラリーを作成して本発明の方法でスクリーニングすることができる。この実施形態で特に好ましいのは、バクテリア、菌類、ウイルス、及び哺乳類のタンパク質のライブラリーであり、哺乳類が好ましく、ヒトのタンパク質が特に好ましい。

ある好ましい実施形態では、候補生物活性物質は、約5乃至約30アミノ酸から成るペプチドであり、約5乃至約20アミノ酸が好ましく、約7乃至約15アミノ酸が特に好ましい。ペプチドは、上述のような天然に見られるタンパク質の消化物であっても、ランダム・ペプチドであっても、“偏りのある”ランダム・ペプチドであってもよい。本明細書で用いられる“ランダム化された”という用語、又は文法的に同等なもの、は、各核酸又はペプチドが、それぞれ、本質的にランダムなヌクレオチド又はアミノ酸から成るということを意味する。一般に、これらのランダムなペプチド（又は、後で述べる核酸）は化学的に合成されるものであるから、どんなヌクレオチド又はアミノ酸をどんな位置に含むこともできる。ランダム化されたタンパク質又は核酸を生成し、全部又はほとんどの可能な組み合わせがシーケンスの長さによって形成されるように合成プロセスを設計して、ランダムな候補生物活性タンパク質様物質のライブラリーを作ることができる。

ある実施形態では、ライブラリーは完全にランダムであって、どの位置にも優先されるシーケンスや一定のシーケンスはない。ある実施形態では、ライブラリーは偏りがある。すなわち、シーケンスの中のある位置は一定に保たれるか、又は限られた数の可能性の中から選択される。例えば、ある好ましい実施形態では、ヌクレオチド又はアミノ酸残基は、一定の部類の中でランダム化され、例えば、疎水性アミノ酸、親水性残基、立体的に偏った（小さな又は大きな）残基、の範囲内で、核酸結合ドメインの形成、システインの形成、架橋のために、SH-3ドメインのためのプロリン、リン酸化のためのセリン、スレオ

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ニン、チロシン、又はヒスチジン、等を作る方向に、又はプリン等を作る方向に、ランダム化される。

ある好ましい実施形態では、候補生物活性物質は上で定義されたような核酸である。

上でタンパク質について一般的に述べたように、核酸の候補生物活性物質も、天然に見られる核酸、ランダムな核酸、又は“偏った”ランダムな核酸、がある。

上でタンパク質について述べたように、原核細胞又は真核細胞のゲノムの消化物を用いることもできる。

ある好ましい実施形態では、候補生物活性物質は有機化学分子であり、多種多様な有機化学分子が文献で利用できる。

候補物質を加えて、そのまま細胞をある時間培養した後、分析しようとする標的シーケンスを含むサンプルがバイオチップに加えられる。必要なら、標的シーケンスは既知の方法で調製される。当業者には理解されるように、例えば、サンプルを処理して既知の溶解バッファー、エレクトロポレーション、等を用いて細胞を溶かし、必要に応じてPCRを行って精製／増幅する。例えば、ヌクレオシドにラベルを共有結合で付着させてインビトロ (in vitro) 転写を行う。一般に、核酸はビオチン-FITC又はPE、又はcy3又はcy5でラベルされる。 10

ある好ましい実施形態では、プローブと標的シーケンスの特異的結合を検出する手段を提供するために、標的シーケンスは蛍光、化学発光、化学的、又は放射性信号でラベルされる。ラベルは、また、アルカリ性ホスファターゼ、ホースラディッシュ・ペルオキシダーゼなどの酵素であってもよく、これらは適当な基質が与えられれば検出できる生成物を生ずる。あるいはまた、ラベルは、結合するが酵素によっては触媒又は変性されない酵素阻害物質などの標識された化合物または小さな分子であってもよい。ラベルはまた、エピトープ・タグ又はストレプトタビジンと特異的に結合するビオチンなど、半量の化合物であってもよい。ビオチンの例では、ストレプトタビジンが上述のようにラベルされて、結合した標的シーケンスを検出できる信号を提供する。当業者には公知のように、分析の前に結合しないラベルされたストレプトタビジンが除去される。 20

当業者には理解されるように、この分析は、直接のハイブリダイゼーション分析であっても、複数のプローブを用いる“サンドウィッチ分析”であっても良く、後者については、米国特許第5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, 及び 5,681,697号に一般的に記載されており、これらは全てここで参照することによって本明細書に取り込まれる。この実施形態では、一般に、核酸が上述のように調製され、ハイブリダイゼーション複合体の形成を可能にする条件の下で、複数の核酸プローブを含むバイオチップに加えられる。 30

本発明では、上述のように高、中及び低ストリンジェンシー条件を含むいろいろなハイブリダイゼーション条件が用いられる。分析は一般に、標的の存在下でのみラベル・プローブ・ハイブリダイゼーション複合体の形成が可能になるようなストリンジェンシー条件の下で行われる。ストリンジェンシーは、温度、フォルムアミド濃度、塩濃度、カオトロピック塩濃度 pH、有機溶剤濃度、等、これだけに限定されないが、熱力学的変数であるステップ・パラメータを変えることによって制御される。 40

これらのパラメータは、また、非特異的な結合を制御するのににも利用される。これは、米国特許第5,681,697号に一般的に述べられている。したがって、非特異的な結合を減少させるためにいくつかのステップを高いストリンジェンシー条件の下で行うことが望ましいかもしれない。

当業者には理解されるように、本明細書で述べる反応はいろいろな仕方で遂行することができる。反応の成分は、同時に加えても、任意の順序で順次加えてもよいが、好ましい実施形態は以下で述べる。さらに、分析では、他のいろいろな試薬も反応に含まれる。それらは、塩、緩衝剤、中性タンパク質、例えばアルブミン、洗浄剤、等の試薬であり、最適 50

なハイブリダイゼーション及び検出を助け、及び／又は、非特異的な又はバックグラウンド相互作用を減らすために用いられることがある。その他に分析の効率を高める試薬、例えばプロテアーゼ阻害因子、ヌクレアーゼ阻害因子、抗菌剤、等も、サンプル調製方法や標的の純度によっては用いられることがある。

分析を行ったら、データを解析して、発現レベル、状態間の発現レベルの差を個々の遺伝子について決定して、遺伝子発現プロファイルが作成される。

スクリーニングを行って、乳癌表現型を変調する薬剤又は生物活性物質を同定する。具体的には、いくつかのタイプのスクリーニングを行うことができる。好ましい実施形態は、ある特定発現プロファイルを誘発又は抑制することができ、好ましくは関連表現型を生成する候補物質のスクリーニングである。すなわち、正常乳組織の発現プロファイルと同様な発現プロファイルを乳癌において模倣又は生成できる候補物質は、乳癌表現型の抑制につながると期待される。このように、この実施形態では、ある発現プロファイルを模倣すること、又はあるプロファイルを別のプロファイルに変えることが目標である。

ある好ましい実施形態では、診断及び予後判定への応用の場合のように、何らかの状態で重要な差動的に発現する遺伝子を同定したら、スクリーニングは遺伝子の発現を個別に変化させるように行うことができる。すなわち、ある単一遺伝子の発現の調節の変調に関してスクリーニングすることができる；すなわち、ある発現プロファイルの全部又は一部を模倣しようとするのではなく、個別遺伝子の調節に関するスクリーニングを行うことができる。例えば、特に標的遺伝子が存在するかどうか二つの状態の間でユニークである標的遺伝子の場合、標的遺伝子の発現の変調因子に関するスクリーニングが行われる。

ある好ましい実施形態では、スクリーニングは、差動的に発現される遺伝子の発現産物の生物学的機能を変化させるように行われる。やはり、ある特定状態におけるある遺伝子の重要性が同定されたら、その遺伝子産物に結合する及び／又はその生物活性を変調する物質に関するスクリーニングを以下で詳しく述べるように行うことができる。

すなわち、遺伝子発現レベル又はタンパク質レベルで乳癌表現型を変調する候補物質のスクリーニングを行うことができる。

さらに、候補物質に応答して誘導される新しい遺伝子に関するスクリーニングも行うことができる。乳癌発現パターンを抑制して正常発現パターンにする能力、又は単一乳癌遺伝子の発現プロファイルを変調して正常組織からの遺伝子の発現を模倣させる能力に基づいてある候補物質を同定した後、その物質に応答して特異的に変調される遺伝子を同定するために上述のようなスクリーニングを行うことができる。正常組織とその物質で処理された乳癌組織の発現プロファイルを比較することによって、正常組織又は乳癌組織では発現されないが、その物質で処理された組織で発現される遺伝子が明らかにされる。乳癌遺伝子又はタンパク質について本明細書で述べた方法によって、これらの物質特異的シーケンスを同定し利用することができる。特に、これらのシーケンス及びそれがコード化しているタンパク質はその物質で処理された細胞をマークしたり同定したりするのに利用できる。さらに、その物質で誘導されたタンパク質に対する抗体を見つけて、新しい治療法の標的を処理された乳癌組織サンプルに絞るのに用いることができる。

このように、ある実施形態では候補物質がある乳癌細胞集団に投与され、それは関連乳癌発現プロファイルをもつことになる。本明細書で用いる“投与”又は“接触”という用語は、候補物質が、細胞に対して、取り込まれて細胞内部で作用する形であれ、細胞表面で作用する形であれ、作用を及ぼすことができるような仕方で細胞に加えられることを意味する。いくつかの実施形態では、タンパク質様の候補物質（すなわち、ペプチド）をコードする核酸は、レトロウイルス構造などのウイルス構造にして細胞に加えてペプチド物質の発現が遂行されるようにする；PCT US 97/01019を参照、これは、ここで参照することにより本明細書にはっきりと取り込まれる。

候補物質が細胞に投与されたら、細胞は、所望するなら洗浄して、好ましくは生理的条件下である期間培養させる。その後、細胞を収穫して、新しい遺伝子発現プロファイルをここで述べているように生成する。

このようにして、例えば、乳癌組織をスクリーニングして乳癌表現型を減少又は抑制する

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物質を探ることができる。少なくとも一つの遺伝子における発現プロファイルの変化は、その物質が乳癌に影響を及ぼすことを示す。乳癌表現型に関するこのようなシグナチャーを定めることによって、表現型を変化させる新しい薬剤のためのスクリーニングを考案することができる。このアプローチでは、薬剤のターゲットを知る必要はなく、最初の発現スクリーニング・プラットフォームに表す必要もなく、ターゲット・タンパク質の転写レベルが変化する必要もない。

上述のように、ある好ましい実施形態では、スクリーニングは個々の遺伝子および遺伝子産物（タンパク質）について行うことができる。すなわち、ある特定の差動的に発現される遺伝子がある特定状態で重要であると同定したら、その遺伝子の発現又は遺伝子産物自身の変調因子のスクリーニングを行うことができる。差動的に発現される遺伝子の遺伝子産物は、本明細書において、“乳癌タンパク質”、“乳癌変調タンパク質”、“BCP”、又は“BCMP”と呼ばれることがある。ある実施形態では、BCMPはBCH1と呼ばれる。ある実施形態では、BCH1は、ここで乳癌タンパク質の同定について述べたように同定することができる。ある好ましい実施形態では、BCH1は図34に示されている。BCMPは、断片であっても、あるいはここに示された断片に対する全長タンパク質であってもよい。好ましくは、BCMPはほぼ14乃至24アミノ酸という長さの断片である。さらに好ましくは、BCMPは可溶性の断片である。

本明細書における別の好ましい実施形態では、乳癌タンパク質又は乳癌タンパク質をコードする核酸は、図に示されているシーケンスから、アクセス番号が示されているものも含めて、選択される。好ましいシーケンスは図10にあり、さらに好ましくは図11にあり、最も好ましくは図12にある。好ましいシーケンスは、また、BCH1、BCA2、BCJ7、BCN1、BCN5、BCO2、BCQ5、BCR2、BCR3、BCO8、BCN2、BCX3、BCX2及びBCY3から成る群から選択される。最も好ましくは、シーケンスはBCH1、BCA2、BCJ7、BCN1、BCN5、BCO2、BCQ5、BCR2、BCX2及びBCY3から成る群から選択される。タンパク質は、このタンパク質の群の任意の部分集合から選択することもできる、例えばBCH1は群全体から選択することも、BCH1とBCN1という部分集合から選択することもできる、ということと言うまでもない。

ある実施形態では、乳癌タンパク質はここで述べられる免疫原物質と結合している。ある実施形態では、乳癌タンパク質はBSAと結合している。

すなわち、ある好ましい実施形態では、複数の特定遺伝子の発現変調因子のスクリーニングを行うことができる。これは上述のように行われるが、しかし一般には唯一つ又は少数の遺伝子の発現だけが評価される。

ある好ましい実施形態では、スクリーニングが、まず差動的に発現されるタンパク質に結合できる候補物質を見つけるように設計され、次にそれらの物質を用いて、候補物質が差動的に発現される活性を変調する能力を評価する分析を行う。したがって、当業者には理解できるように、いくつかの異なる分析が、すなわち、結合分析と活性分析が、行われる。

ある好ましい実施形態では、結合分析が行われる。一般に、精製又は単離された遺伝子産物が用いられる；すなわち、一つ以上の差動的に発現される核酸の遺伝子産物が作られる。一般に、これは当業者には公知の方法で行われる。例えば、そのタンパク質遺伝子産物に対する抗体を生成し、標準的な免疫分析を行ってタンパク質の存在量を決定する。あるいはまた、乳癌タンパク質を含む細胞を分析に用いることもできる。

すなわち、ある好ましい実施形態では、方法は、乳癌タンパク質と候補生物活性物質を結合するステップと、乳癌タンパク質への候補物質の結合を決定するステップとを含む。好ましい実施形態はヒトの乳癌タンパク質が用いるが、他の哺乳類タンパク質も、例えばヒトの疾病の動物モデルを開発するために、用いることができる。本明細書で述べるいくつかの実施形態では、乳癌タンパク質の変異体又は誘導体が用いられる。

一般に、本明細書におけるこの方法の好ましい実施形態では、乳癌タンパク質又は候補物質は、隔離されたサンプル受容区域を有する不溶性サポートに（例えば、マイクロタイタ

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・プレート、アレー、等) 拡散しないように結合される。不溶サポートは、組成物が結合できるどんな組成でもよく、可溶物質から容易に分離され、その他の点でもスクリーニングの方法全体と共用できるものである。このようなサポートの表面は、固体又は多孔質であり、好適な形を有する。適当な不溶性のサポートの例としては、マイクロタイタ・プレート、アレー、膜、ビーズ、などがある。これらは普通、ガラス、プラスチック（例えば、ポリスチレン）、多糖類、ナイロン、ニトロセルローズ、テフロン（商標）、等から作られる。マイクロタイタ・プレート、及びアレーは少量の試薬とサンプルを用いて多数の分析を同時に行うことができるので特に好都合である。試薬及び本発明の方法全体と両立でき、組成物の活性が保たれ、拡散しないものであれば組成物の具体的な結合の仕方は重要でない。好ましい結合方法には、抗体の利用（これはタンパク質がサポートに結合したときに、リガンド結合部位も活性シーケンスも立体的にブロックしない）、“粘着性の”又はイオン性のサポートへの直接結合、化学的架橋、表面でのタンパク質又は作用物質の合成、などがある。タンパク質又は物質の結合の後、過剰な結合していない物質は洗浄によって除去される。サンプル受容部はその後ウシ血清アルブミン（BSA）、カゼイン、又は他の無害なタンパク質又は他の半量体と共にインキュベーションすることでブロックされる。

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ある好ましい実施形態では、乳癌タンパク質がサポートに結合され、候補生物活性物質が分析に加えられる。あるいはまた、候補物質がサポートに結合され、乳癌タンパク質がそれに加えられる。新しい結合物質としては、特異的抗体、化学ライブラリーのスクリーニングで同定された非天然結合物質、ペプチド類似体、などがある。特に興味深いのは、ヒトの細胞に対する毒性が低い物質に関するスクリーニング分析である。この目的にいろいろな分析を用いることができる、例えば、標識インビトロ・タンパク質-タンパク質結合分析、電気泳動移動度シフト分析、タンパク質結合に関する免疫分析、機能的分析（リン酸化分析、等）、などがある。

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乳癌タンパク質との候補生物活性物質の結合はいくつかの仕方で行うことができる。ある好ましい実施形態では、候補生物活性物質をラベルで標識して結合を直接測定する。例えば、これは乳癌タンパク質の全部又は一部を固体サポートに付着させ、ラベル標識（例えば、蛍光ラベル）された候補物質を加え、固体サポートにラベルが存在するかどうかを決定することで行うことができる。当業者には周知のいろいろなブロック及び洗浄ステップが用いられる。

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本明細書では“標識された”という用語は、化合物が直接又は間接に、検出可能な信号を与えるラベル、例えば、放射性同位元素、蛍光物質、酵素、抗体、磁性粒子などの粒子、化学発光物質、又は特異的結合分子、などで標識されることを意味する。特異的結合分子には、対、例えばビオチンとストレプトタビジン、ダイオキシシンとアンチダイオキシシン、などの対が含まれる。特異的結合メンバーでは、通常、相補的メンバーが上述のように既知の手順に従って検出できるような分子で標識される。ラベルは直接又は間接に検出できる信号を与える。

いくつかの実施形態では、一方の成分だけがラベル標識される。例えば、タンパク質（又はタンパク質様候補物質）は、チロシンの位置で^{1 2 5} Iを用いて、又は蛍光体によって標識できる。あるいはまた、二つ以上の成分を異なるラベルで標識することもできる：例えばタンパク質を^{1 2 5} Iを用いて標識し、候補物質を蛍光体で標識することができる。ある好ましい実施形態では、候補生物活性物質の結合は競合結合分析を用いて決定される。この実施形態では、競合物質は標的分子（すなわち、乳癌）に結合することが知られている結合半片、例えば、抗体、ペプチド、結合パートナー、リガンド、等、である。場合によっては、生物活性物質と結合半片との間に競合的な結合が行われて結合半片が生物活性物質を追い出してしまう。

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ある実施形態では、候補生物活性物質がラベル標識される。まず、候補生物活性物質、又は競合物質、又はその両方、がタンパク質に、結合があるならそれを可能にするに十分な時間加えられる。インキュベーションは、活性を最適にする任意の温度、普通4から40℃の間、で行われる。インキュベーション時間は活性を最適にするように選ばれるが、迅

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速で高効率のスクリーニングができるようにも最適化される。普通、0.1から1時間までの間で十分である。過剰な試薬は、一般に、除去又は洗い流される。次に第二の成分を加え、ラベル標識された成分が存在するかどうかを追跡して結合を示す。

ある好ましい実施形態では、競合物質が最初に加えられ、その後で候補生物活性物質が加えられる。競合物質が追い出されることが、候補生物活性物質が乳癌タンパク質に結合しており、したがって、乳癌タンパク質に結合することができ、その活性を変調できるということを示す証左である。この実施形態では、どちらの成分をラベル標識することもできる。すなわち、例えば、競合物質をラベル標識した場合、洗浄溶液中にラベルが存在することが生物活性物質による追い出しを示す。あるいは、生物活性物質をラベル標識した場合、サポートにラベルが存在することが追い出しを示す。

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別の実施形態では、候補生物活性物質が最初に加えられ、インキュベーションと洗浄が行われ、その後競合物質が加えられる。競合物質による結合が存在しないことは、生物活性物質が乳癌タンパク質に高い親和度で結合していることを示すであろう。したがって、もしも候補生物活性物質をラベル標識した場合、サポートにラベルが存在することは、競合物質の結合が見られないことと合わせて、候補生物活性物質が乳癌タンパク質と結合できるということを示す。

ある好ましい実施形態では、この方法は乳癌タンパク質の活性を変調できる生物活性物質を同定する差動的なスクリーニングを含む。この実施形態では、方法は、第一のサンプルで乳癌タンパク質と競合物質を結合させるステップを含む。第二のサンプルは、候補生物活性物質、乳癌タンパク質、及び競合物質を含む。両方のサンプルについて競合物質の結合を測定すると、二つのサンプルの間の結合の変化又は差が、乳癌タンパク質に結合でき、その活性を変調する可能性がある物質の存在を示す。すなわち、競合物質の結合が第一のサンプルに比べて第二のサンプルで異なる場合、その生物活性物質は乳癌タンパク質に結合できる。

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あるいはまた、ある好ましい実施形態は差動的スクリーニングを用いて、自生乳癌タンパク質には結合するが、変性した乳癌タンパク質には結合しない薬剤候補を同定する。乳癌タンパク質の構造をモデル化し、合理的な薬剤デザインでそれを用いてその部位と相互作用する物質を合成することができる。乳癌の活性に影響を及ぼす薬剤候補も、そのタンパク質の活性を強化又は減少させる能力に関して薬剤をスクリーニングして同定される。

分析ではポジティブ対照とネガティブ対照が用いられる。統計的に有意な結果を得るために、全ての対照及びテスト・サンプルは、少なくとも三重にして調べるのが好ましい。全てのサンプルのインキュベーションは、タンパク質への物質の結合に十分な時間にわたって行う。インキュベーションの後、全てのサンプルを洗浄して非特異的に結合した物質を除去して結合した、一般にラベル標識された、生物活性物質の量を決定する。例えば、放射性標識を用いる場合、サンプルをシンチレーション・カウンタで計測したがって結合した化合物の量を決定する。

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スクリーニング分析には他のいろいろな試薬が含まれる。それは例えば、最適なタンパク質-タンパク質結合を助けるために及び／又は非特異的なバックグラウンド相互作用を減らすために用いられる塩、中性タンパク質、例えば、アルブミン、洗浄剤、などの試薬である。また、別の仕方で分析の効率を高める試薬、例えばプロテアーゼ阻害物質、ヌクレアーゼ阻害物質、抗菌剤、等も用いられることがある。成分の混合物は必要な結合を可能にするようなどんな順序で加えてもよい。

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乳癌タンパク質の活性を変調する作用物質のスクリーニングも行うことができる。ある好ましい実施形態では、乳癌タンパク質の活性を変調できる生物活性物質をスクリーニングする方法は、上記のように乳癌タンパク質のサンプルに候補生物活性物質を加えるステップと、乳癌タンパク質の生物活性の変化を決定するステップとを含む。“乳癌の活性を変調すること”には、活性の増加、活性の減少、又は存在している活性のタイプや種類の変化も含まれる。したがって、この実施形態では、候補作用物質は乳癌タンパク質に結合し（これは必要でないかもしれない）、かつ、ここで定義したようにその生物活性又は生化学活性を変化させなければならない。方法は、上で一般的に述べたようなインビトロ（i

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n v i t r o)・スクリーニング方法と、乳癌タンパク質の存在、分布、活性、又は量の変化を細胞で調べるインビボ (i n v i v o)・スクリーニングとを含む。

すなわち、この実施形態では、方法は、乳癌サンプルと候補生物活性物質を結合させるステップと、乳癌活性への影響を評価するステップとを含む。本明細書における“乳癌活性”という用語、又は文法的にそれと同等なもの、は、細胞分裂、好ましくは乳組織におけるもの、細胞増殖、腫瘍増殖、細胞の形質転換、など、ただしそれだけに限定されない乳癌の生物的活動の一つを意味する。ある実施形態では、乳癌活性は、乳癌タンパク質、例えば B C H 1, の活性化又は乳癌タンパク質によるその基質の活性化、を含む。乳癌活性の阻害因子とは一つ以上の乳癌活性の阻害である。

ある好ましい実施形態では、乳癌タンパク質の活性は増加し、別の好ましい実施形態では、乳癌タンパク質の活性は減少する。すなわち、ある実施形態では拮抗物質である生物活性物質が好ましく、別の実施形態では作用物質である生物活性物質が好ましい。

ある好ましい実施形態では、本発明は乳癌タンパク質の活性を変調できる生物活性物質をスクリーニングする方法を提供する。この方法は、上で定義されたような候補生物活性物質を乳癌タンパク質を含む細胞に加えるステップを含む。好ましい細胞のタイプは、ほとんどすべての細胞を含む。細胞は、乳癌タンパク質をコードする組み換え核酸を含む。ある好ましい実施形態では、候補作用物質のライブラリーが複数の細胞でテストされる。

ある態様では、分析は、生理的信号、例えばホルモン、抗体、抗原、サイトカイン、成長因子、作用電位、化学療法を含む薬理物質、放射線、発癌物質、又は他の細胞（すなわち、細胞-細胞接触）、などの存在、又は不在、又は事前又は事後の曝露、という条件下で評価される。別の例では、細胞サイクルの過程の異なる段階で決定が行われる。

このようにして生物活性物質が同定される。薬理活性を有する化合物は乳癌タンパク質の活性を強化したり、又は妨害したりできる。ある実施形態では、この中で用いられる“乳癌タンパク質活性”という語は、以下の少なくとも一つを含む：乳癌活性、乳癌タンパク質との結合、乳癌タンパク質の活性化、又は乳癌タンパク質による乳癌タンパク質の基質の活性化。

ある実施形態では、乳癌の細胞分裂を阻害する方法が提供される。この方法は乳癌阻害物質の投与を含む。

中和とは、あるタンパク質の活性を阻害又はそれに対抗して実質的に細胞に何も影響しないようにすることを意味する。

別の実施形態では、腫瘍の成長を阻害する方法が提供される。この方法は乳癌阻害物質の投与を含む。

さらに別の実施形態では、癌を有する細胞又は人を治療する方法が提供される。この方法は乳癌阻害物質の投与を含む。

ある実施形態では、乳癌阻害物質は上述のような抗体である。別の実施形態では、乳癌阻害物質はアンチセンス分子である。本明細書で用いるアンチセンス分子という用語は、標的の乳癌分子の m R N A (センス)又は D N A (アンチセンス)と結合できる単一鎖核酸シーケンス (R N A 又は D N A) から成るアンチセンス又はセンス・オリゴヌクレオチドを含む。好ましいアンチセンス分子は B C H 1 又はそのリガンド又は活性化剤に関するものである。本発明によると、アンチセンス又はセンス・オリゴヌクレオチドは一般に少なくとも約 1 4 ヌクレオチド、好ましくは約 1 4 乃至 3 0 ヌクレオチドの断片を含む。与えられたタンパク質をコードする c D N A シーケンスに基づいてアンチセンス又はセンス・オリゴヌクレオチドを誘導できる方法は、例えば、Stein and Cohen (Cancer Res. 48:2659, 1988) 及び van der Kroel et al (BioTechniques 6.958, 1988) に記述されている。

アンチセンス分子は、W O 9 1 / 0 4 7 5 3 に記載されているように、リガンド結合分子との接合体を形成することによって標的ヌクレオチド・シーケンスを含む細胞に導入することができる。適当なリガンド結合分子は、細胞表面受容体、成長因子、他のサイトカイン、又は細胞表面受容体に結合する他のリガンド、などであるが、それだけに限定されない。リガンド結合分子との接合は、リガンド結合分子がその対応する分子又は受容体と結

合する能力を実質的に妨げたり、センス又はアンチセンス・オリゴヌクレオチド又はその複合体が細胞に入るのをブロックしたりしないことが好ましい。あるいはまた、センス又はアンチセンス・オリゴヌクレオチドを、WO 90/10448に記載されているように、オリゴヌクレオチド脂質複合体を形成することによって標的ヌクレオチド・シーケンスを含む細胞に導入することもできる。上述のようなスクリーニング分析において、処理の方法の他に、アンチセンス分子又はノックアウト又はノックイン・モデルも利用できることは言うまでもない。

所望の薬理活性を有する化合物は、前述のように、生理的に受容できるキャリアによってホストに投与することができる。作用物質はいろいろな仕方で、経口的に、非経口的に、例えば皮下注射で、腹腔内投与で、血管内注入、等により、投与できる。導入の仕方によって、化合物はいろいろな仕方で調合される。調合物の中の治療的に効力ある化合物の濃度は、約0.1-100重量%にわたっている。作用物質は単独で、又は他の治療、例えば放射線と組み合わせて、投与される。

医薬組成物は、顆粒、錠剤、ピル、座薬、カプセル、懸濁剤、軟膏、ローション、などいろいろな形で調製できる。経口及び局所施用に適した医薬等級の有機又は無機のキャリア及び／又は希釈剤を用いて治療的に活性な化合物を含む組成物を構成することができる。当業者に公知の希釈剤は、水性媒質、植物及び動物の油脂、などである。安定化剤、加湿剤及び乳化剤、浸透圧を変えるための塩、又は十分なpH値を確保するための緩衝剤、及び皮膚浸透強化剤などを補助剤として用いることができる。

理論には拘束されないが、乳癌ではいろいろな乳癌シーケンスが重要であるように思われる。それにより、乳癌遺伝子の突然変異体又は変異体に基づく疾患を決定することができる。ある実施形態では、本発明は乳癌遺伝子変異体を含む細胞を同定する方法を提供し、その方法は細胞における少なくとも一つの乳癌遺伝子のシーケンスの全部又は一部を決定するステップを含む。当業者には理解されるように、これはいくつかのシーケンス決定方法を用いて行うことができる。ある好ましい実施形態では、本発明はある個人の乳癌遺伝子型を同定する方法を提供し、その方法は少なくとも一つのその人の乳癌遺伝子のシーケンスの全部又は一部を決定するステップを含む。これは一般に、少なくとも一つのその人の組織で行われ、いくつかの組織の評価又は同じ組織のいろいろなサンプルの評価も含む。この方法は、シーケンス決定された乳癌遺伝子のシーケンスを既知の乳癌遺伝子、すなわち野生型の遺伝子、と比較するステップを含むことがある。

その場合、その乳癌遺伝子の全部又は一部のシーケンスを既知の乳癌遺伝子のシーケンスと比較して差があるかどうかを決定することができる。これはいくつかの既知の相同（ホモロジー）プログラム、例えばBestfit、等、を用いて行うことができる。ある好ましい実施形態では、患者の乳癌遺伝子と既知の乳癌遺伝子のシーケンスの差が、ここで述べているように、疾病状態又は疾病状態の傾向を示す。

ある好ましい実施形態では、乳癌遺伝子をプローブとして用いてゲノムにおける乳癌遺伝子のコピーの数を決定する。

別の好ましい実施形態では、乳癌遺伝子をプローブとして用いて乳癌遺伝子の染色体上の位置を決定する。染色体上の位置などの情報は、特にトランスロケーションなどの染色体異常が乳癌遺伝子の座に同定されたとき、診断又は予後判定に利用できる。

ある実施形態では、細胞又は生物における乳癌を変調する方法が提供される。ある実施形態では、この方法は、自生的な乳癌タンパク質の生物活性を低下又は消失させる抗乳癌抗体を細胞に投与するステップを含む。あるいは、この方法は、乳癌タンパク質をコードする組み換え核酸を細胞又は生物に投与するステップを含む。当業者には理解されるように、これはいくつかの仕方で行うことができる。ある好ましい実施形態では、例えば乳癌シーケンスが乳癌でダウンレギュレートされる場合、細胞内の乳癌の量を増加させることによって、例えば自生的な乳癌を過剰発現させること又は乳癌シーケンスをコードする遺伝子を、例えば公知の遺伝子治療法を用いて、投与することによって、乳癌遺伝子の活性が高められる。ある好ましい実施形態では、この遺伝子治療法は、例えばPCIT/US93/03868（これは参照によって全体がここに取り入れられる）に記載されているよう

な強化相同組み換え法（EHR）による外来遺伝子の組み込みを含む。あるいはまた、乳癌シーケンスが乳癌においてアップレギュレートされる場合、自生乳癌遺伝子の活性は、例えば乳癌アンチセンス核酸を投与することによって、減少する。

ある実施形態では、本発明の乳癌タンパク質を用いて、ここで述べたように有用な、乳癌タンパク質に対するポリクローナル及びモノクローナル抗体を生成することができる。同様に、乳癌タンパク質は、標準的な方法でアフィニティー・クロマトグラフィー・カラムに結合させることができる。このカラムは乳癌抗体を精製するのに利用できる。ある好ましい実施形態では、抗体は乳癌タンパク質にユニークなエピトープに生成される：すなわち、抗体は他のタンパク質に対する交差感受性をほとんど全く示さない。これらの抗体はいくつかの用途に利用できる。例えば、乳癌抗体は標準的なアフィニティー・クロマトグラフィー・カラムと結合させて、乳癌タンパク質を精製するのに利用できる。これらの抗体は乳癌タンパク質に特異的に結合するので、上述のように、ブロッキング・ポリペプチドとして用いることができる。

ある実施形態では、治療的に有効な量の乳癌又はそのモジュレーターが患者に投与される。本明細書で用いる“治療的に有効な量”とは、そのために投与される効果を生ずる用量を意味する。正確な用量は、治療の目的に依存し、当業者ならば公知の方法で確定することができる。当業者には周知であるが、タンパク質の分解、全身投与 v s . 局所投与、新しいタンパク質分解酵素の合成の速度、ならびに年齢、体重、全般的健康、性別、食事、投与時間、薬物相互作用、及び疾患の重症度、に関する調整が必要であり、当業者は日常的な試験によって確かめることができる。

本発明の目的では“患者”という用語にはヒト及び他の動物、特に哺乳類、及び生物が含まれる。すなわち、この方法は人間の治療及び獣医学の用途に適用できる。好ましい実施形態では、患者は哺乳類である。最も好ましい実施形態では、患者はヒトである。

本発明の乳癌タンパク質及びモジュレーターの投与は、上述のように、経口的に、皮下に、静脈内に、鼻腔内に、皮内注射で、腹腔内に、筋肉注射で、肺内に、子宮内に、直腸に、又は眼内に、などそれだけに限定されないいろいろな仕方で行うことができる。場合によっては、例えば、傷及び炎症の治療で乳癌タンパク質及びモジュレーターは溶液又はスプレーとして直接塗布することができる。

本発明の医薬組成物は、患者に投与するのに適当な形の乳癌タンパク質を含む。好ましい実施形態では、この医薬組成物は、酸及び塩基添加塩の両方を含め、医薬として許容できる塩として存在するような水溶性の形をしている。“医薬として許容できる酸添加塩”とは、自由な塩基の生物学的な効力を保ち、生物学的その他で望ましくないものではなく、塩酸、臭化水素酸、硫酸、硝酸、リン酸、などの無機酸、及び酢酸、プロピオン酸グリコール酸、ピルビン酸、蔞酸、マレイン酸、マロン酸、コハク酸、フマル酸、酒石酸、クエン酸、安息香酸、ケイ皮酸、マンデル酸、メタンスルホン酸、エタンスルホン酸、p-トールエンスルホン酸、サリチル酸、などの有機酸によって形成される塩を指す。“医薬として許容できる塩基添加塩”とは、ナトリウム、カリウム、リチウム、アンモニウム、カルシウム、マグネシウム、鉄、亜鉛、銅、マンガン、アルミニウム塩、などの無機塩基から誘導されるものを指す。特に好ましいのは、アンモニウム、カリウム、ナトリウム、カルシウム、及びマグネシウム塩である。医薬として許容できる有機無毒性塩基から誘導される塩としては、一次、二次、及び三次アミン、天然に見られる置換アミンを含めた置換アミン、環状アミン、及びイソプロピルアミン、トリメチルアミン、ジエチルアミン、トリエチルアミン、トリプロピルアミン、及びエタノールアミンなどの塩基性イオン交換樹脂、の塩がある。

医薬組成物はまた、次のものを一つ以上含むことがある：血清アルブミンなどのキャリア・タンパク質；緩衝剤；微結晶セルローズ、ラクトース、コーンその他の澱粉、などの充填剤；結合剤；甘味料及び他の芳香剤、着色剤；及びポリエチレングリコール。添加剤は当業者には周知であり、いろいろな調合で用いられる。

ある好ましい実施形態では、乳癌タンパク質とモジュレーターは治療用物質として投与され、上述のように調合することができる。同様に、乳癌遺伝子（全長シーケンス、部分シ

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ーケンスの両方、又は乳癌をコードする領域の調節シーケンス、を含む）は、当業者には周知のように、遺伝子治療用途に投与することができる。これらの乳癌遺伝子には、遺伝子治療としての（すなわち、ゲノムに組み込むための）、あるいはアンチセンス組成物としてのアンチセンス応用も含まれる。

ある好ましい実施形態では、乳癌遺伝子はDNAワクチンとして、単一遺伝子又は乳癌遺伝子の組み合わせで、投与される。裸のDNAワクチンは当業者に一般に公知である、Brower, Nature Biotechnology, 16: 1304-1305 (1998)。

ある実施形態では、本発明の乳癌遺伝子はDNAワクチンとして用いられる。遺伝子をDNAワクチンとして利用する方法は当業者には周知であり、乳癌遺伝子又は乳癌遺伝子の一部をプロモータの制御下におき乳癌患者で発現させる、などの方法がある。DNAワクチンとして用いられる乳癌遺伝子は、全長の乳癌タンパク質をコードすることもあるが、乳癌タンパク質から誘導されるペプチドを含む乳癌タンパク質の部分をコードするものがさらに好ましい。ある好ましい実施形態では、患者は、乳癌遺伝子から誘導された複数のヌクレオチド・シーケンスを含むDNAワクチンによって免疫される。同様に、患者を個々で定義されたような複数の乳癌遺伝子又はその部分によって免疫することが可能である。理論によっては拘束されないが、DNAワクチンによってコードされるポリペプチド、細胞毒性T細胞、ヘルパーT細胞及び抗体の発現が誘発されて乳癌タンパク質を発現する細胞を認識し破壊又は除去する。

ある好ましい実施形態では、DNAワクチンは、DNAワクチンとアジュバントな分子をコードする遺伝子を含む。このようなアジュバントな分子としては、DNAワクチンがコードする乳癌ポリペプチドに対する免疫応答を増加させるサイトカインなどがある。その他の又は代替りのアジュバントは当業者に公知であり、本発明で利用できる。

別の好ましい実施形態では、乳癌遺伝子は乳癌の動物モデルを生成するのに利用される。当業者には理解されるように、同定された乳癌遺伝子が乳癌組織で抑圧されている又は減少しているとき、アンチセンスRNAがその乳癌遺伝子に向けられた遺伝子治療技術もその遺伝子の発現を減少又は抑圧する。このように生成された動物は乳癌の動物モデルとして役に立ち、生物活性薬剤候補のスクリーニングに利用できる。同様に、例えば適当な遺伝子標的ベクターによる相同組み換えの結果として、遺伝子ノックアウト技術によってその乳癌タンパク質は不在になる。望まれる場合、乳癌タンパク質の組織特異的な発現又はノックアウトが必要かもしれない。

乳癌で乳癌タンパク質を過剰発現させることも可能である。そのようなものとして、乳癌タンパク質を過剰発現するトランスジェニック動物を生成することができる。所望の発現レベルに応じて、いろいろな強度のプロモータを用いて導入遺伝子を発現させることができる。また、組み込まれた導入遺伝子のコピーの数を決定し比較して導入遺伝子の発現レベルを決定することができる。この方法で生成された動物は、乳癌の動物モデルとして利用でき、さらに乳癌を治療する生物活性分子をスクリーニングするのにも役立つ。

ここに記述される実施例は、いかなる意味でもこの発明の真の範囲を限定するものではなく、例示的な目的で提示されるに過ぎない。全ての参照文献及び引用されたアクセス番号のあるシーケンスはその全体が参照によって本明細書に組み込まれる。

実施例

ここで、発現研究はタンパク質及び核酸レベルの両方で行われた。結果は図に示されている。

BCH1タンパク質とエストロゲン受容体（ER）の発現及び局在位置の間の相関（もしあれば）を調べる実験が行われた。BCH1タンパク質に対する抗体は、ウサギで、BCH1の領域に対応する15-mer合成ペプチドによる免疫化によって得られた。抗ER抗体は商業的に購入した。約50の乳癌腫組織検体（5ミクロン連続切片；パラフィン包埋、ホルマリン固定）が免疫組織化学的に分析された。このうち、～40%がBCH1発現ポジティブであり、～35%がERポジティブであった。タンパク質レベルは免疫組織化学的に1から5までのスコアで採点され、5が最高の発現を表していた。BCH1と

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ERの共発現は図37に示されている。

ER+腫瘍 (n=108) のうち、約半数はERが主に核に局在し、半数は主に細胞質に局在する。興味深いことは、BCH1+/ER+腫瘍は偶然よりも多くなかったが、BCH1のレベルが高い腫瘍 (1HCスコア=4又は5) は例外なく細胞質へのERの局在、及び核からの排除を示した (図38及び39を見よ) (n=16, $p < 5 \times 10^{-7}$)。他方、BCH1の低い発現はERの局在位置と相関がなく、しばしば核内のERと関連していた (図40及び41を見よ)。

現在、ER発現は乳癌の重要な臨床予診マーカーである。多くのエストロゲン応答遺伝子を活性化させるERを通しての信号伝達には活性化されたERを核に転座させることが必要であると考えられるので、BCH1の高い発現がER+腫瘍における機能的にネガティブなERと相関すると予測される。ER-は予後の悪さと相関しているので、BCH1も重要な予診マーカーになる。それも予後の悪さに、又は、抗エストロゲン治療 (例えば、タモキシフェン) に対する不応答と相関するからである (約50%のER+患者はタモキシフェンに応答しない)。タモキシフェンはこれらの細胞へのエストロゲンの作用に対抗して働く。しばしばそれは“抗エストロゲン”と呼ばれる。乳癌の治療として、この薬は、体内に既にある癌細胞の増殖を遅らせ、又は停止させる。補助治療として、タモキシフェンは元の乳癌が戻ってくるのを防ぎ、また反対の胸に新しい癌が発生するのを防ぐのに役立つことが示されている。

最近の研究は、ERがRas/Raf/MAPキナーゼによって信号を伝達できると報告している。この信号伝達カスケードにおけるタンパク質の多くは細胞質にあるので、大きなBCH1発現は、ERと相関し、ERを細胞質にとどまらせる原因にさえなっており、MAPキナーゼ経路によるERの信号伝達を変化させる。これがER+患者の一部にタモキシフェンに応答しない人たちがいる理由かもしれない。

さらに、BCH1はERの核への転座において、ある因果的な役割を演じ、直接又は間接に核への移動を妨げ、その結果エストロゲン又は類似物に対する細胞の応答を消失させたり変化させたりする可能性がある。

【図面の簡単な説明】

【図1】発現遺伝子配列断片を含んだ (ここでそれらの全体及び登録番号が提供されている応用面の全体を組み入れた)、正常乳房組織に比較して腫瘍組織では下降制御を受けている遺伝子の登録番号を提供する。

【図2】発現遺伝子配列断片を含んだ正常乳房組織に比べ腫瘍組織では下降制御を受けている遺伝子の登録番号を提供する。

【図3】発現遺伝子配列断片を含んだ正常乳房組織に比べ腫瘍組織では下降制御を受けている遺伝子の登録番号を提供する。

【図4】発現遺伝子配列断片を含んだ正常乳房組織に比べ腫瘍組織では上昇制御を受けている遺伝子の登録番号を提供する。

【図5】発現遺伝子配列断片を含んだ正常乳房組織に比べ腫瘍組織では上昇制御を受けている遺伝子の登録番号を提供する。

【図6】発現遺伝子配列断片を含んだ正常乳房組織に比べ腫瘍組織では上昇制御を受けている遺伝子の登録番号を提供する。

【図7】発現遺伝子配列断片を含んだ正常乳房組織に比べ腫瘍組織では上昇制御を受けている遺伝子の登録番号を提供する。配列中の読み取り枠はシグナル配列 (SS)、膜貫通ドメイン (TM) 又その他を有することで特徴がある。

【図8】発現遺伝子配列断片を含んだ正常乳房組織に比べ腫瘍組織では上昇制御を受けている遺伝子の登録番号を提供する。特に、一つの欄では遺伝子の乳房腫瘍組織と他の体組織を比較したときの発現比率、他の欄では遺伝子の腫瘍乳房組織と正常乳房組織での発現比率を示す。

【図9】発現遺伝子配列断片を含んだ正常乳房組織より腫瘍乳房組織で上昇制御を受けている遺伝子の登録番号を示す。

【図10】発現遺伝子配列断片を含んだ正常乳房組織より腫瘍乳房組織で上昇制御を受け

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ている遺伝子1007個の登録番号の好ましい群を示す。

【図11】発現遺伝子配列断片を含んだ正常乳房組織より腫瘍乳房組織で上昇制御を受けている遺伝子123個の登録番号の好ましい群を示す。

【図12】発現遺伝子配列断片を含んだ正常乳房組織より腫瘍乳房組織で上昇制御を受けている遺伝子10個の登録番号の好ましい群を示す。

【図13】本明細書で提供した乳癌タンパク質BCR3をコードしている配列を含む核酸(mRNA)の具体例を示した。開始及び終結コドンには下線を付ける。

【図14】BCR3をコードしている核酸の読み取り枠を具体的に示し、開始及び終結コドンには下線を付す。

【図15】BCR3のアミノ酸配列の具体例を示す。シグナルペプチドには下線を引き、膜貫通ドメインには陰影を付けた。好ましい態様では、BCR3の可溶形を提供するが、そこではシグナルペプチドは除かれているか好ましくは自然に開裂しており、そして膜貫通ドメインは削除されるか、非活性化されているかもしくはBCR3が切り詰められ膜貫通ドメインは除かれている。

【図16】BCR3 p1及びBCR3 p2のアミノ酸配列を示す。

【図17】乳癌組織の(黒の棒)及び多くの正常組織タイプ(白の棒)の種々な試料におけるBCR3の発現の対比量を示す。

【図18】本明細書で提示した乳癌タンパク質BCQ8をコードした配列を含んだ核酸(mRNA)の具体例を示す。開始及び終結コドンには下線をする。

【図19】BCQ8をコードしている核酸の読み取り枠の具体例を示し、開始及び終結コドンに下線をする。

【図20】BCQ8のアミノ酸配列の具体例を示す。シグナルペプチドには二重下線を、膜貫通ドメインには一重下線を引く。好ましい態様ではBCQ8の可溶形ではシグナルペプチドは除かれ、膜貫通ドメインは除去され不活性化されるか、BCQ8は望ましい片方の末端が切断され膜貫通ドメインが除かれている。

【図21】BCQ8 p1及びBCQ8 p2のアミノ酸配列を示す。

【図22】乳癌組織(黒の棒)及び多くの正常組織タイプ(白の棒)の種々な試料におけるBCQ8の発現の対比量を示す。

【図23】本明細書に提示した、異なる発現のタンパク質ヒトBCQ5をコードした配列を含む核酸(mRNA)の具体例を示す。

【図24】ヒトBCQ5をコードした核酸の読み取り枠の具体例を示した。

【図25】BCQ5のアミノ酸配列の具体例を並べて示すが、列ではラットの上にマウス、その上がヒトである。

【図26】BCQ5 p1, BCQ5 p2及びBCQ5 p3のアミノ酸配列を示す。

【図27】乳癌組織、結腸直腸癌、上皮細胞から作成した管での血管形成モデル及び正常組織タイプなどの種々な試料におけるBCQ5の発現対比量を示す。

【図28】本明細書で提供した異なる発現をしたタンパク質であるマウスBCQ5の配列を含む核酸(mRNA)の具体例を示す。

【図29】マウスBCQ5をコードした核酸の読み取り枠の具体例を示す。

【図30】本明細書で提供した、異なる発現をしたタンパク質ラットBCQ5をコードしている配列を含む核酸(部分mRNA)の具体例を示す。

【図31】ラットBCQ5をコードしている核酸の部分読み取り枠の具体例を示す。

【図32】本明細書で提供した乳癌タンパク質BCH1の配列を含む核酸(mRNA)の具体例を示す。開始及び終結コドンには下線を付す。

【図33】BCH1をコードした核酸の読み取り枠の具体例を示すが、開始及び終結コドンには下線を引く。

【図34】BCH1のアミノ酸配列の具体例を示す。好ましい具体例では、単離したBCH1はシグナル配列であるアミノ酸1~19を除いてある。

【図35】BCH1 p1及びBCH1 p2(下)のアミノ酸配列を示す。

【図36】乳癌組織(黒の棒)及び多くの正常組織タイプ(白の棒)の種々な試料にお

る B C H 1 の発現の対比量を示す。

【図 3 7】核（ひし形）又は細胞質（四角）に局在化したエストロゲン受容体（E R）（垂直の棒）及び B C H 1（水平の棒）の発現の相互関係を表すグラフを示す。

【図 3 8】抗 B C H 1 抗体で測定したとき高レベルの B C H 1 を発現した乳癌発現検体を示す。

【図 3 9】それぞれ図 3 8 A 及び図 3 8 B で示した組織から採取した試料を示すが、抗エストロゲン受容体抗体はエストロゲン受容体が全て細胞質に局在していることを示す。

【図 4 0】抗 B C H 1 抗体によれば乳癌組織検体では B C H 1 発現は低レベルであることを示す。

【図 4 1】それぞれ図 4 0 A と図 4 0 B に示した組織から得た試料を示すが、抗エストロゲン受容体抗体によれば低 B C H 1 発現組織でのエストロゲン受容体はエストロゲン受容体局在性とは関係ないことを示す。 10

【図 4 2】本明細書で提供した乳癌タンパク質 B C N 1 をコードした配列を含む核酸（m R N A）の具体例を示す。開始及び終結コドンは陰影を付け、登録番号 A A 1 9 6 2 2 配列には下線を付した。

【図 4 3】B C N 1 のアミノ酸配列の具体例を示す。推定貫通膜ドメインは少なくともほぼ位置 2 0 1 ～ 2 1 7 及び 6 7 ～ 8 3 にあると予測される。当該タンパク質は I I I a 型膜タンパク質で、付加的膜貫通ドメインを有するようである。

【図 4 4】B C N 1 p 1 及び B C N 1 p 2 のアミノ酸配列を示す。

【図 4 5】乳癌組織（黒の棒）、結腸癌組織（白の棒）及び多くの正常組織タイプ（中間 20
白の点印の棒）の種々な試料における B C N 1 の発現の対比量を示す。

【図 4 6】本明細書で提供した乳癌タンパク質 B C N 2 をコードした配列を含む核酸（m R N A）につき具体例を示す。開始及び終結コドンには陰影、登録番号 A A 4 2 8 0 9 0 配列には下線を付した。

【図 4 7】B C N 2 のアミノ酸配列の具体例を示す。

【図 4 8】乳癌組織（黒の棒）、結腸癌組織（白の棒）及び多数の正常組織タイプ（中間白の点印の棒）など種々な試料における B C N 2 の発現の対比量を示す。

【図 4 9】本明細書で提供した乳癌タンパク質 B C N 5 をコードした配列を含む核酸（m R N A）の具体例を示す。開始及び終結コドンには陰影を付け、登録番号 R 5 1 3 0 9 配列には下線を付した。 30

【図 5 0】B C N 5 のアミノ酸配列の具体例を示す。推定シグナル配列には陰影を付け、好ましい配列には下線を付す。

【図 5 1】乳癌組織（黒の棒）、結腸癌組織（白の棒）及び多数の正常組織タイプ（中間白の点印の棒）など種々な試料における B C N 5 の発現の対比量を示す。

【図 5 2】本明細書で提供した乳癌タンパク質 B C N 2 をコードした配列を含む核酸（m R N A）の具体例を示す。開始及び終結コドンには下線を付した。

【図 5 3】B C O 2 をコードした核酸の読み取り枠の具体例を示す。

【図 5 4】B C O 2 のアミノ酸配列の具体例を示す。

【図 5 5】マウス B C O 2 の上部にヒト B C O 2 のアミノ酸の列を示す。

【図 5 6】乳癌組織（黒の棒）及び多くの正常組織タイプ（白の棒）など種々な試料にお 40
ける B C O 2 の発現の対比量を示す。

【図 5 7】本明細書で提供した乳癌タンパク質 B C X 2 をコードした配列を含む核酸（m R N A）の具体例を示す。開始及び終結コドンには下線を付した。

【図 5 8】B C X 2 をコードした核酸の読み取り枠の具体例を示す。

【図 5 9】B C X 2 のアミノ酸配列の具体例を示す。

【図 6 0】乳癌組織（黒の棒）及び多くの正常組織タイプ（白の棒）など種々な試料における B C X 2 の発現の対比量を示す。

【図 6 1】結腸癌組織（白の棒）、非癌細胞系（黒の棒）及び多数の細胞系（中間白の棒）など種々な試料における B C X 2 の発現の対比量を示す。

【図 6 2】本明細書で提供した乳癌タンパク質 B C X 3 をコードした配列を含む核酸（m 50

R N A) の具体例を示す。開始及び終結コドンには下線を付した。

【図 6 3】 B C X 3 をコードした核酸の読み取り枠の具体例を示す。

【図 6 4】 B C X 2 のアミノ酸配列の具体例を示す。

【図 6 5】 乳癌組織（黒の棒）及び多くの正常組織タイプ（白の棒）など種々な試料における B C X 2 の発現の対比量を示す。

【図 6 6】 本明細書で提供した乳癌タンパク質 B C A 2 をコードした配列を含む核酸（m R N A）の具体例を示す。開始及び終結コドンには陰影を付し，登録番号 D 1 2 4 8 5 配列には下線を付した。

【図 6 7】 B C A 2 のアミノ酸配列の具体例を示す。

【図 6 8】 本明細書で提供した乳癌タンパク質 B C R 2 をコードした配列を含む核酸（m R N A）の具体例を示す。開始及び終結コドンには陰影を付し，登録番号 A A 6 0 9 7 7 3 配列には下線を付した。 10

【図 6 9】 B C R 2 のアミノ酸配列の具体例を示す。

【図 7 0】 乳癌組織の種々な試料中にある B C R 2 の発現の対比量を示す。

【図 7 1】 正常組織タイプ（白の棒）の種々な試料中にある B C R 2 の発現の対比量を示す。

【図 7 2】 本明細書で提供した乳癌タンパク質 B C J 7 をコードした配列を含む核酸の具体例を示す。

【図 7 3】 本明細書で提供した乳癌タンパク質 B C Y 3 をコードした配列を含む核酸の具体例を示す。 20

【国際公開パンフレット】

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<table border="1"><caption>Relative Expression Levels (Estimated from Chart)</caption><thead><tr><th>Gene/Tissue</th><th>Breast Cancer (Solid)</th><th>Normal Tissues (Hatched)</th></tr></thead><tbody><tr><td>11CLA Tum</td><td>~3500</td><td>~1000</td></tr><tr><td>12COO Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>13COO Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>14CRO Tum</td><td>~2500</td><td>~1000</td></tr><tr><td>16FOR Mel</td><td>~4000</td><td>~1000</td></tr><tr><td>26GL Tum</td><td>~1500</td><td>~1000</td></tr><tr><td>33MAM Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>38MCI Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>38MCI Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>41OHA Tum</td><td>~2500</td><td>~1000</td></tr><tr><td>59VAL Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>57MCI Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>71WCH Tum</td><td>~1000</td><td>~1000</td></tr><tr><td>Tum Pool</td><td>~1000</td><td>~1000</td></tr><tr><td>Brain</td><td>~1000</td><td>~1000</td></tr><tr><td>Breast</td><td>~1000</td><td>~1000</td></tr><tr><td>Breast nom 38MCI</td><td>~1000</td><td>~1000</td></tr><tr><td>bulb CD14</td><td>~1000</td><td>~1000</td></tr><tr><td>bulb mena</td><td>~1000</td><td>~1000</td></tr><tr><td>Colon</td><td>~1000</td><td>~1000</td></tr><tr><td>Colon Epithelium</td><td>~1000</td><td>~1000</td></tr><tr><td>Endometrium</td><td>~1000</td><td>~1000</td></tr><tr><td>Kidney</td><td>~1000</td><td>~1000</td></tr><tr><td>Liver</td><td>~1000</td><td>~1000</td></tr><tr><td>Lung</td><td>~1000</td><td>~1000</td></tr><tr><td>Prostate</td><td>~1000</td><td>~1000</td></tr><tr><td>sm. intestine</td><td>~1000</td><td>~1000</td></tr><tr><td>Spleen</td><td>~1000</td><td>~1000</td></tr><tr><td>Testis</td><td>~1000</td><td>~1000</td></tr></tbody></table>				Gene/Tissue	Breast Cancer (Solid)	Normal Tissues (Hatched)	11CLA Tum	~3500	~1000	12COO Tum	~1000	~1000	13COO Tum	~1000	~1000	14CRO Tum	~2500	~1000	16FOR Mel	~4000	~1000	26GL Tum	~1500	~1000	33MAM Tum	~1000	~1000	38MCI Tum	~1000	~1000	38MCI Tum	~1000	~1000	41OHA Tum	~2500	~1000	59VAL Tum	~1000	~1000	57MCI Tum	~1000	~1000	71WCH Tum	~1000	~1000	Tum Pool	~1000	~1000	Brain	~1000	~1000	Breast	~1000	~1000	Breast nom 38MCI	~1000	~1000	bulb CD14	~1000	~1000	bulb mena	~1000	~1000	Colon	~1000	~1000	Colon Epithelium	~1000	~1000	Endometrium	~1000	~1000	Kidney	~1000	~1000	Liver	~1000	~1000	Lung	~1000	~1000	Prostate	~1000	~1000	sm. intestine	~1000	~1000	Spleen	~1000	~1000	Testis	~1000	~1000
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(57) Abstract Described herein are methods that can be used for diagnosis and prognosis of breast cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate breast cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in breast and other cancers are described.																																																																																													

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**NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER, COMPOSITIONS, AND
METHODS OF SCREENING FOR BREAST CANCER MODULATORS**

FIELD OF THE INVENTION

- 5 The invention relates to the identification of expression profiles and the nucleic acids involved in breast cancer, and to the use of such expression profiles and nucleic acids in diagnosis, prognosis and treatment of breast cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate breast cancer.

BACKGROUND OF THE INVENTION

- 10 Breast cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal breast epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in breast cancer. However, there is a need to identify all of the genetic alterations involved in the development of breast cancer.
- 15 Imaging of breast cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence
- 20 of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast majority of breast cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

- Thus, methods that can be used for diagnosis and prognosis of breast cancer would be desirable. While academia and industry has made an effort to identify novel sequences, there has not been an
- 25 equal effort exerted to identify the function of the novel sequences. For example, databases show the

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sequence of accession number W72838, but there no data correlating this sequence with a function, much less a disease state. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of breast cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate breast cancer. Additionally, provided herein are molecular targets for therapeutic intervention in breast and other cancers.

SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate breast cancer. Also provided herein are methods of inhibiting proliferation of a cell, preferably a breast cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

10 In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably breast cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, 15 BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2; fragments of the proteins of this group are also preferred. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

20 In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or 25 decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to a breast cancer modulator protein (BCMP), the method comprising combining the BCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the BCMP. Preferably the BCMP is a protein or fragment thereof selected from the group consisting of BCR3, BCQ8, BCQ5,

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BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

- 5 Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a BCMP. In one embodiment, the method comprises combining the BCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the BCMP. Preferably the BCMP is a protein or fragment thereof selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2. In
10 another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

- Also provided is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the BCMP, or an animal
15 lacking the BCMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate breast cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

- 20 Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a breast cancer protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9,
25 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

Furthermore, a method of diagnosing a disorder associated with breast cancer is provided. The method comprises determining the expression of a gene which encodes a breast cancer protein preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5,

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BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12.

5 Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. A difference in the expression indicates that the first individual has a disorder associated with breast cancer.

In another aspect, the present invention provides an antibody which specifically binds to a breast cancer protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another
10 embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. In a preferred embodiment, the fragment of BCH1 is selected from BCH1p1 and BCH1p2. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the
15 antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a breast cancer protein (BCMP) or a fragment thereof and an antibody which binds to said BCMP or
20 fragment thereof. In a preferred embodiment, the method comprises combining a BCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said BCMP or fragment thereof. The method further includes determining the binding of said BCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The
25 interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits breast cancer.

In a further aspect, a method for inhibiting breast cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another embodiment,
30 the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

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The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting breast cancer is provided to an individual with cancer. As described herein, methods of inhibiting breast cancer can be performed by administering an inhibitor of breast cancer protein activity, including an antisense molecules, and preferably small molecules.

5 Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 10
8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 15
4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, 20
BCX2, BCJ7, BCY3, BCX3, BCA2 and BCR2, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a breast modulating protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, 25
BCX3, BCA2 and BCR2, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

A method of neutralizing the effect of a breast cancer protein, preferably selected from the group consisting of BCR3, BCQ8, BCQ5, BCH1, BCN1, BCN2, BCN5, BCO2, BCX2, BCJ7, BCY3, BCX3, 30
BCA2 and BCR2, or a fragment thereof, is also provided. Preferably, the method comprises

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contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. Preferred nucleic acids are in Figure 10, more preferably Figure 11, and most preferably in Figure 12.

- 5 In another aspect of the invention, a method of treating an individual for breast cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of BCH1. In another embodiment, the individual is non-responsive to an anti-estrogen and is positive for estrogen receptor. Optionally, the method further comprises administering an anti-estrogen to said individual.

- Also provided herein is method for determining the prognosis of an individual with breast cancer comprising determining the level of BCH1 in a sample, wherein a high level of BCH1 indicates a poor prognosis. Moreover, in yet another aspect of the invention, a method is provided for determining whether an individual with breast cancer will be non-responsive to anti-estrogen therapies comprising determining the level of BCH1 wherein a high level of BCH1 indicates that an individual will be non-responsive. Preferably, the methods herein are used to identify persons who are tamoxifen resistant.
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- 15 Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

DETAILED DESCRIPTION OF THE FIGURES

- Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), downregulated in tumor tissue compared to normal breast tissue.
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Figure 2 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal breast tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal breast tissue.

- 25 Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

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Figure 5 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 6 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

- 5 Figure 7 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- 10 Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue. Specifically, one column shows the ratio of expression of the indicated gene in breast tumor tissue compared to other body tissues, and another column shows the ratio of expression of the indicated gene in breast tumor tissue compared to normal breast tissue.

Figure 9 depicts the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

- 15 Figure 10 depicts a preferred group of 1007 Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 11 depicts a preferred group of 123 Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

- 20 Figure 12 depicts a preferred group of 10 Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal breast tissue.

Figure 13 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCR3. The start and stop codons are underlined.

Figure 14 shows an embodiment of an open reading frame of a nucleic acid encoding BCR3, wherein the start and stop codons are underlined.

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Figure 15 shows an embodiment of an amino acid sequence of BCR3. The signal peptide is underlined and the transmembrane domain is shaded. In a preferred embodiment, a soluble form of BCR3 is provided wherein the signal peptide is deleted or preferably naturally cleaved, and the transmembrane domain is deleted, inactivated, or BCR3 is truncated to exclude the transmembrane domain.

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Figure 16 shows the amino acid sequence of BCR3p1 and BCR3p2.

Figure 17 shows the relative amount of expression of BCR3 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 18 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCQ8. The start and stop codon are underlined.

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Figure 19 shows an embodiment of an open reading frame of a nucleic acid encoding BCQ8, wherein the start and stop codons are underlined.

Figure 20 shows an embodiment of an amino acid sequence of BCQ8. The signal peptide is underlined twice and the transmembrane domain is underlined. In a preferred embodiment, a soluble form of BCQ8 is provided wherein the signal peptide is deleted, and the transmembrane domain is deleted, inactivated, or BCQ8 is truncated on either end as desired, to exclude the transmembrane domain.

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Figure 21 shows the amino acid sequence of BCQ8p1 and BCQ8p2.

Figure 22 shows the relative amount of expression of BCQ8 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

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Figure 23 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a differentially expressed protein provided herein, human BCQ5.

Figure 24 shows an embodiment of an open reading frame of a nucleic acid encoding human BCQ5.

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Figure 25 shows embodiments of amino acid sequences of BCQ5 by providing an alignment wherein human is above mouse which is above rat.

Figure 26 shows the amino acid sequence of BCQ5p1, BCQ5p2 and BCQ5p3.

- 5 Figure 27 shows the relative amount of expression of BCQ5 in various samples of breast cancer tissue, colorectal cancer tissue, angiogenesis models wherein tubes are formed from endothelial cells, and normal tissue types.

Figure 28 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a differentially expressed protein provided herein, mouse BCQ5.

Figure 29 shows an embodiment of an open reading frame of a nucleic acid encoding mouse BCQ5.

- 10 Figure 30 shows an embodiment of a nucleic acid (partial mRNA) which includes a sequence which encodes a differentially expressed protein provided herein, rat BCQ5.

Figure 31 shows an embodiment of a partial open reading frame of a nucleic acid encoding rat BCQ5.

Figure 32 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCH1. Start and stop codons are underlined.

- 15 Figure 33 shows an embodiment of an open reading frame of a nucleic acid encoding BCH1, wherein start and stop codons are underlined.

Figure 34 shows an embodiment of an amino acid sequence of BCH1. In a preferred embodiment, isolated BCH1 excludes the signal sequence, amino acids 1-19.

Figure 35 shows the amino acid sequence of BCH1p1 and BCH1p2 (below).

- 20 Figure 36 shows the relative amount of expression of BCH1 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

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Figure 37 shows a graph correlating expression of estrogen receptor (ER) (vertical bar) and BCH1 (horizontal bar) with localization to the nucleus (diamonds) or the cytoplasm (squares).

Figures 38A and 38B show breast carcinoma tissue specimens having high levels of BCH1 expression as indicated by anti-BCH1 antibodies.

- 5 Figures 39A and 39B show samples taken from the tissues shown in Figures 38A and 38B respectively, wherein anti-estrogen receptor antibodies indicate that estrogen receptor is localized exclusively to the cytoplasm.

Figures 40A and 40B show breast carcinoma tissue specimens having low levels of BCH1 expression as indicated by anti-BCH1 antibodies.

- 10 Figures 41A and 41B show samples taken from the tissues shown in Figures 40A and 40B respectively, wherein anti-estrogen receptor antibodies indicate that estrogen receptor in low BCH1 expression tissue does not correlate with estrogen receptor localization.

- 15 Figure 42 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCN1. Start and stop codons are shaded, and Accession number AA419622 sequence is underlined.

Figure 43 shows an embodiment of an amino acid sequence of BCN1. A putative transmembrane domain is predicted to be at least at approximately positions 201-217 and 67-83. The protein may be a type IIIa membrane protein and may have additional transmembrane domains.

Figure 44 shows the amino acid sequence of BCN1p1 and BCN1p2.

- 20 Figure 45 shows the relative amount of expression of BCN1 in various samples of breast cancer tissue (dark bars), colon cancer tissue (light bars) and many normal tissue types (medium light dotted bars).

Figures 46A-46D show an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCN2. Start and stop codons are shaded, and Accession number AA428090 sequence is underlined.

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- Figure 47 shows an embodiment of an amino acid sequence of BCN2.
- Figure 48 shows the relative amount of expression of BCN2 in various samples of breast cancer tissue (dark bars), colon cancer tissue (light bars) and many normal tissue types (medium light dotted bars).
- Figures 49A-49B show an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCN5. Start and stop codons are shaded, and Accession number R51309 sequence is underlined.
- Figure 50 shows an embodiment of an amino acid sequence of BCN5. A putative signal sequence is shaded and preferred sequence is underlined.
- Figure 51 shows the relative amount of expression of BCN5 in various samples of breast cancer tissue (dark bars), colon cancer tissue (light bars) and many normal tissue types (medium light dotted bars).
- Figure 52 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCO2. Start and stop codons are underlined.
- Figure 53 shows an embodiment of an open reading frame of a nucleic acid encoding BCO2.
- Figure 54 shows an embodiment of an amino acid sequence of BCO2.
- Figure 55 shows an alignment of amino acids for human BCO2 above mouse BCO2.
- Figure 56 shows the relative amount of expression of BCO2 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).
- Figure 57 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCX2. Start and stop codons are underlined.
- Figure 58 shows an embodiment of an open reading frame of a nucleic acid encoding BCX2.
- Figure 59 shows an embodiment of an amino acid sequence of BCX2.

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Figure 60 shows the relative amount of expression of BCX2 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 61 shows the relative amount of expression of BCX2 in various samples of colon cancer tissue (light bars), non-cancer cell lines (dark bars) and many cell lines (medium light bars).

- 5 Figure 62 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCX3. Start and stop codons are underlined.

Figure 63 shows an embodiment of an open reading frame of a nucleic acid encoding BCX3.

Figure 64 shows an embodiment of an amino acid sequence of BCX3.

- 10 Figure 65 shows the relative amount of expression of BCX3 in various samples of breast cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 66 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCA2. Start and stop codons are shaded, and Accession number D12485 sequence is underlined.

Figure 67 shows an embodiment of an amino acid sequence of BCA2.

- 15 Figure 68 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCR2. Start and stop codons are shaded, and Accession number AA609773 sequence is shown underlined.

Figure 69 shows an embodiment of an amino acid sequence of BCR2.

- 20 Figure 70 shows the relative amount of expression of BCR2 in various samples of breast cancer tissue.

Figure 71 shows the relative amount of expression of BCR2 in various samples of normal tissue types (light bars).

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Figure 72 shows an embodiment of a nucleic acid which includes a sequence which encodes a breast cancer protein provided herein, BCJ7.

Figure 73 shows an embodiment of a nucleic acid which includes a sequence which encodes a breast cancer protein provided herein, BCY3.

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DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for breast cancer, as well as methods for screening for compositions which modulate breast cancer. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from breast cancer tissue, and within breast cancer tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of breast tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in breast cancer versus normal breast tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the breast cancer expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important breast cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the breast cancer proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the breast cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the breast cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in breast cancer, breast cancer, herein termed "breast cancer sequences". As outlined below, breast cancer sequences include those that are up-regulated (i.e. expressed at a higher level) in breast cancer, as well as those that are down-regulated (i.e. expressed at a lower level) in breast cancer. In a preferred embodiment, the breast cancer sequences are from humans; however, as will be appreciated by those in the art, breast cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other breast cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). Breast cancer sequences from other organisms may be obtained using the techniques outlined below.

Breast cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the breast cancer sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a breast cancer protein from one organism in a

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different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the breast cancer sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, breast cancer sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the breast cancer sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzi et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 9(1986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphosphoramidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also

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included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

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A breast cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the breast cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

- 5 The breast cancer sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.
- 10 In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the breast cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some
- 15 embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

- In a preferred embodiment, breast cancer sequences are those that are up-regulated in breast cancer; that is, the expression of these genes is higher in breast carcinoma as compared to normal breast tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least
- 20 about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited relative amount or not at all in heart, brain, lung, liver, kidney, prostate, small intestine, testes, fibroblasts and spleen.
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In a preferred embodiment, breast cancer sequences are those that are down-regulated in breast cancer; that is, the expression of these genes is lower in breast carcinoma as compared to normal breast tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

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Breast cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the breast cancer protein is an intracellular protein. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or dysregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

10 An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner.

15 PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus,

20 an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the breast cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins

25 may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for

30 additional SH2 domain containing proteins.

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Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions. It is understood that the transmembrane domains may be removed to create soluble proteins herein.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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Breast cancer proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

5 In a preferred embodiment, the breast cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or
10 or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Breast cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

15 A breast cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the breast cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

20 As used herein, a nucleic acid is a "breast cancer nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be
25 determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics
30 Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by

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Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); [http://blast.wustl.edu/blast/ README.html](http://blast.wustl.edu/blast/README.html). WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the se. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

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The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the proteins identified in the figures, or their complements, are considered a breast cancer sequence. High stringency conditions are known in the art; see for example Maniatis et al., *Molecular Cloning: A Laboratory Manual*, 2d Edition, 1989, and *Short Protocols in Molecular Biology*, ed. Ausubel, et al., both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

In addition, the breast cancer nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding

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regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the breast cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., supra, hereby expressly incorporated by reference.

Once the breast cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire breast cancer nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant breast cancer nucleic acid can be further-used as a probe to identify and isolate other breast cancer nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant breast cancer nucleic acids and proteins.

The breast cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the breast cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene therapy and/or antisense applications. Alternatively, the breast cancer nucleic acids that include coding regions of breast cancer proteins can be put into expression vectors for the expression of breast cancer proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to breast cancer nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the breast cancer nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

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A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of

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possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled A Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

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Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent
5 Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, breast cancer nucleic acids encoding breast cancer proteins are used to make a variety of expression vectors to express breast cancer proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating
10 extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the breast cancer protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter,
15 optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA
20 for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However,
25 enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the breast cancer protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to
30 express the breast cancer protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

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In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The breast cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a breast cancer protein, under the appropriate conditions to induce or cause expression of the breast cancer protein. The conditions appropriate for breast cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation.

For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

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Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

5 In a preferred embodiment, the breast cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as
10 mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription
15 terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct
20 microinjection of the DNA into nuclei.

In a preferred embodiment, breast cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial
25 promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the breast cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located
30 between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that

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- have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors.
- 5 Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.
- 10 In one embodiment, breast cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.
- In a preferred embodiment, breast cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.
- 15 The breast cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the breast cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the breast cancer protein may be made as a fusion protein to increase expression, or for other reasons.
- 20 For example, when the breast cancer protein is a breast cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.
- In one embodiment, the breast cancer nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes:
- 25 a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the breast cancer nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as
- 30 fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-

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galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

5 Accordingly, the present invention also provides breast cancer protein sequences. A breast cancer protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by
10 comparing it to known sequences to search for homology to provide a frame, assuming the breast cancer protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is
15 "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of breast cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about
20 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined
25 using standard techniques known in the art as are outlined above for the nucleic acid homologies.

Breast cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of breast cancer proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the
30 breast cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

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In a preferred embodiment, the breast cancer proteins are derivative or variant breast cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative breast cancer peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the breast cancer peptide.

Also included in an embodiment of breast cancer proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the breast cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant breast cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the breast cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed breast cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of breast cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small

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alterations in the characteristics of the breast cancer protein are desired, substitutions are generally made in accordance with the following chart:

		Chart I	
		Original Residue	Exemplary Substitutions
5	Ala		Ser
	Arg		Lys
	Asn		Gln, His
	Asp		Glu
	Cys		Ser
10	Gln		Asn
	Glu		Asp
	Gly		Pro
	His		Asn, Gln
	Ile		Leu, Val
15	Leu		Ile, Val
	Lys		Arg, Gln, Glu
	Met		Leu, Ile
	Phe		Met, Leu, Tyr
	Ser		Thr
20	Thr		Ser
	Trp		Tyr
	Tyr		Trp, Phe
	Val		Ile, Leu

- Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.
- The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the breast cancer proteins as needed. Alternatively, the variant may be designed

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such that the biological activity of the breast cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of breast cancer polypeptides are included within the scope of this invention.

One type of covalent modification includes reacting targeted amino acid residues of a breast cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a breast cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking breast cancer to a water-insoluble support matrix or surface for use in the method for purifying anti-breast cancer antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutaminy and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the breast cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence breast cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence breast cancer polypeptide.

Addition of glycosylation sites to breast cancer polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence breast cancer polypeptide (for O-linked glycosylation sites). The breast cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the breast

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cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the breast cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, breast cancer Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the breast cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of breast cancer comprises linking the breast cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Breast cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a breast cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a breast cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the breast cancer polypeptide. The presence of such epitope-tagged forms of a breast cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the breast cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a breast cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

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Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

Also included with the definition of breast cancer protein in one embodiment are other breast cancer proteins of the breast cancer family, and breast cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related breast cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the breast cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, breast cancer proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Breast cancer proteins may also be identified as being encoded by breast cancer nucleic acids. Thus, breast cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the breast cancer protein is to be used to generate antibodies, for example for immunotherapy, the breast cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller breast cancer protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a

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unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from BCH1p1, BCH1p2, BCR3p1, BCR3p2, BCQ8p1, BCQ8p2, BCQ5p1, BCQ5p2, BCN1p1, BCN1p2, wherein BCH1p1 and BCH1p2 are preferred. In one embodiment the epitope or fragment of BCH1p1 is conjugated to KLH or BSA.

- 5 In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab₂, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.
- 10 Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the BCH1 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic
- 15 proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.
- 20 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in*
- 25 *vitro*. The immunizing agent will typically include the BCH1 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and
- 30 Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or

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5 mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

10 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the breast cancer protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

15 In a preferred embodiment, the antibodies to breast cancer are capable of reducing or eliminating the biological function of breast cancer, as is described below. That is, the addition of anti-breast cancer antibodies (either polyclonal or preferably monoclonal) to breast cancer (or cells containing breast cancer) may reduce or eliminate the breast cancer activity. Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

20 In a preferred embodiment the antibodies to the breast cancer proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will

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comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

5 Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *BioTechnology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.*, 13 65-93 (1995).

30 By immunotherapy is meant treatment of breast cancer with an antibody raised against breast cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as

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defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide
5 against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the breast cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment,
10 bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted breast cancer protein.

In another preferred embodiment, the breast cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the breast cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the
15 transmembrane breast cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the breast cancer protein. The antibody is also an antagonist of the breast cancer protein. Further, the antibody prevents activation of the transmembrane breast cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the breast cancer protein,
20 the antibody prevents growth of the cell. The antibody also sensitizes the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, breast cancer is treated by administering to a patient
25 antibodies directed against the transmembrane breast cancer protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the breast cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the breast cancer protein. The therapeutic moiety may inhibit enzymatic activity such as
30 protease or protein kinase activity associated with breast cancer.

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In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with breast cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against breast cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane breast cancer proteins not only serves to increase the local concentration of therapeutic moiety in the breast cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

The breast cancer antibodies of the invention specifically bind to breast cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^4 - 10^9 M⁻¹, with a preferred range being 10^7 - 10^9 M⁻¹.

In a preferred embodiment, the breast cancer protein is purified or isolated after expression. Breast cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the breast cancer protein may be purified using a standard anti-breast cancer antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the breast cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the breast cancer proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the breast cancer phenotype; that is, the expression levels of genes in normal breast tissue and in breast cancer tissue (and in some cases, for varying severities of breast cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or

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point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or breast cancer tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus breast cancer tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the breast cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the

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proteins corresponding to breast cancer genes, i.e. those identified as being important in a breast cancer phenotype, can be evaluated in a breast cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the breast cancer protein are detected. Although DNA or RNA encoding the breast cancer protein may be detected, of particular interest are methods wherein the mRNA encoding a breast cancer protein is detected. The presence of mRNA in a sample is an indication that the breast cancer gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a breast cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput

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screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, breast cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of breast cancer. Detection of these proteins in putative breast cancer tissue or patients allows for a determination or diagnosis of breast cancer. Numerous methods known to those of ordinary skill in the art find use in detecting breast cancer. In one embodiment, antibodies are used to detect breast cancer proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the breast cancer protein is detected by immunoblotting with antibodies raised against the breast cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the breast cancer protein find use in *in situ* imaging techniques. In this method cells are contacted with from one to many antibodies to the breast cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the breast cancer protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of breast cancer proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing breast cancer from blood samples. As previously described, certain breast cancer proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted breast cancer proteins. Antibodies can be used to detect the breast cancer by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

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In a preferred embodiment, in situ hybridization of labeled breast cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including breast cancer tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

5 It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

10 In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to breast cancer severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the breast cancer probes are attached to biochips for the detection and quantification of breast cancer sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

15 In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing breast cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

20 In a preferred embodiment, the breast cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified breast cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the breast cancer phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

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Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in breast cancer, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the breast cancer protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the breast cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of breast cancer sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates breast cancer, modulates breast cancer proteins, binds to a breast cancer protein, or interferes between the binding of a breast cancer protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the breast cancer phenotype or the expression of a breast cancer sequence, including both

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5 nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a breast cancer phenotype, for example to a normal breast tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe breast cancer phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

10 Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

20 Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

25 In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means

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both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration.

5 If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of

10 procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15

15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The

20 synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the

25 sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for

30 phosphorylation sites, etc., or to purines, etc.

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In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

- 5 In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

- 1.0 After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

- 1.5 In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also
2.0 can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

- 2.5 As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared

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as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

5 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

10 These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

15 The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

20 Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

25 The screens are done to identify drugs or bioactive agents that modulate the breast cancer phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in breast cancer similar to the expression profile of normal breast tissue is expected to result in a suppression of the breast cancer phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

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In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the breast cancer phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a breast cancer expression pattern leading to a normal expression pattern, or modulate a single breast cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated breast cancer tissue reveals genes that are not expressed in normal tissue or breast cancer tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for breast cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated breast cancer tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of breast cancer cells, that thus has an associated breast cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be

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put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

5 Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

1.0 Thus, for example, breast cancer tissue may be screened for agents that reduce or suppress the breast cancer phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on breast cancer activity. By defining such a signature for the breast cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

1.5 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "breast cancer proteins", "breast cancer modulating proteins" "BCP" or a "BCMP". In one embodiment, BCMP is termed BCH1. In one embodiment, BCH1 can be identified as described for identifying breast cancer proteins herein. In a preferred embodiment, BCH1 is depicted in Figure 34.

2.0 The BCMP may be a fragment, or alternatively, be the full length protein to the fragment shown herein. Preferably, the BCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

2.5 In other preferred embodiments herein, the breast cancer protein or nucleic acid encoding a breast cancer protein may be selected from any sequence provided in the figures including those wherein the accession numbers are provided. Preferred sequences are in Figure 10, more preferably Figure 11 and most preferably Figure 12. Preferred sequences are also selected from the group consisting of BCH1, BCA2, BCJ7, BCN1, BCN5, BCO2, BCQ5, BCR2, BCR3, BCQ8, BCN2, BCX3, BCX2 and BCY3. Most preferably, the sequence is selected from the group consisting of BCH1, BCA2, BCJ7, BCN1, BCN5, BCO2, BCQ5, BCR2, BCX2 and BCY3. It is understood that any protein can also be

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selected from any subset of this group of proteins, for example, BCH1 can be selected from the whole group, or from the subset of BCH1 and BCN1.

In one embodiment the breast cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the breast cancer protein is conjugated to BSA.

- 5 Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

- 10 In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

- 15 In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the breast cancer proteins can be used in the assays.

- 20 Thus, in a preferred embodiment, the methods comprise combining a breast cancer protein and a candidate bioactive agent, and determining the binding of the candidate agent to the breast cancer protein. Preferred embodiments utilize the human breast cancer protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative breast cancer proteins may be used.

- 25 Generally, in a preferred embodiment of the methods herein, the breast cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates,

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arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the breast cancer protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the breast cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the breast cancer protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labelled, and binding determined directly. For example, this may be done by attaching all or a portion of the breast cancer protein to a solid support, adding a labelled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support.

Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for

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detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I , or with fluorophores.

5 Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophore for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. breast cancer), such as an antibody, peptide, binding partner, ligand, etc.

10 Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present.

15 Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent.

20 Displacement of the competitor is an indication that the candidate bioactive agent is binding to the breast cancer protein and thus is capable of binding to, and potentially modulating, the activity of the breast cancer protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

25 Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the breast cancer protein with a higher affinity. Thus, if the candidate

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bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the breast cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the breast cancer proteins. In this embodiment, the methods comprise combining a breast cancer protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a breast cancer protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the breast cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the breast cancer protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native breast cancer protein, but cannot bind to modified breast cancer proteins. The structure of the breast cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect breast cancer bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of breast cancer proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity

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of breast cancer proteins comprise the steps of adding a candidate bioactive agent to a sample of breast cancer proteins, as above, and determining an alteration in the biological activity of breast cancer proteins. "Modulating the activity of breast cancer" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to breast cancer proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of breast cancer proteins.

Thus, in this embodiment, the methods comprise combining a breast cancer sample and a candidate bioactive agent, and evaluating the effect on breast cancer activity. By "breast cancer activity" or grammatical equivalents herein is meant one of the breast cancer's biological activities, including, but not limited to, cell division, preferably in breast tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, breast cancer activity include activation of breast cancer protein, Bcl-1, for example, or a substrate thereof by the breast cancer protein. An inhibitor of breast cancer activity is the inhibition of any one or more breast cancer activities.

In a preferred embodiment, the activity of the breast cancer protein is increased; in another preferred embodiment, the activity of the breast cancer protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a breast cancer protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising breast cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a breast cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

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In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the breast cancer protein. In one embodiment, "breast cancer protein activity" as used herein includes at least one of the following: breast cancer activity, binding to a breast cancer protein, activation of a breast cancer protein or activation of substrates of a breast cancer protein by a breast cancer protein.

In one embodiment, a method of inhibiting breast cancer cell division is provided. The method comprises administration of a breast cancer inhibitor.

Neutralizing means that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on the cell.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a breast cancer inhibitor.

In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a breast cancer inhibitor.

In one embodiment, a breast cancer inhibitor is an antibody as discussed above. In another embodiment, the breast cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for breast cancer molecules. A preferred antisense molecule is for BCH1 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind

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to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt %. The agents may be administered alone or in combination with other treatments, i.e., radiation.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various breast cancer sequences are important in breast cancer. Accordingly, disorders based on mutant or variant breast cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant breast cancer genes comprising determining all or part of the sequence of at least one endogeneous breast cancer genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the breast cancer genotype of an individual comprising determining all or part of the sequence of at least one breast cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced breast cancer gene to a known breast cancer gene, i.e. a wild-type gene.

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The sequence of all or part of the breast cancer gene can then be compared to the sequence of a known breast cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the breast cancer gene of the patient and the known breast cancer gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the breast cancer genes are used as probes to determine the number of copies of the breast cancer gene in the genome.

In another preferred embodiment breast cancer genes are used as probed to determine the chromosomal localization of the breast cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in breast cancer gene loci.

Thus, in one embodiment, methods of modulating breast cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-breast cancer antibody that reduces or eliminates the biological activity of an endogenous breast cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a breast cancer protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the breast cancer sequence is down-regulated in breast cancer, the activity of the breast cancer gene is increased by increasing the amount of breast cancer in the cell, for example by overexpressing the endogenous breast cancer or by administering a gene encoding the breast cancer sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the breast cancer sequence is up-regulated in breast cancer, the activity of the endogenous breast cancer gene is decreased, for example by the administration of a breast cancer antisense nucleic acid.

In one embodiment, the breast cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to breast cancer proteins, which are useful as described herein. Similarly, the breast cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify breast cancer antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a breast cancer protein;

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that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the breast cancer antibodies may be coupled to standard affinity chromatography columns and used to purify breast cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the breast cancer protein.

In one embodiment, a therapeutically effective dose of a breast cancer or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for protein degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

The administration of the breast cancer proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the breast cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a breast cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as

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acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, breast cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, breast cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the breast cancer coding regions) can be administered in gene therapy applications, as is known in the art. These breast cancer genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

In a preferred embodiment, breast cancer genes are administered as DNA vaccines, either single genes or combinations of breast cancer genes. Naked DNA vaccines are generally known in the art. Brower, *Nature Biotechnology*, 16:1304-1305 (1998).

In one embodiment, breast cancer genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a breast cancer gene or portion of a breast cancer gene under the control of a promoter for expression in a breast cancer patient. The breast cancer gene used for DNA vaccines can encode full-length breast cancer proteins, but more preferably encodes portions of the breast cancer proteins including peptides derived from the breast cancer protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived

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from a breast cancer gene. Similarly, it is possible to immunize a patient with a plurality of breast cancer genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing breast cancer proteins.

5 In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the breast cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

10 In another preferred embodiment breast cancer genes find use in generating animal models of breast cancer. As is appreciated by one of ordinary skill in the art, when the breast cancer gene identified is repressed or diminished in breast cancer tissue, gene therapy technology wherein antisense RNA directed to the breast cancer gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of breast cancer that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the breast cancer protein. When desired, tissue-specific expression or knockout of the breast cancer protein may be necessary.

15 It is also possible that the breast cancer protein is overexpressed in breast cancer. As such, transgenic animals can be generated that overexpress the breast cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of breast cancer and are additionally useful in screening for bioactive molecules to treat breast cancer.

20 It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLE

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Expression studies were performed herein on both the protein and nucleic acid level. Results are provided in the figures.

An experiment was performed to examine the correlation (if any) between BCH1 protein and estrogen receptor (ER) expression and localization. Antibodies against BCH1 protein were obtained by immunization in rabbits with 15-mer synthetic peptides corresponding to regions of BCH1. Anti-ER antibodies were purchased commercially. Approximately 50 breast carcinoma tissue specimens (5 micron serial sections; paraffin-embedded, formalin-fixed) were analyzed by immunohistochemistry. Of these, ~40% were positive for BCH1 expression; ~35% were positive for ER. Protein levels were scored from 1 to 5 by immunohistochemistry, with 5 representing the highest expression. Co-expression of BCH1 and ER is shown in Figure 37.

Of the ER+ tumors (n=108), about one-half have predominantly nuclear localizations of ER, one-half predominantly cytoplasmic. Interestingly, while the BCH1+/ER+ tumors were no more prevalent than by chance, without exception tumors with high levels of BCH1 (IHC score = 4 or 5) showed exclusively localization of ER to the cytoplasm, with exclusion from the nucleus (see Figures 38 and 39) (n=16, $p < 5 \times 10^{-3}$), whereas low expression of BCH1 had no correlation with ER localization and was often associated with nuclear ER (see Figures 40 and 41).

Currently, ER expression is an important clinical prognostic marker for breast cancer. Because signaling through ER to activate most estrogen-responsive genes is believed to require translocation of activated ER to the nucleus, high expression of BCH1 is predicted to correlate with functionally-negative ER in ER+ tumors. Since ER- correlates with poor prognosis, BCH1 may also be a valuable prognostic marker, as it may also correlate with poor prognosis, or to no-responsiveness to anti-estrogen therapies (e.g., tamoxifen), since approximately 50% of the ER+ patients do not respond to tamoxifen. Tamoxifen works against the effects of estrogen on these cells. It is often called an "anti-estrogen." As a treatment for breast cancer, the drug slows or stops the growth of cancer cells that are already present in the body. As adjuvant therapy, tamoxifen has been shown to help prevent the original breast cancer from returning and also prevent the development of new cancers in the opposite breast.

Recent publications report that ER can signal through the Ras/Raf/MAP kinase. Since many of the proteins in this signaling cascade reside in the cytoplasm, increased BCH1 expression may correlate with, or even cause, ER to remain in the cytoplasm, thereby altering the signaling of ER through the

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MAP kinase pathway. This may be an explanation for the subset of ER+ patients who do not respond to tamoxifen.

Furthermore, BCH1 may have a casual role in ER translocation to the nucleus, by either directly or indirectly preventing nuclear translocation, thereby eliminating or altering responsiveness of the cell to estrogens or their analogs.

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CLAIMS

We claim:

1. A method of screening drug candidates comprising:
 - a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of BCH1, BCA2, BCJ7, BCN1, BCN5, BCQ2, BCQ5, BCR2, BCX2 and BCY3 or a fragment thereof;
 - b) adding a drug candidate to said cell; and
 - c) determining the effect of said drug candidate on the expression of said expression profile gene.
2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.
3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.
4. A method of screening for a bioactive agent capable of binding to a breast cancer modulator protein (BCMP), wherein said BCMP is BCH1 or a fragment thereof, said method comprising combining said BCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said BCMP.
5. A method for screening for a bioactive agent capable of modulating the activity of a breast cancer modulator protein (BCMP), wherein said BCMP is BCH1 or a fragment thereof, said method comprising combining said BCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said BCMP.
6. A method of evaluating the effect of a candidate breast cancer drug comprising:
 - a) administering said drug to a patient;
 - b) removing a cell sample from said patient; and
 - c) determining the expression profile of said cell.

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7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.
8. A biochip comprising a nucleic acid segment encoding BCH1 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.
- 5 9. A method of diagnosing breast cancer comprising:
 - a) determining the expression of a gene encoding BCH1 or a fragment thereof in a first tissue type of a first individual; and
 - b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;
- 10 wherein a difference in said expression indicates that the first individual has breast cancer.
10. An antibody which specifically binds to BCH1, or a fragment thereof.
11. The antibody of Claim 10 wherein said fragment is BCH1p1 or BCH1p2.
12. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.
13. The antibody of Claim 10, wherein said antibody is a humanized antibody.
- 15 14. The antibody of Claim 10, wherein said antibody is an antibody fragment.
15. A method for screening for a bioactive agent capable of interfering with the binding of a breast cancer modulator protein (BCMP) or a fragment thereof and an antibody which binds to said BCMP or fragment thereof, said method comprising:
 - a) combining a BCMP or fragment thereof, a candidate bioactive agent and and an antibody
 - 20 which binds to said BCMP or fragment thereof; and
 - b) determining the binding of said BCMP or fragment thereof and said antibody.
16. A method for inhibiting breast cancer, said method comprising administering to a cell a composition comprising an antibody to BCH1 or a fragment thereof.
17. The method of Claim 16 wherein said cell is a cell of an individual.

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18. The method of Claim 17 wherein said individual has cancer.
19. The method of Claim 16 wherein said fragment is selected from the group consisting of BCH1p1 and BCH1p2.
20. The method of Claim 16 wherein said antibody is a humanized antibody.
- 5 21. The method of Claim 16 wherein said antibody is an antibody fragment.
22. A method for inhibiting breast cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to BCH1.
23. A peptide consisting essentially of BCH1p1.
24. A composition comprising the peptide of Claim 23.
- 10 25. A peptide consisting essentially of BCH1p2.
26. A composition comprising the peptide of Claim 25.
27. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising BCH1 or a fragment thereof.
28. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding BCH1 or a fragment thereof.
- 15 29. A composition capable of eliciting an immune response in an individual, said composition comprising BCH1 or a fragment thereof and a pharmaceutically acceptable carrier.
30. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding BCH1 or a fragment thereof and a pharmaceutically acceptable carrier.
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31. A method of treating an individual for breast cancer comprising administering to said individual an inhibitor of BCH1.
32. The method of Claim 31 wherein said inhibitor is an antibody.
33. The method of Claim 31 wherein said individual is non-responsive to an anti-estrogen and is positive for estrogen receptor.
- 5 34. The method of Claim 33 wherein said method further comprises administering an anti-estrogen.
35. A method for determining the prognosis of an individual with breast cancer comprising determining the level of BCH1 in a sample, wherein a high level of BCH1 indicates a poor prognosis.
- 10 36. A method for determining whether an individual with breast cancer will be non-responsive to anti-estrogen therapies comprising determining the level of BCH1 wherein a high level of BCH1 indicates that an individual will be non-responsive.
37. A method of neutralizing the effect of a BCH1, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.
- 15

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FIGURE 1

Accession	Gene Name	Ratio breast v. tumor
RC_AA023277	ESTs	10.0
RC_H49425	ESTs	10.0
RC_N51657	EST	10.0
RC_P16733	ESTs	10.0
RC_P079072	Insulin-like growth factor binding protein 6	10.0
HG1428-HT1428	EST - HG1428-HT1428	10.0
HG3157-HT2227	EST - HG3157-HT2227	10.0
HG3841-HT2969	EST - HG3841-HT2969	10.0
J03874	EST - HG3841-HT2969	10.0
J03474	Fatty acid binding protein 4 adipocyte	10.0
L19871	SERUM AMYLOID A PROTEIN PRECURSOR	10.0
L49169	Activating transcription factor 3	10.0
M12963	Human GOS3 mRNA complete cds	10.0
M21305	Alcohol dehydrogenase 1 (class I) alpha polypeptide	10.0
M22430	EST - M21305	10.0
M25079	Phospholipase A2 group IIA (platelet synovial)	10.0
M27826	Human endogenous retroviral protease mRNA	10.0
M30185	Cholesteryl ester transfer protein plasma	10.0
U22961	EST - L122961	10.0
U48251	Homo sapiens protein kinase C-binding protein	10.0
U88902	EST - U88902 cds1_f	10.0
X00129	PLASMA RETINOL-BINDING PROTEIN	10.0
X04602	Interleukin 6 (B cell stimulatory factor 2)	10.0
X14141	SERUM AMYLOID A PROTEIN PRECURSOR	10.0
X24559	Tetranectin (plasminogen-binding protein)	10.0
X75938	TR43 (alternatively spliced) (human brain mRNA)	10.0
X87344	H.sapiens DMA DMB HLA-Z1 JPP2 LMP2 TAP1	10.0
X99142	H.sapiens mRNA for hHKb1 protein	10.0
Z49269	Homo sapiens MIP-1 delta mRNA complete cds	10.0
AA081995	EST - AA081995	10.0
AA090439	ESTs	10.0
AA137107	ESTs	10.0
AA203296	ESTs	10.0
AA285284	ESTs highly similar to ISOCITRATE	10.0
AA310850	ESTs	10.0

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FIGURE 1 (CONT.)

AA418143	AA418143	ESTs	10.0
AA425719	AA425719	ESTs	10.0
AA427379	AA427379	ESTs	10.0
AA452705	AA452705	ESTs Weakly similar to D2045.9 [C-elegans]	10.0
AB002328	AB002328	Human mRNA for KIAA0339 gene partial cds	10.0
AF000575_s	AF000575	Homo sapiens clone 17.11 immunoglobulin-like	10.0
M12272_s	M12272	Alcohol dehydrogenase 3 (class I) gamma	10.0
M26315_cds2_s	M26315	CD8 antigen alpha polypeptide (p32)	10.0
M64936_1	M64936	Homo sapiens retinoic acid-inducible endogenous	10.0
M81349	M81349	SERUM AMYLOID A-4 PROTEIN PRECURSOR	10.0
M84526	M84526	D component of complement (autosol)	10.0
N73185	N73185	EST	10.0
N79074_s	N79074	ESTs	10.0
N88827	N88827	ESTs	10.0
N91071_s	N91071	ESTs	10.0
R21149	R21149	ESTs Highly similar to RAB GDP	10.0
R69417	R69417	ESTs	10.0
RC_AA009764	AA009764	ESTs	10.0
RC_AA017254	AA017254	ESTs	10.0
RC_AA019300	AA019300	ESTs	10.0
RC_AA026280	AA026280	ESTs	10.0
RC_AA115253	AA115253	ESTs	10.0
RC_AA128617	AA128617	ESTs	10.0
RC_AA179338	AA179338	ESTs	10.0
RC_AA223237	AA223237	ESTs Moderately similar to retrovirus-related pol	10.0
RC_AA234308	AA234308	ESTs	10.0
RC_AA251772	AA251772	H. sapiens mRNA for HES1 protein	10.0
RC_AA279673	AA279673	Homo sapiens mRNA for HscGAK complete cds	10.0
RC_AA411443	AA411443	ESTs	10.0
RC_AA416947	AA416947	ESTs	10.0
RC_AA426584	AA426584	ESTs	10.0
RC_AA434113	AA434113	ESTs	10.0
RC_AA433303	AA433303	ESTs	10.0
RC_AA446005	AA446005	ESTs	10.0
RC_AA449471	AA449471	ESTs	10.0
RC_AA451877	AA451877	ESTs	10.0

FIGURE 1 (CONT.)

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RC_AA47847 AA47847	ESTs	10.0
RC_AA491001_f AA491001	ESTs Weakly similar to ORF YOR173w	10.0
RC_AA620446 AA620446	ESTs	10.0
RC_AA621131 AA621131	ESTs	10.0
RC_AA621414 AA621414	Homo sapiens transmembrane protein mRNA	10.0
RC_AA621680 AA621680	Homo sapiens Kruppel-like zinc finger protein	10.0
RC_D25786 D25786	EST	10.0
RC_D56989_f D56989	ESTs	10.0
RC_D56989_i D56989	ESTs	10.0
RC_D59420 D59420	EST - RC_D59420	10.0
T87593 T87593	EST - T87593	10.0
U25265 U25265	Human MEK5 mRNA complete cds	10.0
U81787 U81787	Human Wnt10B mRNA complete cds	10.0
W19098 W19098	ESTs	10.0
W26097 W26097	ESTs	10.0
W28601 W28601	Human mRNA for rab GDI alpha complete cds	10.0
W28648 W28648	ESTs	10.0
W28931 W28931	ESTs	10.0
W38002_s W38002	ESTs Weakly similar to D2030.9 [C.elegans]	10.0
X04602_s X04602	EST - W38002_s	10.0
X55019_s X55019	Interleukin 6 (B cell stimulatory factor 2)	10.0
RC_AA01576 AA01576	Cholinergic receptor nicotinic delta polypeptide	10.0
RC_AA015736 AA015736	ESTs	10.0
RC_AA017462 AA017462	ESTs Weakly similar to C27H6.5 [C.elegans]	10.0
RC_AA017547_f AA017547	ESTs	10.0
RC_AA025061 AA025061	ESTs	10.0
RC_AA037388 AA037388	ESTs	10.0
RC_AA043675 AA043675	EST	10.0
RC_AA047229 AA047229	ESTs Weakly similar to HYPOTHETICAL 41.9 KD	10.0
RC_AA059473 AA059473	ESTs	10.0
RC_AA071193 AA071193	ESTs	10.0
RC_AA075124 AA075124	EST - RC_AA075124	10.0
RC_AA079079 AA079079	EST - RC_AA079079	10.0
RC_AA079120 AA079120	EST - RC_AA079120	10.0
RC_AA083070 AA083070	EST - RC_AA083070_s	10.0
RC_AA121820 AA121820	ESTs	10.0
RC_AA126583 AA126583	ESTs	10.0

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FIGURE 1 (CONT.)

RC_AA131571_AA131571	ESTs	10.0
RC_AA171426_AA171426	ESTs	10.0
RC_AA219555_AA219555	ESTs	10.0
RC_H05645_H05645	ESTs Weakly similar to R07B7.10 [C.elegans]	10.0
RC_H10761_H10761	ESTs	10.0
RC_H18299_H18299	ESTs	10.0
RC_H51276_H51276	ESTs	10.0
RC_H58934_H58934	ESTs Moderately similar to TRANSIENT	10.0
RC_H69547_H69547	RECEPTOR POTENTIAL LOCUS C PROTEIN	10.0
RC_N49409_N49409	ESTs Weakly similar to HYPOTHETICAL 46.1 KD	10.0
RC_N62889_s_N62889	ESTs	10.0
RC_N69541_N69541	ESTs	10.0
RC_R00144_R00144	EST - RC_R00144	10.0
RC_R07324_R07324	ESTs	10.0
RC_R16157_R16157	Homo sapiens clone 23770 mRNA sequence	10.0
RC_R33146_R33146	ESTs	10.0
RC_R42333_R42333	ESTs	10.0
RC_R43977_R43977	ESTs Moderately similar to H11 ALU SUBFAMILY	10.0
RC_R49568_R49568	ESTs	10.0
RC_R66992_R66992	ESTs	10.0
RC_R77302_R77302	ESTs	10.0
RC_T03803_T03803	ESTs	10.0
RC_T51588_T51588	Human mRNA for KIAA0226 gene complete cds	10.0
RC_T58756_T58756	ESTs	10.0
RC_T67285_T67285	EST	10.0
RC_T79768_T79768	ESTs	10.0
RC_T91047_T91047	ESTs	10.0
RC_W04657_W04657	ESTs	10.0
RC_W33178_W33178	ESTs	10.0
RC_W86195_W86195	ESTs Weakly similar to retrovirus-related pol	10.0
RC_Z39319_Z39319	EST	10.0
RC_AA43580_AA43580	ESTs	10.0
RC_AA43800_AA43800	ESTs	10.0
RC_AA43968_AA43968	ESTs	10.0
RC_AA481427_AA481427	ESTs	10.0

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FIGURE 1 (CONT.)

RC_C21161_C21161	EST	10.0
RC_D20860_D20860	Homo sapiens intermediate conductance calcium-activated potassium channel (hKCa4) mRNA	10.0
RC_H02848_s_H02848	TYROSINE-PROTEIN KINASE RECEPTOR TIE-	10.0
RC_N20468_N20468	ESTs Weakly similar to Itic-1 protein ORF2	10.0
RC_N39426_N39426	ESTs	10.0
RC_N49285_f_N49285	ESTs	10.0
RC_N50034_N50034	ESTs	10.0
RC_N65972_N65972	ESTs	10.0
RC_N70907_N70907	EST	10.0
RC_T47418_T47418	ESTs	10.0
RC_T48075_f_T48075	Hemoglobin alpha 1	10.0
RC_T52813_s_T52813	Human G0S2 protein gene contig	10.0
RC_W38051_W38051	EST - RC_W38051	10.0
RC_A437323_f_A437323	MYO-INOSITOL-1(OR 4)-	10.0
RC_A437323_f_A437323	EST	10.0
RC_A437323_f_A437323	ESTs Weakly similar to RETROVIRUS-RELATED	10.0
RC_A437323_f_A437323	ESTs	10.0
RC_A443137_A443137	EST	10.0
RC_A447555_A447555	EST	10.0
RC_A448945_A448945	EST	10.0
RC_A4485421_f_A4485421	ESTs	10.0
RC_A4621529_f_A4621529	EST	10.0
RC_H15814_s_H15814	Human apM1 mRNA for GS3109 (novel adipose	10.0
RC_H90310_f_H90310	ESTs Moderately similar to nuclear autoantigen	10.0
RC_N22392_N22392	Homo sapiens oligodendrocyte-specific protein	10.0
RC_N22730_s_N22730	P35-C-FOS PROTO-ONCOGENE PROTEIN	10.0
RC_N50809_N50809	ESTs Highly similar to HYPOTHETICAL 58.2 KD PROTEIN IN BEM2 SPT2 INTERGENIC	10.0
RC_N48732_s_N48732	ESTs	10.0
RC_T47089_s_T47089	Cytochrome P450 subfamily XXI (steroid 21-	10.0
RC_T61256_s_T61256	H.sapiens KHK mRNA for ketohexokinase clone	10.0

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FIGURE 1 (CONT.)

RC_T04447_s_T04447	ESTs	10.0
RC_T08109_f_T08109	ESTs	10.0
RC_W72887_W72887	ESTs	10.0
RC_W04688_W04688	ESTs	10.0
AF000959_AF000959	Homo sapiens transmembrane protein mRNA	5.0
HG2147-TIGR-HG2147-HT2217	EST - HG2147-HT2217_f	5.0
HG2796-HT2904-TIGR-HG2796-HT2904	EST - HG2796-HT2904	5.0
HG3236-TIGR-HG3236-HT3413	EST - HG3236-HT3413_f	5.0
HG537-HT537-TIGR-HG537-HT537	EST - HG537-HT537	5.0
L07738_L07738	DIHYDROPYRIDINE-SENSITIVE L-TYPE	5.0
L10373_L10373	CELL SURFACE GLYCOPROTEIN AL5	5.0
L13197_L13197	Pregnancy-associated plasma protein A	5.0
L14927_L14927	Lipocalin 1 (protein migrating faster than albumin)	5.0
M57731_M57731	GRO2 oncogene	5.0
M62402_M62402	Insulin-like growth factor binding protein 6	5.0
M72885_ma1_M72885	Human GGS1 protein gene complete cds	5.0
S68874_S68874	Prostaglandin E receptor 3 (subtype EP3)	5.0
U32674_U32674	Homo sapiens skeletal muscle LIM1 protein FHL1	5.0
U60115_U60115	EST - U32674	5.0
U92457_U92457	Glutamate receptor metabotropic 4	5.0
X03350_X03350	Alcohol dehydrogenase 2 (class I) beta polypeptide	5.0
X98085_X98085	Tenascin R (retrocin janusin)	5.0
Z84721_cds2_Z84721	Hemoglobin alpha 1	5.0
AA044622_AA044622	ESTs Weakly similar to ZINC FINGER PROTEIN	5.0
AA059327_f_AA059327	Homo sapiens clone Z3718 mRNA sequence	5.0
AA062932_AA062932	Homo sapiens mRNA for GNAS1 protein (IMAGE)	5.0
AA082561_s_AA082561	EST - AA082561_s	5.0
AA093348_AA093348	Homo sapiens secreted fittzled related protein	5.0
AA166651_AA166651	ESTs Weakly similar to HYPOTHETICAL 39.7 KD	5.0
AA191072_AA191072	EST - AA191072	5.0

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FIGURE 1 (CONT.)

AA210757	AA210757	Transcription factor 3 (E2A immunoglobulin	5.0
AA232121	AA232121	Human tyrosyl-RNA synthetase mRNA complete	5.0
AA247434	AA247434	ESTs Highly similar to OVARIAN GRANULOSA	5.0
AA252752	AA252752	ESTs	5.0
AA278194	AA278194	Human DNA sequence from clone 71L16 on	5.0
		chromosome Xp11. Contains a probable Zinc Finger	
		protein (pseudo)gene an unknown putative gene a	
AA291786_s	AA291786	ESTs Weakly similar to HYPOTHETICAL	5.0
AA400044	AA400044	Human clone 23803 nuRNA partial cds	5.0
AA402109	AA402109	ESTs	5.0
AA402971_s	AA402971	ESTs Moderately similar to serine protease	5.0
AA416829	AA416829	ESTs	5.0
AA418214	AA418214	ESTs Weakly similar to APK1 antigen [H.sapiens]	5.0
AA422123_j	AA422123	ESTs Weakly similar to eukaryotic initiation factor	5.0
AA448946_r	AA448946	ESTs	5.0
AA461426_r	AA461426	ESTs	5.0
AB002361	AB002361	Human mRNA for KIAA0363 gene partial cds	5.0
AF001900	AF001900	Homo sapiens secreted frizzled related protein	5.0
C16161_s	C16161	ESTs	5.0
C17282	C17282	ESTs Weakly similar to L8083.1 gene product	5.0
D10216_s	D10216	POU domain class 1 transcription factor 1 (Ptl	5.0
D31381	D31381	ESTs Weakly similar to cytoplasmic dynein light	5.0
D88213	D88213	Amino oxidase copper containing 2 (retina-specific)	5.0
F5201	F5201	EST - F15201	5.0
H30278	H30278	ESTs	5.0
L34155	L34155	Laminin alpha 3 (necin (150kD) kalium (165kD)	5.0
N39361	N39361	ESTs Highly similar to GLYCINE-RICH	5.0
N40774	N40774	ESTs	5.0

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FIG. 1

FIGURE 1 (CONT.)

N99542	N99542	Homo sapiens exportin 1 mRNA, complete cds	EST	5.0
R19997	R19997	ESTs Moderately similar to H1: ALU SUBFAMILY Y	ESTs	5.0
R24011	R24011	ESTs Moderately similar to H1: ALU SUBFAMILY Y	ESTs	5.0
R25944	f R25944	ESTs Moderately similar to H1: ALU SUBFAMILY Y	ESTs	5.0
R68735	R68735	H. sapiens mRNA for phosphoinositide 3-kinase	ESTs	5.0
R81474	R81474	Acyl-Coenzyme A dehydrogenase very long chain	ESTs	5.0
R88038	R88038	ESTs	ESTs	5.0
RC_AA007153	AA007153	ESTs	ESTs	5.0
RC_AA019031	AA019031	ESTs	ESTs	5.0
RC_AA025351	AA025351	ESTs	ESTs	5.0
RC_AA033749	AA033749	ESTs	ESTs	5.0
RC_AA066626	AA066626	ESTs	ESTs	5.0
RC_AA126429	AA126429	ESTs	ESTs	5.0
RC_AA151872	AA151872	ESTs	ESTs	5.0
RC_AA215643	AA215643	ESTs	ESTs	5.0
RC_AA402268	AA402268	ESTs	ESTs	5.0
RC_AA402613	AA402613	ESTs	ESTs	5.0
RC_AA405449	AA405449	ESTs	ESTs	5.0
RC_AA422146	AA422146	ESTs	ESTs	5.0
RC_AA427627	AA427627	ESTs	ESTs	5.0
RC_AA446027	AA446027	Early growth response 2 (Krox-20) (Drosophila)	ESTs	5.0
RC_AA459944	AA459944	ESTs	ESTs	5.0
RC_AA463929	AA463929	ESTs	ESTs	5.0
RC_AA478305	AA478305	Homo sapiens chromosome 19 cosmid R27216	ESTs	5.0
RC_AA482546	AA482546	Human mRNA for KIAA0124 gene partial cds	ESTs	5.0
RC_AA485409	AA485409	ESTs	ESTs	5.0
RC_AA487576	AA487576	ESTs	ESTs	5.0
RC_AA489499	AA489499	ESTs	ESTs	5.0
RC_AA496980	AA496980	ESTs	ESTs	5.0
RC_AA521454	AA521454	ESTs	ESTs	5.0
RC_AA608802	AA608802	ESTs	ESTs	5.0
RC_AA609785	AA609785	Homo sapiens mRNA for doublecortin	ESTs	5.0
RC_AA621430	AA621430	Human LMP1 associated protein mRNA complete cds	ESTs	5.0
U15637	U15637	ESTs	ESTs	5.0
U15704	U15704	Homo sapiens killer cell receptor (KIR103) mRNA	ESTs	5.0
U73394	f U73394			

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FIGURE 1 (CONT.)

U76456	U76456	Human tissue inhibitor of metalloproteinase 4	5.0
U83171	U83171	Human macrophage-derived chemokine precursor	5.0
W26652	W26652	ESTs	5.0
W29012	W29012	ESTs	5.0
W37319	W37319	ESTs	5.0
W37398	W37398	ESTs	5.0
W44533	W44533	MAP KINASE PHOSPHATASE-1	5.0
X72308	X72308	MONOCYTE CHEMOTACTIC PROTEIN 3	5.0
RC_AA025837	AA025837	ESTs	5.0
RC_AA029927	AA029927	ESTs	5.0
RC_AA045306	AA045306	ESTs	5.0
RC_AA063174	AA063174	ESTs	5.0
RC_AA070500	AA070500	EST - RC_AA070500	5.0
RC_AA074885	AA074885	Homo sapiens macrophage receptor MARCO	5.0
RC_AA099820	AA099820	ESTs	5.0
RC_AA113289	AA113289	EST - RC_AA113289	5.0
RC_AA207059	AA207059	ESTs Moderately similar to H11 ALU SUBFAMILY	5.0
RC_F01449	F01449	ESTs	5.0
RC_H41380	H41380	ESTs	5.0
RC_H52172	H52172	EST - RC_H52172	5.0
RC_H58222	H58222	ESTs	5.0
RC_N52176	N52176	ESTs	5.0
RC_N66616	N66616	ESTs Moderately similar to CMRF35 ANTIGEN	5.0
RC_N67583	N67583	ESTs	5.0
RC_N73988	N73988	ESTs Weakly similar to No definition line found	5.0
RC_N92239	N92239	ESTs Highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA	5.0
RC_R26065	R26065	ESTs	5.0
RC_R43035	R43035	ESTs	5.0
RC_R51898	R51898	ESTs	5.0
RC_R84968	R84968	ESTs	5.0
RC_R96306	R96306	ESTs	5.0
RC_R98491	R98491	ESTs	5.0
RC_T10142	T10142	ESTs	5.0

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FIGURE 1 (CONT.)

RC_T34659	T54659	EST	5.0
RC_T37857	T37857	ESTs	5.0
RC_T86674	T86674	ESTs	5.0
RC_T89160.f	T89160	ESTs	5.0
RC_T91185	T91185	ESTs	5.0
RC_Z39975	Z39975	ESTs	5.0
RC_Z41480	Z41480	ESTs	5.0
RC_AA020736	AA020736	EST - RC_AA020736	5.0
RC_AA034378.f	AA034378	ESTs	5.0
RC_AA065096	AA065096	EST - RC_AA065096	5.0
RC_AA084362.f	AA084362	EST - RC_AA084362.f	5.0
RC_AA24826	AA24826	EST	5.0
RC_AA24839	AA24839	ESTs	5.0
RC_AA26534	AA26534	ESTs	5.0
RC_AA405791	AA405791	ESTs	5.0
RC_AA406050	AA406050	Homo sapiens Tax interaction protein 33 mRNA	5.0
RC_AA412707	AA412707	ESTs	5.0
RC_AA428964	AA428964	Homo sapiens serine protease-like protease (nest)	5.0
RC_AA463902	AA463902	ESTs	5.0
RC_AA485080	AA485080	ESTs	5.0
RC_AA488839	AA488839	ESTs	5.0
RC_F04052	F04052	Homo sapiens clone 23763 unknown mRNA, partial	5.0
RC_F10528.f	F10528	ESTs Moderately similar to H1 ALU CLASS B	5.0
RC_H90434	H90434	EST	5.0
RC_H95958	H95958	ESTs	5.0
RC_H97387.s	H97387	ESTs	5.0
RC_N23399	N23399	ESTs	5.0
RC_N33978	N33978	ESTs	5.0
RC_N50937	N50937	EST	5.0
RC_N59860.s	N59860	Human clone 23947 mRNA partial cds	5.0
RC_N69476	N69476	ESTs	5.0
RC_N90744	N90744	ESTs	5.0
RC_R95132	R95132	EST - RC_R95132	5.0
RC_T41144	T41144	ESTs	5.0
RC_T77892	T77892	EST - RC_T77892	5.0
RC_T81824	T81824	EST	5.0
RC_W74257	W74257	EST - RC_W74257	5.0

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FIGURE 1 (CONT.)

RC_W78168	W78168	ESTs	5.0
RC_W86214	W86214	ESTs	5.0
RC_W87535	W87535	ESTs	5.0
RC_AA297532	AA297532	ESTs	5.0
RC_AA299629	AA299629	ESTs	5.0
RC_AA383038	AA383038	ESTs	5.0
RC_AA398531	AA398531	ESTs	5.0
RC_AA401695	AA401695	ESTs	5.0
RC_AA405763	AA405763	ESTs	5.0
RC_AA421483	AA421483	ESTs	5.0
RC_AA435746	AA435746	ESTs	5.0
RC_AA456975	AA456975	ESTs	5.0
RC_AA459658	AA459658	ESTs	5.0
RC_AA609122	AA609122	ESTs	5.0
RC_AA609214	AA609214	ESTs	5.0
RC_F04387	F04387	ESTs	5.0
RC_H59063	H59063	ESTs	5.0
RC_H79007	H79007	ESTs	5.0
RC_H83465	H83465	ESTs	5.0
RC_N27118	N27118	ESTs	5.0
RC_N56898	N56898	ESTs	5.0
RC_R01398	R01398	ESTs	5.0
RC_R44214	R44214	ESTs	5.0
RC_R71403	R71403	ESTs	5.0
RC_T61561	T61561	ESTs	5.0
RC_T94357	T94357	ESTs	5.0
RC_W61260	W61260	ESTs	5.0
RC_W87480	W87480	ESTs	5.0
RC_T55547	T55547	ESTs	3.3
RC_W44733	W44733	ESTs	3.3
RC_AA401564	AA401564	ESTs	3.3
RC_N34417	N34417	ESTs	3.3
RC_N53145	N53145	ESTs	3.3
RC_N81130	N81130	ESTs	3.3
RC_R02384	R02384	ESTs	3.3
RC_W73194	W73194	ESTs	3.3
RNA-BINDING PROTEIN FUS/TLS			
Homo sapiens mRNA for KIAA0538 protein partial			
Apolipoprotein D			
ESTs Weakly similar to ADAM 20 [H. sapiens]			
AXL receptor tyrosine kinase			
EST - RC_H59063			
EST - RC_H83465			
ESTs Highly similar to HYPOTHETICAL 64.3 KD			
GTP-BINDING PROTEIN C32F5.3 IN			
Glutathione S-transferase M5			
EST - RC_R01398			
VON WILLEBRAND FACTOR PRECURSOR			
Homo sapiens STAT-induced STAT inhibitor-2			
Pregnancy-specific beta-1 glycoprotein 6			
EST - RC_N53145			

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FIGURE 1 (CONT.)

RC W73889.s W73889	
RC W92278 W92278	
RC R48540.s R48540	
YEL024w/RIP1	
Tetaneccin (plasminogen binding protein)	3.3
ESTs	3.3
ESTs	3.3
ESTs	3.3
EST - YEL024w/RIP1	3.3

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FIGURE 2

Accession	Gene Name	Ratio breast v. tumor
AA023277	ESTs	10.0
U88902	ESTs	10.0
RC_H49425	EST	10.0
RC_N51657	ESTs	10.0
RC_R16733	Insulin-like growth factor binding protein	10.0
AA079072	EST - HG1428-HT1428	10.0
RC_AA079072_s	Human GOS3 mRNA complete cds	10.0
HG1428-HT1428	SERUM AMYLOID A PROTEIN	10.0
U88902	D component of complement (adipsin)	10.0
X51441	ESTs	10.0
M84526	Homo sapiens Kruppel-like zinc finger	10.0
R69417	ESTs	10.0
RC_AA621680	ESTs	10.0
RC_AA071193	ESTs	10.0
RC_N66951	ESTs	10.0
RC_R33146	P53-C-FOS PROTO-ONCOGENE	10.0
RC_N23730_s	Homo sapiens mRNA for perlepin	10.0
RC_W94688	EST - HG2157-HT2227	10.0
HG2157-HT2227	EST - HG2841-HT2969	10.0
HG2841-HT2969	Fatty acid binding protein class 1	10.0
J02874	SERUM AMYLOID A PROTEIN	10.0
J03474	Activating transcription factor 3	10.0
L19871	Alcohol dehydrogenase 1 (class I) alpha	10.0
M12963	EST - M21305	10.0
M21305	Phospholipase A2 group IIA (platelets)	10.0
M22430	Hemoglobin beta	10.0
M25079	Human endogenous retroviral protease	10.0
M27826	Cholesteryl ester transfer protein plasma	10.0
M27826	EST - U22961	10.0
M30185	Homo sapiens protein kinase C-binding	10.0
U22961	EST - U88902_cds1_f	10.0
U48251	PLASMA RETINOL-BINDING	10.0
U88902_cds1_f	Interleukin 6 (B cell stimulatory factor 2)	10.0
X00129	Tetranectin (plasminogen-binding)	10.0
X04602	TrkB (alternatively spliced) [human	10.0
X64559	H.sapiens DMB DMB HLA-Z1 JPP2	10.0
X75958	H.sapiens mRNA for hHRb1 protein	10.0
X87344	Homo sapiens MIP-1 delta mRNA	10.0
cds10_f	EST - AA081995	10.0
X99142	EST	10.0
Z49269	EST	10.0
AA081995	EST	10.0
AA090439	EST	10.0

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FIGURE 2 (CONT.)

AA137107	AA137107	ESTs	10.0
AA203296	AA203296	ESTs	10.0
AA285284	AA285284	ESTs Highly similar to ISOCITRATE	10.0
AA310850	AA310850	ESTs	10.0
AA418143	AA418143	ESTs	10.0
AA425719	AA425719	ESTs	10.0
AA427379	AA427379	ESTs	10.0
AA452705	AA452705	ESTs Weakly similar to D2045.9	10.0
AB002328	AB002328	Human mRNA for KIAA0330 gene	10.0
AF000573	AF000573	Human alpha 3 (class I) gamma	10.0
M12272.s	M12272.s	Alcohol dehydrogenase 3 (class I) gamma	10.0
M64936	M64936	CD8 antigen alpha polypeptide (c32)	10.0
M81349	M81349	Human sapiens retinoic acid-inducible	10.0
N73185	N73185	SERUM AMYLOID A-4 PROTEIN	10.0
N79674	N79674	EST	10.0
N86845	N86845	ESTs	10.0
N88827	N88827	ESTs	10.0
N91071	N91071	ESTs Highly similar to RAB GDP	10.0
R21149	R21149	ESTs	10.0
AA009764	AA009764	ESTs	10.0
AA017254	AA017254	ESTs	10.0
AA019300	AA019300	ESTs	10.0
AA026280	AA026280	ESTs	10.0
AA115253	AA115253	ESTs	10.0
AA128617	AA128617	ESTs	10.0
AA179338	AA179338	ESTs Moderately similar to retrovirus	10.0
AA223237	AA223237	ESTs	10.0
AA234308	AA234308	ESTs	10.0
AA251772	AA251772	H.sapiens mRNA for HES1 protein	10.0
AA279673	AA279673	Human sapiens mRNA for HES1	10.0
AA411443	AA411443	ESTs	10.0
AA416947	AA416947	ESTs	10.0
AA426384	AA426384	ESTs	10.0
AA441113	AA441113	ESTs	10.0
AA445383	AA445383	ESTs	10.0
AA446005	AA446005	ESTs	10.0
AA449471	AA449471	ESTs	10.0
AA451877	AA451877	ESTs	10.0
AA478487	AA478487	ESTs	10.0
AA491001	AA491001	ESTs Weakly similar to ORF YOR173w	10.0
RC_AA009764	RC_AA009764		
RC_AA017254	RC_AA017254		
RC_AA019300	RC_AA019300		
RC_AA026280	RC_AA026280		
RC_AA115253	RC_AA115253		
RC_AA128617	RC_AA128617		
RC_AA179338	RC_AA179338		
RC_AA223237	RC_AA223237		
RC_AA234308	RC_AA234308		
RC_AA251772	RC_AA251772		
RC_AA279673	RC_AA279673		
RC_AA411443	RC_AA411443		
RC_AA416947	RC_AA416947		
RC_AA426384	RC_AA426384		
RC_AA441113	RC_AA441113		
RC_AA445383	RC_AA445383		
RC_AA446005	RC_AA446005		
RC_AA449471	RC_AA449471		
RC_AA451877	RC_AA451877		
RC_AA478487	RC_AA478487		
RC_AA491001_f	RC_AA491001_f		

RC_AA620446	AE620446	100	ESTs
RC_AA621131	AE621131	100	ESTs
RC_AA621416	AE621416	100	ESTs
RC_D25786	D25786	100	EST
RC_D56989 f	D56989	100	ESTs
RC_D56989 j	D56989	100	ESTs
RC_D59420	D59420	100	EST - RC_D39420
T87593	T87593	100	EST - RC_D39420
U25265	U25265	100	Human MER5 mRNA complete cds
U81787	U81787	100	Human Wnt10B mRNA complete cds
W19098	W19098	100	ESTs
D26097	D26097	100	ESTs
W28390	W28390	100	Human mRNA for rah (CD) alpha
W28348	W28348	100	ESTs
D28511	D28511	100	ESTs Weakly similar to D20261
AF042268	AF042268	50	Human sapiens Sec and fringed related
RC_AA608802	AA608802	50	Human sapiens mRNA for KIAA0652
RC_F01449	F01449	50	ESTs
RC_AA034378 f	AA034378	50	ESTs
RC_AA456975 f	AA456975	50	ESTs
RC_AA456975 s	AA456975	50	Apolipoprotein D

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FIGURE 3

Atymatrix ID	Accession	Gene Name	ratio breast vs tumor
PC_A2073072_s	AA073072	Insulin-like growth factor binding protein 5	10.0
L49169	L49169	Human GOS3 mRNA complete cds	10.0
X51441	X51441	SERUM AMYLOID A PROTEIN PRECURSOR	10.0
PC_N65951	N65951	ESTs	10.0
PC_R33146	R33146	ESTs	10.0
M30185	M30185	Cholesteryl ester transfer protein plasma	10.0
U22981	U22981	EST - U22981	10.0
X64559	X64559	Tetranectin (glutaminogen-binding protein)	10.0
Z49269	Z49269	Homo sapiens MIP-1 delta mRNA complete cds	10.0
AA427379	AA427379	ESTs	10.0

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FIGURE 4

Accession	Gene Name	Ratio tumor v. breast
RC_AA453640	ESTs	135.3
RC_AA453640	ESTs	121.4
RC_AA453638	EST - RC_AA453638	107.3
RC_AA461322	EST	81.8
RC_AA461510	EST - RC_AA461510	75.3
RC_AA461510	Collagen type XI alpha 1	72.9
RC_AA453518	ESTs	61.5
RC_AA453518	EST - RC_N27351	57.1
RC_AA466737	Haptens mRNA for Sm protein F	53.9
RC_AA466737	Human focal adhesion kinase (FAK) mRNA complete cds	53.2
RC_AA466737	ESTs Weakly similar to zinc-finger protein Znf72D	52.0
RC_AA291468	ESTs	46.8
RC_AA291468	ESTs	45.7
RC_AA169440	ARYLAMINE N-ACETYLTRANSFERASE	38.9
RC_AA169440	ESTs	33.6
RC_AA621202	ESTs	33.5
RC_AA621202	EST - RC_AA232294	32.6
RC_AA232294	EST - RC_R86839	31.4
RC_R86839	GLYCOPROTEIN HORMONES ALPHA CHAIN	31.1
RC_R86839	EST	31.1
RC_AA453641	EST	30.6
RC_AA453641	EST - RC_AA211831	28.3
RC_AA609955	ESTs	28.1
RC_AA283905	Inhibin beta A (activin A activin AB alpha polypeptide)	25.5
RC_AA211831	ESTs Weakly similar to ZINC FINGER PROTEIN MFG1	25.5
RC_AA412090	ESTs	25.1
RC_N27159	EST	23.9
RC_AA421289	EST	23.8
RC_AA421289	Human TFIIID subunits TAF20 and TAF15 mRNA	23.6
RC_AA421289	ESTs	22.8
RC_AA421289	EST - RC_AA232940	21.7
RC_AA232940	ESTs	20.9
RC_AA463189	ESTs	19.5
RC_AA421171	ESTs	19.4
RC_AA251875	ESTs Moderately similar to POL POLYPROTEIN [elaine	17.7
RC_AA054228	ESTs	17.4
RC_D51215	EST - RC_D51215	17.1
RC_AA621462	CARCINOEMBRYONIC ANTIGEN PRECURSOR	17.1
RC_AA505133	ESTs	17.1

RC_AA0232508		ESTs	17.0
RC_AA0232508	H sapiens mRNA for MUK1 protein	ESTs	16.9
RC_AA024659		ESTs	16.8
RC_AA483191	EST - RC_AA211158	ESTs	16.8
RC_AA211158	Human 4E-binding protein 1 mRNA complete cds	ESTs	16.3
RC_AA290674		ESTs	16.2
RC_AA481853		ESTs	16.1
RC_AA481853	ESTs Highly similar to thyroid disease hypothetical	ESTs	16.1
RC_AA196768	EST - RC_AA196721	ESTs	15.9
RC_AA196721	Homo sapiens clone Z3967 alphaB nuclear cdc	ESTs	15.8
RC_Z3967	Inhibin beta A (activin A activin AB alpha polypeptide)	ESTs	15.7
RC_Z3967	TRANSLOCALIZATION PRECURSOR	ESTs	15.7
RC_Z3967	ESTs Moderately similar to H1 ALU SUBFAMILY 1 SP	ESTs	15.4
RC_Z3967		ESTs	15.2
RC_Z3967	ESTs Weakly similar to J03334.4 [C-epsilon]	ESTs	14.9
RC_Z3967	Human fibroblast activation protein mRNA complete cds	ESTs	14.7
RC_Z3967		ESTs	14.6
RC_Z3967	Interferon regulatory factor 5	ESTs	14.6
RC_Z3967	ESTs Moderately similar to PTTG gene product	ESTs	14.4
RC_Z3967		ESTs	14.4
RC_Z3967	Carboxypeptidase B1 (tissue)	ESTs	14.4
RC_Z3967	ESTs Highly similar to HYPOPHYSICAL_213 KD	ESTs	14.3
RC_Z3967	Human effector cell protease receptor-1 (EPK-1) ESTs	ESTs	14.2
RC_Z3967		ESTs	14.0
RC_Z3967	Chromogranin A (parathyroid secretory protein 1)	ESTs	14.0
RC_Z3967	ESTs Moderately similar to Z45H3 [D melanogaster]	ESTs	13.9
RC_Z3967	ESTs Weakly similar to TH1 protein [D melanogaster]	ESTs	13.9
RC_Z3967	Androgen receptor (dihydrotestosterone receptor testicular	ESTs	13.9
RC_Z3967		ESTs	13.9
RC_Z3967	ESTs Weakly similar to hypothalamic protein 1 [H sapiens]	ESTs	13.7
RC_Z3967		ESTs	13.5
RC_Z3967	Homo sapiens histone macroH2A1.2 mRNA complete cds	ESTs	13.4
RC_Z3967	ESTs Moderately similar to T1UG6.8 [C.elegans]	ESTs	13.4
RC_Z3967	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen	ESTs	13.4
RC_Z3967	EST - RC_AA023243	ESTs	13.4
RC_Z3967	Homo sapiens KIAA0040 mRNA pool cds	ESTs	13.4
RC_Z3967	F01444		

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FIGURE 4 (CONT.)

AA401324	ESTs	13.3
T8922.3	Homo sapiens mRNA for SCGF-beta complete cds	13.3
U0354	Human mRNA for KIAA0007 gene partial cds	13.3
AA431350	ESTs Moderately similar to [H] ALU SUBFAMILY SC	13.1
AA412065	EST - RC_AA412065	13.1
AA406655	ESTs	13.1
AA431738	EST	13.1
AA435178	Homo sapiens regulator of G-protein signalling 12	13.0
B61740	EST	12.8
R54950	ESTs	12.7
AA405488	EST	12.7
AA418749	Homo sapiens mRNA for A+U-rich element RNA binding	12.5
AA037285	ESTs	12.5
AA233796	EST	12.4
AA219305	ESTs	12.4
AA222245	ESTs	12.4
AA041276	ESTs Weakly similar to [H] ALU SUBFAMILY SX	12.3
AA463874	Homo sapiens EST130 mRNA complete cds	12.3
AA461528	ESTs	12.2
AA099404	ESTs	12.2
AA443985	ESTs	12.2
AA214305	ESTs	12.1
AA220223	Fibroblast growth factor receptor 2 (bacteria-expressed	12.1
AA478571	Glutamine-fructose-6-phosphate transaminase	12.1
U31875	Human Hep27 protein mRNA complete cds	11.8
RC_AA235217	ESTs	11.5
AA440674	ESTs	11.4
RC_AA236010	ESTs	11.4
J03589	UBIQUITIN-LIKE PROTEIN GDX	11.4
D82307	ESTs Weakly similar to TH1 protein [D.melanogaster]	11.4
AA430002	ESTs	11.3
R22952	ESTs	11.3
AA179298	Homo sapiens chromosome 9 P1 clone 11659	11.3
W56363	ESTs Weakly similar to extracellular protein [H.sapiens]	11.2
AA449232	EST	11.2
AA444054	ESTs Weakly similar to transmembrane protein [H.sapiens]	11.1
AA281733	ESTs	11.0
AA452601	EST	11.0
AA035630	Homo sapiens U4/U6 small nuclear ribonucleoprotein	10.9
AA235117	ESTs Weakly similar to eapin [R.norvegicus]	10.9
AA279418	ESTs	10.9

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FIGURE 4 (CONT.)

RC_AA432069	AA432069	ESTs	10.8
RC_AA453630	AA453630	EST	10.7
RC_W44657	W44657	EST	10.7
RC_R40431	R40431	ESTs	10.6
RC_AA405098	AA405098	ESTs	10.6
RC_AA411425	AA411425	ESTs	10.5
RC_AA423956	AA423956	ESTs	10.5
RC_AA599259	AA599259	Human splicing protein (SAP 61) mRNA, complete cds	10.4
RC_AA253170	AA253170	GANGLIOSIDE GM2 ACTIVATOR PRECURSOR	10.4
RC_AA459347	AA459347	EST	10.4
RC_AA251430	AA251430	ESTs: Highly similar to RAS-RELATED PROTEIN RAB-	10.3
RC_AA470156	AA470156	ESTs Weakly similar to dyx11 74K chain cytosolic	10.3
RC_T64933.f	T64933.f	ESTs	10.3
RC_AA281290	AA281290	ESTs Highly similar to ZINC FINGER PROTEIN 85	10.2
RC_AA286069	AA286069	ESTs Weakly similar to K02B2.3 gene product [C.elegans]	10.2
RC_AA49832	AA49832	ESTs	10.1
RC_AA427898	AA427898	ESTs Weakly similar to trabecular meshwork inducible	10.0
RC_AA609867	AA609867	ESTs Weakly similar to No definition line found	10.0
RC_R49198	R49198	H.sapiens DAP-3 mRNA	9.9
RC_AA465158	AA465158	EST	9.9
RC_AA112396	AA112396	ESTs	9.8
RC_AA207015	AA207015	ESTs	9.8
RC_R06986.f	R06986	ESTs	9.7
RC_M14338	M14338	Spermidine synthase	9.7
RC_AA228030	AA228030	ESTs	9.7
RC_AA447982	AA447982	ESTs Weakly similar to R01H10.6 [C.elegans]	9.7
RC_Z14982.mal	Z14982.mal	PROTEASOME COMPONENT C13 PRECURSOR	9.7
RC_AA176247	AA176247	EST	9.6
RC_T97341	T97341	EST - RC_T97341	9.6
RC_W26392	W26392	ESTs Highly similar to ONCOSTATIN PRECURSOR	9.6
RC_AA143190	AA143190	ESTs Highly similar to HYPOTHETICAL 23.1 KD	9.5
RC_AA452578	AA452578	ESTs	9.5
RC_W92713	W92713	ESTs	9.4
RC_AA282914	AA282914	ESTs	9.4
RC_AA461476	AA461476	ESTs Highly similar to PUTATIVE ATP-DEPENDENT	9.4
RC_AA258057	AA258057	ESTs	9.4
RC_W81731	W81731	ESTs	9.3
RC_N21678	N21678	ESTs	9.3
RC_AA262111	AA262111	ESTs	9.3

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FIGURE 4 (CONT.)

RC_AA490929	AA490929	EST	9.3
RC_NT0690	N70690	ESTs	9.3
RC_NB0716	N80716	ESTs	9.3
RC_AA007344	AA007344	ESTs	9.2
RC_W73140	W73140	ESTs	9.2
DI4657	DI4657	ESTs	9.2
RC_T16308.1	T16308	ESTs	9.1
RC_AA47666	AA47666	ESTs	9.1
RC_AA243020	AA243020	ESTs	9.1
RC_AA33418	AA33418	ESTs	9.1
RC_R38919.1	R38919	ESTs	9.1
RC_R60223.5	R60223	ESTs	9.0
RC_R70379.5	R70379	ESTs	9.0
RC_RG2981.1	RG2981	ESTs	9.0
RC_RG2981.1	RG2981	ESTs	9.0
RC_AA347209	AA347209	ESTs	8.9
RC_AA485041	AA485041	ESTs	8.8
RC_AA443342	AA443342	ESTs	8.8
RC_AA481281	AA481281	ESTs	8.7
RC_T96361.5	T96361	ESTs	8.7
RC_H18027.5	H18027	ESTs	8.6
RC_AA608723	AA608723	ESTs	8.6
RC_AA457018	AA457018	ESTs	8.5
RC_AA113011	AA113011	ESTs	8.5
RC_H96237.5	H96237	ESTs	8.4
RC_AA024835	A024835	ESTs	8.4
RC_S85655	S85655	ESTs	8.4
RC_N99976	N99976	ESTs	8.4
RC_T65004	T65004	ESTs	8.3
RC_N91197	N91197	ESTs	8.3
RC_H72948	H72948	ESTs	8.3
RC_AA489510	AA489510	ESTs	8.3
RC_Z39971.5	Z39971	ESTs	8.2
RC_AA236037	AA236037	ESTs	8.2
RC_J05070	J05070	ESTs	8.2
RC_H98621.5	H98621	ESTs	8.1
RC_R40177	R40177	ESTs	8.1
RC_D60302	D60302	ESTs	8.1

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FIGURE 4 (CONT.)

RC_AA419225	AA419225	Human nurin-like element-containing mRNA clone	8.1
RC_W03659	W03659	ESTs	8.0
RC_AA233545	AA233545	ESTs Weakly similar to HYPOTHETICAL 26.1 KD	8.0
RC_N99415	N99415	ESTs Highly similar to OSTEOINDUCTIVE FACTOR	8.0
RC_AA436370	AA436370	ESTs Highly similar to ADP-RIBOSYLATION FACTOR-RAP1 GTPase activating protein	8.0
RC_F01538	F01538	ESTs	7.9
RC_AA053319	AA053319	ESTs	7.9
RC_N69464	N69464	ESTs Weakly similar to LINE-1 REVERSE	7.9
RC_AA458882	AA458882	Replication protein A (E coli RecA homolog RAD51)	7.9
RC_N33011	N33011	EST	7.9
RC_AA421750	AA421750	ESTs	7.9
RC_AA235009	AA235009	ESTs	7.9
RC_AA47574	AA47574	ESTs	7.9
RC_R01634	R01634	ESTs	7.9
RC_R01634	R01634	ESTs	7.9
RC_N53950	N53950	EST - RC_N53950	7.9
RC_AA150182	AA150182	EST - RC_N53950	7.9
RC_AA446486	AA446486	ESTs Weakly similar to HYPOTHETICAL 88.1 KD	7.8
RC_AA342684	AA342684	Homo sapiens Ran binding protein 2 (RanBP2alpha)	7.8
RC_AA47213	AA47213	EST - RC_AA472084	7.8
RC_AA609170	AA609170	ESTs	7.8
RC_N46435	N46435	EST	7.8
RC_N54916	N54916	EST - RC_N46435	7.8
RC_T88814	T88814	Human mRNA for KIAA0136 gene partial cds	7.8
RC_AA459389	AA459389	Homo sapiens mRNA for tyrosyl sulfotransferase-2	7.7
RC_AA463693	AA463693	ESTs	7.7
RC_H99879	H99879	ESTs Highly similar to EPIDERMAL GROWTH	7.6
RC_U19796	U19796	Human melanoma antigen p15 mRNA complete cds	7.6
RC_T68871	T68871	ESTs	7.6
RC_AA446008	AA446008	EST	7.6
RC_T03306	T03306	Homo sapiens clone 24703 beta-tubulin mRNA complete	7.6
RC_HG2981	HG2981	EST - HG2981-IT3938	7.6
RC_N67119	N67119	ESTs	7.5
RC_AA442767	AA442767	Tyrosine 3-monooxygenase/tyrosolase 5-monooxygenase	7.5
RC_AA454566	AA454566	Human mRNA for KIAA0170 gene complete cds	7.5
RC_AA476937	AA476937	ESTs	7.5
RC_W01296	W01296	EST - W01296	7.5
RC_AA282074	AA282074	ESTs	7.5
RC_AA094752	AA094752	Calcineurin B	7.5
RC_D13666	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-	7.5

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FIGURE 4 (CONT.)

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RC_N67889	N67889	ESTs	7.4
RC_AA609309	AA609309	ESTs	7.4
RC_AA12477	AA12477	EST	7.4
RC_AA459392	AA459392	ESTs	7.4
RC_AA390042	AA390042	EST	7.4
RC_W7320	W7320	ESTs Highly similar to HYPOTHETICAL 28.5 KD	7.4
RC_AA069476	AA069476	H.sapiens mRNA for surface glycoprotein	7.4
RC_AA237061	AA237061	ESTs	7.4
RC_AA237061	AA237061	Homo sapiens mRNA for GalT4 protein	7.4
RC_AA411952	AA411952	ESTs	7.4
RC_AA411952	AA411952	ESTs Moderately similar to breast cancer suppressor	7.4
RC_AA486250	AA486250	Interferon (gamma)-induced cell line protein 10 from	7.4
RC_X02530	X02530	ESTs	7.4
RC_D59489	D59489	ESTs Highly similar to CHROMOSOME	7.5
RC_AA283006	AA283006	ESTs	7.5
RC_AA43794	AA43794	ESTs	7.5
RC_F13642	F13642	Human mRNA for histone H1x complete cds	7.3
RC_AA426372	AA426372	ESTs	7.3
RC_AA446869	AA446869	ESTs	7.3
RC_N21321	N21321	ESTs	7.2
RC_AA121315	AA121315	ESTs	7.2
RC_R65593	R65593	Homo sapiens mRNA for kynurenine 3-monooxygenase	7.2
RC_AA427950	AA427950	EST - RC_AA427950	7.2
RC_AA088458	AA088458	ESTs Weakly similar to H11 ALU SUBFAMILY J	7.2
RC_AA088458	AA088458	ESTs Moderately similar to H11 ALU SUBFAMILY SX	7.2
RC_AA432130	AA432130	ESTs	7.1
RC_AA234921	AA234921	ESTs Weakly similar to T04A8.11 [C.elegans]	7.1
RC_AA310967	AA310967	ESTs	7.1
RC_AA256177	AA256177	H.sapiens mRNA for melanoma growth regulatory protein	7.1
RC_AA282143	AA282143	ESTs	7.1
RC_AA283003	AA283003	ESTs	7.1
RC_AA21158	AA21158	ESTs	7.1
RC_T10082	T10082	ESTs	7.1
RC_C00225	C00225	ESTs Highly similar to HYPOTHETICAL 52.8 KD	7.1
RC_AA258482	AA258482	Human mRNA for zinc finger protein complete cds	7.1
RC_AA287870	AA287870	Lymphotoxin-beta	7.1
RC_AA410373	AA410373	ESTs	7.1
RC_F13694	F13694	ESTs	7.1
RC_N29431	N29431	EST - RC_N29431	7.1
RC_N67239	N67239	ESTs	7.1
RC_AA449351	AA449351	ESTs Weakly similar to similar to deoxyribose-phosphate	7.0
RC_Z40345	Z40345	ESTs Weakly similar to T06D8.5 [C.elegans]	7.0

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FIGURE 4 (CONT.)

RC_N34686	N34686	Homo sapiens clone 23915 mRNA sequence	7.0
RC_AA310499	AA310499	ESTs	7.0
RC_D57389_f	D57389	EST	7.0
RC_N71704	N71704	ESTs	6.9
RC_AA410441	AA410441	ESTs	6.9
RC_AA505093	AA505093	ESTs	6.9
U48705_mal	U48705	Receptor protein-tyrosine kinase EDOR1	6.8
RC_AA419461	AA419461	ESTs	6.8
RC_AA411204	AA411204	ESTs	6.8
RC_AA496569	AA496569	ESTs Highly similar to VALYL-TRNA SYNTHETASE	6.8
RC_AA346385	AA346385	ESTs Highly similar to putative hydrophobic domain in	6.8
RC_D51229_f	D51229	Human clone Z5589 mRNA sequence	6.8
RC_AA127818	AA127818	ESTs	6.8
RC_H18428_s	H18428	ESTs Weakly similar to (III) ALU SUBFAMILY J	6.8
RC_F02254_s	F02254	ESTs	6.8
RC_AA416876	AA416876	ESTs Weakly similar to TRANSFORMATION-EST	6.8
RC_AA446966	AA446966	ESTs	6.7
RC_N50550	N50550	Homo sapiens mRNA for Ets1 complete cds	6.7
L27841	L27841	Human autotransgenic pericentriolar material 1 (PCM-1)	6.7
U30246	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter	6.7
RC_AA034699	AA034699	ESTs	6.7
RC_AA034699	AA034699	ESTs	6.7
RC_T92935	T92935	ESTs	6.7
RC_T92935	T92935	Human JTV-1 (JTV-1) mRNA complete cds	6.7
RC_U24169	U24169	Interleukin 6 signal transducer (gp130 oncostatin M	6.7
RC_H09935_s	H09935	ESTs Moderately similar to unknown protein [H.sapiens]	6.7
RC_AA435849	AA435849	ESTs	6.7
RC_AA127058	AA127058	Collagen type V alpha	6.6
RC_AA127058	AA127058	ESTs	6.6
RC_M11718	M11718	ESTs	6.6
RC_AA283198	AA283198	ESTs	6.6
RC_R51988	R51988	ESTs	6.6
RC_AA505141	AA505141	ESTs	6.6
RC_D60341	D60341	ESTs Highly similar to FK506-BINDING PROTEIN	6.6
RC_N26904	N26904	ESTs Highly similar to SKD3 [H.musculi]	6.6
RC_R40606	R40606	ESTs	6.6
RC_T03790	T03790	ESTs	6.6
RC_W72455	W72455	Nuclear factor of kappa light polypeptide gene enhancer in	6.6
RC_AA098334	AA098334	ESTs	6.6
RC_AA421782	AA421782	ESTs Highly similar to COP1 REGULATORY PROTEIN	6.5
RC_AA236384	AA236384	EST	6.5
RC_AA431085	AA431085	Human prollyl 4-hydroxylase alpha (II) subunit mRNA	6.5
RC_W49521	W49521		6.5

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FIGURE 4 (CONT.)

RC_AA446591	AA446591	ESTs	6.5
RC_R06700	R06700	ESTs	6.5
RC_AA100364	AA100364	ESTs	6.5
X54326	X54326	MULTIFUNCTIONAL AMINOACYL-TRNA	6.4
U89606	U89606	Human pyridoxal kinase mRNA complete cds	6.4
RC_AA119551	AA119551	EST	6.4
RC_AA115991	AA115991	ESTs	6.4
RC_AA130211	AA430211	ESTs	6.4
RC_T17119	T17119	ESTs	6.4
RC_AA157814	AA157814	ESTs	6.3
X70649	X70649	Homo sapiens DDX1 gene complete CDS	6.3
RC_H57330	H57330	EST	6.3
D81608	D81608	H sapiens mRNA for RNA polymerase II subunit	6.3
R65826	R65826	Homo sapiens mRNA for KIAA0549 protein partial cds	6.3
RC_AA621169	AA621169	ESTs	6.3
L77701	L77701	Homo sapiens COX17 mRNA complete cds	6.3
AA443658	AA443658	Homo sapiens lamin B receptor homolog TMPS2	6.3
W19662	W19662	ESTs	6.3
RC_D20168	D20168	Human mRNA for KIAA0050 gene complete cds	6.3
RC_N48166	N48166	ESTs	6.3
RC_AA024664	AA024664	Human NADH ubiquinone oxidoreductase subunit B13	6.2
RC_AA279943	AA279943	ESTs	6.2
RC_AA093874	AA093874	ESTs	6.2
X36018	X36018	ESTs	6.2
RC_AA412106	AA412106	H sapiens mRNA for MUF1 protein	6.2
RC_AA621721	AA621721	ESTs	6.2
U40271	U40271	ESTs	6.2
X52150	X52150	Protein-tyrosine kinase 7	6.2
RC_AA152178	AA152178	Arylsulfatase A	6.2
RC_N38959	N38959	ESTs	6.2
L37747	L37747	ESTs	6.2
U78525	U78525	Homo sapiens chaperonn containing t-complex	6.1
RC_T77733	T77733	LAMIN B1	6.1
RC_D20280	D20280	Tubulin gamma polypeptide	6.1
RC_V69807	V69807	ESTs	6.1
RC_AA405505	AA405505	ESTs	6.1
RC_AA133199	AA133199	ESTs highly similar to GOLIAITH PROTEIN [Drosophila	6.1
RC_H55748	H55748	Homo sapiens mRNA for putative RNA helicase	6.1
RC_AA479933	AA479933	ESTs	6.1
RC_AA448349	AA448349	ESTs	6.1

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FIGURE 4 (CONT.)

RC_AA600257	AA600257	ERGIC-53 PROTEIN PRECURSOR	6.1
RC_R99978	R99978	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	6.1
AA455331	AA455331	ESTs	6.1
RC_H55915	H55915	ESTs Weakly similar to LINE-1 REVERSE	6.1
RC_AA398740	AA398740	ESTs	6.1
RC_AA521080	AA521080	ESTs	6.1
RC_AA416568	AA416568	ESTs	6.1
RC_N92593	N92593	Human germline oligomeric matrix protein (COMP)	6.1
RC_AA609277	AA609277	ESTs	6.0
RC_R33663_s	R33663_s	ESTs	6.0
RC_AA321103	AA321103	ESTs	6.0
RC_AA406137	AA406137	EST	6.0
RC_U73514	U73514	Homo sapiens short chain L-3-hydroxyacyl-CoA	6.0
RC_T16660	T16660	ESTs	6.0
RC_J04177	J04177	Collagen type XI alpha 1	5.9
RC_W38407	W38407	ESTs	5.9
RC_N26391	N26391	ESTs	5.9
RC_AA292655	AA292655	ESTs	5.9
RC_Z41619_s	Z41619_s	ESTs Weakly similar to keratin 8 type II cytoskeletal	5.9
RC_AA223730	AA223730	ESTs	5.9
RC_T88953	T88953	ESTs	5.9
RC_N50744	N50744	ESTs	5.9
RC_W63563_s	W63563_s	Homo sapiens scaffold attachment factor B (SAF-B)	5.9
RC_HG37748-	HG37748-	EST - HG3748-H1018	5.9
RC_AA430673	AA430673	ESTs	5.8
RC_AA463740	AA463740	ESTs	5.8
RC_M25753	M25753	Cyclin B1	5.8
RC_AA279292	AA279292	ESTs	5.8
RC_AA427925	AA427925	ESTs Weakly similar to PROCOLLAGEN ALPHA 1(I)	5.8
RC_AA387665	AA387665	ESTs	5.8
RC_AA422007	AA422007	ESTs	5.8
RC_AA425379	AA425379	ESTs	5.8
RC_T67463_s	T67463_s	CATHEPSIN K PRECURSOR	5.8
RC_AA441801	AA441801	ESTs	5.8
RC_H89987_s	H89987_s	Human multidrug resistance-associated protein homolog	5.8
RC_H94843	H94843	ESTs	5.8
RC_N80183	N80183	ESTs	5.8
RC_U65932	U65932	Human extracellular matrix protein 1 (ECM1) mRNA	5.8
RC_N27563	N27563	ESTs	5.7

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FIGURE 4 (CONT.)

RC_F09058	F09058	ESTs	5.7
RC_R02572	R02572	Fibronectin 1	5.7
RC_AA442763	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC	5.7
RC_AA148624	AA148624	Homo sapiens mRNA for follistatin-related protein (FRP)	5.7
RC_AA59945	AA59945	Homo sapiens mRNA for KIAA0585 protein partial cds	5.7
RC_R09166	R09166	ESTs	5.7
RC_K34677	K34677	FACTOR VIII INTRON 22 PROTEIN	5.7
RC_AA478794	AA478794	ESTs	5.7
RC_AA192334	AA192334	ESTs	5.7
RC_AA454562	AA454562	ESTs	5.7
RC_U56402	U56402	Homo sapiens clone 24522 mRNA sequence	5.7
RC_AA443251	AA443251	ESTs	5.7
RC_AA207105	AA207105	EST	5.7
RC_AA609473	AA609473	ESTs	5.7
RC_H54430	H54430	ESTs	5.7
RC_R85829	R85829	EST	5.7
RC_HG2981-	HG2981-	EST - HG2981-HT3125	5.7
RC_AA232956	AA232956	EST - U91327	5.6
RC_U91327	U91327	ESTs	5.6
RC_N51590.s	N51590.s	ESTs	5.6
RC_AA406169	AA406169	Homo sapiens KIAA0431 mRNA partial cds	5.6
RC_AA147884	AA147884	ESTs	5.6
RC_AA453987	AA453987	ESTs	5.6
RC_AA040154	AA040154	ESTs	5.6
RC_T23528	T23528	ESTs Moderately similar to TYK1 protein [M. musculus]	5.6
RC_D50914	D50914	Human mRNA for KIAA0124 gene partial cds	5.6
RC_X76105	X76105	Human mRNA for KIAA0124 gene partial cds	5.6
RC_AA149754	AA149754	H. sapiens DAP-1 mRNA	5.6
RC_AA397919	AA397919	EST	5.6
RC_AA398212	AA398212	ESTs	5.6
RC_AA416986	AA416986	ESTs	5.6
RC_AA435936	AA435936	Guanine nucleotide binding protein (G protein) beta	5.6
RC_T95057.F	T95057.F	EST	5.6
RC_AA116095	AA116095	ESTs	5.6
RC_AA477214	AA477214	ESTs Weakly similar to T12D8.i [C. elegans]	5.6
RC_AA398264	AA398264	ESTs	5.6
RC_AA435742	AA435742	Homo sapiens clone 23736 mRNA sequence	5.6
RC_AA452842	AA452842	Human fatty acid amide hydrolase mRNA complete cds	5.6
RC_AA482269	AA482269	Integral transmembrane protein 1	5.6

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FIGURE 4 (CONT.)

RC_AA436819	AA436819	ESTs	5.6
RC_N93797	N93797	ESTs	5.6
RC_AA43602	AA43602	ESTs	5.5
RC_AA609996	AA609996	ESTs Highly similar to Surt-4 protein [Mammalia]	5.5
RC_AA075200	AA075200	Homo sapiens Chromosome 16 BAC clone C198783	5.5
RC_AA195517	AA195517	ESTs Weakly similar to Hs. ALU SUBFAMILY 1	5.3
RC_X02874	X02874	(2-5') oligoadenylate synthetase E	5.3
RC_AA085589	AA085589	ESTs Highly similar to TRANSLATION INITIATION	5.3
RC_H99500	H99500	Homo sapiens mRNA for folistatin-related protein (FRP)	5.5
RC_R43883	R43883	ESTs	5.5
RC_M24486	M24486	Procollagen-proline 2-oxoglutarate 4-dioxygenase (proline	5.5
RC_AA115535	AA115535	ESTs	5.5
RC_AA280840	AA280840	ESTs	5.5
RC_N22015	N22015	ESTs	5.5
RC_AA021182	AA021182	EST	5.5
RC_N21022	N21022	EST	5.5
RC_U09278	U09278	Human fibroblast activation protein mRNA complete cds	5.5
RC_AA251973	AA251973	ESTs	5.4
RC_H75933	H75933	Laminin receptor (2H5 epitope)	5.4
RC_T81310	T81310	EST	5.4
RC_M07936	M07936	SIGNAL TRANSDUCER AND ACTIVATOR OF	5.4
RC_AA242757	AA242757	ESTs	5.4
RC_W92001	W92001	ESTs	5.4
RC_AA398721	AA398721	EST - RC_AA398721	5.4
RC_AA448410	AA448410	ESTs	5.4
RC_AA479348	AA479348	H.sapiens mRNA for STT	5.4
RC_C02170	C02170	ESTs Weakly similar to weak similarity to ribosomal	5.4
RC_AA437225	AA437225	ESTs	5.4
RC_N51917	N51917	ESTs	5.4
RC_AA293773	AA293773	Homo sapiens clone 23870 mRNA sequence	5.4
RC_AA49357	AA49357	ESTs	5.4
RC_R41294	R41294	ESTs	5.4
RC_W45275	W45275	CD44 antigen (cell adhesion molecule)	5.4
RC_AA447213	AA447213	ESTs Weakly similar to 5S RIBOSOMAL PROTEIN L20	5.3
RC_AA133809	AA133809	ESTs	5.3
RC_AA191324	AA191324	ESTs	5.3
RC_AA399477	AA399477	ESTs	5.3
RC_H80749	H80749	Human germline oligomeric matrix protein (COMP)	5.3
RC_N94383	N94383	EST - RC_AA157811	5.3
RC_AA157811	AA157811		5.3

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FIGURE 4 (CONT.)

Y09912_mal	Y09912	H.sapiens mRNA for AP-2 beta transcription factor	5.1
RC_AA491465	AA491465	ESTs	5.1
RC_AA436673	AA436673	ESTs	5.0
RC_N73898_f	N73898	ESTs	5.0
RC_F10496_f	J05614	EST - J05614	5.0
RC_AA085676	J00314	H.sapiens 40 kDa protein kinase related to rat ERK2	5.0
RC_AA236356	AA085676	Homo sapiens clone 24703 beta-tubulin mRNA complete	5.0
RC_AA232195	AA232195	ESTs Weakly similar to TYL [H.sapiens]	5.0
RC_N33927_s	N33927	ESTs	5.0
RC_AA211400	AA211400	"Homo sapiens mRNA for histone H2B clone p104-5-	5.0
RC_AA211400	M80244	ESTs	5.0
RC_AA211400	M16336	ESTs	5.0
RC_AA479995	AA479995	INTEGRAL MEMBRANE PROTEIN E16	5.0
RC_AA055892	AA055892	CD2 antigen (T cell surface antigen T11)	5.0
RC_AA281451	D82419	Homo sapiens mRNA for KIAA0383 protein partial cds	5.0
RC_AA172056	U62392	ESTs Highly similar to UBIQUITIN-CONJUGATING	5.0
RC_AA287095	AA287095	ESTs	5.0
RC_AA425691	AA425691	Homo sapiens zinc finger protein mRNA complete cds	5.0
RC_AA426376	AA426376	EST - RC_AA287095	5.0
RC_AA446000	AA446000	ESTs	5.0
RC_AA478951	AA478951	EST	5.0
RC_F02080_f	F02080	ESTs Weakly similar to H1 ALU SUBFAMILY J	5.0
RC_F09815_f	T79815	Polypyrimidine tract binding protein (hnRNP I)	4.9
RC_F10945	F10945	Homo sapiens clone 23915 mRNA sequence	4.9
RC_F01169	C01169	ESTs	4.9
RC_AA490830	AA490830	ESTs	4.9
RC_AA133756	AA133756	Protein phosphatase 2 (formerly 2A) catalytic subunit	4.9
RC_H24044	H24044	EST	4.9
RC_R41772	R41772	EST - RC_T39338	4.9
RC_T59338	T59338	Cadherin 11 (OB-cadherin)	4.9
RC_D21255	D21255	ESTs	4.9
RC_AA234559	AA234559	ESTs Highly similar to HYPOTHETICAL 47.8 KD	4.8
RC_N34893	N34893	ESTs	4.8
RC_AA191512	AA191512	Human mRNA for KIAA0203 gene complete cds	4.8
RC_W60007_s	W60007		4.8

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FIGURE 4 (CONT.)

RC_AA400513	AA400513	ESTs	4.8
RC_N94362	N94362	EST	4.8
RC_AA406081	AA406081	ESTs	4.8
RC_AA448158	AA448158	EST	4.7
RC_AA404352	AA404352	ESTs	4.7
RC_AA075599	AA075599	ESTs highly similar to NADH-UBIQUINONE	4.7
RC_AA026356	AA026356	ESTs	4.7
RC_AA157836	AA157836	ESTs	4.7
RC_AA196549	AA196549	ESTs	4.7
RC_AA417321	AA417321	ESTs Weakly similar to CALMODULIN [D melanogaster]	4.7
RC_AA418074	AA418074	ESTs	4.7
RC_N32919	N32919	ESTs	4.7
RC_AA620795	AA620795	ESTs	4.7
RC_U18321	U18321	ESTs	4.6
RC_H97012	H97012	H sapiens DAP-3 mRNA	4.6
RC_AA177051	AA177051	ESTs Weakly similar to L8004.7 gene product	4.6
RC_AA45483	AA45483	EST - RC_AA177051	4.6
RC_X17059	X17059	ESTs	4.6
M34453_mal	M34453	ARYLAMINE N-ACETYLTRANSFERASE	4.6
RC_X68921	N68921	LAMIN B1	4.6
RC_AA466535	AA46653	ESTs	4.6
RC_AA40722	AA210722	ESTs Weakly similar to T01G9.4 [C.elegans]	4.5
RC_AA461507	AA461507	EST	4.5
RC_T40841	T40841	ESTs	4.5
RC_N71076	N71076	EST	4.5
RC_X57766	X57766	Human stromelysin-3 mRNA	4.5
RC_AA255605	AA255605	Homo sapiens spindle pole body protein spc97 homolog	4.5
RC_AA443634	AA443634	Homo sapiens ubiquitin conjugating enzyme G2	4.5
RC_T97307	T97307	EST - RC_T97307	4.4
X02419	X02419	Urokinase-type plasminogen activator	4.4
RC_AA430124	AA430124	ESTs	4.4
RC_AA405569	AA405569	Human fibroblast activation protein mRNA complete cds	4.4
RC_AA227900	AA227900	H.sapiens mRNA homologous to S. cerevisiae RAD54	4.4
RC_AA422025	AA422025	ESTs	4.4
RC_AA346495	AA346495	ESTs Moderately similar to H1 ALU SUBFAMILY J	4.4
RC_AA386260	AA386260	EST	4.4
RC_AA398155	AA398155	ESTs	4.4
RC_AA453466	AA453466	Homo sapiens mRNA for JM27 protein complete CDS	4.4
RC_AA463726	AA463726	ESTs Highly similar to CHOLINE DEHYDROGENASE	4.4
RC_C20981	C20981		4.4

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FIGURE 4 (CONT.)

RC_R70801_s	R70801	EST	4.4
U28386	U28386	RAG (recombination activating gene) cohort 1	4.4
RC_AA206497	AA206497	PROTEASOME COMPONENT C9	4.4
RC_U21090	U21090	Human DNA polymerase delta small subunit mRNA	4.3
RC_AA453176	AA453176	Human protein kinase ATR mRNA complete cds	4.3
RC_AA235112	AA235112	ESTs	4.3
U73359	U73359	Human cyclin-selective ubiquitin carrier protein mRNA	4.3
U74489	U74489	Human lysyl oxidase-like protein mRNA complete cds	4.3
D42073	D42073	Human mRNA for reticulocalbin complete cds	4.3
U24389	U24389	ESTs	4.2
D42073	D42073	ESTs	4.2
H18947	H18947	ESTs	4.2
H90161	H90161	ESTs Highly similar to CYTOCHROME P450 17B1	4.2
H25577	H25577	Cellular retinoic acid-binding protein (human skin mRNA)	4.2
S74445	S74445	ESTs	4.2
AA419200	AA419200	Human cysteine protease Me12 isoform alpha (M12)	4.2
AA227959	AA227959	ESTs	4.2
AA416931	AA416931	ESTs	4.2
U74612	U74612	Human putative M phase phosphoprotein 2 (MP2) mRNA	4.2
R46482	R46482	ESTs	4.2
X62534	X62534	High-mobility group (nonhistone chromosomal) protein 2	4.2
M15796	M15796	Protein kinase cell nuclear antigen	4.1
D54296	D54296	Human mRNA for KIAA0255 gene complete cds	4.1
AA398369	AA398369	ESTs	4.1
AA464707	AA464707	ESTs	4.1
AA478799	AA478799	ESTs	4.1
AA496369	AA496369	ESTs	4.1
U50648	U50648	Protein kinase interferon-inducible double stranded RNA	4.1
RC_N66818	N66818	ESTs	4.1
RC_AA448347	AA448347	Annexin XI (56kD autoantigen)	4.1
AA193297	AA193297	ESTs	4.0
RC_AA387596	AA387596	ESTs	4.0
RC_AA228026	AA228026	ESTs Highly similar to PBDX protein [H.sapiens]	4.0
AA421041	AA421041	ESTs	4.0
RC_AA48347	AA48347	Small inducible cytokine A5 (RANTES)	4.0
W87752	W87752	EST - X94562_xp12_f	4.0
X94563	X94563	Cytochrome B561	4.0
U29463	U29463	ESTs	3.9
AA287325	AA287325	ESTs	3.9
RC_AA287325	AA287325	Human sapiens mRNA for RB18A protein	3.9
RC_R44709	R44709	ADP-ribosylation factor 1	3.9
RC_AA256837	AA256837	ESTs	3.9
RC_W45572_f	W45572	ESTs Weakly similar to No definition line found	3.9
RC_AA482224	AA482224	ESTs	3.9

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FIGURE 4 (CONT.)

RC_AA112063	AA112063	ESTs Weakly similar to PRE-MRNA SPLICING	3.5
RC_AA034365	R70167	ESTs	3.5
RC_AA034365	AA034365	NUCLEAR PORE GLYCOPROTEIN P62	3.5
RC_AA034365	X75346	H.sapiens mRNA for MAP kinase activated protein kinase	3.5
RC_AA034365	AA034365	EST - RC_AA034365	3.5
RC_AA034365	AA034365	ESTs	3.5
RC_AA034365	AA034365	EST	3.5
RC_AA034365	AA034365	EST	3.5
RC_AA034365	AA034365	Human TFIIB related factor hBRF (HBRF) mRNA	3.5
RC_AA034365	AA034365	EST - RC_AA034365	3.5
RC_AA034365	AA034365	Human mRNA for KIAA0265 gene partial cds	3.5
RC_AA034365	AA034365	ESTs	3.5
RC_AA034365	AA034365	Integral transmembrane protein 1	3.5
RC_AA034365	AA034365	FARNESYL-DIPHOSPHATE	3.5
RC_AA034365	AA034365	ESTs	3.5
RC_AA034365	AA034365	Homo sapiens ERM1 RNA binding protein Grp-ebp (GRY)	3.4
RC_AA034365	AA034365	Homo sapiens mRNA for putative Glucosyltransferase	3.4
RC_AA034365	AA034365	ESTs	3.4
RC_AA034365	AA034365	ESTs	3.4
RC_AA034365	AA034365	ESTs	3.4
RC_AA034365	AA034365	ESTs	3.4
RC_AA034365	AA034365	ESTs	3.4
RC_AA034365	AA034365	Phosphothiosyl pyrophosphate amidotransferase	3.4
RC_AA034365	AA034365	Homo sapiens mRNA for putative methyltransferase	3.4
RC_AA034365	AA034365	EST	3.4
RC_AA034365	AA034365	H.sapiens mRNA for diubiquitin	3.4
RC_AA034365	AA034365	ESTs	3.4
RC_AA034365	AA034365	EST	3.4
RC_AA034365	AA034365	Human hSLAH2 mRNA complete cds	3.4
RC_AA034365	AA034365	EST - L47276	3.4
RC_AA034365	AA034365	DNA topoisomerase I	3.4
RC_AA034365	AA034365	L-lysine	3.4
RC_AA034365	AA034365	ESTs Weakly similar to LINE-1 REVERSE	3.3
RC_AA034365	AA034365	ESTs	3.3
RC_AA034365	AA034365	Homo sapiens cDNA similar to RNA binding protein C	3.3
RC_AA034365	AA034365	ESTs	3.3
RC_AA034365	AA034365	Homo sapiens sodium/myo-inositol cotransporter	3.3
RC_AA034365	AA034365	ESTs	3.3
RC_AA034365	AA034365	ESTs	3.3
RC_AA034365	AA034365	ESTs	3.3

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FIGURE 4 (CONT.)

RC_AA451159	AA451159	Human kinesin-like spindle protein HKSP (HKSP) mRNA	3.3
RC_AA496051	AA496051	ESTs	3.3
RC_W85861	W85861	ESTs Weakly similar to ZK1058.4 [C.elegans]	3.3
RC_R24237_f	R24237	ESTs	3.3
AD000092_cds	AD000092	ESTs	3.3
RC_W44735	W44735	ESTs	3.3
RC_AA435847	AA435847	EST - RC_AA435847	3.3
RC_N34059	N34059	EST - RC_N34059	3.3
RC_N58172	N58172	ESTs Weakly similar to tttt ALU SUBFAMILY SC	3.3
AA421213	AA421213	ESTs Weakly similar to P28F8.5 [C.elegans]	3.2
N35385	N35385	ESTs	3.2
T15665	T15665	ESTs Weakly similar to HYPOTHETICAL 139.1 KD	3.2
W46255	W46255	ESTs	3.2
AA490969	AA490969	Homo sapiens mRNA for KIAA0583 protein partial cds	3.2
RC_F09315	F09315	ESTs	3.2
RC_AA169379	AA169379	ESTs	3.2
RC_AA211941	AA211941	Homo sapiens polyadenylate binding protein-interacting	3.2
RC_N68931	N68931	ESTs	3.2
RC_AA134965	AA134965	Peroxisomal membrane protein 3 (35kD Zellweger	3.2
RC_R01092_s	R01092	ESTs	3.2
RC_D84145	D84145	Peroxisomal biogenesis factor 7	3.2
Z97054_392	Z97054	Human WS-3 mRNA complete cds	3.2
RC_AA232939	AA232939	Human mRNA for KIAA0312 gene partial cds	3.2
RC_T65797	T65797	ESTs	3.2
RC_W33134_s	W33134	ESTs Weakly similar to Ftn1 protein [H.sapiens]	3.2
RC_AA609423	AA609423	ESTs	3.2
L07515	L07515	ESTs	3.2
RC_R67996	R67996	HETEROCHROMATIN PROTEIN 1 HOMOLOG	3.2
RC_AA422079	AA422079	ESTs	3.2
RC_AA422079	AA422079	ESTs Weakly similar to RAR-RESPONSIVE PROTEIN	3.2
U37547	U37547	Human stat binding protein 1 (StatBP1) mRNA partial cds	3.2
U81554	U81554	Human IAP homolog B (NIBB) mRNA complete cds	3.2
U81554	U81554	Human IAP homolog B (NIBB) mRNA complete cds	3.2
T40327_s	T40327	Homo sapiens signal recognition particle 72 (SRP72)	3.2
RC_N78572	N78572	ESTs	3.2
RC_AA448213	AA448213	EST - RC_N78572	3.2
AA047036	AA047036	Human myogenic repressor 1-nf (MEF1) mRNA complete	3.1
RC_W72967	W72967	ESTs	3.1
RC_N69331	N69331	ESTs	3.1
RC_W44928	W44928	Peptidylprolyl isomerase C (cyclophilin C)	3.1
RC_AA150043	AA150043	ESTs	3.1

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FIGURE 4 (CONT.)

RC_D60208_f	D60208	Homo sapiens ribonuclease P protein subunit p20 (RPP20)	ESTs	3.1
RC_AA401687	AA401687		ESTs	3.1
RC_N21626	N21626		ESTs	3.1
S66431	S66431	Homo sapiens clone 23592 mRNA sequence		3.1
X17620	X17620	NUC1 FOSIDE DIPHOSPHATE KINASE A		3.1
X59798	X59798	Cyclin D1 (PRAD1 parathyroid adenomatosis 1)	EST	3.1
RC_AA223874	AA223874		ESTs	3.1
RC_AA291259	AA291259	Human mRNA for KIAA0276 gene partial cds	EST	3.1
RC_AA398360	AA398360		EST	3.1
RC_AA398360	D87466		EST	3.1
RC_AA398360	AA398360	PTB-ASSOCIATED SPLICING FACTOR	EST	3.0
RC_AA099719	AA099719		ESTs	3.0
RC_AA251738	S50223		ESTs	3.0
RC_AA251738	AA251738	H sapiens mRNA for TAF1100 protein		3.0
RC_AA406577	Y12065	Homo sapiens mRNA for nucleolar protein hNop56	ESTs	3.0
RC_N47204	AA406577		ESTs	3.0
RC_W80482	N47204	ESTs Weakly similar to C50F4.12 [C.elegans]	ESTs	3.0
RC_AA423827	W80482		ESTs	3.0
RC_AA227932	AA227932		ESTs	3.0
RC_W46286_s	W46286	ESTs Weakly similar to ZK1058.5 [C.elegans]	ESTs	3.0
RC_AA386264	AA386264	ESTs Highly similar to the C. elegans protein p14		3.0
RC_AA152305	X74801	H sapiens Cdc mRNA for clathronin		3.0
RC_R36548	AA152305	Interferon (gamma)-induced cell line protein 10 from	ESTs	2.9
RC_N32333	R36548		ESTs	2.9
RC_N36881	N32333	Homo sapiens M962 protein spliced isoform 2 mRNA	ESTs	2.9
RC_H16790	N36881		ESTs	2.9
RC_AA399164_s	AA399164	Homo sapiens transferrin B precursor mRNA complete	ESTs	2.9
RC_AA164293	AA164293		ESTs	2.9
RC_AA164293	D60061		ESTs	2.9
RC_AA203523	AA203523	ESTs Weakly similar to coded for by C. elegans cDNA		2.9
RC_AA195936	AA195936	ESTs Weakly similar to W02D9.2 [C.elegans]		2.9
RC_T25732_f	T25732	Human mRNA for KIAA0252 gene partial cds		2.9
RC_AA426120	AA426120	EST - RC_AA426120		2.9
RC_AA485214	AA485214	DNA-BINDING PROTEIN NEFA PRECURSOR		2.9
RC_AA485214	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds	ESTs	2.9
RC_AA213506	AA213506		ESTs	2.9
RC_R50840	R50840	H sapiens mRNA for ras-related GTP-binding protein		2.9

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FIGURE 4 (CONT.)

RC_R97040	R97040	Homo sapiens GTP-binding protein (RAB4) mRNA	ESTs	2.9
M32211	M32211	ESTs Highly similar to deduced protein product shows	ESTs	2.9
AA452011	AA452011	Homo sapiens splicing factor (CCL3) mRNA complete cds	ESTs	2.9
RC_AA228020	AA228020	Homo sapiens splicing factor (CCL3) mRNA complete cds	ESTs	2.9
T54762_s	T54762	ESTs	ESTs	2.9
RC_AA242834	AA242834	ESTs	ESTs	2.9
RC_F13779	F13779	ESTs	ESTs	2.9
RC_AA206088	AA206088	ESTs	ESTs	2.9
RC_AA292747	AA292747	ESTs	ESTs	2.9
RC_AA400725	AA400725	ESTs	ESTs	2.9
RC_H97677_s	H97677	EST - HG110-HT110	ESTs	2.9
HG110-HT110	HG110	EST - HG110-HT110	ESTs	2.9
D00596	D00596	Thymidylate synthase	ESTs	2.9
RC_AA279420	AA279420	ESTs Weakly similar to T08A11.2 [C. elegans]	ESTs	2.9
RC_AA179845	AA179845	ESTs Moderately similar to rabkinin-6 [M. musculus]	ESTs	2.9
RC_AA111532	AA111532	ESTs Weakly similar to ORF YOR285w [S. cerevisiae]	ESTs	2.8
RC_AA292765	AA292765	H. sapiens mRNA for M-phase phosphoprotein mpp5	ESTs	2.8
RC_AA609501	AA609501	HEAT SHOCK 70 KD PROTEIN 1	ESTs	2.8
RC_AA478596	AA478596	ESTs	ESTs	2.8
RC_N48715	N48715	ESTs	ESTs	2.8
RC_AA412497	AA412497	ESTs Weakly similar to H11 ALL SUBFAMILY J	EST	2.8
RC_AA480103	AA480103	Homo sapiens eps8 binding protein e3B1 mRNA complete	ESTs	2.8
AF06516	AF06516	ESTs	ESTs	2.8
RC_AA128407	AA128407	ESTs Weakly similar to Similar to S. cerevisiae	ESTs	2.8
RC_AA425606	AA425606	ESTs	ESTs	2.8
RC_AA323231	AA323231	EST - RC_TG3857	ESTs	2.8
RC_TG3857	TG3857	EST - RC_TG3857	ESTs	2.8
RC_AA488432	AA488432	Natural resistance-associated macrophage protein 2	ESTs	2.8
RC_R49327	R49327	ESTs	ESTs	2.8
RC_AA405512	AA405512	ESTs	ESTs	2.8
RC_F79617	F79617	Human mRNA for clathrin-like protein complete cds	ESTs	2.8
RC_AA310729	AA310729	EST - RC_AA446572	ESTs	2.8
RC_AA446572	AA446572	EST - RC_AA446572	ESTs	2.8
RC_AA486407	AA486407	ESTs Weakly similar to elastin like protein	ESTs	2.8
RC_R39234_f	R39234	ESTs Weakly similar to elastin like protein	ESTs	2.8
RC_AA425900	AA425900	UTASE-DNA glycosylase	ESTs	2.8
RC_AA425900	AA425900	PUTATIVE 60S RIBOSOMAL PROTEIN	ESTs	2.8
RC_F03605	F03605	Human neutral amino acid transporter B mRNA complete	ESTs	2.8
RC_U53347	U53347	Human splicing factor SRP30c mRNA complete cds	ESTs	2.8
U30825	U30825	Human splicing factor SRP30c mRNA complete cds	ESTs	2.8

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FIGURE 4 (CONT.)

RC_N21159	N21159	Homo sapiens forkhead protein (FKHL1) mRNA	2.8
RC_H24460.s	H24460	FK-506-binding protein 4 (59kD)	2.8
RC_D80710.1	D80710	ESTs Weakly similar to transmembrane protein [H.sapiens]	2.8
X76732	X76732	DNA-BINDING PROTEIN NEFA PRECURSOR	2.8
RC_AA001409	AA001409	ESTs	2.8
RC_N92915	N92915	ESTs	2.8
RC_N93325	N93325	ESTs	2.8
RC_AA609200	AA609200	ESTs Highly similar to 47 KD PROTEIN [Pseudomonas	2.8
RC_R41933	R41933	EST - RC_AA609200	2.8
RC_AA262768	AA262768	ESTs	2.8
RC_R46025	R46025	ESTs	2.8
RC_AA164687	AA164687	ESTs	2.7
RC_AA424031	AA424031	ESTs	2.7
RC_N23663	N23663	ESTs	2.7
RC_W69160	W69160	ESTs	2.7
RC_N25798	N25798	ESTs	2.7
RC_AA431333	AA431333	ESTs Highly similar to Ras inhibitor [H.sapiens]	2.7
RC_R54112	R54112	ESTs	2.7
RC_F02863	F02863	ESTs Moderately similar to [H.sapiens]	2.7
RC_W80750	W80750	ESTs	2.7
RC_AA461509	AA461509	ESTs Weakly similar to putative p150 [H.sapiens]	2.7
RC_AA620586	AA620586	ESTs	2.7
RC_L11669	L11669	Human tetracycline transporter-like protein mRNA	2.7
RC_AA291269	AA291269	ESTs	2.7
RC_W87747	W87747	ESTs	2.7
RC_K02777	K02777	T cell receptor alpha-chain	2.7
RC_X89986	X89986	H.sapiens mRNA for NBK apoptotic inducer protein	2.7
RC_AA125969	AA125969	ESTs Weakly similar to F35G12.9 [C.elegans]	2.7
RC_AA449718	AA449718	ESTs Weakly similar to ZINC FINGER PROTEIN 42	2.7
RC_R02354	R02354	ESTs	2.7
RC_AA425725	AA425725	ESTs Weakly similar to serine protein kinase SRPK1	2.7
RC_R71481	R71481	ESTs	2.7
RC_D63391	D63391	Human mRNA for platelet activating factor	2.7
RC_AA126743	AA126743	ESTs	2.7
RC_U33052	U33052	Human lipid-activated protein kinase PRK2 mRNA	2.7
RC_M96982	M96982	SPLICING FACTOR U2AF 35 KD SUBUNIT	2.7
RC_X16396	X16396	NAD-DEPENDENT	2.7
RC_L12350	L12350	Thrombospondin 2	2.7
RC_AA215333	AA215333	ESTs	2.7
RC_AA102520	AA102520	ESTs Highly similar to HYPOTHETICAL 31.6 KD	2.7

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FIGURE 4 (CONT.)

RC_N63869	N68609	ESTs Weakly similar to PROCOLLAGEN ALPHA 2(IV)	ESTs	2.6
RC_W85712	W85712		ESTs	2.6
RC_AA176121	AA176121	Homo sapiens 15 kDa telopeptide mRNA complete cds	ESTs	2.6
RC_AA001402	AA001402	ESTs Highly similar to elastin like protein		2.6
RC_N51316	N51316	ESTs		2.6
	L03411	Radin blood group		2.6
	D79997			2.6
	L04490			2.6
RC_AA412112	AA412112	Human mRNA for KIAA0175 gene complete cds		2.6
RC_AA417956	AA417956	Homo sapiens (clone CG6) NADH-ubiquinone		2.6
RC_AA433624	AA433624	EST - RC_AA412112		2.6
RC_N63210	N63210	ESTs		2.6
RC_N92948	N92948	Human terminal transferase mRNA complete cds		2.6
RC_AA447553	AA447553	ESTs		2.6
RC_AF001294	AF001294	Human IEF SSP 9502 mRNA complete cds		2.6
RC_AA598648	AA598648	Homo sapiens IPL (IPL) mRNA complete cds		2.6
RC_AA447617	AA447617	H. sapiens mRNA for spermine synthase		2.6
RC_AA293300	AA293300	Human mRNA for transcriptional activator hSNF2b		2.6
RC_R20333_i	R50333	ESTs		2.6
RC_AB000115	AB000115	ESTs Weakly similar to semaphorin C [M.musculus]		2.6
	D63881	Homo sapiens mRNA expressed in osteoblast complete cds		2.6
	T39176_s	Human mRNA for KIAA0160 gene partial cds		2.6
RC_N46252	N46252	ESTs Weakly similar to ZK1058.4 [C.elegans]		2.6
RC_N33516	N33516	ESTs		2.6
RC_N48790	N48790	Homo sapiens ribirin (NBS) mRNA complete cds		2.6
RC_H98655	H98655	ESTs Moderately similar to the ALU SUBFAMILY SX		2.6
RC_AA242758	AA242758	Homo sapiens ribirin (NBS) mRNA complete cds		2.6
RC_AA130349	AA130349	Human breast cancer estrogen regulated L1V-1 protein		2.5
RC_AA262491	AA262491	ESTs		2.5
RC_N70646	N70646	ESTs		2.5
RC_N70646	N70646	ESTs		2.5
RC_N70646	N70646	ESTs		2.5
RC_AA490832	AA490832	ESTs		2.5
RC_AA610073	AA610073	ESTs		2.5
RC_N67187	N67187	ESTs		2.5
RC_AA400957	AA400957	Matrix Gla protein		2.5
RC_T70541	T70541	ESTs		2.5
RC_AA236489	AA236489	ESTs		2.5
RC_AA284372	AA284372	EST - RC_D60374_f		2.5
RC_D60374_f	D60374	EST - RC_AA069547		2.5
RC_AA069547	AA069547			2.5

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FIGURE 4 (CONT.)

RC_AA398280	AA398280	ESTs	2.5
RC_N93000	N93000	ESTs	2.5
RC_AA291503	AA291503	EST	2.5
RC_AA446100	AA446100	ESTs	2.5
RC_W47183	W47183	ESTs	2.5
RC_L00205	L00205	ESTs	2.5
RC_AA369027	AA369027	ESTs	2.5
RC_N66158	N66158	ESTs	2.5
RC_AA428179	AA428179	EST	2.5
RC_X70218	X70218	EST	2.5
AB002308	AB002308	Protein phosphatase 4 (formerly X) catalytic subunit	2.5
RC_AA416877	AA416877	Human mRNA for KIAA0310 gene complete cds	2.5
RC_AA262730	AA262730	ESTs	2.5
X54941	X54941	ESTs	2.5
D43948	D43948	ESTs	2.5
N23379	N23379	ESTs	2.5
X83373	X83373	ESTs	2.5
U16306	U16306	ESTs	2.5
T13963	T13963	ESTs	2.5
T39763.1	T39763.1	ESTs	2.5
RC_H12634	H12634	ESTs	2.5
RC_AA423867	AA423867	ESTs	2.5
RC_AA160890	AA160890	ESTs	2.5
RC_X21677	X21677	ESTs	2.5
RC_AA191424	AA191424	ESTs	2.5
RC_AA451707	AA451707	ESTs	2.5
RC_AA045083	AA045083	ESTs	2.5
RC_AA252672	AA252672	ESTs	2.4
RC_W79060	W79060	ESTs	2.4
RC_AA262651	AA262651	ESTs	2.4
RC_AA399047	AA399047	ESTs	2.4
RC_AA456646	AA456646	ESTs	2.4
RC_AA258601	AA258601	ESTs	2.4
RC_N51260	N51260	ESTs	2.4
RC_N51260.1	N51260.1	ESTs	2.4
RC_X13482	X13482	ESTs	2.4
RC_AA504223	AA504223	ESTs	2.4
RC_R37778	R37778	ESTs	2.4
RC_W31919	W31919	ESTs	2.4
RC_AA487207	AA487207	ESTs	2.4
RC_AA599674	AA599674	ESTs	2.4
RC_Z40898	Z40898	ESTs	2.4

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FIGURE 4 (CONT.)

RC_AA286942	AA286942	Human Rho-associated coiled-coil containing protein	EST - RC_AA286942	2.4
RC_AA371604	AA371604	ESTs Weakly similar to D9481.16 gene product	ESTs Weakly similar to D9481.16 gene product	2.4
RC_AA223209	AA223209	ESTs Weakly similar to U1 SMALL NUCLEAR R	ESTs Weakly similar to U1 SMALL NUCLEAR R	2.4
RC_AA218663	AA218663	ESTs	ESTs	2.4
RC_AA449458	AA449458	Human mRNA for KIAA0079 gene complete cds	Human mRNA for KIAA0079 gene complete cds	2.4
D38555	D38555	HLA-DR ASSOCIATED PROTEIN 1	HLA-DR ASSOCIATED PROTEIN 1	2.4
U73477	U73477	COL10A1	COL10A1	2.4
X60382	X60382	NUCLEAR FACTOR RIP140	NUCLEAR FACTOR RIP140	2.4
X84373	X84373	Guanylate binding protein 1, interferon-inducible GTPD	Guanylate binding protein 1, interferon-inducible GTPD	2.4
M55542	M55542	Human mRNA for UDP-GalNAc:polypeptide N-	Human mRNA for UDP-GalNAc:polypeptide N-	2.4
S82397	S82397	Glucose-fructose-6-phosphate transaminase	Glucose-fructose-6-phosphate transaminase	2.4
M90516	M90516	Human mRNA for KIAA0242 gene partial cds	Human mRNA for KIAA0242 gene partial cds	2.4
D87684	D87684	Human mRNA for 5-aminomidazole-4-carboxamide-1-	Human mRNA for 5-aminomidazole-4-carboxamide-1-	2.4
D82348	D82348	ESTs	ESTs	2.4
AA190693	AA190693	Homo sapiens mRNA for ATP-dependent RNA helicase	Homo sapiens mRNA for ATP-dependent RNA helicase	2.4
RC_N96953	N96953	ESTs	ESTs	2.4
AA434329	AA434329	Human serine kinase mRNA complete cds	Human serine kinase mRNA complete cds	2.4
RC_T29681	T29681	ESTs	ESTs	2.4
RC_AA279799	AA279799	ESTs Highly similar to VACUOLAR ATP SYNTHASE	ESTs Highly similar to VACUOLAR ATP SYNTHASE	2.4
RC_T25896	T25896	ESTs	ESTs	2.4
RC_AA147708	AA147708	ESTs Highly similar to CHROMOSOME	ESTs Highly similar to CHROMOSOME	2.4
RC_AA039887	AA039887	ESTs Moderately similar to ZINC FINGER PROTEIN	ESTs Moderately similar to ZINC FINGER PROTEIN	2.3
RC_AA455239	AA455239	Human protein-tyrosine phosphatase (HU-IP-1) mRNA	Human protein-tyrosine phosphatase (HU-IP-1) mRNA	2.3
RC_Z39909	Z39909	ESTs	ESTs	2.3
AA330771	AA330771	Homo sapiens breast cancer putative transcription factor	Homo sapiens breast cancer putative transcription factor	2.3
AA173223	AA173223	ESTs	ESTs	2.3
R81830	R81830	ESTs Weakly similar to R01H10.8 (C-elegans)	ESTs Weakly similar to R01H10.8 (C-elegans)	2.3
RC_AA031814	AA031814	CH22A protein	CH22A protein	2.3
RC_AA010065	AA010065	ESTs Highly similar to HYPOTHETICAL TRP-ASP	ESTs Highly similar to HYPOTHETICAL TRP-ASP	2.3
W23625	W23625	ESTs	ESTs	2.3
F02907	F02907	ESTs	ESTs	2.3
N94581	N94581	ESTs Weakly similar to PROBABLE UBIQUITIN	ESTs Weakly similar to PROBABLE UBIQUITIN	2.3
RC_N94581	N94581	ESTs	ESTs	2.3
RC_AA069285	AA069285	ESTs	ESTs	2.3
RC_AA450116	AA450116	ESTs Highly similar to GAG POLYPROTEIN (Avian	ESTs Highly similar to GAG POLYPROTEIN (Avian	2.3
RC_N33063	N33063	ESTs	ESTs	2.3
RC_T87807	T87807	ESTs Moderately similar to H11 ALU SUBFAMILY SQ	ESTs Moderately similar to H11 ALU SUBFAMILY SQ	2.3
RC_W495174	W495174	ESTs	ESTs	2.3
RC_AA450371	AA450371	ESTs	ESTs	2.3
RC_AA250737	AA250737	Human mRNA for EB1-ligand chemokine complete cds	Human mRNA for EB1-ligand chemokine complete cds	2.3
RC_AA425749	AA425749			2.3
U77180	U77180			2.3

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RC_AA024658	RC_AA024658	AA024658	ESTs	2.3
D00591	D00591	D00591	Chromosome condensation 1	2.3
X94453	X94453	X94453	Pyruvate-5-carboxylate synthetase (glutamate gamma-lysine) highly similar to CHROMOSOME	2.3
RC_AA459673	RC_AA459673	AA459673	ESTs	2.3
RC_AA428648	RC_AA428648	AA428648	ESTs Highly similar to CHROMOSOME	2.3
RC_AA54199	RC_AA54199	R32088	EST - RC R32088	2.3
RC_N92984.5	RC_N92984.5	X54109	Phosphoribosyl-vanillamide formyltransferase	2.3
RC_N92984.5	RC_N92984.5	N49284	MYB PROTO-ONCOGENE PROTEIN	2.3
U37022_mal	U37022_mal	U37022	Human cyclin-dependent protein kinase mRNA complete	2.3
U37022_mal	U37022_mal	U37022	Human mRNA for transcriptional activator hSN27b	2.3
D26156	D26156	D26156	Human C21 mRNA complete cds	2.3
U72514	U72514	U72514	Lysosomal-associated membrane protein 2	2.3
S79873	S79873	S79873	Human DNA-dependent protein kinase catalytic subunit	2.3
U47077	U47077	U47077	Human chromosome 4 Mad homolog Smad1 mRNA	2.3
U59423	U59423	U59423	Integrin beta-5 subunit	2.3
JO5633	JO5633	JO5633	H sapiens mRNA encoding GFP-anchored protein ESTs	2.3
Z48042	Z48042	Z48042	Human NAD+-specific isocitrate dehydrogenase beta	2.3
RC_AA037657	RC_AA037657	AA037657	ESTs	2.3
RC_N29888	RC_N29888	N29888	Human NAD+-specific isocitrate dehydrogenase beta	2.3
RC_AA251776	RC_AA251776	AA251776	ESTs	2.3
RC_AA236951	RC_AA236951	AA236951	ESTs weakly similar to F25H2.6 [C.elegans]	2.3
RC_AA464423	RC_AA464423	AA464423	ESTs	2.3
RC_AA074010	RC_AA074010	AA074010	ESTs Weakly similar to ¹⁰⁰ ALU SUBFAMILY J	2.3
RC_R63652	RC_R63652	R63652	Human DNA sequence from PAC 127B20 on chromosome	2.3
RC_N66857	RC_N66857	N66857	ESTs	2.3
RC_AA280588	RC_AA280588	AA280588	ESTs	2.3
RC_AA436477	RC_AA436477	AA436477	ESTs	2.3
RC_AA028028	RC_AA028028	AA028028	ESTs	2.3
RC_N39148	RC_N39148	N39148	ESTs	2.3
RC_AA485223	RC_AA485223	AA485223	ESTs	2.3
RC_AA011556	RC_AA011556	AA011556	ESTs	2.3
RC_AA003636	RC_AA003636	AA003636	ESTs	2.3
RC_AA148516	RC_AA148516	AA148516	ESTs	2.3
RC_AA495924	RC_AA495924	AA495924	ESTs	2.3
RC_AA131692	RC_AA131692	AA131692	ESTs	2.3
RC_N90401	RC_N90401	N90401	ESTs	2.3
RC_AA436613	RC_AA436613	AA436613	ESTs	2.3
RC_AA397921	RC_AA397921	AA397921	Homo sapiens mRNA transcriptional unit N143	2.3
RC_AA251766	RC_AA251766	AA251766	ESTs Moderately similar to metastasis-associated gene	2.3
RC_F093128	RC_F093128	F093128	ESTs	2.3

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FIGURE 4 (CONT.)

RC_T15674 f	T15674	ESTs	2.2
RC_AA416735	AA416735	ESTs	2.2
RC_AA423827	AA423827	ESTs	2.2
RC_AA600200	AA600200	ESTs	2.2
RC_H84658 s	H84658	ESTs	2.2
RC_H99261 s	H99261	ESTs	2.2
RC_T10060	T10060	ESTs	2.2
RC_AA043160	AA043160	ESTs	2.2
RC_AA059214	AA059214	ESTs	2.2
RC_AA490237	AA490237	EST - RC_AA490237	2.2
RC_AA227856	AA227856	II sapiens mRNA for HOXC9 protein exon 1	2.2
RC_H28428	H28428	ESTs	2.2
RC_AA076328	AA076328	Cyclin-dependent kinase inhibitor 2A (melanoma p16)	2.2
RC_F13690 s	F13690	ESTs Weakly similar to ZNF127-Xp [H.sapiens]	2.2
RC_AA237340	AA237320	ESTs	2.2
RC_AA378753	AA378753	ESTs	2.2
RC_AA430726	AA430726	EST - RC_AA430726	2.2
RC_N93618	N93618	ESTs	2.2
RC_T59686 s	T59686	ESTs	2.2
RC_U09770	U09770	Human cysteine-rich heart protein (hCRHP) mRNA	2.2
RC_R72008	R72008	ESTs Weakly similar to D1033 gene product [H.sapiens]	2.2
RC_N94606	N94606	ESTs	2.2
RC_D80237 s	D80237	Homo sapiens Anp2/3 protein complex subunit p20-Arc	2.2
RC_U09510	U09510	Glycyl-tRNA synthetase	2.2
U86782	U86782	COATOMER BETA SUBUNIT	2.2
X70476	X70476	Human z6S proteasome-associated protein (PUB1)	2.2
RC_AA417030	AA417030	Homo sapiens protein regulating cytokinesis 1 (PRC1)	2.2
RC_AA446949	AA446949	ESTs Weakly similar to ISOLEUCYL-tRNA	2.2
RC_AA236516	AA236516	ESTs	2.2
R78119	R78119	Homo sapiens vesicle transport related protein mRNA	2.2
RC_AA150088	AA150088	ESTs Highly similar to UBIQUITIN-CONJUGATING	2.2
RC_AA043353	AA043353	ESTs	2.1
RC_AA126719	AA126719	ESTs	2.1
RC_AA403121	AA403121	ESTs	2.1
RC_N64378	N64378	ESTs	2.1
RC_AA158132	AA158132	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces	2.1
RC_AA225031	AA225031	Homo sapiens RRM RNA binding protein Gyr-bp (GRY-	2.1
RC_Z99394 s	AA25031	ESTs Moderately similar to H11 ALU SUBFAMILY SP	2.1
RC_AA400820	AA400820	ESTs	2.1
RC_W20391 L3	W20391	Human mRNA for kinsin-related protein partial cds	2.1

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[illegible]

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FIGURE 4 (CONT.)

RC_R68425	R68425	ESTs	2.0
RC_W80467	W80467	ESTs	2.0
RC_U53192_f	D31392	ESTs Weakly similar to PEREGRIN [H.sapiens]	2.0
RC_Z39053	Z39053	ESTs	2.0
RC_N91246	N91246	ESTs	2.0
RC_Z90909	Z90909	PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC	2.0
AA443460	AA443460	ESTs	2.0
AA045481	AA045481	ESTs	2.0
W28362	W28362	ESTs	2.0
AA233177	AA233177	ESTs	2.0
T90746	T90746	H.sapiens mRNA for novel member of serine-arginine	2.0
H78241	H78241	ESTs	2.0
AA443596	AA443596	ESTs	2.0
AA453253	AA453253	ESTs	2.0
X69636	X69636	Human mRNA for KIAA0393 gene complete cds	2.0
AA047265	AA047265	Homo sapiens mRNA for osteoblast specific cysteine-rich	2.0
AA188981	AA188981	Homo sapiens retinol dehydrogenase-associated protein HEC	2.0
H11938	H11938	EST - RC_H11938	2.0
RC_H11938	RC_H11938	EST - RC_H11938	2.0
AA405838	AA405838	ESTs Highly similar to zinc finger protein [M.musculus]	2.0
AA406375	AA406375	ESTs Highly similar to PRE-MRNA SPLICING FACTOR	2.0
N24954	N24954	ESTs	2.0
D78586	D78586	CAD PROTEIN	2.0
U34044	U34044	Human selenium donor protein (seld) mRNA complete cds	2.0
AA621122	AA621122	ESTs	2.0
Z40810	Z40810	ESTs	2.0
AA127716	AA127716	Homo sapiens unknown mRNA complete cds	2.0
AA237022	AA237022	ESTs	2.0
AA479139	AA479139	Acid phosphatase 1 soluble	2.0
U05340	U05340	Human p55CDC mRNA complete cds	2.0
AA417909	AA417909	ESTs	2.0
AA181657	AA181657	ESTs	2.0
L37347	L37347	Natural resistance-associated macrophage protein 2	2.0
X92896	X92896	H.sapiens mRNA for ITBA2 protein	2.0
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular)	2.0
U37519	U37519	Aldehyde dehydrogenase 8	2.0
D28364	D28364	EST - D28364	2.0
D86978	D86978	Human mRNA for KIAA0225 gene partial cds	2.0
Z24724	Z24724	H.sapiens poly(A) site DNA	2.0
U39840	U39840	Human hepatocyte nuclear factor-3 alpha (HNF-3 alpha)	2.0

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FIGURE 4 (CONT.)

RC_AA136884	AA136884	ESTs	2.0
T63174.5	ESTs	ESTs	2.0
RC_N50963	N50963	ESTs	2.0
D80000	D80000	Human mRNA for KIAA0178 gene partial cds	2.0
RC_N73567	R73567	Human mRNA for KIAA0178 gene partial cds	2.0
RC_N81670	N81670	Human mRNA for KIAA0178 gene partial cds	2.0
RC_N72162	N72162	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA176312	AA176312	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA521474	AA521474	Human mRNA for KIAA0178 gene partial cds	2.0
L20298	L20298	Human mRNA for KIAA0178 gene partial cds	2.0
Z47727	Z47727	Human mRNA for KIAA0178 gene partial cds	2.0
U91932	U91932	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA173417	AA173417	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA287834	AA287834	Human mRNA for KIAA0178 gene partial cds	2.0
RC_W80763	W80763	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA112679	AA112679	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA233261	AA233261	Human mRNA for KIAA0178 gene partial cds	2.0
RC_T77464	T77464	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA227463	AA227463	Human mRNA for KIAA0178 gene partial cds	2.0
D50920	D50920	Human mRNA for KIAA0178 gene partial cds	2.0
D13645	D13645	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA233168	AA233168	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA227963	AA227963	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA451898	AA451898	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA302745	AA302745	Human mRNA for KIAA0178 gene partial cds	2.0
RC_N23393	N23393	Human mRNA for KIAA0178 gene partial cds	2.0
RC_W97931	W97931	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA504832	AA504832	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA46918	AA46918	Human mRNA for KIAA0178 gene partial cds	2.0
RC_N47469	N47469	Human mRNA for KIAA0178 gene partial cds	2.0
RC_T89703	T89703	Human mRNA for KIAA0178 gene partial cds	2.0
X55448	X55448	Human mRNA for KIAA0178 gene partial cds	2.0
RC_AA257972	AA257972	Human mRNA for KIAA0178 gene partial cds	2.0
RC_Z40715	Z40715	Human mRNA for KIAA0178 gene partial cds	2.0
AA464013	AA464013	Human mRNA for KIAA0178 gene partial cds	2.0
RC_W95063	W95063	Human mRNA for KIAA0178 gene partial cds	2.0
RC_X12791	X12791	Human mRNA for KIAA0178 gene partial cds	2.0
X81788	X81788	Human mRNA for KIAA0178 gene partial cds	2.0
L13689	L13689	Human mRNA for KIAA0178 gene partial cds	2.0
L33801	L33801	Human mRNA for KIAA0178 gene partial cds	2.0

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FIGURE 4 (CONT.)

U76638	Human BRCA1-associated RING domain protein	1.9
TIGR - HG174	EST - HG174-H174	1.9
X58072	GATA-binding protein 3	1.9
U05237	Human fetal ALe-50-reactive clone 1 (FAC1) mRNA	1.9
M2159	Small nuclear ribonucleoprotein polypeptide E	1.9
AA149585	ESTs	1.9
AA115058	ESTs	1.9
AA236453	ESTs	1.9
T25867	EST	1.9
U26312	Human heterochromatin protein HP1H-gamma mRNA	1.9
U41387	Human Gu protein mRNA partial cds	1.9
AA496000	ESTs	1.9
AA489046	ESTs	1.9
AA278653	ESTs	1.9
X82153	CATHEPSIN K PRECURSOR	1.9
AA403008	ESTs	1.9
D12485	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1	1.9
H44386	ESTs	1.9
N55583	ESTs	1.9
N55136	ESTs	1.9
AA497052	ESTs	1.9
N26855	ESTs Moderately similar to H1; ALU SUBFAMILY SQ	1.8
N52006	ESTs	1.8
Z40332	Homo sapiens mRNA for p15 complete cds	1.8
AA028074	ESTs	1.8
AA279171	ESTs Weakly similar to F25D7.1 [C.elegans]	1.8
AA251982	Homo sapiens clone Z3770 mRNA sequence	1.8
AA455001	ESTs	1.8
AA599219	ESTs Moderately similar to ALR [H.sapiens]	1.8
W84790	Human mRNA for KIAA0208 gene complete cds	1.8
H94248	ESTs	1.8
AA234765	ESTs	1.8
N35583	ESTs Weakly similar to PROBABLE E3 PROTEIN	1.8
AA099241	ESTs Moderately similar to 6S RIBOSOMAL PROTEIN	1.8
AA436192	ESTs	1.8
AA420988	ESTs	1.8
F02990	ESTs Highly similar to DOSAGE COMPENSATION	1.8
U14518	Centonate protein A (U78D)	1.8
AA22103	ESTs	1.8
AA398319	ESTs	1.8

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FIGURE 4 (CONT.)

RC_W52225	W52225	ESTs	1.8
RC_AA063460	AA063460	Gastrin-releasing peptide	1.8
RC_AA447603	AA447603	EST	1.8
RC_AA401274	AA401274	Homo sapiens REM RNA binding protein Gyr-rbp (GRY-)	1.8
RC_F04989	F04989	ESTs	1.8
RC_T96595	T96595	EST - RC_T96595	1.8
AF000430	AF000430	Homo sapiens mRNA for Dam1p/Vps1p-like protein	1.8
L76937	L76937	Homo sapiens Werner syndrome gene complete cds	1.8
U72263	U72263	Exostoses (multiple) 2	1.8
L25876	L25876	Human protein phosphatase (KAP1) mRNA complete cds	1.8
W68502	W68502	ESTs	1.8
AA005108	AA005108	ESTs	1.8
W72876	W72876	ESTs	1.8
RC_W72876	RC_W72876	ESTs	1.8
RC_AA457566	AA457566	OX40L RECEPTOR PRECURSOR	1.8
X75962	X75962	ESTs Highly similar to transcript from ARF6 chain B	1.8
RC_AA232104	AA232104	ESTs Highly similar to GERANYLGERANYL	1.8
RC_AA417962	AA417962	ESTs	1.8
RC_D59894	D59894	ESTs Moderately similar to HYPOTHETICAL 52.2 KD	1.8
RC_AA328988	AA328988	Human RNA-binding protein CUG-BP/hNab50 (NAB50)	1.8
RC_W88983	W88983	Human transducin beta-2 subunit mRNA complete cds	1.8
L16642	M63629	H. sapiens mRNA for transmembrane protein mp24	1.8
X92098	X92098	Human transporin (TRN) mRNA complete cds	1.8
X92098	U70322	Human transporin (TRN) mRNA complete cds	1.8
U70322	M63180	Thrombolytic RNA synthetase	1.8
U32986	U32986	Damage-specific DNA binding protein 1 (127 kD)	1.8
U65928	U65928	V-jun avian sarcoma virus 17 oncogene homolog	1.8
L10910	L10910	Homo sapiens splicing factor (CCL3) mRNA complete cds	1.8
RC_R41281	R41281	Homo sapiens DN13/CPR3 mRNA complete cds	1.8
RC_N50050	N50050	ESTs	1.8
RC_AA460350	AA460350	ESTs Weakly similar to C01H6.7 [C.elegans]	1.8
RC_AA292066	AA292066	ESTs	1.8
RC_AA291923	AA291923	ESTs	1.8
RC_AA411144	AA411144	ESTs	1.8
RC_AA436171	AA436171	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3)	1.8
RC_AA251758	AA251758	ESTs	1.8
RC_AA406478	AA406478	ESTs	1.8
RC_AA191353	AA191353	ESTs	1.8
D13630	D13630	Human mRNA for KIAA0005 gene complete cds	1.8
X65488	X65488	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN	1.8
D13630	D13630	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces	1.8
RC_AA131584	AA131584		

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FIGURE 4 (CONT.)

RC_AA283743	AA283743	ESTs Moderately similar to YY1-associated factor 2	1.8
RC_AA056588	AA056588	ESTs	1.7
RC_AA180321	AA180321	ESTs Weakly similar to W04D2.6 [C.elegans]	1.7
RC_AA262957	AA262957	ESTs	1.7
RC_AA234767	AA234767	ESTs	1.7
RC_AA479961	AA479961	ESTs	1.7
RC_T03865	T03865	ESTs	1.7
RC_N51226	N51226	ESTs	1.7
RC_AA056249	AA056249	Collagen type IV alpha 3	1.7
RC_H17620	H17620	ESTs	1.7
RC_H73608_s	H73608	ESTs	1.7
RC_H23230	H23230	ESTs	1.7
RC_AA171529	AA171529	ESTs	1.7
RC_AA470140	AA470140	ESTs	1.7
RC_AA459005	AA459005	ESTs	1.7
RC_AA425439	AA425439	EST	1.7
RC_AA695364	AA695364	EST	1.7
RC_N31598	N31598	ESTs	1.7
RC_T57317	T57317	ESTs	1.7
RC_H55890	W55890	Human Chromosome 16 BAC clone C1987/SK-A-73556	1.7
RC_N50831	N50831	ESTs	1.7
RC_AA280687	AA280687	ESTs	1.7
RC_AA11879	AA11879	EST	1.7
RC_AA116075	AA116075	ESTs	1.7
RC_U95367	U95367	Human GABA-A receptor pi subunit mRNA complete cds	1.7
RC_AA598447	AA598447	Homo sapiens exportin 1 mRNA complete cds	1.7
RC_W38150	W38150	EST - RC_W38150	1.7
RC_AA232315	AA232315	Homo sapiens clone 23797 and 23917 mRNA partial cds	1.7
RC_R39923	R39923	ESTs	1.7
RC_AA410972	AA410972	ESTs	1.7
RC_W23469	W23469	Homo sapiens vesicle trafficking protein sec22b mRNA	1.7
RC_AA287091	AA287091	ESTs highly similar to C10 [H.sapiens]	1.7
RC_AA291260	AA291260	ESTs	1.7
RC_AA465690	AA465690	Human arginine-rich nuclear protein mRNA complete cds	1.7
RC_AA453465	AA453465	ESTs	1.7
RC_D78151	D78151	H sapiens mRNA for 55.11 binding protein	1.7
RC_L19161	L19161	TRANSLATION INITIATION FACTOR 2 GAMMA	1.7
RC_U90551	U90551	Human histone 2A-like protein (H2A.L) mRNA complete	1.7
RC_L76703	L76703	Homo sapiens protein phosphatase 2A, B56-epsilon (PP2A)	1.7
RC_HG4557	HG4557	EST - HG4557-HT4962	1.7

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FIGURE 4 (CONT.)

RC_N58561_s	N58561	Cathepsin B	1.7
RC_H15436	H15436	ESTs	1.7
RC_W58888	W58888	Chaperonin containing T-complex subunit 6	1.6
RC_AA479362	AA479362	ESTs	1.7
RC_D31161_s	D31161	ESTs	1.7
RC_AA035143	AA035143	ESTs	1.7
RC_AF002668	AF002668	Homo sapiens putative fatty acid desaturase MLD mRNA	1.7
RC_AA416733	AA416733	ESTs	1.7
RC_N92860_s	N92860	Proto-oncogene AML1 (alternative products)	1.7
RC_R93068	R93068	ESTs	1.7
RC_W19222	W19222	ESTs	1.7
RC_AA599267	AA599267	EST - RC_AA599267	1.7
RC_AA410894	AA410894	ESTs	1.7
RC_AA609053	AA609053	ESTs	1.7
RC_AA400080	AA400080	EST	1.7
RC_AA286891	AA286891	EST	1.7
RC_N31952	N31952	ESTs	1.7
RC_AA421773	AA421773	ESTs Moderately similar to HYPOTHETICAL 66.5 KD	1.7
RC_N90029	N90029	ESTs	1.7
RC_AA150142	AA150142	Homo sapiens clone 1400 unknown protein mRNA partial	1.7
RC_AA132514	AA132514	ESTs	1.7
RC_AA462222	AA462222	ESTs	1.6
RC_AA426716	AA426716	Homo sapiens drp1 mRNA complete cds	1.6
RC_AA15803	AA15803	ESTs Weakly similar to Similar to S. cerevisiae	1.6
RC_AA14937	AA14937	ESTs	1.6
RC_AA24052	AA24052	Homo sapiens thyroid receptor interactor (TRIP3) mRNA	1.6
RC_AA456437	AA456437	ESTs Highly similar to GONADOTROPIN-RELEASING	1.6
RC_AA424524	AA424524	ESTs Weakly similar to CLEAVAGE STIMULATION	1.6
RC_AA253360	AA253360	Homo sapiens mRNA for KIAA0286 gene partial cds	1.6
RC_W58247_s	W58247	EST	1.6
RC_AA599622	AA599622	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4	1.6
RC_X39059	X39059	ESTs	1.6
RC_W04698	W04698	II sapiens mRNA for unknown protein expressed in	1.6
RC_N73865	N73865	ESTs	1.6
RC_T23820	T23820	ESTs Weakly similar to L8004.7 gene product	1.6
RC_AA099589	AA099589	Homo sapiens cyclin 12a mRNA complete cds	1.6
RC_U61145	U61145	Homo sapiens mRNA for GDP dissociation inhibitor beta	1.6
RC_AA151708	AA151708	Human enhancer of zeste homolog 2 (EZH2) mRNA	1.6
RC_H19378	H19378	EST	1.6
		ESTs	1.6

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RC_AA417970	AA417970	ESTs	1.6
RC_R10720	R10720	ESTs	1.6
RC_A256106	A256106	ESTs	1.6
RC_A12424_s	A12424	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	1.6
RC_W17820	W17820	ESTs	1.6
RC_AA167708	AA167708	ESTs	1.6
RC_AA187579	AA187579	ESTs	1.6
RC_AA187579	AA187579	ESTs Weakly similar to Ya007-cap1 [C.eerevisiae]	1.6
RC_B15743	B15743	ESTs	1.6
RC_N69014_1	N69014	Homo sapiens SOX22 protein (SOX22) mRNA, complete cds	1.6
RC_N38919	N38919	ESTs	1.6
RC_Z3919	Z3919	1 human mRNA for KIAA0345 gene complete cds	1.6
AB0021343	AB002134	ESTs	1.6
RC_AA321186	AA321186	Homo sapiens DNA polymerase zeta catalytic subunit	1.6
RC_AA258205	AA258205	Human mRNA for KIAA0110 gene complete cds	1.6
DI4811	DI4811	Homo sapiens interferon stimulated 1-cell protein 1	1.6
U39286	U39286	Probable 26S PROTEASE SUBUNIT TPST1	1.6
M34079	M34079	ESTs	1.6
AA072618	AA072618	ESTs, Weakly similar to NADH+UBIQUINONE	1.6
RC_N026259	N026259	Human mRNA for ceramide glucosyltransferase complete cds	1.6
D50840	D50840	Nuclear autologous sperm protein (histone-binding)	1.6
N973516	N973516	Human nuclear protein NF45 mRNA complete cds	1.6
U10323	U10323	Human nuclear protein p53 (L1-Fraumeni syndrome)	1.6
N22898	N22898	Tumor protein p53 (L1-Fraumeni syndrome)	1.6
U90549	U90549	Human non-histone chromosomal protein (NH2) mRNA	1.6
Q03934	Q03934	NAD(P)H:menadiene oxidoreductase	1.6
X33793	X33793	MULTIFUNCTIONAL PROTEIN ADE2	1.6
U76992	U76992	Human Tax-SFI mRNA complete cds	1.6
U09820	U09820	X-LINKED HELICASE II	1.6
X38321	X38321	NUCLEAR PORE GLYCOPROTEIN P62	1.6
AA121127	AA121127	ESTs Weakly similar to ZK1058.4 [C.elegans]	1.6
RC_AA243007	AA243007	ESTs	1.6
RC_AA463195	AA463195	Human clone 23772 mRNA sequence	1.6
U09099	U09099	ESTs	1.6
RC_W15528	W15528	ESTs	1.6
R70621	R70621	Human clone 23772 mRNA sequence	1.6
RC_AA456598	AA456598	ESTs Highly similar to hypothetical protein 100K	1.6
RC_AA161375	AA161375	ESTs	1.6
RC_AA27967	AA27967	Homo sapiens mRNA for KIAA0530 protein partial cds	1.6
RC_AA07378	AA07378	Cathepsin B	1.6
RC_AA148855	AA148855	ESTs	1.6
RC_W00856_f	W00856	Homo sapiens UDP-glucose dehydrogenase (UGDH)	1.6

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RC_AA101811	AA101811	Human Ecd Ahr-50-reactive clone 1 (FAC1) mRNA	EST	1.6
RC_AA347967	AA347967	ESTs Highly similar to POP2 PROTEIN [Schoenmayers	ESTs	1.6
RC_AA256678	U05237	H.sapiens p63 mRNA for transmembrane protein	ESTs	1.6
RC_AA256678	X69910	H.sapiens KIAA0442 mRNA partial cds	ESTs	1.6
RC_H95039	H95039	Human sapiens importin beta subunit mRNA complete cds	ESTs	1.6
RC_H95039	AA115890	ESTs	ESTs	1.5
RC_AA183038	AA219699	ESTs Weakly similar to DES70 [H.sapiens]	ESTs	1.5
RC_AA226662	AA236672	ESTs	ESTs	1.5
RC_AA276319	AA476319	ESTs	ESTs	1.5
RC_AA041551	AA041551	ESTs	ESTs	1.5
RC_AA195179	AA195179	ESTs	ESTs	1.5
RC_AA256492	AA256492	Protein tyrosine phosphatase non-receptor type-4	ESTs	1.5
RC_W93640	W93640	ESTs	ESTs	1.5
RC_R07016	R07016	ESTs	ESTs	1.5
RC_AA232644	AA232644	ESTs Weakly similar to mouse MMR1	ESTs	1.5
RC_N37065	N37065	ESTs	ESTs	1.5
RC_T10258	T10258	ESTs	ESTs	1.5
RC_AA279757	AA279757	ESTs	ESTs	1.5
RC_N67590	N67590	ESTs	ESTs	1.5
RC_W72138	W72138	ESTs	ESTs	1.5
RC_AA804071	AA804071	ESTs	ESTs	1.5
RC_AA002171	AA002171	ESTs	ESTs	1.5
RC_AA113309	AA113309	ESTs	ESTs	1.5
RC_N21978	N21978	ESTs Highly similar to CALCIUM-TRANSPORTING	ESTs	1.5
RC_AA47970	AA47970	Human mRNA for phosphatidylinositol-4-oxo-3-phosphatase	ESTs	1.5
RC_AA433925	AA433925	Human mRNA for phosphatidylinositol-4-oxo-3-phosphatase	ESTs	1.5
RC_AA166888	AA166888	EST - AA113913	ESTs	1.5
RC_D31764	D31764	ESTs	ESTs	1.5
RC_AA146888	AA146888	Human mRNA for KIAA0064 gene complete cds	ESTs	1.5
RC_AA293568	AA293568	ESTs	ESTs	1.5
RC_AA293568	AA293568	ESTs	ESTs	1.5
RC_N48677	N48677	ESTs	ESTs	1.5
RC_AA226922	AA226922	ESTs Highly similar to CLATHRIN COAT ASSEMBLY	ESTs	1.5
RC_N53271	N53271	Human sapiens LIM protein mRNA complete cds	ESTs	1.5
RC_N31253	N31253	Transcription factor 3/2A, immunoglobulin enhancer	ESTs	1.5

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FIGURE 4 (CONT.)

D38521	D38521	Human mRNA for KIAA0077 gene partial cds	1.5
M63167	M63167	V-akt thymine thymoma viral oncogene homolog 1	1.5
U50939	U50939	EST - HG884-H1864	1.5
U35451	U35451	Human ankyrin precursor protein-binding protein 1	1.5
U94836	U94836	Homo sapiens heterochromatin protein p25 mRNA	1.5
L33881	L33881	Human ERPOT 213-21 mRNA complete cds	1.5
L18960	L18960	Protein kinase C, α isoform	1.5
AA496257	AA496257	Eukaryotic translation initiation factor-4C (EIF4C)	1.5
AA262942	AA262942	ESTs Weakly similar to DIPEPTIDYL PEPTIDASE IV	1.5
AA056735	AA056735	ESTs Weakly similar to HYPOTHETICAL PROTEIN	1.5
AA482014	AA482014	ESTs Weakly similar to HYPOTHETICAL PROTEIN	1.5
U09564	U09564	H. sapiens mRNA for centrin gene	1.5
AA609738	AA609738	Human serine kinase mRNA complete cds	1.5
N54450	N54450	ESTs	1.5
Z70955	Z70955	ESTs	1.5
N78717	N78717	ESTs	1.5
R87660	R87660	H. sapiens mRNA for translin	1.5
T98843	T98843	EST - RC_R87660	1.5
Z39211	Z39211	ESTs Moderately similar to H11 ALU SUBFAMILY J	1.5
AA412528	AA412528	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPF)	1.5
AA399550	AA399550	ESTs Weakly similar to QRF2 consensus sequence	1.5
AA621580	AA621580	ESTs Weakly similar to DPY-30 PROTEIN [C.elegans]	1.5
AA422160	AA422160	ESTs Highly similar to HYPOTHETICAL 66.5 KD	1.5
AA156542	AA156542	H. sapiens NAP (nucleosome assembly protein) mRNA	1.4
H59417	H59417	ESTs	1.4
AA460246	AA460246	ESTs Weakly similar to similar to tyrosyl-RNA	1.4
F04982	F04982	ESTs	1.4
AA285277	AA285277	Homo sapiens brain expressed ring finger protein mRNA	1.4
R09196	R09196	ESTs Moderately similar to M-phase phosphoprotein 11	1.4
F09983	F09983	ESTs	1.4
AA057193	AA057193	ESTs	1.4
AA449068	AA449068	Homo sapiens TFAR19 mRNA complete cds	1.4
AA452724	AA452724	Zinc finger protein 7 (KOX 4 clone HF 16)	1.4
M25380	M25380	ESTs	1.4
AA417895	AA417895	ESTs	1.4
AA425100	AA425100	ESTs	1.4
RC_AA237879	RC_AA237879	ESTs Highly similar to GTP-BINDING PROTEIN SARA	1.4
RC_T17440_L	RC_T17440_L	ESTs	1.4

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FIGURE 4 (CONT.)

RC_AA25554	AA25554	ESTs	1.4
RC_AA40297	AA40297	ESTs	1.4
RC_N92253	N92253	EST	1.4
RC_AA292128	AA292128	ESTs	1.4
RC_N61243	N61243	ESTs	1.4
RC_U0727	U0727	ESTs	1.4
RC_D38498	D38498	Cyclin-dependent kinase inhibitor 2A (melanoma p16)	1.4
RC_M62810	M62810	Human PMS5 mRNA (yeast mismatch repair gene PMS1)	1.4
RC_AA279991	AA279991	Transcription factor 6-like 1 (mitochondrial transcription)	1.4
RC_N66569	N66569	ESTs	1.4
RC_AA287138	AA287138	ESTs Weakly similar to ASPARTYL-TRNA	1.4
RC_AA278755	AA278755	ESTs Weakly similar to HLA ALU SUBFAMILY SBI	1.4
RC_AA195515	AA195515	ESTs	1.4
RC_R63925	R63925	ESTs	1.4
RC_N23972	N23972	ESTs	1.4
RC_W93379	W93379	U. sapiens nek2 mRNA for protein kinase	1.4
RC_L06419	L06419	Lyss) hydroxylase	1.4
RC_AA411882	AA411882	ESTs	1.4
RC_AA085918	AA085918	H. sapiens HUNK1 mRNA	1.4
RC_U12595	U12595	Human tumor necrosis factor type 1 receptor associated	1.4
RC_AA262943	AA262943	ESTs	1.4
RC_AA135095	AA135095	Homo sapiens Sox-like transcriptional factor mRNA	1.4
RC_T10626	T10626	ESTs	1.4
RC_AA497015	AA497015	Homo sapiens chromosome 19 cosmid R32469	1.4
RC_AA171939	AA171939	ESTs	1.4
RC_AB064884	AB064884	Homo sapiens mRNA for PKU-alpha partial cds	1.4
RC_N94700	N94700	Homo sapiens mRNA export protein (RAE1) mRNA	1.4
RC_Z40041	Z40041	ESTs	1.4
RC_W60473	W60473	ESTs	1.4
RC_Z38501	Z38501	ESTs Weakly similar to PROBABLE E5 PROTEIN	1.4
RC_H93708	H93708	CLEAVAGE SIGNAL-1 PROTEIN	1.4
RC_AA025086	AA025086	ESTs	1.4
RC_N64244	N64244	ESTs	1.4
RC_U07418	U07418	DNA mismatch repair protein MLH1	1.4
RC_R64660	R64660	ESTs	1.4
RC_AA400093	AA400093	ESTs Weakly similar to HYPOTHETICAL 48.8 KD	1.4
RC_AA490949	AA490949	ESTs	1.4
RC_D80921	D80921	Homo sapiens clone 23965 mRNA sequence	1.4
RC_N26722	N26722	ESTs	1.4
RC_W90146	W90146	ESTs	1.4

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FIGURE 4 (CONT.)

RC_AA114250	AA114250	Homo sapiens mRNA for KIAA0512 protein complete cds	1.4
RC_AA031357	AA031357	ESTs	1.3
RC_T68510	T68510	ESTs	1.3
RC_W67567	W67567	DI-N-ACETYL CHITOBIASE PRECURSOR	1.3
RC_W67524	W67524	Human protein-tyrosine phosphatase (HU/PP-1) mRNA	1.3
RC_AA465093	AA465093	ESTs	1.3
RC_H26417	H26417	ESTs	1.3
RC_T64438	T64438	ESTs	1.3
RC_D11718	D11718	ESTs Weakly similar to C01A2.4 [C.elegans]	1.3
RC_Z11963.f	Z11963	ESTs	1.3
RC_AA22079	AA22079	Homo sapiens HP protein (HP) mRNA complete cds	1.3
RC_AA262889	AA262889	Homo sapiens mRNA for dachshund protein	1.3
RC_AA487492	AA487492	Homo sapiens clone 23592 mRNA sequence	1.3
RC_AA464428	AA464428	ESTs	1.3
RC_H38328.s	H38328	H sapiens RBQ-1 mRNA	1.3
RC_AA040696	AA040696	ESTs	1.3
RC_AA231169	AA231169	Zinc finger protein 139 (clone pHZ-37)	1.3
RC_AA443294	AA443294	ESTs	1.3
RC_T166561	T166561	ESTs	1.3
RC_X69398	X69398	Homo sapiens putative transcriptional repressor E2F-6	1.3
RC_AA122394	AA122394	Human Kruppel-related zinc finger protein (ZNF184)	1.3
RC_T40707	T40707	CD47 antigen (Rb-related antigen integrin-associated	1.3
RC_AA45536	AA45536	ESTs	1.3
RC_AA206800	AA206800	ESTs	1.3
RC_AA001386	AA001386	ESTs	1.3
RC_AA428992	AA428992	ESTs	1.3
RC_R49886	R49886	ESTs	1.3
RC_T95591	T95591	ESTs	1.3
RC_AA338760	AA338760	ESTs	1.3
RC_AA098864	AA098864	ESTs	1.3
RC_AA234817	AA234817	ESTs	1.3
RC_AA059051	AA059051	ESTs	1.3
RC_AA046619	AA046619	ESTs	1.3
RC_AA461169	AA461169	ESTs	1.3
RC_AA449071	AA449071	ESTs	1.3
RC_N24732	N24732	ESTs	1.3
RC_AA400195	AA400195	ESTs	1.3
RC_AA029264	AA029264	ESTs	1.3
RC_W86978	W86978	ESTs	1.3

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FIGURE 4 (CONT.)

RC_H18086	H38086	Human N-ethylmaleimide-sensitive factor mRNA partial	1.3
RC_F11663	F11663	ESTs	1.3
AA458542	AA458542	Homo sapiens chromosome 19 cosmid R32469	1.3
RC_AA101601	AA101601	ESTs Highly similar to Polio virus receptor protein	1.3
RC_AA598675	AA598675	ESTs	1.3
AA156670	AA156670	Homo sapiens agrin precursor mRNA partial cds	1.3
AA059415	AA059415	ESTs Moderately similar to H11 ALU SUBFAMILY SB	1.3
RC_AA485424	AA485424	ESTs	1.3
M64929	M64929	Protein phosphatase 2 (formerly 2A) regulatory subunit B	1.3
U28686	U28686	Human putative RNA binding protein RNPL mRNA	1.3
U02680	U02680	Human protein tyrosine Kinase mRNA complete cds	1.3
U96113	U96113	EST - U96113	1.3
X97544	X97544	H. sapiens mRNA for TIM17 precursor transcript	1.3
Z46629	Z46629	SRX (sex-determining region Y) gene family member	1.3
RC_H60061	H60061	ESTs Moderately similar to H11 ALU SUBFAMILY SB	1.3
RC_AA007234	AA007234	ESTs	1.3
AA329211_s	AA329211	Homo sapiens RBM RNA binding protein GRY-1p (GRY-	1.3
RC_AA132007	AA132007	Down-regulator of transcription 1 TBP-binding (negative	1.3
RC_AA417569	AA417569	ESTs	1.3
RC_AA236200	AA236200	ESTs	1.3
RC_AA126426	AA126426	Human brain secretory protein hSec10p (HSEC10) mRNA	1.3
RC_AA304499	AA304499	ESTs Highly similar to probable chloride channel 3	1.3
RC_AA51471	AA51471	ESTs	1.3
H83438	H83438	Homo sapiens mRNA for DDS1beta protein complete cds	1.3
T23932	T23932	ESTs	1.3
T59859	T59859	ESTs	1.3
N20630	N20630	ESTs	1.3
D87466	D87466	Human mRNA for KIAA0276 gene partial cds	1.3
AA083339	AA083339	ESTs	1.3
AA598506	AA598506	Human mRNA for KIAA0179 gene partial cds	1.3
AA278650	AA278650	ESTs	1.3
AA599718	AA599718	H. sapiens mRNA for translin associated protein X	1.3
AA398243	AA398243	ESTs Highly similar to RSP7 PROTEIN (Saccharomyces	1.3
N51855	N51855	ESTs Moderately similar to NAD(P) dehydrogenase	1.3
W52065	W52065	ESTs Highly similar to KIAA0539 protein complete cds	1.3
L38961	L38961	Homo sapiens mRNA for KIAA0539 protein complete cds	1.2
N55304	N55304	Integral transmembrane protein 1	1.2
AA147543	AA147543	ESTs	1.2
T32794	T32794	ESTs	1.2
U51698	U51698	ESTs	1.2

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FIGURE 4 (CONT.)

RC_AA464758	AA464758	ESTs	1,2
RC_X02751	X02751	Neuroblastoma RAS viral (v-ra) oncogene homolog	1,2
RC_W87544	W87544	ESTs	1,2
RC_AA025746	AA025746	ESTs	1,2
RC_R62444	R62444	ESTs	1,2
RC_H05635	H05635	ESTs	1,2
RC_AA433943	AA433943	ESTs Highly similar to 50S RIBOSOMAL PROTEIN L13	1,2
RC_N42440	N42440	ESTs Weakly similar to luteal RNA-binding protein M4	1,2
RC_W03007	W03007	ESTs	1,2
RC_T99364	T99364	ESTs Weakly similar to 1101 ALU SUBFAMILY J	1,2
RC_AA411708	AA411708	Human segment clone 23685 mRNA sequence	1,2
RC_U25239	U25239	CCAAT/enhancer binding protein (C/EBP) gamma	1,2
RC_A112222	A112222	EST - AA112222	1,2
RC_W61011	W61011	ESTs	1,2
RC_AA010188	AA010188	ESTs	1,2
RC_N67104	N67104	ESTs	1,2
RC_N71027	N71027	ESTs	1,2
RC_AA398222	AA398222	EST - RC_T85190	1,2
RC_T85190	T85190	ESTs	1,2
RC_N74635	N74635	ESTs	1,2
RC_Z38839	Z38839	Human endonuclease III homolog mRNA complete cds	1,2
RC_U79718	U79718	ESTs	1,2
RC_AA355201	AA355201	YY1 transcription factor	1,2
RC_Z14077_5	Z14077_5	ESTs Highly similar to HYPOTHETICAL 275 KD	1,2
RC_N68622	N68622	ESTs	1,2
RC_T17498	T17498	ESTs	1,2

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FIGURE 5

Accession	Gene Name	Ratio tumor v. breast
AF010616.1		
RC_T79956		135.3
RC_AA453638	ESTs	107.3
AA453638	EST - RC_AA453638	81.8
AA461322	EST	75.3
RC_AA461322	EST - RC_AA461322	72.9
RC_AA461310	Collagen type XI alpha 1	61.5
RC_R67275.5	ESTs	57.1
RC_AA453518	EST - RC_N27351	53.9
RC_N27351	Human focal adhesion kinase (FAK) mRNA complete cds	53.2
RC_AA486737	ESTs	46.8
RC_AA453479	Human focal adhesion kinase (FAK) mRNA complete cds	38.9
RC_AA453479	ESTs	33.6
RC_AA453479	EST - RC_AA453479	32.4
RC_AA453479	EST - RC_R68339	30.6
RC_AA453479	EST	28.3
RC_AA453479	EST - RC_AA211831	28.1
RC_AA453479	ESTs	25.5
RC_AA453479	Inhibin beta A (activin A activin AB alpha polypeptide)	23.9
RC_AA453479	ESTs	22.8
RC_AA453479	EST - RC_AA232940	21.7
RC_AA453479	ESTs	20.9
RC_AA453479	ESTs	19.5
RC_AA453479	ESTs	19.4
RC_AA453479	ESTs	17.7
RC_AA453479	CARCINOEMBRYONIC ANTIGEN PRECURSOR	17.1
RC_AA453479	ESTs	16.8
RC_AA453479	ESTs	16.8
RC_AA453479	EST - RC_AA211158	16.2
RC_AA453479	ESTs	16.1
RC_AA453479	ESTs	16.1
RC_AA453479	ESTs Highly similar to thyroid disease hypothetical	16.1

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FIGURE 5 (CONT.)

RC_AA196721	AA196721	Homo sapiens clone 23967 unknown mRNA partial cds	EST - RC_AA196721	16.1
RC_T23875	T23875	Inhibin beta A (activin A activin AB alpha polypeptide)	ESTs	15.8
RC_X57579	X57579	ESTs	ESTs	15.2
RC_AA191404	AA191404	ESTs Weakly similar to R0334.4 [C elegans]	ESTs	14.9
RC_AA436869	AA436869	Human fibroblast activation protein mRNA complete cds	ESTs	14.7
RC_AA436611	AA436611	ESTs	ESTs	14.6
RC_R51309	R51309	ESTs Moderately similar to PTTG gene product	ESTs	14.4
RC_AA461297	AA461297	ESTs Highly similar to HYPOPHYSAL 21.5 KD	ESTs	14.2
RC_AA430032	AA430032	Carboxypeptidase B1 (tissue)	ESTs	14.3
RC_AA280679	AA280679	ESTs	ESTs	14.1
RC_R07976	R07976	Chromograinin A (parathyroid secretory protein 1)	ESTs	14.1
RC_R46627	R46627	ESTs Moderately similar to 25E8.1 [D melanogaster]	ESTs	14.0
RC_AA461559	AA461559	ESTs Weakly similar to TH1 protein [D melanogaster]	ESTs	13.9
RC_AA092129	AA092129	Androgen receptor (dihydrotestosterone receptor) testicular	ESTs	13.9
RC_AA436893	AA436893	ESTs Weakly similar to hypothetical protein 1 [H. sapiens]	ESTs	13.7
RC_M23263	M23263	Homo sapiens histone macroH2A1.2 mRNA complete cds	ESTs	13.5
RC_AA486538	AA486538	ESTs Weakly similar to KIAA0007 gene partial cds	ESTs	13.4
RC_D20379	D20379	Human mRNA for KIAA0007 gene partial cds	ESTs	13.3
RC_AA076138	AA076138	Homo sapiens mRNA for SCGP-beta complete cds	ESTs	13.3
RC_AA045074	AA045074	ESTs Moderately similar to H1 ALU SUBFAMILY SC	ESTs	13.1
RC_D60354	D60354	EST - RC_AA412065	ESTs	13.1
RC_T78922_s	T78922_s	Homo sapiens regulator of G-protein signalling 12	ESTs	12.8
RC_AA401334	AA401334	Homo sapiens mRNA for A+U-rich element RNA binding	ESTs	12.5
RC_AA431350	AA431350	ESTs	ESTs	12.5
RC_AA412065	AA412065	ESTs	ESTs	12.4
RC_R61740	R61740	ESTs	ESTs	12.4
RC_R54950	R54950	ESTs	ESTs	12.3
RC_AA037285	AA037285	ESTs	ESTs	12.3
RC_AA233796	AA233796	ESTs	ESTs	12.2
RC_AA219305	AA219305	ESTs	ESTs	12.2
RC_AA252245	AA252245	ESTs	ESTs	12.1
RC_AA041276	AA041276	ESTs Weakly similar to H1 ALU SUBFAMILY SX	ESTs	12.1
RC_AA463874	AA463874	Homo sapiens ES/130 mRNA complete cds	ESTs	12.1
RC_AA461528	AA461528	ESTs	ESTs	12.1
RC_AA099404	AA099404	ESTs	ESTs	12.1
RC_AA214305	AA214305	Fibroblast growth factor receptor 2 (bacteria-expressed	ESTs	12.1
RC_AA220223	AA220223	ESTs	ESTs	12.1

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FIGURE 5 (CONT.)

RC_AA478571	AA478571	Glutamine-fructose-6-phosphate transaminase	12.1
RC_AA253217	AA253217	ESTs	11.8
RC_AA470074	AA470074	ESTs	11.5
RC_AA256010	AA256010	ESTs	11.4
RC_AA256010	AA256010	UBIQUITIN-LIKE PROTEIN GDX	11.4
RC_R22922_s	R22922	ESTs	11.3
RC_W56538	W56538	ESTs	11.3
RC_AA179298	AA179298	ESTs Weakly similar to extracellular protein [H.sapiens]	11.3
RC_AA48232	AA48232	Homo sapiens chromosome 9 P1 clone 11659	11.3
RC_AA281733	AA281733	EST	11.2
RC_AA452601	AA452601	ESTs	11
RC_AA035630	AA035630	Homo sapiens U4/U6 small nuclear ribonucleoprotein	11
RC_AA453630	AA453630	EST	10.9
RC_R40431	R40431	ESTs	10.7
RC_AA405098	AA405098	ESTs Weakly similar to MOESIN/EZRIN/RADIXIN	10.6
RC_AA599259	AA599259	Human splicedomal protein (SAP 61) mRNA complete cds	10.6
RC_X62078	X62078	GANGLIOSIDE GN2 ACTIVATOR PRECURSOR	10.4
RC_AA233170	AA233170	EST	10.4
RC_AA470156	AA470156	ESTs Weakly similar to dynein 74K chain cytosolic	10.4
RC_AA281290	AA281290	ESTs Highly similar to ZINC FINGER PROTEIN	10.3
RC_AA449832	AA449832	ESTs	10.3
RC_AA427898	AA427898	ESTs Weakly similar to trabecular meshwork inducible	10.1
RC_AA609867	AA609867	ESTs Weakly similar to No definition line found	10
RC_R49198_1	R49198	H.sapiens DAP-3 mRNA	9.9
RC_AA112596	AA112596	ESTs	9.8
RC_AA207013	AA207013	ESTs	9.7
RC_R06986_1	R06986	ESTs	9.7
RC_R06986_1	R06986	Spermidine synthase	9.7
RC_AA24338	AA24338	ESTs	9.7
RC_AA228030	AA228030	ESTs Weakly similar to R01H10.6 [C.elegans]	9.7
RC_AA447982	AA447982	PROTEASOME COMPONENT C13 PRECURSOR	9.7
RC_AA447982	AA447982	EST - RC_T97341	9.6
RC_Z14982_mal	Z14982	ESTs Highly similar to HYPOTHETICAL 23.1 KD	9.5
RC_T97341	T97341	ESTs	9.4
RC_AA143190	AA143190	ESTs	9.3
RC_AA282914	AA282914	ESTs	9.3
RC_N21678	N21678	ESTs	9.3
RC_AA262111	AA262111	Human mRNA for KIAA0101 gene complete cds	9.2
RC_AA262111	AA262111	ESTs	9.2
RC_D14657	D14657	ESTs	9.2
RC_AA007344	AA007344	ESTs	9.2

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FIGURE 5 (CONT.)

RC_W71140	W71140	ESTs Highly similar to TRYPTOPHAN ANIONIC	9.2
RC_T16308	T16308	ESTs	9.1
RC_AA47666	AA47666	Human CENP-F kinetochore protein mRNA complete cds	9.1
RC_AA47666	AA47666	EST - HG2981-HT3127	9
RC_R38919	R38919	EST	9
RC_M86757	M86757	S100 calcium-binding protein A7 (psortasin 1)	8.9
RC_X72755	X72755	H.sapiens Humig mRNA	8.8
RC_AA43342	AA43342	ESTs	8.7
RC_AA481281	AA481281	ESTs	8.7
RC_AA608723	AA608723	ESTs	8.6
RC_AA457018	AA457018	ESTs	8.5
RC_AA113011	AA113011	Human mRNA for KIAA0314 gene partial cds	8.5
RC_H96237	H96237	Collagen type XI alpha 1	8.5
RC_AA024835	AA024835	Homo sapiens Shab-related delayed-rectifier K channel	8.4
RC_S85655	S85655	Prohibitin	8.4
RC_N99976	N99976	ESTs	8.4
RC_T65004	T65004	EST - RC_T65004	8.4
RC_N93197	N93197	ESTs	8.3
RC_J03070	J03070	Matrix metalloproteinase 2 (gelatinase A collagenase type	8.2
RC_R40177	R40177	ESTs	8.1
RC_W93659	W93659	ESTs	8.1
RC_N69464	N69464	ESTs	8
RC_AA458882	AA458882	ESTs	7.9
RC_AA421750	AA421750	ESTs Weakly similar to LINE-1 REVERSE	7.9
RC_N33011	N33011	EST	7.9
RC_AA47574	AA47574	Replication protein A (E coli RecA homolog RAD51	7.9
RC_R47948	R47948	ESTs	7.9
RC_AA235009	AA235009	ESTs	7.9
RC_R01634	R01634	ESTs	7.9
RC_AA150182	AA150182	ESTs	7.9
RC_AA446486	AA446486	ESTs Weakly similar to HYPOTHETICAL 88.1 KD	7.8
RC_AA342084	AA342084	Homo sapiens Ran binding protein 2 (RanBP2alpha)	7.8
RC_AA609170	AA609170	EST - RC_AA42084	7.8
RC_N46435	N46435	EST	7.8
RC_AA417213	AA417213	EST - RC_N46435	7.8
RC_T88814	T88814	ESTs	7.8
RC_AA459389	AA459389	Homo sapiens mRNA for tyrosyl sulfotransferase-2	7.7

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FIGURE 5 (CONT.)

RC_H99879	H99879	ESTs Highly similar to EPIDERMAL GROWTH	7.6
RC_T08871	T08871	ESTs	7.6
U09706	U09706	Human melanoma antigen p15 mRNA complete cds	7.6
U09706	U09706	EST - HG2981-HT3918	7.6
U09706	U09706	EST	7.6
RC_AA46008	AA46008	Human sapiens mRNA for osteoblast specific factor 2 (OSF-	7.5
RC_AA46008	AA46008	Human mRNA for KIAA0170 gene complete cds	7.5
RC_AA45466	AA45466	ESTs	7.5
RC_AA476937	AA476937	EST - W01296	7.5
RC_AA476937	W01296	EST - W01296	7.5
RC_AA428074	AA428074	Interferon (gamma)-induced cell line protein 10 from	7.4
RC_AA428074	X02530	ESTs	7.4
RC_NG7889	NG7889	ESTs	7.4
RC_AA609309	AA609309	ESTs	7.4
RC_AA412477	AA412477	EST	7.4
RC_AA459392	AA459392	ESTs	7.4
RC_AA599042	AA599042	EST	7.4
RC_AA443794	AA443794	ESTs	7.3
RC_AA121315	AA121315	ESTs	7.2
RC_R65593_s	R65593	Homo sapiens mRNA for kynurenine 3-monooxygenase	7.2
RC_AA427950	AA427950	EST - RC_AA427950	7.2
RC_AA088458	AA088458	EST - RC_AA427950	7.2
RC_NG7239	NG7239	ESTs Weakly similar to H1 ALU SUBFAMILY J	7.1
RC_AA310967_s	AA310967	ESTs	7.1
RC_AA226177	AA226177	ESTs Weakly similar to T04A8.11 [C.elegans]	7.1
RC_AA282143	AA282143	ESTs	7.1
RC_AA233068	AA233068	H sapiens mRNA for melanoma growth regulatory protein	7.1
RC_AA421158	AA421158	ESTs	7.1
RC_AA421158	AA421158	ESTs	7.1
RC_T06045	T06045	ESTs Weakly similar to T0608.5 [C.elegans]	7
RC_Z00345	Z00345	ESTs	7
RC_AA310499	AA310499	Homo sapiens clone 23915 mRNA sequence	6.9
RC_N34686	N34686	ESTs	6.9
RC_N71704	N71704	Receptor protein-tyrosine kinase EDDRI	6.8
U48705	U48705	ESTs	6.8
RC_AA419461	AA419461	ESTs	6.8
RC_AA411204	AA411204	ESTs Highly similar to putative hydrophobic domain in	6.8
RC_AA346385	AA346385	Human clone 23589 mRNA sequence	6.8
RC_D51229_F	D51229	Collagen type V alpha	6.7
RC_M11718	M11718		6.7

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FIGURE 5 (CONT.)

RC_N50550	N50550	Homo sapiens mRNA for Ets1 complete cds	6.7
RC_L27841	L27841	Human autoantigen pericentriol material 1 (PCM-1)	6.7
RC_T92935	T92935	ESTs	6.7
RC_U30246	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter	6.7
RC_AA034069	AA034069	ESTs	6.7
RC_U24169	U24169	Human JTV-1 (JTV-1) mRNA complete cds	6.7
RC_AA435849	AA435849	ESTs Moderately similar to unknown protein [H.sapiens]	6.7
RC_H99935	H99935	Interleukin 6 signal transducer (gp130 oncostat M)	6.7
RC_R51988	R51988	ESTs	6.6
RC_AA505141	AA505141	ESTs	6.6
RC_AA236384	AA236384	ESTs Highly similar to COP1 REGULATORY PROTEIN	6.5
RC_AA431085	AA431085	MULTIFUNCTIONAL AMINOACYL-TRNA	6.4
RC_X54326	X54326	Human pyridoxal kinase mRNA complete cds	6.4
RC_U89606	U89606	EST	6.4
RC_AA195651	AA195651	ESTs	6.4
RC_AA430211	AA430211	H.sapiens mRNA for RNA polymerase II subunit	6.3
RC_D81608	D81608	Homo sapiens CDX17 mRNA complete cds	6.3
RC_L77701	L77701	Homo sapiens lamin B receptor homolog TM7SF2	6.3
RC_AA445658	AA445658	ESTs	6.2
RC_AA024664	AA024664	Human NADH ubiquinone oxidoreductase subunit B13	6.2
RC_AA275943	AA275943	ESTs	6.2
RC_AA098874	AA098874	ESTs	6.2
RC_AA412106	AA412106	ESTs	6.2
RC_U40271	U40271	Protein-tyrosine kinase 7	6.2
RC_L37747	L37747	LAMIN B1	6.1
RC_U78525	U78525	Human eukaryotic translation initiation factor (eIF3)	6.1
RC_T77733	T77733	Tubulin gamma polypeptide	6.1
RC_D20280	D20280	ESTs	6.1
RC_W69807	W69807	ESTs Highly similar to GOLIA1H PROTEIN [Drosophila]	6.1
RC_AA133199	AA133199	ESTs	6.1
RC_H55748	H55748	ESTs	6.1
RC_AA479933	AA479933	ESTs	6.1
RC_L32137	L32137	Human germline oligomeric matrix protein (COMP)	6.1
RC_AA448349	AA448349	ESTs	6.1
RC_AA600257	AA600257	ERGIC-53 PROTEIN PRECURSOR	6.1
RC_R99978	R99978	ESTs Weakly similar to line-1 protein ORF7 [H.sapiens]	6.1
RC_J04177	J04177	Collagen type XI alpha 1	6
RC_AA406137	AA406137	EST	6

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FIGURE 5 (CONT.)

U73514	Homo sapiens short chain L-3-hydroxyacyl-CoA	6
W38407	ESTs	5.9
AA292655	ESTs	5.9
U65932	Human extracellular matrix protein 1 (ECM1) mRNA	5.8
AA463740	ESTs	5.8
M25753	Cyctin B1	5.8
AA279292	ESTs	5.8
AA287665	ESTs	5.8
AA425379	ESTs	5.8
AA422007	ESTs	5.8
TIGR -	EST - HG2981-HT345	5.7
R02572	Human cytochrome P-450 1	5.7
AA442763	ESTs Highly similar to G3MITOTIC-SPECIFIC	5.7
AA149624	Homo sapiens mRNA for follicle-related protein (FRP)	5.7
AA459945	Homo sapiens mRNA for KIAA0585 protein partial cds	5.7
M34677	FACTOR VIII INTRON 22 PROTEIN	5.7
AA454562	ESTs	5.7
W30943	ESTs	5.6
AA232956	ESTs	5.6
U91327	EST - U91327	5.6
AA453987	ESTs	5.6
AA40154	ESTs	5.6
T23528	ESTs Moderately similar to TYK1 protein [M.musculus]	5.6
AA398212	H.sapiens DAP-1 mRNA	5.6
X76105	ESTs	5.6
AA416986	Guanine nucleotide binding protein (G protein) beta	5.6
T95057	ESTs	5.6
U09278	Human fibroblast activation protein mRNA complete cds	5.5
AA443602	ESTs	5.5
AA075200	Homo sapiens Chromosome 16 BAC clone C17987SK-A-	5.5
X02874	(2-5') oligoadenylate synthetase	5.5
R43883	ESTs	5.5
T81310	EST	5.4
H75933	Laminin receptor (LHS epitope)	5.4
M97936	SIGNAL TRANSDUCER AND ACTIVATOR OF	5.4
AA398721	EST - RC_AA398721	5.4
AA448410	ESTs	5.4
AA242757	ESTs	5.4

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FIGURE 5 (CONT.)

RC_AA479348	AA479348	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE	5.4
RC_X03363	X03363	Human low-Mr GTP-binding protein (RAB31) mRNA	5.3
RC_U59877	U59877	Human germline oligomeric matrix protein (COMP)	5.3
RC_N94385_s	N94385	Thymidine kinase 1, soluble	5.3
RC_AA287022	AA287022	Homo sapiens Jak2 kinase mRNA complete cds	5.2
RC_AA464860	AA464860	EST - RC_AA464860	5.2
RC_AA488280	AA488280	EST - RC_AA488280	5.2
RC_AA403116	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USC)	5.2
RC_H96392	H96392	ESTs	5.1
RC_W59961_s	W59961	Human mRNA for KIAA0389 gene complete cds	5.1
RC_AA487449	AA487449	EST - RC_AA487449	5.1
RC_R43343	R43343	EST - RC_AA487449	5.1
RC_J05614	J05614	EST - J05614	5
RC_AA262179	AA262179	ESTs	5
RC_AA281451	AA281451	ESTs	5
RC_AA425691	AA425691	ESTs	5
RC_AA425691	AA425691	ESTs	5
RC_AA425691	AA425691	ESTs	5
RC_AA466000	AA466000	ESTs	5
RC_AA479995	AA479995	Homo sapiens mRNA for KIAA0583 protein partial cds	5
RC_AA055892	AA055892	ESTs	5
RC_AA172056	AA172056	ESTs	5
RC_C01169	C01169	Homo sapiens clone 23915 mRNA sequence	4.9
RC_AA075599	AA075599	ESTs Highly similar to NADH-LIBQUINONE	4.7
RC_AA026356	AA026356	ESTs	4.7
RC_X17059	X17059	ARYLAMINE N-ACETYLTRANSFERASE	4.6
RC_U18321	U18321	Human stromelysin-3 mRNA	4.6
RC_X57766	X57766	ESTs	4.6
RC_AA464853	AA464853	ESTs Weakly similar to T01G9.4 [C-degus]	4.5
RC_AA227900	AA227900	ESTs Highly similar to S. cerevisiae R0504	4.5
RC_AA422025_s	AA422025_s	ESTs	4.4
RC_AA346495	AA346495	ESTs Moderately similar to H. ALL SUBFAMIL V	4.4
RC_U73379	U73379	Human cyclin-selective ubiquitin carboxyl protein mRNA	4.3
RC_U24389	U24389	Human lysyl oxidase-like protein mRNA complete cds	4.3
RC_U21090	U21090	Human DNA polymerase delta small subunit mRNA	4.3
RC_H25377	H25377	ESTs Highly similar to CYTOCHROME P450 IVB1	4.2
RC_S74445	S74445	Cellular retinoic acid binding protein [human skin mRNA	4.2
RC_AA419200	AA419200	ESTs	4.2
RC_AA192297	AA192297	ESTs	4

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FIGURE 5 (CONT.)

U29463	Cytochrome B561	4
RC_R44709	Homo sapiens mRNA for EB18A protein	3.9
AA459960	ESTs Weakly similar to D9481.16 gene product	3.8
M25077	Human 60-kdal ribonucleoprotein (Ro) mRNA complete	3.7
AA321240	ESTs	3.6
RC_N63823	ESTs	3.6
AA034365	NUCLEAR PORE GLYCOPROTEIN P62	3.5
R70167	ESTs	3.5
L47276	EST - L47276	3.4
RC_AA442070	Phosphoribosyl pyrophosphate amidotransferase	3.4
AA116036	ESTs	3.3
R24237	ESTs	3.3
RC_AA116036	Homo sapiens DNA from chromosome 19p13.2 contig	3.3
AD000092	Peroxisomal membrane protein 3 (3kD Zellweger)	3.2
M86852	ESTs	3.2
AA232939	Cyclin D1 (PRAD1 parathyroid adenomatosis 1)	3.1
RC_N59798	ESTs	3.1
RC_AA401682	Homo sapiens ribonuclease P protein subunit p20 (RPP20)	3.1
RC_AA423827	ESTs	3
AA401687	Homo sapiens M062 protein spliced isoform 2 mRNA	2.9
RC_N32333	Thymidylate synthase	2.9
D00596	ESTs	2.9
RC_AA399164	ESTs	2.9
RC_AA164293	ESTs Weakly similar to coded for by C. elegans cDNA	2.9
AA203523	ESTs Weakly similar to W02D9.2 [C.elegans]	2.9
RC_AA195936	DNA-BINDING PROTEIN NEFA PRECURSOR	2.9
RC_AA482114	H. sapiens mRNA for ras-related GTP-binding protein	2.9
R50840	ESTs	2.9
R97040	ESTs	2.9
N21159	Homo sapiens forkhead protein (FKHL1) mRNA	2.8
RC_AA292765	H. sapiens mRNA for M-phase phosphoprotein mpp5	2.8
AA480103	ESTs Weakly similar to t11 ALU SUBFAMILY J	2.8
AA412497	ESTs	2.8
H24460	ESTs	2.8
R39234	ESTs	2.8
R79617	ESTs	2.8
U33052	ESTs	2.8
RC_R79617	ESTs	2.8
D63391	ESTs	2.7
RC_W69160	Human lipid-activated protein kinase PRK2 mRNA	2.7
	Human mRNA for platelet activating factor	2.7
	ESTs	2.7

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FIGURE 5 (CONT.)

RC_F02863	F02863	ESTs Moderately similar to 1111 ALU SUBFAMILY SQ	2.7
L11669	L11669	Human testis cDNA	2.7
M96982	M96982	Human testis cDNA	2.7
Z49099	Z49099	SPLICING FACTOR UDAF 35 KD SUBUNIT	2.6
RC_AA59648	AA59648	H sapiens mRNA for apurine synthase	2.6
RC_AA447617	AA447617	Human mRNA for transcriptional activator USNF2b	2.6
RC_AA59648	AA59648	ESTs	2.6
RC_AA130349	AA130349	Human JEF SSP 9502 mRNA complete cds	2.5
RC_AA130349	AA130349	ESTs	2.5
RC_AA02308	AA02308	Human mRNA for KIAA0310 gene complete cds	2.5
RC_AA02308	AA02308	KERATIN TYPE II CYTOSKELETAL 6D	2.5
RC_AA49458	AA49458	ESTs	2.4
RC_AA59674	AA59674	ESTs Weakly similar to F08G12.1 [C.elegans]	2.4
R81830	R81830	Homo sapiens breast cancer putative transcription factor	2.3
RC_N49284_s	N49284	MYB PROTO-ONCOGENE PROTEIN	2.3
RC_AA069285	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN	2.3
RC_N33063	N33063	ESTs Highly similar to GAG POLYPROTEIN (Avian	2.3
RC_AA250737	AA250737	ESTs	2.3
RC_U77180	U77180	Human mRNA for EB11-ligand chemokine complete cds	2.3
RC_AA028028	AA028028	ESTs	2.2
RC_AA485223	AA485223	ESTs	2.2
RC_AA148516	AA148516	ESTs	2.2
RC_X70683	X70683	SRY (sex determining region Y) box 4	2.1
RC_AA609869	AA609869	ESTs	2.1
RC_N23263	N23263	Human mRNA for kinesin-related protein partial cds	2.1
RC_AA487202	AA487202	Androgen receptor (dihydrotestosterone receptor) testicular	2
RC_F02651	F02651	ESTs	2
RC_AA476582	AA476582	ESTs	2
RC_W80467	W80467	ESTs Highly similar to SIGNAL RECOGNITION	2
RC_U37519	U37519	Aldehyde dehydrogenase 8	2
RC_W28362	W28362	ESTs	2
RC_AA045481	AA045481	ESTs	2
RC_AA443460	AA443460	ESTs	2
RC_U76638	U76638	Human BRCA1-associated RING domain protein	1.9
RC_W80763	W80763	ESTs Highly similar to FK506-BINDING PROTEIN	1.9
RC_AA464013	AA464013	ESTs Weakly similar to Y33C12A.3 [C.elegans]	1.9
RC_AA599219	AA599219	ESTs Moderately similar to ALR [H.sapiens]	1.8
RC_Z40332	Z40332	Homo sapiens mRNA for p115 complete cds	1.8

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FIGURE 6

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Accession	Gene Name	ratio tumor vs breast	Associated with chromosomal gain (by CGH)?
RC_TT9855	ESTs	135.3	
RC_AA453538	EST - RC_AA453538	107.3	
RC_AA461322	EST	81.8	
RC_AA461510	EST - RC_AA461510	75.3	
RC_R67275_s	Collagen type XI alpha 1	72.9	
RC_AA453518	ESTs	61.5	
RC_N27351	EST - RC_N27351	57.1	
RC_AA486737	H sapiens mRNA for Sm protein F	53.9	
RC_AA453479_s	Human focal adhesion kinase (FAK) mRNA, complete cds	52	YES
RC_AA455050_s	ESTs Weakly similar to zinc finger protein Zn720 (D.melanogaster)	46.8	
RC_AA291468	ESTs	45.7	
RC_Z40805	ESTs	39.9	
RC_AA169440	ESTs	31.1	
RC_AA453641	EST	30.6	
RC_AA450955	EST	28.3	
RC_AA453505_s	ESTs	28	
RC_AA412090	ESTs	25.5	
RC_N27159_s	Inhibin beta A (activin A activin AB alpha polypeptide)	23.9	
RC_R65753	EST	20.9	
RC_R97053	ESTs	17.1	
RC_AA463189	ESTs	16.1	
RC_AA505133	ESTs	15.8	YES
H83327_s	ESTs Highly similar to thyroid disease hypothyroid autoantigen (H.sapiens)	15.2	
RC_AA196768_s	Inhibin beta A (activin A activin AB alpha polypeptide)	14.9	
X57579	ESTs	14.7	
RC_AA191404	ESTs Weakly similar to RC334.4 (C elegans)	8.9	
RC_AA262969	Human fibroblast activation protein mRNA, complete cds	8.8	
RC_AA435611_s	S100 calcium-binding protein A7 (psoriasin 1)	7.6	
M86757	H sapiens Homo sapiens n15 mRNA, complete cds	7.5	
X72755	Human melanoma cell line n15 mRNA, complete cds	7.4	
U19796	Human melanoma cell line n15 mRNA, complete cds	6.9	
D13666	Interferon (gamma)-induced cell line protein 10 from	6.8	
X02530	Interferon (gamma)-induced cell line protein 10 from	6.1	
U48705	Receptor protein tyrosine kinase EDDR1		
U48705_n1	ESTs Highly similar to putative hydrophobic domain in amino acid positions 373		
RC_AA446385	Human gamma oligomeric matrix protein (COMP) mRNA complete cds		
L32137			

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FIGURE 6 (CONT.)

AA422025	ESTs	4.4	YES
H25577	ESTs Highly similar to CYTOCHROME P450 11B1 [Drosophila curcubitae]	4.2	YES
T15916	ESTs Highly similar to COXATOMER GAMMA SUBUNIT [Saccharomyces cere	3.2	YES
AA203523	ESTs Weakly similar to coiled for by C. elegans cDNA y10c10.3 [C.elegans]	2.9	YES
R50640	H.sapiens mRNA for rat isolated GTP-binding protein	2.9	YES
H24460	FKBP5-binding protein - (BBD)	2.8	YES
AA125989	ESTs Weakly similar to F35G13.0 [C.elegans]	2.7	YES
A293300	ESTs Weakly similar to Semaphorin C [H.musculus]	2.6	YES
AA447617	ESTs	2.6	YES
R00333	Glucose-6-phosphate dehydrogenase	2.6	YES
X55448	ESTs Weakly similar to monocytic leukemia zinc finger protein [H.sapiens]	1.9	YES
AA443952	ESTs	1.8	YES
AA203588	ESTs	1.5	YES
D02042	Human mRNA for Tob complete cds	1.2	YES

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Accession	Gene Name	ratio tumor vs breast	ORF structural info
RC_178956	ESTs	135.3	?
RC_AA453640	ESTs	121.4	other
RC_AA453638	EST - RC_AA453638	107.3	?
RC_AA461322	EST	81.8	?
RC_AA461510	EST - RC_AA461510	75.3	other
RC_R67275_1	R67275 Collagen type XI alpha 1	72.9	other
RC_A453518	ESTs	61.5	other
RC_A453518	EST - RC_A453518	57.1	?
RC_AA46737	H.sapiens mRNA for Sn protein F	53.9	TM
RC_AA45479_5	Human focal adhesion kinase (FAK) mRNA complete cds	53.2	other
RC_AA455050_5	ESTs Weakly similar to zinc-finger protein ZNF220 (D melanogaster)	52	other
RC_AA291468	ESTs	46.8	TM
RC_Z40806	Z40806	45.7	other
RC_AA169440	AA169440	38.9	other
Q90041_3	D90041 ARYLAMINE N-ACETYLTRANSFERASE MONOMORPHIC	33.6	?
RC_AA621202	AA621202	33.5	other
RC_AA232284	AA232284	32.4	other
RC_R86839	R86839	31.3	?
S70585_maf	S70585 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR	31.1	SS
RC_AA453641	AA453641	30.6	TM
RC_AA209955	AA209955	28.3	?
RC_AA283905	AA283905	28.1	?
RC_AA211831	AA211831	28	TM
RC_AA12090	AA12090	25.5	other
RC_AA421289	AA421289	25.5	other
RC_A427159_1	A427159 Human beta A (actinin A actinin AB alpha polypeptide)	25.1	other
RC_T16687	T16687	23.9	?
RC_R65763	R65763	23.8	TM
RC_AA487987	AA487987	23.6	other
RC_H99309	H99309 Human TFIIID subunits TAF20 and TAF15 mRNA complete cds	22.6	other
RC_R87063	R87063	21.7	other
RC_AA232940	AA232940	20.9	TM
RC_AA453189	AA453189	19.5	other
RC_AA421171	AA421171	19.4	other
RC_AA251875_1	AA251875	17.7	other
RC_AA251875_1	AA251875	17.4	other
RC_AA251875_1	AA251875	17.1	other
RC_AA251875_1	AA251875	17.1	other
RC_AA251875_1	AA251875	17	other
RC_AA251875_1	AA251875	16.9	other
RC_AA251875_1	AA251875	16.8	other
RC_AA251875_1	AA251875	16.6	other
RC_AA251875_1	AA251875	16.3	other
RC_AA251875_1	AA251875	16.2	TM
RC_AA251875_1	AA251875	16.1	other
RC_AA251875_1	AA251875	15.9	other
RC_AA251875_1	AA251875	15.8	other
RC_AA251875_1	AA251875	15.8	?
RC_AA251875_1	AA251875	15.7	SS
RC_AA251875_1	AA251875	15.6	TM
RC_AA251875_1	AA251875	15.4	other
RC_AA251875_1	AA251875	15.2	other
RC_AA251875_1	AA251875	14.9	?
RC_AA251875_1	AA251875	14.7	SS
RC_AA251875_1	AA251875	14.6	?
RC_AA251875_1	AA251875	14.6	other
RC_AA251875_1	AA251875	14.6	other
RC_AA251875_1	AA251875	14.4	?
RC_AA251875_1	AA251875	14.4	other
RC_AA251875_1	AA251875	14.4	?

FIGURE 7
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MB1057	MB1057	Carboxypeptidase B1 (tissue)	14.4	SS
RC_A037876	R07916	ESTs Highly similar to HYPOTHETICAL 21.5 KD PROTEIN CORB11.9 IN CHROMOSOME II [Caenorhabditis elegans]	14.9	?
U75285_mml	U75285	Human effector cell protease receptor-1 (EPR-1) gene partial cds	14.3	?
RC_A046027	R46627	ESTs	14.2	other
RC_AA01559	AA01559	Chromogranin A (parathyroid secretory protein 1)	14.1	?
AA092129_1	AA092129	ESTs Moderately similar to 25E8.1 [D.melanogaster]	14	?
RC_AA436893	AA436893	ESTs Weakly similar to TH1 protein [D.melanogaster]	13.9	other
RC_AA05345	AA05345	ESTs	13.9	other
RC_AA095538	AA095538	ESTs Weakly similar to hypothetical protein 1 [H.sapiens]	13.9	TM
M23263	M23263	Androgen receptor (dihydrotestosterone receptor) testicular feminization spinal and bulbar muscular atrophy Kennedy disease	13.9	TM
RC_020379	G20379	ESTs	13.7	other
RC_AA076138	AA076138	Homo sapiens histone macroH2A1.2 mRNA complete cds	13.5	other
RC_V05046	V05046	ESTs Moderately similar to T1106.8 [C.elegans]	13.5	other
RC_AA032243	AA032243	EST - RC_AA032243	13.4	other
RC_AA045074_s	AA045074	ESTs Weakly similar to 524D SS-A/Ro autoantigen [H.sapiens]	13.4	other
RC_FD1444_1	F01444	Homo sapiens KIAA0440 mRNA partial cds	13.4	other
AA01334	AA01334	ESTs	13.3	other
RC_060354_1	G06034	Human mRNA for KIAA0007 gene partial cds	13.3	other
RC_T78222_5	T78222	Homo sapiens mRNA for SCGF-beta complete cds	13.3	other
RC_AA069535	AA069535	ESTs	13.1	other
RC_AA112065	AA112065	EST - RC_AA112065	13.1	other
RC_AA01350	AA01350	ESTs Moderately similar to H1 ALU SUBFAMILY SC WARNING ENTRY H1 [H.sapiens]	13.1	?
RC_AA013738	AA013738	EST	13	other
RC_R01740_1	R01740	Homo sapiens regulator of G-protein signaling 12 (RGS12) mRNA complete cds	12.8	other
RC_R54950	R54950	ESTs	12.8	other
RC_AA05468	AA05468	ESTs	12.7	TM
RC_AA018749	AA018749	EST	12.7	other
AA037285	AA037285	Homo sapiens mRNA for A+U-rich element RNA binding factor complete cds	12.5	other
RC_AA020796	AA020796	ESTs	12.4	?
RC_AA018955	AA018955	EST	12.4	?
RC_AA025245	AA025245	ESTs	12.4	TM
RC_AA041276	AA041276	ESTs Weakly similar to H1 ALU SUBFAMILY SX WARNING ENTRY H1 [H.sapiens]	12.3	?
RC_AA03874	AA03874	Homo sapiens EST130 mRNA complete cds	12.2	TM
RC_AA099404_s	AA099404	ESTs	12.2	other
RC_AA439985	AA439985	ESTs	12.2	?
RC_AA01528	AA01528	ESTs	12.2	TM
RC_AA214305	AA214305	ESTs	12.1	other
AA020223	AA020223	Fibroblast growth factor receptor 2 (bacteria-expressed kinase keratinocyte growth factor receptor craniotactal dysplasia 1 Crizotinib syndrome Pfeiffer syndrome Jackson-Weiss syndrome)	12.1	SS, TM
RC_AA478571	AA478571	Glutamine-fructose-6-phosphate transaminase	12.1	TM
U31875	U31875	Human Hep27 protein mRNA complete cds	12.1	TM
RC_AA253217	AA253217	ESTs	11.8	other
RC_AA470074	AA470074	ESTs	11.5	other
RC_AA236010	AA236010	ESTs	11.4	other
RC_AA430002	AA430002	ESTs	11.4	other
D82307	D82307	ESTs Weakly similar to TH1 protein [D.melanogaster]	11.4	?
J03589	J03589	UBIQUITIN-LIKE PROTEIN GDX	11.3	other
RC_AA179298	AA179298	Homo sapiens chromosome 9 P1 clone 11659	11.3	?
RC_Q22662_3	Q22662	ESTs	11.3	TM
RC_V06363	V06363	ESTs Weakly similar to extracellular protein [H.sapiens]	11.3	TM
RC_AA449232	AA449232	EST	11.2	?
RC_AA44054	AA44054	ESTs Weakly similar to transmembrane protein [H.sapiens]	11.1	?
RC_AA081733	AA081733	ESTs	11	other
RC_AA052601	AA052601	EST	11	?
RC_AA035630	AA035630	Homo sapiens (A4)IC small nuclear ribonucleoprotein hPrp4 mRNA complete cds	10.9	other
RC_AA235117	AA235117	ESTs Weakly similar to espin [R.novogigae]	10.9	other
RC_AA279418	AA279418	ESTs	10.9	TM
RC_AA432069	AA432069	ESTs	10.8	?
RC_AA453630	AA453630	EST	10.7	?
RC_V04637	V04637	EST	10.7	?
RC_AA05509	AA05509	ESTs Weakly similar to MDESINYEZINRADUXIN HOMOLOG [D.melanogaster]	10.6	other
RC_R04031	R04031	ESTs	10.6	other
RC_AA11425	AA11425	ESTs	10.5	other

FIGURE 7 (cont.)

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RC_AA423956	AA423956	ESTs	10.5	other
RC_AA253170	AA253170	EST	10.4	?
RC_AA459347	AA459347	ESTs	10.4	other
RC_AA599259_s	AA599259	Human splicing protein (SAP 61) mRNA complete cds	10.4	SS
X82078	X82078	GANGLIOSIDE GAG ACTIVATOR PRECURSOR	10.3	other
RC_AA351430	AA351430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 (Carni tamianis)	10.3	SS
RC_AA470156	AA470156	ESTs Weakly similar to dymin 74K chain cytosolic (R norvegicus)	10.3	other
RC_T64933_1	T64933	ESTs	10.2	other
RC_AA280609	AA280609	ESTs Weakly similar to K2B2.3 gene product (C. elegans)	10.2	?
RC_AA281290	AA281290	ESTs Highly similar to ZINC FINGER PROTEIN 85 (Homo sapiens)	10.1	other
RC_AA449632	AA449632	ESTs	10	other
RC_AA427899	AA427899	ESTs Weakly similar to tubular meshwork inducible glucocorticoid response protein (H. sapiens)	10	other
RC_AA059967	AA059967	ESTs Weakly similar to No deletion line found (C. elegans)	9.9	?
RC_AA465158	AA465158	EST	9.9	?
RC_AA112396	AA112396	H. sapiens DAP-3 mRNA	9.8	other
RC_AA207015	AA207015	ESTs	9.8	TM
RC_AA228030	AA228030	ESTs	9.7	other
RC_AA447982	AA447982	ESTs Weakly similar to RD1H10.6 (C. elegans)	9.7	other
M34338	M34338	Openmide synthase	9.7	?
RC_R08986_1	R08986	ESTs	9.7	?
Z14982_mai	Z14982	PROTEASOME COMPONENT C13 PRECURSOR	9.7	?
RC_AA176247	AA176247	EST	9.6	?
RC_T87341	T87341	EST - RC_T87341	9.6	other
V026392	V026392	ESTs Highly similar to OVOSTATIN PRECURSOR (Gallus gallus)	9.5	TM
RC_AA143190_s	AA143190	ESTs Highly similar to HYPOTHETICAL 23.1 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION (Saccharomyces cerevisiae)	9.5	other
RC_AA452578	AA452578	ESTs	9.4	other
RC_AA058057	AA058057	ESTs	9.4	other
RC_AA382914	AA382914	ESTs	9.4	other
RC_AA461476	AA461476	ESTs Highly similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C31A2 D7C (Drosophila melanogaster)	9.4	other
RC_V087751	V087751	ESTs	9.4	other
RC_V092713	V092713	ESTs	9.3	other
RC_AA262111	AA262111	ESTs	9.3	?
RC_AA490929	AA490929	EST	9.3	?
RC_N21678	N21678	ESTs	9.3	other
RC_N179596	N179596	ESTs	9.3	other
RC_N80716	N80716	ESTs	9.2	other
RC_AA007344	AA007344	ESTs	9.2	other
D14657	D14657	Human mRNA for KIAA0101 gene complete cds	9.2	other
RC_W073140	W073140	ESTs Highly similar to TRYPSINOGEN ANIONIC PRECURSOR (Carni familiaris)	9.2	SS, TM
RC_AA243020	AA243020	H. sapiens mRNA for disintegrin-metalloprotease (partial)	9.1	other
RC_AA431478	AA431478	ESTs	9.1	other
RC_AA447666_s	AA447666	Human CENP-F kinetochore protein mRNA complete cds	9.1	other
RC_T16308_1	T16308	ESTs	9	other
RC_R38919_1	R38919	EST	9	other
RC_R60223_s	R60223	ESTs	9	?
RC_R70379_s	R70379	Human germline IgD chain gene C-region C-delta-1 domain	9	?
HG2981-HT3127	HG2981-HT3127	EST - HG2981-HT3127	8.9	SS, TM
M08757	M08757	S100 calcium-binding protein A7 (protein 1)	8.8	other
RC_AA472029_s	AA472029	Human mRNA for KIAA0324 gene partial cds	8.8	other
RC_AA485041	AA485041	ESTs	8.8	TM
X72755	X72755	H. sapiens Hunting mRNA	8.7	other
RC_AA443342_s	AA443342	ESTs	8.7	other
RC_AA481281	AA481281	ESTs	8.7	other
RC_T96361_3	T96361	MULTIFUNCTIONAL AMINOACYL-tRNA SYNTHETASE	8.6	other
RC_AA0608723	AA0608723	ESTs	8.6	SS
RC_H18027_s	H18027	Homo sapiens clone 23785 mRNA sequence	8.6	other
M06762	M06762	TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521	8.5	other
RC_AA113011_s	AA113011	Human mRNA for KIAA0314 gene partial cds	8.5	SS
RC_AA457018	AA457018	ESTs	8.5	other
RC_H06237_s	H06237	Collagen type XI alpha 1	8.4	TM
RC_AA24835	AA24835	Homo sapiens (Telo-related delayed rectifier K+ channel alpha subunit (KCNT3)) mRNA complete cds	8.4	TM

FIGURE 7 (cont.)
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RC_N59976	N59976	ESTs	0.4	other
S65655	S65655	Protein	0.4	other
RC_T65004	T65004	EST - RC_T65004	0.4	other
RC_AA489510_1	AA489510	Homo sapiens clone 23715 mRNA sequence	0.3	?
RC_H72948_1	H72948	ESTs Highly similar to BONE/CARTILAGE PROTEOGLYCAN I [Bos taurus]	0.3	SS
RC_N93197	N93197	ESTs	0.3	other
RC_Z39971_1	Z39971	ESTs	0.3	other
RC_AA236037	AA236037	ESTs Highly similar to HYPOTHETICAL 37.8 KD PROTEIN B0285.4 IN CHROMOSOME III [Caenorhabditis elegans]	0.2	?
J05070	J05070	Matrix metalloproteinase 2 (gelatinase A collagenase type IV)	0.2	TM
RC_AA118225	AA118225	Human matrix-like element-containing mRNA clone pcHMT1	0.1	other
RC_D60302	D60302	ESTs	0.1	other
RC_H98621_1	H98621	Homo sapiens mRNA for KIAA0617 protein complete cds	0.1	?
RC_R40177	R40177	ESTs	0.1	other
RC_AA233545	AA233545	ESTs Weakly similar to HYPOTHETICAL 20.1 KD PROTEIN IN RIB5-SHIM1 INTERGENIC REGION [Saccharomyces cerevisiae]	0.1	TM
RC_AA436370	AA436370	ESTs Highly similar to ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 4 [Rattus norvegicus]	0.1	other
RC_F01538_1	F01538	RAP1 GTPase activating protein 1	0.1	SS
RC_N39415	N39415	ESTs Highly similar to GSTEINDUCTIVE FACTOR PRECURSOR [Bos taurus]	0.1	other
RC_V93659	V93659	ESTs	0.1	TM
RC_AA053319	AA053319	ESTs	0.1	?
RC_AA255029	AA255029	ESTs	0.1	?
RC_AA421750	AA421750	EST	0.1	TM
RC_AA447574	AA447574	ESTs	0.1	other
RC_AA458882	AA458882	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]	0.1	?
RC_N33011_1	N33011	Replication protein A [E. coli RacA homolog RAD51 homolog]	0.1	other
RC_N53950	N53950	EST - RC_N53950	0.1	other
RC_M89464	M89464	ESTs	0.1	other
RC_R01834	R01834	ESTs	0.1	other
RC_R47949_1	R47949	ESTs	0.1	other
RC_AA150182	AA150182	ESTs Weakly similar to HYPOTHETICAL 68.1 KD PROTEIN K02210.1 IN CHROMOSOME III [C. elegans]	0.1	other
RC_AA342084	AA342084	EST - RC_AA342084	0.1	other
RC_AA417213	AA417213	ESTs	0.1	other
RC_AA464486	AA464486	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds	0.1	?
RC_AA609170	AA609170	EST	0.1	?
RC_N46435	N46435	EST - RC_N46435	0.1	other
RC_N54916	N54916	Human mRNA for KIAA0136 gene partial cds	0.1	TM
RC_AA455389	AA455389	Homo sapiens mRNA for tyrosyl sulfoltransferase-2	0.1	other
RC_AA463653	AA463653	ESTs	0.1	TM
RC_T88814	T88814	ESTs	0.1	?
RC_AA46008	AA46008	EST	0.1	other
RC_H98879	H98879	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]	0.1	?
RC_T03306	T03306	Homo sapiens clone 24702 beta-tubulin mRNA complete cds	0.1	?
RC_T08871	T08871	ESTs	0.1	?
RC_Z3911-H73938	TIGR - HG22881	EST - HG22881-H73938	0.1	?
U19796	U19796	Human melanoma antigen p15 mRNA complete cds	0.1	other
AA024752	AA024752	Calnexin B	0.1	other
RC_AA282074	AA282074	ESTs	0.1	other
RC_AA442767	AA442767	Tyrosine 3-monooxygenase/hydrophan 5-monooxygenase activation protein beta polypeptide	0.1	?
RC_AA454566	AA454566	Human mRNA for KIAA0170 gene complete cds	0.1	other
RC_AA476937_1	AA476937	ESTs	0.1	SS
D13666	D13666	Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)	0.1	?
RC_N57119	N57119	ESTs	0.1	TM
V01296	V01296	EST - V01296	0.1	other
RC_AA069476_1	AA069476	H. sapiens mRNA for surface glycoprotein	0.1	?
RC_AA287061	AA287061	ESTs	0.1	other
RC_AA410190	AA410190	ESTs	0.1	?
RC_AA411952	AA411952	Homo sapiens mRNA for GaT4 protein	0.1	?
RC_AA412477	AA412477	EST	0.1	other
RC_AA439392	AA439392	ESTs	0.1	?
RC_AA480256	AA480256	ESTs Moderately similar to breast cancer suppressor element [human Upper RP2]	0.1	?
RC_AA590042	AA590042	[H. sapiens]	0.1	?
RC_AA029309	AA029309	ESTs	0.1	other

FIGURE 7 (cont.)

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RC_D59488	D59489	ESTs	7.4	SS TM
RC_N67869	N67869	ESTs	7.4	other
RC_W73520	W73520	ESTs Highly similar to HYPOTHETICAL 28.5 KD PROTEIN ZK1236.7 IN CHROMOSOME II (Caenorhabditis elegans)	7.4	other
X02530	X02530	Interferon (gamma)-induced cell line protein 10 from (Caenorhabditis elegans)	7.3	SS
RC_AA283006	AA283006	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 (Caenorhabditis elegans)	7.3	other
RC_AA283772_3	AA283772	Human mRNA for histone H1x complete cds	7.3	other
RC_AA443784	AA443784	ESTs	7.3	TM
RC_AA468809	AA468809	ESTs	7.3	other
RC_F13642	F13642	ESTs	7.3	?
RC_N21321_1	N21321	ESTs	7.3	?
RC_A068458	A068458	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY H1 (H sapiens)	7.2	other
RC_AA121315	AA121315	ESTs	7.2	other
RC_AA234921	AA234921	ESTs	7.2	?
RC_AA427950	AA427950	EST - RC_AA427950	7.2	?
RC_AA432130	AA432130	ESTs Moderately similar to H1 ALU SUBFAMILY SX WARNING ENTRY H1 (H sapiens)	7.2	?
RC_R65593_1	R65593	Homo sapiens mRNA for kynurenine 3-monooxygenase	7.2	TM
RC_AA236177	AA236177	ESTs	7.1	?
RC_AA258482_1	AA258482	Human mRNA for zinc finger protein complete cds	7.1	SS
RC_AA282143_1	AA282143	H sapiens mRNA for melanoma growth regulatory protein MGA	7.1	other
RC_AA282003	AA282003	ESTs	7.1	other
RC_AA281870_1	AA281870	Lymphoblastoid-beta	7.1	other
AA310957_1	AA310957	ESTs Weakly similar to T04A8.11 (C. elegans)	7.1	other
RC_AA410373	AA410373	ESTs	7.1	SS
RC_AA421158	AA421158	ESTs	7.1	TM
C00225_1	C00225	ESTs Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV (Caenorhabditis elegans)	7.1	?
RC_F13694_1	F13694	ESTs	7.1	?
RC_N29431	N29431	EST - RC_N29431	7.1	other
RC_N67239	N67239	ESTs	7.1	other
RC_T10092_1	T10092	ESTs	7	other
RC_AA310469	AA310469	ESTs	7	other
RC_AA448351	AA448351	ESTs Weakly similar to similar to deoxyribose phosphate aldolase (C. elegans)	7	other
RC_D57389_1	D57389	EST	7	?
RC_N34686	N34686	Homo sapiens clone 22915 mRNA sequence	7	TM
RC_Z40345	Z40345	ESTs Weakly similar to T06D8.5 (C. elegans)	6.9	other
RC_AA410441	AA410441	ESTs	6.9	other
RC_AA505093	AA505093	ESTs	6.9	other
RC_N71704	N71704	ESTs	6.9	other
U48705_ma1	U48705	Receptor protein-tyrosine kinase EDDR1	6.9	?
RC_AA127818_1	AA127818	ESTs	6.8	other
RC_AA346385	AA346385	ESTs Highly similar to putative hydrophobic domain in amino acid phosphatase 373.390 (H sapiens)	6.8	TM
RC_AA411204	AA411204	ESTs	6.8	other
RC_AA416676	AA416676	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 (H sapiens)	6.8	other
RC_AA419461	AA419461	ESTs	6.8	other
RC_AA446968	AA446968	EST	6.8	other
RC_AA495569	AA495569	ESTs Highly similar to VALYL-TRNA SYNTHETASE (Fugu rubripes)	6.8	other
RC_D51228_1	D51228	Human clone 23589 mRNA sequence	6.8	TM
RC_F00254_1	F00254	H sapiens mRNA for FAST kinase	6.8	other
RC_H18428_1	H18428	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY H1 (H sapiens)	6.8	?
RC_AA034069	AA034069	ESTs	6.7	other
RC_AA127058	AA127058	ESTs	6.7	TM
RC_AA433849	AA433849	ESTs Moderately similar to unknown protein (H sapiens)	6.7	other
RC_H09935_1	H09935	Interleukin 6 signal transducer (gp130 oncostatin M receptor)	6.7	TM
L27841	L27841	Human autoantigen pendericid material 1 (PCM-1) mRNA complete cds	6.7	other
M11718	M11718	Collagen type V alpha	6.7	?
RC_N50550	N50550	Homo sapiens mRNA for Est1 complete cds	6.7	other
RC_T02835	T02835	ESTs	6.7	other
U24169	U24169	Human JTV-1 (JTV-1) mRNA complete cds	6.7	other
U30246	U30246	Human tumetamide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	6.7	TM
RC_AA208834_1	AA208834	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	6.6	TM
RC_AA283198	AA283198	ESTs	6.6	other
RC_AA421782	AA421782	ESTs	6.6	other
RC_AA505141	AA505141	ESTs	6.6	other

FIGURE 7 (cont.)

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RC_D60341	D60341	ESTs	6.6	SS.
RC_K26904	K26904	ESTs Highly similar to FK506-BINDING PROTEIN PRECURSOR (Mus musculus)	6.6	TM
RC_R40606	R40606	ESTs Highly similar to SKD3 (M. musculus)	6.6	other
RC_R51988	R51988	ESTs	6.6	other
RC_T03790	T03790	ESTs	6.6	TM
RC_V072455	V072455	ESTs	6.5	other
RC_AA100364	AA100364	ESTs Highly similar to COP1 REGULATORY PROTEIN (Arabidopsis thaliana)	6.6	?
AA236364	AA236364	EST	6.5	other
RC_AA431085	AA431085	ESTs	6.5	other
RC_AA446591	AA446591	ESTs	6.5	?
RC_R06700	R06700	ESTs	6.4	?
W49521	W49521	Human prol 4-hydroxylase alpha [l] subunit mRNA complete cds	6.4	other
RC_AA195651	AA195651	EST	6.4	TM
RC_AA430211	AA430211	ESTs	6.4	TM
RC_T15991	T15991	ESTs	6.4	other
RC_T17119	T17119	ESTs	6.4	other
U89606	U89606	Human pyridoxal kinase mRNA complete cds	6.3	other
X54326	X54326	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE	6.3	TM
RC_AA157814	AA157814	ESTs	6.3	other
RC_AA443650	AA443650	Human sapient beta n B receptor homolog TM7SF2 (TM7SF2) mRNA complete cds	6.3	other
RC_AA621169	AA621169	ESTs	6.3	TM
RC_D02159	D02159	Human mRNA for KIAA0050 gene complete cds	6.3	?
D81608	D81608	H. sapiens mRNA for RNA polymerase II subunit	6.3	other
RC_H57330	H57330	EST	6.3	other
L77701	L77701	Human sapient COX17 mRNA complete cds	6.3	SS.
RC_N48166	N48166	ESTs	6.3	other
RC_R85826	R85826	Human sapient mRNA for KIAA0549 protein partial cds	6.3	?
V01969	V01969	ESTs	6.2	other
X70549	X70549	Human sapient DDX1 gene complete CDS	6.2	other
RC_AA024664_s	AA024664	Human NADH ubiquinol oxidoreductase subunit B13 (B13) mRNA complete cds	6.2	other
RC_AA098874	AA098874	ESTs	6.2	other
RC_AA152178	AA152178	ESTs	6.2	other
RC_AA279943	AA279943	ESTs	6.2	other
RC_AA412106	AA412106	ESTs	6.2	other
RC_AA621721	AA621721	ESTs	6.2	other
RC_N38959_f	N38959	Human sapient chaperonin containing 1 complex polypeptide 1 beta subunit (Cob) mRNA complete cds	6.2	TM
U40271	U40271	Protein-tyrosine kinase 7	6.2	?
X52150_nal_s	X52150	Arylsulfatase A	6.2	other
X86018	X86018	H. sapiens mRNA for MUE-1 protein	6.1	?
RC_AA133199	AA133199	ESTs	6.1	other
RC_AA388740	AA388740	ESTs	6.1	other
RC_AA403505	AA403505	Human sapient mRNA for putative RNA helicase 3' end	6.1	?
RC_AA416568	AA416568	ESTs	6.1	TM
RC_AA448349	AA448349	ESTs	6.1	other
AA455331	AA455331	ESTs	6.1	other
RC_AA479933_f	AA479933	ESTs	6.1	TM
RC_AA621080	AA621080	ESTs	6.1	other
RC_AA680257_s	AA680257	EROC-53 PROTEIN PRECURSOR	6.1	other
RC_D20280	D20280	ESTs	6.1	?
RC_H55748	H55748	ESTs	6.1	other
RC_H55815	H55815	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (H sapiens)	6.1	?
L32137	L32137	Human gamma oligomeric matrix protein (COMP) mRNA complete cds	6.1	SS.
L37747_s	L37747	LAMN B1	6.1	?
RC_H62593	H62593	ESTs	6.1	?
RC_R99978	R99978	ESTs Weakly similar to line-1 protein ORF2 (H sapiens)	6.1	other
RC_T77733_s	T77733	Tubulin gamma polypeptide	6.1	other
U78525	U78525	Human eukaryotic translation initiation factor (eIF3) mRNA complete cds	6.1	?
RC_W69807	W69807	ESTs Highly similar to GOLATH PROTEIN (Drosophila melanogaster)	6	?
RC_AA409137	AA409137	EST	6	other
RC_AA521103	AA521103	ESTs	6	other
RC_AA609277	AA609277	ESTs	6	other
J04177	J04177	Collagen type XI alpha 1	6	?
RC_R33663_s	R33663	ESTs	6	?

FIGURE 7 (cont.)

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RC_T16660	T16660	ESTs	6	other
UT3514	UT3514	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase (SCHAD) mRNA complete cds	6	other
RC_AA223730	AA223730	ESTs	5.9	other
RC_AA252655	AA252655	ESTs	5.9	other
RC_N03091	N03091	ESTs	5.9	other
RC_N00744	N00744	ESTs	5.9	TM
RC_T88953	T88953	ESTs	5.9	?
HQ3748-HT4018	TIGR - HQ3748-HT4018	EST - HQ3748-HT4018	5.9	?
RC_W03407	W03407	ESTs	5.9	other
RC_W63563_s	W63563	Homo sapiens scaffold attachment factor B (SAF-B) mRNA partial cds	5.9	?
RC_Z41619_s	Z41619	ESTs Weakly similar to keratin 6 type II cytoskeletal embryonic (M. nodulosus)	5.9	other
RC_AA079282	AA079282	ESTs	5.8	other
RC_AA001665	AA001665	ESTs	5.8	other
RC_AA422007	AA422007	ESTs	5.8	TM
RC_AA425379	AA425379	ESTs	5.8	TM
RC_AA427525_s	AA427525	ESTs Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR (Homo sapiens)	5.8	?
RC_AA430573	AA430573	ESTs	5.8	other
RC_AA441801	AA441801	ESTs	5.8	other
RC_AA463740_s	AA463740	ESTs	5.8	TM
RC_H89987_s	H89987	Human multidrug resistance-associated protein homolog (MRP5) mRNA partial cds	5.8	other
RC_H54843	H54843	ESTs	5.8	other
M25753	M25753	Cyclin B1	5.8	other
RC_N80183	N80183	ESTs	5.8	other
RC_T67463_s	T67463	CATHEPSIN K PRECURSOR	5.8	?
U65932	U65932	Human extracellular matrix protein 1 (ECM1) mRNA complete cds	5.7	TM
RC_AA149624	AA149624	Homo sapiens mRNA for forixin-related protein (FRP) complete cds	5.7	other
RC_AA182334	AA182334	ESTs	5.7	other
RC_AA207105	AA207105	EST	5.7	?
RC_AA42763	AA42763	ESTs Highly similar to G2MITOTIC-SPECIFIC CYCLIN B2 (Mesocricetus auratus)	5.7	other
AA443251	AA443251	ESTs	5.7	other
RC_AA454562	AA454562	ESTs	5.7	other
RC_AA459945	AA459945	Homo sapiens mRNA for KIAA0585 protein partial cds	5.7	other
RC_AA478794	AA478794	ESTs	5.7	other
RC_AA05473	AA05473	ESTs	5.7	other
RC_F09058	F09058	ESTs	5.7	other
RC_H54430	H54430	ESTs	5.7	?
M34677	M34677	FACTOR VIII INTRON 22 PROTEIN	5.7	other
RC_N27563	N27563	ESTs	5.7	other
RC_N02572	N02572	Fibronectin 1	5.7	?
RC_R09166	R09166	ESTs	5.7	other
RC_R85829	R85829	EST	5.7	?
HQ2981-HT3125	TIGR - HQ2981-HT3125	EST - HQ2981-HT3125	5.7	?
U56402	U56402	Homo sapiens clone 24522 mRNA sequence	5.7	other
W00943	W00943	ESTs	5.6	other
RC_AA40154	AA40154	ESTs	5.6	other
AA116095	AA116095	ESTs Weakly similar to T12DB-1 (C. elegans)	5.6	TM
RC_AA447884	AA447884	ESTs	5.6	?
RC_AA449754_s	AA449754	EST	5.6	?
RC_AA232856	AA232856	ESTs	5.6	other
RC_AA397919	AA397919	ESTs	5.6	other
RC_AA398212	AA398212	ESTs	5.6	other
RC_AA398264	AA398264	Homo sapiens clone 23736 mRNA sequence	5.6	other
RC_AA406169	AA406169	Homo sapiens KIAA0431 mRNA partial cds	5.6	TM
RC_AA446565	AA446565	Guanine nucleotide binding protein (G protein) beta polypeptide 1	5.6	TM
RC_AA435742_s	AA435742	Human fatty acid amide hydrolase mRNA complete cds	5.6	?
RC_AA435936	AA435936	EST	5.6	other
RC_AA436819	AA436819	ESTs	5.6	other
RC_AA432642	AA432642	ESTs	5.6	other
RC_AA452987	AA452987	ESTs	5.6	other
AA477214	AA477214	ESTs	5.6	TM
RC_AA482269	AA482269	Integral transmembrane protein 1	5.6	TM
D05914	D05914	Human mRNA for KIAA0124 gene partial cds	5.6	TM

FIGURE 7 (cont.)
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RC_N51590_s	N51590	ESTs	5.6	other
RC_N90297	N90297	ESTs	5.6	SS
RC_T23528	T23528	ESTs Moderately similar to Tyk protein (R. musculus)	5.6	other
RC_T95057_s	T95057	ESTs	5.6	other
U91327	U91327	EST - U91327	5.6	?
X76105	X76105	H sapiens OAP-1 mRNA	5.6	other
RC_AA021182	AA021182	ESTs	5.5	other
RC_A075200	A075200	Homo sapiens Chromosome 16 BAC clone C17807SK-A-31968	5.5	other
RC_AA065589	AA065589	ESTs Highly similar to TRANSLATION INITIATION FACTOR EIF-2B DELTA SUBUNIT [Chyrotogus cuniculus]	5.5	other
RC_AA115535	AA115535	ESTs	5.5	other
RC_AA195517	AA195517	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY H1 [H sapiens]	5.5	TM
RC_AA280840	AA280840	ESTs	5.5	SS
RC_AA443602	AA443602	ESTs	5.5	TM
RC_AA609996	AA609996	ESTs Highly similar to Surf4 protein (R. musculus)	5.5	?
RC_H09500	H09500	Homo sapiens mRNA for folate-inhibited protein (FIP) complete cds	5.5	other
M24486	M24486	Procollagen-proline 3-hydroxylase 4-oxoglutarate (proline 4-hydroxylase) alpha polypeptide	5.5	SS
RC_N021032	N021032	EST	5.5	?
RC_N20115	N20115	ESTs	5.5	TM
RC_R43883	R43883	ESTs	5.5	other
U09278	U09278	Human fibroblast activation protein mRNA complete cds	5.5	SS
X02874	X02874	(Z-5) oligoadenylate synthetase E	5.5	other
RC_AA242757	AA242757	ESTs	5.4	?
RC_AA251973	AA251973	ESTs	5.4	other
RC_AA293773	AA293773	Homo sapiens clone Z3870 mRNA sequence	5.4	other
RC_AA398721	AA398721	EST - RC_AA398721	5.4	other
RC_AA437225	AA437225	ESTs	5.4	other
RC_AA4458410	AA4458410	ESTs	5.4	other
RC_AA449357	AA449357	ESTs	5.4	other
RC_AA479348_s	AA479348	H sapiens mRNA for SVT	5.4	other
C02170	C02170	ESTs Weakly similar to weak similarity to ribosomal protein L14 [C. elegans]	5.4	other
RC_N175933_s	N175933	Laminin receptor (2HS epitope)	5.4	other
M97306	M97306	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	5.4	other
RC_N51917	N51917	ESTs	5.4	other
RC_R41294_s	R41294	ESTs	5.4	?
RC_T81310	T81310	EST	5.4	TM
RC_V45275_s	V45275	CD44 antigen (cell adhesion molecule)	5.4	other
RC_V92001	V92001	ESTs	5.3	other
RC_AA135809	AA135809	ESTs	5.3	TM
RC_AA157811	AA157811	EST - RC_AA157811	5.3	other
RC_AA191524	AA191524	ESTs	5.3	?
RC_AA195036_s	AA195036	Human RofGSA ribonucleoprotein homolog (RofG) mRNA complete cds	5.3	other
RC_AA284565_s	AA284565	ESTs	5.3	other
RC_AA287022_s	AA287022	Thymidine kinase 1 soluble	5.3	other
RC_AA394071	AA394071	Homo sapiens gamma2-adaptin (G2AD) mRNA complete cds	5.3	?
RC_AA399477	AA399477	ESTs	5.3	TM
RC_AA401428_s	AA401428	NUCLEAR PORE COMPLEX PROTEIN NUP214	5.3	other
RC_AA425154	AA425154	ESTs	5.3	other
RC_AA447213_s	AA447213	ESTs Weakly similar to SOS RIBOSOMAL PROTEIN L20 [E. coli]	5.3	other
RC_AA454850	AA454850	Homo sapiens Jab2 kinase mRNA complete cds	5.3	other
RC_AA485191	AA485191	ESTs	5.3	other
RC_AA476293	AA476293	ESTs Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT [Plasmodium falciparum]	5.3	TM
RC_H80749	H80749	ESTs	5.3	other
RC_N94385_s	N94385	Human germine oligomeric matrix protein (COMP) mRNA complete cds	5.3	other
U59877	U59877	Human low-affinity GTP-binding protein (RAB31) mRNA complete cds	5.3	other
X03363	X03363	ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR	5.3	TM
RC_AA025262	AA025262	Homo sapiens DNA sequence from PAC 263D12 on chromosome 12 (3-24.3). Contains a Terasaki (Heterochromatin Cytoplasmic Neuronectin Myeloidin antigen)-LIKE gene and a mitochondrially encoded 30S ribosome	5.2	other
RC_AA025370	AA025370	ESTs	5.2	?
RC_AA026682_s	AA026682	Topoisomerase (DNA) II alpha (170kD)	5.2	other
RC_AA279160	AA279160	ESTs	5.2	?
RC_AA403116	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA complete cds	5.2	other
RC_AA452857	AA452857	ESTs	5.2	?
RC_AA488280	AA488280	EST - RC_AA488280	5.2	other

FIGURE 7 (cont.)

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RC_AA599140	AA599140	ESTs Moderately similar to ZINC FINGER PROTEIN 7 (Homo sapiens)	5.2	other
RC_AA629991	AA629991	EST	5.2	?
RC_AA621714	AA621714	ESTs	5.2	other
H87319	H87319	Protein kinase C substrate BOK-H	5.2	TM
RC_H96392	H96392	ESTs	5.2	other
RC_N54321	N54321	SST	5.2	?
RC_N73861	N73861	EST - RC_N73861	5.2	other
RC_R05312_s	R05312	ESTs	5.2	other
RC_R59183_s	R59183	ESTs	5.2	other
RC_R92205	R92205	ESTs	5.2	TM
RC_VW4502	VW4502	ESTs Highly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III (Caenorhabditis elegans)	5.2	other
X17644	X17644	G1 to S phase transition 1	5.2	other
RC_AA284518	AA284518	ESTs	5.1	other
RC_AA434152	AA434152	ESTs	5.1	SS
RC_AA436673	AA436673	ESTs	5.1	other
RC_AA481463	AA481463	ESTs	5.1	other
RC_AA487449	AA487449	EST - RC_AA487449	5.1	other
RC_AA491465	AA491465	ESTs	5.1	other
RC_N79612	N79612	ESTs	5.1	other
RC_N98461	N98461	ESTs	5.1	TM
RC_R42036	R42036	ESTs	5.1	other
RC_R43543	R43543	ESTs	5.1	other
RC_V59961_s	V59961	Human mRNA for KIAA0389 gene complete cds	5.1	other
RC_V605180	V605180	ESTs	5.1	other
Y09912_rna1	Y09912	H.sapiens mRNA for AP-2 beta transcription factor	5.1	?
RC_AA055892	AA055892	ESTs	5	other
RC_AA065676	AA065676	ESTs Weakly similar to TYL (H.sapiens)	5	other
RC_AA172056	AA172056	ESTs	5	other
RC_AA211400	AA211400	ESTs	5	other
RC_AA236356	AA236356	ESTs	5	other
RC_AA252385	AA252385	ESTs	5	?
RC_AA262179	AA262179	ESTs	5	other
RC_AA281451	AA281451	ESTs	5	?
RC_AA287095	AA287095	EST - RC_AA287095	5	other
RC_AA325691	AA325691	ESTs	5	other
RC_AA426376	AA426376	ESTs	5	other
RC_AA446000	AA446000	ESTs	5	?
RC_AA478951	AA478951	EST	5	?
AA478995	AA478995	Homo sapiens mRNA for KIAA0583 protein partial cds	5	other
D82419	D82419	ESTs Highly similar to UBQUITIN-CONJUGATING ENZYME E2-28 4 KD (Saccharomyces cerevisiae)	5	TM
RC_F02080_f	F02080	ESTs	5	other
RC_F10496_f	F10496	H.sapiens 40 kDa protein kinase related to rat ERK2	5	other
J02314	J02314	Homo sapiens clone 247C3 beta-tubulin mRNA complete cds	5	?
J05614	J05614	EST - J05614	5	?
M16336	M16336	CD2 antigen (T cell surface antigen T11)	5	TM
M80244	M80244	INTEGRAL MEMBRANE PROTEIN E16	5	TM
RC_N33927_s	N33927	Homo sapiens mRNA for histone H2B clone pJG4-5-15'''	5	SS
RC_N73959_s	N73959	ESTs	5	?
RC_T75915	T75915	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY H1 (H.sapiens)	5	other
U62392	U62392	Homo sapiens zinc finger protein mRNA complete cds	5	other
RC_AA133756	AA133756	ESTs	4.9	other
RC_AA234559	AA234559	ESTs	4.9	other
RC_AA490830	AA490830	ESTs	4.9	other
C01169	C01169	Homo sapiens clone Z9815 mRNA sequence	4.9	other
G21255	G21255	Cadherin 11 (CD-133/cadherin)	4.9	SS, TM
RC_F10945	F10945	Polyomidine tract binding protein (pRNP 1) (alternative products)	4.9	other
RC_H24044	H24044	Protein phosphatase 2 (formerly 2A) catalytic subunit alpha isoform	4.9	other
RC_N34893	N34893	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0280.9 IN CHROMOSOME III (Caenorhabditis elegans)	4.9	other
RC_R41772	R41772	EST	4.9	?
RC_T59338	T59338	EST - RC_T59338	4.8	other
RC_AA191512	AA191512	ESTs	4.8	?
RC_AA400513_s	AA400513	ESTs	4.8	other
RC_AA490581	AA490581	ESTs	4.8	other

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RC_AA48158	AA48158	EST	4.8	?
RC_N94362	N94362	EST	4.8	?
RC_JM5007_1	JM5007	Human mRNA for KIAA0203 gene complete cds	4.8	other
RC_AA026256	AA026256	ESTs	4.7	?
AA075599	AA075599	ESTs Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT [Bos taurus]	4.7	other
RC_AA157836	AA157836	ESTs	4.7	other
RC_AA196549	AA196549	ESTs	4.7	other
RC_AA04352	AA04352	ESTs	4.7	SS.
RC_AA417321	AA417321	ESTs Weakly similar to CALMODULIN [D.melanogaster]	4.7	other
RC_AA18074	AA18074	ESTs	4.6	?
RC_N32919	N32919	EST - RC_AA177051	4.6	TM
RC_AA177051	AA177051	ESTs	4.6	SS, TM
RC_AA453483	AA453483	ESTs	4.6	other
RC_AA020795	AA020795	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	4.6	other
RC_H97012	H97012	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	4.6	other
M34458_ma1	M34458	LAMIN B1	4.6	other
RC_N68921	N68921	ESTs	4.6	?
U18321	U18321	H.sapiens DAP-3 mRNA	4.5	?
X17059	X17059	ARYLAMINE N-ACETYLTRANSFERASE MONOMORPHIC	4.5	other
X17059	AA210722	EST	4.5	?
RC_AA210722	AA210722	Homo sapiens spindle pole body protein spb87 homolog GCP2 mRNA complete cds	4.5	?
RC_AA256055	AA256055	Homo sapiens ubiquitin conjugating enzyme U2 (UBE2G2) mRNA complete cds	4.5	TM
RC_AA443634	AA443634	Homo sapiens ubiquitin conjugating enzyme U2 (UBE2G2) mRNA complete cds	4.5	other
RC_AA461507	AA461507	ESTs	4.5	?
RC_AA464853	AA464853	ESTs Weakly similar to T0109.4 [C.elegans]	4.5	other
RC_H11076	H11076	EST	4.5	other
RC_T40841	T40841	ESTs	4.4	other
X57766	X57766	Human stromelysin-3 mRNA	4.4	other
RC_AA206497_1	AA206497	PHOTOLASOME COMPONENT D9	4.4	?
RC_AA227500_1	AA227500	H.sapiens mRNA homologous to S. cerevisiae RAD54	4.4	?
RC_AA346495	AA346495	ESTs Moderately similar to H1 ALU SUBFAMILY J VARIATION ENTRY III [H.sapiens]	4.4	other
RC_AA396260	AA396260	EST	4.4	other
RC_AA396155	AA396155	ESTs	4.4	SS.
RC_AA405569_1	AA405569	Human fibroblast activation protein mRNA complete cds	4.4	other
AA422025_1	AA422025	ESTs	4.4	other
RC_AA430124	AA430124	ESTs	4.4	other
RC_AA433466	AA433466	ESTs	4.4	other
RC_AA63726_1	AA63726	Homo sapiens mRNA for JAD7 protein complete CDS (clone IMAGE 145745 and IMAGE 257878)	4.4	other
RC_C20981	C20981	ESTs Highly similar to CHOLINE DEHYDROGENASE [Escherichia coli]	4.4	other
RC_R10801_1	R10801	EST	4.4	?
RC_T97307	T97307	EST - RC_T97307	4.4	TM
U28386	U28386	RAG (recombination activating gene) cohort 1	4.4	?
X02419_ma1	X02419	Urokinase-type plasminogen activator	4.3	other
RC_AA235112	AA235112	ESTs	4.3	TM
RC_AA453176_1	AA453176	Human protein kinase ATR mRNA complete cds	4.3	SS.
D40573	D40573	Human mRNA for reticulocalbin complete cds	4.3	other
U21090	U21090	Human DNA polymerase delta small subunit mRNA complete cds	4.3	?
U24389	U24389	Human lysyl oxidase-like protein mRNA complete cds	4.3	other
U73379	U73379	Human cyclin-selective ubiquitin carrier protein mRNA complete cds	4.2	other
RC_AA227959_1	AA227959	Human cyclin-selective ubiquitin carrier protein mRNA complete cds	4.2	other
RC_AA416931	AA416931	ESTs	4.2	SS.
RC_AA419200	AA419200	ESTs	4.2	other
RC_H18947	H18947	ESTs	4.2	TM
RC_H25577	H25577	ESTs Highly similar to CYTOCHROME P450 IVS1 [Drosophila melanogaster]	4.2	SS.
RC_H90161_1	H90161	ESTs	4.2	?
M15796	M15796	Proliferating cell nuclear antigen	4.2	other
RC_R46482	R46482	ESTs	4.2	other
S74445	S74445	Cellular retinoic acid-binding protein [human skin mRNA 735 nt]	4.2	TM
U74612	U74612	Human putative M phase phosphoprotein 2 (MPP2) mRNA complete cds	4.2	other
X62534	X62534	High-mobility group (nonhistone chromosomal) protein 2	4.1	other
RC_AA390369	AA390369	ESTs	4.1	TM
RC_AA48347	AA48347	Annexin XI (S61D subunit)	4.1	TM
RC_AA484707	AA484707	ESTs	4.1	TM
RC_AA478799_1	AA478799	H.sapiens mRNA for B569 protein	4.1	TM

FIGURE 7 (cont.)
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RC_AA496369	AA496369	ESTs	4.1	other
RC_DS4296_f	DS4296	Human mRNA for KIAA0255 gene complete cds	4.1	TM
RC_N56918	N56918	ESTs	4.1	TM
US0648	US0648	Protein kinase interferon-inducible double stranded RNA dependent	4.1	?
AA193287	AA193287	ESTs	4	SS
RC_AA228026	AA228026	ESTs Highly similar to PBDK protein (H sapiens)	4	TM
RC_AA287325_1	AA287325	ESTs	4	?
RC_AA287896	AA287896	ESTs	4	other
RC_AA421041	AA421041	ESTs	4	other
U29463	U29463	Cytochrome B561	4	?
RC_V87752_s	V87752	Small inducible cytokine A5 (RANTES)	4	TM
X94563_x02_f	X94563	EST - X94563_x02_f	4	?
RC_AA256637_1	AA256637	ESTs	3.9	?
RC_AA18627_3	AA18627	ESTs	3.9	other
RC_AA483224_f	AA483224	ESTs Weakly similar to No definition line found [C elegans]	3.9	?
RC_AA483360	AA483360	EST	3.9	?
RC_R44709	R44709	Homo sapiens mRNA for RB18A protein	3.9	other
RC_V45572_f	V45572	ADP-ribosylation factor 1	3.9	other
RC_AA132366	AA132366	Homo sapiens mRNA for SPDP	3.8	?
RC_AA133527	AA133527	ESTs Moderately similar to The KIAA0138 gene product is novel. (H sapiens)	3.8	other
RC_AA232324	AA232324	ESTs	3.8	other
RC_AA287842_s	AA287842	Human mRNA for KIAA0078 gene complete cds	3.8	other
RC_AA226552	AA226552	ESTs	3.8	other
RC_AA59960_s	AA59960	ESTs Weakly similar to DS481.16 gene product [S cerevisiae]	3.8	other
RC_AA65094	AA65094	ESTs Weakly similar to nemo form II (D melanogaster)	3.8	other
RC_AA485451	AA485451	EST	3.8	other
RC_AA599244	AA599244	Homo sapiens mRNA for KIAA2530 protein partial cds	3.8	other
RC_N41018	N41018	Human mRNA for prepro cortistatin like peptide complete cds	3.8	?
RC_N74501	N74501	ESTs	3.8	other
RC_N95525	N95525	Homo sapiens tumorous marginal discs protein TMD5 homolog (TMD1) mRNA complete cds	3.8	other
VW46488	VW46488	Homo sapiens Amplified in Breast Cancer (AIB1) mRNA complete cds	3.8	other
RC_AA232183	AA232183	ESTs Weakly similar to H ¹⁹ ALU SUBFAMILY J WARNING ENTRY H ¹⁹ (H sapiens)	3.7	other
RC_AA399547	AA399547	ESTs	3.7	other
RC_AA424486	AA424486	ESTs	3.7	TM
RC_AA596661	AA596661	ESTs	3.7	other
RC_H04339	H04339	ESTs	3.7	TM
M14219	M14219	Desorin	3.7	other
M25077	M25077	Human 60-kdal ribonuclease protein (Rn) mRNA complete cds	3.7	?
RC_N67102_s	N67102	ESTs	3.7	other
RC_V45728	V45728	ESTs Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN L (Homo sapiens)	3.7	other
Y12394	Y12394	Homo sapiens importin-alpha homolog (SRP1 gamma) mRNA complete cds	3.7	other
RC_AA401758_1	AA401758	ESTs Weakly similar to H ¹⁹ ALU SUBFAMILY SQ WARNING ENTRY H ¹⁹ (H sapiens)	3.6	SS
RC_AA435840	AA435840	Homo sapiens mRNA for high mobility group protein HMGB2a	3.6	other
RC_AA461492	AA461492	ESTs	3.6	other
RC_AA521240	AA521240	ESTs	3.6	TM
RC_F02450	F02450	ESTs Moderately similar to unknown protein (H sapiens)	3.6	TM
RC_N63823	N63823	ESTs	3.6	other
RC_N67603	N67603	ESTs Weakly similar to hypothetical L1 protein (H sapiens)	3.6	?
RC_N59187_s	N59187	Homo sapiens mRNA for NB thymosin beta complete cds	3.6	other
RC_N93967	N93967	EST	3.6	other
RC_V073788	V073788	ESTs	3.6	other
RC_AA034365	AA034365	NUCLEAR PORE GLYCOPROTEIN P92	3.5	other
RC_AA083069	AA083069	EST - RC_AA083069	3.5	?
RC_AA112063	AA112063	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 (S cerevisiae)	3.5	other
RC_AA1126951	AA1126951	ESTs Weakly similar to DNA-directed RNA polymerase (D melanogaster)	3.5	other
RC_AA1129181	AA1129181	ESTs Weakly similar to Lda1p (S cerevisiae)	3.5	other
RC_AA398450	AA398450	H sapiens mRNA for synaptonemal complex lateral element protein	3.5	other
RC_AA404593	AA404593	ESTs	3.5	other
RC_AA412739	AA412739	EST	3.5	other
RC_AA447626	AA447626	EST	3.5	?
RC_AA453787_s	AA453787	Human TF108 related factor hBRF (hBRF) mRNA complete cds	3.5	other
RC_AA599106	AA599106	EST - RC_AA599106	3.5	other
D82558	D82558	Homo sapiens K807 protein mRNA partial cds	3.5	other

FIGURE 7 (cont.)

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RC_H27283_s	H27283	Human mRNA for KIAA0265 gene partial cds	3.5	other
L38901	L38901	Integral transmembrane protein 1	3.5	TM
RC_N30635	N30635	ESTs	3.5	other
RC_N90859	N90859	ESTs	3.5	other
RC_R63734	R63734	ESTs	3.5	TM
R70167	R70167	ESTs	3.5	other
X69141	X69141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	3.5	TM
X75346	X75346	H sapiens mRNA for MAP kinase activated protein kinase	3.5	other
RC_AA028042	AA028042	Human HSIH2 mRNA complete cds	3.4	other
RC_AA100470	AA100470	ESTs	3.4	other
AA115397	AA115397	Homo sapiens mRNA for putative methyltransferase	3.4	other
RC_AA164209	AA164209	Homo sapiens RRM RNA binding protein GRY-1p (GRY-RBP) mRNA complete cds	3.4	other
RC_AA256203	AA256203	ESTs	3.4	other
RC_AA411440_s	AA411440	ESTs	3.4	TM
RC_AA429917	AA429917	ESTs	3.4	TM
RC_AA442070_s	AA442070	Phosphoribosyl pyrophosphate amidotransferase	3.4	other
RC_AA449417	AA449417	Homo sapiens mRNA for putative glucosyltransferase partial cds	3.4	TM
RC_AA453164	AA453164	EST	3.4	?
RC_F10326_f	F10326	EST	3.4	?
RC_H68639	H68639	ESTs	3.4	other
L47276	L47276	EST - L47276	3.4	other
RC_N29740	N29740	ESTs	3.4	other
RC_N33920	N33920	H sapiens mRNA for duobiquitin	3.4	other
RC_N34855	N34855	ESTs	3.4	other
S81003	S81003	L-UBC	3.4	other
U07606	U07606	DNA topoisomerase I	3.4	other
RC_AA447896	AA447896	ESTs	3.3	other
RC_AA116036	AA116036	ESTs	3.3	other
RC_AA323535_s	AA323535	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [homo sapiens]	3.3	other
RC_AA435847	AA435847	EST - RC_AA435847	3.3	other
RC_AA453159_s	AA453159	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	3.3	other
RC_AA490899	AA490899	ESTs	3.3	other
RC_AA490501	AA490501	ESTs	3.3	TM
AD000092_cds7	AD000092	Homo sapiens DNA from chromosome 19p13.2 cosmid R21240 R22272 and R28549 containing the EKLFC GCDH CRTCA and RAD23A genes genomic sequence	3.3	?
RC_F09353	F09353	Homo sapiens sodiummyo-inositol cotransporter (SLC5A3) gene complete cds	3.3	other
RC_N34029	N34029	EST - RC_N34029	3.3	other
RC_N56172	N56172	ESTs Weakly similar to H1 ALU SUBFAMILY SC WARMING ENTRY III [H sapiens]	3.3	TM
RC_N67437	N67437	ESTs	3.3	TM
RC_R24237_f	R24237	ESTs	3.3	?
RC_R45356	R45356	Homo sapiens cDNA similar to RNA binding protein C. elegans complete	3.3	other
RC_W44735	W44735	ESTs	3.3	?
RC_V85961	V85961	ESTs Weakly similar to ZK1058.4 [C elegans]	3.3	5S, TM
RC_AA134965_s	AA134965	ESTs	3.2	other
RC_AA169379	AA169379	ESTs	3.2	other
RC_AA211941	AA211941	Homo sapiens poly(ADP-ribose) binding protein-interacting protein-1 (PAIP-1) mRNA complete cds	3.2	other
RC_AA232939	AA232939	ESTs	3.2	other
AA421213	AA421213	ESTs Weakly similar to F28F8.3 [C elegans]	3.2	other
RC_AA422079	AA422079	ESTs Weakly similar to RAR-RESPONSIVE PROTEIN TIG1 [H sapiens]	3.2	TM
RC_AA448213_s	AA448213	Human myogenic repressor hMRF1 (MRF1) mRNA complete cds	3.2	other
RC_AA490969	AA490969	ESTs	3.2	other
RC_AA609429	AA609429	ESTs	3.2	other
D84145	D84145	Human WS-3 mRNA complete cds	3.2	other
RC_F09315	F09315	Homo sapiens mRNA for KIAA0583 protein partial cds	3.2	other
L07515	L07515	HETEROCHROMATIN PROTEIN 1 HOMOLOG	3.2	other
M86852	M86852	Peroxisomal membrane protein 3 (35AD Zellweger syndrome)	3.2	TM
RC_N30385	N30385	ESTs	3.2	other
RC_U078572	N78572	EST - RC_U078572	3.2	other
RC_R60192_s	R60192	Peroxisomal biogenesis factor 7	3.2	other
RC_R67996	R67996	ESTs	3.2	other
RC_T15665	T15665	ESTs Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN COBB11.3 IN CHROMOSOME II [C elegans]	3.2	other
T40327_s	T40327	ESTs	3.2	other
RC_T65797	T65797	ESTs Weakly similar to Pin1 protein [H sapiens]	3.2	TM

FIGURE 7 (cont.)

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U37547	U37547	Human IAP homolog B (MIH2) mRNA complete cds	3.2	other
U51586	U51586	Human stah binding protein 1 (StahBP1) mRNA partial cds	3.2	other
U81554	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	3.2	other
RC_V03134_s	W03134	ESTs	3.2	?
RC_W46255	W46255	ESTs	3.2	?
Z97054_x02	Z97054	Human mRNA for KIAA0312 gene partial cds	3.1	other
RC_AA041035	AA041035	ESTs	3.1	TM
RC_AA150043	AA150043	ESTs	3.1	TM
RC_AA232874	AA232874	EST	3.1	TM
RC_AA291259	AA291259	ESTs	3.1	?
RC_AA388350	AA388350	EST	3.1	other
RC_AA401687_s	AA401687	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	3.1	other
RC_D60208_s	D60208	ESTs	3.1	other
D87466	D87465	Human mRNA for KIAA0276 gene partial cds	3.1	other
RC_N21626	N21626	ESTs	3.1	other
RC_N69331	N69331	Peptidylprolyl isomerase C (cyclophilin C)	3.1	TM
S66431	S66431	Homo sapiens clone 23592 mRNA sequence	3.1	TM
RC_W44928	W44928	ESTs	3.1	other
RC_W72967	W72967	ESTs	3.1	other
X17620	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	3.1	other
X59798	X59798	Cyclin D1 (PRAD1; parathyroid adenomatosis 1)	3.1	other
RC_AA099719	AA099719	ESTs	3	other
RC_AA152305_s	AA152305	Interferon (gamma)-induced cell line protein 10 from	3	SS,
RC_AA227932	AA227932	ESTs	3	other
RC_AA251738	AA251738	H. sapiens mRNA for TAF1100 protein	3	other
RC_AA386264	AA386264	ESTs Highly similar to ribosome-binding protein p34 [R.norvegicus]	3	other
RC_AA406577	AA406577	ESTs	3	other
RC_AA423827_s	AA423827	ESTs	3	other
RC_N47204	N47204	ESTs Weakly similar to C50F4.12 [C.elegans]	3	other
RC_R36548	R36548	ESTs	3	TM
S50223	S50223	HRR-T1	3	other
RC_W48505_s	W48505	ESTs Weakly similar to ZK1008.5 [C.elegans]	3	TM
RC_W80482	W80482	ESTs	3	other
X70944_s	X70944	PTB-ASSOCIATED SPLICING FACTOR	3	other
X74801	X74801	H.sapiens. Ccig mRNA for chaperonin	3	other
Y12065	Y12065	Homo sapiens mRNA for nucleolar protein hNop56	3	?
RC_AA164293_s	AA164293	ESTs	2.9	?
RC_AA178845	AA178845	ESTs Moderately similar to rathemson-6 [R.musculus]	2.9	other
RC_AA185639	AA185639	ESTs Weakly similar to W0209.2 [C.elegans]	2.9	TM
AA203523	AA203523	ESTs Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]	2.9	other
RC_AA206088	AA206088	ESTs	2.9	other
RC_AA213506	AA213506	ESTs	2.9	other
RC_AA228020	AA228020	Homo sapiens splicing factor (CC1.3) mRNA complete cds	2.9	other
RC_AA242634	AA242634	ESTs	2.9	other
RC_AA279420	AA279420	ESTs Weakly similar to T08A11.2 [C.elegans]	2.9	TM
RC_AA282747	AA282747	ESTs	2.9	other
AA393164_s	AA393164	Homo sapiens marnmaglobin B precursor mRNA complete cds	2.9	TM
RC_AA395184	AA395184	ESTs	2.9	other
RC_AA399264	AA399264	ESTs	2.9	other
RC_AA400725	AA400725	ESTs	2.9	other
RC_AA426120	AA426120	EST - RC_AA426120	2.9	other
AA452011	AA452011	ESTs Highly similar to deduced protein product shows significant homology to scabactin from Dictyostelium discoideum [H.sapiens]	2.9	other
RC_AA485214_s	AA485214	DNA-BINDING PROTEIN NEFA PRECURSOR	2.9	SS,
D00596	D00596	Thymidylate synthase	2.9	?
RC_D60061_s	D60061	ESTs	2.9	other
RC_F13778	F13778	ESTs	2.9	SS,
RC_H16790	H16790	ESTs	2.9	other
RC_H87677_s	H87677	ESTs	2.9	other
A28211	A28211	Homo sapiens GTP-binding protein (RAB4) mRNA complete cds	2.9	other
RC_N32333	N32333	Homo sapiens M92 protein spliced isoform 2 mRNA complete cds	2.9	other
RC_N36881	N36881	ESTs	2.9	other
RC_R50840	R50840	H.sapiens mRNA for ras-related GTP-binding protein	2.9	other
RC_R93740	R93740	ESTs	2.9	other

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RC_T25732_f	T25732	Human mRNA for KIAA0252 gene partial cds	2.9	?
T54762_s	T54762	ESTs	2.9	?
HG110-HT110	TIGR - HG110-HT110	EST - HG110-HT110	2.9	?
U40714	U40714	Human lysozyme mRNA complete cds	2.9	other
RC_AA001409_f	AA001409	ESTs	2.9	other
RC_AA128407	AA128407	ESTs	2.8	other
RC_AA232231	AA232231	ESTs	2.8	other
RC_AA262768	AA262768	ESTs	2.8	TM
RC_AA292765	AA292765	H sapiens mRNA for M-phase phosphoprotein map5	2.8	other
RC_AA310729_s	AA310729	Human mRNA for clathrin-like protein complete cds	2.8	TM
RC_AA426512	AA426512	ESTs	2.8	other
RC_AA411532	AA411532	ESTs Weakly similar to ORF YOR285w [S cerevisiae]	2.8	other
RC_AA412497	AA412497	EST	2.8	?
RC_AA425606	AA425606	ESTs Weakly similar to Similar to S cerevisiae hypothetical protein L3111 [H sapiens]	2.8	TM
RC_AA425900_s	AA425900	Uracil-DNA glycosylase	2.8	other
RC_AA446572	AA446572	EST - RC_AA446572	2.8	other
RC_AA478596	AA478596	ESTs	2.8	?
RC_AA480103	AA480103	ESTs Weakly similar to ttt ALU SUBFAMILY J WARNING ENTRY ttt [H sapiens]	2.8	TM
RC_AA486407	AA486407	ESTs	2.8	other
RC_AA488432	AA488432	ESTs	2.8	?
RC_AA509200	AA509200	EST - RC_AA509200	2.8	other
RC_AA609501	AA609501	HEAT SHOCK 70 KD PROTEIN s	2.8	other
AF095516	AF095516	Homo sapiens ep58 binding protein s381 mRNA complete cds	2.8	other
RC_D02710_f	D02710	ESTs Weakly similar to transmembrane protein [H sapiens]	2.8	?
RC_F03605_f	F03605	POTENTIAL EOS RIBOSOMAL PROTEIN	2.8	other
RC_H24460_s	H24460	FK506-binding protein 4 [S96D]	2.8	other
RC_H21159	H21159	Homo sapiens forkhead protein (FKHL1) mRNA complete cds	2.8	other
RC_H29325	H29325	ESTs Highly similar to 47 KD PROTEIN (Pseudomonas citrorubra)	2.8	other
RC_H48715	H48715	ESTs	2.8	SS, TM
RC_H92915	H92915	ESTs	2.8	other
RC_R38234_f	R38234	ESTs Weakly similar to elastin like protein [D melanogaster]	2.8	TM
RC_R41933	R41933	ESTs	2.8	?
RC_R46025	R46025	ESTs	2.8	SS
RC_R49327	R49327	Natural resistance-associated macrophage protein 2	2.8	TM
RC_R73617	R73617	ESTs	2.8	other
RC_T63857	T63857	EST - RC_T63857	2.8	?
U30825	U30825	Human splicing factor SRS30c mRNA complete cds	2.8	other
U53347	U53347	Human neutral amino acid transporter 8 mRNA complete cds	2.8	TM
X76732	X76732	DNA-BINDING PROTEIN NEFA PRECURSOR	2.8	SS
RC_AA102520	AA102520	ESTs Highly similar to HYPOPHYSICAL 31.6 KD PROTEIN F54F2.9 IN CHIRONOMUS THUMMUS [C. elegans]	2.7	TM
RC_AA125969	AA125969	ESTs Weakly similar to F36G12.9 [C. elegans]	2.7	?
RC_AA126743	AA126743	ESTs	2.7	other
RC_AA154687	AA154687	ESTs	2.7	other
RC_AA215333	AA215333	ESTs	2.7	TM
RC_AA291269	AA291269	ESTs	2.7	other
RC_AA424031	AA424031	ESTs	2.7	other
RC_AA425725	AA425725	ESTs Weakly similar to serine protein kinase SRPK1 [H sapiens]	2.7	other
RC_AA431333_s	AA431333	ESTs Highly similar to Ras inhibitor [H sapiens]	2.7	other
RC_AA449718	AA449718	ESTs Weakly similar to ZINC FINGER PROTEIN 42 [H sapiens]	2.7	other
RC_AA451529	AA451529	ESTs Weakly similar to putative p150 [H sapiens]	2.7	other
RC_AA620580	AA620580	ESTs	2.7	?
D63391	D63391	Human mRNA for platelet activating factor acetylhydrolase IB gamma subunit complete cds	2.7	other
RC_F02863	F02863	ESTs Moderately similar to ttt ALU SUBFAMILY SQ WARNING ENTRY ttt [H sapiens]	2.7	TM
K02777	K02777	T cell receptor alpha chain	2.7	TM
L11069	L11069	Human telomerase transporter-like protein mRNA complete cds	2.7	SS, TM
L12350	L12350	Thrombospondin 2	2.7	other
M06992	M06992	SPINNING FACTOR UDAF 35 KD SUBUNIT	2.7	?
RC_N22963	N22963	ESTs	2.7	other
RC_N25788	N25788	ESTs	2.7	TM
RC_R02354	R02354	ESTs	2.7	other
RC_R54112	R54112	ESTs	2.7	other
RC_R71481	R71481	ESTs	2.7	TM
U33052	U33052	Human lipid-activated protein kinase PRK2 mRNA complete cds	2.7	other

FIGURE 7 (cont.)

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RC_W69160	W69160	ESTs	2.7	other
RC_W80750	W80750	ESTs	2.7	other
RC_W87747	W87747	ESTs	2.7	other
X16396	X16396	NAO-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	2.7	SS
X39966	X39966	H sapiens mRNA for N8K apolipoprotein protein	2.7	TM
RC_AA001403	AA001403	Homo sapiens 15 kDa selenoprotein mRNA complete cds	2.6	other
RC_AA176121	AA176121	ESTs	2.6	other
RC_AA242758_1	AA242758	Human breast cancer estrogen regulated LVI-1 protein (LVI-1) mRNA partial cds	2.6	SS, TM
RC_AA255300_3	AA255300	ESTs Weakly similar to semaphorin C (M musculus)	2.6	SS
RC_AA412112	AA412112	EST - RC_AA412112	2.6	?
RC_AA417956	AA417956	ESTs	2.6	other
RC_AA447553	AA447553	ESTs	2.6	other
RC_AA447617	AA447617	ESTs	2.6	other
RC_AA453624	AA453624	Human terminal transferase mRNA complete cds	2.6	other
RC_AA596948_5	AA596948	Human mRNA for transcriptional activator hSNF2o complete cds	2.6	other
AB000115	AB000115	Homo sapiens mRNA expressed in osteoblast complete cds	2.6	other
AF001294	AF001294	Homo sapiens (PL (PL)) mRNA complete cds	2.6	other
DE3981	DE3981	Human mRNA for KIAA0160 gene partial cds	2.6	SS
D79997	D79997	Human mRNA for KIAA0175 gene complete cds	2.6	TM
U09655	U09655	Homo sapiens ribon (HBS) mRNA complete cds	2.6	TM
L03411	L03411	Rabbit blood group	2.6	other
L04490	L04490	Homo sapiens (clone CC6) NADH-ubiquinone oxidoreductase subunit mRNA 3' end cds	2.6	other
RC_N33516	N33516	Homo sapiens ribon (HBS) mRNA complete cds	2.6	TM
RC_N46252	N46252	ESTs	2.6	TM
RC_N48790	N48790	ESTs Moderately similar to H1 ALU SUBFAMILY SX WARNING ENTRY H1 (H sapiens)	2.6	other
RC_N51316	N51316	ESTs Highly similar to elastin like protein (D melanogaster)	2.6	other
RC_N63210	N63210	ESTs	2.6	other
RC_N63669	N63669	ESTs	2.6	other
RC_N92948_1	N92948	Human REF SSP 9502 mRNA complete cds	2.6	other
RC_R50333_1	R50333	ESTs	2.6	?
T39176_1	T39176	ESTs Weakly similar to ZK1058.4 (C elegans)	2.6	SS, TM
RC_W85712	W85712	ESTs Weakly similar to PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR (H sapiens)	2.6	TM
Z49099	Z49099	H sapiens mRNA for spermine synthase	2.6	other
RC_AA045083	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	2.5	other
RC_AA095647	AA095647	EST - RC_AA095647	2.5	other
RC_AA130343	AA130343	ESTs	2.5	?
RC_AA160890_1	AA160890	Human mRNA for KIAA0389 gene complete cds	2.5	other
RC_AA191424	AA191424	ESTs	2.5	other
RC_AA236489	AA236489	ESTs	2.5	other
RC_AA251587	AA251587	Homo sapiens mRNA for KIAA2530 protein partial cds	2.5	other
RC_AA262491	AA262491	ESTs	2.5	other
RC_AA282730	AA282730	ESTs	2.5	?
RC_AA284372	AA284372	ESTs	2.5	other
RC_AA291503	AA291503	EST	2.5	?
RC_AA369027	AA369027	ESTs	2.5	SS
RC_AA398280	AA398280	ESTs	2.5	other
RC_AA404937	AA404937	Matrix Gs protein	2.5	other
RC_AA416877	AA416877	ESTs	2.5	other
RC_AA428179	AA428179	EST	2.5	?
RC_AA446100	AA446100	ESTs	2.5	other
RC_AA451707	AA451707	ESTs	2.5	other
RC_AA490882_1	AA490882	ESTs	2.5	other
RC_AA610073	AA610073	ESTs	2.5	other
AB000308	AB000308	Human mRNA for KIAA0310 gene complete cds	2.5	other
D43946	D43946	Human mRNA for KIAA0097 gene complete cds	2.5	TM
RC_D60374_1	D60374	EST - RC_D60374_1	2.5	other
RC_H12834	H12834	ESTs	2.5	other
L00205	L00205	KERATIN TYPE II CYTOSKELETAL 60	2.5	?
M23379	M23379	GTPase-activating protein ras p21 (RAS)	2.5	TM
RC_N21677	N21677	ESTs	2.5	other
RC_N66158	N66158	ESTs	2.5	TM
RC_N67187_1	N67187	ESTs	2.5	other
RC_N70646	N70646	ESTs	2.5	TM

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RC_N93000	N93000	ESTs	2.5	other
T39763_s	T39763	ESTs	2.5	other
RC_T77641	T77641	ESTs	2.5	SS
U16306	U16306	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR	2.5	SS
RC_W47163	W47163	ESTs	2.5	other
X54941	X54941	CDC28 protein kinase 1	2.5	other
X70218	X70218	Protein phosphatase 4 (formerly X) catalytic subunit	2.5	other
X85373	X85373	H sapiens mRNA for Sm protein G	2.5	other
RC_AA039897	AA039897	ESTs	2.4	other
RC_AA147708	AA147708	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D (Bos taurus)	2.4	other
RC_AA190993	AA190993	ESTs	2.4	other
RC_AA216663	AA216663	ESTs Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (Xenopus laevis)	2.4	other
RC_AA223209	AA223209	ESTs Weakly similar to D9481.16 gene product [S cerevisiae]	2.4	other
RC_AA252672_s	AA252672	Homo sapiens diaphanide biosynthesis protein-2 (DPY102) mRNA complete cds	2.4	other
RC_AA258601	AA258601	EST - RC_AA258601	2.4	?
RC_AA262051	AA262051	ESTs	2.4	other
RC_AA278799	AA278799	ESTs	2.4	?
RC_AA286942	AA286942	EST - RC_AA286942	2.4	?
RC_AA31604	AA31604	Human Rho-associated coiled-coil containing protein kinase p160ROCK mRNA complete cds	2.4	other
RC_AA329047	AA329047	ESTs	2.4	other
AA434329	AA434329	ESTs	2.4	other
RC_AA445458	AA445458	ESTs	2.4	TM
RC_AA452239	AA452239	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 (Caenorhabditis elegans)	2.4	other
RC_AA456646	AA456646	ESTs	2.4	other
RC_AA487207	AA487207	EST - RC_AA487207	2.4	other
AA040423	AA040423	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 (Caenorhabditis elegans)	2.4	other
RC_AA599674	AA599674	ESTs Weakly similar to F08G12.1 (C. elegans)	2.4	SS
D38555	D38555	Human mRNA for KIAA0079 gene complete cds	2.4	other
D82348	D82348	Human mRNA for 5-aminocrotonate-4-epimerase-1-beta D-ribonucleoside diphosphate lyase/nucleoside complete cds	2.4	other
D87684	D87684	Human mRNA for KIAA0242 gene partial cds	2.4	TM
M35542	M35542	Guanylate binding protein 1 interferon-inducible 67kD	2.4	TM
M30516	M30516	Glutamine-fructose-6-phosphate transaminase	2.4	other
RC_N51260_s	N51260	Human mRNA for KIAA0240 gene partial cds	2.4	other
RC_N69352	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds	2.4	other
RC_R37778	R37778	ESTs	2.4	?
S82597_ma1	S82597	H sapiens mRNA for UDP-GalNAc polypeptide N-acetyl-galactosaminyltransferase (T1)	2.4	other
RC_T25996	T25996	ESTs	2.4	other
RC_T29681	T29681	Human serine kinase mRNA complete cds	2.4	other
U73477	U73477	HLA-DR ASSOCIATED PROTEIN I	2.4	other
RC_V31919	V31919	EST	2.4	other
W79060	W79060	ESTs Highly similar to ribosome-binding protein p34 (R. norvegicus)	2.4	other
X13482	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A	2.4	?
X62392_ma1	X62392	COL10A1	2.4	other
X84373	X84373	NUCLEAR FACTOR RIP140	2.4	other
RC_Z40898	Z40898	ESTs	2.3	other
RC_AA010065_s	AA010065	CDC28 protein kinase 2	2.3	SS, TM
RC_AA024656	AA024656	ESTs	2.3	?
RC_AA031814	AA031814	ESTs Weakly similar to R01H10.8 (C. elegans)	2.3	other
RC_AA037410_s	AA037410	Human DNA sequence from PAC 127B20 on chromosome 22q11.2, other contains GTPase-activating protein similar to rhoGAP protein ribosomal protein L5 pseudogene ESTs and CA repeat	2.3	other
RC_AA037657_s	AA037657	ESTs	2.3	TM
RC_AA069285	AA069285	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (C. elegans)	2.3	other
RC_AA173223	AA173223	ESTs	2.3	other
RC_AA236951_s	AA236951	ESTs	2.3	other
RC_AA250737	AA250737	ESTs	2.3	other
RC_AA251776	AA251776	ESTs	2.3	other
RC_AA262566	AA262566	ESTs Weakly similar to F25H2.6 (C. elegans)	2.3	other
AA330771_s	AA330771	Human protein-tyrosine phosphatase (R3-PP-1) mRNA partial sequence	2.3	TM
RC_AA425749	AA425749	ESTs	2.3	TM
RC_AA428647	AA428647	ESTs	2.3	other
RC_AA450116	AA450116	ESTs	2.3	other

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RC_AA459673	AA459673	ESTs Highly similar to CHROMOSOME SEGREGATION PROTEIN CUT3 [Schistosoma mansoni]	2.3	other
RC_AA464423	AA464423	ESTs Weakly similar to H1 ALU SUBFAMILY J VARIING ENTRY III [H sapiens]	2.3	other
D00591	D00591	Chromosome condensation 1	2.3	?
D06156	D06156	Human mRNA for transcriptional activator hSNF2b complete cds	2.3	other
RC_F02907	F02907	ESTs	2.3	TM
J05633	J05633	Integrin beta-5 subunit	2.3	SS, TM
RC_N03688	N03688	Human NAD+-specific isocitrate dehydrogenase beta subunit precursor mRNA nuclear gene encoding mitochondrial protein complete cds	2.3	other
RC_N03063	N03063	ESTs Highly similar to GAG POLYPROTEIN [Avian spleen neorosis virus]	2.3	other
RC_N49284_s	N49284	MYB PROTO-ONCOGENE PROTEIN	2.3	other
RC_N65857	N65857	ESTs	2.3	?
RC_N94581	N94581	ESTs	2.3	TM
RC_R02088	R02088	EST - RC_R02088	2.3	other
RC_R03652	R03652	ESTs	2.3	other
R01830	R01830	Human sapiens breast cancer putative transcription factor (ZABC1) mRNA complete cds	2.3	other
S79873	S79873	Lysosomal-associated membrane protein 2	2.3	SS, TM
RC_T87807_s	T87807	ESTs	2.3	other
U07022_mel	U07022	Human cyclin-dependent protein kinase mRNA complete cds	2.3	?
U47077	U47077	Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA complete cds	2.3	TM
U59423	U59423	Human chromosome 4 Mac homolog Smad1 mRNA complete cds	2.3	other
U72514	U72514	Human G21 mRNA complete cds	2.3	other
U77140	U77140	Human mRNA for EBI1-ligand chemokine complete cds	2.3	TM
RC_X02925_s	X02925	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN (X PRITE-PC1) INTERGENIC REGION [Saccharomyces cerevisiae]	2.3	SS, TM
RC_X49574	X49574	ESTs Moderately similar to H1 ALU SUBFAMILY G2 VARIING ENTRY III [H sapiens]	2.3	other
X54199	X54199	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylaminoimidazole synthetase	2.3	?
X94453	X94453	Pyrimidine-Carboxylester synthetase (glutamate gamma-semialdehyde synthetase)	2.3	other
RC_Z39609	Z39609	ESTs Moderately similar to ZKAC FINGER PROTEIN ZFP-36 [Homo sapiens]	2.3	other
Z48042	Z48042	H sapiens mRNA encoding GPI-anchored protein p137	2.3	other
RC_AA011556	AA011556	ESTs	2.2	other
RC_AA028028	AA028028	ESTs	2.2	other
AA043160	AA043160	ESTs	2.2	other
RC_AA043353_s	AA043353	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]	2.2	other
RC_AA053636	AA053636	ESTs	2.2	other
RC_AA059214	AA059214	ESTs Moderately similar to neurospodin 2 [M musculus]	2.2	SS
RC_AA076328_s	AA076328	Cyclin-dependent kinase inhibitor 2A (melanoma p16 inhibits CDK4)	2.2	TM
RC_AA126719	AA126719	ESTs	2.2	other
RC_AA131692	AA131692	ESTs	2.2	other
RC_AA148516	AA148516	ESTs	2.2	TM
RC_AA150098	AA150098	Human sapiens vesicle transport related protein mRNA partial cds	2.2	other
RC_AA027856	AA027856	H sapiens mRNA for HDXCB protein exon 1	2.2	other
RC_AA029516	AA029516	ESTs Weakly similar to ISOLEUCYL-TRNA SYNTHETASE MITOCHONDRIAL [S cerevisiae]	2.2	other
RC_AA251706	AA251706	ESTs Moderately similar to metastasis-associated gene [H sapiens]	2.2	other
RC_AA280588	AA280588	ESTs	2.2	other
RC_AA287320	AA287320	ESTs	2.2	other
RC_AA287833	AA287833	ESTs	2.2	other
RC_AA397821	AA397821	Human sapiens mRNA transcriptional unit N143	2.2	TM
RC_AA416735	AA416735	ESTs	2.2	other
RC_AA417030	AA417030	Human sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	2.2	other
RC_AA420927_1	AA420927	ESTs	2.2	other
RC_AA430726	AA430726	EST - RC_AA430726	2.2	SS
RC_AA436477	AA436477	ESTs	2.2	TM
RC_AA436613	AA436613	ESTs	2.2	other
RC_AA446949	AA446949	ESTs	2.2	other
RC_AA455223	AA455223	ESTs	2.2	TM
RC_AA490237	AA490237	EST - RC_AA490237	2.2	other
RC_AA495924	AA495924	ESTs	2.2	other
RC_AA600200	AA600200	ESTs	2.2	SS
RC_D00237_s	D00237	Human sapiens Arp2/3 protein complex subunit p20-Arc (ARPC20) mRNA complete cds	2.2	?
RC_F09328	F09328	ESTs	2.2	other
RC_F13090_s	F13090	ESTs Weakly similar to ZNF127-Xp [H sapiens]	2.2	other
RC_H08426	H08426	ESTs	2.2	other
RC_H08458_s	H08458	ESTs	2.2	other

FIGURE 7 (cont.)
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RC_H99281_4	H99281	Human DNA from overlapping chromosome 19 cosmids R31396 F25421 and R31076 containing COX2B and UPKA genomic sequen	2.2	TM
RC_H39148	H39148	ESTs	2.2	other
RC_H90401	H90401	ESTs	2.2	TM
RC_H93618	H93618	ESTs	2.2	other
RC_H94506	H94506	ESTs	2.2	other
RC_R72008	R72008	ESTs Weakly similar to Dnf33 gene product (H sapiens)	2.2	other
R78119	R78119	ESTs	2.2	other
RC_T10060	T10060	ESTs	2.2	TM
RC_T15674_2	T15674	ESTs	2.2	?
RC_T09685_3	T09685	ESTs	2.2	other
U09510	U09510	Glycyl-tRNA synthetase	2.2	other
U09770	U09770	Human cysteine-rich heart protein (hCRHP) mRNA complete cds	2.2	SS, TM
U06782	U06782	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	2.2	other
XT0476	XT0476	COATOMER BETA' SUBUNIT	2.2	?
RC_AA018587	AA018587	ESTs Weakly similar to H1 ALU SUBFAMILY SP WARNING ENTRY "" (H sapiens)	2.1	?
RC_AA154053	AA154053	ESTs	2.1	other
RC_AA158132	AA158132	ESTs Highly similar to YSA1 PROTEIN (Saccharomyces cerevisiae)	2.1	other
RC_AA251909	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete cds	2.1	other
RC_AA253031	AA253031	Homo sapiens RRM RNA binding protein Gry-bp (GRY-BBP) mRNA complete cds	2.1	other
RC_AA281780	AA281780	ESTs Weakly similar to HYPOTHETICAL 46.4 KD PROTEIN TIGR12.5 IN CHROMOSOME III (C. elegans)	2.1	other
RC_AA291137	AA291137	ESTs	2.1	other
RC_AA339395	AA339395	LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR	2.1	other
RC_AA400320_3	AA400320	ESTs	2.1	other
RC_AA403121	AA403121	ESTs	2.1	SS
RC_AA426000	AA426000	ESTs	2.1	other
RC_AA427662	AA427662	ESTs	2.1	other
RC_AA451712	AA451712	ESTs	2.1	other
AA460077	AA460077	ESTs	2.1	other
RC_AA463148	AA463148	ESTs	2.1	other
RC_AA465989	AA465989	ESTs	2.1	other
RC_AA470039	AA470039	ESTs	2.1	other
RC_AA620454	AA620454	Human mRNA for KIAA2311 gene complete cds	2.1	?
D13888	D13888	Homo sapiens mRNA for GDP dissociation inhibitor beta	2.1	TM
RC_F01896_7	F01896	EST	2.1	?
RC_H38246_5	H38246	ESTs Weakly similar to similar to S. cerevisiae LAG1 (C. elegans)	2.1	TM
RC_H80737_1	H80737	ESTs	2.1	TM
K30538	K30538	ATP-DEPENDENT DNA HELICASE II 85 KD SUBUNIT	2.1	other
K74099	K74099	Cut (Drosophila)-like 1 (CCAAT displacement protein)	2.1	?
RC_H22222	N22222	ESTs	2.1	other
RC_H24958	N24958	Homo sapiens vacuolar H(+)-ATPase subunit mRNA complete cds	2.1	other
RC_H64378	N64378	ESTs	2.1	other
RC_H72113	N72113	ESTs	2.1	other
RC_H92837	N92837	Homo sapiens clone 24551 mRNA sequence	2.1	TM
RC_R91380_5	R91380	H. sapiens RNA for CLGN3	2.1	TM
U51205	U51205	Human COP9 homolog (hCOP9) mRNA complete cds	2.1	other
U58090	U58090	Human Hs-ou-4A mRNA partial cds	2.1	TM
U60808	U60808	Human GDP-diacetylglucosyl synthase (GDS) mRNA complete cds	2.1	other
U61232	U61232	Human tubulin-binding cofactor E mRNA complete cds	2.1	other
U61722	U61722	Human ubiquitin-homology domain protein PIC1 mRNA complete cds	2.1	other
RC_V02091_3	V02091	Human mRNA for kinesin-related protein partial cds	2.1	other
RC_V02470	V02470	ESTs	2.1	other
RC_V07384_1	V07384	Homo sapiens testis-specific nm22 homolog mRNA complete cds	2.1	other
X70683	X70683	SRY (sex determining region Y)-box 4	2.1	TM
X70944	X70944	PTB-ASSOCIATED SPLICING FACTOR	2.1	other
RC_Z99394_3	Z99394	ESTs Moderately similar to H1 ALU SUBFAMILY SP WARNING ENTRY "" (H sapiens)	2	TM
RC_AA045481	AA045481	ESTs	2	SS
RC_AA047265	AA047265	Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds	2	TM
RC_AA127716	AA127716	Homo sapiens unknown mRNA complete cds	2	other
RC_AA136884	AA136884	ESTs	2	other
RC_AA181657	AA181657	ESTs	2	?
RC_AA186861	AA186861	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds	2	other
RC_AA233177	AA233177	ESTs	2	other
RC_AA237022	AA237022	ESTs	2	other

FIGURE 7 (cont.)

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RC_AA287388	AA287388	ESTs	2	other
RC_AA405838	AA405838	ESTs	2	other
RC_AA417909	AA417909	ESTs	2	other
RC_AA426375	AA426375	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 (Saccharomyces cerevisiae)	2	other
AA443460	AA443460	ESTs	2	other
RC_AA443596	AA443596	ESTs	2	other
RC_AA453255	AA453255	ESTs	2	other
RC_AA476312	AA476312	ESTs	2	TM
RC_AA476582	AA476582	ESTs Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (Mus musculus)	2	other
RC_AA479139_3	AA479139	Acid phosphatase 1 soluble	2	other
RC_AA487202	AA487202	ESTs	2	other
RC_AA521474	AA521474	ESTs	2	?
RC_AA586452	AA586452	ESTs	2	other
RC_AA621122	AA621122	ESTs	2	other
AF015913	AF015913	Homo sapiens SKB1Hs mRNA complete cds	2	other
D28364	D28364	EST - D28364	2	other
RC_DS3392_1	DS3392	ESTs Weakly similar to PEREGRIN (H. sapiens)	2	TM
D78695	D78695	CAD PROTEIN	2	other
D80000	D80000	Human mRNA for KIAA0178 gene partial cds	2	TM
D86978	D86978	Human mRNA for KIAA0225 gene partial cds	2	other
RC_F02651	F02651	ESTs	2	other
RC_H11938	H11938	EST - RC_H11938	2	?
RC_H78241_5	H78241	H sapiens mRNA for novel member of serine-arginine domain protein SRP129	2	other
L20288	L20288	Core-binding factor beta subunit	2	TM
L37347	L37347	Natural killer cell-associated macrophage protein 2	2	TM
M23263	M23263	Androgen receptor (dihydrotestosterone receptor testicular feminization spiral and butyral muscular atrophy Kennedy disease)	2	other
RC_N22160	N22160	ESTs	2	other
RC_N24954	N24954	ESTs	2	TM
RC_N50960	N50960	ESTs	2	TM
RC_N70520	N70520	ESTs	2	SS
RC_N91246	N91246	ESTs	2	?
RC_R68425	R68425	ESTs	2	TM
RC_R73567	R73567	Homo sapiens matrilin-1 precursor (ADAM12) mRNA complete cds	2	other
RC_T23539	T23539	ESTs Highly similar to zinc finger protein (M. musculus)	2	?
T63174_3	T63174	ESTs	2	other
RC_T90746	T90746	ESTs	2	other
U05340	U05340	Human p55CDC mRNA complete cds	2	other
U34044	U34044	Human selenium donor protein (srd) mRNA complete cds	2	TM
U37519	U37519	Aldhyde dehydrogenase 8	2	other
U38940	U38940	Human hepatocyte nuclear factor-3 alpha (HNF-3 alpha) mRNA complete cds	2	other
U91932	U91932	Human mRNA for calnexin opal assembly protein-like complete cds	2	other
V028362	V028362	ESTs	2	other
RC_V02467	V02467	ESTs	2	other
X69636	X69636	Human mRNA for KIAA0293 gene complete cds	2	other
X92896	X92896	H sapiens mRNA for ITBA2 protein	2	?
Z24724	Z24724	H sapiens polyA site DNA	2	other
Z29090	Z29090	PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT ALPHA ISOFORM	2	other
RC_Z39053	Z39053	ESTs	2	TM
RC_Z40910	Z40910	ESTs	2	?
Z47727	Z47727	H sapiens mRNA for RNA polymerase II subunit	1.9	TM
RC_AA112679	AA112679	ESTs	1.9	other
AA119058_3	AA119058	ESTs	1.9	other
RC_AA146985	AA146985	ESTs	1.9	other
RC_AA173417	AA173417	ESTs	1.9	other
RC_AA227463	AA227463	ESTs Weakly similar to No definition line found (C. elegans)	1.9	?
RC_AA227963	AA227963	ESTs	1.9	TM
RC_AA233166	AA233166	ESTs Highly similar to HYPOTHETICAL 16.5 KD PROTEIN IN PASS-EGT2 INTERGENIC REGION (Saccharomyces cerevisiae)	1.9	other
RC_AA233261	AA233261	ESTs	1.9	other
RC_AA236453	AA236453	ESTs	1.9	other
RC_AA257972	AA257972	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 (Arabidopsis thaliana)	1.9	other
RC_AA278653_1	AA278653	ESTs	1.9	other
RC_AA287834	AA287834	ESTs	1.9	other

FIGURE 7 (cont.)

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RC_AA302745	AA302745	ESTs	1.9	?
RC_AA403009	AA403009	ESTs	1.9	?
RC_AA446918	AA446918	EST	1.9	?
RC_AA451888	AA451898	ESTs	1.9	other
AA464013	AA464013	ESTs Weakly similar to Y53C12A.3 [C. elegans]	1.9	TM
RC_AA485045	AA485046	ESTs	1.9	TM
RC_AA496000	AA496000	ESTs	1.9	SS
RC_AA497052	AA497052	ESTs	1.9	other
RC_AA504932	AA504932	ESTs Weakly similar to Sp140 protein [H.sapiens]	1.9	other
D12485	D12485	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1	1.9	TM
D13645	D13645	Human mRNA for KIAA0200 gene complete cds	1.9	other
D50520	D50520	Human sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA complete cds	1.9	TM
H44396_s	H44396	ESTs	1.9	other
L13689	L13689	Mouse leukemia viral (Dml-1) oncogene homolog	1.9	other
L33801	L33801	Human protein kinase mRNA complete cds	1.9	other
M21259	M21259	Small nuclear ribonucleoprotein polypeptide E	1.9	?
RC_N23393	N23393	ESTs	1.9	other
RC_NH8423	N46423	ESTs	1.9	other
RC_N47489	N47489	ESTs	1.9	other
RC_N55336	N55336	ESTs	1.9	TM
RC_T25867	T25867	EST	1.9	?
RC_T77464	T77464	H.sapiens mRNA for transcriptional intermediary factor 2	1.9	other
RC_T89703	T89703	ESTs Weakly similar to siah binding protein 1 [H.sapiens]	1.9	other
HG174-HT174	TIGR - HG174-HT174	EST - HG174-HT174	1.9	?
U06237	U06237	Human fetal Atr-5D-reactive clone 1 (FAC1) mRNA complete cds	1.9	other
U26312	U26312	Human heterochromatin protein HP1Hs-gamma mRNA complete cds	1.9	other
U41387	U41387	Human Gu protein mRNA partial cds	1.9	other
U15638	U15638	Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds	1.9	other
RC_V07933	V07933	EST - RC_V07933	1.9	?
RC_V08783	V08783	ESTs Highly similar to FK506-BINDING PROTEIN PRECURSOR [Mus musculus]	1.9	other
RC_V06063	V06063	ESTs Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2 OSC IN CHROMOSOME 1 [Schistosoma mansoni]	1.9	TM
X12791	X12791	Signal recognition particle 19 kD protein	1.9	other
X55448_cds1	X55448	H.sapiens mRNA for 2.19 gene	1.9	?
X58072	X58072	GATA-binding protein 3	1.9	other
X81788	X81788	Human sapiens ICT1 (alias DS-1) mRNA	1.9	other
X82153	X82153	CATHEPSIN K PRECURSOR	1.9	other
RC_Z40715	Z40715	ESTs Weakly similar to T13F2.1 [C. elegans]	1.9	TM
RC_AA005108	AA005108	ESTs	1.9	other
RC_AA028074	AA028074	ESTs	1.9	other
RC_AA063460_s	AA063460	Gastrin-releasing peptide	1.9	SS
AA099241	AA099241	ESTs Moderately similar to R55 RIBOSOMAL PROTEIN L25 [H.sapiens]	1.9	other
RC_AA131584	AA131584	ESTs Weakly similar to SGP1 PROTEIN [Saccharomyces cerevisiae]	1.9	other
RC_AA191353	AA191353	ESTs	1.9	TM
RC_AA232103	AA232103	ESTs	1.9	other
RC_AA232104	AA232104	ESTs Highly similar to transcription factor ARF5 chain B [M.musculus]	1.9	other
RC_AA234765	AA234765	ESTs	1.9	TM
RC_AA251758	AA251758	Human sapiens spleen mitotic checkpoint (BUB3) (BUB3) mRNA complete cds	1.9	other
RC_AA251982	AA251982	Human sapiens clone 237D mRNA sequence	1.9	other
RC_AA279171	AA279171	ESTs Weakly similar to F25D7.1 [C. elegans]	1.9	other
RC_AA283743_s	AA283743	ESTs Moderately similar to YY1-associated factor 2 [H.sapiens]	1.9	other
RC_AA291923	AA291923	ESTs	1.9	TM
RC_AA292066_s	AA292066	ESTs Weakly similar to CD1H6.7 [C. elegans]	1.9	TM
RC_AA388319	AA388319	ESTs	1.9	other
RC_AA401274	AA401274	Human sapiens RRM RNA binding protein Grr-abp (GRY-RBP) mRNA complete cds	1.9	other
RC_AA406478	AA406478	ESTs	1.9	TM
RC_AA411144	AA411144	ESTs	1.9	TM
RC_AA417962	AA417962	ESTs Highly similar to GERANYLGERANYL PYROPHOSPHATE SYNTHETASE [Neurospora crassa]	1.9	other
RC_AA420098	AA420098	ESTs	1.9	other
RC_AA436171	AA436171	ESTs	1.9	other
RC_AA438192	AA438192	ESTs	1.9	other
RC_AA447803	AA447803	EST	1.9	?
AA455001_s	AA455001	ESTs	1.9	other

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RC_AA457566	AA457566	ESTs	1.8	other
RC_AA450350	AA450350	ESTs	1.8	other
RC_AA598988	AA598988	ESTs Moderately similar to HYPOTHETICAL 52.3 KD PROTEIN IN MPRI-GCN20 INTERGENIC REGION (Saccharomyces cerevisiae)	1.8	SS
RC_AA599219	AA599219	ESTs Moderately similar to ALR (H.sapiens)	1.8	other
AF000430	AF000430	Homo sapiens mRNA for Dnm1p/Vps1p-like protein complete cds	1.8	TM
D13630	D13630	Human mRNA for KIAA0005 gene complete cds	1.8	other
RC_D59894	D59894	ESTs	1.8	?
RC_F02990	F02990	ESTs Highly similar to DOSAGE COMPENSATION REGULATOR (Ereophila melanoscelus)	1.8	other
RC_F04989	F04989	ESTs	1.8	other
RC_H94248	H94248	ESTs	1.8	other
L10910	L10910	Homo sapiens splicing factor (CC1.3) mRNA complete cds	1.8	other
L25876	L25876	Human protein phosphatase (KAP1) mRNA complete cds	1.8	other
L76937	L76937	Homo sapiens Werner syndrome gene complete cds	1.8	?
M36429	M36429	Human transducin beta-2 subunit mRNA complete cds	1.8	other
M83190	M83190	Thymidylate synthetase	1.8	other
RC_N32855	N32855	ESTs Moderately similar to [H] ALU SUBFAMILY SQ WARNING ENTRY [H] (H.sapiens)	1.8	other
RC_N35583	N35583	ESTs Weakly similar to PROBABLE E5 PROTEIN (Human papillomavirus type 56)	1.8	?
RC_N50050	N50050	ESTs	1.8	other
RC_N52006	N52006	ESTs	1.8	other
RC_R41281	R41281	Homo sapiens DNU/CPI3 mRNA complete cds	1.8	TM
RC_T96595	T96595	EST - RC_T96595	1.8	TM
U14518	U14518	Centromere protein A (17kD)	1.8	other
U32986	U32986	Damage-specific DNA binding protein 1 (127 kD)	1.8	TM
U65828	U65828	V-jun avian sarcoma virus 17 oncogene homolog	1.8	other
U70322	U70322	Human transportin (TRN) mRNA complete cds	1.8	other
U72263	U72263	Exonuclease (multi-sub)	1.8	TM
RC_V85225	V85225	ESTs	1.8	other
V86502	V86502	ESTs	1.8	other
RC_W72876	W72876	ESTs	1.8	SS
RC_X84790_s	X84790	Human mRNA for KIAA2028 gene complete cds	1.8	?
RC_X86983	X86983	Human RNA-binding protein CUG-BP/NA50 (NA50) mRNA complete cds	1.8	other
X05488	X05488	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U	1.8	other
X75962	X75962	OX40 RECEPTOR PRECURSOR	1.8	SS, TM
X82058	X82058	H.sapiens mRNA for transmembrane protein mp24	1.8	SS, TM
RC_Z40332	Z40332	Homo sapiens mRNA for p115 complete cds	1.8	other
RC_AA035143	AA035143	ESTs	1.7	other
RC_AA056249	AA056249	Collagen type IV alpha 3	1.7	other
RC_AA056568	AA056568	ESTs	1.7	other
RC_AA111879	AA111879	EST	1.7	?
RC_AA116075	AA116075	ESTs	1.7	other
RC_AA132514	AA132514	Homo sapiens drp1 mRNA complete cds	1.7	other
RC_AA156142_s	AA156142	ESTs	1.7	TM
RC_AA171529	AA171529	ESTs	1.7	TM
RC_AA180321	AA180321	ESTs Weakly similar to WCHD2.6 (C.allegans)	1.7	other
RC_AA222315	AA222315	Homo sapiens clone Z3797 and Z3917 mRNA partial cds	1.7	other
RC_AA234767	AA234767	ESTs	1.7	TM
RC_AA252557	AA252557	ESTs	1.7	TM
RC_AA280687	AA280687	ESTs	1.7	other
RC_AA286891	AA286891	ESTs	1.7	other
RC_AA287091_s	AA287091	ESTs Highly similar to C10 (H.sapiens)	1.7	other
RC_AA291280	AA291280	ESTs	1.7	?
RC_AA400080	AA400080	EST	1.7	other
RC_AA410894	AA410894	ESTs	1.7	other
RC_AA410872	AA410872	ESTs	1.7	other
RC_AA416733	AA416733	ESTs	1.7	TM
RC_AA421773	AA421773	ESTs	1.7	other
RC_AA429439	AA429439	ESTs	1.7	other
RC_AA433465	AA433465	ESTs	1.7	other
RC_AA459005	AA459005	ESTs	1.7	other
RC_AA465890_s	AA465890	Human arginine-rich nuclear protein mRNA complete cds	1.7	other
RC_AA470140	AA470140	ESTs	1.7	?
RC_AA479362	AA479362	ESTs	1.7	SS
RC_AA479961	AA479961	ESTs	1.7	other

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RC_AA588447	AA588447	Homo sapiens exportin 1 mRNA complete cds	1.7	other
RC_AA59267	AA59267	EST - RC_AA59267	1.7	other
RC_AA609053	AA609053	ESTs	1.7	SS
RC_AA69584	AA69584	EST	1.7	?
AF002668	AF002668	Homo sapiens putative fatty acid desaturase MLD mRNA complete cds	1.7	TM
D31161.1	D31161	ESTs	1.7	TM
D78151	D78151	H.sapiens mRNA for 5S.11 binding prot"n	1.7	TM
RC_H15436	H15436	ESTs	1.7	other
RC_H17620	H17620	ESTs	1.7	TM
RC_H22220	H22220	ESTs	1.7	other
RC_H3608.1	H3608	ESTs	1.7	other
L19161	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	1.7	other
L27706	L27706	Chaperonin containing T-complex subunit 6	1.7	?
L76703	L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds	1.7	?
RC_N31598	N31598	ESTs	1.7	SS
RC_N31952	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A3.5 IN CHROMOSOME II (Caenorhabditis elegans)	1.7	other
RC_N50831	N50831	ESTs	1.7	TM
RC_N51220	N51220	ESTs	1.7	other
RC_N5551.1	N5551	Cathepsin B	1.7	other
RC_N60029	N60029	Homo sapiens clone 1400 unknown protein mRNA partial cds	1.7	?
RC_N92860.1	N92860	Proto-oncogene AML1 (alternative products)	1.7	other
RC_R39923	R39923	ESTs	1.7	TM
RC_R93006	R93006	ESTs	1.7	other
RC_T03865	T03865	ESTs	1.7	other
RC_T37317	T37317	ESTs	1.7	?
HQ4557-H14362	TIGR - HQ4557	EST - HQ4557-H14362	1.7	?
U95551	U95551	Human histone 2A-like protein (H2AF) mRNA complete cds	1.7	other
U95367	U95367	Human GABA-A receptor pi subunit mRNA complete cds	1.7	TM
RC_Y18222	Y18222	ESTs	1.7	other
W23469	W23469	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	1.7	other
RC_W08150	W08150	EST - RC_W08150	1.7	?
V05890	V05890	Human Chromosome 16 BAC clone C178073K-A-73505	1.7	other
RC_V05898	V05898	ESTs	1.7	other
RC_AA028418	AA028418	ESTs	1.6	other
RC_AA095689.1	AA095689	Homo sapiens mRNA for GDP dissociation inhibitor beta	1.6	TM
RC_AA101811	AA101811	EST	1.6	SS
RC_AA121127	AA121127	ESTs Weakly similar to ZK1058.4 (C.elegans)	1.6	SS, TM
RC_AA148855	AA148855	ESTs	1.6	?
RC_AA141708	AA141708	EST	1.6	other
RC_AA155803	AA155803	ESTs	1.6	other
RC_AA167375	AA167375	Homo sapiens mRNA for KIAA0550 protein partial cds	1.6	other
RC_AA167708	AA167708	ESTs	1.6	other
RC_AA181590.1	AA181580	Homo sapiens importin beta subunit mRNA complete cds	1.6	other
AA187579	AA187579	ESTs Weakly similar to Yw007-ap (S.cerevisiae)	1.6	other
RC_AA243007	AA243007	ESTs	1.6	?
RC_AA243052	AA243052	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR (Rattus norvegicus)	1.6	other
RC_AA252360	AA252360	EST	1.6	?
AA256106	AA256106	ESTs	1.6	other
RC_AA256678	AA256678	ESTs Highly similar to POP2 PROTEIN (Saccharomyces cerevisiae)	1.6	other
RC_AA258205	AA258205	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA complete cds	1.6	other
RC_AA279667.1	AA279667	Cathepsin B	1.6	other
RC_AA347967	AA347967	ESTs	1.6	SS
RC_AA417970	AA417970	ESTs	1.6	?
RC_AA424524	AA424524	Homo sapiens mRNA for KIAA0286 gene partial cds	1.6	?
AA426176	AA426176	ESTs Weakly similar to Similar to S.cerevisiae hypothetical protein L3111 (H.sapiens)	1.6	other
RC_AA456437	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT (H.sapiens)	1.6	other
RC_AA456598	AA456598	ESTs	1.6	other
RC_AA463195	AA463195	ESTs	1.6	other
RC_AA465222	AA465222	ESTs	1.6	TM
RC_AA521186	AA521186	ESTs	1.6	TM
RC_AA599622	AA599622	ESTs	1.6	other
AB002343	AB002343	Human mRNA for KIAA0345 gene complete cds	1.6	TM

FIGURE 7 (cont.)
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D14811	D14811	Human mRNA for KIAA0110 gene complete cds	1.6	other
D50840	D50840	Human mRNA for carboxide glucosyltransferase complete cds	1.6	TM
RC_D60866_f	D60866	Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA complete cds	1.6	other
RC_F03738_f	F03738	ESTs	1.6	other
H19378	H19378	ESTs	1.6	TM
RC_H95039	H95039	Homo sapiens KIAA0442 mRNA partial cds	1.6	other
J03904	J03904	NAD(P)H:menadiol oxidoreductase	1.6	other
A22599	A22599	Tumor protein p53 (Li-Fraumeni's syndrome)	1.6	?
M34079	M34079	PROBABLE 26S PROTEASE SUBUNIT TBP-1	1.6	other
M97856	M97856	Nuclear autoantigenic sperm protein (histone-binding)	1.6	other
RC_N26259	N26259	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (Paramecium tetraurum)	1.6	?
RC_M99014_s	M99014	Homo sapiens SOX22 protein (SOX22) mRNA complete cds	1.6	?
RC_N73865	N73865	ESTs Weakly similar to U0047 gene product (S. cerevisiae)	1.6	other
RC_R10720	R10720	EST	1.6	?
RC_R15743	R15743	EST	1.6	?
R70621	R70621	ESTs Highly similar to hypothetical protein 100K (R. norvegicus)	1.6	?
RC_T23820	T23820	Homo sapiens cyclin T2a mRNA complete cds	1.6	other
RC_T64937_s	T64937	Homo sapiens thyroid receptor interactor (TRIP3) mRNA 3' end of cds	1.6	?
U05237	U05237	Human fetal Aiz-50-reactive clone 1 (FAC1) mRNA complete cds	1.6	other
U09820	U09820	X-LINKED HELICASE II	1.6	other
U10323	U10323	Human nuclear factor NF-45 mRNA complete cds	1.6	TM
U12424_s	U12424	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	1.6	other
U59286	U59286	Homo sapiens interferon stimulated T-cell alpha chemotractor precursor mRNA complete cds	1.6	SS
U61145	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	1.6	other
U76992	U76992	Human Tat-SF1 mRNA complete cds	1.6	other
U90549	U90549	Human non-telomere chromosomal protein (NHC) mRNA complete cds	1.6	other
U90909	U90909	Human clone 23722 mRNA sequence	1.6	other
RC_V04898	V04898	ESTs	1.6	other
RC_W15528	W15528	ESTs	1.6	other
V06247_s	V06247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 (Mus musculus)	1.6	other
RC_W73820	W73820	ESTs	1.6	other
X53793	X53793	MULTIFUNCTIONAL PROTEIN ADE2	1.6	other
X58521	X58521	NUCLEAR PORE GLYCOPROTEIN P62	1.6	other
X99910	X99910	H. sapiens p63 mRNA for transmembrane protein	1.6	TM
X99029	X99029	H. sapiens mRNA for unknown protein expressed in macrophages	1.6	other
RC_Z36919	Z36919	ESTs	1.6	other
RC_AA041551	AA041551	ESTs	1.5	other
RC_AA056735	AA056735	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0079 (H. sapiens)	1.5	other
AA113913	AA113913	EST - AA113913	1.5	other
RC_AA133309	AA133309	EST	1.5	other
AA146888_s	AA146888	ESTs Highly similar to COATOMER ZETA SUBUNIT (Box tauros)	1.5	other
AA195179_s	AA195179	ESTs	1.5	other
RC_AA219699	AA219699	ESTs	1.5	other
RC_AA226922	AA226922	ESTs Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 (Mus musculus)	1.5	?
RC_AA232644_s	AA232644	Protein tyrosine phosphatase non-receptor type 4	1.5	other
RC_AA236672	AA236672	ESTs Weakly similar to DFST0 (H. sapiens)	1.5	?
RC_AA256492	AA256492	ESTs	1.5	other
RC_AA259492	AA259492	ESTs	1.5	other
RC_AA279757	AA279757	ESTs Weakly similar to similar to mouse MMR1 (C. elegans)	1.5	other
RC_AA293568	AA293568	ESTs	1.5	other
RC_AA309550	AA309550	ESTs	1.5	other
RC_AA400271	AA400271	ESTs Highly similar to CALCIUM-TRANSPORTING ATPASE 1 (Saccharomyces cerevisiae)	1.5	TM
RC_AA412528	AA412528	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH (R. norvegicus)	1.5	other
RC_AA433925	AA433925	ESTs	1.5	TM
RC_AA447970	AA447970	EST	1.5	TM
RC_AA476319	AA476319	ESTs	1.5	SS
RC_AA482014	AA482014	H. sapiens mRNA for centrin gene	1.5	other
RC_AA489085	AA489085	ESTs	1.5	other
RC_AA496257	AA496257	ESTs Weakly similar to DIPTEPTIDYL PEPTIDASE IV (H. sapiens)	1.5	other
RC_AA609738	AA609738	ESTs	1.5	other
RC_AA621580	AA621580	ESTs Highly similar to HYPOTHETICAL 66.5 KD PROTEIN IN ADE12-RAP1 INTERGENIC REGION (Saccharomyces cerevisiae)	1.5	other
D31764	D31764	Human mRNA for KIAA0054 gene complete cds	1.5	other

FIGURE 7 (cont.)

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D38521	D38521	Human mRNA for KIAA0077 gene partial cds	1.5	other
RC_D51177	D51177	ESTs	1.5	TM
D85418	D85418	Human mRNA for phosphatidylinositol-glycan-4-ase C (PIG-C) complete cds	1.5	TM
L18960	L18960	Eukaryotic translation initiation factor 4C (eIF-4C)	1.5	other
L33881	L33881	Protein kinase C iso	1.5	?
M31523	M31523	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	1.5	other
M63167	M63167	V-akt murine thymoma viral oncogene homolog 1	1.5	other
RC_N21978	N21978	ESTs	1.5	other
RC_N28101	N28101	ESTs Weakly similar to GPF-30 PROTEIN [C.elegans]	1.5	other
RC_N307055	N30705	ESTs	1.5	other
RC_N48677	N48677	ESTs	1.5	TM
RC_N52271	N52271	Homo sapiens LIM protein mRNA complete cds	1.5	other
RC_N54450_1	N54450	ESTs	1.5	?
RC_N67380	N67380	ESTs	1.5	TM
RC_N68640	N68640	ESTs	1.5	other
RC_N78717_3	N78717	H. sapiens mRNA for tracinin	1.5	?
RC_R07018	R07018	ESTs	1.5	other
RC_R87660	R87660	EST - RC_R87660	1.5	TM
RC_T10258	T10258	EST	1.5	?
RC_T98043	T98043	ESTs Moderately similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]	1.5	TM
HG884-HT884	TIGR - HG884-HT884	EST - HG884-HT884	1.5	?
U09564	U09564	Human serine kinase mRNA complete cds	1.5	other
U35451	U35451	Homo sapiens heterochromatin protein p25 mRNA complete cds	1.5	?
U41868	U41868	Oecyganostine kinase	1.5	other
U50939	U50939	Human amyloid precursor protein-binding protein 1 mRNA complete cds	1.5	other
U94836	U94836	Human ERROT 213-21 mRNA complete cds	1.5	other
V02806	V02806	Homo sapiens clone 24800 mRNA sequence	1.5	other
RC_W72138	W72138	Homo sapiens putative transcriptional repressor E2F-6 mRNA partial cds	1.5	other
RC_W93640	W93640	ESTs	1.5	other
RC_Z39211	Z39211	Homo sapiens GDP-L-Lucose pyrophosphorylase (GPP) mRNA complete cds	1.5	other
RC_Z39255_1	Z39255	ESTs	1.5	other
RC_AA025086	AA025086	ESTs	1.4	other
RC_AA057193	AA057193	ESTs	1.4	other
RC_AA085918	AA085918	H.sapiens HUNKI mRNA	1.4	other
RC_AA114250_5	AA114250	Homo sapiens mRNA for KIAA0512 protein complete cds	1.4	other
RC_AA135095	AA135095	Homo sapiens Sov-like transcriptional factor mRNA complete cds	1.4	other
RC_AA156542	AA156542	ESTs	1.4	other
RC_AA171839	AA171839	ESTs	1.4	other
RC_AA195515	AA195515	ESTs	1.4	TM
RC_AA235554	AA235554	ESTs	1.4	TM
RC_AA252943	AA252943	ESTs	1.4	other
RC_AA278755	AA278755	ESTs Weakly similar to [H] ALU SUBFAMILY SBT WARNING ENTRY [H] [H.sapiens]	1.4	other
RC_AA279091	AA279091	ESTs	1.4	other
AA285277	AA285277	Homo sapiens brain expressed ring finger protein mRNA complete cds	1.4	other
RC_AA287138	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus (Ventosphaera)]	1.4	other
RC_AA287879	AA287879	ESTs Highly similar to GTP-BINDING PROTEIN SARA [Mus musculus]	1.4	?
RC_AA292128	AA292128	ESTs	1.4	other
RC_AA400093	AA400093	ESTs Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRN2-4MR54 INTERGENIC REGION [Saccharomyces cerevisiae]	1.4	other
AA402937	AA402937	ESTs	1.4	other
RC_AA411882	AA411882	ESTs	1.4	other
RC_AA417895	AA417895	ESTs	1.4	SS
AA422160	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds	1.4	other
RC_AA425100	AA425100	ESTs	1.4	other
RC_AA449068	AA449068	ESTs	1.4	TM
AA452724	AA452724	Homo sapiens TFAR19 mRNA complete cds	1.4	other
RC_AA460246	AA460246	ESTs Weakly similar to similar to tyrosyl-RNA synthetase [C.elegans]	1.4	other
RC_AA460949	AA460949	ESTs	1.4	other
RC_AA467015	AA467015	Homo sapiens chromosome 19 contig R32469	1.4	?
A3004804	A3004804	Homo sapiens mRNA for POU-alpha partial cds	1.4	other
D38498_1	D38498	Human PM55 mRNA (yeast mismatch repair gene PMS1 homolog) partial cds (C-terminal region)	1.4	?
RC_D80921_3	D80921	Homo sapiens clone Z3965 mRNA sequence	1.4	other
RC_F04982	F04982	ESTs	1.4	other

FIGURE 7 (cont.)

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RC_F05983	P09963	ESTs	1.4	other
H59417_s	H59417	ESTs	1.4	other
RC_H53708_s	H53708	CLEAVAGE SIGNAL-1 PROTEIN	1.4	other
L06419	L06419	Lysyl hydroxylase	1.4	SS
M29580	M29580	Zinc finger protein 7 (KOK 4 clone HF.16)	1.4	other
M62810	M62810	Transcription factor 64-ka 1 (mitochondrial transcription factor 1-like)	1.4	other
RC_N23872	N23872	ESTs	1.4	other
RC_N28722	N28722	ESTs	1.4	other
RC_N64244	N64244	ESTs	1.4	TM
RC_N66569	N66569	ESTs	1.4	?
RC_N692393	N692393	EST	1.4	?
RC_R01243	R01243	ESTs	1.4	other
RC_R09196	R09196	ESTs Moderately similar to M-phase phosphoprotein 11 [H sapiens]	1.4	other
RC_R63925	R63925	ESTs	1.4	other
RC_R64660	R64660	ESTs	1.4	?
RC_T16228	T16228	ESTs	1.4	other
RC_T17440_s	T17440	ESTs	1.4	other
U07418	U07418	DNA mismatch repair protein MLH1	1.4	other
U12595	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds	1.4	other
U26727	U26727	Cyclin-dependent kinase inhibitor 2A (melanoma p16 inhibits CDK4)	1.4	TM
U84720	U84720	Human sapiens mRNA export protein (RAE1) mRNA complete cds	1.4	other
RC_W60473	W60473	ESTs	1.4	other
RC_W60146_s	W60146	ESTs	1.4	other
RC_W60379_s	W60379	H sapiens nak2 mRNA for protein kinase	1.4	other
RC_Z38501	Z38501	ESTs Weakly similar to PROBABLE ES PROTEIN [Human papillomavirus type 56]	1.4	other
RC_Z40041	Z40041	ESTs	1.4	other
RC_AA001386	AA001386	EST	1.3	other
RC_AA007234_s	AA007234	ESTs	1.3	other
RC_AA029264_s	AA029264	ESTs	1.3	other
RC_AA031357	AA031357	ESTs	1.3	other
RC_AA040696_s	AA040696	ESTs	1.3	other
RC_AA046619	AA046619	ESTs	1.3	other
RC_AA059051	AA059051	ESTs	1.3	other
AA059415	AA059415	ESTs Moderately similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!! [H sapiens]	1.3	other
AA063339	AA063339	ESTs	1.3	other
RC_AA068864	AA068864	ESTs	1.3	other
RC_AA101601	AA101601	ESTs Highly similar to Polo virus receptor protein [H sapiens]	1.3	other
RC_AA122394	AA122394	ESTs	1.3	other
RC_AA126428_s	AA126428	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	1.3	other
RC_AA132007_s	AA132007	Down-regulator of transcription 1 TBP-binding (negative cofactor 2)	1.3	other
AA156670_s	AA156670	Homo sapiens agrin precursor mRNA partial cds	1.3	SS
RC_AA206800	AA206800	ESTs Weakly similar to ZINC FINGER PROTEIN 135 [H sapiens]	1.3	TM
AA234817	AA234817	ESTs	1.3	other
RC_AA236200	AA236200	ESTs	1.3	other
RC_AA252079	AA252079	Homo sapiens mRNA for dachshund protein	1.3	other
RC_AA258189	AA258189	ESTs	1.3	other
RC_AA262889_s	AA262889	ESTs	1.3	other
RC_AA278650	AA278650	ESTs	1.3	other
AA329211_s	AA329211	Homo sapiens RRM RNA binding protein Gry-dp (GRY-RBP) mRNA complete cds	1.3	other
RC_AA336750	AA336750	ESTs	1.3	?
RC_AA339243	AA339243	ESTs Highly similar to RSP15 PROTEIN [Saccharomyces cerevisiae]	1.3	other
RC_AA400195	AA400195	ESTs	1.3	other
RC_AA417589_s	AA417589	ESTs	1.3	TM
RC_AA428992	AA428992	ESTs	1.3	other
RC_AA435536	AA435536	ESTs	1.3	other
RC_AA448294	AA448294	Homo sapiens putative transcriptional repressor E2F-6 mRNA partial cds	1.3	other
RC_AA449071	AA449071	ESTs	1.3	TM
AA458542	AA458542	Homo sapiens chromosome 19 cosmid R32469	1.3	other
RC_AA461189	AA461189	ESTs	1.3	other
RC_AA464428	AA464428	ESTs	1.3	other
RC_AA465093	AA465093	ESTs	1.3	other
RC_AA485424	AA485424	ESTs	1.3	other
RC_AA487492_s	AA487492	Homo sapiens clone 23592 mRNA sequence	1.3	other

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RC_AA504499	AA504499	ESTs Highly similar to probable chloride channel 3 (H sapiens)	1.3	other
RC_AA521471	AA521471	ESTs	1.3	other
RC_AA595956_s	AA595956	Human mRNA for KIAA0179 gene partial cds	1.3	other
RC_AA598675	AA598675	ESTs	1.3	other
RC_AA599718	AA599718	H sapiens mRNA for transin associated protein X	1.3	other
RC_D11718	D11718	ESTs	1.3	?
D87466	D87466	Human mRNA for KIAA0276 gene partial cds	1.3	other
RC_F13663	F13663	ESTs	1.3	other
RC_H26417	H26417	ESTs	1.3	other
RC_H38086	H38086	Human N-ethylmaleimide-sensitive factor mRNA partial cds	1.3	other
RC_H38828_s	H38828	H sapiens RBQ-1 mRNA	1.3	other
RC_H50061	H50061	ESTs Moderately similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!! (H sapiens)	1.3	other
RC_H71863_s	H71863	Zinc finger protein 139 (clone pHZ-37)	1.3	other
RC_H83438_s	H83438	Homo sapiens mRNA for DOB1beta protein complete cds	1.3	other
M64629	M64629	Fruzen phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	1.3	other
M95767	M95767	DI-N-ACETYLCHITOBINASE PRECURSOR	1.3	SS
RC_N20630_J	N20630	ESTs	1.3	other
RC_N24732	N24732	ESTs	1.3	other
RC_N51855	N51855	ESTs Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D melanogaster]	1.3	other
RC_R49896	R49896	ESTs	1.3	SS
RC_T23932_J	T23932	ESTs	1.3	other
RC_T420707	T420707	ESTs	1.3	other
RC_T59859	T59859	ESTs	1.3	other
RC_T64438	T64438	ESTs Weakly similar to CO1A2.4 (C. elegans)	1.3	TM
T68510	T68510	ESTs	1.3	other
RC_T95581	T95581	ESTs	1.3	other
U05580	U05580	Human protein tyrosine kinase mRNA complete cds	1.3	other
U28686	U28686	Human putative RNA binding protein RNPL1 mRNA complete cds	1.3	other
U66561	U66561	Human knuppel-related zinc finger protein (ZNF164) mRNA partial cds	1.3	other
U96113	U96113	EST - U96113	1.3	other
RC_V52005_J	V52005	Homo sapiens mRNA for KIAA0539 protein complete cds	1.3	?
RC_V67524	V67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	1.3	TM
RC_V66576	V66576	ESTs	1.3	other
X59398	X59398	CD47 antigen (Rb-related antigen integrin-associated signal transducer)	1.3	SS, TM
X97544	X97544	H sapiens mRNA for TIM17 preprotein translocase	1.3	TM
RC_Z41963_J	Z41963	Homo sapiens HP protein (HP) mRNA complete cds	1.3	?
Z46629	Z46629	SRY (sex-determining region Y)-box 9 (compensable dysplasia autosomal sex-reversal)	1.3	other
RC_AA010188	AA010188	ESTs	1.2	other
RC_AA025746	AA025746	ESTs	1.2	other
AA112222	AA112222	EST - AA112222	1.2	other
AA147543	AA147543	ESTs	1.2	SS
AA355201	AA355201	ESTs	1.2	SS, TM
RC_AA398222	AA398222	ESTs	1.2	other
RC_AA411708	AA411708	Homo sapiens clone 23685 mRNA sequence	1.2	other
RC_AA433843	AA433843	ESTs Highly similar to SCS RIBOSOMAL PROTEIN L13 [Mycobacterium leprae]	1.2	other
RC_AA464758	AA464758	ESTs	1.2	other
RC_H05635	H05635	ESTs	1.2	TM
L38961	L38961	Integrin transmembrane protein 1	1.2	TM
N42440	N42440	ESTs Weakly similar to hcrRNA-binding protein M4 (H sapiens)	1.2	other
RC_N55304_s	N55304	ESTs	1.2	other
RC_N67104	N67104	ESTs	1.2	other
RC_N68622	N68622	ESTs Highly similar to HYPOTHETICAL 27.5 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION [Saccharomyces cerevisiae]	1.2	other
RC_N71027	N71027	ESTs	1.2	other
RC_N74835	N74835	ESTs	1.2	other
RC_R62444	R62444	ESTs	1.2	other
RC_T17489	T17489	ESTs	1.2	TM
RC_T32794_s	T32794	ESTs	1.2	other
RC_T85190	T85190	EST - RC_T85190	1.2	?
RC_T89364	T89364	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! (H sapiens)	1.2	other
U02040	U02040	COAATenhancer binding protein (CIEBP) gamma	1.2	other
U51698	U51698	ESTs	1.2	?
U79718	U79718	Human endonuclease III homolog mRNA complete cds	1.2	other
W03007	W03007	ESTs	1.2	other

FIGURE 7 (cont.)

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RC_W61011	W61011	ESTs	1,2	other
RC_W97544	W97544	ESTs	1,2	other
X02751	X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	1,2	?
Z14077.1	Z14077	YY1 transcription factor	1,2	other
RC_Z38939	Z38939	ESTs	1,2	?

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Title	Accession	PROBESET	EST count	EST total
fibronectin 1	T78889	RC_T78889_s	3.1	44.4
ESTs	AA393803	RC_AA393803	3.9	24.6
Human heart mRNA for heat shock protein 9; partial cds	H88540	RC_H88540	2.8	22.0
ESTs	W31478	RC_W31478_s	1.5	20.8
ESTs; Weakly similar to (define not available 4454131) [D.melanogaster]	W79424	RC_W79424_s	1.8	19.7
Homo sapiens RGS-GAP interacting protein GIPC mRNA; complete cds	AA149940	RC_AA149940	1.2	17.5
collagen, type I; alpha 2	J03464	J03464_s	8.7	17.3
Homo sapiens mRNA for actin-related protein; complete cds	W48638	RC_W48638	3.0	17.3
MYOSIN REGULATORY LIGHT CHAIN 2; NONSARCOMERIC	W92462	RC_W92462	1.1	16.1
ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]	D63079	D63079_s	1.9	15.9
ESTs	AA255874	RC_AA255874	1.7	15.8
fibronectin 1	X02781	X02781	3.6	15.2
TFAR19 novel apoptosis-related gene	R71082	RC_R71082_s	2.5	15.2
ESTs; Highly similar to FRIZZLED PROTEIN PRECURSOR [Drosophila melanogaster]	AA449749	RC_AA449749	10.8	14.7
ESTs	AA243721	RC_AA243721	1.5	14.0
Homo sapiens mRNA for KIAA886 protein; complete cds	AA600169	RC_AA600169	1.2	13.9
ESTs	AA182001	RC_AA182001_i	1.2	13.8
dihydropyrimidinase-like 2	T10322	RC_T10322	0.8	13.5
ESTs	M97935	AFFX-HUMISGF3A/M97935_3	2.3	13.5
lactate dehydrogenase B	AA186897	RC_AA186897	4.5	13.5
ESTs; Weakly similar to SAS [H.sapiens]	T16206	RC_T16206_i	0.6	13.1
ESTs	AA365742	AA365742_s	3.2	13.0
ESTs; Highly similar to GALECTIN-1 [Homo sapiens]	AA621274	RC_AA621274_i	1.1	12.8
H.sapiens gene from PAC 295C6; similar to rat PO44	H25999	RC_H25999_s	2.5	12.7
Human CCAAT-box-binding factor (CBF) mRNA; complete cds	AA281132	RC_AA281132	1.9	12.6
ESTs; Moderately similar to 25E8 [D.melanogaster]	T47491	RC_T47491	1.4	12.3
ESTs; Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-25 KD [Bos taurus]	W79421	RC_W79421	1.2	12.0
ESTs	H78385	RC_H78385_s	1.7	11.7
desmoplakin (DPI; DPL)	F13673	RC_F13673	14.8	11.5
immunoglobulin gamma 3 (Gm marker)	AA247685	AA247685	4.3	11.5
Pantophysin [human; keratinocyte line HaCaT; mRNA; 216 nt]	H64493	RC_H64493_f	1.6	11.4
ESTs	R72029	RC_R72029_f	1.4	11.4
ESTs	D79891	D79891	2.7	11.4
ESTs	AA167393	RC_AA167393_s	2.0	11.3
Human transcriptional coactivator PC4 mRNA; complete cds	D57317	RC_D57317	1.9	11.2
ESTs	N67607	RC_N67607	1.3	11.2
neurotrophic tyrosine kinase; receptor-related 1	C15347	RC_C15347	1.2	11.2
ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UBP5-SPT15 INTERGENIC REGION [Saccharomyces cerevisiae]	AA027086	RC_AA027086	2.3	11.2
ESTs; Weakly similar to EBNA-2 NUCLEAR PROTEIN [Human herpesvirus 4 (strain b95-8)]	AA598781	RC_AA598781	4.0	11.2
Homo sapiens actin-related protein Arp2 (ARP2) mRNA; complete cds	C16379	C16379	1.5	11.1

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tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; eta polypeptide	H69844	RC_H69844_s	1.5	11.1
Homo sapiens mRNA for DCRA; complete cds	R97540	RC_R97540_f	1.0	11.1
Homo sapiens chaperonin containing t-complex polypeptide 1; beta subunit (Cctb) mRNA; complete cds	AA488991	RC_AA488991_s	1.5	10.9
Homo sapiens actin-related protein Arp2 (ARP2) mRNA; complete cds	AF006082	AF006082	1.6	10.9
ESTs	T23457	RC_T23457	3.7	10.8
Human (clone E5.1) RNA-binding protein mRNA; complete cds	T33593	RC_T33593_s	2.0	10.8
Homo sapiens clone 24416 mRNA sequence	AA417761	RC_AA417761	1.4	10.7
ESTs	N39152	RC_N39152	1.5	10.7
ESTs	AA429539	AA429539_f	1.8	10.7
ESTs	T30617	T30617	1.1	10.6
small inducible cytokine A5 (RANTES)	AA486072	RC_AA486072_i	1.4	10.6
ESTs	R79392	RC_R79392	3.3	10.5
calumenin	AA477316	RC_AA477316	2.8	10.5
ESTs	R54421	RC_R54421_s	1.4	10.4
UDP-N-acetylglucosamine pyrophosphorylase 1; Sperm associated antigen 2	AA447549	RC_AA447549	1.9	10.3
Homo sapiens HRIH-FB2115 mRNA; partial cds	H11320	RC_H11320_s	2.0	10.3
ESTs; Moderately similar to putative G-binding protein [H.sapiens]	H94877	RC_H94877	1.8	10.2
protein kinase; cAMP-dependent; catalytic; alpha	H89514	RC_H89514_s	1.0	10.2
ESTs	F10354	RC_F10354_f	1.0	10.1
ESTs	AA173981	RC_AA173981	1.2	10.0
zn13e4.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547326 5' similar to gb:J2683 ADP.ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (HUMAN); mRNA sequence	AA084874	AA084874_f	0.9	10.0
ESTs; Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]	AA452161	RC_AA452161	1.8	9.9
ESTs	N93521	RC_N93521	1.5	9.9
small inducible cytokine A5 (RANTES)	M21121	M21121_s	0.9	9.9
ESTs	AA490112	RC_AA490112_s	2.1	9.9
ESTs; Highly similar to HYPOTHETICAL 16.3 KD PROTEIN IN DURI1.2-NGR1 INTERGENIC REGION [Saccharomyces cerevisiae]	AA053139	RC_AA053139	3.2	9.7
ESTs	AA448461	RC_AA448461	1.1	9.7
C-terminal binding protein 2	N50048	RC_N50048	2.1	9.7
Homo sapiens mRNA for putative progesterone binding protein	N66130	RC_N66130	1.4	9.6
ESTs	AA490341	RC_AA490341_s	1.4	9.5
transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)	R38044	RC_R38044_f	9.4	9.4
ESTs; Highly similar to (define not available 468665) [H.sapiens]	W73805	W73805	1.2	9.4
cathepsin B	AA608751	RC_AA608751_i	2.1	9.3
ESTs; Highly similar to heat shock factor binding protein 1 HSBP1 [H.sapiens]	D59525	RC_D59525_f	1.8	9.3
ESTs	AA280409	RC_AA280409_s	2.1	9.3
ESTs; Weakly similar to similar to yeast adenylate cyclase [H.sapiens]	N77542	N77542	1.6	9.2
ESTs	D60296	RC_D60296	1.7	9.2
ESTs; Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	Z39349	RC_Z39349	1.6	9.2
solute carrier family 12 (sodium/potassium/chloride transporters); member 2	AA262080	RC_AA262080	1.4	9.2
iduronate 2-sulfatase (Hunter syndrome)	H14810	RC_H14810_s	1.0	9.1

FIGURE 8
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ESTs	T90531	RC_T90531	1.5	9.1
ESTs	Z40959	RC_Z40959_f	1.0	8.9
collagen-binding protein 2 (collagen 2)	H27188	RC_H27188_f	2.6	8.9
HMT1 (hnRNP methyltransferase; <i>S. cerevisiae</i>)-like 1	T81393	RC_T81393_s	1.8	8.8
Homo sapiens lysophospholipase (LPL1) mRNA; complete cds	AA252436	AA252436	1.6	8.8
Homo sapiens TACC1 (TACC1) mRNA; complete cds	N46837	RC_N46837	2.4	8.7
ESTs	AA122386	RC_AA122386	6.6	8.7
ESTs; Highly similar to LEUCYL-TRNA SYNTHETASE; CYTOPLASMIC [<i>Saccharomyces cerevisiae</i>]	R32993	R32993_s	1.6	8.6
NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 6 (17kD; B17)	C16329	C16329	0.9	8.6
ESTs; Weakly similar to transporter protein [H.sapiens]	R80048	R80048	1.2	8.5
ESTs	AA102644	RC_AA102644	1.8	8.5
ESTs; Weakly similar to (define not available 4234) [D.melanogaster]	AA393805	RC_AA393805	1.1	8.4
ESTs; Weakly similar to putative Rab5-interacting protein (clone L1-94) [H.sapiens]	H68794	RC_H68794	1.5	8.4
ESTs	AA399445	RC_AA399445	0.9	8.4
Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) mRNA; complete cds	AF006088	AF006088	1.5	8.3
ESTs	AA278329	RC_AA278329_f	3.1	8.3
ESTs	AA187490	RC_AA187490	3.6	8.3
ESTs	N90933	RC_N90933	1.0	8.2
ESTs	D31058	D31058_s	2.1	8.2
ESTs; Weakly similar to predicted using GeneFinder [C.elegans]	T67053	RC_T67053_f	1.2	8.2
epithelial membrane protein 2	T88721	RC_T88721_s	1.3	8.2
Homo sapiens actin-related protein Arp3 (ARP3) mRNA; complete cds	AF006083	AF006083	1.8	8.1
ESTs	AA040923	RC_AA040923	1.8	8.1
INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN	AA161292	RC_AA161292_s	1.5	8.0
ESTs	W85875	RC_W85875	0.9	8.0
Human mRNA for KIAA336 gene; complete cds	AA608903	RC_AA608903	1.4	7.9
ESTs; Moderately similar to KIAA438 [H.sapiens]	H81379	RC_H81379_s	1.3	7.9
H. sapiens cDNA for RFG	AA194075	RC_AA194075_f	0.4	7.9
ESTs; Weakly similar to cDNA EST EMBL:T1157 comes from this gene [C.elegans]	N67312	RC_N67312	1.7	7.9
Fibronectin, Alt. Splice 1	M10098	AFFX-HUMRGE/M10098_5	1.1	7.9
cytochrome c oxidase subunit VII-related protein	HG3044-HT3742	HG3044-HT3742	3.0	7.8
CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	AA025213	RC_AA025213	1.3	7.8
ESTs; Weakly similar to neural differentiation-associated protein [M.musculus]	W67577	RC_W67577_s	1.2	7.8
ESTs	AA233342	RC_AA233342	3.8	7.7
ESTs	AA291159	RC_AA291159_f	0.7	7.7
ESTs	N63604	RC_N63604	3.6	7.7
HEAT SHOCK 7 KD PROTEIN 1	T66307	RC_T66307_f	1.3	7.6
Human DNA sequence from clone 3M3 on chromosome 6p22.1-22.3. Contains three novel genes; one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant; worm; yeast and archaea bacterial genes; and the first exon of the KIAA319 gene. Contains E	AA243497	RC_AA243497	1.7	7.6
Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT)	AA600134	RC_AA600134	1.7	7.6
ESTs	H61476	RC_H61476_s	1.6	7.6
transforming growth factor; beta receptor II (7-8kD)	H90886	RC_H90886_s	0.8	7.6

FIGURE 8
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ESTs; Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]	AA449320	RC_AA449320	1.0	7.5
ESTs; Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]	N48787	RC_N48787	1.9	7.5
Homo sapiens heterogeneous nuclear ribonucleoprotein R mRNA; complete cds	C16574	C16574	1.7	7.5
Homo sapiens mRNA for CMP-sialic acid transporter; complete cds	AA481542	RC_AA481542_s	1.2	7.5
ESTs; Weakly similar to F15D4.3 [C.elegans]	N89563	N89563_s	2.0	7.5
ESTs	AA490282	RC_AA490282	2.9	7.5
ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	AA621349	RC_AA621349	1.3	7.5
ESTs; Highly similar to (define not available 412715) [H.sapiens]	C01782	C01782	1.9	7.4
ESTs	AA402492	RC_AA402492	1.7	7.4
ESTs; Weakly similar to C17H11.6 [C.elegans]	AFEX-M27830	AFEX-M27830_s	0.5	7.4
ESTs	AA194237	RC_AA194237	1.7	7.4
ESTs	H10933	RC_H10933	4.6	7.4
Human spliceosomal protein (SAP 49) gene; complete cds	AA463934	RC_AA463934	1.6	7.3
Human mRNA for KIAA174 gene; complete cds	R16097	RC_R16097_s	1.2	7.2
ESTs	AA128486	RC_AA128486	1.5	7.2
ESTs; Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN AT51-TPD3 INTERGENIC REGION [Saccharomyces cerevisiae]	R59694	RC_R59694_s	1.4	7.1
ESTs	AA428090	AA428090	7.0	7.0
ESTs	H88486	RC_H88486_f	1.5	7.0
ESTs; Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT [Canis familiaris; Mus musculus]	D79052	D79052_s	3.1	7.0
C-terminal binding protein 2	AA417287	RC_AA417287	2.8	7.0
protein kinase; mitogen-activated 6 (extracellular signal-regulated kinase; p97)	T32837	RC_T32837_s	1.1	6.9
tumor rejection antigen (gp96) 1	D51235	RC_D51235_f	1.2	6.9
ESTs; Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]	F04258	RC_F04258_s	3.3	6.9
Human mRNA for KIAA35 gene; partial cds	D51272	RC_D51272_s	3.2	6.9
Homo sapiens mRNA from chromosome 5q31-33 region	T99196	RC_T99196_s	1.4	6.9
H.sapiens mRNA for serine palmitoyltransferase; subunit I	T39740	T39740_s	1.3	6.9
Homo sapiens calcium binding protein (ALG-2) mRNA; complete cds	AA122332	RC_AA122332	1.7	6.9
ESTs	T92245	RC_T92245_i	0.9	6.9
ESTs	F01813	RC_F01813_s	3.1	6.9
ESTs; Highly similar to putative Rab5-interacting protein (clone L1-37) [H.sapiens]	AA292533	RC_AA292533	1.3	6.9
ESTs; Moderately similar to POSSIBLE DNA-REPAIR PROTEIN XP-E [Cercopithecus aethiops]	AA287961	RC_AA287961	1.6	6.8
ESTs	AA053883	RC_AA053883	0.7	6.8
peptidylprolyl isomerase B (cyclophilin B)	H96655	RC_H96655_s	2.2	6.8
connective tissue growth factor	AA449789	RC_AA449789_f	1.9	6.8
Homo sapiens exportin t mRNA; complete cds	H99877	RC_H99877	4.0	6.8
ESTs; Weakly similar to Ydr372cp [S.cerevisiae]	AA191014	RC_AA191014	1.7	6.8
ESTs; Highly similar to (define not available 4426952) [H.sapiens]	H82061	RC_H82061	1.2	6.8
ESTs	AA433947	RC_AA433947	1.8	6.8
ESTs	AA236280	RC_AA236280	1.5	6.8
ESTs	AA521303	RC_AA521303	0.8	6.7
ESTs; Highly similar to DTPD-4-DEHYDRORHAMNOSE REDUCTASE [Salmonella typhimurium]	W94289	RC_W94289	1.1	6.7
N-acetylglucosaminyl transferase component Gpi1				

FIGURE 8
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proteasome (prosome; macropain) 26S subunit; non-ATPase; 1	AA460532	RC_AA460532	1.5	6.6
ESTs	AA398197	RC_AA398197	1.9	6.6
cytochrome c oxidase subunit IV	AA236361	RC_AA236361	1.2	6.6
Thymosin; beta 1	T59181	RC_T59161_s	2.6	6.6
Homo sapiens mRNA for KIAA733 protein; partial cds	H88033	H88033_s	1.2	6.6
ESTs	H86543	RC_H86543_f	1.8	6.6
glucan (1,4-alpha-); branching enzyme 1 (glycogen branching enzyme; Andersen disease; glycogen storage disease type IV)	H71861	RC_H71861_s	0.9	6.6
ESTs	T95333	RC_T95333	5.3	6.6
ESTs; Moderately similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens]	AA425447	RC_AA425447	1.7	6.6
Homo sapiens GA17 protein mRNA; complete cds	AA147725	RC_AA147725	2.5	6.5
lactate dehydrogenase A	AA112012	RC_AA112012_s	2.0	6.5
ESTs	AA621159	RC_AA621159	1.8	6.5
ESTs; Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	AA429228	AA429228	1.6	6.5
collagen; type I; alpha 2	Z74616	Z74616	9.9	6.5
ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	AA608668	RC_AA608668	1.0	6.5
ESTs	N93155	RC_N93155_j	1.8	6.5
ESTs	D51401	RC_D51401_s	1.4	6.3
Homo sapiens mRNA for KIAA96 protein; partial cds	AA250870	AA250870_s	2.3	6.3
ESTs	AA429636	RC_AA429636	0.9	6.3
ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	H73484	RC_H73484_s	1.3	6.3
ESTs	AA488091	RC_AA488091	1.4	6.3
ESTs; Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]	H84891	RC_H84891_j	1.1	6.3
ESTs	AA001049	RC_AA001049	1.1	6.3
ESTs; Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	N20066	RC_N20066	1.2	6.2
ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1 [Canis familiaris]	AA428870	RC_AA428870	1.8	6.2
ESTs	W16836	RC_W16836_s	2.2	6.2
ESTs	H07873	RC_H07873	1.2	6.2
ESTs	W58619	RC_W58619	1.7	6.2
Homo sapiens mRNA for KIAA737 protein; complete cds	N66219	RC_N66219	1.3	6.2
bone morphogenetic protein 6	AA092596	AA092596	1.1	6.2
Homo sapiens DNA from chromosome 19-cosmid R3879 containing USF2; genomic sequence	R36881	RC_R36881_s	1.5	6.2
ESTs	AA179387	RC_AA179387	4.0	6.1
ESTs; Moderately similar to fibronectin [H.sapiens]	AA279397	RC_AA279397	1.3	6.1
ESTs; Highly similar to MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE [Xenopus laevis]	T96374	RC_T96374	0.8	6.1
ESTs	AA465194	RC_AA465194	1.7	6.1
Human amino acid transport-related protein mRNA; complete cds	AA152418	RC_AA152418	1.1	6.1
ESTs	AA447971	RC_AA447971	5.1	6.1
ESTs	V28419	RC_V28419_f	0.9	6.1
ESTs	AA111889	RC_AA111889	1.5	6.1
pigment epithelium-derived factor	W42508	RC_W42508	1.1	6.1
ESTs	N91023	RC_N91023	3.3	6.1
ESTs	AA186666	RC_AA186666	2.4	6.0
membrane fatty acid (lipid) desaturase				

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collagen, type I, alpha 2	H88574	RC_H88674_s	3.0	6.0
Homo sapiens 3-phosphoglycerate dehydrogenase mRNA; complete cds	T83646	RC_T83646	0.9	6.0
HMT1 (hnRNP methyltransferase; S. cerevisiae)-like 2	V46810	RC_V46810_s	3.2	5.9
LYMPHOCYTE-SPECIFIC PROTEIN LSP1	T49291	RC_T49291_s	1.0	5.9
Homo sapiens secreted cement gland protein XAG-2 homolog (hAG-2/R) mRNA; complete cds	AA421562	RC_AA421562	1.3	5.9
Homo sapiens clone 23956 mRNA; partial cds	W69452	RC_W69452	1.1	5.9
ESTs; Moderately similar to Similar to S.cerevisiae hypothetical protein L3111 [H.sapiens]	N79531	RC_N79531_s	3.1	5.9
ESTs	AA406163	RC_AA406163	1.1	5.9
ESTs	AA454157	RC_AA454157	1.2	5.9
Homo sapiens clone 2394 mRNA sequence	AA609773	RC_AA609773	5.5	5.9
ESTs	AA156897	AA156897_s	3.7	5.8
Homo sapiens insulin induced protein 1 (INSIG1) gene; complete cds	AA021623	RC_AA021623_s	1.1	5.8
biliverdin reductase A	D51072	RC_D51072_s	1.8	5.8
ESTs; Weakly similar to hypothetical protein [H.sapiens]	T97257	RC_T97257_f	1.4	5.8
quinoid dihydropteridine reductase	T69009	RC_T69009_s	0.5	5.8
ESTs	AA489459	RC_AA489459	1.1	5.7
ESTs; Highly similar to follistatin-related protein [H.sapiens]	D51110	RC_D51110_s	2.1	5.7
ESTs	AA452855	RC_AA452855	2.0	5.7
ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	AA442125	RC_AA442125	1.3	5.7
cell division cycle 42 (GTP-binding protein; 25kD)	N63172	RC_N63172	2.1	5.7
ESTs; Highly similar to EUKARYOTIC INITIATION FACTOR 4 GAMMA [Oryctolagus cuniculus]	W84870	RC_W84870_s	1.2	5.7
ESTs	AA121121	RC_AA121121	1.3	5.7
ESTs	AA436027	RC_AA436027	1.9	5.7
ESTs; Moderately similar to HN1 [M.musculus]	AA441923	RC_AA441923	5.6	5.7
ESTs	AA460049	AA460049_s	1.2	5.7
ESTs; Weakly similar to brain-specific L-proline transporter	AA181911	RC_AA181911	0.7	5.6
ESTs	AA053962	RC_AA053962	1.2	5.6
ESTs	AA453783	RC_AA453783_s	3.7	5.6
ESTs	N32811	RC_N32811	1.8	5.6
Human transposon-like element mRNA	M23161	M23161	0.8	5.6
ESTs	AA485655	RC_AA485655	2.3	5.6
ESTs; Weakly similar to (define not available 446577) [H.sapiens]	Z41803	RC_Z41803	1.1	5.6
Homo sapiens short form transcription factor C-MAF (c-maf) mRNA; complete cds	AA496914	RC_AA496914	0.8	5.6
glioblastoma amplified sequence	AA095021	AA095021	1.0	5.6
karyopherin alpha 1 (importin alpha 5)	N35247	RC_N35247	1.2	5.6
Human mRNA for KIAA69 gene; partial cds	AA148318	RC_AA148318_s	2.3	5.6
Homo sapiens clone Z3675 mRNA sequence	Z39978	RC_Z39978	1.1	5.6
ESTs	H73161	RC_H73161_f	1.2	5.6
Homo sapiens clone Z3585 mRNA sequence	AA453461	RC_AA453461	1.6	5.5
ESTs	H98153	RC_H98153	7.0	5.5
desmoplakin (DPI; DPII)	H90899	RC_H90899	5.4	5.5
sterol regulatory element binding transcription factor 2	AA053886	RC_AA053886_s	1.2	5.5
ESTs; Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]	AA134138	RC_AA134138	1.4	5.5

FIGURE 8
(Cont.)

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ESTs; Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus]	AA082057	RC_AA082057	1.1	5.5
ESTs; Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMA4-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]	AA609710	RC_AA609710	5.5	5.5
heterogeneous nuclear ribonucleoprotein A1	AA416785	RC_AA416785_f	2.2	5.5
Human Chromosome 16 BAC clone CIT987SK-A-362G6	U95740	U95740_nna1	0.9	5.5
Homo sapiens Arp2/3 protein complex subunit p21-Arc (ARPC21) mRNA; complete cds	AF006086	AF006086	1.4	5.4
ESTs	AA478387	RC_AA478387	1.0	5.4
Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA; complete cds	AA455970	RC_AA455970	1.8	5.4
ESTs; Weakly similar to NIPSNAP2 protein [H.sapiens]	R49052	RC_R49052	1.3	5.4
ESTs	AA235803	RC_AA235803_i	2.5	5.4
ESTs	T15482	RC_T15482_f	0.7	5.4
NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 3 (12kD; B12)	AA040759	RC_AA040759_s	1.0	5.4
Human mRNA for KIAA263 gene; complete cds	T16989	RC_T16989_f	1.2	5.4
ESTs	R27975	RC_R27975	1.2	5.4
ESTs; Moderately similar to (define not available 445515) [H.sapiens]	AA047187	RC_AA047187	0.8	5.4
ESTs	W45417	RC_W45417	1.0	5.4
ESTs; Weakly similar to zinc finger protein [H.sapiens]	AA487297	RC_AA487297	1.6	5.4
ESTs	M27830	AFFX-M27830_5	0.6	5.4
ESTs	AA258614	RC_AA258614_s	2.0	5.3
ESTs; Weakly similar to cDNA EST EMBL:T1157 comes from this gene [C.elegans]	AA313414	AA313414_s	1.5	5.3
secreted frizzled-related protein 4	AA291725	RC_AA291725	5.3	5.3
ESTs	AA282179	RC_AA282179	0.9	5.3
Human pim-2 protooncogene homolog pim-2h mRNA; complete cds	AA227480	RC_AA227480_s	0.8	5.3
ESTs; Weakly similar to ORF YOR126c [S.cerevisiae]	AA249311	AA249311	1.4	5.3
ESTs	W36290	W36290_s	1.7	5.3
Homo sapiens hJTB mRNA; complete cds	AA071387	AA071387	1.7	5.3
Homo sapiens mRNA for putative vacuolar proton ATPase membrane sector associated protein M8-9	D51241	RC_D51241_s	2.2	5.3
ESTs	T92735	RC_T92735	1.7	5.3
splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated)	T64923	RC_T64923_f	1.2	5.3
ESTs	W20404	RC_W20404_s	1.1	5.2
high-mobility group (nonhistone chromosomal) protein 1	AA486201	RC_AA486201_s	1.1	5.2
ESTs	T15386	RC_T15386	0.9	5.2
ESTs	AA608657	RC_AA608657_f	2.1	5.2
ESTs	AA236276	RC_AA236276	1.4	5.2
ESTs; Weakly similar to cDNA EST EMBL:T1585 comes from this gene [C.elegans]	AA598439	RC_AA598439	1.4	5.2
ubiquitin-specific protease 1	D62657	RC_D62657	0.5	5.2
ESTs	AA419507	AA419507	1.0	5.2
ESTs	AA496962	RC_AA496962	0.9	5.2
Homo sapiens clone 23596 mRNA sequence	AA425741	RC_AA425741	0.7	5.2
Homo sapiens clone 23714 mRNA sequence	AA147364	RC_AA147364	0.9	5.2
ESTs; Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Z21420	Z21420	1.3	5.2

FIGURE 8
(Cont.)

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ESTs	T15434	RC_T15434_s	0.9	5.1
ESTs	W95416	RC_W95416	1.1	5.1
Homo sapiens clone 23675 mRNA sequence	AA018804	AA018804	2.9	5.1
Homo sapiens mRNA for KIAA447 protein; complete cds	C02016	C02016	1.4	5.1
apolipoprotein H (beta-2-glycoprotein I)	T83356	RC_T83356_s	0.3	5.1
ESTs; Moderately similar to weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [C.elegans]	D31544	D31544_s	3.2	5.1
Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA; complete cds	AF010193	AF010193	1.0	5.1
ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	AA155779	RC_AA155779	1.7	5.1
ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L26 [Homo sapiens; Mus musculus]	D80128	RC_D80128_f	1.6	5.1
ESTs	AA018907	RC_AA018907_s	2.0	5.1
immunoglobulin gamma 3 (Gm marker)	J00231	J00231_f	1.4	5.1
ESTs	N81162	N81162	2.0	5.1
ESTs	AA598850	RC_AA598850	1.3	5.1
ESTs	AA460935	RC_AA460935	1.8	5.0
ESTs; Highly similar to heat shock factor binding protein 1 HSBP1 [H.sapiens]	AA490864	RC_AA490864	1.4	5.0
ESTs	W80516	W80516	1.0	5.0
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA046939	RC_AA046939_s	1.2	5.0
Human DNA sequence from clone 149A16 on chromosome 22q12-13. Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene; the RFPL3 and RFPL3S genes for Rat finger protein-like 3 and Rat finger protein-like 3 antisense respectively; a gene for a novel imm	AA151882	RC_AA151882	1.4	5.0
ESTs	T72867	RC_T72867	1.2	5.0
myosin VI	AB002387	AB002387	4.5	5.0
GM2 ganglioside activator protein	AA167512	RC_AA167512	1.3	5.0
ESTs; Moderately similar to putative p15 [H.sapiens]	AA481060	RC_AA481060	1.3	5.0
ESTs	N69086	RC_N69086	1.5	5.0
ESTs; Highly similar to heat shock factor binding protein 1 HSBP1 [H.sapiens]	C14243	RC_C14243_f	1.7	5.0
neuroblastoma RAS viral (v-ras) oncogene homolog	AA431977	RC_AA431977	1.4	5.0
Homo sapiens mRNA for putative vacuolar proton ATPase membrane sector associated protein M5-9	R25326	R25326	0.9	5.0
butyrate response factor 1 (EGF-response factor 1)	H40424	RC_H40424_s	1.4	5.0
H factor (complement)-like 1	AA235873	RC_AA235873_s	0.6	5.0
ESTs; Weakly similar to predicted using Genefinder [C.elegans]	AA252040	RC_AA252040	1.5	5.0
ESTs	R62589	RC_R62589_f	1.2	5.0
Human mRNA for KIAA171 gene; complete cds	AA028889	RC_AA028889_s	1.1	5.0
ESTs; Highly similar to G protein-coupled receptor kinase 6; splice variant B [H.sapiens]	AA040699	RC_AA040699	1.0	4.9
ESTs; Highly similar to (define not available 45813) [H.sapiens]	AA488414	RC_AA488414	1.2	4.9
CYTOCHROME C	M22877	M22877	0.8	4.9
ESTs; Highly similar to synapsin I [R.norvegicus]	T15663	RC_T15663_s	0.8	4.9
lysosome (renal amyloidosis)	J03801	J03801_f	0.9	4.9
ESTs	W88642	RC_W88642	1.0	4.9
ESTs	W57813	RC_W57813_f	0.8	4.9
ESTs	AA046405	RC_AA046405	1.6	4.9
Homo sapiens metalloprotease 1 (MP1) mRNA; complete cds	AA132969	RC_AA132969_s	2.0	4.9

FIGURE 8
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Homo sapiens mRNA for KIAA829 protein; partial cds	H01766	H01766_s	1.3	4.9
ESTs; Weakly similar to synapse associated protein sap47-2 [D.melanogaster]	N51752	RC_N51752	2.5	4.9
secreted phosphoprotein 1 (osteopontin; bone sialoprotein I; early T-lymphocyte activation 1)	U20758	U20758_ma1	1.9	4.9
ESTs	AA263085	RC_AA263085_s	0.6	4.9
ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	M23114	M23114	2.0	4.9
Deleted in oral cancer-1	AA600140	RC_AA600140	2.4	4.9
ESTs	W88755	RC_W88755	1.3	4.8
synuclein; alpha (non A4 component of amyloid precursor)	C13990	RC_C13990_f	0.6	4.8
ESTs; Weakly similar to KIAA638 protein [H.sapiens]	R73882	R73882	0.7	4.8
ESTs	AA281949	RC_AA281949	1.3	4.8
ESTs	AA134767	RC_AA134767_s	1.5	4.8
ESTs	AA453593	RC_AA453593_s	0.9	4.8
fizzled (Drosophila) homolog 1	AA358618	RC_AA358618_s	2.4	4.8
ESTs	H93552	RC_H93552	0.9	4.8
cyclin G2	D53233	RC_D53233	2.7	4.8
peptidylprolyl isomerase B (cyclophilin B)	H15847	RC_H15847_s	1.8	4.8
ESTs; Highly similar to (define not available 439889) [H.sapiens]	AA256210	RC_AA256210	2.0	4.8
Homo sapiens clone 23698 mRNA sequence	R32440	RC_R32440	0.5	4.8
ESTs	C15078	RC_C15078_i	0.8	4.8
ESTs; Weakly similar to CH-TOG PROTEIN [H.sapiens]	AA486092	RC_AA486092	2.8	4.8
ESTs	C00038	RC_C00038_s	2.8	4.8
ESTs	AA450281	RC_AA450281	1.0	4.8
Homo sapiens mRNA for KIAA863 protein; complete cds	N57577	RC_N57577	1.1	4.8
ferritin; light polypeptide	T73572	RC_T73572_f	1.1	4.8
ESTs; Highly similar to 5'-AMP-ACTIVATED PROTEIN KINASE; GAMMA-1 SUBUNIT [Rattus norvegicus]	AA114970	RC_AA114970_i	1.3	4.8
ESTs; Highly similar to ZYXIN [Gallus gallus]	H25769	RC_H25769_s	1.2	4.8
tubulin-specific chaperone a	AA504095	AA504095	1.6	4.8
ESTs	N25576	RC_N25576	1.1	4.8
Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23) mRNA; nuclear gene encoding mitochondrial protein; complete cds	AA442768	RC_AA442768_i	1.9	4.8
ESTs	AA235289	RC_AA235289	2.4	4.8
ESTs	N27198	RC_N27198	2.5	4.8
ESTs	AA479132	AA479132	1.7	4.8
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA450228	RC_AA450228	1.5	4.7
calmodulin 1 (phosphorylase kinase; delta)	AA085590	RC_AA085590_s	1.3	4.7
Homo sapiens actin-related protein Arp3 (ARP3) mRNA; complete cds	AA199588	RC_AA199588	1.8	4.7
Human TAR DNA-binding protein-43 mRNA; complete cds	H16390	RC_H16390_s	1.3	4.7
Human TAR RNA loop binding protein (TRP-185) mRNA; complete cds	N70678	RC_N70678_s	1.5	4.7
Human transformer-2 alpha (htra-2 alpha) mRNA; complete cds	AA455812	AA455812	1.3	4.7
ESTs	AA057287	AA057287	0.7	4.7
ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	AA070801	RC_AA070801	6.3	4.7
ESTs; Highly similar to COMPLEMENT C1Q SUBCOMPONENT; A CHAIN PRECURSOR [Homo sapiens]	W87494	RC_W87494	1.2	4.7

FIGURE 8
(Cont.)

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ESTs	AA480264	RC_AA480264	0.8	4.7
TAP binding protein (tapasin)	AA303745	AA303745_s	1.8	4.7
UDP-glucose dehydrogenase	AA454086	RC_AA454086_f	1.3	4.7
protein tyrosine phosphatase; receptor type: c polypeptide	Y00062	Y00062	0.6	4.6
ESTs	AA449333	RC_AA449333	2.9	4.6
ESTs; Highly similar to TURNED ON AFTER DIVISION; 64 KD PROTEIN [Rattus norvegicus]	AA058664	RC_AA058664	1.5	4.6
ESTs	R51913	RC_R51913	1.3	4.6
protein tyrosine phosphatase type IVA; member 2	AA329274	AA329274_f	1.9	4.6
calumenin	W84712	RC_W84712	3.5	4.6
ESTs	AA173597	AA173597	1.8	4.6
H.sapiens mRNA for Fas/Apo-1 (clone pCRTM111-Fasdelta(4,7))	X83492	X83492	0.8	4.6
ESTs	AA404427	RC_AA404427	1.3	4.6
ESTs	W65477	RC_W65477	1.2	4.6
ESTs	AA040270	RC_AA040270	1.3	4.6
hemoglobin; gamma A	R92458	RC_R92458_f	0.5	4.6
ESTs	F01831	RC_F01831	0.2	4.6
ESTs	Z41372	RC_Z41372_s	2.0	4.6
ESTs; Weakly similar to PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 [H.sapiens]	AA410336	RC_AA410336	2.0	4.6
ESTs; Highly similar to GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 2 [Saccharomyces cerevisiae]	AA010686	AA010686	1.6	4.6
ESTs; Weakly similar to keratin 1 [H.sapiens]	AA037386	RC_AA037386_s	1.1	4.6
H1 histone family; member 2	T90190	RC_T90190_s	1.5	4.5
lysosome (renal amyloidosis)	X14008	X14008_ma1_f	0.9	4.5
ESTs	Z39622	RC_Z39622_s	2.1	4.5
ribosomal protein L22	T23926	RC_T23926	1.5	4.5
tumor necrosis factor (ligand) superfamily; member 1	H25836	RC_H25836	3.2	4.5
ESTs	R60952	RC_R60952_i	1.0	4.5
Homo sapiens clone 23636 mRNA sequence	T17428	RC_T17428_s	1.0	4.5
NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 7 (18kD; B18)	AA609299	RC_AA609299_s	1.1	4.5
SET PROTEIN	AA205665	RC_AA205665_s	1.7	4.5
Human mRNA for KIAA349 gene; partial cds	AB002347	AB002347	0.7	4.5
protease; serine; 11 (IGF binding)	T82292	RC_T82292_s	2.1	4.5
ESTs	AA465218	RC_AA465218	1.6	4.5
ESTs	AA236018	RC_AA236018	1.2	4.5
SRP (sex determining region Y)-box 4	AA479953	RC_AA479953	8.7	4.5
LIVER CARBOXYL ESTERASE PRECURSOR	T68878	RC_T68878_f	0.3	4.4
Human mRNA for KIAA228 gene; partial cds	AA431206	RC_AA431206_s	1.5	4.4
ESTs	AA489012	RC_AA489012	2.4	4.4
ESTs; Highly similar to NUCLEAR FACTOR 1 A1 [Gallus gallus]	F08945	RC_F08945	1.5	4.4
zinc finger protein 27	H80409	RC_H80409	1.5	4.4
ESTs	T86337	RC_T86337	1.2	4.4
ESTs	AA459245	RC_AA459245	0.9	4.4
ribosomal protein L22	N83380	RC_N83380	1.3	4.4
ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	W61297	RC_W61297	0.4	4.4
ESTs	AA291749	RC_AA291749_s	4.4	4.4
tubulin; beta polypeptide	T03651	RC_T03651_s	1.0	4.4
regulator of G-protein signalling 5	AA348466	RC_AA348466_s	1.4	4.4

FIGURE 8
(Cont.)

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ESTs; Highly similar to ARGINYL-TRNA SYNTHETASE;	R12777	RC_R12777_s	1.5	4.4
MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]	Z14244	Z14244	0.9	4.4
cytochrome c oxidase subunit VIIb	T92718	RC_T92718	1.1	4.3
ESTs	T96379	RC_T96379_s	1.4	4.3
protein phosphatase 2; regulatory subunit B (B56); delta isoform	T74571	RC_T74571_s	1.2	4.3
LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1	M34516	M34516_s	1.1	4.3
PRECURSOR	N23222	RC_N23222	2.2	4.3
immunoglobulin lambda-like polypeptide 2	Z38688	RC_Z38688	0.3	4.3
ESTs; Moderately similar to unknown [H.sapiens]	W42412	RC_W42412	1.1	4.3
ESTs	W20487	RC_W20487_s	1.4	4.3
ESTs; Highly similar to HEMOPOIETIC-SPECIFIC EARLY	N21407	RC_N21407	1.8	4.3
RESPONSE PROTEIN [Mus musculus]	H97159	RC_H97159	1.2	4.3
ESTs	R69293	RC_R69293	1.0	4.3
ESTs; Weakly similar to deduced amino acid sequence is highly	AA253459	RC_AA253459	0.9	4.3
homologous to hypothetical proteins of C.elegans (T23g5.4 and	AA452248	RC_AA452248	0.9	4.3
T23G5.2). [H.sapiens]	AA608649	RC_AA608649	1.2	4.3
poly (ADP-ribose) glycohydrolase	AA393432	AA393432_s	1.5	4.3
ESTs	AA398318	RC_AA398318	1.5	4.3
ESTs	R79723	RC_R79723_s	1.5	4.3
H.sapiens mRNA for translin associated zinc finger protein-1	Z38874	RC_Z38874	1.1	4.3
ESTs	AA079500	RC_AA079500	1.1	4.3
testis enhanced gene transcript	N48000	RC_N48000	2.7	4.3
ESTs	W31600	RC_W31600_f	2.3	4.3
von Hippel-Lindau syndrome	AA156230	RC_AA156230	1.0	4.3
ESTs	H69138	RC_H69138	0.9	4.3
v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	T34527	T34527	2.6	4.3
UDP-N-acetyl-alpha-D-galactosamine:polypeptide	AA029288	RC_AA029288	1.5	4.2
N-acetylgalactosaminyltransferase 1 (GaIIAa-T1)	AA458959	RC_AA458959	1.7	4.2
ESTs; Highly similar to ZINC FINGER PROTEIN 91 [Homo	T10108	RC_T10108_s	1.4	4.2
sapiens]	H04753	RC_H04753_f	3.2	4.2
ESTs	W63747	RC_W63747	1.8	4.2
ESTs	AA094989	AA094989	0.7	4.2
ras homolog gene family; member H	H05631	RC_H05631_f	1.2	4.2
Homo sapiens voltage dependent anion channel protein mRNA;	R44357	RC_R44357	1.8	4.2
complete cds	N34482	RC_N34482	1.4	4.2
ESTs; Weakly similar to Bat2 [H.sapiens]	U37283	U37283	1.1	4.2
ESTs	AA418985	RC_AA418985	2.3	4.2
Microfibril-associated glycoprotein-2	AA252765	RC_AA252765	1.0	4.2
ESTs; Weakly similar to CH-TOG PROTEIN [H.sapiens]	R24483	RC_R24483_s	0.6	4.2
ESTs; Moderately similar to (define not available 4589678)	AA481428	RC_AA481428	1.0	4.2
[H.sapiens]	AA279811	RC_AA279811_s	0.9	4.2
Homo sapiens mRNA for KIAA214 protein; complete cds				
zinc finger protein 262				
CAAX box 1				

FIGURE 8
(Cont.)

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ESTs; Weakly similar to (define not available 46333)	AA452082	AA452082	1.0	4.2
[H.sapiens]	T03441	RC_T03441_f	1.2	4.2
cytochrome b-561	AA040945	RC_AA040945	0.8	4.2
ESTs	H82632	RC_H82632	1.1	4.2
FSHD region gene 1	AA093977	AA093977	1.2	4.2
ESTs	R26589	RC_R26589_f	1.0	4.2
ESTs	U56833	U56833	1.4	4.2
von Hippel-Lindau binding protein 1	M21005	M21005	0.9	4.2
S1 calcium-binding protein A8 (calgranulin A)				
ESTs; Highly similar to POLYADENYLATE-BINDING PROTEIN	W95592	RC_W95592_i	1.3	4.1
[Homo sapiens]	AA620962	RC_AA620962	1.2	4.1
ESTs	L05512	L05512	0.8	4.1
histatin 1	AA293426	RC_AA293426	0.7	4.1
ESTs	T89627	RC_T89627_s	1.3	4.1
cyclin F				
ESTs; Weakly similar to Similarity to Serpentine stricoidine	AA256171	RC_AA256171	1.9	4.1
synthase precursor [C.elegans]	AA311352	AA311352_s	1.6	4.1
ESTs	AA405654	RC_AA405654_s	1.5	4.1
ESTs	AA040263	RC_AA040263	1.1	4.1
ESTs; Highly similar to ACTIN II [Plasmodium falciparum]	C01552	C01552	1.0	4.1
ESTs	N95507	N95507	1.3	4.1
ESTs; Weakly similar to KIAA319 [H.sapiens]	N63706	RC_N63706	1.0	4.1
ESTs	AA152312	RC_AA152312	1.1	4.1
ESTs	M81916	M81916	1.5	4.1
laminin; beta 1	AA063431	RC_AA063431_f	0.8	4.1
ESTs	N39016	RC_N39016	1.3	4.1
ESTs; Moderately similar to neuronal thread protein AD7c-NTP	W45457	RC_W45457	1.2	4.1
[H.sapiens]	C15324	RC_C15324_f	4.2	4.1
ESTs	N46086	N46086_s	1.6	4.1
ESTs	W45494	RC_W45494	1.0	4.1
bone morphogenetic protein 6	AA598702	RC_AA598702	1.6	4.1
cadherin 11 (DE-cadherin; osteoblast)	D21254	D21254_s	3.2	4.1
ESTs; Weakly similar to ribokinase [E.coli]	T69020	RC_T69020_s	0.9	4.1
ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING	AA120783	RC_AA120783	1.4	4.1
ENTRY !!!! [H.sapiens]	H27442	RC_H27442_s	1.0	4.1
erythrocyte membrane protein band 7.2 (stomat)				
solute carrier family 7 (cationic amino acid transporter, y+	R51116	RC_R51116_f	0.8	4.1
system); member 6	T69728	RC_T69728	1.1	4.1
ESTs	R44163	RC_R44163_f	0.9	4.1
Homo sapiens clone 2377 mRNA sequence	W80739	RC_W80739_f	1.0	4.1
ESTs	H82424	RC_H82424	1.7	4.0
ESTs; Moderately similar to LNXp7 [M.musculus]	AA487193	RC_AA487193	4.7	4.0
secreted frizzled-related protein 4				
ESTs; Moderately similar to neuronal thread protein AD7c-NTP	AA428607	RC_AA428607	1.3	4.0
[H.sapiens]	W79422	RC_W79422_s	1.3	4.0
fumarylacetoacetate	N20178	RC_N20178	1.2	4.0
MATRIN 3	W67727	RC_W67727	1.4	4.0
ESTs	AA011510	RC_AA011510	1.8	4.0
ESTs				

FIGURE 8
(Cont.)

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ESTs	AA069569	RC_AA069569	1.5	4.0
cysteine-rich protein 1 (intestinal)	N92934	RC_N92934_s	2.5	4.0
ESTs	AA004415	RC_AA004415	1.2	4.0
ESTs	W81205	RC_W81205	1.5	4.0
ESTs	N56993	RC_N56993	2.0	4.0
ESTs	AA256943	RC_AA256943_s	0.8	4.0
ESTs	N68133	RC_N68133	0.7	4.0
ESTs	R08615	RC_R08615_s	0.5	4.0
homogentisate 1,2-dioxygenase (homogentisate oxidase)	N95243	RC_N95243_s	0.9	4.0
Meis1 (mouse) homolog	K01160	K01160	1.7	4.0
Accession not listed in Genbank	T33489	RC_T33489_s	1.3	4.0
ESTs	M37583	M37583	2.8	4.0
H2A histone family, member Z	T72268	RC_T72268_s	1.3	4.0
B-factor, properdin	AA133457	RC_AA133457	1.2	4.0
ESTs	AA287681	RC_AA287681_s	1.3	4.0
ESTs				
ESTs; Highly similar to HYPOTHETICAL 84.7 KD PROTEIN ZK198.1 IN CHROMOSOME III [Caenorhabditis elegans]	AA481403	RC_AA481403	4.0	4.0
ESTs	AA233445	RC_AA233445	1.9	4.0
ESTs; Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]	AA452256	RC_AA452256	1.2	4.0
ESTs; Weakly similar to deduced amino acid sequence is highly homologous to hypothetical proteins of C.elegans (T23g5.4 and T23g5.2). [H.sapiens]	AA488433	RC_AA488433	1.1	4.0
Homo sapiens mRNA for KIAA719 protein; complete cds	R60689	RC_R60689	1.9	4.0
ESTs	AA016306	RC_AA016306	0.6	4.0
H.sapiens mRNA for nuclear protein SA-2	AA489057	RC_AA489057	6.2	4.0
ESTs	AA431191	RC_AA431191_s	1.8	4.0
protein kinase C, zeta	R24258	RC_R24258_s	0.7	4.0
ESTs	N66847	RC_N66847	1.4	4.0
ESTs	AA233548	RC_AA233548	1.5	4.0
ESTs	AA400229	RC_AA400229	1.7	4.0
ESTs; Weakly similar to SAS [H.sapiens]	H07011	H07011	1.8	3.9
Human mRNA for KIAA96 gene; partial cds	D60769	RC_D60769_s	0.9	3.9
cell division cycle 42 (GTP-binding protein; 25kD)	AA031548	AA031548	3.1	3.9
ESTs	H29293	RC_H29293_f	1.6	3.9
ESTs	AA032067	RC_AA032067_s	2.0	3.9
Rho GTPase activating protein 1				
ESTs; Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]	AA234533	AA234533	1.4	3.9
calpain; large polypeptide L2	R39610	RC_R39610_s	1.3	3.9
ESTs	AA456845	RC_AA456845	1.4	3.9
ESTs; Highly similar to ATP SYNTHASE EPSILON CHAIN; MITOCHONDRIAL PRECURSOR [Bos taurus]	W72685	RC_W72685	1.3	3.9
Homo sapiens mRNA for KIAA886 protein; complete cds	W58081	RC_W58081	1.0	3.9
ESTs; Highly similar to (define not available 467918) [H.sapiens]	AA026962	RC_AA026962	1.4	3.9
Human DNA from overlapping chromosome 19 cosmids R31396; F25451; and R3176 containing COX6B and UPKA; genomic sequence	T15852	RC_T15852_f	2.0	3.9
ESTs	AA256317	RC_AA256317	1.3	3.9
ESTs	AA504492	RC_AA504492	2.4	3.9
ESTs	R78224	RC_R78224	1.0	3.9
ESTs	W74728	RC_W74728	0.2	3.9

FIGURE 8
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Human mRNA for KIAA263 gene; complete cds	T90946	RC_T90946_f	1.1	3.9
ESTs	D59711	RC_D59711_f	2.8	3.9
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA428364	RC_AA428364_s	1.3	3.9
ESTs	AA342457	RC_AA342457_s	2.1	3.9
ATPase; H+ transporting; lysosomal (vacuolar proton pump) 9kD	AA214710	AA214710	1.4	3.9
Homo sapiens mRNA for nuclear protein; NP22; complete cds	AA147532	RC_AA147532_s	2.8	3.9
Homo sapiens mRNA for KIAA75 protein; complete cds	AA157623	AA157623_s	1.2	3.9
ESTs	T90345	RC_T90345	1.2	3.9
ESTs	AA410424	RC_AA410424	1.3	3.9
ESTs; Highly similar to (define not available 467914) [H.sapiens]	N26691	RC_N26691	1.6	3.9
Homo sapiens mRNA for KIAA99 protein; partial cds	N51651	RC_N51651	0.9	3.9
ESTs; Highly similar to MICROSOMAL SIGNAL PEPTIDASE 21 KD SUBUNIT [Canis familiaris]	AA234347	RC_AA234347	1.3	3.9
ATPase; H+ transporting; lysosomal (vacuolar proton pump); beta polypeptide; 56/58kD; isoform 2	M60346	M60346_s	0.9	3.9
RAB4; member RAS oncogene family	X82554	X82554_ma1	0.8	3.9
ESTs; Highly similar to TISSUE ALPHA-L-FUCOSIDASE PRECURSOR [Homo sapiens]	AA234925	RC_AA234925	1.4	3.9
heterogeneous nuclear ribonucleoprotein A2/B1	AA131165	RC_AA131165_s	2.0	3.9
Human mariner-like element-containing mRNA; clone pCHMT1	AA487508	RC_AA487508	1.9	3.9
ESTs	AA489618	RC_AA489618_s	1.5	3.9
ESTs	AA436158	RC_AA436158	3.9	3.9
ESTs	AA256688	RC_AA256688_s	1.0	3.8
ESTs	H14982	RC_H14982_f	1.0	3.8
ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	J03473	J03473	2.1	3.8
ESTs	W60310	RC_W60310	1.3	3.8
ESTs	AA040397	RC_AA040397	1.5	3.8
ESTs	T15457	RC_T15457_f	1.0	3.8
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	N67343	RC_N67343	2.1	3.8
ESTs; Highly similar to HYPOTHETICAL 3.5 KD PROTEIN C3A5.3 IN CHROMOSOME III [Caenorhabditis elegans]	AA348925	RC_AA348925_s	2.4	3.8
protocadherin 2 (cadherin-like 2)	T65540	RC_T65540_s	1.0	3.8
ESTs	AA404421	RC_AA404421	1.2	3.8
ESTs	AA237009	RC_AA237009	1.3	3.8
ESTs; Moderately similar to ATP-CITRATE [Rattus norvegicus]	D51405	RC_D51405	1.4	3.8
Human Ig J chain gene	M12759	M12759	0.5	3.8
ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	H90314	RC_H90314_s	1.2	3.8
NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	AA063581	RC_AA063581	0.8	3.8
H.sapiens OZF mRNA	T25747	RC_T25747_s	1.8	3.8
lumican	U21128	U21128	2.2	3.8
heterogeneous nuclear ribonucleoprotein G	AA173143	RC_AA173143_s	1.6	3.8
ESTs	N63165	RC_N63165	1.1	3.8
ESTs; Weakly similar to KIAA62 [H.sapiens]	AA233763	RC_AA233763	0.8	3.8
Human high density lipoprotein binding protein (HBP) mRNA; complete cds	H28100	RC_H28100_s	1.9	3.8
ESTs	AA074350	RC_AA074350	1.3	3.8
ESTs	W46632	RC_W46632	1.1	3.8

FIGURE 8
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ESTs	AA491278	RC_AA491278_r	1.0	3.8
ESTs; Highly similar to GASTRULA ZINC FINGER PROTEIN XLGFB.2DB [Xenopus laevis]	T58753	RC_T58753_f	1.4	3.8
Homo sapiens lysophospholipase (LPL1) mRNA; complete cds	AA251902	RC_AA251902	2.2	3.8
interferon stimulated gene (2kD)	AA504805	RC_AA504805_s	1.3	3.8
Homo sapiens mRNA for KIAA446 protein; complete cds	AA416723	RC_AA416723	1.0	3.8
Homo sapiens mRNA for KIAA92 protein; complete cds	T65396	RC_T65396_f	1.0	3.8
ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	H95569	RC_H95569_i	0.5	3.7
ESTs; Highly similar to ZINC FINGER PROTEIN ZFP-92 [Mus musculus]	T26494	RC_T26494_f	1.3	3.7
ESTs	AA174183	AA174183_s	2.0	3.7
cellular retinoic acid-binding protein 1	R53950	RC_R53950_s	1.1	3.7
erythrocyte membrane protein band 4.1-like 2	AA427955	RC_AA427955	0.5	3.7
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA425378	RC_AA425378_r	0.9	3.7
yd73e9.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113896 3', mRNA sequence	T77525	RC_T77525	1.5	3.7
ESTs	AA477445	RC_AA477445	1.4	3.7
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA071089	RC_AA071089	1.2	3.7
ferritin; light polypeptide	T63769	RC_T63769_f	1.1	3.7
ESTs	R63173	RC_R63173_s	2.0	3.7
Homo sapiens mRNA for DnaJ protein	W72906	RC_W72906	2.7	3.7
ESTs	R32393	RC_R32393_s	1.2	3.7
Homo sapiens mRNA for KIAA878 protein; complete cds	H98653	RC_H98653	2.8	3.7
procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	U84573	U84573	1.8	3.7
ESTs	AA156335	RC_AA156335	4.6	3.7
zn13d5.a1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:54735 3' similar to gb:L8441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN); mRNA sequence	AA085374	RC_AA085374	1.6	3.7
fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	AA489375	RC_AA489375_f	1.6	3.7
ESTs; Weakly similar to eyelid [D.melanogaster]	Z38897	RC_Z38897_s	1.2	3.7
ESTs	AA235040	RC_AA235040	1.5	3.7
collagen; type III; alpha 1 (Ehlers-Danlos syndrome type IV; autosomal dominant)	X06700	X06700	4.7	3.7
ESTs; Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]	T26471	RC_T26471	4.5	3.7
ESTs	R27006	RC_R27006_f	1.6	3.7
H.sapiens mRNA for putative progesterone binding protein	H60595	RC_H60595_s	1.3	3.7
fibroblast growth factor receptor 2 (bacteria-expressed kinase; keratinocyte growth factor receptor; craniofacial dysostosis 1; Crouzon syndrome; Pfeiffer syndrome; Jackson-Weiss syndrome)	AA460450	RC_AA460450	1.5	3.7
ATPase; H+ transporting; lysosomal (vacuolar proton pump); alpha polypeptide; 7kD; isoform 1	AA228122	RC_AA228122	1.1	3.7
ribosomal protein; large; P	AA416866	RC_AA416866_f	1.3	3.7
ESTs	R21443	R21443	1.6	3.7
Homo sapiens mRNA for KIAA564 protein; partial cds	AA053020	RC_AA053020_i	1.0	3.7

FIGURE 8
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ESTs; Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]	N91377	RC_N91377	2.8	3.7
ESTs	H95989	RC_H95989_s	2.0	3.7
ESTs; Weakly similar to B-cell growth factor [H.sapiens]	T88817	RC_T88817	1.0	3.7
ESTs; Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]	AA394126	RC_AA394126	1.8	3.6
ESTs	R38547	RC_R38547	0.9	3.6
ESTs; Weakly similar to uroporphyrinogen III synthase; UROIII [H.sapiens]	AA476237	RC_AA476237	1.5	3.6
ESTs	R53062	RC_R53062	0.8	3.6
ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	AA452237	RC_AA452237_i	3.6	3.6
ESTs; Weakly similar to hypothetical protein [H.sapiens]	AA040465	RC_AA040465	1.2	3.6
ESTs	AA350781	RC_AA350781	1.1	3.6
ESTs	AA121313	RC_AA121313	1.4	3.6
ESTs	AA234966	RC_AA234966	1.6	3.6
ESTs	W58461	RC_W58461	1.0	3.6
ESTs	AA252372	RC_AA252372	1.2	3.6
ESTs	W31470	RC_W31470	1.5	3.6
ESTs; Weakly similar to hypothetical protein [H.sapiens]	D80076	RC_D80076_f	1.7	3.6
ubiquitin specific protease 7 (herpes virus-associated)	R54935	RC_R54935_s	1.7	3.6
ESTs; Weakly similar to SH3BGR PROTEIN [H.sapiens]	D30930	D30930_s	1.1	3.6
Homo sapiens mRNA for low molecular mass ubiquinone-binding protein; complete cds	N77716	N77716_s	1.2	3.6
ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	R56485	RC_R56485	1.0	3.6
ESTs	AA135894	RC_AA135894	1.3	3.6
zm8716 s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:545895 3'; mRNA sequence	AA079487	RC_AA079487	1.5	3.6
ESTs	N22152	RC_N22152_f	1.9	3.6
ESTs	AA114893	RC_AA114893	1.2	3.6
Homo sapiens HRIHFB2115 mRNA; partial cds	AA278400	RC_AA278400_f	1.5	3.6
ESTs; Weakly similar to similar to SP:YR4_BACSU [C.elegans]	W67789	RC_W67789	1.2	3.6
ESTs; Weakly similar to cDNA EST EMBL:C1359 comes from [this gene] [C.elegans]	N89819	RC_N89819	1.4	3.6
ESTs; Moderately similar to (define not available 446549) [H.sapiens]	AA488658	RC_AA488658	2.4	3.6
Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence	H88535	RC_H88535_f	1.3	3.6
ESTs	AA459255	RC_AA459255	1.3	3.6
immunoglobulin gamma 3 (Gm marker)	M87789	M87789	1.2	3.6
Homo sapiens signalosome subunit 2 (SGN2) mRNA; complete cds	AA458919	RC_AA458919	1.2	3.6
sorting nexin 3	W49551	RC_W49551	1.2	3.6
ESTs; Highly similar to (define not available 3915613) [H.sapiens]	W38597	W38597_s	1.1	3.6
ESTs	AA446451	RC_AA446451	1.1	3.6
hemoglobin; gamma A	H74317	RC_H74317_s	0.2	3.6
neuromedin B	X76534	X76534	2.2	3.6
ESTs; Highly similar to 26S PROTEASE REGULATORY SUBUNIT 6 [Homo sapiens]	AA441978	RC_AA441978	1.2	3.6
ESTs; Moderately similar to histone H2B [H.sapiens]	AA610040	RC_AA610040	1.1	3.6
Homo sapiens clone 2477 mRNA sequence	T15703	RC_T15703	1.4	3.6

FIGURE 8
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Human glutamate dehydrogenase (GDH) mRNA; complete cds	T85978	RC_T85978_s	1.0	3.6
Homo sapiens mRNA for leptin receptor gene-related protein	AA393825	RC_AA393825	1.1	3.6
ESTs	R49385	RC_R49385	1.5	3.6
ESTs	W16996	W16996_s	1.1	3.6
ESTs	AA351254	RC_AA351254	0.9	3.6
ESTs; Weakly similar to neuronal tyrosine threonine phosphatase 1 [M.musculus]	T88897	RC_T88897	0.9	3.6
ESTs	N70873	RC_N70873	1.1	3.5
ESTs	AA238532	RC_AA238532_s	1.0	3.5
APOLIPOPROTEIN AI REGULATORY PROTEIN-1	AA393876	RC_AA393876_s	0.9	3.5
ESTs	AA027229	RC_AA027229	1.3	3.5
ESTs; Weakly similar to The KIAA147 gene product is related to adenylyl cyclase. [H.sapiens]	AA131394	RC_AA131394	1.4	3.5
ESTs	AA235505	RC_AA235505	1.4	3.5
ESTs	N21207	RC_N21207	1.6	3.5
protease; serine; 11 (IGF binding)	D87258	D87258	2.4	3.5
Homo sapiens SMC73 protein (SMC73) mRNA; complete cds	H27498	RC_H27498_f	1.1	3.5
ESTs	AA621788	RC_AA621788	1.1	3.5
Human mRNA for KIAA249 gene; complete cds	T95515	RC_T95515_s	1.6	3.5
ESTs	AA043960	RC_AA043960	1.1	3.5
ribosomal protein; large; P	W32281	RC_W32281_f	1.3	3.6
ESTs; Highly similar to POTASSIUM CHANNEL PROTEIN KV2.1 [Rattus norvegicus]	T89084	RC_T89084	1.0	3.5
ESTs	T52700	RC_T52700	0.9	3.5
ESTs	H16772	RC_H16772	1.2	3.5
ATP synthase; H+ transporting; mitochondrial F complex; subunit c (subunit 9) isoform 3	AA112059	RC_AA112059_s	1.1	3.5
ESTs; Highly similar to HYPOTHETICAL 17.2 KD PROTEIN F44E2.6 IN CHROMOSOME III [Caenorhabditis elegans]	R49920	RC_R49920	1.5	3.5
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	N54909	RC_N54909_s	2.3	3.5
ESTs	AA033974	RC_AA033974	1.6	3.5
ESTs; Weakly similar to Weak similarity with Salmonella typhimurium RFBU protein [C.elegans]	AA057832	RC_AA057832	1.2	3.5
synaptophysin	R42172	RC_R42172	0.6	3.5
ESTs	W27770	W27770	0.9	3.6
EST	AA164676	RC_AA164676	1.2	3.5
ESTs; Highly similar to THROMBOXANE A2 RECEPTOR [Homo sapiens]	AA253424	RC_AA253424	1.0	3.5
ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]	N23761	RC_N23761	1.8	3.5
GLUCOSYLCERAMIDASE PRECURSOR	T48672	RC_T48672_s	1.1	3.5
collagen; type VI; alpha 3	X52022	X52022	2.6	3.5
ESTs; Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION [Saccharomyces cerevisiae]	T35725	T35725_s	2.1	3.5
ESTs; Weakly similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]	T40145	T40145	1.1	3.5
Human mRNA for KIAA9 gene; complete cds	H86350	RC_H86350_s	1.3	3.5
ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	R81173	RC_R81173	1.3	3.5
fatty-acid-Coenzyme A ligase; long-chain 3	AA316272	AA316272	1.7	3.5
ESTs	R46209	RC_R46209	1.4	3.5

FIGURE 8
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ESTs	AA397916	RC_AA397916_J	1.4	3.5
ESTs	T89379	RC_T89379	1.1	3.5
ESTs	H98714	RC_H98714_s	1.6	3.5
ESTs	N69552	RC_N69552	1.2	3.5
Human alpha satellite and satellite 3 junction DNA sequence	M21305	M21305	29.9	0.3
transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)	AA458761	AA458761_J	13.9	0.8
Prolactin-Induced Protein	HG1763-HT1780	HG1763-HT1780	11.9	0.4
ESTs	AA164586	RC_AA164586_s	6.2	0.8
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA; partial cds	AA447146	RC_AA447146_s	5.9	1.6
H4 histone family; member G	X60486	X60486	5.8	1.5
ESTs	AA424798	RC_AA424798	5.5	2.9
ESTs	AA425309	RC_AA425309	5.4	1.2
ESTs	R55185	RC_R55185	5.3	1.2
Homo sapiens mRNA for KIAA48 protein; complete cds	AA412149	RC_AA412149	5.0	2.0
ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	AA621557	RC_AA621557	5.0	1.3
desmoplakin (DPI; DPL)	W95070	RC_W95070	5.0	2.8
ESTs	R49482	RC_R49482	4.6	2.0
ESTs	AA406145	RC_AA406145_f	4.6	3.0
dual specificity phosphatase 4	U48807	U48807	4.5	0.5
ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	N22107	RC_N22107	4.5	2.4
golgi SNAP receptor complex member 1	AA481414	RC_AA481414	4.4	0.9
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA; partial cds	U28831	U28831	4.4	0.6
matrix metalloproteinase 7 (matrilysin; uterine)	L22524	L22524	4.4	0.6
Homo sapiens clone 24629 mRNA sequence	AA419386	RC_AA419386	4.3	1.3
EST	W86779	RC_W86779	4.3	0.7
ser-Thr protein kinase related to the myotonic dystrophy protein kinase	N39214	RC_N39214	4.3	0.5
ESTs	T10100	RC_T10100_f	4.3	0.9
ESTs	AA251297	RC_AA251297	4.3	2.9
mammaglobin 1	U33147	U33147	4.2	0.7
ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	N66845	RC_N66845	4.2	0.5
Sjogren syndrome antigen A2 (SKD; ribonucleoprotein autoantigen SS-A/Ro)	AA075182	RC_AA075182	4.2	2.0
ESTs	AA411621	RC_AA411621	4.1	1.2
ESTs	AA255933	RC_AA255933	4.0	1.4
ESTs	H88496	H88496_s	4.0	1.3
ESTs	HG2167-HT2237	HG2167-HT2237	3.8	1.2
Protein Kinase H31, Camp-Dependent	J03460	J03460_s	3.8	0.5
prolactin-induced protein	W81552	RC_W81552	3.8	1.0
ESTs	AA398892	RC_AA398892	3.8	1.9
X-box binding protein 1	M31627	M31627	3.8	0.8
ESTs	H48032	RC_H48032	3.7	3.3
protein tyrosine phosphatase; receptor type; F	Y00815	Y00815	3.7	1.2
homolog of mouse quaking QKI (KH domain RNA binding protein)	AA280004	RC_AA280004	3.7	1.5
ESTs	F10707	RC_F10707	3.7	1.3

FIGURE 8
(Cont.)

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ESTs	AA255991	RC_AA255991	3.7	1.0
cadherin 3; P-cadherin (placental)	X83629	X83629	3.7	0.5
ESTs	N67149	RC_N67149	3.5	3.3
Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region	L33930	L33930	3.5	1.1
copine III	W66835	RC_W66835	3.5	1.9
Homo sapiens mRNA for semaphorin E; complete cds	AA042990	RC_AA042990_s	3.5	1.0
Homo sapiens clone 23967 unknown mRNA; partial cds	AA070485	RC_AA070485	3.4	2.6
Homo sapiens mRNA for KIAA882 protein; partial cds	Z39762	RC_Z39762_s	3.4	0.9
ESTs	AA419622	RC_AA419622	3.4	3.2
SRX (sex determining region Y)-box 4	AA458584	AA458584	3.4	0.4
Human gastrointestinal tumor-associated antigen GA733-1 protein gene, complete cds, clone 5516	JD4152	JD4152_ma1	3.4	0.4
ESTs; Highly similar to RING3 PROTEIN [Homo sapiens]	AA188647	RC_AA188647	3.3	2.8
ESTs; Weakly similar to Numblike (M.musculus)	AA463254	RC_AA463254_s	3.3	1.6
wee1+ (S. pombe) homolog	T16282	RC_T16282_f	3.3	1.1
SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily s; member 4	U29175	U29175	3.3	3.4
Homo sapiens mRNA for squalene epoxidase, partial cds	D78129	D78129	3.3	1.4
ESTs	AA456687	AA456687	3.3	2.2
ESTs; Weakly similar to NF-kB subunit [H.sapiens]	AA487561	RC_AA487561	3.3	1.2
hepatocyte growth factor activator inhibitor	AA157857	RC_AA157857_s	3.3	2.4
MITOCHONDRIAL 6S RIBOSOMAL PROTEIN L3	X06323	X06323	3.3	2.1
ESTs	AA496053	RC_AA496053	3.3	1.8
ESTs	AA058846	RC_AA058846	3.3	3.3
ESTs; Highly similar to N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG [Leishmania donovani]	C02582	C02582	3.3	3.3
stanniocalcin 2	AA126474	RC_AA126474	3.2	0.2
STATHMIN	D51276	RC_D51276_f	3.2	3.0
collagen; type I; alpha 1	Z74615	Z74615	3.2	3.0
ESTs	AA485431	RC_AA485431_s	3.2	2.4
ESTs	H89575	H89575_s	3.2	0.6
ESTs	T17185	RC_T17185	3.2	3.0
ESTs	R39044	RC_R39044	3.2	0.8
ESTs	D60411	RC_D60411_s	3.2	0.8
ESTs; Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]	T91518	RC_T91518_f	3.2	2.5
3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1	AA165526	RC_AA165526	3.2	1.8
androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	M35851	M35851	3.2	1.8
Human mRNA for calgizzarin; complete cds	D38583	D38583	3.2	2.3
Human 26S proteasome-associated pad1 homolog (POH1) mRNA; complete cds	AA621752	RC_AA621752	3.2	2.5
heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	R99599	RC_R99599_s	3.2	3.4
ESTs	AA088228	RC_AA088228	3.2	1.4
ESTs	W72838	RC_W72838	3.2	1.0
ESTs	AA485212	RC_AA485212	3.1	1.4
keratin 19	Y00503	Y00503	3.1	1.1
collagen; type XV; alpha 1	L25286	L25286	3.1	3.4
ESTs; Weakly similar to predicted using GeneFinder [C.elegans]	AA416886	RC_AA416886	3.1	3.1

FIGURE 8
(Cont.)

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ESTs	AA406294	RC_AA406294	3.1	3.1
Human alpha-1 collagen type I gene, 3' end	M55998	M55998	3.1	1.7
ESTs	W02734	RC_W02734	3.1	1.4
KERATIN; TYPE II CYTOSKELETAL 7	M13955	M13955	3.1	1.1
H.sapiens mRNA for retrotransposon	AA598453	RC_AA598453_s	3.1	0.7
ESTs; Weakly similar to DREBRINS E1 AND E2 [Gallus gallus]	N69879	RC_N69879_s	3.1	1.6
ESTs	N48603	RC_N48603	3.1	1.2
ESTs; Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	N51488	RC_N51488	3.0	1.6
ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	N67422	RC_N67422_s	3.0	1.5
ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L3A [Saccharomyces cerevisiae]	AA045365	RC_AA045365	3.0	1.7
ESTs	T32108	RC_T32108	3.0	1.1
ESTs; Weakly similar to FUN9 transcript; essential gene; similar to Schizosaccharomyces pombe unknownorf SPAC24B11.8c; GenBank Accession Number Z67757 [S.cerevisiae]	AA504631	RC_AA504631	3.0	3.0

FIGURE 8 (Cont.)

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Accession	Title
Z29083	5T4 Oncofetal antigen
AA443962	Homo sapiens histone acetyltransferase (HBO1) mRNA, complete cds
AA055656	ESTs
D20342	transducer of erbB-2 (TOB)
AA130273	ESTs; Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]
U23070	Human putative transmembrane protein (nma) mRNA; complete cds
AA235448	ESTs
AA256162	ESTs
AA436880	ESTs; Moderately similar to similar to rat integral membrane glycoprotein; PIR Accession Number A467 [H.sapiens]
AA256485	ESTs

FIGURE 9

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FIGURE 10

Accession	UniGene ID	UniGene Title	ratio tumor/ body	90%ile tumor	75%ile body	ratio tumor/ normal breast
AA126474	Hs.155223	stanniocalcin 2	72.2	722	1	1.8
U020758	Hs.313	secreted phosphoprotein 1 (osteopontin; bone sialoprotein)	45.7	457	1	39.7
AA434329	Hs.36563	ESTs	40.2	402	1	4
AA250737	Hs.72472	ESTs	35.9	359	10	29.7
X82153	Hs.83942	cathepsin K (pycnodystosis)	34.3	411	12	5.1
X03635	Hs.1657	estrogen receptor 1	32.2	322	1	4.7
H09290	Hs.76550	ESTs; Weakly similar to unknown [H.sapiens]	30.6	306	4	26.5
AA428090	Hs.26102	ESTs	29	290	1	26.8
AA419547	Hs.11713	ESTs	28.3	356	14	1
AA256485	Hs.182471	ESTs	25.4	508	20	3
N67239	Hs.10760	ESTs	23.1	288	12	6.7
Z38595	Hs.125019	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING BCU3	24.2	242	10	5.6
H25836	Hs.83429	tumor necrosis factor (ligand) superfamily, member 10	22.8	228	9	12.4
HG1763-HT1760		Prolactin-Induced Protein	22.7	760	34	1.4
C01714	Hs.3838	serum-inducible kinase	22.6	226	10	0.9
U26686	Hs.182225	RNA binding motif protein 3	22.1	221	9	17.8
AA411621	Hs.8895	ESTs	21.2	212	6	17.4
N46252	Hs.29724	ESTs	20.9	209	1	19.5
U05237	Hs.99872	fatal Alzheimer antigen	20.6	206	4	19.1
U48907	Hs.2359	dual specificity phosphatase 4	20.2	202	5	1.3
AA070801	Hs.51615	ESTs; Weakly similar to !!! ALU SUBFAMILY SQ WARN	18.7	187	1	17
U28831	Hs.44566	Human protein immuno-reactive with anti-PTH polyclonal	18.6	186	10	1.5
AA292066	Hs.240802	ESTs; Weakly similar to Br140 [H.sapiens]	17.5	175	2	12.8
AA291725	Hs.105700	secreted frizzled-related protein 4	17.4	409	24	7.8
N26722	Hs.42645	ESTs	17.4	174	9	6.9
AA256323	Hs.25264	ESTs	16.6	166	8	12.7
AA065217	Hs.169874	ESTs	16.2	162	1	4.2
AA446650	Hs.27680	ESTs	16	255	16	6.6
D13666	Hs.136348	osteoblast specific factor 2 (fascilin I-like)	15.7	1030	66	5
AA621169	Hs.8687	ESTs	15.6	156	7	10.8
L07615		"Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exo	15.3	153	1	14.1
AA456598	Hs.240190	ESTs	15.2	152	1	12.6
AA007234	Hs.30095	ESTs	14.9	149	1	6.4
F01831	Hs.14838	ESTs	14.6	219	15	7.5
N65818	Hs.42179	ESTs	14.5	145	1	2.4
HG2167-HT2237		"Protein Kinase H131, Camp-Dependent"	14.4	144	9	4.7
Z39621	Hs.107295	ESTs	14.2	142	1	9.5
N05509	Hs.24638	ESTs	14.2	142	6	9.4
T00821	Hs.109052	chromosome 14 open reading frame 2	14.2	390	28	22.5
AA171913	Hs.5338	carbonic anhydrase XII	13.7	137	1	8.9
AA149007	Hs.243954	ESTs	13.5	135	1	5.1
N22222		"yw34b05.s1 Morton Fetal Cochlea Homo sapiens cDNA	13.3	133	8	3.2
AA480975	Hs.44829	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WA	13.3	415	34	6
D62633	Hs.8238	ESTs	13.2	244	19	9.9
D12485	Hs.11951	phosphodiesterase 1nucleotide pyrophosphatase 1 (homo	13.2	331	25	12.4
AA490262	Hs.15485	ESTs; Moderately similar to APXL gene product [H.sapien	13.1	131	1	5.1
V093640	Hs.4779	ESTs	12.8	128	1	11.7
D48396	Hs.75454	Human mRNA for Apo1_Human (MERS(Aop1-Mouse)-like	12.8	141	11	12.2
H94892	Hs.6906	v-rat simian leukemia viral oncogene homolog A (ras relat	12.7	311	25	2.4
AA458751	Hs.18387	ESTs	12.6	126	7	7.5
AA436158	Hs.190013	ESTs	12.6	126	8	9.9
AA444369	Hs.177537	ESTs	12.6	126	1	10.8
X14787	Hs.87409	thrombospondin 1	12.5	156	13	2.9
T40327	Hs.80680	ESTs	12.4	124	6	10.8
Z48633	Hs.6940	H.sapiens mRNA for retrotransposon	12.3	123	1	11.3
AA227219	Hs.110826	Homo sapiens CAGF9 mRNA; partial cds	12.3	129	11	11.7
T97307	Hs.161720	ESTs; Moderately similar to !!! ALU SUBFAMILY J WARN				

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FIGURE 10

(CONT.)

M86849		"Homo sapiens connexin 26 (GJB2) mRNA, complete cds	CBC2	12	120	8	9
AA417152	Hs.5101	ESTs; Highly similar to protein regulating cytokinesis 1 [H. CQA4		11.8	201	17	18.1
D31352	Hs.31433	ESTs; Weakly similar to HIII ALU SUBFAMILY SQ WARNI		11.7	117	1	10.1
AA251089	Hs.94576	ESTs; Weakly similar to phosducin, retinal [H.sapiens]		11.5	115	1	6.9
AA224180	Hs.127579	ESTs; Weakly similar to HIII ALU SUBFAMILY J WARNING		11.5	115	1	10
F11019	Hs.12686	ESTs		11.4	114	1	10
L19872	Hs.170087	aryl hydrocarbon receptor		11.3	113	8	3.9
AA471525	Hs.97496	YY1 transcription factor		11.3	124	11	9.7
AA487557	Hs.10705	ESTs; Weakly similar to (define not available 3882221) [H		11.3	113	8	2.5
M24594	Hs.20315	interferon-induced protein 56		11.2	112	8	5.9
AA279112	Hs.86594	ESTs		11.2	112	1	10.3
AA490969	Hs.168147	ESTs	CQA8	11	187	17	10.4
X17059	Hs.155953	N-acetyltransferase 1 (arylamine N-acetyltransferase)		10.8	706	66	9.2
W85765	Hs.30504	ESTs		10.7	123	12	7
AA405569	Hs.418	fibroblast activation protein; alpha	CZA9	10.7	433	41	7.2
N31952	Hs.167531	ESTs; Weakly similar to (define not available 3875448) [C		10.5	105	4	7.1
H93575	Hs.227146	ESTs		10.5	105	1	9.9
F03969	Hs.16940	ESTs; Weakly similar to tumorous imaginal discs protein T		10.5	105	1	9
N22157	Hs.226573	Homo sapiens Ikb kinase-b (IKK-beta) mRNA; complete c		10.5	121	12	1.6
F13673	Hs.99769	ESTs	BCN4	10.4	860	85	5.3
AA131692	Hs.26204	ESTs		10.3	103	1	3.9
AA411745	Hs.239691	ESTs; Weakly similar to KIAA0554 protein [H.sapiens]		10.3	103	1	9.3
D86957	Hs.80712	Human mRNA for KIAA0202 gene; partial cds		10.2	102	1	4.8
AA408542	Hs.71520	ESTs		10.2	506	50	2.8
U65932	Hs.81071	extracellular matrix protein 1	CBC3	10.2	628	62	17.2
AA236813	Hs.72324	ESTs; Highly similar to unknown [H.sapiens]		10.1	111	11	10.2
M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1		10	100	1	7.6
AA425309	Hs.33287	nuclear factor I/B	BCD1	9.9	463	49	1.8
AA487468	Hs.100686	ESTs; Moderately similar to secreted cement gland protei	BCX3	9.9	351	36	13.9
AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1; ca		9.8	123	13	5
AA398913	Hs.45231	ESTs		9.8	98	1	8.8
HG3748-HT4018		"Basic Transcription Factor, 44 Kda Subunit"		9.7	97	10	7.2
X91868	Hs.54416	sine oculis homeobox (Drosophila) homolog 1		9.7	97	1	9.3
AA599267	Hs.154554	ESTs; Weakly similar to ANKYRIN; BRAIN VARIANT 1 [H		9.7	102	11	6
M23379	Hs.758	RAS p21 protein activator (GTPase activating protein) 1		9.6	96	1	8.5
T26867	Hs.7549	ESTs	BCY9	9.6	124	13	9
U11313	Hs.75760	sterol carrier protein 2		9.5	95	4	8.8
R63542	Hs.110488	ESTs		9.5	95	1	8.5
M69225	Hs.620	bulbosus pemphigoid antigen 1 (230/240kd)		9.4	94	1	0.3
AA250775	Hs.87747	ESTs		9.4	94	8	7.3
AI039722	Hs.171205	ESTs		9.4	94	3	5.3
U14550	Hs.107573	sialyltransferase		9.3	93	4	3
U18321	Hs.159627	Death associated protein 3		9.3	93	5	8
X89308	Hs.78853	uracil-DNA glycosylase		9.3	93	8	8.2
AA283006	Hs.50758	chromosome-associated polypeptide C		9.3	93	1	8.4
U44378	Hs.76862	MAD (mothers against decapentaplegic; Drosophila) hom		9.3	93	1	7.8
AA187490	Hs.21941	ESTs	AAD1	9.3	436	47	5.8
AA487202	Hs.17962	ESTs		9.2	234	26	16.8
T33637	Hs.6841	ESTs		9.1	91	6	8.3
AA235112	Hs.106227	ESTs; Moderately similar to similar to murine RNA-binding		9.1	91	1	7.6
M83822	Hs.62354	Human beige-like protein (BGL) mRNA; partial cds		9	144	16	13
AA256680	Hs.181104	ESTs		9	117	13	10.6
AA028028	Hs.61460	ESTs	BCX5	9	90	1	5.5
M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein		8.9	89	5	8
AA898097	Hs.173594	pigment epithelium-derived factor		8.8	110	13	10.5
AA179845	Hs.73625	RAB6 interacting; kinesin-like (rabkinesin)		8.8	199	23	16.1
AA112396	Hs.44276	ESTs; Moderately similar to HOMEBOX PROTEIN HOX		8.7	247	29	5.7
U16306	Hs.81800	"Human chondroitin sulfate proteoglycan versican V splice		8.6	568	66	22.4
HG2981-HT3125		"Epican, Alt. Splice 1"		8.5	85	1	3.2
AA280036	Hs.145374	ESTs; Weakly similar to W01A6.c [C.elegans]		8.5	127	15	1.6

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FIGURE 10

(CONT.)

D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yeast U	8.5	85	1	7.2
AA609200	Hs.162686	ESTs	8.5	85	1	4.3
U33147	Hs.46452	mammaglobin 1	8.5	2058	243	1.4
N30855	Hs.30245	ESTs	8.4	84	1	5.3
AA446887	Hs.42911	ESTs	8.4	101	12	8.7
N90526	Hs.54529	ESTs	8.4	84	10	0.8
AA383876	Hs.1255	transcription factor COUP 2 (chicken ovalbumin upstream	8.4	169	20	4.6
AA257971	Hs.21214	ESTs	8.3	83	3	1.8
D60799	Hs.189391	ESTs	8.3	83	8	1.9
AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene h	8.3	87	11	0.4
AA047896	Hs.49169	ESTs	8.3	145	18	3.7
U59863	Hs.146847	TRAF family member-associated NFkB activator	8.2	82	1	6.8
H95094	Hs.75187	KIAA0016 gene product	8.2	124	15	11.5
H13108	Hs.107968	ESTs	8.2	82	1	7.4
AA236324	Hs.92381	ESTs; Weakly similar to !!!!! ALU CLASS A WARNING EN CVA1	8.2	114	14	9.8
L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin; uterine)	8.2	395	48	0.9
T16387	Hs.65328	ESTs	8.2	82	1	6.4
W42451	Hs.92260	high-mobility group protein 2-like 1	8.1	94	12	8.5
Z38501	Hs.8768	ESTs; Weakly similar to neuronal thread protein AD7c-NT	8.1	81	9	5.5
W04517	Hs.18442	ESTs	8.1	81	3	2.8
D31161	Hs.68613	ESTs	8.1	81	1	4.6
AA452000	Hs.94030	ESTs	8.1	101	13	7.9
R40057	Hs.112260	prominin (mouse)-like 1	8.1	328	41	1.7
AA451992	Hs.247127	ESTs; Weakly similar to similar to Schizosaccharomyces p	8	84	11	6.3
AA227428	Hs.9728	ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	8	80	6	7.3
AA620599	Hs.24766	ESTs	8	100	13	2.9
N32919	Hs.27931	ESTs	7.9	79	1	6.2
AA398155	Hs.97600	ESTs	7.9	79	1	2.7
R79723	Hs.69997	H.sapiens mRNA for translin associated zinc finger protein	7.9	234	30	18.9
Z29083	Hs.82128	ST4 oncofetal tropoblast glycoprotein	7.9	79	2	6.9
A1267886	Hs.148027	polymerase (RNA) II (DNA directed) polypeptide B (140kD	7.9	137	16	11.9
N38213	Hs.78305	RAB2; member RAS oncogene family	7.8	78	1	5.6
R56678	Hs.88959	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SP WARNIN	7.7	77	8	6.9
AA031357	Hs.31803	ESTs	7.7	77	1	5.1
N68857	Hs.14808	ESTs; Weakly similar to !!!!! ALU CLASS C WARNING EN	7.7	77	1	5
Z38436	Hs.102720	ESTs	7.7	81	11	7.6
T90037	Hs.16686	ESTs	7.6	76	1	4.2
AA167268	Hs.62349	ESTs	7.6	92	12	1.4
R34631	Hs.243068	KIAA0480 gene product	7.6	76	1	5
AA416997	Hs.59622	ESTs	7.6	144	19	13.9
AA211400	Hs.193172	ESTs	7.5	112	15	2.5
D60237	Hs.14368	SH3-binding domain glutamic acid-rich protein like	7.5	75	1	6.5
W37145	Hs.30029	ESTs	7.5	136	18	3.4
AA054228	Hs.23165	ESTs	7.4	74	1	6
AA455875	Hs.227602	Homo sapiens mRNA for KIAA0727 protein; partial cds	7.4	74	3	1.7
AA043562	Hs.62637	ESTs	7.4	74	8	6
D62657	Hs.35065	ubiquitin-specific protease 1	7.4	103	14	6.5
AA044842	Hs.95280	ESTs	7.4	74	5	2.4
AA159181	Hs.184013	ESTs	7.4	137	19	1.8
M99701	Hs.95243	transcription elongation factor A (SII)-like 1	7.3	73	1	5.3
Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dyspl	7.3	73	1	5.2
AA165333	Hs.24808	ESTs	7.3	73	1	3.8
N90719	Hs.94445	ESTs	7.3	73	3	5.4
L38608	Hs.10247	activated leucocyte cell adhesion molecule	7.3	106	15	5
R87634	Hs.3688	acid-insoluble phosphoprotein	7.3	73	1	1.2
AA042990	Hs.171921	sema domain; immunoglobulin domain (Ig); short basic do	7.3	271	37	2.3
N54378	Hs.13149	ESTs; Weakly similar to ARI protein [D.melanogaster]	7.2	72	10	6.1
AA476446	Hs.69559	ESTs; Weakly similar to Bat2 [H.sapiens]	7.2	72	1	5.7
U83908	Hs.247134	Homo sapiens nuclear antigen H731-like protein mRNA; c	7.2	72	1	5.8
W60913	Hs.30738	ESTs	7.2	72	4	5.7

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FIGURE 10

(CONT.)

AA393164	Hs.97644	mannaglobin 2		7.2	498	69	9.3
F10577	Hs.70312	ESTs; Moderately similar to neuronal thread protein AD7c		7.1	71	9	6.9
AA211941	Hs.109643	polyadenylate binding protein-interacting protein 1		7.1	71	1	6.2
X57985	Hs.2179	H2B histone family; member Q		7.1	100	14	7.5
M57230	Hs.82065	interleukin 6 signal transducer (gp130; oncostatin M recep		7.1	71	4	6.4
D61676	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone BCB9		7.1	392	56	3.6
H18027	Hs.184697	receptor for virally-encoded semaphorin	BCY7	7.1	150	21	14.5
AA195828	Hs.188662	ESTs	BCY8	7.1	71	1	6.5
AA032147	Hs.23296	ESTs		7	70	1	6.5
AA436244	Hs.17240	ESTs		7	70	3	1.3
AA400080	Hs.97774	EST		7	70	1	0.9
U25435	Hs.57419	transcriptional repressor		7	115	17	5.4
M74524	Hs.80512	ubiquitin-conjugating enzyme E2A (RAD6 homolog)		7	97	14	7.5
U47183	Hs.153468	ESTs; Weakly similar to !!! ALU SUBFAMILY SB2 WARN		7	70	6	6
M60752	Hs.121017	H2A histone family; member A		6.9	103	15	8.4
J03460	Hs.99949	prolactin-induced protein		6.9	1494	218	1.3
AA292701	Hs.5364	ESTs		6.9	69	1	4.4
AA219699	Hs.184245	ESTs		6.9	69	5	6.2
H64938	Hs.36331	ESTs		6.9	69	10	2.4
Z38839	Hs.125019	ESTs; Weakly similar to !!! ALU SUBFAMILY J WARNING		6.9	319	47	2.1
Y086779	Hs.241582	EST		6.9	162	24	2.6
AA361852	Hs.192905	ESTs		6.8	68	1	0.2
AJ283493	Hs.75722	ribophorin II		6.8	223	33	2.8
H17861	Hs.17767	ESTs		6.8	129	19	12.1
J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)		6.8	68	1	5.6
AA608955	Hs.109053	ESTs		6.8	68	10	6.1
U39840	Hs.105440	hepatocyte nuclear factor 3; alpha		6.7	67	9	6.3
AA425367	Hs.32094	ESTs		6.7	94	14	8
H48502	Hs.28212	ESTs		6.7	78	12	3
Z38763	Hs.15740	ESTs		6.7	67	1	6.3
AA598803	Hs.111496	ESTs		6.7	67	2	2.1
AJ287461	Hs.164950	ESTs		6.7	67	1	6
N45219	Hs.48320	ESTs		6.7	155	23	1.4
AA195260	Hs.204151	ESTs; Moderately similar to !!! ALU SUBFAMILY SX WAR		6.7	67	1	5.7
F09012	Hs.181326	ESTs		6.7	67	6	1.9
L11066	Hs.3069	heat shock 70kD protein 98 (mortalin-2)		6.7	93	14	8.4
AA453783	Hs.76550	ESTs; Weakly similar to unknown [H.sapiens]		6.7	304	46	7.8
T25508	Hs.81057	ESTs		6.7	67	9	5.7
L40391	Hs.6445	Homo sapiens (clone s153) mRNA fragment		6.6	135	21	13.1
AA147719	Hs.159441	ESTs		6.6	66	1	5.4
AA126433	Hs.173242	sorting nexin 4		6.6	69	11	6.3
M21305	Hs.247946	Human alpha satellite and satellite 3 junction DNA sequen		6.5	878	135	0.8
AA041551	Hs.48644	ESTs		6.5	65	2	6
R42036	Hs.6763	ESTs		6.5	65	10	1.5
T40530	Hs.231577	ESTs		6.5	65	6	4.8
N29888	Hs.169539	ESTs		6.5	65	4	5.3
AA490862	Hs.55901	ESTs; Moderately similar to !!! ALU SUBFAMILY SQ WA		6.5	65	1	5.6
R09599	Hs.103904	heterogeneous nuclear ribonucleoprotein U (scaffold attac		6.5	162	25	14.7
M63256	Hs.75124	cerebellar degeneration-related protein (62kD)		6.4	64	2	4.9
U37519	Hs.87539	aldehyde dehydrogenase 8		6.4	428	67	2.3
AB002367	Hs.21355	doublecortin and CaM kinase-like 1		6.4	64	8	3
AA284755	Hs.214742	CDWS2 antigen (CAMPATH-1 antigen)		6.4	64	8	6
AA243012	Hs.75928	ESTs		6.4	67	11	5
AJ366250	Hs.4779	ESTs		6.4	74	12	6.8
X06700	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danlos syndrome type I		6.4	1111	175	5
U51166	Hs.173824	thymine-DNA glycosylase		6.4	100	16	4.4
W23525	Hs.8739	ESTs		6.4	64	1	5.1
M15796	Hs.78996	proliferating cell nuclear antigen		6.4	249	39	22.4
HG4390-HT4650	Hs.78996	Ribosomal Protein L18a Homolog		6.3	63	4	5.7
X92098	Hs.75914	H.sapiens mRNA for transmembrane protein mp24		6.3	98	16	9.1

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FIGURE 10
(CONT.)

N67711	Hs.151046	Homo sapiens clone Z3859 mRNA sequence	6.3	63	1	5.8
W37999	Hs.24336	ESTs	6.3	63	6	5
AA149894	Hs.20815	erythroblast macrophage protein	6.3	165	26	3.2
H10933	Hs.10967	ESTs	6.3	693	110	7.2
AA609723	Hs.30652	ESTs	6.3	63	1	5.4
AA122386	Hs.82965	collagen; type V; alpha 2	6.3	1075	171	3.8
AA243052	Hs.172643	Homo sapiens mRNA; cDNA DKFZp564J1616 (from clone	6.2	62	6	5.6
R39995	Hs.25925	Homo sapiens clone Z3860 mRNA sequence	6.2	62	2	5.9
AA430124	Hs.234607	ESTs	6.2	62	1	5.4
T68510	Hs.76704	ESTs	6.2	600	97	4.1
R79750	Hs.83623	constitutive androstane receptor-beta; orphan nuclear hor	6.1	493	81	0.7
U35835	Hs.155637	protein kinase; DNA-activated; catalytic polypeptide	6.1	61	1	5.7
AA046405	Hs.5306	ESTs; Weakly similar to KIAA0597 protein [H.sapiens]	6.1	61	2	5.9
AA359268	Hs.95464	ESTs; Moderately similar to transcription factor RTEF-1 [H	6.1	61	1	5.1
D31058	Hs.24375	ESTs	6.1	343	56	16.4
U70322	Hs.168075	karyopherin (importin) beta 2	6.1	126	21	2.4
R46025	Hs.7413	ESTs	6.1	185	31	6.6
W68845	Hs.24095	ESTs	6.1	110	18	10.2
AA176690	Hs.4084	ESTs	6	60	6	4.6
N67390	Hs.43226	ESTs	6	60	5	3.7
U09717	Hs.8262	lysosomal-associated membrane protein 2	6	60	5	5.9
F03819	Hs.173094	ESTs	6	202	34	3.7
D38491	Hs.247463	Human mRNA for KIAA0117 gene; partial cds	5.9	59	1	2.8
F02582	Hs.14474	ESTs	5.9	59	10	4.2
AA347193	Hs.62180	ESTs	5.9	59	1	4.2
AA504642	Hs.28436	ESTs; Weakly similar to coded for by C. elegans cDNA CE	5.9	59	1	4.4
AA476594	Hs.9817	arg/Abi-interacting protein ArgBP2	5.9	186	32	3.7
Z81326	Hs.78589	protease inhibitor 12 (neuroserpin)	5.9	59	1	3.3
F10707	Hs.181104	ESTs	5.9	203	36	1.8
X07698	Hs.80342	keratin 15	5.8	753	131	0.4
X53793	Hs.117950	multifunctional polypeptide similar to SAICAR synthetase	5.8	218	38	13
AB000221	Hs.16530	small inducible cytokine subfamily A (Cys-Cys); member 1	5.8	58	1	3.2
AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapiens]	5.8	58	5	3.1
W63793	Hs.75744	S-adenosylmethionine decarboxylase 1	5.8	151	26	11.4
AA262491	Hs.186572	ESTs	5.8	58	1	5
AA429038	Hs.40541	ESTs	5.8	58	1	4.4
AA608531	Hs.170313	ESTs	5.8	58	1	4.9
L19161	Hs.211539	eukaryotic translation initiation factor 2; subunit 3 (gamma	5.8	171	30	2.9
R27296	Hs.23240	ESTs	5.8	115	20	2.5
AA610085	Hs.32990	ESTs	5.8	91	16	1.4
D87685	Hs.78893	Human mRNA for KIAA0244 gene; partial cds	5.8	58	1	4.9
AA262943	Hs.23552	ESTs	5.8	336	58	2
D60302	Hs.108977	ESTs	5.8	321	55	17
AA194882	Hs.19522	ESTs	5.7	57	8	5.3
AA287097	Hs.244443	transcription factor 4	5.7	57	8	4.1
AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDENT R	5.7	57	10	4.8
AA490814	Hs.24170	ESTs	5.7	94	17	7.3
AA094677	Hs.54558	ESTs; Weakly similar to !!!!! ALU CLASS C WARNING EN	5.7	57	1	4.9
Z38301	Hs.7859	ESTs	5.7	57	1	4.9
AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis; secreted cement glan	5.7	368	65	28.5
AA044095	Hs.3402	ESTs	5.7	57	1	4.5
AA092376	Hs.90606	15 kDa selenoprotein	5.7	67	1	5
R51309	Hs.70823	KIAA1077 protein	5.7	567	100	6.7
X16396	Hs.154672	methylenetetrahydrofolate dehydrogenase (NAD+ depen	5.7	251	44	6.6
AA024835	Hs.47504	potassium voltage-gated channel; delayed-rectifier; subfa	5.7	85	15	7.8
D87448	Hs.91417	Homo sapiens mRNA for DNA topoisomerase II binding p	5.6	76	14	2
U90914	Hs.5057	carboxypeptidase D	5.6	56	1	5.3
X72841	Hs.31314	H.sapiens IEF 7442 mRNA	5.6	191	34	3.5
AA281591	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (from clone	5.6	101	18	1.6
AA464428	Hs.119394	ESTs	5.6	108	20	1.8

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FIGURE 10

(CONT.)

AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapiens]	5.6	73	13	6.1
X52003	Hs.1406	retinol factor 1 (breast cancer; estrogen-inducible sequenc	5.6	1346	239	5.4
AA121286	Hs.34641	ESTs	5.6	95	17	9.1
AA521472	Hs.73435	ESTs	5.6	108	19	9
D87469	Hs.57652	EGF-like-domain; multiple 2	5.5	145	27	2.2
AA452411	Hs.29679	ESTs	5.5	147	27	4.4
AA504631	Hs.26813	ESTs; Weakly similar to (define not available 4689108) [H	5.5	130	24	12.5
AA621557	Hs.58633	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WA	5.5	315	58	3.1
A1051902	Hs.4112	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coen	5.5	55	10	4.2
AA418089	Hs.241391	natural killer-tumor recognition sequence	5.5	63	12	1
T26989	Hs.121376	aspartate beta-hydroxylase	5.5	79	15	4.4
AA143019	Hs.182667	ESTs; Highly similar to surface 4 integral membrane prote	5.5	90	17	2.9
W90146	Hs.35962	ESTs	5.5	168	31	4.4
N37065	Hs.44856	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WA	5.5	323	59	10.5
T23983	Hs.7365	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WA	5.5	186	34	16.5
AA130273	Hs.7584	ESTs; Weakly similar to (define not available 4240269) [H BCF3	5.5	55	1	5.2
AA262942	Hs.79741	ESTs	5.5	343	62	2.5
M86546	Hs.155691	pre-B-cell leukemia transcription factor 1	5.4	160	34	15.9
U15632	Hs.2126	dual specificity phosphatase 5	5.4	137	26	2.5
AA338760	Hs.15169	ESTs	5.4	54	1	4.4
AA460350	Hs.22370	ESTs	5.4	75	14	0.8
AA133250	Hs.62180	ESTs	5.4	54	1	4
N22414		*yvw39a07.s1 Weizmann Olfactory Epithelium Homo sapie	5.4	54	1	3.7
N63623	Hs.220470	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WA	5.4	54	1	4.3
W60473	Hs.57787	ESTs	5.4	54	1	4.1
AA287115	Hs.99697	ESTs	5.4	54	10	2.5
AA313639	Hs.185793	ESTs	5.4	73	14	8.8
M14219	Hs.76152	discom	5.4	144	27	13.3
N79749	Hs.87627	ESTs	5.4	81	15	2.6
H89575	Hs.93468	ESTs	5.4	259	48	1.4
D59894	Hs.34782	ESTs	5.4	483	90	4
AA485223	Hs.34892	ESTs	5.4	192	36	4.4
U43189	Hs.82143	Human Ets transcription factors NERF-1a and NERF-1b (	5.3	53	1	4.8
AA347973	Hs.221132	ESTs	5.3	67	13	5.3
AA459657	Hs.12311	Homo sapiens clone 23570 mRNA sequence	5.3	166	32	14.9
AA130596	Hs.71331	ESTs; Weakly similar to potent heat-stable protein phosph	5.3	53	1	2.8
RA5175	Hs.117183	ESTs	5.3	53	6	2.3
Z39549	Hs.153746	ESTs	5.3	53	5	0.9
AA292655	Hs.96557	ESTs	5.3	58	11	3.3
F02641	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.3	53	9	3.6
AA610070	Hs.151469	ESTs; Highly similar to CASK [H.sapiens]	5.3	53	9	3.2
W52493	Hs.13531	ESTs	5.3	53	1	4.1
H46617	Hs.172241	*yp19h1.r1 Soares breast 3NbhBst Homo sapiens cDNA	5.3	144	27	13.1
AA449887		ESTs	5.2	52	1	4.3
AA101416	Hs.107149	ESTs	5.2	52	3	2.3
AA406546	Hs.71968	ESTs	5.2	405	78	10.1
AA465701	Hs.108646	ESTs	5.2	52	4	3.9
W80702	Hs.58461	ESTs	5.2	52	6	1.8
AA837495	Hs.69851	ESTs; Weakly similar to Wiskott-Aldrich syndrome protein	5.2	81	16	1.1
AA090695	Hs.181385	ESTs	5.2	75	15	6.4
AA132007	Hs.167420	ESTs	5.2	251	48	21
Y00503	Hs.182265	keratin 19	5.2	1320	256	3.2
AA418230	Hs.8172	ESTs; Weakly similar to alternatively spliced product using	5.2	52	1	4.9
M22995	Hs.855	RAP1A; member of RAS oncogene family	5.2	52	1	3
U89328	Hs.87223	bone morphogenetic protein receptor; type IB	5.2	52	5	3.5
X53629	Hs.2977	cadherin 3; P-cadherin (placental)	5.2	331	64	1.5
AA122147	Hs.64691	Homo sapiens mRNA for KIAA0483 protein; partial cds	5.2	117	23	5
D14878	Hs.82043	D123 gene product	5.1	106	21	9.2
AA236859	Hs.8788	ESTs; Weakly similar to neuronal thread protein AD7c-NT	5.1	181	36	15.8
AA598710	Hs.23740	ESTs	5.1	298	59	4.4

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FIGURE 10

(CONT.)

AA252663	Hs. 67729	ESTs	5.1	51	1	4.2
AA456099	Hs. 176376	ESTs	5.1	51	1	2
AA479382	Hs. 47144	ESTs	5.1	190	35	17.9
AA398302	Hs. 127437	ESTs	5.1	51	1	2.4
V68502	Hs. 190201	ESTs; Weakly similar to Hs. ALU CLASS C WARNING EN	5.1	58	12	5.7
RS1273	Hs. 79020	ESTs	5.1	51	9	3.8
N46085	Hs. 92308	ESTs	5.1	150	30	7.2
N33236	Hs. 28555	ESTs	5.1	51	1	3.9
N22898	Hs. 1846	tumor protein p53 (Li-Fraumeni syndrome)	5.1	87	19	9.3
W44735	Hs. 9286	ESTs	5.1	51	5	4.5
Z39053	Hs. 27263	ESTs	5.1	113	22	6.1
U67319	Hs. 6216	caspace 7, apoptosis-related cysteine protease	5	66	13	5.3
AA004415	Hs. 106106	ESTs	5	468	94	4.7
F10770	Hs. 180378	Homo sapiens clone 669 unknown mRNA; complete sequ	5	50	5	4.1
N26101	Hs. 7838	ESTs	5	50	1	4.3
N36421	Hs. 107854	ESTs; Moderately similar to Hs. ALU SUBFAMILY SQ WA	5	50	1	4.7
N57773	Hs. 93560	ESTs; Weakly similar to Similar to Rat trg gene product [C	5	50	2	3.1
N93839	Hs. 39288	ESTs; Weakly similar to Hs. ALU SUBFAMILY SB WARNIN	5	50	5	4.7
AA608679	Hs. 108327	damage-specific DNA binding protein 1 (127kD)	5	121	25	5.9
AI362972	Hs. 82128	ST4 oncofetal trophoblast glycoprotein	5	285	58	1.2
V78968	Hs. 241880	H3 histone; family 3A	5	264	53	3.4
AA129465	Hs. 106843	ESTs; Weakly similar to hypothetical protein [H.sapiens]	5	50	1	3.3
H88033	Hs. 106727	Homo sapiens mRNA for KIAA0733 protein; partial cds	5	64	13	6.3
UB4573	Hs. 41270	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine h	5	225	45	9.1
N59764	Hs. 5398	GUANINE-MONOPHOSPHATE SYNTHETASE	5	50	1	4.1
H06195	Hs. 7194	ESTs	5	110	22	9.7
U47414	Hs. 79069	cyclin G2	5	50	1	3.2
HG3510-HT3704		V-Erba Related Ear-3 Protein	5	62	17	6.9
U24576		LIM domain only 4	4.9	49	1	3.8
X65724	Hs. 2839	Nerrie disease (pseudoglioma)	4.9	49	5	3.8
X98263	Hs. 152720	M-phase phosphoprotein 6	4.9	153	31	2.4
AA315807	Hs. 106227	ESTs; Weakly similar to (define not available 4200325) [H	4.9	49	1	4.2
AA349014	Hs. 23412	ESTs	4.9	49	1	4.5
AA446949	Hs. 6236	ESTs	4.9	337	70	2.7
AA456981	Hs. 35349	ESTs	4.9	49	1	4.1
AA193592	Hs. 42300	ESTs; Moderately similar to Hs. ALU SUBFAMILY SQ WA	4.9	121	25	10.4
H28581	Hs. 92711	ESTs	4.9	108	22	9
N51058	Hs. 38991	ESTs	4.9	49	1	4.4
AA430487	Hs. 95424	ESTs	4.9	49	7	3.7
AA442868	Hs. 12531	ESTs; Weakly similar to (define not available 5081652) [H	4.9	68	14	1.4
AA435633	Hs. 16879	Homo sapiens clone 23965 mRNA sequence	4.9	49	1	4.3
RS5185	Hs. 3321	ESTs; Highly similar to iroquois-class homeodomain prote	4.9	632	129	1.7
AA257056	Hs. 7972	Homo sapiens mRNA for KIAA0871 protein; complete cds	4.9	49	1	4.1
AA455917	Hs. 50785	SEC22, vesicle trafficking protein (S. cerevisiae)-like 1	4.9	49	1	4.4
AA329274	Hs. 82911	protein tyrosine phosphatase type IVA; member 2	4.9	153	34	15.1
D87969	Hs. 82921	CMP-sialic acid transporter	4.9	49	3	3.8
AA461712	Hs. 171581	ESTs	4.9	49	1	3.7
X95585	Hs. 180139	H. sapiens mRNA for SMT3B protein	4.9	261	53	3.7
M21389	Hs. 195850	keratin 5 (epidermolysis bullosa simplex; Dowling-Meara/K	4.8	622	130	0.7
AA001049	Hs. 24713	ESTs	4.8	231	49	7.3
AA280670	Hs. 24968	ESTs	4.8	79	17	5.2
AA398533	Hs. 22209	ESTs	4.8	134	28	3.2
DS1095	Hs. 35861	ESTs	4.8	48	8	3.1
AA132983	Hs. 44155	ESTs; Moderately similar to C-1-TETRAHYDROFOLATE	4.8	96	20	6.5
N69514	Hs. 28877	ESTs; Weakly similar to predicted using GeneFinder [C. ele	4.8	51	13	5.6
R73468	Hs. 140996	ESTs	4.8	48	2	3.4
AA258030	Hs. 55356	ESTs; Weakly similar to (define not available 3874821) [C	4.8	48	1	4.4
AA489046	Hs. 94109	ESTs	4.8	179	38	2.8
H88261	Hs. 120093	ESTs	4.8	48	1	2.5
H97225	Hs. 38592	ESTs	4.8	48	1	0.9

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FIGURE 10

(CONT.)

AA236010	Hs.26513	ESTs	4.8	48	1	0.5
AA748483	Hs.191355	Homo sapiens basic transcription factor 2 p44 (bt2p44) g	4.8	48	5	4.1
AA412106	Hs.191803	ESTs	4.8	106	22	1
AA513722	Hs.173729	collagen, type XI, alpha 1 (Schmid metaphyseal chondrodysplasia)	4.8	312	65	30.9
X74987	Hs.12013	ribonuclease L (2',5'-oligoadenylate synthetase-dependent)	4.8	48	8	3.8
AA609427	Hs.210706	ESTs; Moderately similar to Hs.111 ALU SUBFAMILY SP WAR	4.8	48	1	4.1
AA459555	Hs.31921	Homo sapiens mRNA for KIAA0648 protein; partial cds	4.8	48	1	4.6
W79865	Hs.58367	glypican 4	4.8	48	1	3.6
X06323	Hs.79086	Human MRL3 mRNA for ribosomal protein L3 homologue	4.8	246	51	3.9
AA165231	Hs.8184	ESTs	4.8	53	11	3.7
R38185	Hs.83954	ESTs; Moderately similar to (define not available 4335943)	4.8	153	32	4.3
AA129390	Hs.5285	ESTs	4.8	93	20	3.1
D14651	Hs.119	gene predicted from cDNA with a complete coding sequence	4.7	119	26	3
D25538	Hs.172199	adenylate cyclase 7	4.7	47	1	4.3
D26361	Hs.3104	KIAA0042 gene product	4.7	47	4	0.7
HQ4557-HT4962	Hs.109253	"Small Nuclear Ribonucleoprotein U1, 1snp"	4.7	47	1	4.2
C02582	Hs.32478	ESTs; Highly similar to (define not available 5114045) [H]	4.7	229	49	7.9
AA040154	Hs.28423	ESTs	4.7	201	43	4.5
AA286809	Hs.25880	ESTs	4.7	152	33	5.3
AA412473	Hs.12244	ESTs	4.7	47	1	4
AA026594	Hs.26885	ESTs; Weakly similar to Hs.111 ALU CLASS B WARNING EN	4.7	47	4	4.3
N24716	Hs.122576	ESTs	4.7	47	4	4.2
R68425	Hs.131189	ESTs; Moderately similar to Hs.111 ALU SUBFAMILY SQ WA	4.7	54	12	4.5
AA055768	Hs.122576	ESTs	4.7	770	166	5.8
AA165313	Hs.131189	ESTs	4.7	57	12	4.7
AA478625	Hs.241676	stromal cell-derived factor 1	4.7	59	13	4.7
AA044840	Hs.227459	ESTs; Moderately similar to Hs.111 ALU SUBFAMILY SP WAR	4.7	114	25	0.9
N90960	Hs.137947	ESTs	4.7	151	32	9.3
AA873285	Hs.75337	Human mRNA for KIAA0035 gene; partial cds	4.7	47	3	4.4
D21262	Hs.76173	ESTs	4.7	47	1	4
AA214305	Hs.9946	ESTs	4.7	47	1	4.1
AA235803	Hs.168017	ESTs; Weakly similar to heat shock protein hsp40 homologue BCL2	4.7	710	151	2.5
AA102520	Hs.26792	ESTs	4.7	556	119	4.5
AA491465	Hs.16869	ESTs	4.7	391	81	6.4
AA393803	Hs.82643	protein tyrosine kinase 9	4.7	747	158	5.7
U02680	Hs.1592	CDC16 (cell division cycle 16; S. cerevisiae, homolog)	4.6	148	32	11.3
U18291	Hs.247244	Homo sapiens Tiro mRNA, complete cds	4.6	151	33	2
AA476473	Hs.32793	ESTs	4.6	46	1	4
AA609943	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetyltransferase	4.6	71	16	3.6
T34527	Hs.7041	ESTs; Weakly similar to Hs.111 ALU SUBFAMILY SQ WARNING	4.6	199	44	19.2
W19222	Hs.42173	ESTs	4.6	46	4	4.3
AA400247	Hs.101174	microtubule-associated protein tau	4.6	46	2	1.8
H29532	Hs.136102	Homo sapiens mRNA for KIAA0853 protein; partial cds	4.6	163	35	7.3
N49406	Hs.53565	ESTs; Weakly similar to Hs.111 ALU SUBFAMILY J WARNING	4.6	46	1	3.9
W02102	Hs.57987	ESTs	4.6	60	13	4.8
W69134	Hs.48820	ESTs	4.6	46	7	0.5
AA412488	Hs.100261	ESTs	4.6	46	3	0.8
AA447504	Hs.11500	ESTs	4.6	46	8	3.9
AA437116	Hs.173542	ESTs	4.6	199	44	2.3
AA421139	Hs.29379	ESTs	4.6	239	93	3.5
N64405	Hs.47783	ESTs	4.6	46	7	3.8
AA431459	Hs.5070	ESTs	4.6	46	1	4.3
AA447230	Hs.71573	ESTs	4.6	46	1	4.4
AA135466	Hs.50421	KIAA0203 gene product	4.6	46	5	3.5
R38102	Hs.82777	collagen, type XI, alpha 1	4.6	69	15	5.8
J04177	Hs.176588	ESTs; Weakly similar to (define not available 4519535) [H] BCB1	4.6	1216	287	4.4
H25577	Hs.62817	ESTs	4.6	913	199	2.9
AA047036	Hs.154443	minichromosome maintenance deficient (S. cerevisiae) 4	4.6	427	93	10.4
AA148885	Hs.245174	a disintegrin and metalloproteinase domain 12 (matrin alpha)	4.6	195	43	10
AA190993			4.6	132	29	9.7

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FIGURE 10

(CONT.)

D37965	Hs.170040	platelet-derived growth factor receptor-like	4.5	45	4	4
U33052	Hs.69171	protein kinase C-like 2	4.5	45	1	3.6
U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.5	45	1	2.8
AA195399	Hs.24641	ESTs	4.5	45	1	3.6
AA233168	Hs.3585	ESTs; Weakly similar to coded for by C. elegans cDNA CE	4.5	45	10	0.5
AA281623	Hs.7625	ESTs; Weakly similar to (define not available 3882205) [H	4.5	45	1	3.7
AA435542	Hs.25796	ESTs	4.5	116	26	4.5
AA489790	Hs.167496	Homo sapiens Ran-GTP binding protein mRNA; partial cd	4.5	45	1	3.8
AA036811	Hs.169030	ESTs	4.5	45	4	2.6
W94942	Hs.177534	ESTs; Weakly similar to dual-specificity protein tyrosine ph	4.5	45	2	3
Z40861	Hs.6540	ESTs	4.5	290	65	3.7
AA253217	Hs.41271	ESTs	4.5	96	21	7.8
AA279943	Hs.122579	ESTs	4.5	45	9	3.4
AA459956	Hs.49183	ESTs	4.5	96	22	6.9
F04816	Hs.92127	ESTs	4.5	211	47	5
N39214	Hs.44708	ser-Thr protein kinase related to the myotonic dystrophy p	4.5	45	2	3.6
AA621785	Hs.170008	ESTs	4.5	45	1	2.4
X56199	Hs.244401	constitutive androstane receptor-beta; orphan nuclear hor	4.5	45	1	2.5
Z38919	Hs.21929	ESTs	4.5	137	31	12
AA430008	Hs.8117	ESTs	4.5	45	2	3.4
D38073	Hs.178565	minichromosome maintenance deficient (S. cerevisiae) 3	4.5	1472	330	2.1
U41060	Hs.79136	Human breast cancer; estrogen regulated LIV-1 protein (L. BCR4	4.5	129	29	3.1
D78611	Hs.79284	mesoderm specific transcript (mouse) homolog CBC1	4.5	390	87	5.3
T17185	Hs.4299	ESTs	4.4	255	58	1.6
U85658	Hs.61796	transcription factor AP-2 gamma (activating enhancer-bind	4.4	174	40	1.6
AA412059	Hs.26864	ESTs	4.4	222	51	1.8
AA452590	Hs.30349	ESTs	4.4	371	84	3.2
AA484708	Hs.249247	ESTs; Weakly similar to alternatively spliced product using	4.4	73	17	6.2
AA005528	Hs.42743	ESTs; Weakly similar to predicted using GeneFinder [C.ile	4.4	103	24	3.8
H97678	Hs.31319	ESTs	4.4	44	6	2.3
W02713	Hs.11732	ESTs	4.4	104	24	5.1
Z39211	Hs.150926	fucose-1-phosphate guanylyltransferase	4.4	44	1	3
AA024804	Hs.26102	ESTs	4.4	44	7	1.1
AA401474	Hs.209414	ESTs	4.4	44	1	3.1
W72967	Hs.191361	ESTs	4.4	48	11	0.9
AA425887	Hs.98502	ESTs	4.4	76	18	1
A1334393	Hs.18113	ESTs	4.4	44	1	3.8
N59212	Hs.236081	C-terminal binding protein 2	4.4	44	1	4.1
L07493	Hs.1608	replication protein A3 (14kD)	4.4	53	12	2.1
AA281770	Hs.184081	seven in absentia (Drosophila) homolog 1	4.4	44	1	4.1
X54199	Hs.82285	phosphoribosylglycylamide formyltransferase; phosphorib	4.3	77	16	7.2
X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glutamate gamma-sem	4.3	43	1	3.9
AA226968	Hs.22826	ESTs	4.3	772	179	1.7
AA268892	Hs.24391	ESTs	4.3	43	1	3.7
AA395414	Hs.28332	ESTs	4.3	101	24	1.6
AA465093	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein	4.3	43	10	2.2
AA489636	Hs.25253	ESTs	4.3	43	10	2.7
AA025728	Hs.61307	ESTs	4.3	43	1	2
N59543	Hs.15456	POZ domain containing 1	4.3	43	1	1
N69113	Hs.110655	ESTs	4.3	43	5	2.2
N69820	Hs.14659	ESTs	4.3	45	11	4.4
RS3439	Hs.194149	ESTs	4.3	43	8	3.6
W00439	Hs.119370	ESTs; Moderately similar to cbp145 [M.musculus]	4.3	819	191	1.2
V81552	Hs.242943	constitutive androstane receptor-beta; orphan nuclear hor	4.3	162	38	12.1
N79820	Hs.50854	ESTs	4.3	65	15	5.7
T78274	Hs.10175	ESTs	4.3	43	1	3.5
Z36290	Hs.173933	ESTs; Weakly similar to NUCLEAR FACTOR 1/K [H.sapie	4.3	66	18	2.8
R25607	Hs.23978	scaffold attachment factor B	4.3	152	35	12.5
AA916752	Hs.244697	ESTs; Highly similar to MEM3 [M.musculus]	4.3	43	1	3.9
N79516	Hs.73287	ESTs				

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FIGURE 10

(CONT.)

F13665	Hs.65841	ESTs	4.3	190	44	5.4
AB003103	Hs.4295	proteasome (prosome; macropain) 26S subunit; non-ATP	4.2	152	36	12.2
L37936	Hs.3273	Ts translation elongation factor; mitochondrial	4.2	50	12	4.4
U14518	Hs.1594	centromere protein A (17kD)	4.2	42	7	3.4
U90919	Hs.7137	Human clones 23657 and 23775 zinc finger protein mRNA	4.2	42	7	3.7
AA058946	Hs.33363	ESTs	4.2	135	32	4
AA171736	Hs.35947	ESTs; Highly similar to methyl-CpG binding protein MBD4	4.2	90	22	2.6
AA227145	Hs.209473	ESTs; Moderately similar to transformation-related protein	4.2	56	14	2.2
H08778	Hs.133521	ESTs	4.2	58	14	0.8
R40576	Hs.21590	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SC WARNIN	4.2	125	30	7.4
R06634	Hs.28403	ESTs	4.2	42	6	3.6
Z39898	Hs.21948	ESTs	4.2	46	11	1.4
AA251524	Hs.44649	ESTs	4.2	42	9	1.1
P08813	Hs.97410	ret finger protein-like 3 antisense	4.2	42	1	2.7
AA191353	Hs.22385	ESTs	4.2	124	30	1.8
AA412494	Hs.98152	ESTs	4.2	77	19	1.4
AA599786	Hs.112110	ESTs	4.2	42	7	2.9
R01073	Hs.191202	ESTs	4.2	42	7	3
AA504343	Hs.183475	ESTs; Moderately similar to !!!!! ALU SUBFAMILY J WARN	4.2	104	25	7.8
N30436	Hs.11356	ESTs	4.2	42	1	3.8
U38847	Hs.151518	TAR (HIV) RNA-binding protein 1	4.2	46	11	1.1
AA608856	Hs.431	murine leukemia viral (bmi-1) oncogene homolog	4.2	42	1	2.2
W85888	Hs.47334	ESTs; Moderately similar to !!!!! ALU SUBFAMILY SQ WA	4.2	159	38	7.1
AA453614	Hs.5460	Homo sapiens mRNA for KIAA0776 protein; partial cds	4.2	171	41	12.8
X57025	Hs.85112	insulin-like growth factor 1 (somatomedin C)	4.2	42	5	2.6
D63391	Hs.6793	platelet-activating factor acetylhydrolase; isoform Ib; gamm	4.2	187	44	5.4
AA427861	Hs.59503	ESTs	4.2	79	19	1.9
D14657	Hs.81892	KIAA0101 gene product	4.1	320	78	10.6
D29677	Hs.3085	KIAA0054 gene product	4.1	84	16	3
HG2755-HT262		T-Plastin	4.1	259	63	1.9
L05425		Homo sapiens autoantigen mRNA; complete cds	4.1	53	13	4
U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cytidyltrans	4.1	41	1	3.3
U79293	Hs.159264	Human clone 23948 mRNA sequence	4.1	41	1	2.4
X75042	Hs.44313	v-rel avian relictendotheliosis viral oncogene homolog	4.1	53	13	4.9
AA236950	Hs.8115	ESTs	4.1	41	2	3.3
H08748	Hs.20072	ESTs	4.1	41	7	1.7
N80430	Hs.6616	ESTs	4.1	41	1	2.6
AA436475	Hs.190104	ESTs	4.1	43	11	1.6
D82808	Hs.17820	Rho-associated; coiled-coil containing protein kinase 1	4.1	41	1	3.6
N77151	Hs.61638	Homo sapiens mRNA for KIAA0799 protein; partial cds	4.1	62	15	4.9
AA093348	Hs.7306	secreted frizzled-related protein 1	4.1	374	91	1.1
W95070	Hs.74316	desmoplakin (DPI; DPK)	4.1	640	158	3
AA243746	Hs.211577	ESTs; Highly similar to CG1 protein [H.sapiens]	4.1	301	73	6.1
AA169379	Hs.72695	ESTs	4.1	334	82	3.4
AA490890	Hs.105273	ESTs	4.1	72	18	1.5
O86961	Hs.79259	lipome HMGIC fusion partner-like 2	4	40	1	3.8
L28997	Hs.77102	ADP-ribosylation factor-like 1	4	110	28	10.7
AA281245	Hs.23317	ESTs	4	75	19	1.7
AA393793	Hs.110347	ESTs; Highly similar to (define not available 4465913) [H.	4	40	3	3.2
AA171755	Hs.181915	ESTs	4	40	7	1.1
R51818	Hs.104222	ESTs	4	70	18	6.8
W72471	Hs.23920	ESTs	4	48	12	4
T23820	Hs.155478	cyclin T2	4	40	4	1.2
T56679	Hs.865	RAP1A; member of RAS oncogene family	4	40	1	3.4
H03688	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding prote	4	40	4	3.2
N78483	Hs.24809	ESTs	4	95	24	1.1
U90551	Hs.28777	H2A histone family; member L	4	350	88	3
AA010163	Hs.3383	upstream regulatory element binding protein 1	4	140	35	1.8
W60186	Hs.169487	ESTs	4	452	114	2
L04656		carbonic anhydrase VIII	3.9	39	8	3.6

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FIGURE 10

(CONT.)

M27492	Hs.82112	interleukin 1 receptor, type I	3.9	39	2	3.5
X87613	Hs.155944	H.sapiens mRNA for skeletal muscle abundant protein	3.9	43	11	1
Y09443	Hs.22550	alkylglycerone phosphate synthase	3.9	49	13	2.5
AA227448	Hs.5003	Homo sapiens mRNA for KIAA0456 protein; partial cds	3.9	39	6	3.2
AA235303	Hs.8645	ESTs	3.9	79	20	6.5
AA398197	Hs.30029	ESTs	3.9	371	54	4.6
AA609210	Hs.19221	ESTs	3.9	98	25	8.6
N36001	Hs.17348	ESTs; Weakly similar to alternatively spliced product using	3.9	353	90	1.2
N67437	Hs.24375	ESTs	3.9	145	37	9.8
AA427528	Hs.114547	ESTs; Weakly similar to ZINC FINGER PROTEIN 84 [H.s]	3.9	39	8	2.2
AA521080	Hs.46765	ESTs	3.9	39	10	0.8
AA255923	Hs.109111	ESTs	3.9	161	42	2
AA400412	Hs.97794	ESTs	3.9	39	1	0.2
AA425374	Hs.193063	ESTs	3.9	39	1	0.2
AA600121	Hs.190253	ESTs	3.9	39	1	3.2
AA609471	Hs.112712	ESTs	3.9	39	5	3.7
AA370120	Hs.7870	ESTs; Weakly similar to Yhr350wp [S.cerevisiae]	3.9	47	12	4.4
H02692	Hs.99189	ESTs; Weakly similar to novel stromal cell protein [M.mus]	3.9	220	57	2.5
M28679	Hs.1051	granzyne B (granzyme 2; cytotoxic T-lymphocyte-associa	3.9	43	11	1.8
D13435	Hs.166982	phosphatidylinositol glycan; class F	3.9	54	14	5.1
N21679	Hs.180059	ESTs	3.9	39	1	1.9
D31263	Hs.15929	ESTs	3.9	39	1	2.6
AA477739	Hs.246856	ESTs	3.9	39	1	3.4
R49035	Hs.25176	ESTs	3.9	116	30	0.5
U66815	Hs.172280	SWI/SNF related; matrix associated; actin dependent regu	3.9	39	1	2.5
U23070	Hs.78776	Human putative transmembrane protein (msa) mRNA; co BCH9	3.9	442	114	1.3
N22107	Hs.172241	ESTs; Moderately similar to HIII ALU SUBFAMILY SC WARBCN7	3.9	322	83	4.4
AA609651	Hs.112742	ESTs	3.9	60	16	4.8
K01160		Accession not listed in Genbank	3.9	390	100	11.1
AA057193	Hs.25252	ESTs	3.9	280	72	3.3
D28137	Hs.118110	bone marrow stromal cell antigen 2	3.8	350	93	1.9
J05249	Hs.79411	replication protein A2 (32kD)	3.8	115	30	7.1
S80562	Hs.194682	calporin 3; acidic	3.8	399	105	3.3
U28368	Hs.34853	inhibitor of DNA binding 4; dominant negative helix-loop-h	3.8	163	43	0.5
U57721	Hs.81771	kynureninase; L-kynurenine hydrolase	3.8	38	1	1.5
Z74615	Hs.172928	collagen; type I; alpha 1	3.8	1612	429	3.1
R89920	Hs.127585	ESTs	3.8	38	4	1.2
AA027317	Hs.221929	ESTs; Weakly similar to HIII ALU SUBFAMILY J WARNING	3.8	40	11	3.8
AA084602	Hs.29669	ESTs	3.8	38	1	2.4
AA179826	Hs.32058	ESTs	3.8	38	2	3.2
AA233790	Hs.4104	ESTs	3.8	93	25	7.5
AA424006	Hs.22972	ESTs; Weakly similar to steroid 5-alpha-reductase Z [H.s]	3.8	38	1	3.3
AA429951	Hs.21104	ESTs	3.8	63	22	7.5
AA436836	Hs.35560	ESTs	3.8	38	1	1.9
AA456646	Hs.28661	ESTs	3.8	263	69	3.9
AA489009	Hs.26994	ESTs	3.8	38	1	1.6
AA079468	Hs.94631	ESTs	3.8	38	1	3.2
AA179387	Hs.25264	ESTs	3.8	233	62	3.8
H42396	Hs.107872	ESTs	3.8	38	7	2.8
Z38909	Hs.22265	ESTs	3.8	73	19	1.8
AA478729	Hs.76450	ESTs	3.8	38	7	2.1
AA347422	Hs.238040	ESTs; Weakly similar to hypothetical protein [H.sapiens]	3.8	35	7	0.2
AA485458	Hs.181957	ESTs; Moderately similar to laminin-binding protein [H.sap	3.8	207	55	5.5
H05323	Hs.247496	ESTs	3.8	58	19	5.5
AA512802	Hs.7337	ESTs	3.8	38	1	3
N75007	Hs.199009	ESTs; Weakly similar to (define not available 4589652) [H	3.8	38	1	0.9
AA232276	Hs.22806	ESTs; Weakly similar to HIII ALU SUBFAMILY J WARNING	3.8	42	11	0.6
AA465527	Hs.23853	ESTs	3.8	38	1	3.3
AA418039	Hs.26155	ESTs	3.8	38	1	3
AA262821	Hs.28578	ESTs	3.8	79	21	6.9

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FIGURE 10
(CONT.)

AA599853	Hs.30695	transcription factor-like 5 (basic helix-loop-helix)	3.8	51	14	1.7
AA448297	Hs.237825	calcium/calmodulin-dependent protein kinase (CaM kinase)	3.8	38	1	3
AA174183	Hs.63072	ESTs	3.8	240	64	3.2
C00038	Hs.23576	ESTs	3.8	585	153	3.7
N91023	Hs.170057	ESTs	3.8	425	111	4
AA007160	Hs.14846	ESTs	3.8	82	22	3.1
AI167942	Hs.61835	Homo sapiens BAC clone RG041D11 from 7q21	3.8	38	1	2.7
AA569531	Hs.162859	ESTs	3.8	38	7	3.4
HG4297-HT4567		Transcriptional Coactivator Pcd	3.7	477	130	3.1
X53961	Hs.347	lactotransferrin	3.7	1421	388	1.9
AA434508		zwd1c1.1 Scores ovary tumor NbHOT Homo sapiens cD	3.7	37	7	2.1
R04534	Hs.101469	ESTs	3.7	37	5	2.5
AA126855	Hs.13268	ESTs	3.7	157	43	3.6
AA128548	Hs.90847	ESTs; Weakly similar to Similarity with yeast transcription	3.7	37	1	3.2
H03627	Hs.245209	ESTs	3.7	37	4	2
H53572	Hs.32407	ESTs	3.7	37	1	2.1
N68869	Hs.15119	ESTs	3.7	119	33	6.7
R52949	Hs.25978	ESTs	3.7	37	1	3
W80763	Hs.3849	ESTs; Moderately similar to FK506-binding protein 65kD [	3.7	239	65	3.6
AA504116	Hs.62501	ESTs	3.7	37	1	1.8
N04475	Hs.227342	H. sapiens mRNA similar to Xenopus laevis mRNA for KDE	3.7	37	6	0.5
R46061	Hs.92482	ESTs	3.7	37	4	3
W84767	Hs.58698	ESTs; Weakly similar to [H] ALU SUBFAMILY J WARNING	3.7	37	4	1.9
W86835	Hs.14158	copine III	3.7	590	159	3.8
AA280738	Hs.128879	ESTs	3.7	37	1	0.5
AA389441	Hs.104699	ESTs	3.7	37	10	1
AA495812	Hs.105384	ESTs	3.7	41	11	1.6
R28587	Hs.11000	Homo sapiens brain myo47 protein mRNA; complete cds	3.7	39	11	3.2
N87339	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.7	37	1	3.4
F09788	Hs.3622	procollagen-proline; 2-oxoglutarate 4-dioxygenase (prolin	3.7	37	9	2.8
X75535	Hs.168670	peroxisomal farnesylated protein	3.7	37	1	2.2
D15050	Hs.232088	*Human mRNA for transcription factor AREB6, complete c	3.7	91	25	2.8
W58612	Hs.173840	ESTs	3.7	41	11	0.6
AA121315	Hs.70823	KIAA1077 protein	3.7	625	168	3.8
AA477445	Hs.105341	ESTs	3.7	162	44	12.4
AA477571	Hs.152901	UDP-glucose ceramide glucosyltransferase	3.7	224	61	21
D89978	Hs.84790	Human mRNA for KIAA0225 gene; partial cds	3.6	36	7	3.2
M55542	Hs.62681	guanylate binding protein 1; interferon-inducible; 67kD	3.6	36	1	2.6
M81057	Hs.180884	carboxypeptidase B1 (tissue)	3.6	824	227	1.4
U90304	Hs.28351	iroquois-class homeodomain protein	3.6	142	39	1.6
AA282138	Hs.11325	ESTs	3.6	36	1	0.1
AA398346	Hs.21898	ESTs	3.6	68	19	9
AA399623	Hs.23505	ESTs	3.6	36	7	3.1
AA400517	Hs.22983	ESTs; Moderately similar to UDP-GLUCOSE-GLYCOPRO	3.6	45	13	1.3
AA417287	Hs.171391	C-terminal binding protein 2	3.6	444	125	4.6
AA417761	Hs.5957	Homo sapiens clone 24418 mRNA sequence	3.6	365	103	6.9
AA481495	Hs.14512	ESTs	3.6	210	58	4.7
AA489665	Hs.25245	ESTs	3.6	36	1	1.2
D59368	Hs.159872	ESTs	3.6	36	5	0.5
H53829	Hs.36823	ESTs	3.6	36	10	2.5
T93830	Hs.17207	ESTs	3.6	36	4	2.6
AA459020	Hs.50848	ESTs; Weakly similar to (define not available 4239895) [H	3.6	36	1	2
F01601	Hs.117485	ESTs	3.6	36	1	1.9
H09959	Hs.42768	ESTs; Weakly similar to (define not available 4689264) [H	3.6	41	12	2.8
N66413	Hs.172466	ESTs; Weakly similar to (define not available 3882271) [H	3.6	89	25	0.9
W73788	Hs.43213	ESTs	3.6	36	1	2.9
AA280794	Hs.241328	ESTs	3.6	36	8	0.2
AA426270	Hs.145696	ESTs	3.6	150	42	3.2
AA465196	Hs.107233	ESTs	3.6	36	1	3.4
W38240		Accession not listed in Genbank	3.6	36	11	2.6

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FIGURE 10

(CONT.)

AA714635	Hs.181287	ESTs		3.6	36	6	2.9
AA305536		EST176522 Colon carcinoma (Caco-2) cell line II Homo s		3.6	121	34	11.8
AA129640	Hs.128065	ESTs		3.6	36	10	1.9
D00763	Hs.243746	proteasome (prosome, macropain) subunit, alpha type; 4		3.6	130	36	3.5
D86959	Hs.105751	KIAA0204 gene product		3.6	36	5	1.5
X55330	Hs.207776	asparnylglucosaminidase		3.6	36	1	2.7
M95767	Hs.135578	chitinase: di-N-acetyl-		3.6	36	1	1.2
AA248405	Hs.19347	ESTs		3.6	100	28	8.8
AA234767	Hs.246093	ESTs		3.6	141	39	12.6
AA479933	Hs.46967	ESTs		3.6	96	1	3.1
AA287107	Hs.172945	ESTs: Weakly similar to ZINC FINGER PROTEIN 135 [H.		3.6	146	41	1.1
U69811	Hs.64311	a disintegrin and metalloproteinase domain 17 (tumor nec		3.6	36	1	3.1
AA284143	Hs.194369	Homo sapiens chromosome 1 atrophin-1 related protein (		3.6	39	11	0.4
U30827	Hs.166976	Human splicing factor SRp40-1 (SRp40) mRNA: complete		3.6	35	1	0.4
X76040	Hs.250165	Lon protease-like protein		3.6	36	1	2.8
N68921	Hs.34806	ESTs: Weakly similar to neogenin [H.sapiens]	BOW3	3.6	402	112	4.9
T95333	Hs.122730	ESTs: Weakly similar to Strabismus (D.melanogaster)	CVA9	3.6	224	63	4
H95039	Hs.32168	ESTs		3.6	282	79	1.7
AA509710	Hs.42562	ESTs: Weakly similar to similar to GTP-binding protein [C.		3.6	256	72	3.7
DA2084	Hs.82007	Human mRNA for KIAA0094 gene; partial cds		3.5	96	28	1.3
D80604	Hs.75009	Human mRNA for KIAA0182 gene; partial cds		3.5	78	23	4.8
D87453	Hs.122669	Human mRNA for KIAA0264 gene; partial cds		3.5	35	9	3.1
HG371-HT1053		"Mucin 1, Epithelial, Alt. Splice 6"		3.5	37	11	2.8
U90651	Hs.151461	embryonic ectoderm development protein		3.5	35	1	2.7
AA232215	Hs.14600	ESTs		3.5	35	7	2.7
AA258873	Hs.25242	ESTs		3.5	73	21	1.6
AA417034	Hs.23019	ESTs: Weakly similar to ZINC FINGER PROTEIN 135 [H.		3.5	53	15	1.2
AA482035	Hs.28070	KIAA0753 gene product		3.5	58	17	1.6
AA504144	Hs.22315	ESTs		3.5	180	52	2.3
T74445	Hs.5957	"yc826.r1 Soares infant brain 1N1B Homo sapiens cDNA		3.5	35	1	2.6
AA018021	Hs.173091	Homo sapiens HCG-1 protein (HCG-1) mRNA: complete c		3.5	282	80	3.7
AA025315	Hs.61184	ESTs		3.5	35	1	1
AA129968	Hs.49376	ESTs: Weakly similar to PROTEIN PHOSPHATASE PP2A		3.5	35	1	3.2
H89315		"yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA		3.5	35	8	1.9
N51374	Hs.96870	ESTs		3.5	35	9	3.2
R08850	Hs.9786	ESTs		3.5	35	1	2.1
R33468	Hs.24651	ESTs		3.5	105	30	9.6
R49482	Hs.5637	ESTs		3.5	507	145	3.3
R49483	Hs.22159	ESTs: Weakly similar to finger protein HZF10; Krueppel-re		3.5	40	12	2.5
R54822	Hs.26244	ESTs		3.5	41	12	3.7
T66847	Hs.194040	ESTs		3.5	35	1	1.4
W96222	Hs.34192	ESTs		3.5	35	6	3.2
AA459703	Hs.79070	ESTs: Moderately similar to coded for by C. elegans cDNA		3.5	35	8	3.3
N24954	Hs.42502	ESTs		3.5	72	21	1.3
N89881	Hs.44577	ESTs		3.5	35	1	2.9
AA377296	Hs.97104	ESTs		3.5	37	11	0.1
AA410383	Hs.100431	B-cell-homing chemokine (ligand for Burkitt's lymphoma re		3.5	35	1	2.6
AA412151	Hs.235402	ESTs		3.5	143	41	2.6
AA428213	Hs.98523	ESTs		3.5	35	3	2.3
AA454103	Hs.110031	ESTs		3.5	35	1	3
AI479264	Hs.13058	ESTs		3.5	35	4	3.3
AA936428	Hs.128638	ESTs		3.5	35	1	3.1
AI369594		aryl sulfatase D		3.5	113	33	1.7
U68522	Hs.155485	"Human huntingtin interacting protein (HIP2) mRNA, comp		3.5	79	23	2.5
U25997	Hs.25590	stanniocalcin		3.5	402	114	2.1
AA090617	Hs.247614	ESTs		3.5	35	1	2.5
AA599801	Hs.239507	ESTs		3.5	73	21	6.3
AA496037	Hs.60293	ESTs		3.5	110	32	2.1
N30704	Hs.238797	ESTs		3.5	35	7	2.1
X72755	Hs.77367	monokine induced by gamma interferon	BCA6	3.5	796	228	3.2

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FIGURE 10

(CONT.)

W72838	Hs.58213	ESTs	BCR1	3.5	2073	595	2.1
R45698	Hs.21893	ESTs	CZA1	3.5	124	35	6.5
X54941	Hs.77550	CDC28 protein kinase 1		3.5	332	94	3.1
Y00815	Hs.75216	protein tyrosine phosphatase; receptor type; F		3.5	564	162	1.7
D31888	Hs.78398	Homo sapiens clone 24709 mRNA sequence		3.4	77	23	5.9
D87470	Hs.75400	Human mRNA for KIAA0280 gene; partial cds		3.4	34	1	1.2
X85750	Hs.79889	H.sapiens mRNA for transcript associated with monocyte		3.4	34	8	2.3
AA004211	Hs.30977	ESTs; Weakly similar to putative p150 [H.sapiens]		3.4	154	45	3
AA292711	Hs.29131	ESTs		3.4	34	1	3.1
AA400093	Hs.32271	ESTs; Weakly similar to [Hs] ALU SUBFAMILY SP WARNIN		3.4	34	8	2.9
AA401633	Hs.22390	ESTs		3.4	34	1	1.5
AA412505	Hs.10653	ESTs		3.4	49	15	4.4
AA417067	Hs.13055	ESTs		3.4	116	35	2.2
D51235	Hs.82689	tumor rejection antigen (gp96) 1		3.4	251	74	23.7
AA044181	Hs.82677	ESTs		3.4	34	1	2.3
AA129933	Hs.71168	Homo sapiens clone 24674 mRNA sequence		3.4	34	1	2.8
AA156460	Hs.44229	ESTs		3.4	34	1	2.6
AA167708	Hs.52184	ESTs		3.4	71	21	2.4
N48603	Hs.14947	ESTs		3.4	115	34	2.4
N95837	Hs.169111	ESTs		3.4	314	91	2.4
AA406968	Hs.82689	ESTs		3.4	34	8	1
N79496	Hs.50824	EST		3.4	740	217	2.8
T78324	Hs.90905	ESTs		3.4	34	3	2.4
W73057	Hs.58272	ESTs; Moderately similar to alternatively spliced product u		3.4	34	1	2.5
AA171739	Hs.101590	ESTs		3.4	34	1	1.7
AA251973	Hs.143853	ESTs		3.4	34	4	0.1
AA406293	Hs.193498	ESTs		3.4	34	1	0.8
AA418988	Hs.96514	ESTs		3.4	34	10	0.7
AA598899	Hs.112493	ESTs		3.4	34	1	2.6
AA621348	Hs.227933	ESTs; Highly similar to (define not available 5281121) [H.		3.4	80	24	3.8
R41933	Hs.140237	ESTs; Weakly similar to neuronal threat protein AD7c-NT		3.4	210	63	3.3
T91518		*ye2005.s1 Stratagene lung (#937210) Homo sapiens cD		3.4	985	286	2.8
R56892	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase		3.4	234	68	10.7
AA219081	Hs.242396	ESTs; Moderately similar to [Hs] ALU SUBFAMILY SB2 WA		3.4	107	32	9.9
W46810	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2		3.4	525	154	5.3
X96098	Hs.3238	adenovirus 5 E1A binding protein		3.4	115	34	9.1
H96225	Hs.42151	ESTs		3.4	59	17	4
N41849	Hs.119410	Homo sapiens cytokine receptor related protein 4 (CYTOR		3.4	34	2	3
AA386284	Hs.5337	ESTs		3.4	193	58	12.3
X78627	Hs.75066	translin		3.4	178	53	8.8
C02374	Hs.7822	ESTs		3.4	91	27	8.5
C06270	Hs.8078	Homo sapiens clone FBD3 Cri-du-chat critical region mRN		3.4	34	5	2.6
AA481414	Hs.8868	golgi SNAP receptor complex member 1		3.4	179	52	1.5
AA262727	Hs.12144	ESTs		3.4	88	26	1.4
N77698	Hs.97498	YY1 transcription factor		3.4	475	142	2.5
AA215333	Hs.97101	ESTs	CXA1	3.4	169	50	9.1
X70683	Hs.83484	SRY (sex determining region Y)-box 4		3.4	495	144	1.6
N81017	Hs.42679	ESTs		3.4	118	35	2.3
HG2874-HT3018		Ribosomal Protein L39 Homolog		3.3	116	36	2.2
HG4036-HT4306		Retinoblastoma 1		3.3	33	1	0.8
M84805	Hs.957	Human putative opioid receptor mRNA; complete cds		3.3	36	11	2.4
U43286	Hs.118725	Human selenophosphate synthetase 2 (SPS2) mRNA; co		3.3	111	34	7.5
X88733	Hs.234725	alpha-1-antitrypsin		3.3	1497	458	2.1
Z35402	Hs.194657	H.sapiens gene encoding E-cadherin, exon 3 and joined		3.3	745	229	1.8
AA251297	Hs.23439	ESTs		3.3	206	63	2.2
AA350771	Hs.17850	ESTs		3.3	98	30	4.7
AA427816	Hs.11803	ESTs		3.3	95	29	4.4
AA434441	Hs.173859	frizzled (Drosophila) homolog 7		3.3	97	30	6.4
AA487561	Hs.5566	ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1A		3.3	606	214	1.8
AA598820	Hs.3530	TLS-associated serine-arginine protein		3.3	228	69	2.8

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FIGURE 10

(CONT.)

AA137078	Hs.173848	ESTs	3.3	33	5	1.7
AA171525	Hs.183867	ESTs	3.3	33	1	2.9
AA227119	Hs.171558	sex comb on midleg (Drosophila)-like 2	3.3	39	12	1.5
H61560	Hs.161011	EST	3.3	33	1	1.8
H86553	Hs.188006	Homo sapiens mRNA for KIAA0878 protein; complete cds	3.3	138	42	3.6
N69287	Hs.21943	ESTs	3.3	33	1	1.1
R44538	Hs.140889	ESTs	3.3	33	10	2.3
W37382	Hs.11090	ESTs	3.3	744	227	2.5
W42845	Hs.14611	dual specificity phosphatase 11 (RNA-RNP complex 1-inte	3.3	180	54	2.1
Z39742	Hs.247047	ESTs	3.3	33	1	2.4
AA150043	Hs.11498	ESTs	3.3	168	51	7.3
AA261819	Hs.88367	ESTs	3.3	33	1	3
AA481256	Hs.88201	ESTs; Weakly similar to (define not available 3859560) [H	3.3	106	33	9.8
D51276	Hs.81915	leukemia-associated phosphoprotein p18 (statthmin)	3.3	931	279	5.6
H91164	Hs.237404	ESTs; Moderately similar to [!!!] ALU SUBFAMILY SQ WA	3.3	33	1	2.3
N67889	Hs.49397	ESTs	3.3	81	25	1.5
N98488	Hs.161545	EST	3.3	35	11	0.6
R39281	Hs.90750	ESTs	3.3	167	51	2.6
W43000	Hs.159225	ESTs	3.3	33	8	0.9
W52480	Hs.56148	ESTs; Moderately similar to (define not available 5350125	3.3	33	10	0.5
AA227837	Hs.210566	ESTs; Moderately similar to [!!!] ALU SUBFAMILY SC WAR	3.3	33	10	2.8
AA347419	Hs.96870	ESTs	3.3	33	3	0.2
AA446190	Hs.99051	ESTs	3.3	53	16	4
AA480103	Hs.111730	ESTs	3.3	207	63	3.5
N53976	Hs.179864	ESTs	3.3	33	1	1.7
W72949	Hs.77495	Human mRNA for KIAA0242 gene; partial cds	3.3	34	11	3.2
H22147	Hs.245474	ESTs; Moderately similar to [!!!] ALU SUBFAMILY SP WAR	3.3	33	9	0.9
U31875	Hs.152677	short-chain alcohol dehydrogenase family member	3.3	105	32	3
W15528	Hs.106390	ESTs	3.3	288	87	7.9
X84373	Hs.155017	nuclear receptor interacting protein 1	3.3	354	108	4
X60486	Hs.46423	H4 histone family; member G	3.3	979	298	2.2
AA176475	Hs.4864	Homo sapiens mRNA for KIAA0892 protein; partial cds	3.3	33	4	2.9
AA253330	Hs.5344	ESTs	3.3	908	274	3.2
N26645	Hs.58220	Homo sapiens clone 24723 cDNA sequence	3.3	61	19	5.1
AA142857	Hs.234898	ESTs; Highly similar to geminin [H. sapiens]	3.3	106	33	2.6
AA218562	Hs.68855	neuroblastoma RAS viral (v-ras) oncogene homolog	3.3	33	1	2.9
M33882	Hs.76391	myxovirus (influenza) resistance 1; homolog of murine (in	3.3	380	114	4.9
W84712	Hs.7753	calumenin	3.3	889	267	5
S80437	Hs.83190	*fatty acid synthase (3' region) [human, breast and HepG2	3.3	710	217	2
N21407	Hs.247471	ESTs	3.3	33	1	2
C15324	Hs.93668	ESTs	3.3	1296	394	2.2
D30756	Hs.244822	membrane component; chromosome 17; surface marker 2	3.3	33	1	2.6
T32108	Hs.153315	ESTs	3.3	571	171	2
AA455687	Hs.25057	ESTs	3.3	775	233	2.4
D86969	Hs.82292	KIAA0215 gene product	3.2	32	2	2.9
X06272	Hs.75730	signal recognition particle receptor ('docking protein')	3.2	58	18	5
X15875	Hs.198166	activating transcription factor 2	3.2	32	4	2.6
Z35491	Hs.41714	BCL2-associated athanogene	3.2	41	13	2.8
Z60781	Hs.249216	H2B histone family; member J	3.2	32	5	2.8
AA314389	Hs.203994	ESTs; Weakly similar to (define not available 4502227) [H	3.2	32	9	2.7
D55869	Hs.173138	ESTs	3.2	32	7	2.4
AA088228	Hs.18272	ESTs	3.2	522	165	1.9
AA112361	Hs.10592	ESTs	3.2	32	4	2.9
AA148859	Hs.179909	ESTs; Moderately similar to [!!!] ALU SUBFAMILY J WARN	3.2	32	1	3
AA255874	Hs.23458	ESTs	3.2	466	146	8.4
AA255996	Hs.3862	ESTs	3.2	32	6	1.5
AA279991	Hs.124691	ESTs	3.2	32	1	1
AA369245	Hs.17448	ESTs; Moderately similar to [!!!] ALU SUBFAMILY SC WAR	3.2	143	46	3.6
AA419609	Hs.170121	ESTs; Weakly similar to ETX1 (alternatively spliced) [H.sa	3.2	267	83	2.3
AA439623	Hs.158249	KIAA0406 gene product	3.2	37	12	2.6

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FIGURE 10

(CONT.)

T63174	Hs.193700	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WAR	3.2	110	35	9.6
AA004806	Hs.60090	ESTs	3.2	32	5	2.1
AA111879	Hs.69507	EST	3.2	32	5	1.7
AA180453	Hs.73643	ESTs	3.2	32	1	2.2
AA233342	Hs.90680	ESTs; Weakly similar to Unknown gene product [H.sapien]	3.2	286	91	5.7
F10024	Hs.220640	ESTs	3.2	41	13	3.3
H09594	Hs.10299	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WA	3.2	136	43	3.6
R38436	Hs.21181	ESTs	3.2	37	12	3.5
T23860	Hs.7312	ESTs	3.2	99	31	3.1
W60002	Hs.4114	plastin 3 (T isoform)	3.2	238	75	2.1
AA258116	Hs.191533	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNII	3.2	49	16	4.2
AA435946	Hs.50831	ESTs	3.2	40	13	0.7
AA496000	Hs.4084	ESTs	3.2	173	55	3
N30205	Hs.93740	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WAR	3.2	35	11	0.7
N65763	Hs.43080	ESTs	3.2	378	117	2.8
Z41050	Hs.108787	Homo sapiens Mod4p homolog mRNA; complete cds	3.2	106	34	3.3
AA279654	Hs.194524	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WAR	3.2	32	5	0.6
AA287389	Hs.98267	ESTs	3.2	32	8	3
AA416568	Hs.98203	ESTs	3.2	32	1	0.6
AA431751	Hs.105711	eukaryotic translation initiation factor 4E binding protein 3	3.2	88	28	1.2
AA449121	Hs.99210	ESTs	3.2	291	91	4
AA454149	Hs.99357	EST	3.2	32	10	3.1
AA460324	Hs.99527	ESTs	3.2	38	11	2.5
H90150	Hs.13366	Homo sapiens mRNA; cDNA DKFZp566F133 (from clone	3.2	32	1	1.5
W78134	Hs.122647	N-myristoyltransferase 2	3.2	37	12	3.6
AA488132	Hs.62741	ESTs	3.2	32	10	2.9
L12350	Hs.108823	thrombospondin 2	3.2	814	257	2.4
J04076	Hs.1395	early growth response 2 (Krox-20 (Drosophila) homolog)	3.2	32	1	0.2
D60074	Hs.169833	ESTs; Highly similar to (define not available 4689144) [H.	3.2	87	27	1.7
H44396	Hs.22666	ESTs	3.2	210	66	3.8
U28174	Hs.3066	granzyme K (serine protease; granzyme 3; tryptase II)	3.2	82	26	6.6
N51260	Hs.196275	ESTs	3.2	207	64	5.5
X52947	Hs.74471	gap junction protein; alpha 1; 43kD (connexin 43)	3.2	351	111	5.2
Y00264	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II; Alz	3.2	226	71	2.8
L08044	Hs.169224	tretinoin factor 3 (intestinal)	3.2	1872	592	3.3
X04011	Hs.88574	cytochrome b-245; beta polypeptide (chronic granulomato	3.2	143	45	13.9
X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	3.2	153	48	4.7
L14622	Hs.166563	replication factor C (activator 1) 1 (145kD)	3.2	32	1	2.4
M23263	Hs.99915	androgen receptor (dihydrotestosterone receptor; testicula	3.2	117	37	9.4
AA156897	Hs.72157	ESTs; Highly similar to (define not available 4884194) [H. BCW1	3.2	725	227	3.2
AA521354	Hs.24758	ESTs	3.2	266	83	1.8
D21255	Hs.75929	cadherin 11 (OB-cadherin; osteoblast)	3.2	560	174	2.6
AA404352	Hs.178603	ESTs	3.2	372	115	2.1
D43772	Hs.86859	growth factor receptor-bound protein 7	3.1	306	98	1.5
L20320	Hs.184288	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cd	3.1	118	38	2
M55996	Hs.692	*human alpha-1 collagen type I gene, 3' end	3.1	2898	923	2.2
M53036	Hs.32943	membrane component; chromosomal 4; surface marker (3	3.1	353	116	2.8
U27185	Hs.35156	retinoic acid receptor responder (tazarotene induced) 1	3.1	31	1	1.3
AA148516	Hs.25320	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARN	3.1	31	1	2.5
AA447223	Hs.17138	ESTs	3.1	72	23	5
AA448850	Hs.4029	Glioma-amplified sequence-41	3.1	165	54	1.6
AA449741	Hs.247309	eukaryotic translation elongation factor 1 delta (guanine n	3.1	31	1	2.6
AA599472	Hs.18720	ESTs; Highly similar to (define not available 4323587) [H.	3.1	55	18	3.8
AA609053	Hs.35198	ESTs	3.1	75	24	2.2
AA025782	Hs.61284	ESTs	3.1	367	119	2.3
AA135894	Hs.194691	retinoic acid induced 3	3.1	31	9	2.2
N29454	Hs.27552	ESTs; Weakly similar to putative p150 [H.sapiens]	3.1	529	170	4.1
N40981	Hs.9856	ESTs	3.1	31	1	2.7
T92735	Hs.17061	ESTs	3.1	31	1	1.3
			3.1	453	148	7

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FIGURE 10

(CONT.)

Z38239	Hs.26962	ESTs	3.1	31	5	1.5	
AA417375	Hs.76917	ESTs; Weakly similar to KIAA0522 protein [H.sapiens]	3.1	58	19	2.5	
AA620761	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (from clone	3.1	119	39	2	
C20652	Hs.60501	ESTs	3.1	31	4	1.9	
H95785	Hs.167652	ESTs; Highly similar to CENP-E protein [H.sapiens]	3.1	38	13	1.7	
H98153	Hs.42500	ESTs	3.1	295	96	27.9	
N49667	Hs.46624	ESTs	3.1	31	1	2.7	
N66845	Hs.165411	ESTs; Weakly similar to !!!!! ALU CLASS B WARNING EN	3.1	199	64	1	
AA382275	Hs.97126	ESTs	3.1	31	1	0.4	
AA436890	Hs.98918	ESTs	3.1	31	1	1	
AA449453	Hs.192915	ESTs; Weakly similar to !!!!! ALU SUBFAMILY J WARNING	3.1	31	6	0.8	
AA608598	Hs.193534	ESTs	3.1	927	295	2.1	
H69206	Hs.5123	ESTs; Weakly similar to (define not available 4960208) [H	3.1	41	14	2.7	
N50641	Hs.80285	ESTs	3.1	31	1	1.8	
T90297	Hs.140571	ESTs	3.1	31	6	2.4	
W42680	Hs.95941	ESTs	3.1	31	1	2.8	
AA643322		*nr59c06.s1 NCL_CGAP_Lym3 Homo sapiens cDNA clon	3.1	31	1	2.5	
AA625690	Hs.190272	ESTs	3.1	33	11	2.3	
AI354332	Hs.72365	ESTs	3.1	31	3	2	
AA093378	Hs.101810	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SC WARNIN	3.1	172	55	3.1	
RA6843	Hs.10315	solute carrier family 7 (cationic amino acid transporter; y*	3.1	31	1	2.2	
W93562	Hs.105749	Homo sapiens mRNA for KIAA0553 protein; partial cds	3.1	34	11	2.7	
F11087	Hs.236668	ESTs	3.1	31	2	2.5	
T71333	Hs.13854	ESTs	3.1	31	3	3	
M31627	Hs.149923	X-box binding protein 1	3.1	1336	434	1.4	
AA121127	Hs.181307	ESTs	3.1	197	63	18.7	
W01996	Hs.3945	ESTs; Highly similar to (define not available 4929583) [H.	3.1	227	73	16.8	
AA393804	Hs.67052	H beta 58 homolog	3.1	359	118	2.5	
AA235289	Hs.247630	ESTs; Highly similar to rap2 gene product [H.sapiens]	3.1	234	76	8.6	
D63477	Hs.84087	Human mRNA for KIAA0143 gene; partial cds	3.1	147	48	12.7	
AC000115	Hs.9030	Human DNA sequence from PAC 196E23 on chromosom	3.1	31	1	2.3	
U84011	Hs.904	amylase-1,6-glucosidase; 4-alpha-glucanotransferase (glyco	3.1	31	1	2.6	
M74093	Hs.9700	cyclin E1	3.1	31	1	2.3	
N75308	Hs.99433	ESTs	3.1	31	10	1.7	
X54925	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	AAC1	3.1	94	30	5.8
X12876	Hs.65114	keratin 18	3.1	815	266	1.7	
M34309	Hs.199067	v-erbB-2 avian erythroblastic leukemia viral oncogene hom	3	68	23	2.8	
AA283300	Hs.9598	ESTs; Weakly similar to semaphorin C [M.musculus]	BCF1	3	30	10	0.9
AA609773	Hs.250175	Homo sapiens clone 23904 mRNA sequence	BCR2	3	816	275	3.9
AA505133	Hs.62273	ESTs	CAA2	3	380	127	5.5
HG2981-HT3127		*Epican. Alt. Splice 11*	3	594	201	2.3	
AA195936	Hs.76362	general transcription factor IIA; 1 (37kD and 19kD subunit	BCF5	2.9	114	39	9.9
AA419622	Hs.104800	ESTs	BCN1	2.9	214	74	3.7
R53457	Hs.26040	ESTs	BCX1	2.8	751	270	1.3
AA234561	Hs.22862	ESTs	BCZ1	2.8	131	47	3.9
AA428062	Hs.98558	ESTs	BCU7	2.7	864	321	0.6
AA620795	Hs.8207	ESTs	BCQ8	2.5	382	155	4.3
AA449749	Hs.31386	ESTs; Highly similar to secreted apoptosis related protein	BCW8	2.1	1561	757	1.7
C13992	Hs.93868	ESTs	BCQ7	1.8	1047	596	1.6
H85169	Hs.172455	solute carrier family 5 (inositol transporters); member 3	BCW2	1	1	1	1

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FIGURE 11

Accession	UniGene ID	UniGene Title	ratio tumor/ body	90%ile tumor	75%ile body	ratio tumor/ normal breast
AA126474	Hs.159223	stannocalcin 2	72.2	722	1	1.9
AA434329	Hs.36963	ESTs	BCJ7	40.2	402	4
AA250737	Hs.72472	ESTs	BCY2	35.9	359	10
X82153	Hs.63942	cathepsin K (pycnodysostosis)	34.3	411	12	5.1
X03635	Hs.1657	estrogen receptor 1	BCQ3	32.2	322	1
H09290	Hs.76550	ESTs: Weakly similar to unknown [H.sapiens]	30.6	306	4	26.5
AA428090	Hs.26102	ESTs	BCN2	29	290	1
AA419547	Hs.11713	ESTs	26.3	366	14	1
AA256485	Hs.182471	ESTs	BCQ2	25.4	508	20
N87239	Hs.10760	ESTs	BCX9	25.1	280	12
Z38595	Hs.129019	ESTs: Weakly similar to [H] ALU SUBFAMILY J WARNING	24.2	242	10	5.6
H25836	Hs.83429	tumor necrosis factor (ligand) superfamily, member 10	22.8	228	9	12.4
HG11763-HT1780		Prolactin-induced Protein	22.7	760	34	1.4
AA411621	Hs.8895	ESTs	21.2	212	6	17.4
N46252	Hs.29724	ESTs	BCX6	20.9	209	1
U05237	Hs.99872	fetal Alzheimer antigen	20.6	206	4	19.1
U48807	Hs.2359	dual specificity phosphatase 4	20.2	202	5	1.3
AA070801	Hs.51615	ESTs: Weakly similar to [H] ALU SUBFAMILY SQ WARN	18.7	187	1	17
U28831	Hs.44566	Human protein immuno-reactive with anti-PTH polyclonal antibodies	18.6	186	10	1.5
AA292066	Hs.240802	ESTs: Weakly similar to Br140 [H.sapiens]	17.5	175	2	12.8
N26722	Hs.42645	ESTs	BCY5	17.4	174	9
AA291725	Hs.105700	secreted frizzled-related protein 4	BCX2	17.4	409	24
AA065217	Hs.189674	ESTs	16.2	162	1	4.2
D13666	Hs.136348	osteoblast specific factor 2 (fascilin I-like)	BCA4	15.7	1030	66
AA621169	Hs.8687	ESTs	BCX8	15.6	156	7
L07615		"Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exo	15.3	153	1	14.1
AA007234	Hs.30098	ESTs	14.9	149	1	6.4
F01831	Hs.14838	ESTs	BCX4	14.6	219	15
N66818	Hs.42179	ESTs	BCY6	14.5	145	1
H05690	Hs.24639	ESTs	14.2	142	1	9.5
AA149007	Hs.243954	ESTs	13.7	137	1	8.9
D12485	Hs.11951	phosphodiesterase 1/nucleotide pyrophosphatase 1 (homo	BCA2	13.2	244	19
AA490262	Hs.15485	ESTs: Moderately similar to APXL gene product [H.sapien	BCU8	13.2	331	25
W93640	Hs.4779	ESTs	13.1	131	1	5.1
AA455761	Hs.18387	ESTs	12.7	311	25	2.4
Z48633	Hs.6940	H.sapiens mRNA for retrotransposon	12.4	124	6	10.8
AA227219	Hs.110826	Homo sapiens CACF9 mRNA; partial cds	12.3	123	1	11.3
T97507	Hs.161720	ESTs: Moderately similar to [H] ALU SUBFAMILY J WARN	12.3	129	11	11.7
D31352	Hs.31433	ESTs: Weakly similar to [H] ALU SUBFAMILY SQ WARN	11.7	117	1	10.1
AA251089	Hs.94576	ESTs: Weakly similar to phosducin; retinal [H.sapiens]	11.5	115	1	6.9
AA224180	Hs.187579	ESTs: Weakly similar to [H] ALU SUBFAMILY J WARNING	11.5	115	1	10
F11019	Hs.12696	ESTs	11.4	114	1	10
X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltransferase)	10.8	706	66	9.2
H93575	Hs.227146	ESTs	10.5	105	1	9.9
F13673	Hs.99769	ESTs	BCN4	10.4	680	85
AA411745	Hs.235881	ESTs: Weakly similar to KIAA0554 protein [H.sapiens]	10.3	103	1	9.3
M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1	10	100	1	7.6
AA425309	Hs.33287	nuclear factor I/B	BCQ1	9.9	483	49
AA487468	Hs.100686	ESTs: Moderately similar to secreted cement gland protei	BCX3	9.9	351	36
M23379	Hs.756	RAS p21 protein activator (GTPase activating protein) 1	9.6	96	1	8.5
T28867	Hs.7549	ESTs	BCY9	9.6	124	13
R63542	Hs.110488	ESTs	9.5	95	1	8.5
M89225	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	9.4	94	1	0.3
A039722	Hs.171205	ESTs	9.4	94	3	5.3
U18321	Hs.159627	Death associated protein 3	9.3	93	5	8
AA283006	Hs.50758	chromosome-associated polypeptide C	9.3	93	1	8.4
U44378	Hs.75862	MAD (mothers against decapentaplegic; Drosophila) hom	9.3	93	1	7.8

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FIGURE 11

(CONT.)

AA235112	Hs.106227	ESTs: Moderately similar to similar to murine RNA-binding	9.1	91	1	7.6
AA028028	Hs.61460	ESTs	9	90	1	5.5
M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein	8.9	89	5	8
HG2581-HT3125	Hs.46452	"Epicon, Alt. Splice 1"	8.5	85	1	3.2
U33147	Hs.145374	mammaglobin 1	8.5	2058	243	1.4
AA280036	Hs.162686	ESTs: Weakly similar to W01A6.c [C.elegans]	8.5	127	15	1.6
AA609200	Hs.75355	ESTs	8.5	85	1	4.3
D83004	Hs.21214	ubiquitin-conjugating enzyme E2N (homologous to yeast U	8.5	85	1	7.2
AA257971	Hs.146847	ESTs	8.3	83	3	1.8
U58663	Hs.65328	TRAF family member-associated NFKB activator	8.2	82	1	6.8
T18387	Hs.107968	ESTs	8.2	82	1	6.4
H13108	Hs.68613	ESTs	8.2	82	1	7.4
D31161	Hs.78305	ESTs	8.1	81	1	4.6
N28213	Hs.31803	RAB2, member RAS oncogene family	7.8	78	1	5.6
AA031357	Hs.14808	ESTs	7.7	77	1	5.1
N86857	Hs.59622	ESTs: Weakly similar to !!! ALU CLASS C WARNING EN	7.7	77	1	5
AA416997	Hs.243068	ESTs	7.6	144	19	13.9
R34531	Hs.30029	KIAA0480 gene product	7.6	76	1	5
W37145	Hs.14368	ESTs	7.5	135	18	3.4
D60227	Hs.23165	SH3-binding domain glutamic acid-rich protein like	7.5	75	1	6.5
AA054228	Hs.95243	ESTs	7.4	74	1	6
N99701	Hs.23116	transcription elongation factor A (SII)-like 1	7.3	73	1	5.3
Z46629	Hs.65559	SRY (sex-determining region Y)-box 9 (campomelic dyspl	7.3	73	1	5.2
AA476446	Hs.247134	ESTs: Weakly similar to Bat2 [H.sapiens]	7.2	72	1	5.7
U83908	Hs.189628	Homo sapiens nuclear antigen HT31-like protein mRNA; c	7.2	72	1	5.8
AA199828	Hs.21851	ESTs	7.1	71	1	6.5
D61676	Hs.109643	Homo sapiens mRNA; cDNA DKFZp596J2118 (from clone BCY8	7.1	392	56	3.6
AA211941	Hs.184697	polyadenylate binding protein-interacting protein 1	7.1	71	1	6.2
H18027	Hs.23296	receptor for virally-encoded semaphorin	7.1	150	21	14.5
AA032147	Hs.5384	ESTs	7	70	1	6.5
AA292701	Hs.156346	ESTs	6.9	69	1	4.4
J04098	Hs.15740	topoisomerase (DNA) II alpha (170KD)	6.8	68	1	5.6
Z38763	Hs.164950	ESTs	6.7	67	1	6.3
A1287461	Hs.204151	ESTs	6.7	67	1	6
AA195260	Hs.169539	ESTs: Moderately similar to !!! ALU SUBFAMILY SX WAR	6.7	67	1	5.7
N29888	Hs.55901	ESTs	6.5	65	4	5.3
AA490862	Hs.87539	ESTs: Moderately similar to !!! ALU SUBFAMILY SQ WA	6.5	65	1	5.6
U37519	Hs.30652	aldehyde dehydrogenase 6	6.4	428	67	2.3
W23625	Hs.10067	ESTs	6.4	64	1	5.1
AA609723	Hs.151046	ESTs	6.3	63	1	5.4
H10933	Hs.234607	ESTs	6.3	693	110	7.2
N67711	Hs.155637	Homo sapiens clone 23859 mRNA sequence	6.3	63	1	5.8
AA430124	Hs.186572	ESTs	6.2	62	1	5.4
U35835	Hs.109977	protein kinase; DNA-activated; catalytic polypeptide	6.1	61	1	5.7
AA262491	Hs.70823	ESTs	5.8	58	1	5
D60302	Hs.90506	ESTs	5.8	58	1	5
RS1309	Hs.5057	KIAA1077 protein	5.8	321	55	17
AA092376	Hs.28792	15 kDa selenoprotein	5.7	567	100	6.7
U90914	Hs.62817	carboxypeptidase D	5.7	57	1	5
AA130273	Hs.79136	ESTs: Weakly similar to (define not available 4240269) [H BCF3	5.6	56	1	5.3
AA491465	Hs.72965	ESTs	5.5	55	1	5.2
AA047036	Hs.112241	ESTs	4.7	381	61	6.4
U41060	Hs.112742	Human breast cancer; estrogen regulated LIV-1 protein (L	4.6	427	93	10.4
AA168379	Hs.112742	ESTs	4.5	1472	330	2.1
N22107	Hs.170057	ESTs	4.1	334	82	3.4
AA609651	Hs.23579	ESTs: Moderately similar to !!! ALU SUBFAMILY SC WARBCN7	3.9	322	83	4.4
N91023	Hs.34806	ESTs	3.9	60	16	4.8
C00038	Hs.58213	ESTs	3.8	425	111	4
N89921		ESTs: Weakly similar to neogenin [H.sapiens]	3.8	585	153	3.7
W72838		ESTs	3.6	402	112	4.9
			3.5	2073	595	2.1

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AA609773	Hs.250175	Homo sapiens clone 23904 mRNA sequence	BCR2	3	816	275	3.8
AA419622	Hs.104800	ESTs	BCN1	2.9	214	74	3.7
AA234501	Hs.22862	ESTs	BC21	2.8	131	47	3.9
AA620795	Hs.8207	ESTs	BC08	2.5	392	155	4.3
C13992	Hs.93669	ESTs	BC07	1.8	1047	596	1.6
H85169	Hs.172455	solute carrier family 5 (inositol transporters), member 3	BCW2	1	1	1	1

FIGURE 11
(CONT.)

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FIGURE 12

Accession	UniGene ID	UniGene Title		ratio tumor/ body	90%ile tumor	75%ile body	ratio tumor/ normal breast
W72838	Hs.58213	ESTs	BCH1	3.5	2073	595	2.1
D12485	Hs.11951	phosphodiesterase 1 (PC-1)	BCA2	13.2	244	19	9.9
AA434329	Hs.36563	ESTs	BCJ7	40.2	402	1	4
AA419922	Hs.104900	ESTs	BCN1	2.9	214	74	3.7
RS1399	Hs.70823	KIAA1077 protein	BCN5	5.7	587	100	6.7
AA256455	Hs.182471	ESTs	BCO2	25.4	508	20	3
C00038	Hs.23579	ESTs	BCQ5	3.8	585	153	3.7
AA609773	Hs.250175	Homo sapiens clone Z3904 mRNA sequence	BCR2	3	916	275	3.9
AA291725	Hs.105700	secreted frizzled-related protein 4	BCX2	17.4	409	24	7.8
Z38595	Hs.125019	ESTs	BCY3	24.2	242	10	5.6

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GGGACAGGGCTGAGGATGAGGAGAAACCTGGGGACCCAGAAAGACCGTGGCTTGCCCGGAAGTCCTGCCTGTAGGCCTGAA
 GGAATTCGCCCTAACAGAGCCTCAACAACCTACCTGGTATTCTCTACTTCAGCCCTTGCTGTGAGCAGCTTCTCAACATGA
 ACTACAGCCTCCACTTGGCCCTCGTGTGCTGAGTCTCTTCACTGAGAGGATGTGCATCCAGGGGAGTCAGTTCAACGTG
 GAGGTGCGCAGAGGTGACAGCTTTCCCTGCTGGCTTTCAGAACCTCAGCAGGATATAACAAATTTCTCAGGCCCAA
 TTTTGGTGAGGAACCCGTACAGATAGCGCTGACTCTGGACATTGCAAGTATCTCTAGCATTTCAGAGAGTAACATGGACT
 ACACAGCCACCATATACCTCCGACAGCGCTGGATGGACAGCGCTGGTGTGAAGGCAACAGAGCTTCACTCTGGAT
 GCCCGCCTCGTGGAGTTCTCTGGGTGCCAGATACTTACATTGTGGAGTCCAAAGTCCCTCCTCCATGAAGTCACTGT
 GGGAAACAGGCTCATCCGCTCTTCTCCAAATGGCACGGTCTGTATGCCCTCAGAATCAGCAGAACTTTGCATGTATACA
 TGGATCTGCTTAAATACCCATGGACACAGACATGCAAGTTGACAGTGGAAAGCTGGGGCTATGATGGAATGATGTG
 GAGTTCACCTGGCTGAGAGGGAACGACTCTGTGCTGGACTGGAACACCTGGCGCTTGTCTAGTACACCATAGAGCGGTA
 TTTACACCTTAGTCACAGATCGCAGCAGGAGACAGGAAATACACTAGATTGGTCTTACAGTTTGAGCTTCGGAGGAATG
 TTCTGTATTTTCAATTTGGAAACCTACGTTCTTCCACTTTCTGGTGGTGTGTCTCGGGTTTCAATTTGGATCTCTCTC
 GATTCACTCCCTGCAAGAACCTGCAATTGGAGTGACGACCGTGTATCAATGACCACACTGATGATCGGGTCCCGCACTTC
 TCTTCCCAACCAACTGCTTCATCAAGGCCATCGATGTGTACTGGGATCTGCTTTAGCTTTGTGTTTGGGGCTTGC
 TAGAATATGCAATTTGCTCACTACAGTTCTTACAGCAGATGGCAGCCAAAGATAGGGGGACAAACAAGGAGTGAAGAA
 GTCAGIATTAATATATCACTACAGCTTCTCTCAGCTTTAAACGGAAGATCAGCTTTGCCAGCATTTGAATTTCCAG
 CGACAGCTTGTACTACAGTACTTGCAATGAAGAACCCAGCGACAGTTCAAGTTTGTCTTCCAGAAAGATGGGCAAGGA
 TTGTGTATTTTTCACAAATTCAAAACCCAGTAATGTGATCACTATTCCAAACTACTGTTTCTTGAATTTTATGCTA
 GCCAATGTATTTTACTGGGCATACTACATGATTTTGTAGTCAATGTTAAATTTCTTGATGCCATAGGCTTCAACAGG
 ACAAGATTAATGATGTAAGTGTATTTTAGGCCAAGTGTGACCCACATCCAATGGTGTACAAAGTGAATGAATAATAT
 TGAGTCTTTCTGTCTCAAGAAATGAAGCTCCAAACCATTTGTTCTAAGCTGTGTAGAAGTCTTAGCATTTATAGGATCTTGTAA
 TAGAATCATCAGTCCATTCCTCTTCACTTAATCAAGGACATTCCCATGGAGCCCAAGATTACAATGTACTCAGGGCT
 GTTTATCGGGTGGCTCCCTGTTTGCATTTTACCTCATATAAAGAAATGGGAAGGAGACCATTTGGTAACCCCTCAAGTGTCA
 GAAGTTGTTTCTAAGTACTATACATGTTTTTTTACTAAATCTCTGAGTGTCTATAAAATACATTTGTGCTTATTTAGG
 GAGTAACTATTTCTAGTTTTTGTCTTCTGTTTAAATGAATATGGGCTTATGTCAATTCATTGGAAGTCAATGCATTAAC
 TCAATACCAAGATGAGTTTTTAAATATGAATATTATTTAATACCAACAGAAATATCCCAATTTCCAAATAGTCCCTA
 TCATTGAAATTCATATATAGTGAAGAAAAATTAGTAGTCAACAATCTAAACAATCCCTCGGTTCTAGATACAAAT
 GGATTCCTCATCTGGAAGGACTCTGAGGCTTTATTCCTCCACTATGCATATCTTATCATTATTATATACACACATC
 CATCTAACTATACATAAGCCCTTTTCCATGCATGGATGGAAATGGAAGATTTTGTGAATTTGTCTAGAAAGTCTT
 AATATGGCTGTGGCATGAGGCTTCAGAAATGAGTCCATTTCTAGTGCCTTTATTCACATAGTGTGGGGTACTA
 AAGTACTGGGTGACTCAGAGAGTCGTGTCATTCTGCTATTGCTGCTACTCTAACACTGAGCAACACTCTCCAGTGG
 CAGATCCCTGTATCATTTCCAAAGAGGAGCAATTCATCCCTTTGCTCTAATGATCAGGAATGATGCTTATTAGAAAAACAAC
 TGCTTGACCCGGAACAAGTGGCTTAGCTTAAGTAACTTGGCTTTGCTCAGATCCCTGATCCTTCCAGCTGGTCTGCTC
 TGAGTGGCTTATCCCGCATGAGCAGGAGCGTGTGGCCCTGAGTACTGAACCTTCTGAGTAACATGAGACAGCTTACAG
 AACCTATGTTCAAGTTGCGGGTGGAGCTGCCCTCTCCAAATCCAGCCAGAGATGCACATTTCTCGGCCGCTCTCAGCCAC
 AGTACCAAAAGTGATTTTGAAGTGTGCCAGGTAAGGCTTCCAGTTCAGCCTCAGTTATTTAGACATCTCCGATCT
 TTAATTTCTAGCTTCTGTTCTAATAATGACGGCTTTACCTTTCTGCTCAGAAATAACGAGGCTCTAAAAGATGA
 TTGCTCTGTTAGTCTTCTAGAGCGACGGTCTCATTCTCTTCCCAATTAATCTCTCACAATTCAGTTCTTATGAT
 TTGATCACTGATTTTTTAAACAAATTTCTAACGGAAATGGGTGGGAGTGTGCTGGTGAAGAGGATGAATGTGGTTG
 TATGAGCCATCATATTTGTGATTTTTTAAAGAAAGTTTAAAGGAATATCTGTTCTGAAGCCCACTTAAGCATTTGT
 TTTATATAAAACAATGATAAGATGTGAAGTGAAGTAAATATACCATATTAGCTACCCACC

FIGURE 13

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FIGURE 14

ATGAACACAGCCTCCACTTGGCCTTCGTGTCTGAGTCTCTTCACTGAGAGGATGTCATCCAGGGGAGTCAGTTCAA
CGTCGAGGTCGGCAGAGTGACAAGCTTCCCTGCTGGCTTTGAGAACCTCAGCAGGATATAACAAATTTCTCAGGC
CCAAATTTTGGTGGAGAACCCGTACAGATAGCCCTGACTCTGGACATTCGACATCTCTAGCATTTCAGAGAGTACATG
GACTACACAGCCACCATATACCTCCGACAGCCGCTGGATGGACCCAGCGGCTGGTGTGGAGGCACACAGAGCTTCACTCT
GGATGCCCGCCTCGTGGAGTTCCTCTGGGGTCCAGATACTTACATTGTGGAGTCCAGAAGTCCCTCCATGAAGTCA
CTGTGGGAAACAGGCTCATCGCCCTCTTCCCAATGGCAAGGCTCTGTATGCCCTCAGAATCAGGCAACTGTTGATGT
AACATGGATCTCTTAATAGTACCCCATGGACACACAGCATGCAAGTTCAGCTGGAAGCTGGGGCTATGATGGAATGA
TGTGAGTTCACCTGGCTGAGAGGGGAACGACTCTGTGCGTGGACTGGAACACCTGGGGCTTGTCTAGTACACCATAGAGC
GGTATTTACACTTAGTCACAGATCGCAGCAGGAGACAGGAAATTACACTAGATTGGTCTTACAGTTTGAAGCTTCGGAGG
AATGTTCTGTATTTCAATTTGAAACCTACGTTCCCTCCACTTTCCTGGTGGTGTGCTCCTGGGTTTCAATTTGGATCTC
TCTCGATTCACTCCCTGCAAGAACCTGCATTGGAGTACGACCGCTGTATCAATGACACACTGATGATCGGGTCCCGCA
CTTCTCTTCCCAACACCACTGCTTCATCAAGGCCATCGATGTGTACCTGGGGATCTGCTTTAGCTTTGTGTTGGGGCC
TTGCTAGAAATATGCAAGTGTCTCACTACAGTTCCTTACAGCAGATGGCAGCCAAAGATAGGGGGACACAAAGGAAGTGA
AGAAGTCAGTATTACTATATCATCAACAGCTCCATCTCCAGCTTTAAACGGAAGATCAGCTTTGCCAGCATGAAATTT
CCAGCGACACGTTGACTACAGTACTTGACATGAAACACGACAGTTCAGGTTTGTCTCCGAGAAAGATGGGC
AGGATTGTTGATTATTTACAAATTCAAAACCCAGTAATGTTGATCACTATTCAAAACACTGTTTCCCTTGTATTTTAT
GCTAGCCAATGATTTTACTGGGCATACATGATTTTGA

FIGURE 15

MNYSLLHAFVCLSLFTECMCIQSSQFNVEVGRSKLSLPGFENLTAGYNKFLRPNFGGEPVOIALTLDIASISSISESNM
DYTATITLQRWMDQRLVFEKNKSFILDLARLVEFLNVPOTYIVESKKSFLHEVTGHNRLRLFSNGTVLYALRITTTVAC
NMDSLKYPMDTQCTCKLQLESWGYDGNDEFTWLRGNDVSRGLEHLRLAQYTLERYFTLVTRSQOETGNVTRLVLOFELRR
NVLYFILETYVPSFTLVLSWVSFWISLDSVPARTICIGVTTLVSMHTLWIGSRTSLPNTNCFKAIIDVLEKAGGSGSGSGSG
RIVDYFTIQNPSNVDRYSKLLFLFIEMLANVYWAYMYWF.

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FIGURE 16

BCR3p1

Ac-Ala-Cys-Asn-Met-Asp-Leu-Ser-Lys-Tyr-Pro-
Met-Asp-Thr-Gln-Thr-NH₂

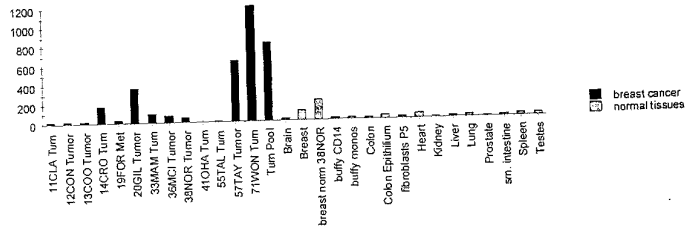
Ac-Cys-Lys-Leu-Gln-Leu-Glu-Ser-Trp-Gly-Tyr
-Asp-Gly-Asn-Asp-Val-NH₂

BCR3p2

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FIGURE 17

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FIGURE 19

ATGAAAGCCTTCCACACTTCTGTGTTGTCCTTCTGGTGTGGAGTGTCTCTGAAGCCAAGTTGATGATTTGAGGA
TGAGGAGGACATAGTAGATGATGATGACTTCGCTGAATTTGAGGATCTCATGGAAGACTCTGTTACTGAATCTC
CTCAACGGGTCTATATCACTGAGATGATGAGATGAGACCACTGTGGAGTTGGAAGGGCAGGATGAAAACCAAGAAGGA
GATTTTGAAGTGCAGATACCCAGGAGGAGATCTGAGAGTGAACCATATGATGATGAAGAATTTGAAGTTATGAAGA
CAAAACAGATCTCTTTAGCAAAAATAAGGACCCCAATAACGATTGTTGATGTTCTGCACACCTCCAGAACAGCTGGG
AGAGTTATTATCTAGAAATTTGATGGTGAAGTCTGCTTGTCTTATATCATGAATTACATCATTGGGAAGAATAAAAC
AGTCGCTTGCACAGGCTGGTTTAACTCTATAGGGAGCTTTGGAGAGCAACTTACTTTAGTGGGGGATGATGGAAC
TAACAAGAAGCCACAGCACAGGAAGTTGAACCGAGAGATGAGCACATCTATAACCTGTGGTGTCTGTCGAGTGT
GCTGTGAGGCGATGCTTATCCAGCTGAGGTTCTCAAGAGACAGACTTACTGAATGCTGGCCGGATGATGAGGCCA
GTGAGTGATCAAGTGCAATAAAGTAACCATGAATGATGAAGACATGGATACCTACGTATTGCTGTTGGCACAGGAA
AGCCTTGGTGGGACTACAGAAAGATGAGGATTTGAGTGAGTTTGTAGTGATAAACCTAAGTCTGGAGCAAGTATG
GACTGCCGGACTCTTTGGCCATCCTGTGAGAGATGGGAGAGTCAAGACGGAATGATGGATACAAAGATGGTTCACTTC
TTACACACCTATGCTGACAAGATTGAATCTGTTCAATTTTACAGACAGTCTCTGGTCCAAAATTTATGCAAGAGGAAGG
TCAGCCTTTAAAGCTACCTGACACTAAGAGGACACTGTTGTTTACATTTAATGTGCTGGCTCAGGTAACTTACCCAA
AGGATATGGAGGCACTGCTACCCCTGATGAACATGGTGATTTATTCTATTGATAAAGCCAAAAGTTCCGACTCAACAGA
GAAGGCCAAACAAAAGCGATAGAACCGTGCCCGAGTAGAAGAGAACTTTTGAAGTACACATGTGCAAGACAGGA
AGCAGCACATCTCGGCGGAGGAGAAAAAGAGCAGAGAGGAGCGAATCATGAATGAGGAAGATCTGAGAAACAGC
GCAGGCTGGAGGAGGCTGATTTGAGGCGTGACGAAAAAGAGTTGGAAAAAGCAAAATGAAAATGAACAAATCAAAAT
GAAAGCCATGTAAGCCATCCAGAGATTTGAGTTCTGA

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FIGURE 20

MKAFHTFCVLLVFGSVSEAKFDDFEDAEIOIVEYDDNOFAEFEDVMEDSVTESPQRVIITEDDEDETTVELEGQDENQEG
DFEDADTQEGOTESEPYDDEEFEGYEDKPTOTSSSKNKOPITIVDVPALQNSWE STYLETIMVTGLLAYIMNYTTG KNKN
SRLAQAWFNTHRELLESNTLVGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCGMLIQLRFLKRQDLLNLVLRMMRP
VSDQVQIKVTMNDMDTYVFAVGTRKALVRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMMDTKMHF
LHTYADKIESVHFSDQFSGPKIMQEGQPLKLPOTKRTLLFTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFLNR
EGKQKADKNRARVEENFLKLTHVQRQEAASRREKKRAEKERIMNEEDPEKQRRLEEAALRRDEKEVGKDEANENETNQS
ESHVKPSQRFEF.

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FIGURE 2 1

Peptide Name: BCQ8p1

Sequence: Ac-Cys-Lys-Pro-Asp-Thr-Ser-Ser-Ser-Lys-Asn-Lys
-Asp-Pro-Ile-Thr-NH₂

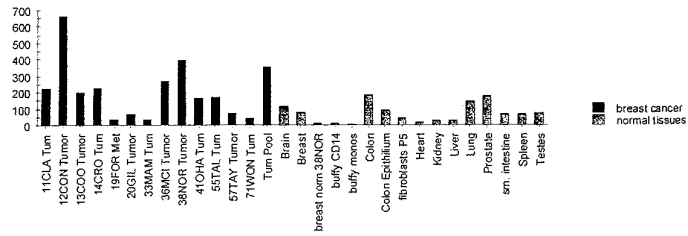
Peptide Name: BCQ8p2

Sequence: H-Lys-Phe-Asp-Asp-Phe-Glu-Asp-Glu-Glu-Asp
-Ile-Val-Glu-Tyr-Cys-NH₂

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FIGURE 22



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FIGURE 23

FIGURE 24

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```
human_BCQ5 1 MIRCGLACERCRWILPLLLLSAIAFDIIALAGRGWLQSSDHGQTSSLWVK 50
mouse_BCQ5 1 MLRCGLACERCRWILPLLLLSAIAFDIIALAGRGWLQSSNHIQTSSLWVR 50
rat_BCQ5 1 0

human_BCQ5 51 CSQEGGGSGSYEEGCCQSLMEYAWGAAAAAMLFCGFIILVICFILSFFALC 100
mouse_BCQ5 51 CFDEGGGSGSYDDGCCQSLMEYAWGAAAAATLFCGFIILVICFILSFFALC 100
rat_BCQ5 1 EYAWGAAAAATLFCGFIILVICFILSFFALC 31

human_BCQ5 101 GPQMLVFLRVIGLLALAAVEQIIISLVYIPVKYTTQTFTLHANPAVYIYN 150
mouse_BCQ5 101 GPQMLVFLRVIGLLALAAIFQIIISLVYIPVKYTTQTFRLHDNPAVNYIYN 150
rat_BCQ5 32 GPQMLVFLRVIGLLALAAVEQIIISLVYIPVKYTTQTFRLHDNPAVNYIYN 81

human_BCQ5 151 WAYGFGWAATIIILIGCAFFFCCLPNYEDDLLGNAKPRYFYTSA 193
mouse_BCQ5 151 WAYGFGWAATIIILIGCSFFFCCLPNYEDDLLGAAPRYFYPPA 193
rat_BCQ5 82 WAYGFGWAATIIILIGCSFFFCCLPNYEDDLLGNAKPRYFYTSA 124
```

FIGURE 25

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BCQ5p1

Ac-Cys-Ser-Tyr-Ser-Ala-Pro-Ser-Pro-Ser-Thr
-Ser-Ser-Arg-Trp-Pro-NH₂

BCQ5p2

Ac-Cys-Leu-Pro-Asn-Tyr-Glu-Asp-Asp-Leu
-Leu-Gly-Asn-Ala-Lys-Pro-NH₂

BCQ5p3

Ac-Cys-Gly-Gly-Asn-Ala-Pro-Lys-Arg-Gly-Gly
-Gly-Arg-Gly-Ser-Tyr-NH₂

FIGURE 26

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GTACCCGAATCAAGGTGTGGCTGGAGGCGCGCTCCCGCGCYCAGCCGKGGCCGCGCTTCGGGGGAGCCGCTCTTCCTTWTTC
 GGCCKYGAACGCGCTCGAGGACCACTCTTGGCGGCTGCTCTGCCCGCGCTTCTCCGCTCCGCGCCCGCCGACGACATGCTG
 CGCTGGCGGCTGGCTCGAGGCGCTGAGGTGGATCCTGCCCTGCTGCTGCTCAGCGCCATCGCTTCGACATCATCGCGCTGGCGCG
 CGCGGCTGGCTGAGCTTAGCAACACATCCAGACATCGTCCCTTGGTGGAGGTGTTCCGACAGGGGGGCGAGCGCTCTACGC
 GATGGCTCCAGAGGCTCAGGAGTACGATGGGGACGAGCGCTGCGAGCCAGCTTTCTGTGGCTTATCATCTCTGTGCAATCTGCTTC
 ATCTCTGCTGCTTCCGCGCTGGTGGACCCAGATGCTTGTTCCTGAGAGTCATTGGAGGCGCTCTCGCACTGGCTGCCATTTCCAG
 ATCATCTCCCTGGTAACTACCCCGTGAAGTACACACAGACCTTCAGGCTTCAGGATAACCTCTGTTAAATTACATCTATAACTGGGCG
 TATGGCTTCGATGGGGGCGCCACCATCATCTTGAATGGTGTGCTCTCTCTCTGCTGCTCCCACTAGAGGATGACTTTTGGGG
 CGCGCCAGCGCGAGTACCTTATCCCGACCTTATGTGGGAGGAGAGCGCTGAGAAAGCGCTGCTGCAAGATGGATCTGAGGAGGAAA
 CTCTTCTCCAGGACACAGGAGCTACGTTTGGGCAATGTTCATATGATCAGAAATGTTAGAATAAATGCTAAAGAAATCTTCATAAT
 TAGTGTTAAGTTTCAATGTATGCTGTGGAGTTAAAAGACTTGAATCTGTTTGTAGTATATGCTAATTTTCTTATGTCAATCTCT
 ATACCATTTAAGCTTCATTTGTAAAGAAATGCCCTGTAATCTGTATAGSTAGAAATGACAGCGCTCTCAATTTAATATCTGTATGG
 GCTTCGTTTTTCCACATAGATGGTTTTCTCTTAGGGCTACAGAGGAGGAAAGTCACTGGCAAACTTCCATGACCAATATCTCT
 GAATTAATTTGTTTTTTTAAAGACCTTATTTTGAATTTTCAATTAAGAGGAGGAGGAGGATTTGGTTTTCTTAAGTGAGCATC
 ATTGTGAGAAATTTTAGTCAAGTGTTTTGAACAAATTTATTTTCTTAGCTTCATGTTGACTTTCTCTGATGCTAGAAAAGTGTCTA
 ACGTGGCTGAGGTTAGCGCTGTATCTAGTAAATGCTAGAGATTTCTCTTTTCCCTAGTGTAGAGGGGTAGGCTGTGGGAGAG
 CGGTGTAGACATCTTAGTATGTGTGTATCTTAGAGAGGCTACAGAGGAGGAAAGTCACTGGCAAACTTCCATGACCAATATCTCT
 TGGTGTGTAGAGAGGCTCAGTAGGAGGACACAGGAGGCTCAACACTGTACAGAGGAGGCAATGCAAGACTCTTAGGAGAGAGATGGC
 AGTGTTCCTCTCAGTCTCTTCCCTTAAGTCACTGCTGTGCTACAGAGAGGCTAGAAATGATTTTAAGTGAACAGAAACCTAAATGTAA
 TTAAGAACTGGCTCTCTTGGTAAAGAGCTTAAATATCTGTATAGTACATCGAGTGGAAATTTGGGATAGGCTCTCTGTATAC
 ATACCGAAGGCTACTTTTACCTTTTCTTACCTTTATCTTCTAATGGAAGCGCTTGTTTAAGTATCAGAACACTATTTTGT
 AAGTCTTCGAAGACAGTTGAAGTTTTCATTACCAATTTCCCAATTAAGCAGGTGTCAATCTGAAAAAAGGCG

FIGURE 28

ATGCTGCGCTCGCGGCTGGCTCGAGGCTGAGGTGGATCTGCCCTGCTGCTCAGGCGCATCGCTTCGACATCATCGCGCTG
 GCGCGCGCGGCTGGCTGAGCTTAGCAACACATCCAGACATCGTCCCTTGGTGGAGGTGTTCCGACAGGGGCGCGGCGAGCGGCTCC
 TAGACGATGCTGCTGAGGCTCAGAGGCTCAGGATGAGGAGGAGGAGGCTGAGGAGGAGGCTTTTCTGTGGCTTTATCATCTCTGTGATC
 TGGTTCATCTCTGCTCTGCGCTGTGTGGAGGCGGAGATCTGTTTCTGAGATCATTTGGAGGCTCTCGCACTGGCTGCAAT
 TTCCAGATCATCTCCCTGGTATCTACCCCGTGAAGTACACAGAGGCTCAGGCTTCAGGATAGCCCTGCTGTTAATTACATCTATAAC
 TGGGCTATGGCTTCGGATGGGCGGCGACCATCATCTGATGGTGTGTTCTCTCTCTGCTGCTGCCCACTACAGGATGACCTT
 TGGGGGCGCGCAAGGCTACTTCTATCTCCCGAGCTAA

FIGURE 29

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GAATACGCCTGGGGCCGAGCAGCTGCTGCCACTCTCTTCTGTGGATTGATCATCTGCTGCTCATCTGCTTCTTCTGGCCCTG
TGTGGACCCAGATGCTTGTCTTCTGAGAGTGAATTGGAGCCCTTCTGGACTGGCTGCTGTAATCCAGATCATCTCCCTGCTTATCTAT
CCCTGAAATACACACAACTTCCAGCTTCTATGATATCCGCTGTTAATTACATCTACAACTGGGCTATGGCTTCGGATGGGAGCC
ACGATCTCTTCTGATGGTGGCTCTTCTTCTCTGCTGCTCCCACTACGAGGATGACCTTCTGGGCAATGCAGGCCCCAGGTACTTC
TATACATCTGCTTAATGTGGAGGAGATCCTGAGAAAGCTGCTGCAAGATGCTATGAGGAGGAAATGCTTCTGAGGAGGCTAAGAA
CCTATGTTTGGGCACTGTTCAATATGATGGAAATGCTAGATTAATGCTAAGAAATTCCTCTAATAAAAAAAAAAAAAAAAAA

FIGURE 30

GAATACGCCTGGGGCCGAGCAGCTGCTGCCACTCTCTTCTGTGGATTGATCATCTGCTGCTCATCTGCTTCTTCTGGCCCTG
TGTGGACCCAGATGCTTGTCTTCTGAGAGTGAATTGGAGCCCTTCTGGACTGGCTGCTGTAATCCAGATCATCTCCCTGCTTATCTAT
CCCTGAAATACACACAACTTCCAGCTTCTATGATATCCGCTGTTAATTACATCTACAACTGGGCTATGGCTTCGGATGGGAGCC
ACGATCTCTTCTGATGGTGGCTCTTCTTCTCTGCTGCTCCCACTACGAGGATGACCTTCTGGGCAATGCAGGCCCCAGGTACTTC
TATACATCTGCTTAATGTGGAGGAGATCCTGAGAAAGCTGCTGCAAGATGCTATGAGGAGGAAATGCTTCTGAGGAGGCTAAGAA
CCTATGTTTGGGCACTGTTCAATATGATGGAAATGCTAGATTAATGCTAAGAAATTCCTCTAATAAAAAAAAAAAAAAAAAA

FIGURE 31

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FIGURE 32

CTTTGAAGCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCAACCAATGAAGTTCTTAGCAGTCCTGGTACTCTTGGGAG
TTTCCATCTTTCTGGTCTCTGCCCCAGAATCOGACAACAGCTGCTCCAGGTGACAGGTATCCAGCTACTGGTCTCTGAT
GATGAAGCCCTGATGCTGAAGAACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCAACCGTGC
TTCTACCACTGCTGCTGAAGACATTCCAGTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGCTCCCTGAG
ATGGAATCAGCTTGAGTCTTCTGCAATTGGGTCACACTATTTCATGCTTCCTGTGATTTTCATCCAACTACTTACCTTGCC
TACGATATCCCTTTATCTCTAATCAGTTTATTTCTTTCAAATAAAAAATAACTATGAGCGAGCTAACAT

FIGURE 33

ATGAAGTTCTTAGCACTCCTGGTACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAAATCOGACAACAGCTGCTCC
AGCTGACACGTATCCAGCTACTGGTCTCTGATGATGAAGCCCTGATGCTGAACCACTGCTGCTGCAACCACTGGGA
CCACTGCTGCTCTACCACTGCAACCAACCGTCTTCTACCACTGCTGCTGAAGACATTCAGTTTACCCAAATGGGT
GGGGATCTCCCGAATGGTAGAGTGTGCTCCCTGA

FIGURE 34

MKFLAVLVLLGSVIFLVSQNPPTAAPADTYPATGPADDEAPDAETTAATTTAAPTATTATAASTTARKDIPVLKWW
GOLPNGRVCP.

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FIGURE 35

H-Gln-Asn-Pro-Thr-Thr-Ala-Ala-Pro-Ala-Asp-Thr-
Tyr-Pro-Ala-Cys-NH₂

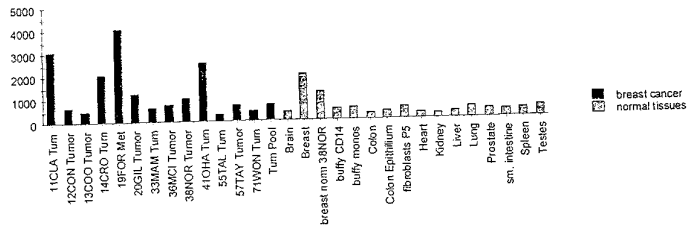
Ac-Leu-Pro-Lys-Trp-Val-Gly-Asp-Leu-Pro-Asn
-Gly-Arg-Val-Cys-Pro-OH

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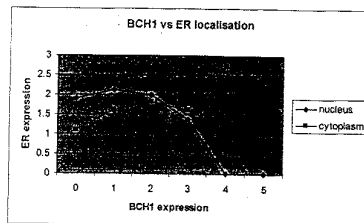
FIGURE 36



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FIGURE 37

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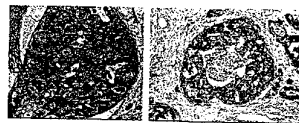
FIGURE38A

FIGURE38B



FIGURE39A

FIGURE39B



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FIGURE 40A

FIGURE 40B



FIGURE 41A

FIGURE 41B



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FIGURE 4 2

GGAGTTTTCTGGAGCTGTGCAATGTGTATGCTGGTGAATCTACTTGAGCATTAAAGCAGTATCTCCAGC
 ATTGTTAGCTACTGAGTGGCAGTCTTCACTAGCCATGTTCTGGGGGACTCAGGCAGAGGTAAAGTGT
 GAAACTTTTCAGCATATACCTAAGAACCAAGGCTCAATTTGGCTGCTTCATTCTTATCTCTCTGCCACA
 GTTCTAACGTGGCTGATCTACTGAGACCAAGCCTACCAATGACTCAGAGGGAAATGGGATTTAAACAC
 CCAAGATCATGGGGAAATTCAGAGGTCATGCCCTCCCTGGACCTTCTTTTTATTTGGTCTTTGGTG
 GTGTCAGAGGATTTCTGAGTATATCTGCAAAAGCAAGCGAACCTGCTATCTTGGTCCAAACAT
 TATTCATCGATTGGAATTTTGGAGGGAATACAACTAGTGGCATGGCTTAACTGGCATGGCTGGGAG
 CAGTTTATCTCTGGAGGGGCCCATCTGATGTATATGACTATAACCAAGGTCACTGGAAATCAACTCCTGGG
 CTGGCATCTTACCATGTATTTCTCTTTGGGCTGTGGGTGTGGCAGATATCTTATGTTTACCATCA
 GTTCACATCCTGTGTCTTAAACCAAGTTAATGTTGTCAATGCCTTATTTGGAGGCCCTTATCTCTAC
 AAGCCACTCATGGCCGGGAAATGCTGGACATCTTGTGCACCAAGCTGCTGGTTTTGGTCTCTTCTGAC
 AGGCCTCGTTGGCTTCTTAGAGTTCTTGTTCGGAACAATGACTTCTGGAGCTATTGGGTCAGTCTCA
 TTCTGCTTCAGGGGAGCTGGTTCTTTCAGATTGGATTGTCTCTGATCCGCCAGTGGAGGTCCTGATGG
 GATCTGATGGATCATGAAAAATTTTGGTTCTCACCATATGCTTTTGGTCATTATGAGTAACCATGT
 CATCGTTGGAATGAATTAATGCTTTCATTACCTGGTGGTTAAATCTAGACTTAAGAGGCTCTGCTCTCAG
 AAGTTGAAAAAGACTTCTGTGCTGAACGAGAACAAGAAATCAGAAGAGAAATGCTTTGATGAGCTTCC
 AGTTTTCTAGATAAACCTTTCTTTTTTACATTGTTCTTGGTTTTGTTTCTCGATCTTTTGGAGAGAA
 CAGCTGGCTAAGGATGACTCTAAGTTGACTGTTTGCATTTCCAATTTGGTTAAAGTATTGAATTTAAATA
 TTTTCTTTTAGCTTTGAAAAATTTTGGGTGATCTTTCATTTTGCACATCATGCACATCATGGTATTCA
 GGGGCTAGAGTGAATTTTTCAGATTATCTAAAGTTGGATGCCACACTATGAAGAAATATTGTTTTA
 TTTGCTTATAGATATGCTCAAGGTTACTGGGCTTGCTACTATTGTAACCTCTTGACCATGGAATTATAC
 TTGTTTATCTTGTGCTCAATGAGAAATAAATGAATGATGATTTTGGTGCAGAAAAAAA

FIGURE 4 3

MTNDSGKMGFKHPKIMGNFRGHALPGTFFFIIGLWCTKSILKYICKKQKRTCYLGSKTLFYRLEILEGI
 TIVGMALTMAGEQFIPGGPHMLDYDKQSHWNQLLGNHFTMYFFGLGVADILCPTISSLPVSLTKLM
 LSNALFVEAFIFYNTHGREMLDIFVHQLLVVFLTGLVAFLEFLVRNVLELLRSSILLQGSWFFQI
 GVLVYPPSGGPANDLMDHENILFTICFCWHYAVTIVVGMNYAFITWLKSRKLRKCSSEVGLLKNARE
 QESEEM.

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**BCN1p1**

Ac-Tyr-Pro-Pro-Ser-Gly-Gly-Pro-Ala-Trp-
Asp-Leu-Met-Asp-His-Cys-NH₂

BCN1p2

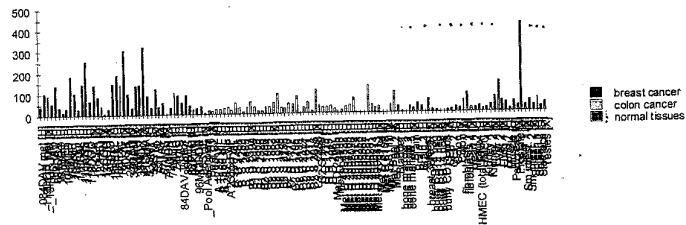
Ac-Cys-Leu-Lys-Asn-Ala-Glu-Arg-Glu-Gln-Glu-Ser
-Glu-Glu-Glu-Met-OH

FIGURE 44

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FIGURE 15

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FIGURE 46A

TTCTCCGCGAAGGCTCCTTTGATATTAATAGTGTGGTGTCTTGAACTGACGTAATGCGCGG
AGACTGAGGTCTCTGACAAGCGATAACATTTCTGATAAAGACCCGATCTTACTGCAATCTCTAG
CGTCTCTCTTTTGGTGCTGCTGGTTTCTCCAGACCTCGCGTCTCTCGATTGCTCTCGCCTT
CCTATTCTCTTTTCTTTTAAACAAAAACAACACCCCTCCCTCTCCACCCGCGACCG
GGCACATCTTGTCTATTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTTTTAAATAAG
GGTGGGGGAGGGAAGGGGGGGGATGACGAAAGACCTTTTCTCTCCCGCCGCAATAATC
CAAGATCAACTCTGCAAAACAACAGAAAGCGTTTCATGGCTTTGGCCGCGCGCCACCATCTTT
CGGGCTGGCGAGGGTGTCTTGACGATTAAATCAACAGATGTACAGATCAGCTCTCAAAATGTC
TTCTGTGTCTCTGAGCGTCTTAAGACAATTGCATTAGCTCTGCTAGTTGACTAATAGAA
TTAATAATTGTAAAAGCACTCTAAAGCCACATGCCTTAGAAGTCAATGCTGGGTATGATT
TACAAATGCTCCGAAAAAGAACCCCTCTGAGAAACGTTGCAAGTGAAGGCGAGGGCC
AGATCTGGAGCTATAGGTACAGAAAGCAAGGTATCTGGAAGAAACAAGAAATTTCTGCA
GATCAGATGTACAGAAATACGGATCAGAGTGATGCTGCAAACTAAATCATAAGGAGGAACA
TAGCTTGCATGTTCAAGATCCATCTTCTAGCAGTAAGAAAGGACTTGAAGCGCAGTTCTGAG
TGAGAAAGCTGGCTTCAATTATGAAAGCCCAAGTAAGGAGGAAACTTTCCCTCTTCCGCA
TGATGAGGTGACAGACAGAAATATGTTGGCTTTCTCATCTCCAGCTGCTGGGGAGTCTGTGA
GCCCTTGAAGTCTCCGCAAGAGCAGAGGCAGATGACCTCAAGATATGGCTGCAACCCCTC
AGGGGACTCACTGGAGACAAAGGAAGATCAGAAAGTGTACCAAGGCTACAGAGGAAACA
GGGCAAGGACAGAGTGGTCAAGCCAAATTGTCAAGGTTTGAGCCAGTTTCAAGTGGCTCAAA
AAACCCACAAGTCCCTCAGATGGGGGTGTAAAGACTGAATAATCCAAAAGTACTTACTGG
TGAAATGACAACCCAGAGCCCGGACCTCTGTCTCCAGAGCTTCAGGACTTTAAATGCAATATCT
GTGGATATGGTTACTACGGCAACGACCCACAGATCTGATTAAAGCACTTCCGAAAGTATCACT
TAGGACTGCATAACCGCACCGGCAAGATGCTGAGCTGGACAGCAAAATCTTGGCCCTTCAAT
AACAATGGTGAAGTTCAGCCATTCCAAAGACTTCCAGAAAGTCAACCGTTCTGTGTTTCTGGT
GTGCTGCAGGACATCAATCTTCAAGGCTGTCTTACTAAATGGGACCTATGATGTGAGGGT
ACTTCAGGTGGAACATTCATTGGCAATGGACGAAACACCAAGTTGCCAAGGGAACACCAA
GTATTTCCGCTGTAAATTTCTGCAATTTCACTTATATGGGCACTTCCACCGAATTAGAACAA
CATTTTCTTCAGACTCACCCAAACAAATAAAGCTTCTCTCCCTCTGAGGTTGCAAAAC
CTTCAGAGAAACTCTAACAAGTCCATCCCTGCACTTCAATCAGTGATTCTGGAGACTTGG
GAAAATGGCAGGACAAAGATAACAGTCAAGCAGGAGATGACACTCCTGTTGGGTACTCAGTG
CCATAAAGCCCTCGATTCTCTAGACAAATGGTACAGAGGCCACCAAGTTACTACTGGTGT
AAATTTTGTAGTTTCAGTGTGAGTCACTAGCTCACTTAACTGCTAGAACATATATGGCAAG
CAGCAGGAGCAGTGCAGTCAAGGCGCTTAATCCAGAGTTAAATGATAAGCTTTCAGGGG
CTCTGTCTAATATCAGAAATGATCTAGCCAAAAGTTCAAGAGGAGAGCAATGACCAAGACAG
ACAAGAGCTCGAGTGGGGCTAAAAAGAGGACTTCCAGCAAGGAGCCGAGGATAATATG
ATAACAGGCTATAATTTGAGTTCTGTGACTTCCGATTTCCAAAAGGCAATGGCCCTGATGTA
ATTGTAGTGGGGCACTTCTCGCTATTATCAACAGCTCCATAACATTCACAAGTGTACCATTA
AACACTGTCCATTCTGTCCAGAGGACTTTGCAAGCCAGAAAAGCACCTTGGAGAAATTAATT
ATCCGTTTGTGTGTAAGAAAGTAATTTGCCACTGTGCACTTCTGTCTTGCACCTGTCTCC
TGGGGCGGCTGGAAGCTCGCGAGTCAAAACATCAGTGCCATCAGTGTTCATTACCAACCCCTGA
CGTAGATGTACTCTCTTCACTATGAAAGTGTGATGAGTCCCAAGCATCGGATGTCAAAACA
AGAAAGCAAAATCACTGCAAGGATCGGATGGGACAGCTGTCTCAAGGAAAGCAAAAGAACACT
CATGTACCAAAATGTATTTATACCCAAGTGGAAAGAGATTCCCGACACTACAGGAGAG
CACACAGCTGCTACAAATGCCGTCAGTGCACTTTACAGCTGCCGATCTCAGTCACTACTGG
AGCACTTCAACACTGTTCACTGCCAGGAACAGGACATCACTACAGCCAACGGCGAAGAGGAC
GGTCATGCCATATCCACCATCAAAGAGGAGGCCAAAATTGACTTCAGGGTCTACAACTCTGCTA
ACTCCAGACTCTAAATGGGAGAGCCAGTTTCTGAGAGTGTGGTGAAGAGAGAGAAAGCTGGA
AGAGAAAGGAGCGGCTCAAAGAGAAAGTTTGGACCGAGGTTCCAGTGATGACCTTCCGCAATG
TGACTTGGAGAGGGGCGAGACATCTGCGGGGGAGTCCGTATACACCCAAGCAAGCCTGGG
CTGCTGACGCTGTGTCTGCAACCAAGAGCAGACAAAGACTCTAAGGGATAGTCCCAATGT
GGAGCGCGCCATCTGGCCGACCTATTTATGGCTGGGTGTGGAAACCAAGGGATCTCTGCA

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FIGURE 46B

GGGGGGCGCAGCTGGCGGAGAGAAAGTCTGGGGCCCTCCCCAGCAGTATCCTGCATCGGGAG
AAAAACAAGTCCAAAGGATGAATCCCAAGTCCCTGTTACGGAGGCGTAGAGGCTCCGGTGTITTT
GTGCCAATTGCCGTACCCACAAAGACCTCTCTCTGGCGAAAGAATGCAATGGCGGATATGTAT
GCCAAGCGCTGTGGCCTCTACCAAGAGCTTCACTCCGACTCCAGGCTTTAAACATCATTAAC
AAAAACAACGGTGAAGCAGATTATTAAGGAGGAGAACAAAGAAAGCGCTTAACCAAGGCACTT
CAGGCTGAGCAGCTCAACAAACAGCAGAGGGGCGAGCAATGAGGAGCAAGTCAATGGAAGCC
CGTTAGAGAGGAGAGTTCAGAAAGATCATCTAAGTGAAGTCAACAGAGAGAAATCCACTCCCC
AGCCTAAGTAAATACGAAGCCAGGGTTCATTGACTAAAGCCATTCTGCTCAGCAGCCAGTCT
CTGGTCAGCCAAACTTTGGATATTACAAAAGGATGCAACCTTTGCACATTCAGATAAAAGT
CCTCAGGAAGTACTGGAGATCCAGGAAATAGTTTATCCGTATCTGAAGGAAAGGAAAGTTC
TGAGAGAGGCACTCTATAGAAAAGTACATGAGACCTTGGGAAACACCCAAATTATTCACAC
CAGGCAGCCCTATTGAAAAGTACCAAGTACCCACTTTTGGACTTCCCTTTGTACATAATGACTT
CCAGAGTGAAGCTGATTGGCTGGGCTTCTGGAGTAAATATAAGCTCTCCGTTCTGGGAATCC
GCATCTACTGAGTCACGTGCTGGCTACCAAACTCTTGGCAAAACTATGTGCTTATCCACC
TTCAATCTGCTCTCTCATTTTTCAGCTGTGGATCAGACAATGACATTCCTCTAGATTGGCGA
TCAAGCATTCACAGCTGGGCACTGCAAAACGGTGCCTCCAAGGAGAAACGAGGCAACCA
CCAAATGTAAAAAATGAAGGCTCCCTTGAATGTAGTAAAAACAGAGAAAGTTGATAGAAATG
TCAAGTGAATCTTCAACAAATGTGTGCACTGTGGCAATGTCTTCTGGATGAAGTGTATGTA
TCTCTGTGATATGAGTTGCCATGGTGACATGGACCTTTCCAGTGCAGCATATGCCAGCATCTT
TGCCAGGACAAATATGACTTCAACACATATCCAGAGGGGCTGCTAGGAAACAAATGCACA
AGTGAAAAAATGGAAAACTAAAGAGCTTAACTTACCACTAGCACAATTAATAAGAA
ATAGGTTTCTTGTGGGAATTCATAGCTTGTAAATGTCTTATGAAGACCTATTAATAAAAAATA
CTTCATAGAGCCTGCTTATCCACATGAAATTCCTCTCTTTTGTATTCTTTCTTTGTATGAGT
AGGTTACCAAGATTAAAAAGTGAGATAAATGGTCAATGAGAAAAAGATGGAAGATGGTAAAC
AATCACTTTTAAAACTGTAAAGTCAAAACCATCTTGGCTAATATGTACTGGGGAATAATCT
CATAAGAGATATCAACAGACTAGAATTAATATTTATAAGAAAGAGACCAAACTGTCTA
GAAATTGAAAGGTTTACATATTATTATACTAAAGCAGTACTGGACTGGCCATTGGACCATTT
GTTCAAAAACCCATAAATTTGTTCCTAAATTTATAATGATCATGAACCTCAGGAGAGGAGG
AGAAATTGAAGGTCCAGGGCAATGAAAGAAAAATGGCGCCTTCAATTTAGTCTTCTCTCAT
TGGCCATGTTTCAGATTTTGACCTAGAAATGCGAGCTGTGGTTAGGCTTGGTTAGAGTGACG
AAGCAACATGACAGATGGTGGCACGCTGTTTTACCCAGCCCTGGCTGTACATACACATGCAC
ACCTCTCTGATATTTTGTCTTATAGATGTTCAAAATACCTAGTGTCTTTTGTGGGTTTA
GATTCATTTTGGCCACATGATCCCATTTAAAAACAATGTCTCGATGCTCTGTAGTGAT
TTCATTTTACGACGATTTCTTCTGTGTGTGATGAACAGTATGGATTGCTTTCTAAAGCC
TCTGTGTGTACTAATCTCACTGGCACATTAATACTAAAGAAATCCCTCAATCAAAAGC
ATAGATGGATACAAATGTACAGCGTGGGTTAATTTGTTTGAACACATGGCATTCTTCAC
AAGGTAACCTGTGTATTTATTTCTTTTGGTTAAATATAATTTCCAACTTTGTGTGTCAG
GCAGCGCTCTAAGGTTACGTTACCAAGACTGACAGTTGGTATATGTACCAAGCAATCCCTTCA
TAAATGTATACAGATTAGTTAAGTAGCATTAAATAGGATTCTTGAAGTATGTCTCATAG
AACTTTATACTAAGGCTTTGTAAAAACTATCCATGAAGGGAAGCTCCTCAGCATAACTG
CTCAGGGAAATAGGGCTAAATAACTGAACATTAATAATTTGGTTAAAGGTGCTGTAGTCGA
GCCTCAATGCTGTGCTACAAGGATGTATGTACAAGGACTGACTTAAATAATTTGCATTATATTGT
CCCAACCAAGTATTTATTTTGGCCAGGAGATGTAGAAGATATTACAAGTCTAGGATGCAC
TGTCAGATTAACTTATTTTCAATTAAGAGTGGGAGAACAAATAGGAAAAAAACTTATTT
TCTAGTAAATATTAATGTATTACATTTCAAATAATGGTGCCTGACATATTGAATAATTTATTT
CTACAGTGTACGTATGCAACAAAGATATCCATCATGCAATTAGAGTCACTTCTGGCTCTGCCT
AGCTGTTTACATTTGCAATGTAGCAACAAAGGTAATGAAGCAACTATTTCTATTGCAGTGA
TATCCTTTTGTGTGTGTGTGTGCTTAAAGTTGTAACGGTAACATGAAACAAATGAAAGT
TCTTGCTATAATGGTATGGAAAAACAAGGAAATGAAATATTTTATGCTACTTAGGAAA
AAAAGGGTAGCACTTATTCATTCCAAGTACTTTTTTTTTTAAATTTTAAAGCTCTTAACCTACA
TTGTTATGCTTAAAGATATAACATATATCTCTTTTATTGCTTTGTCTATGTTTCATATGAAA
CATTTTCAGAAATTTTGTATAAGTGTGTGCTGGAATCTGCAACGCTGATTTTTTTTGCATTCT
GTAGTCGATTTGCATCCATTTTACATTAATTOGCAAGTGTCTTGTATCATTTTGTGTGTGG
GTTTGTGTCTTTTACAGTGGCGGCTCTCGTTTCTTAAAGTTGGATGGCAGGTAGAGTTCA
ACCAAGTCTGTGCTGTGTAGCGAATGAAGTTAAAAAATGTCTTCTGATGTGTGTGTCAT
TTTCATTTTGTGATTTTGTGTGATATTAATAAAGAGAAAGAGAAAGCAAGAGACAGA

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FIGURE 46C

AATCAGGACTAAGTCCCTCTGCTTCAGTTTCATTGTAAACGGGCTTATTTCTGATCTCACCTGTC
 GCGTAGCTCTAATATTCACATAAACTGAAATAAAGAAAGTGGAAATGAGGAGCTTTGACATTCA
 AATTATGTGATGTAATTTATCTTCTTAGGGAATTTGATGGATGCACTCTCAAAATGTATAGCCA
 GACCTTGAGAGGTGACAATTAAAGATCTAAAAAGAGAGAGAGATTTCCCCAAACAAATATT
 TAATTTTCTAGTAAAAAGAAATACAGAAATGCAATGCTGGCAATCTCTTAAGCAACATTATCTAT
 GTGGAAGTCTTAAATCAGCAAAACACCAAGAGTTGGTTAACTTGGCAATATGACAAGTATT
 ACTTTTGGGCAAAATCTACTCTAATAAGCAATTTCTCTAGTGTGTGGGACACAAATAGGTCCTTT
 ATTTTGGGCAATGATGCTTTTATTTTCAATCAATTTTCTCTCAGACAGACATAGTAG
 TATCAACATAGCAATGGGAAATACATATCACTATCTTGGAAATATTATGGTCAGTCACTTTT
 AGTAAATATTTTGGATAGGCTTGACAGATAGATCTTATCCATCTCTTTATTATTGATA
 ATTTTATTTTCAATTTTGGCTTCAATATTATACATATTTGGTGGAGAGAGGTTGGGCTTTT
 TGAAGAGACAAAAATTTATTAACACTAACACTCTTTTGGACATATTAAGGCTTTTATT
 CCACTCTCAAGATATATTATAAAATTTATTTTAAATTAAGATTCTGAATTTTATCTT
 AAATTTGATTTTAAACGAGCTATTATGGTAAGGAACTTTTAAATGAGGAATTTTATGATGA
 TTTAGGAAATTTCTCTCTTGGAAAGGCTTCCCTGTGATGAAATGATGTGCCAGCTAAATAT
 GTGTGCCATTTAAACACTGAAATATTTTAAATTTATTTGCTATATCTCAATTTGAGCTTTGG
 ATCAAACTTTAGGCCAGGACCACTCATGCGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 CACTCACTCTGTATTCTCTGTGTTGGGATAGAAAAATCATAAAGAGCCAAACCATCTC
 AGAAGCTTTGGATTGAGAGAGACACTACATGACTCCAGTATATGAGAAAAGGACAGAGCT
 CTAATTGATAACTCTGTAGTTCAAAAGGAAAGAGTATGCCCAATCTCTCTACATGACATAT
 TGAGATTTTATTAACACTTTTAAAGATAGTATGTTCTGTCTAAACTGTCTGTCTTTAGTGA
 AGGTAGATTTTATAAAACAGCATGGGGATCTTTCTTAAAGGTAAATATTAATGAGAAAGGGA
 AAAAGTATCTTTTAAACAGCTCTTTGTTGAAAGCTGTGGTAGCACATTTATTTATAATTGCACAT
 GTGCACATAATCTATTATGATCCCAATGCAAAATACAGCTCCAAAAATATTAAATGTATATAT
 TTTAAATGCTGAGGAAATACATTTTCTTAAATAAAGTGAAGAGTCTCAGTATGGCTATTAA
 AATAATTATTAGCTCTCTGTGTGTGGTGCAAAACATCAAAAGTGACCGGTCTTGAGAGCT
 GTGAAGTCTGCTGCTGTGTTAGTAAATAAAATTAATGCATTTCTAGAGGGGGAATATCTGCCAT
 CCAAGTGTGGAAATGTGGAGTAAAGAAAGCTGGTGGTCTGCTCTGTGCTGTATGCCAGCTTT
 TGCTTAAAGTTGAGAGGAGGTCAACTTTAGCTACTGTCTTTGGTTGAGAGGCAATGGCAAAAA
 AAAAAAGAAAAAGATCAAGTCTCTTTGGTGGCCAGTAAAGTGAAGCTTTGCTGACT
 GTCCAGGGCACAAGAGAAAAATTGAGGAATTTGAAATGCAACTGAGTATCAAACTAAATATTC
 TAATCAAGGTAGGTACTGTGTTAGGTGAAATCTATCAAGGCAACTGCAATGAGAAAG
 ATAGAAGGACGCCCTGCGGACTTTGGAGGGCATTGTTATTTTCCAAAGAAAGACGGCCAA
 GGGCAGAGGCAATGCTGATAGTGTGCAAGTGTCTGAAAGCAATCCAGTAAATTTGAGTAA
 ATTGAAGCTCTGGAAATAGCTAGGGCAGAAGTATGTCAAGTATGTACATGAAGAAATGT
 GAAATTCAGAGTAATCCACAGTGAGAAACTAGACAATGTACATTATCTGTCTCTTGAAA
 GGAAGGGAGAGCTGTAAGCTTCACTCTGTCTACACCGAGAAAAAGCAGGAATAACTTTAC
 CGTGGAAATTAATGTTAGCTTTTATCAGAGAAATTTGCTCTAGAGCATAGAGTCCCAAAA
 CTCAATCTGGTTTTCCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT
 ATCACTTTTCTTTTGTGCTCAGGTTCTCTCAGTGTAAAAATGAAAAATATATGTATTA
 ATAAATATTATTAATAATAATATGTAATGTAGTACTTGTGTTGTAAGCACTTTGAGATC
 CTTGGTTGAAAGGCCACCATAGGAGTGCCAAATATTATGTGGCCAAAGGGGTTATTT
 AAATCTCAGTTCCCAAGGCCAGGAAAGGTTGGGGTCAATTTTCTTAAAGACGAGCTG
 TAAATATCAACTAGGCAAGCAATAGTGTGACTAGAGATGCAAACTATTACTAGGCT
 GATAAAATCATAGTTTCTTAATGGCTACCAATAAGGCAAAATATCAATAATAAAACGCCA
 AATTCCTTAGGGCGGACTATTGACAAACCATGGAAAACTTTGGGGGAGGCAATGAGGG
 GGGAACTCTCAAAATGCCAATGTAATAATTAACCTTACAGCAATATTACCAGCAGAAAA
 TGTCTTTTATAGGAATGATTTAGTTGCTAAGAAAAAGAAATTCATTTTGTAGTCTGA
 TTTGAATACTAGAAATGTTGGCTATAATAGTTCTGTTCTTACAACACATGAAATTTTTCGT
 TTTATTTTATTTGTTTTCATAGTGATGTTCTTCTACTCACAAACATGTTCTTGGTGT
 ATTCTTATGCAAAACAATCTTACGGCAGCAAGAGTGTCTGTTACATCTAAACTTGAATAA
 TAAAGTTTACACCAAGTTACACATAACGGCGTTGGTATGGTTTATATGGATTCACTTTC
 ATCTCTTAGGCAATAGGGAAATACAGATCATTTGTAATATATATATATATATACAGGC
 TCTGCTGAANTGAAATGGTGAATCAAAATCACCATTCTAAAAAATTTATCTTATATGGA
 TAAAGCTGGANTCTCAACTGTGTTGCTTTGCTTTTCTTTAACCAATCAATCTCT

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TACTGATAGATTTTGTGTAAGATATATACTAGTTTCTTCAGAAAGATTAACAATAAA
AATTGTGTTTATTTCAAAAA

FIGURE 46D

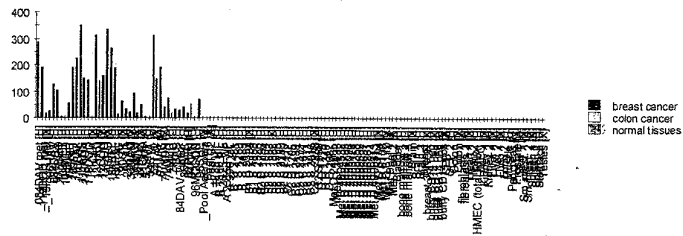
MVRKKNPPLRNVASEGEGQILEPIGTESKVSCKNKEFSADQMSENTDQSDAAELNHKEEHSLSHVQ
DPSSSSKKDLKSAVLSEKAGFNYEFSKGGNFPSPHDEVTDNRNMLAFSSPAAGGVCEPLKSPORA
EADDPODMACTPSGDSLETQKMSKATEETQQAQSGQANCOGLSPVSVAKNPQVPSDGGV
RLNKSCTDLLVNDNDPAPLSPQLQDFKCNIGYGYGNDPTDLIKHFRKYHLGLHNRTQDAEL
DSKILALHNMVQFHSKDFOKVNRSVFSGVLQDINSSRPVLLNGTYDVQVTSGGTFIGRKTTPDC
QGNTRYFRCKFCNFTYMGNSTELQHFLOTHPNKIKASLPSEVAKPSEKNSNKSIPALQSSDSGD
LGKWDQKITVKAGDDTPVGYSVPIKPLDSSRQNGTEATSYWCKFCFSCESSSLKLEHYGKQ
HGAVQSGGLNPELNDKLSRGSVINQNDLAKSSEGETMTKTDKSSSGAKKKDFSSKGAEDNMVTS
YNCQCFDFRYSKSHGPDVIVVGPILLRHYQQLHNHCKCTKHCPFCPRGLCSPEKHLGEITYPFACRK
SNCSHCALLLHLSPGAAGSSRVKHQCHQCSFTTPDQVLLFHYESVHESQASDVKQEANHLQGS
DGOQSVKESKESCTKCDFITQVEEISRHVRRASCYKCRQCSFTAADTQSLLEHFTVHCOEQD
ITTANGEEDGHAISTIKKEPKIDFRVYNLLTPDSKMGEVSVESVVKREKLEEKDGLKEKVWTESSD
DLRNVTVRGADILRGSPSYTQASLGLLTPVSGTQEQTKTLRDSNVAAHLARPIYGLAVETKGL
QGAPAGGEKSGALPQQYPASGENKSKDESQSLRRRRRGSGVFCANCLTTKTSWLRKNANGGYVC
NACGLYQKLHSTPRPLNIIKQNNGEIURRTRKRLNPEALQAEQLNKQQRGSNEEQVNGSPLERR
SEDLTESHQREIPLPSLSKYEAQGSLLKSHSAQQPVLVSQLDIHKRMQPLHIQKSPQESTGDPGN
SSSVSEGGSSERGSPIEKYMRPAKHPNYPSPGSPIEKYQYPLFGLPFVHNDQSEADWLRFSKY
KLSVPGNPHYLSHVPGLPNPCQNYVPYPTFNLPPIHSAVGSNDIPDLALIKHSRPGPTANGASKEK
TKAPPNVKNEGPLNVKTEKVDSTQDELSTKCVHCGIVLDEVMYALHMSCHGDSGPFQCSICQ
HLCTDKYDFTTHIQRLHRNNAQVEKNGKPKKE

FIGURE 47

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FIGURE 48

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FIGURE 49A

ACTCACTATAGGGCTCGAGCGGCGCGCGGGCAGGTGGCCACCCACCATCATCTAAAGAAGA
 TAAACTTGGCAAATGACATGCAGGTTCTTCAAGGCAGAATAATTGCAGAAAAATCTTCAAAGG
 ACCCTATCTGCAATGTTCTGAATACCTCTGAGAAATAGAGATTGATTATCAACCCAGGATACC
 TAATTCAAGAACTCCAGAAATCAGGAGACGGAGACATTTTGTCAGTTTTGCAACATTGGACCA
 AATACAAGTAATCTTGTGTGCTCTGTTTGGCTGTCTGGGCACAGAATTGCTGGGA
 AGCTCTGTCTGACTGTACAGATCCCGAGGTTTCAGAGGACGGATACAGCAGGAACGAAAAA
 CATCCGACCCACATTTATTCTGTGCTTACOGATGATCAAGATGTGGAGCTGGGGTCCCTGC
 AAGTCATGAACAAAAACGAGAAAGATTATGGAACATGGGGGGGCCACCTTCATCAATGCC
 TTGTGACTACACCCATGTGCTGCCCCGTACGGTCTCCATGCTCACCCGGGAAGTATGT
 GCACAATCACAAATGTCTACACCAACAACGAGAACTGCTCTTCCCCCTCGTGGCAGGCCA
 TGCATGAGCCTCGGACTTTTGTCTATATCTTAACAACACTGGCTACAGAACAGCCTTTT
 TTGGAAAAATACCTCAATGAATATAATGGCAGCTACATCCCCCTGGGTGGCGAGAAATGG
 CTTGGATTAAACAAGAAATCTCGCTTCTATAATTACACTGTTTGTGCAATGGCATCAAA
 GAAAAGCATGGATTGTATTATGCAAAGGACTACTTCACAGACTTAATCACTAACGAGAG
 CATTAATTACTTCAAAATGTCTAAGAGAATGTATCCCCATAGGCCCGTTATGATGGTGAT
 CAGCCACGCTGCGCCCCACGGCCCCGAGGACTCAGCCCCACAGTTTTCTAAACTGTACC
 CCAATGCTTCCCAACACATAACTCCTAGTTATAACTATGCACCAAAATATGGATAAACACT
 GGATTATGCAGTACACAGGACCAATGCTGCCATCCACATGGAAATTAACAAACATTCTAC
 AGCGCAAAAGGCTCCAGACTTTGATGTGAGTGGATGATTCTGTGGAGAGGCTGTATAAC
 ATGCTCGTGGAGACGGGGGAGCTGGAGAAATACTTACATCTATTACACCGCCGACCATGG
 TTACCATATTGGGCAGTTTGGACTGGTCAAGGGGAAATCCATGCCATATGACTTTGATAT
 TCGTGTGCCCTTTTTTATTCGTGGTCCAAAGTGTAGAACCCAGGATCAATAGTCCACAGAT
 CGTTCTCAACATTGACTTGGCCCCACGATCCTGGATAATGCTGGGGCTCGACACACCTCC
 TGATGTGGACGGCAAGTCTGTCTCAAACTTCTGGACCCAGAAAAAGCCAGGTAAACAGGT
 TTCGAACAAACAGAAGGCCAAAAATTTGGCGTGATACATTCTAGTGGAAAGAGGCCAAA
 TTTCTACGTAAAGAAGGAAGAATCCAGCAAGAATATCCAACAGTCAAAATCACTTGGCCAAA
 TATGAACGGGTCAAAGAACTATGCCACGAGGCCAGGTACAGACAGCCTGTGAACAAAC
 GGGGCAGAAAGTGGCAATGCATTGAGGATACATCTGGCAAGCTTCGAAATTCACAAAGTGA
 AAGGACCCAGTGACTGCTCAGTCCGGCAGAGCAACGGGAACCTCTACCTCTCCCGGC
 TTCCATGCAAAAGACAAAGAGTGCAGTTGTAGGGAGTCTGGTTACCGTGCCACGAGAAG
 CCAAAAGAAAGAGTCAACGGCAATTTTGAGAAACAGGGGACTCCAAAGTACAAGCCCA
 GATTGTTCATACTCGGCAGACACGTTCTTGTCCGTGCAATTGGAAGGTGAATATATG
 ACATAAATCTGGAAGAAGAAGAAGAAATTGCAAGTGTGCAACCAAGAAACATTGCTAAG
 CGTCATGATGAAGGCCACAAGGGGCCAAGAGATCTCCAGGCTTCCAGTGGTGGCAACAG
 GGGCAGGATGCTGGCAGATAGCAGCAACGCGGTGGGCCACCTACCACTGTCCGAGTG
 ACACACAAGTGTATTATTCTTCCCAATGACTCTATCCATTGTGAGAGAGAACTGTACCAA
 TGGGCCAGAGCGTGGAAAGGACCAATAGGCATACATTGACAAAGAGATTGAAGCTCTGCA
 AGATAAAATTAAGAAATTAAGAGAAGTGAGAGGACATCTGAAGAGAAGGAAGCCTGAGG
 AATGATGCTGCAGTAAACAAAGCTATTACAATAAGAGAAAAGGTGTAATAAAGCAAGAG
 AAATTAAGAGCCATCTTCAACCATTTCAAGGAGGCTGCTCAGGAAGTAGATAGCAAACT
 GCAACTTTTTCAAGGAGAACACCCGTAGGAGGAAGAAGGAGAGGAAGGAGAAGAGACGG
 CAGAGGAAGGGGGAAGAGTGACGCTGCTGGCCTCACTTGTTCACGCATGACAAACA
 CCACTGGCAGACAGCCCCGTTCTGGAACCTGGGATCTTTCTGTGCTTGACGAGTTCTA
 ACAATAACACCTACTGGTGTTCGCTACAGTTAATGAGACGCATAATTTCTTTCTGTG
 AGTTTGCTACTGGCTTTTGGAGTATTTGATATGAATACAGATCCTTATCAGCTCACAA
 ATACAGTGACACCGGTAGAAGGAGCATTTTGAATCAGCTACACGTACAACATATGGAG
 CTCAGAAGCTGTCAAGGATATAAGCAGTGCAACCCAAGACCTAAGAACTTTGATGTTGG
 AAATAAAGATGGAGGAAGCTATGACCTACACAGAGGACAGTTATGGGATGGATGGGAAG
 GTTCAGTTCAGCCCCGTCTCACTGCAGACATCACTGGCAAGCCCTAGAGGAGCTACACAG
 TGTGAATGAAAACATCTATGAGTACAGACAAAACCTACAGACTTGTCTGGTGGACTGGA

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CTAATTACTTGAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGAGCAAA
ATAAAACAAATAAGACTCAAACCTGCTCAAAGTGACGGGTTCTTGGTTGCTCTGCTGAGC
ACGCTGTGTCATTAATGGAGATGGCCTCTGCTGACTCAGATGAAGACCCAAGGCATAAGGTT
GGGAAACACCTCATTTGACCTTGCCAGCTGACCTTCAAACCTGCATTTGAACCGACCA
ACATTAAGTCCAGAGAGTAACTTGAATGGAATAACGACATTCAGAAAGTTAATCATTG
AATTCTGAACACTGGAGAAAACCGAAAAATGGACGGGGCATGAAGAGACTAATCATCT
GGAAACCGATTTTCACTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCAGCCCAAGG
CTGCAGCCCATTCGACGGCACCCGAAAGAACTTCCCCAGTATGGTGGTCTGGAAAGGA
CATTTTGAAGATCAACTATATCTTCTGTGCATTCCGATGGAATTCAGITCATCAGAT
GTTCACTGGCCACCGCAGAACCCGAAAGTAAATCCAGCATAGCGGGGAAGATGTTGA
CCAAGGTGGAGAAAGATCAGAAAAGGAGAAAGTCAAGCACCTAGAAGGCAGCGCCTC
CTCTTCACTCTCTGATTAGATGAACTGTTACCTTACCCCTAAACACAGATTTCTTTT
TAACTTTTTTTATTTGTAACTAATAAAGGTAATCACAGCCACCAACATTCAGCTACCC
TGGGTACCTTTGTGAGTAGAAGCTAGTGAGCATGTGAGCAAGCGGTGTGCACACGGAG
ACTCATCGTTATAATTTACTATCTGCAAGAGTAGAAAAGAAAGGCTGGGGATATTTGGGT
TGGCTTGGTTTGTATTTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
AATATCGTAGGGACATAAGTATATACATGTATCCAAATCAAGATGGCTAGAATGGTGCCT
TTCAGTGTCTTAAACTTGACACCCCTGGTAAATCTTTCAACACACTTCCACTGCTGC
GTAATGAAGTTTGAITCATTTTAAACCACTGGAATTTTCAATGCCGTATTTTCAGTTA
GATGATTTTGCACITTGAGATTTAAATGCCATGCTATTTGATTAGTCTTATTTTTTATT
TTTACAGGCTTATCAGTATGGATCACATATTGTTGACATTAAGCTTTTCCAGAAAATGTT
GCATGTGTTTAACTCGACTTGCTAAATCGATTAGCAGAAAAGGCTGGCTAATAATGTT
GGTGGTGAAAATAAATAAATAAGTAAACAAAARAAAWWGCTGCTCTCTGTGCTC
TAGCCTCAAAGCGTTTATCATATCATACCTTTAAGATTGCTATATTTTGGGTTATTTTC
TTGACAGGAGAAAAGATCTAAGATCTTTTATTTTCATCTTTTGGTGTCTTGGCATG
ACTAAGAAAGCTTAAATGTTGATAAATATGACTAGTTTGAATTTACACCAAGAACTTCT
CAATAAAAGAAAATCATGAATGCTCCACAATTTCAACATACCACAAGAGAAAGTTAATTC
TTAATCATGTTCTATGATTATTTGAAGACCTTCAACCAAGTTCTGATATCTTTAAAGA
CATATGTTCAAAATGCTTTTGAATCTGTATCTTGAATAATCTCTGTTGTTGTTAGG
TTTTTAAATACCAGCTAAAGGATTACCTCACTGAGTCATCAGTACCCCTCTATTAGCTC
CCCAAGATGATGTGTTTTGCTTACCCTAAGAGAGGTTTCTCTTATTTTAGATAATTC
AAGTGCTTAGATAAATTATGTTTTCTTTAAGTGTATGGTAACTCTTTTAAAGAAAAT
TAATATGTTATAGCTGAATCTTTTGGTAACTTTAAATCTTTATCATAGACTCTGTACATA
TGTTCAATTAGCTGCTTGCCTGATGTGTGATCATCGGTGGGATGACAGAACAAACATA
TTTATGATCATGAATAATGCTTTTGTAAAAAGATTTCAGTTATTAGGAAGCATACTCT
GTTTTTAAATCATGTATAATATCCATGATACTTTTATAGAACAAATTCGGCTTCAGGAAA
GTCTAGAAAGCAATATTTCTTCAATAAAAGGTGTTTAAACTTTAAAAAAGAAAAA
AAAAA

FIGURE 49B

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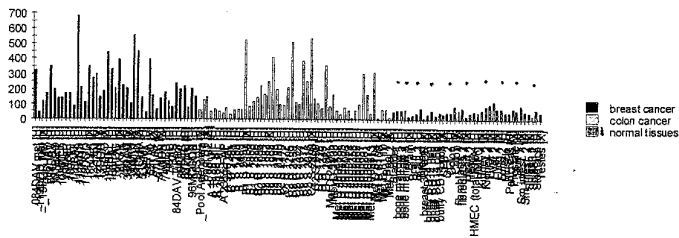
FIGURE 50

MGVSCGALQLVGHGHEGNSKSTVRSFRFRGRIQOERKNIRPNILVLTDDQDVELGSLQVMNKT
RKIMEHGGATFNIAFVITPMCCPSRSSMLTGKYVHNHNYYINNENCSSPSWQAMHEPRITFAVYL
NNTGYRTAFFGKYLNEYNGSYIPPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFTDLI
TNESINYFKMSKRMYPHRPVMVMVISHAAPHGPEDSAPQFSKLYPNASQHIITPSYNYAPNMDKHWI
MQYTGPMLPIHMEFTNILQRKRLQTLMSVDDSVRLYNMLVETGELENTYIITYTADHGYHIGQFG
LVKGKSMPLYDFDIRVFFHRGPSVEPGSIVPQIVLNIDLAPTILDIAGLDTPPDVDGKSVLKLLDPEKP
GNRFRTNKKAKIWRDITFLVERGKFLRKKEESSKNIQSNHLPKYERVKELCQQAQRYQTACEQPGQ
KWQCIEDTSGKLRHKCKGSDLLTVRQSTRNLYARGPHDKKECSCRESGYRASRSORKSQRF
LRNQGTPKYKPRFVHTRQTRSLSVFEGEYDNLLEEEELQVLOPRNTAKRHDEGHKGPRDLOASS
GGNRGRMLADSSNAVGPFTTVRVTHKCFILPNDSHCERELYQSARAWKDHKAYIDKEIALQDKI
KNLREVRGHLKRRKPEECSCSKQSYTNKEKGVKKQEKLSHLHPFKEAAOEVDVKLQLFKENNR
RRKKERKEKRRQKKEECSLPGLTCTFHDNNHWQTAPFWNLGSFCACTSSNNNTYWCRLTVNET
HNFLCFEATGFLFYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQCNPRPKNLDV
GNKDDGSYDLHRGQLWDGWEG

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**FIGURE 51**

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AACCGAGAAAGCGCTCCGTAAAGCCATCCGCACGCTCAGAAAGGCCGCTCCACAGGGAGCAGTTTCCCTCCAGCTCTCAGG
CATGAACCTCGACGTGGCTAAAAAGCTCCCGAACAATCTGAACGCCAGGCAGAGTCTCTGTGGAGTGGGCCAGGGTCATG
CAGAAAACCAATGTGTGAGTTGCAGGGCTGGGACCTATATGATGGAGCACGAGAACGTCATTTTATGTCCAAATGGA
ACCTTCCAAATGAGGAAGGACAAATGACTTGTGAACCATGCCAAGACAGGAAATCTGGGGCCCTGAAGACCCCGAGA
AGCTTGGAAATATGCTGAATGTGGAGGCTGTGTCAACCTACTGAATATTTCTGCAGATGGCTTGCACCTTGCACGCTCT
GTGCCCTGGGCASGTTCCAGCTGTGAAGCTGGTGGAACTTCTGCTTCCCTGTGGAGGAGGCTTGCACCAACACATCAG
GGAGCTACTTCCCTTTCAGGACTGTGAACCCAGAGTTCAATGTTCACCTGGACATTTCTACAACACCCACCTCAACGATG
TATTCGTTGGCCAGTGGGAACATACCCAGCTGAAATTTGGAAAAAATAATTGTGTTTCTTGGCCAGGAAATACTACGACTG
ACTTTGATGGCTCCACAACATACCCAGTGTAAAAACAGAGATGTGGAGGGAGCTGGGAGATTTCACTGGGTACATT
GAATCCCCAACTACCCAGCAATTACCCAGCCACACCGAGTGTACGTGGACCATCAACCCACCCCGAGGCCGCAI
CCTGATCCTGTGCTGAGATCTTCTGCCCATAGAGGACGACTGTGGGACTATCTGGTGTGGGAAACCTCTTCAT
CCAAATCTGTGACAACTATTTGAACCTGCCAGACTACGAACGCCCATCGGCTTCACTCCAGSTCAAGAGAGCTGTGG
ATTCACTTCAAGTCCAAATGAAGGAAACAGCGCTAGAGGGTTCCAGGTCCCATACGTGACATATGATGAGGACTACAGGA
ACTCATTGAAGCATAGTTCCAGATGGCAGGCTCTATGCTATGAGAACCATCAGGAATACTTAAAGATAGAACTTA
TCAAGGCTCTGTGTTGATGTCTTGGCCCATCCCGAACAATTTCAAGTACACAGCCAGGAGTCCCGAGAGATGTTTCCA
AGATCGTTCAATCCGATTGCTACGTTCCAAAGTGTCCAGGTTTTCAGACCTTACAAATGACTCAGCCACGTCCTCA
ATACAAATGTTCTGCTATAGGTTGGTGGGACAGAGCTGTCTTCTTCTGCTATGTCAGCACAGTGGGTATTGCTGCTC
CGATACAGTACTCATTAGAGTTCAATTTTATAGATAATACAGATATTTTGGTAAATGAACTTGGTTTTCTTTCC
AGCATCGTGGATGTAGACTGAGATGGCTTTGAGTGGCATCAGCTTCTCACTGCTGTGGGGGAGTGTCTGGATAGATCA
AGGGCTGGCTGAGCTGGACTTTGGTCAGCTAGGTGAGACTCACTTCTCTCTGGGTCTTACTCTCTCAAGGAGTC
TGATGTGGAAGGAGGCCACAGATAAGCTGCTTATTTCTGAACCTTCACTTCTCTAGCCCGGCCCTCTTAAGGGAGC
CCTCTGCACTCTGTGACAGCTCTGACAGGCAGAACAGGGGAGGGAAGGAGACCCCTGCAGGCTCCCTCCAC
CCACTTGGAGCTGGGAGGACTCAGTTTCTCCACAGCCTTCTCCAGCCTGTGTATCAAGTTTGATCCAGGAACTTG
AGTTCTAAGCAGTCTGCTGAAAAAAGCAGAAAGAAATTAGAAATAAATAAACTAAGCACTTCTGGAGACATAAA
AA

FIGURE 5 2

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FIGURE 53

...ATGAACCTCGACGTGGCTAAAAAGCCTCCAGAACATCTGAACGCCAGGCAGAGTCCTGTGGAGTGGGCCAGGGTCA
TGCAGAAAACCAATGTGTCAAGTTGCAGGGCTGGGACCTATTATGATGGAGCACGAGAACGCTGCATTTTATGTCCAAATG
GAACCTTCCAAATGAGGAAGGACAAATGACTTGTGAACCATGCCAAGACCAGGAAATTCCTGGGSCCTGAAGACCCCA
GAAGCTTGAATATGTCTGAATGTGGAGGCTGTGTCAACCTACTGAATATTCTGCAGATGGCTTTGCACCTTGCACGCT
CTGTGCCCTGGGCASGTTCAGCCTGAGCTGGTGAACCTTCCCTGCTTCCCTGTGGAGGAGGCTTGCACCAAAACATC
AGGAGGCTACTTCCCTTCAGGACTGTGAACCCAGAGTTCAATGTTACCTGGACATTTCTACACACCACCACTCACGSA
TGTATTCGTTGCCAGTGGGACATAACCCAGTGTAAACACAGAAAGATGTGGAGGGGAGCTGGGAGATTTCACTGGGTACA
TGACTTTGATGGCTCCACAAACATAACCCAGTGTAAACACAGAAAGATGTGGAGGGGAGCTGGGAGATTTCACTGGGTACA
TTGAATCCCCAACTACCCAGGCAATTACCCAGCCAAACACCGAGGTACGTGGACCAATCAACCCAGGCTGGGAGATTTCACTGGGTACA
ATCCTGATCGTGGTCCCTGAGATCTTCCCTGCCCATAGAGGACGACTGTGGGAGCTAATCTGGGTGATGGGAAACCTCTTC
ATCCAAATCTGTGACACATATGAACCTTCCAGACCTACGAGCGCCCATGGCTTCCCTGATGGGAAACCTCTTC
GGATTCAGTTCAAGTCCATGAGGGGAAACCGCTAGAGGCTTCCAGGTCCCATACGTGACATATCATGAGGACTACCG
GAATCATTGAAGACATAGTTCCAGATGGGAGGCTCTATGCTCTGAGAACCATCAGGAAATACTTAAGGATAAGAACT
TATCAAGGCTCTTTTATGCTCCTGGCCATCCAGAACTATTTCAAGTACACAGCCAGGAGTCCCGAGAGATGTTTC
CAGATGCTTCATCCGATTGCTACGTTCCAAAGTGTCCAGGTTTTTGAACCTTACAAATGA

FIGURE 54

...MNLDAKKFPRTSERQAESCQVGGQHAENQCVSCRAGTYDGAERERICLPNGTFQNEEGQMTCEPCPREGNSGALK
TPEARNMSECGGLCQPTSEYADGFAPCQLCALGXFPQPEAGRTSCFPCGGGLATKHQGATSFQDCETRVCSPGHFYNTT
HRCIRCPVGTYPQEPFGKNNVSCPGNTTTDFGSTNITQCKNRROGGELGDFTYGIESPNYPGNYPANTECTWTINPPPK
RRILIVVPEIFLPIEDDCG DYLMRKTSSNSVTTYETCQTYERPIAFTSRKKLWQFKSNEGNSARGFQVPTVYDED
YQELIEDIVDRGLYASENHQELKDKKLKALFDVLAHPQNYKYTAQESREMFPSFIRLLRSKVSRLRPYK.

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```
human_BCO2      MNLDVAKKPPRTSERQAESCGVGQGHAEHQVSCRAGTYDGAERECILCPNGTFQNEEG
mouse_BCO2      -----
human_BCO2      QMTCEPCPRPGNSGALKTPAEAWNMECGGLCQPTSEYADGFAPQQLCALGXFPQPEAGRTS
mouse_BCO2      -----
human_BCO2      CFFCGGGLATKHOGATSFQDCETRVQCSFGHFYNTTTHRCIRCFVGTQPEFGKNNVCSC
mouse_BCO2      -----
human_BCO2      PGNTTTDFDGSTNITQCKNRRCGGELGDFTYIESPNYPGNYPANTECTWTINPPFKRRI
mouse_BCO2      -----TINPPFKRRI
                    *****
human_BCO2      LIVVPEIFLPIEDDCGDVLMWKTSSNSVTTYETCQTYERPIAFTSRSKKLWIQFKSNE
mouse_BCO2      LIVVPEIFLPIEDDCGDVLMWKTSSNSVTTYETCQTYERPIAFTSRSKKLWIQFKSNE
                    *****
human_BCO2      GNSARGFQVPYVYDQYQELIEDIVRDGRLYASENHQELKDKKLIKALFDVLAHPQNY
mouse_BCO2      GNSARGFQVPYVYDQYQELIEDIVRDGRLYASENHQELKDKKLIKALFDVLAHPQNY
                    *****
human_BCO2      FKYTAQESREMFPRSFIRLLRSKVSRLRPYK
mouse_BCO2      FKYTAQESREMFPRSFIRLLRSKVSRLRPYK
                    *****
```

FIGURE 55

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FIGURE 57

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ATGTTCTCTCCATCCTAGTGGC
GCTGTGCTGTGGCTGCACCTGGCGCTGGGCGTGGCGGGGGGCGCCCTGCGAGGCGGTGCGCATCCCTATG
TGCCGGCAGATGCCCTGGAAACATCACGGGGATGCCCAACCACTGCAOCACAGCAGCAGGAGAACGCGA
TCCTGGCCATCGAGCAGTACGAGGAGCTGGTGGAGCTGAACCTGCAGCGCCGTGCTGCGCTTCTTCTCTG
TGCCATGTACGGGCCATTGGACCTGGAGTTCTTGACGACCCCTATCAAGCCGTGCAAGTCGGTGTSC
CAACGGCGGGGACGACTGGGAGCCCTCATGAAGATGTACAACCAAGCTGGCCCGAAGCCTGGCCT
GCGACGAGCTGCTGTCTATGACCGTGGCGTGTGCATTTCGCTGAAGCCATCGTCACGGACCTCCGGA
GGATGTTAAGTGGATAGACATCACACAGACATGATGGTACAGGAAAGCCCTCTTGATGTTGACTGTAAA
CGCTTAAGCCCCGATCGGTGCAAGTGTAAAAAGGTGAAGCCAACTTGGCAACGTATCTCAGCAAAAACT
ACAGCTATGTTATTCATGCCAAATAAAACTGTGCGAGGAGTGGCTGCAATGAGGTACACACGGTGT
GGATGTAAAGAGATCTTCAAGTCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCATTACAAATCT
TCTTGCCAGTGTCCACACATCCTGCCCATCAAGATGTTCTCATCATGTGTACGAGTGGCGTTCAAGGA
TGATGCTTCTTGAAAATTGCTTAGTTGAAAAATGGAGAGATCAGCTTAGTAAAAAGATCCATACAGTGGGA
AGAGAGGCTGCAGGAACAGCGGAGAACAGTTCAGGACAGAGAGAAAAACGCGGGCGCACCATGCTGAT
AATCCCCCAACCAAGGGAAAGCTCTGCTCCCAACCCAGCCAGTCCCAAGAGAACATTAAACTA
GGAGTCCCAGAGAGAACCAACCCGAAAAGAGTGTGA

FIGURE 58

MFLSLVALCLNLHLALGVRGAPCEAVRIPMCRHMPWNI TRMPNHLHSTQENAILAIEQYEEVLVDVNC
AVLRFFPCMYAPICTLEFLHDIKPKSVQRRDDCEPLMKYNNHWPESLACDEL PVYDRGVCI SFE
AIVTDLPEVDKIDITPMMVQERPLDVKRLSPDRCKCKVKPTLATYLSKNYSYVIAKIKAVQRSG
CNEVTTVVVVKIEFKSSSPIPTQVPLITNSSCQPHILPHQDVLIMCYENRSRMMLLENCLVEKWRDL
SKRSIQWEERLQEQRTVQDKKKTAGRTSRSNPPKPKGPPAPKFPSPKKNIKTRSAQKRTNPKRV

FIGURE 59

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CGGCACCAAGAGCACTGGCCAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGATGCTACACTCAGCTTTGGGTCT
CTGCCTCTTACTCGTCACAGTTTCTTCCACCTTGCCATTGCAATAAAAAAGGAAAAGAGGCTCTCAGAGACTCTCAA
GAGGATGGGGAGATGACATCACTTGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAGTAAAGAGCCATT
ATGGTTATTCATCAGCTGGAGGATTGTCAATCTCTCAAGCACTAAAGAAAGTATTTGCCCAAATGAAGAAATACAAGA
AATGGCTCAGATAAGTTTCATCATGTGCTAAACCTTATGCATGAACCACTGATAAGATTTATCACCTCATGGGCAATATG
TGCTAGATCATGTTTGTAGACCCCTTCTTTACAGTTAGAGCTGCATAGCTGGAGATCTCTAACAGATTATACACA
TATGAGCCTCGGGATTACCCCTTATGATTAGAAACATGAAGAAAGCATTAGACCTTATTCAGTCAGAGCTATAGAGAT
GATAGAAAAAGCCTTCACTTCAAGAACTCAATTTTCATGAAGAAACCTCTGGCATTGACAAATACTAAATGTGCA
AGTATATAGATTTTGTATATTACTATTAGTTTTTTTAAATGTGTTTGCATAGTCTTATATAAATAAATGTTTTTAA
TCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 62

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ATGATGCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCACCTTGCCATTGCAATAAAAAAGGA
AAAGAGGCTCTCTCAGACACTCTCAAGAGGATGGGAGATGACATCACTTGGGTACAACTTATGAAGAAGGTCTCTTTT
ATGCTCAAAAAAGTAAGAAGCCATTAAATGGTTATTTCATCACCTGGAGGATTGTCRAATCTCTCAGCACTAAGAGAAAGTA
TTTCCCCAAAATGAAGAAATACAAGAAATGGCTCAGAAATAAGTTTCATCATGCTAAACCTTATGCATGAAACCACTGATAA
GAATTTATCACCTGATGGGCAATATGTGCTAGAAATCATGTTTGTAGACCCTTCTTTAACAGTTAGAGCTGACATAGCTG
GAAGATCTCTAACAGATTGTACACATATAGGCTCGGGATTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGA
CTTATTCACTCAGAGCTATAA

FIGURE 63

MMLHSALGLCLLLVTVSSNLAIAIKKEKRPQTLSRGWDDITWVQTYEGLFYAQKSKKPLMVIHHLEDCQYSQALKKV
FAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDPSTVRADIAGRYSNRLTYEPRDLFLLIENMKALR
LIQSEL

FIGURE 64

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AGCGGCCGGGCCACG[REDACTED]GAGCGGACGGCTGCGGGGGGGCGGAGCCGGCGGCGGAG
 GCGCGGCCGCTCCCCGGGAGGCCCCGGCGGGAAACGGCCGGATCGGGGCCGACGCCACG
 CTCCGAGGGCGCCGGGGACCCGACGGCGGCCGCTCTGCTGGCCCTATGGACGTGGGG
 GAGGAGCCGCTGGGAGAAGGGCGCGCGCCCGCACTGCCAAGGACCCCAACACTATAAAGT
 ACTCTCGCTGTTATGTGAGTATGTGTGTTAAACAACAATACITGGTTGTATATTGGGTGAAA
 CCAAGCTGTGCCAAAGAGTTAAAAGTTGCAAAAGGTGCGTGTTCGAGAGAACATTGGGAA
 CTGTGCTGTGATGCTGCTGTGTGTGAGCTTGGAACTGCTGTTAGATTACCAAGAGACGTG
 CATAGAACCAAGACATATATGGACTTGCAACAAATTCAGGTGTGGTGAGAAAAGGTGACCA
 GAAGCCTCTGTGCTGTTTCAAGTACTGCAAGGACCAAGGGCGACTGCTGCATCACTACAGTT
 CTGTGTGTCAAGGTGAGAAAAGTTGGGTAGAGAAGCAATGTGAGAGCATTAATGAGCCACAG
 TGCCACGACGGGTTTGAACGCCCTCTACCCCTCTATTCTTTGGATGGATTACGGGCAGAA
 ATTTACACACTTGGGGTGGACTTCTCTGTTATTAGCAAACTAAAAAATGTGGAAACATATA
 CTAAAAACATGAGACCGGTATATCCAAACAAAACCTTCCCAATCACTACAGCATTTGCAACG
 GATTGTATCCAGAAATCTCATGGCATAATCGAATAAAATGTATGATCCCAAAATGAATGCTT
 CCTTTTCACTTAAAAAGTAAAGAGAAATTTAATCCTGAGTGGTACAAAGGAGAACCAATTTGGG
 TCACAGCTAAGTATCAAGGCCTCAAGTCTGGCACATTTTCTGGCCAGGATCAGATGTGGAAA
 TTAACGGAAATTTTCCAGACATCTATAAAATGTATAATGTTTCAATACCATTTGAAGAAAGGA
 TTTAGCTGTTCTTCAAGTGGCTACAGCTTCTTAAAGATGAAAGACCACTTTTACACTCTGTA
 TTTAGAAAGACAGAAATTTTCAAGTCTTATATGAGCACTGAGCAGTGAAAGTCACTAAAGC
 CTGTCAGAGGGTGTATGTTATGTTGGTATGCTGATGGATGGTCTGAAAGAGCTGAACTTGCA
 CAGATGGCTGAACCTCATCTTATTTTCAAGTATGCGATGGAAACAGGCAAGTTGAAGAAATA
 CATATATCTGAATAAATATTTGGGGGATGTTAAAAATATTAAGTTATCTATGGACCTGCAGC
 TCGATTGAGACCCCTGATGTCCAGATAAAATCTATTTCACTTAACTATGAAGGCAATGGCCG
 AAATCTTCTTGGCCGGGAACCAACCCAGCACTTCAAACTTACCTGAAACATTTCTTACCTAA
 GCCTTTGCACCTTGTCTAAGAGTATAGAAATGAGCCCTTGACATTTCTTTGGACCCCTGAGTG
 CAACTTGCACTTGAATCCCTCAGAAAGGAAATATTTGGAAAGTGGATTTCATGGCTTGACAA
 GTATTTTCAAAATATGCAAGCCCTCTTTGTTGGCTATGGACCTGGATTCAAGCATGGCATTTGAG
 GCTGACACCTTTGAAAACATTGAAAGTCTATAACTTAATGTGTGATTTACTGAAATTTGACACCG
 GCTCTTAATAAGGAACTGATGAAAGTCTTAACCACTCTAAAGAAATCTGTTATACGCCA
 AAGCATCCCAAGAAAGTGCAGCCCTGTGACAGTGCCTTCAAGAAACCCAGAGATAA
 CCTTGGCTGCTCATGTAAACCTTTCGATTTTGGCGATTGAGGATTTCAAAACACAGTTCAATCTG
 ACTGTGGCAGAAAGAGAGATTATTAAGCATGAACTTTACCTATGGAAAGCACTAGAGTTCTC
 CAGAAAGAAACACCACTGTCTTCTTCCAGCACCAAGTTTATGAGTGGATCAGCCAAAGAC
 ATCTTAATGCCCCCTTTGGACATCTTATACCGTGGACAGAAATGACAGTTTCTCTACGGAAGAC
 TTTCTCAACTGTCTGTAACGAGCTTTAGAAATCTCTTATGCTCTGTCCATAAAATGTTCAATTTA
 TAAAAATAACACCAAAAGTGTGTTACGGGTTCTCTCCCCACCACTAAATAAAAAATCAAG
 TGGAAATATATCTGAAGCTTTGCTTACTACAAATATAGTGCCAAATGTACCAAGAGTTTCAAGTT
 ATATGGCGCTACTTTTATGACACCTTACTGCGAAAGTATGCTGAAGAAAGAAATGGTGTCAAT
 GTGCTGAGTGTGCTGTGTTTGAATTTGATTATGATGGACGTGTGATTCTTAGAGAAATCTGA
 GGCAGAAAAGAAAGAGTATCCGTAAACCAAGAAATTTTGAATCCAACTCACTTCTTATTGTGC
 TAACAGGCTGTAAAGATACATCTCAGACGCCCTTGCACGTGTGAAAACCTAGACACCTTAGCTT
 TCATTTTGGCTCAGAGGACTGATAACAGCGAGAGCTGTGTGATGGGAAGCATGACTCTCAT
 GGGTTGAAGAATTTGTTATGTTACACAGGACCGGATCAGAGATGTTGAGCAGATCACTGGA
 CTCAGCTTCTATCAACAAAGAAAGAGCCAGTTTACAGACATTTTAAAGTTGAAAACATTTG
 CCAACCTTAGCCAAAGAGAC[REDACTED]TATGTTTATTTTCCCAACACCATGAACTTTTGGAGA
 GAACCTTATATTTATATAGTCTCTAGCTACACTATGCAATTGTTTCAAGAACTGTGCA-CCA
 AGT-TAGAACGGAGCCCTCGGTGATGCGGACATCTCAGGGAACTTGGCTACTCAGCACAGCA
 GTGGAGAGTGTTCCTGTTGAATCTTGACATATTTGAATGTGTAAGCATTTGATACATTGATCA
 AGTTCGGGGGAATAAGAGACAGACCACTAAACCTGCTTCTGCTTCTTAAAGGAGAAAG
 TAGCTGTGAACATTGTCTGGATACAGATAATTGAATCTTCTTACTATTGGTAATAAACCTTG
 ATGGCATTTGGGCAACAGTAGACTTATAGTAGGGTTGGGGTAGCCCATGTTATGTGACTATCT
 TATGAGAAATTTAAAGTGGTCTGGATATCTTTTAACTTGGAGTTTCAITTTCTTTTCAATTGTA
 TCAAAAAAAATTAACAGAGCCAAATACTTCTGAGACCTTGTTCATCTTTGCTGTATA
 TCCCTCAAAATCCAAGTTATAATCTTATGTGTTTCTTTTAAATTTTGTATTGGATTCTTT
 AGATTTAATGGTTCAATGAGTTCACTTTGAGGGACGATCTTGAATATACTTACCTATTATA
 AAATCTTACTTTGATTTTGTATT

FIGURE 66

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MERDGCAGGSRGGEGGRAPREGPAGNDRDRGRSHAAEAPQDPQAAASLLAPMDVGEEPLEKA
ARARTAKDPNTYKVLSLVLSVCVLTTILGCIIFGLKPSCAKEVKSCRGRCFERTFGNCRCDAAACVEL
GNCCLDYQETCIEPEHIWTCNKFRCEKRLTRSLCACSDCKDKGCCINYSVQCQGEKSWVEEP
CESINEPQCPAGFETPTLLFSLDGFRAEYLHTWGGLLPVISKLLKCGTYTKNMRPVYPTKTPFNI
YSIVTGLYPESHGIIDNKMYDPKMNASFSLKSKEKFNPEWYKGEPIWVTAKYQGLKSGTFFWPGS
DVEINGIFFDIYKMYNGSVPFERILAVLQWLQPKDERPHFYTLYLEEPDSSGHSYGPVSSEVKA
LQRVDGMVGMMLMDGKELNHLRCLNLILISDHGMEQGSCKKYTLNKLCDVKNKVYGAAR
LRPSDVPDKYYSFNYEGIARNLSCREFNQHFYPYLKHLFKRLHFAKSDRIEPLTFYLDPOWQAL
NPSEKRYCGSGFHGSDNVFSNMQALFVGYGPOFKHQBADTFENIEVYNLMCDLLNLTPAPNNGT
HGSLNHLKPNVYTPKHPKEVHPLVQCFFTRNPRDNLGCSCNPSILPIEDFQTQFNLTVAEEKIKHE
TLPYGRPRVLQKENTICLLSQHQFMSGYSDILMPLWTSYTVDRNDSFSTEDFSNCLYQDFRIPLSP
VHKCSFYKNNTKVSYGELSPQLNKNSSGIYSEALLTNIVPMYQSFQVIWRYFHDTLRLKYAEER
NGVNVVSGPVDFDYDGRCDLENLRQKRRVIRNQEILPTHFIVLTSCKDTSQTPLHCENLDTLA
FILPHRTDNSESCVHGKHDSSWVEELMLHRARITDVEHITGLSFYQQRKEPVSDILKCLKHLPTFS
QED.

FIGURE 67

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GGTTTTCAA[REDACTED]GAACATTTTGTGTCATCCTTAGTAOCTATTTCAAGGCATTGCTAGGCCCTC
 GAGATACTAGAGTAAAGGATGGTTTCTTCTGGACAATTATATACCCACATTTATCTGCTCTGT
 CATATATTTACTAATTGTATGGCTGGGACCAAAATACATGAGGAATAAACAGCCATTCTCTTG
 COGGGGGATTTAGTGGTGATAACCTTGGACTCACACTGCTGCTCTGTATATGTTCTGTGAG
 TTAGTAACAGGAGTATGGGAAGGCAAAATACAACCTTCTCTGTGAGGGCACACGCACCGCAGG
 AGAATCAGATATGAAGATTACCGTGTCTCTGTTGGTACTACTTCTCCAAATCATAGAAATTT
 ATGGACACTTTCTTCTCATCTCGCGCAAGAACCAACCAAGATCAGGGTCTGCACTCTAC
 CACCATGCTCGGTGCTGAACATCTGGTGGTTTGTGATGAACCTGGGTCCTGCACTCTAC
 ATTTTGGTGCCACACTTAATAGCTTCAATCCACGTCTCTATGTACTCTTACTATGGTTTGTGTC
 AGTCCCTTCCATGCTGCCATACCTCTGGTGGAAAGAGTACATCTCAGGGGCAGCTGCTTCA
 GTTTGTGCTGACAATCATCCAGACCACTGCGGGGCTCTGAGCCCTGGGCACTCTT
 TGGTTGATTTCCAGATTGGATACATGATTTTCCCTGATTGCTCTCTTCAAACTTCTACATT
 AGACCTACAACAAGAAAGGGGCTCCGGAAGGAAGACCACTGAAGGACCAACAGAAATGG
 GTCCATGGCTGCTGTGAATGGACACACCAACAGCTTTTACCCCTGGAAAAACAATGGAAGCC
 AAGGAAGCTGGGGAAGGAT[REDACTED]AGTCAAAGAATTGAAACCTCCAAACCACTGCTGATT
 GTAAGCACAATATGAGTTGTGCTCCCAATGCTGTTAACAGCTGCTGTAAGTCTGGCTAC
 AATAGTGTGATTCAAAGGGGGAATTTCTATCAATTTCAAACCCCTGAAAACTATACAGA
 TTATATAAGTAGGGATAAGATTTCTAACATTTCTGGGCTCTCTGACCCCTGGCTAGACTGTGG
 AAAGGGAGTATTATATAGTATACAACTGCTGTTGCTTATTAGTTATAACATGATAGGTG
 CTGAATTTGTGATTACAAATTTAAAAACACTGTAATCCAACTTTTTTTTAACTGTAGATCAT
 GCATGTGATTTGTAATGTAAATTTGTACAATGTTGTTATGGTAGAGAAACACACATGCTTAA
 AATTTAAAAAGCAGGGGCCAAAGCTTATTAGTTTAAATTAGGGTATGTTTCAAGTTTGATTA
 ATTTGTAATAGCTCTGTTAGAAAAAATCAAAGACCATGATTTATGAACTAATGTGACATAA
 TTTCAGTGACTTGTGATGTGAAAAACAGACACGACCTTCACTTTTGTACTATTGGCTTTGA
 ATCAAGCAGGCTCAAATCTAGTGGAAACAGTCACTTTTAACTTTTAACTGCTTATTTTAT
 TTTGAGTGGCACTTATTAATGTAATAAGGGGGGGCTCTACAGCAGTGTGATGAACTTAAAT
 ATATATTCTTTCTCTCGAGATTTTAGGAAGGGGTGAGGGTGTAGAGCCATTTTAAATTTCTG
 AAGTGCTAAGTGTTTTATACAGCAACAAAAAGTCAATTTTGTCTTCCCACTGCGAGAGA
 GGATGTATACTTTTCAAGAGAGATGATTGCCTATTTACCGTTTGACAGAGTCCCGTAGATGAG
 CAATGGGGAACTGGTTGCCAGGGTCTAAATTTGGATTGATTTATGCACTGTTATCTGTTTGAC
 ACAGATTTCCTGTGTAATGTGCTGATTTACCAAAATTAACAAAGGGGGGAAAGGACCTTA
 GAACTTTTTAAGGTAAAAATCAATATAGCTACAGCATAAGAGAAATCGAGAAATTTGATAGAG
 GTAACTTGTTAATGTAATCTAATAGTACTGTAAATTTCTTCTGCTTAGAAATTAAGATGT
 GTTTAGAACCTCTTGTAAAAAATAATAGACTGCTTATCATAAAAACACATCTCACACATTGA
 GGCAGTGGTCAAACAGGTAAGCCATGATGTGTGCTTTTAAAGTGTGCGAAATTTAGCCTC
 TGAATACCTTCTCCATTGGGGGAAAGATATCTTGGAAACCACTCATGACATATCTTAGAAGGT
 CATTGCAATGTATAAACTAATTTGTTGGTTGATATTATGTAATATCAAGTTTACCATGCTTT
 AATTTTGCACATTCGTACTATAGGGAGCCTATGGTTCTCTATTAAGTCTGTGTTTCTGTTT
 GAAAAAGGATCATGGCATCTGTTTACATTTACCTTATCAAACTAGAAATGTGTATATTATAA
 ATGTATGTCTCATTTGCTAGGTACTAATTTGCAGATGCTTTACATATTTCAATACAGAACTA
 TAACATTCAATAGTGTGCTGTCAAAAGTGTGCTTAGCTCACTGGATATACCTACATTGTTAAAT
 GTCTAAACAGTAATCATTAACACATTTTGTATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6 8

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MEHFDASLSTYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQPFSCRGLV
VYNLGLTLLSLYMFCELVTVGVWEGKYNFFCQGTIRIAGESDMKIRVLWWYFESKLEFMDTFFFI
LRKNNHQITVLHVYHHASVLNIWWFVNMWVPOGHSYFGATLNSFIHVLMSYVYGLSSVPSMRPY
LWWKKYITQGQLLQFVLTIQTSCGVIWPCIFPLGWLYFQIGYMISLLALFINFYIQTYNKKGASRR
KDHLDHQNQGSMAAVNGHTNSFSPLENNVKPRKLKRD.

FIGURE 69

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TTTTAAAAACAAATCGGGTTTATTTCTCAGATGATGTTTCATCGGTGANTGGTCCAGGGNAGGA
 COTTTACCTTGACIATATGGCATATGTTCTCATCACAGCTCTGAGGCTTCTCCTTTCCATCTGCGTGGAC
 AGCTAAGNCTTCAGTTTCATAGCATCTAGAGCATGGGACTCAGCTGGGGTGATTTGCCCCCCTCTC
 CGGGGGAATGCTGAAAGCAATTTGGTTACCTCATGAGGGAGTGGAGGGATACAGTGCTCTACCAA
 CTACTGNTAAAGSCCAGGGATGCTGCTCAGCTCTACCATCTACAGGGAGCTCTCCCCATTACACTAC
 CCAATCCGAATGTCAACTGTCTCAGGACAAAGAAACCTGGTTTGGTAGAAAGGGCCTGGAAGAGG
 CGAGCCACAAATCTGCTGCTCTCTCAGATTAGTCAATTTGGCAATAGCATTCTGCTCTTTGGCTCTG
 CCTCAGCACAGAGAGCCAGACTCTATCGGGCACCAGATACACTCTCTCAGTGAACAGAGTTGACAAGGC
 CTATGGGAATGCCGTGATGGGATATCTCAGCTTGTGAGCTCTAGTTTCTTCCCTTCAITCTACCC
 TCCAGCCAACTCTCTAAGAGAAATGCTGAGTCTAGCTCAGGTTTCTTACTCTGAATTTAGATCTCC
 AGACCTCTCTGGCCCAATTCAPATTAAGGCACAAACATATACCTTCCATGAAGCACACACAGACTCT
 CAAGCAGGACATGACTGCTTGAATTAAGGCTTGGAGGATGAAGCTTTGAAGGAAAGAAATACTTTCT
 TTCCAGCCCCCTTCCACACTCTTCTATGCTTAACCACTGCTTCTCTGGACCTTGGAGCCACGGTGCTCT
 ATTACATGTTGTTATAGAAACTGATTTAGAGTTCTGTTGTTCAAGGAATGATTAATATACATTTCC
 TACNMAAAAAAAGTCGAG

FIGURE 72

AGAGATGGGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTCTGGGCTCAAGCGATCCTTTGGCCTCG
 GCCTCCCAATGTGCATGAGCCACCATGCTGGCCTGTTAGTTTGTTCAGTTGAATACCTTTCTTGT
 GTTTCTAATTAGAAAGTAATATCTACTCATTTGTAACTCAACAGTGCAGAAATGTAGAAAGTAGAA
 AGTGTAGTCCCTGCTGCTCTCTGCTGAGCACAAGCACTGCTCAGAGTTGATGTATATCTTCCAG
 AGACTCTCAATTTAAGCAAAATATTTTATTCAATGCTTTTATTGAAGACGTACATTTGCTCCAA
 AGTTCAACCAAGTTCACTGACCATATCTTCCATGACCTGANTGATGCTATCTTTATGACCATGCTC
 ANTTGCCTTTGAAGAGAGTAGTCCAGGTATATTTCTGATCAAAATTTGGCAATTTTCAATGATGATCT
 ACACAGATCAGACTCATGTGACAGATCTGCTGCTGGAGAGAGGTTTGTAAACAGAGATTTCTGGAAA
 CATTCAAATTCGAATGGAACCTTGAACCCCAATCTAATGAGGATGACTGGAATAATTTCTGGAAG
 CTGTCAAAATCTGCTGCTGATTTGAACCATGGAATGCAATGCCAATGAGACTTCTGCACTAAACTTAT
 CCTCTAATGTACACATATGCTGCTGATTTATATACAGTGTATGATTTCTGACACCCCAATACATAA
 TATACAGATTTGATTAATGCTACATTTAAATATATATATGACATACAGCTAACATANAATGATGAT
 AGGCTGAGAGATATTACTAGTGCCTAATATTAGATATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 CAGTAAATGTTATANAATTAATCAGTGCAGCCCAATTTATGATCAGATCTTTGMACTGTGAGTA
 GCATATACATATATATTTTAAATACATTTTTCACAGTTTCCAGAGTACTGTTGAATCTGATCACC
 AAAAAAANAAGCAAGATTTTAAACAATGAGAGCTCTTCAAGCCCAATCTGCGTGTGATTT
 CCTATTTGATATTTCCAGAGACTTTAGCAGTCAACAGCCTTAATGATGATGATGATTTATTTGACT
 TAATTTATCTGAGTTTAAATCAATGTAATTTGGGAATTTTAACCGAATTTGGATTAAACCATGCTGCTG
 CTTTCAAGGTTGCAATGTTACATTAATGATTTATGTTGTAATAAAAAA

FIGURE 73

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【国際調査報告】

INTERNATIONAL SEARCH REPORT		International Application No. PCT/US 00/06952															
A. CLASSIFICATION OF SUBJECT MATTER IPC 7 G01N33/574 G01N33/50 According to International Patent Classification (IPC) or to both national classification and IPC																	
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 7 G01N Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used) EPO-Internal, WPI Data, PAJ, STRAND, MEDLINE																	
C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1"> <thead> <tr> <th>Category *</th> <th>Citation of document, with indication, where appropriate, of the relevant passages</th> <th>Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td>X</td> <td>WO 98 18945 A (ABBOTT LAB) 7 May 1998 (1998-05-07) claims 17,20; examples 3,19 page 49, line 1 - line 8 page 33, line 3 -page 38, line 2 ---</td> <td>1-32, 35-37</td> </tr> <tr> <td>A</td> <td>WO 98 34118 A (UNIV YALE) 6 August 1998 (1998-08-06) claims 1,29 ---</td> <td>1-37</td> </tr> <tr> <td>A</td> <td>US 5 514 554 A (BACUS SARAH S) 7 May 1996 (1996-05-07) claim 1 ---</td> <td>1-37</td> </tr> <tr> <td>P, X</td> <td>WO 99 23230 A (ABBOTT LAB) 14 May 1999 (1999-05-14) abstract --- -/--</td> <td>9</td> </tr> </tbody> </table>			Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	X	WO 98 18945 A (ABBOTT LAB) 7 May 1998 (1998-05-07) claims 17,20; examples 3,19 page 49, line 1 - line 8 page 33, line 3 -page 38, line 2 ---	1-32, 35-37	A	WO 98 34118 A (UNIV YALE) 6 August 1998 (1998-08-06) claims 1,29 ---	1-37	A	US 5 514 554 A (BACUS SARAH S) 7 May 1996 (1996-05-07) claim 1 ---	1-37	P, X	WO 99 23230 A (ABBOTT LAB) 14 May 1999 (1999-05-14) abstract --- -/--	9
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X	WO 98 18945 A (ABBOTT LAB) 7 May 1998 (1998-05-07) claims 17,20; examples 3,19 page 49, line 1 - line 8 page 33, line 3 -page 38, line 2 ---	1-32, 35-37															
A	WO 98 34118 A (UNIV YALE) 6 August 1998 (1998-08-06) claims 1,29 ---	1-37															
A	US 5 514 554 A (BACUS SARAH S) 7 May 1996 (1996-05-07) claim 1 ---	1-37															
P, X	WO 99 23230 A (ABBOTT LAB) 14 May 1999 (1999-05-14) abstract --- -/--	9															
☒ Further documents are listed in the continuation of box C. ☒ Patent family members are listed in annex.																	
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document(s) is taken alone "Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "Z" document member of the same patent family																	
Date of the actual completion of the international search 28 November 2000		Date of mailing of the international search report - 5. 12. 00															
Name and mailing address of the ISA European Patent Office, P.O. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer Gundlach, B															

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 00/06952

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO 99 33869 A (CORIXA CORP) 8 July 1999 (1999-07-08) abstract -----	9
P, X	WO 00 08210 A (RECIPON HERVE ; DIADEXUS LLC (US); SUN YONGMING (US); CAFFERKEY ROB) 17 February 2000 (2000-02-17) the whole document -----	9
P, X	WO 99 25877 A (ABBOTT LAB) 27 May 1999 (1999-05-27) page 32, line 32 -page 36, line 9 -----	1-3, 6, 7, 15

INTERNATIONAL SEARCH REPORT		In. .ational application No. PCT/US 00/06952
Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)		
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:		
1. ☒	Claims Nos.: — because they relate to subject matter not required to be searched by this Authority, namely: see FURTHER INFORMATION sheet PCT/ISA/210	
2. ☐	Claims Nos.: — because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:	
3. ☐	Claims Nos.: — because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).	
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)		
This International Searching Authority found multiple inventions in this international application, as follows:		
see additional sheet		
1. ☐	As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.	
2. ☐	As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.	
3. ☒	As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.: 1-3,6,7,15 (partially, in so far as they relate to inventions 1 and 3), 4,5,8-14,16-37 (fully)	
4. ☐	No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:	
Remark on Protest		
☐ The additional search fees were accompanied by the applicant's protest.		
☒ No protest accompanied the payment of additional search fees.		

International Application No. PCT/US 00 06952

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claims 6,7 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
Although claims 28,31-34 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.1

Rule 39.1(iv) PCT - Diagnostic method practised on the human or animal body and/or method for treatment of the human or animal body by therapy

International Application No. PCT/US 00 06952

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-3,6,7,15 (partially) 4,5,8-14,16-37 (fully)
Method of screening drug candidates involving BCH1
2. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCA2
3. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCJ7
4. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCN1
5. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCN5
6. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BC02
7. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCQ5
8. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCR2
9. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCX2
10. Claims: 1-3,6,7,15 (partially)
Method of screening drug candidates involving BCY3

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No.

PCT/US 00/06952

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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(51)Int.Cl. ⁷	F I	テーマコード (参考)
A 6 1 K 48/00	A 6 1 K 48/00	4 C 0 8 5
A 6 1 P 15/00	A 6 1 P 15/00	4 C 0 8 6
A 6 1 P 35/00	A 6 1 P 35/00	4 H 0 4 5
A 6 1 P 37/04	A 6 1 P 37/04	
C 0 7 K 14/82	C 0 7 K 14/82	
C 0 7 K 16/32	C 0 7 K 16/32	
C 1 2 N 15/09	C 1 2 Q 1/02	
C 1 2 Q 1/02	C 1 2 Q 1/68	A
C 1 2 Q 1/68	G 0 1 N 33/15	Z
G 0 1 N 33/15	G 0 1 N 33/53	M
G 0 1 N 33/53	G 0 1 N 33/574	A
G 0 1 N 33/574	G 0 1 N 37/00	1 0 2
G 0 1 N 37/00	A 6 1 K 37/02	
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4B024 AA01 AA12 BA36 CA02 CA12 HA14

4B063 QA01 QA08 QA19 QQ08 QQ43 QQ53 QR40 QR48 QR55 QR62

QR77 QS25 QS34 QX02

4B064 AG27 CA20 DA05 DA14

4C084 AA02 AA07 AA13 AA14 BA01 BA08 BA18 BA20 BA23 BA35

CA17 CA18 NA14 ZA812 ZB092 ZB262

4C085 AA13 BB11 BB50 CC21 EE01

4C086 AA01 AA02 EA16 MA01 MA04 NA14 ZA81 ZB09 ZB26

4H045 AA10 AA11 AA30 BA10 CA41 DA76 DA86 EA28 EA51 FA74