



- (51) **International Patent Classification:**
C12Q 1/68 (2006.01) *G01N 33/574* (2006.01)
- (21) **International Application Number:**
PCT/US2012/043852
- (22) **International Filing Date:**
22 June 2012 (22.06.2012)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
61/500,085 22 June 2011 (22.06.2011) US
- (71) **Applicant:** ONCOCYTE CORPORATION [US/—].
- (72) **Inventors; and**
- (75) **Inventors/Applicants (for US only):** CHAPMAN, Karen [US/US]; 1301 Harbor Bay Parkway, Alameda, CA 94502 (US). WEST, Michael [US/US]; 1301 Harbor Bay Parkway, Alameda, CA 94502 (US). WAGNER, Joseph [US/US]; 1301 Harbor Bay Parkway, Alameda, CA 94502 (US). LACHER, Marcus [CH/US]; 1301 Harbor Bay Parkway, Alameda, CA 94502 (US). KIDD, Jennifer Lorie [US/US]; 1301 Harbor Bay Parkway, Alameda, CA 94502 (US).
- (74) **Agent:** MITTLER, E. Stewart; BioTime, Inc., 1301 Harbor Bay Parkway, Alameda, CA 94502 (US).

(81) **Designated States** (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report (Art. 21(3))
- with sequence listing part of description (Rule 5.2(a))

(54) **Title:** METHODS AND COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BLADDER CANCER

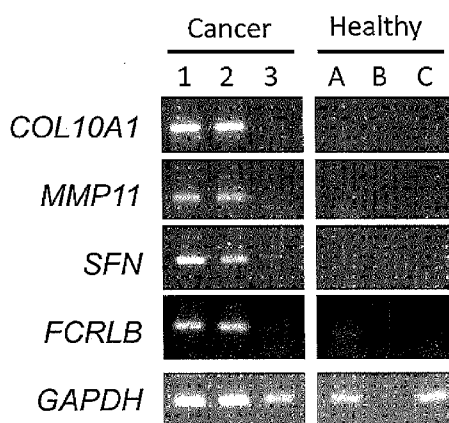


Fig. 75. Agarose gel analysis of markers of cells in voided urine.

(57) **Abstract:** Embodiments of the disclosure are directed to methods of diagnosis, prognosis and treatment of cancer. The methods are particularly suited for bladder cancer. The methods include targeting a marker that is expressed at abnormal levels in bladder cancer tissue in comparison to normal somatic tissue. Also disclosed are methods of treating cancer comprising administering a composition including a therapeutic that affects the expression or function of a target marker.



METHODS AND COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BLADDER CANCER

This application claims priority to U.S. Provisional Application Serial No. 61/500,085 filed June 22, 2011, the entire contents of which is hereby incorporated by reference.

Field of the Invention

[0001] The field of the invention relates to cancer and the diagnosis and treatment of cancer.

BACKGROUND

[0002] Bladder cancer is a type of malignant growths of the urinary bladder. The most common type of bladder cancer begins in cells lining the inside of the bladder and is called transitional cell carcinoma (sometimes urothelial cell carcinoma). Types of bladder cancers include transitional cell carcinoma, squamous cell carcinoma, adenocarcinoma, sarcoma, small cell carcinoma and secondary deposits from cancers elsewhere in the body. Bladder cancer characteristically causes blood in the urine; this may be visible to the naked eye (gross hematuria) or detectable only by microscope (microscopic hematuria). Other possible symptoms include pain during urination, frequent urination (polyuria) or feeling the need to urinate without results

[0003] The gold standard for diagnosing bladder cancer is biopsy obtained during cystoscopy. Sometimes it is an incidental finding during cystoscopy. Urine cytology can be obtained in voided urine or at the time of the cystoscopy ("bladder washing"). Cytology is very specific (a positive result is highly indicative of bladder cancer) but suffers from low sensitivity (inability of a negative result to reliably exclude bladder cancer). There are newer urine bound markers for the diagnosis of bladder cancer. These markers are not currently used routinely in clinical practice due to absence of clear professional guidelines. They are much more expensive as well. Bladder cancer may also be diagnosed with a Cysview™ guided fluorescence cystoscopy, as an adjunct to conventional white-light cystoscopy. This procedure improves the detection of bladder cancer and reduces the rate of early tumor recurrence, compared with white-light cystoscopy alone.

[0004] Many patients with a history, signs, and symptoms of bladder cancer are referred to a urologist or other physician trained in cystoscopy, a procedure in which a flexible tube

bearing a camera and various instruments is introduced into the bladder through the urethra. Suspicious lesions may be biopsied and sent for pathologic analysis. These procedures are invasive.

[0005] There is a need in the field of cancer diagnostics for a highly specific, highly sensitive, rapid, inexpensive, and relatively non-invasive method of diagnosing bladder cancer. Various embodiments of the invention described below meet this need as well as other needs in the field of diagnosing and treating bladder cancer.

SUMMARY OF THE INVENTION

[0001] Embodiments of the disclosure provide for methods of diagnosis, prognosis and treatment of bladder cancer.

[0002] In certain embodiments the invention provides a method of detecting bladder cancer in a subject comprising a) contacting a sample obtained from the subject with one or more agents that detect one or more markers expressed by a bladder cancer cell b) contacting a non-cancerous cell with the one or more agents from a); and c) comparing the expression level of the marker in the sample obtained from the subject with the expression level in the non-cancerous cell, wherein a higher level of expression of the marker in the sample compared to the non-cancerous cell indicates that the subject has bladder cancer.

[0003] In certain embodiments the invention provides a method of detecting bladder cancer in a subject comprising a) contacting a sample obtained from the subject with one or more agents that detect expression of at least one of the markers listed in Table 2 or 3; b) contacting a non-cancerous cell, e.g. a non-cancerous cell from bladder tissue or a noncancerous bladder cell line, with the one or more agents from a); and c) comparing the expression level of one or more of the markers listed in Table 2 or 3 in the sample obtained from the subject with the expression level of one or more of the markers listed in Table 2 or 3 in the non-cancerous cell, wherein a higher level of expression of one or more of the markers listed in Table 2 or 3 in the sample compared to the non-cancerous cell indicates that the subject has bladder cancer.

[0004] In some embodiments the invention provides a method of detecting bladder cancer in a subject comprising a) contacting a sample obtained from the subject with one or more agents that detect expression of at least one of the markers chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3,

SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2, IL1A, KRT16 SLC1A6, and SERPINB5; b) contacting a non-cancerous cell, e.g. a non-cancerous cell from bladder tissue or a non-cancerous bladder cell line, with the one or more agents that detect expression of at least one of the markers chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 ; and c) comparing the expression level of one or more of the markers chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A IL1A, KRT16 SLC1A6, and SERPINB52 in the sample obtained from the subject with the expression level of one or more of the markers chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 in the non-cancerous cell, wherein a higher level of expression of one or more of the markers chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3,

SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 in the sample compared to the non-cancerous cell indicates that the subject has bladder cancer.

[0005] With regard to the embodiments described in the preceding paragraphs, the sample may be any sample as described *infra*, for example, a bodily fluid, such as blood, serum or urine. The sample may be a cellular sample, a tissue sample or the extract of a cellular or tissue sample. The agent may be one or more molecules that bind specifically to one or more proteins expressed by the cancer cell or one or more nucleic acids expressed by the cell. For example, the agent may be a protein such as an antibody that binds specifically to the protein expressed by one of the marker genes identified *infra*. The agent may be one or more nucleic acids that hybridize to a nucleic acid expressed by the cancer cell. The nucleic acid expressed by the cancer cell may be an RNA molecule, e.g. an mRNA molecule. The nucleic acid molecule that hybridizes to the nucleic acid expressed by the cancer cell may be a DNA molecule, such as a DNA probe.

[0006] In still other embodiments the invention provides a composition of matter useful in distinguishing a bladder cancer cell from a non-cancerous cell comprising one or more molecules that specifically bind to a molecule expressed at higher levels on a bladder cancer cell compared to a non-cancer cell. As an example, the composition may comprise a protein, that binds to one or more molecules expressed by the cancer cell at higher levels compared to the non-cancer cell. As another example, the composition may comprise a nucleic acid that binds to one or more molecules expressed by the bladder cancer cell at higher levels compared to the non-cancer cell.

[0007] In some embodiments the invention provides a composition of matter comprising a protein, such as an antibody, that specifically binds to a molecule expressed by a bladder cancer cell chosen from the markers listed in Table 3. The molecule expressed by the bladder cancer cell may be expressed by the bladder cancer cell at level that is higher than the level expressed by a non-cancerous cell such as a non-cancerous bladder tissue cell or non-cancerous bladder cell line.

[0008] In certain embodiments the invention provides a composition of matter comprising a protein, such as an antibody, that specifically binds to a molecule expressed by a bladder cancer cell chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5. The molecule expressed by the bladder cancer cell may be expressed by the bladder cancer cell at level that is higher than the level expressed by a non-cancerous cell such as a non-cancerous bladder tissue cell.

[0009] In other embodiments the invention provides a composition of matter comprising a nucleic acid that specifically binds to a molecule, such as an mRNA molecule, expressed by a bladder cancer cell wherein the molecule is chosen from a marker listed in Table 1 or 2. The molecule expressed by the bladder cancer cell may be expressed by the bladder cancer cell at level that is higher than the level expressed by a non-cancerous cell such as a non-cancerous bladder tissue cell.

[0010] In other embodiments the invention provides a composition of matter comprising a nucleic acid that specifically binds to a molecule, such as an mRNA molecule, expressed by a bladder cancer cell wherein the molecule is chosen from a nucleic acid encoding MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5. The molecule expressed by the bladder cancer cell may be expressed by the bladder cancer cell at level that is higher than the level expressed by a non-cancerous cell such as a non-cancerous bladder tissue cell.

[0011] In still further embodiments the invention provides a method of determining if a cancer in a subject is advancing comprising a) measuring the expression level of one or more

markers associated with cancer at a first time point; b) measuring the expression level of the one or more markers measured in a) at a second time point, wherein the second time point is subsequent to the first time point; and c) comparing the expression level measured in a) and b), wherein an increase in the expression level of the one or more markers in b) compared to a) indicates that the subject's cancer is advancing. In certain embodiments the cancer is bladder cancer.

[0012] In some embodiments the invention provides a method of determining if a bladder cancer in a subject is advancing comprising a) measuring the expression level of one or more markers listed in Table 2 or 3 at a first time point; b) measuring the expression level of the one or more markers measured in a) at a second time point, wherein the second time point is subsequent to the first time point; and c) comparing the expression level measured in a) and b), wherein an increase in the expression level of the one or more markers at the second time point compared to the first time point indicates that the subject's bladder cancer is advancing.

[0013] In other embodiments the invention provides a method of determining if a bladder cancer in a subject is advancing comprising a) measuring the expression level of one or more markers chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 at a first time point; b) measuring the expression level of the one or more markers measured in a) at a second time point, wherein the second time point is subsequent to the first time point; and c) comparing the expression level measured in a) and b), wherein an increase in the expression level of the one or more markers at the second time point compared to the first time point indicates that the subject's bladder cancer is advancing.

[0014] In some embodiments the invention provides antigens (i.e. cancer-associated polypeptides) associated with bladder cancer as targets for diagnostic and/or therapeutic antibodies. In some embodiments, the antigen may be chosen from a protein encoded by, a gene

listed in Table 2, a fragment thereof, or a combination of proteins encoded by a gene listed in Table 2.

[0015] In some embodiments the invention provides antigens (i.e. cancer-associated polypeptides) associated with bladder cancer as targets for diagnostic and/or therapeutic antibodies. In some embodiments, the antigen may be chosen from a protein encoded by, a gene chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5, a fragment thereof, or a combination of proteins encoded by a gene chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5.

[0016] In yet other embodiments the invention provides a method of eliciting an immune response to a bladder cancer cell comprising contacting a subject with a protein or protein fragment that is expressed by a bladder cancer cell thereby eliciting an immune response to the cancer cell. As an example the subject may be contacted intravenously or intramuscularly.

[0017] In further embodiments the invention provides a method of eliciting an immune response to a bladder cancer cell comprising contacting a subject with one or more proteins or protein fragments that is encoded by a gene chosen from the genes listed in Table 3, thereby eliciting an immune response to a bladder cancer cell. As an example the subject may be contacted intravenously or intramuscularly.

[0018] In still other embodiments the invention provides a method of eliciting an immune response to a bladder cancer cell comprising contacting a subject with one or more proteins or protein fragments that is encoded by a gene chosen from MAGEA10, DSCR8, MMP12, CXCL9,

DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 , thereby eliciting an immune response to a bladder cancer cell. As an example the subject may be contacted intravenously or intramuscularly.

[0019] In other embodiments the invention provides a kit for detection of cancer in a sample obtained from a subject. The kit may comprise one or more agents that bind specifically to a molecule expressed by a bladder cancer cell. The molecule may be expressed at a higher level in the bladder cancer cell compared to a non-cancerous cell, such as a non-cancerous bladder cell. The kit may comprise one or more containers and instructions for determining if the sample is positive for cancer. The kit may optionally contain one or more multiwell plates, a detectable substance or label such as a dye, a radioactively labeled molecule, a chemiluminescently labeled molecule and the like. The kit may further contain a positive control (e.g. one or more cancerous bladder cells; or specific known quantities of the molecule expressed by the cancer cell) and a negative control (e.g. a tissue or cell sample that is non-cancerous).

[0020] In some embodiments the invention provides a kit for the detection of bladder cancer comprising one or more agents that specifically bind one or more markers chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5. The kit may comprise one or more containers and instructions for determining if the sample is positive for cancer. The kit may optionally contain one or more multiwell plates, a detectable substance such as a dye, a radioactively labeled molecule, a chemiluminescently labeled molecule and the like. The kit may further contain a positive control

(e.g. one or more cancerous cells; or specific known quantities of the molecule expressed by the cancer cell) and a negative control (e.g. a tissue or cell sample that is non-cancerous). As an example the kit may take the form of an ELISA or a DNA microarray.

[0021] Some embodiments herein are directed to a method of treating bladder cancer in a subject, the method comprising administering to a subject in need thereof a therapeutic agent capable of modulating the activity of a cancer associated protein, wherein the cancer associated protein is encoded by gene listed in Table 2, homologs thereof, combinations thereof, or a fragment thereof. In some embodiments, the therapeutic agent binds to the bladder cancer associated protein. In some embodiments, the therapeutic agent is an antibody. In some embodiments, the antibody may be a monoclonal antibody or a polyclonal antibody. In some embodiments, the antibody is a humanized or human antibody.

[0022] Some embodiments herein are directed to a method of treating bladder cancer in a subject, the method comprising administering to a subject in need thereof a therapeutic agent modulating the activity of a cancer associated protein, wherein the cancer associated protein is encoded by gene chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2, IL1A, KRT16, SLC1A6, and SERPINB5, homologs thereof, combinations thereof, or a fragment thereof. In some embodiments, the therapeutic agent binds to the bladder cancer associated protein. In some embodiments, the therapeutic agent is an antibody. In some embodiments, the antibody may be a monoclonal antibody or a polyclonal antibody. In some embodiments, the antibody is a humanized or human antibody.

[0023] In some embodiments, a method of treating bladder cancer in a subject may comprise administering to a subject in need thereof a therapeutic agent that modulates the activity of one or more genes chosen from those listed in Table 2.

[0024] In some embodiments, a method of treating bladder cancer in a subject may comprise administering to a subject in need thereof a therapeutic agent that modulates the activity of one or more genes chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8,

KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 .

[0025] In further embodiments, the invention provides a method of treating bladder cancer may comprise a gene knockdown of one or more genes listed in Table 2. In some embodiments, a method of treating bladder cancer may comprise treating cells to knockdown or inhibit expression of a gene encoding an mRNA of one or more genes chosen from those listed in Table 2.

[0026] In other embodiments, a method of treating bladder cancer may comprise gene knockdown of one or more genes selected from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5. In some embodiments, a method of treating bladder cancer may comprise treating cells to knockdown or inhibit expression of a gene encoding an mRNA of one or more genes chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 .

[0027] In still other embodiments, the present invention provides methods of screening a drug candidate for activity against bladder cancer, the method comprising: (a) contacting a cell that expresses one or more cancer associated genes chosen from those listed in Table 2 with a

drug candidate; (b) detecting an effect of the drug candidate on an expression of the one or more bladder cancer associated genes in the cell from a); and (c) comparing the level of expression of one or more of the genes recited in a) in the absence of the drug candidate to the level of expression of the one or more genes in the presence of the drug candidate; wherein a decrease in the expression of the bladder cancer associated gene in the presence of the drug candidate indicates that the candidate has activity against bladder cancer.

[0028] In further embodiments, the present invention provides methods of screening a drug candidate for activity against bladder cancer, the method comprising: (a) contacting a cell that expresses one or more bladder cancer associated genes chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 with a drug candidate; (b) detecting an effect of the drug candidate on an expression of the one or more bladder cancer associated genes in the cell from a); and (c) comparing the level of expression of one or more of the genes recited in a) in the absence of the drug candidate to the level of expression in the presence of the drug candidate; wherein a decrease in the expression of the bladder cancer associated gene in the presence of the drug candidate indicates that the candidate has activity against bladder cancer.

[0029] In some embodiments, the present invention provides methods of visualizing a bladder cancer tumor in a subject comprising a) targeting one or more bladder cancer associated proteins with a labeled molecule that binds specifically to the bladder cancer tumor, wherein the cancer associated protein is selected from a protein encoded for by one or more genes chosen from those listed in Table 2; and b) detecting the labeled molecule, wherein the labeled molecule visualizes the tumor in the subject.

[0030] In still other embodiments, the present invention provides methods of visualizing a bladder cancer tumor in a subject comprising a) targeting one or more bladder cancer associated proteins with a labeled molecule that binds specifically to the bladder cancer associated protein, wherein the cancer associated protein is selected from a protein encoded for

by one or more genes chosen from MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, GJB2, COL10A1, FCRLB, SFN, S100A2 IL1A, KRT16 SLC1A6, and SERPINB5 ; and b) detecting the labeled molecule, wherein the labeled molecule visualizes the tumor in the subject.

[0031] The invention also provides the use of one or more of the markers disclosed infra in the detection of bladder cancer in a subject.

[0032] The invention also provides the use of one or more of the markers disclosed infra in estimating the risk of morbidity of bladder cancer in a subject.

DESCRIPTION OF DRAWINGS

[0033] For a fuller understanding of the nature and advantages of the present invention, reference should be had to the following detailed description taken in connection with the accompanying drawings, in which:

[0034] FIG. 1 is a chart of the microarray analysis data showing expression of all mRNA probe sequences in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0035] FIGS. 2A-2L is a chart containing the sequence information for the cancer associated sequences including the sequences of the probes used to detect the gene sequences.

[0036] FIG. 3 shows the expression of the MAGEA10 mRNA (SEQ ID NO: 111) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0037] FIG. 4 shows the expression of the DSCR8 mRNA (SEQ ID NO: 112) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0038] FIG. 5 shows the expression of the MMP12 mRNA (SEQ ID NO: 113) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0039] FIG. 6 shows the expression of the CXCL9 mRNA (SEQ ID NO: 114) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0040] FIG. 7 shows the expression of the DSCR8 mRNA (SEQ ID NO: 115) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0041] FIG. 8 shows the expression of the KRT81 mRNA (SEQ ID NO: 116) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0042] FIG. 9 shows the expression of the LOC729826 mRNA (SEQ ID NO: 117) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0043] FIG. 10 shows the expression of the PTHLH mRNA (SEQ ID NO: 118) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0044] FIG. 11 shows the expression of the MMP11 mRNA (SEQ ID NO: 119) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0045] FIG. 12 shows the expression of the S100A7 mRNA (SEQ ID NO: 120) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0046] FIG. 13 shows the expression of the WISP3 mRNA (SEQ ID NO: 121) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0047] FIG. 14 shows the expression of the CXCL10 mRNA (SEQ ID NO: 122) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0048] FIG. 15 shows the expression of the NMU mRNA (SEQ ID NO: 123) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0049] FIG. 16 shows the expression of the GBP5 mRNA (SEQ ID NO: 124) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0050] FIG. 17 shows the expression of the TOP2A mRNA (SEQ ID NO: 125) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0051] FIG. 18 shows the expression of the SERPINB4 mRNA (SEQ ID NO: 126) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0052] FIG. 19 shows the expression of the GLNY mRNA (SEQ ID NO: 127) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0053] FIG. 20 shows the expression of the GTSFI mRNA (SEQ ID NO: 128) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0054] FIG. 21 shows the expression of the PI3 mRNA (SEQ ID NO: 129) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0055] FIG. 22 shows the expression of the S100A7A mRNA (SEQ ID NO: 130) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0056] FIG. 23 shows the expression of the IDO1 mRNA (SEQ ID NO: 131) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0057] FIG. 24 shows the expression of the GJB6 mRNA (SEQ ID NO: 132) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0058] FIG. 25 shows the expression of the CALML3 mRNA (SEQ ID NO: 133) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0059] FIG. 26 shows the expression of the SERPINB3 mRNA (SEQ ID NO: 134) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0060] FIG. 27 shows the expression of the CXCL6 mRNA (SEQ ID NO: 135) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0061] FIG. 28 shows the expression of the OLFM4 mRNA (SEQ ID NO: 136) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0062] FIG. 29 shows the expression of the TCN1 mRNA (SEQ ID NO: 137) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0063] FIG. 30 shows the expression of the VSNL1 mRNA (SEQ ID NO: 138) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0064] FIG. 31 shows the expression of the UBD mRNA (SEQ ID NO: 139) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0065] FIG. 32 shows the expression of the AIM2 mRNA (SEQ ID NO: 140) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0066] FIG. 33 shows the expression of the ABCC9 mRNA (SEQ ID NO: 141) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0067] FIG. 34 shows the expression of the SERPINB13 mRNA (SEQ ID NO: 142) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0068] FIG. 35 shows the expression of the INDO mRNA (SEQ ID NO: 143) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0069] FIG. 36 shows the expression of the KRT5 mRNA (SEQ ID NO: 144) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0070] FIG. 37 shows the expression of the LOC100130897 mRNA (SEQ ID NO: 145) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0071] FIG. 38 shows the expression of the KRT14 mRNA (SEQ ID NO: 146) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0072] FIG. 39 shows the expression of the FAM83A mRNA (SEQ ID NO: 147) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0073] FIG. 40 shows the expression of the FAM181B mRNA (SEQ ID NO: 148) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0074] FIG. 41 shows the expression of the SEQ ID NO: 149 in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0075] FIG. 42 shows the expression of the GZMB mRNA (SEQ ID NO: 150) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0076] FIG. 43 shows the expression of the DSG3 mRNA (SEQ ID NO: 151) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0077] FIG. 44 shows the expression of the TYMP mRNA (SEQ ID NO: 152) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0078] FIG. 45 shows the expression of the KRT6A mRNA (SEQ ID NO: 153) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0079] FIG. 46 shows the expression of the KRT6B mRNA (SEQ ID NO: 154) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0080] FIG. 47 shows the expression of the HLA-DRB1 mRNA (SEQ ID NO: 155) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0081] FIG. 48 shows the expression of the LCN2 mRNA (SEQ ID NO: 156) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0082] FIG. 49 shows the expression of the KRT4 mRNA (SEQ ID NO: 157) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0083] FIG. 50 shows the expression of the IFI30 mRNA (SEQ ID NO: 158) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0084] FIG. 51 shows the expression of the LOC100134370 mRNA (SEQ ID NO: 159) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0085] FIG. 52 shows the expression of the KIAA1618 mRNA (SEQ ID NO: 160) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0086] FIG. 53 shows the expression of the S100A8 mRNA (SEQ ID NO: 161) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0087] FIG. 54 shows the expression of the MMP7 mRNA (SEQ ID NO: 162) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0088] FIG. 55 shows the expression of the MMP7 mRNA (SEQ ID NO: 163) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0089] FIG. 56 shows the expression of the SPRR2A mRNA (SEQ ID NO: 164) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0090] FIG. 57 shows the expression of the GJB2 mRNA (SEQ ID NO: 165) in normal somatic cells, normal tissues, malignant tumors, and cancer cell lines.

[0091] FIG. 58 shows the relative expression of SP100 in diverse cultured normal somatic cell types including coronary artery endothelial cells (mesoderm), astrocytes (ectoderm), bronchial epithelial cells (endoderm), melanocytes (neural crest) as well as diverse clonal hES-derived embryonic progenitor cell lines compared to hES and iPS cells as measured by Illumina microarray analysis. All hES and established iPS cell lines showed no evidence of *SP100* transcripts above background signal.

[0092] Figure 59 shows the expression level of MMP11 in normal bladder tissue and cancerous bladder tissue by qPCR.

[0093] Figure 60 shows the expression level of MMP12 in normal bladder tissue and cancerous bladder tissue by qPCR.

[0094] Figure 61 shows the expression level of COL10A1 in normal bladder tissue and cancerous bladder tissue by qPCR.

[0095] Figure 62 shows the expression level of FCRLBin normal bladder tissue and cancerous bladder tissue by qPCR.

[0096] Figure 63 shows the expression level of SERPINB5in normal bladder tissue and cancerous bladder tissue by qPCR.

[0097] Figure 64 shows the expression level of SFN in normal bladder tissue and cancerous bladder tissue by qPCR.

[0098] Figure 65 shows the expression level of KRT6Ain normal bladder tissue and cancerous bladder tissue by qPCR.

[0099] Figure 66 shows the expression level of FCRLB in normal bladder tissue and cancerous bladder tissue by qPCR.

[00100] Figure 67 shows the expression level of IL1A in normal bladder tissue and cancerous bladder tissue by qPCR.

[00101] Figure 68 shows the expression level of KRT16 in normal bladder tissue and cancerous bladder tissue by qPCR.

[00102] Figure 69 shows the expression level of SLC1A6 in normal bladder tissue and cancerous bladder tissue by qPCR.

[00103] Figure 70 shows the expression level of S100A2 in normal bladder tissue and cancerous bladder tissue by qPCR.

[00104] Figure 71 shows the expression level of S100A7A in normal bladder tissue and cancerous bladder tissue by qPCR.

[00105] Figure 72 shows the expression level of MMP12 in normal bladder tissue and cancerous bladder tissue by ELISA.

[00106] Figure 73 shows the expression level of ColX in normal bladder tissue and cancerous bladder tissue by ELISA.

[00107] Figure 74 shows the expression level of MMP11 in normal bladder tissue and cancerous bladder tissue by ELISA.

[00108] Figure 75 is agarose gel analysis of a qPCR expression data for markers COL10A1, MMP11, SFN, FCRLB in human urine.

[00109] Figure 76 shows the expression level of SERPINB5 in normal bladder tissue and cancerous bladder tissue by qPCR.

DETAILED DESCRIPTION

[00110] Before the present compositions and methods are described, it is to be understood that this invention is not limited to the particular processes, compositions, or methodologies described, as these may vary. It is also to be understood that the terminology used in the description is for the purpose of describing the particular versions or embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims. Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art. Although any methods and materials similar or equivalent to those described herein can be used in the

practice or testing of embodiments of the present invention, specific methods, devices, and materials are now described.

[00111] The invention provides for the rapid, accurate, and cost effective means to detect bladder cancer in a subject. The method comprises detecting one or more markers that are specifically expressed on bladder cancer tumors in a sample as disclosed infra. The sample may be a bodily fluid such as serum, or urine. Thus in some embodiments the invention provides for a non-invasive test for detecting bladder cancer in a subject. In other embodiments the sample may be a tissue or cell sample. Also provided are methods of screening for drugs having activity against bladder cancer, therapeutics for bladder cancer as well as compositions and kits useful in detecting, and prognosing bladder cancer.

DEFINITIONS

[00112] As used herein, the singular forms “a,” “an,” and “the” include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to a “therapeutic” is a reference to one or more therapeutics and equivalents thereof known to those skilled in the art, and so forth.

[00113] As used herein, the term “about” means plus or minus 10% of the numerical value of the number with which it is being used. Therefore, about 50% means in the range of 45% to 55%.

[00114] “Administering,” when used in conjunction with a therapeutic, means to administer a therapeutic directly into or onto a target tissue or to administer a therapeutic to a patient whereby the therapeutic positively impacts the tissue to which it is targeted. Thus, as used herein, the term “administering”, when used in conjunction with elastin digest, can include, but is not limited to, providing an elastin digest into or onto the target tissue; providing an elastin digest systemically to a patient by, e.g., intravenous injection whereby the therapeutic reaches the target tissue; providing an elastin digest in the form of the encoding sequence thereof to the target tissue (e.g., by so-called gene-therapy techniques). “Administering” a composition may be accomplished by oral administration, intravenous injection, intraperitoneal injection, intramuscular injection, subcutaneous injection, transdermal diffusion or electrophoresis, local injection, extended release delivery devices including locally implanted extended release devices such as bioerodible or reservoir-based implants, as protein therapeutics or as nucleic acid therapeutic via gene therapy vectors, topical administration, or by any of these methods in

combination with other known techniques. Such combination techniques include heating, radiation and ultrasound.

[00115] The term “animal,” “patient” or “subject” as used herein includes, but is not limited to mammals, including humans and non-human primates, farm animals such as pigs, goats, horses, sheep, cows, rodents including rats and mice, rabbits, cats, dogs and the like. In some embodiments, the term “subject,” may refer to humans. In some embodiments, the term “subject,” may refer to a male. In some embodiments, the term “subject,” may refer to a female.

[00116] The term “bladder cancer” as used herein, may include transitional cell carcinoma, squamous cell carcinoma, adenocarcinoma, sarcoma, small cell carcinoma, secondary deposits from cancers elsewhere in the body or a combination thereof.

[00117] The term “inhibiting” includes the administration of a compound of the present invention to prevent the onset of the symptoms, alleviating the symptoms, or eliminating the disease, condition or disorder.

[00118] By “pharmaceutically acceptable”, it is meant the carrier, diluent or excipient must be compatible with the other ingredients of the formulation and not deleterious to the recipient thereof.

[00119] In some embodiments, the present disclosure provides for nucleic acid and protein sequences that are associated with cancer, herein termed “cancer associated” or “CA” sequences. In some embodiments, the present disclosure provides nucleic acid and protein sequences that are associated with cancers or carcinomas that originate in bladder or urinary tissue, herein termed “bladder cancer associated” sequences.

[00120] The term “pluripotent stem cells” refers to animal cells capable of differentiating into more than one differentiated cell type. Such cells include hES cells, hED cells, hEG cells, hEC cells, and adult-derived cells including mesenchymal stem cells, neuronal stem cells, and bone marrow-derived stem cells. Pluripotent stem cells may be genetically modified or not genetically modified. Genetically modified cells may include markers such as fluorescent proteins to facilitate their identification.

[00121] The term “embryonic stem cells” (ES cells) refers to cells derived from the inner cell mass of blastocysts, blastomeres, or morulae that have been serially passaged as cell lines while maintaining an undifferentiated state (e.g. expressing *TERT*, *OCT4*, and SSEA and TRA antigens specific for ES cells of the species). Established cell lines may be available from cell

banks such as WiCell. The ES cells may be derived from in vitro fertilization of an egg cell with sperm or DNA, nuclear transfer, parthenogenesis, or by means to generate hES cells with hemizyosity or homozygosity in the MHC region. The term "human embryonic stem cells" (hES cells) refers to human ES cells.

[00122] The term "human embryonic germ cells" (hEG cells) refer to pluripotent stem cells derived from the primordial germ cells of fetal tissue or maturing or mature germ cells such as oocytes and spermatogonial cells, that can differentiate into various tissues in the body. The hEG cells may also be derived from pluripotent stem cells produced by gynogenetic or androgenetic means, i.e., methods wherein the pluripotent cells are derived from oocytes containing only DNA of male or female origin and therefore will comprise all female-derived or male-derived DNA (see U.S. application nos. 60/161,987, filed October 28, 1999; 09/697,297, filed October 27, 2000; 09/995,659, filed November 29, 2001; 10/374,512, filed February 27, 2003; PCT application no. PCT/US/00/29551, filed October 27, 2000; the disclosures of which are incorporated herein in their entirety).

[00123] The term human iPS cells refers to cells with properties similar to hES cells, including the ability to form all three germ layers when transplanted into immunocompromised mice wherein said iPS cells are derived from cells of varied somatic cell lineages following exposure to hES cell-specific transcription factors such as *KLF4*, *SOX2*, *MYC*, and *OCT4* or the factors *SOX2*, *OCT4*, *NANOG*, and *LIN28*. Said iPS cells may be produced by the expression of these gene through vectors such as retroviral vectors as is known in the art, or through the introduction of these factors by permeabilization or other technologies taught by PCT application number PCT/US2006/030632 (WO2007/019398).

[00124] The term "differentiated cells" when used in reference to cells made by methods of this invention from pluripotent stem cells refer to cells having reduced potential to differentiate when compared to the parent pluripotent stem cells. The differentiated cells of this invention comprise cells that could differentiate further (i.e., they may not be terminally differentiated).

[00125] The term embryonal carcinoma ("EC") cells, including human EC cells, refers to embryonal carcinoma cells such as TERA-1, TERA-2, and NTera-2.

[00126] As used herein, the term “naturally occurring” refers to sequences or structures that may be in a form normally found in nature. “Naturally occurring” may include sequences in a form normally found in any animal.

[00127] As used herein, the term “cancer associated sequences” refers to nucleotide or protein sequences that are either differentially expressed, activated, inactivated or altered in cancers as compared to normal tissue. Cancer associated sequences may include those that are up-regulated (i.e. expressed at a higher level), as well as those that are down-regulated (i.e. expressed at a lower level), in cancers when compared to a non-cancerous or normal sample. Cancer associated sequences can also include sequences that have been altered (i.e., translocations, truncated sequences or sequences with substitutions, deletions or insertions, including, but not limited to, point mutations) and show either the same expression profile or an altered profile. In some embodiments, the cancer associated sequences are from humans; however, as will be appreciated by those in the art, cancer associated sequences from other subjects may be useful in animal models of disease and drug evaluation; thus, other cancer associated sequences may be useful such as any subject, e.g., without limitation, sequences from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, and farm animals (including sheep, goats, pigs, cows, horses, etc). Cancer associated sequences from other organisms may be obtained using the techniques outlined below.

[00128] The term “homology,” as used herein, refers to a degree of complementarity. There may be partial homology or complete homology. The word “identity” may substitute for the word “homology.” A partially complementary nucleic acid sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as “substantially homologous.” The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially homologous sequence or hybridization probe will compete for and inhibit the binding of a completely homologous sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of

complementarity (e.g., less than about 30% homology or identity). In the absence of non-specific binding, the substantially homologous sequence or probe will not hybridize to the second non-complementary target sequence.

[00129] The phrases “percent homology,” “% homology,” “percent identity” or “% identity” refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MEGALIGN program (LASERGENE software package, DNASTAR). The MEGALIGN program can create alignments between two or more sequences according to different methods, e.g., the Clustal Method. (Higgins, D. G. and P. M. Sharp (1988) *Gene* 73:237-244.) The Clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no homology between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be calculated by the Clustal Method, or by other methods known in the art, such as the Jotun Hein Method. (See, e.g., Hein, J. (1990) *Methods Enzymol.* 183:626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

[00130] As used herein, a polynucleotide “derived from” a designated sequence refers to a polynucleotide sequence which is comprised of a sequence of approximately at least about 6 nucleotides, at least about 8 nucleotides, at least about 10-12 nucleotides, and at least about 15-20 nucleotides corresponding to a region of the designated nucleotide sequence. “Corresponding” means homologous to or complementary to the designated sequence. Preferably, the sequence of the region from which the polynucleotide is derived is homologous to or complementary to a sequence that is unique to a cancer associated gene.

[00131] In the broadest sense, use of “nucleic acid,” “polynucleotide” or “oligonucleotide” or equivalents herein means at least two nucleotides covalently linked together. In some embodiments, an oligonucleotide is an oligomer of 6, 8, 10, 12, 20, 30 or up to 100 nucleotides. In some embodiments, an oligonucleotide is an oligomer of at least 6, 8, 10, 12,

20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300, 400, or 500 nucleotides. A “polynucleotide” or “oligonucleotide” may comprise DNA, RNA, PNA or a polymer of nucleotides linked by phosphodiester and/or any alternate bonds. The nucleic acid, polynucleotide or oligonucleotide may be modified by linking a detectable substance or label to it.

[00132] Similarly, a “recombinant protein” is a protein made using recombinant techniques, for example, but not limited to, through the expression of a recombinant nucleic acid as depicted above. A recombinant protein may be 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 about 50-75%, about 80%, or 90% by weight of the total protein. In some embodiments, a substantially pure protein comprises about 80-99%, 85-99%, 90-99%, 95-99%, or 97-99% by weight of the total protein. A recombinant protein can also include the production of a cancer associated protein from one organism (*e.g.* human) in a different organism (*e.g.* yeast, *E. coli*, and the like) or host cell (*e.g.* yeast, *E. coli*, and the like). 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 *e.g.* a detectable substance or label, or amino acid substitutions, insertions and deletions, as discussed herein.

[00133] As used herein, the term “tag,” “sequence tag” or “primer tag sequence” refers to an oligonucleotide with specific nucleic acid sequence that serves to identify a batch of polynucleotides bearing such tags therein. Polynucleotides from the same biological source are covalently tagged with a specific sequence tag so that in subsequent analysis the polynucleotide can be identified according to its source of origin. The sequence tags also serve as primers for nucleic acid amplification reactions.

[00134] A “microarray” is a linear or two-dimensional array of, for example, discrete regions, each having a defined area, formed on the surface of a solid support. The density of the

discrete regions on a microarray is determined by the total numbers of target polynucleotides to be detected on the surface of a single solid phase support, preferably at least about $50/\text{cm}^2$, more preferably at least about $100/\text{cm}^2$, even more preferably at least about $500/\text{cm}^2$, and still more preferably at least about $1,000/\text{cm}^2$. As used herein, a DNA microarray is an array of oligonucleotide primers placed on a chip or other surfaces used to identify, amplify, detect, or clone target polynucleotides. Since the position of each particular group of primers in the array is known, the identities of the target polynucleotides can be determined based on their binding to a particular position in the microarray.

[00135] The term “label” or “detectable substance” refers to a composition capable of producing a detectable signal indicative of the presence of the target polynucleotide in an assay sample. Suitable labels include radioisotopes, nucleotide chromophores, enzymes, substrates, fluorescent molecules, chemiluminescent moieties, magnetic particles, bioluminescent moieties, and the like. As such, a label is any composition detectable by a device or method, such as but not limited to, a spectroscopic, photochemical, biochemical, immunochemical, electrical, optical, chemical detection device or any other appropriate device. The label can also be detectable visually without the aid of a device. The term “label” is used to refer to any chemical group or moiety having a detectable physical property or any compound capable of causing a chemical group or moiety to exhibit a detectable physical property, such as an enzyme that catalyzes conversion of a substrate into a detectable product. The term “label” also encompasses compounds that inhibit the expression of a particular physical property. The label may also be a compound that is a member of a binding pair, the other member of which bears a detectable physical property.

[00136] The term “support” refers to conventional supports such as beads, particles, dipsticks, fibers, filters, membranes, and silane or silicate supports such as glass slides.

[00137] The term “amplify” is used in the broad sense to mean creating an amplification product which may include, for example, additional target molecules, or target-like molecules or molecules complementary to the target molecule, which molecules are created by virtue of the presence of the target molecule in the sample. In the situation where the target is a nucleic acid, an amplification product can be made enzymatically with DNA or RNA polymerases or reverse transcriptases, or any combination thereof.

[00138] As used herein, a “biological sample” refers to a sample of tissue or fluid isolated from a subject, including but not limited to, for example, blood, plasma, serum, spinal fluid, lymph fluid, skin, respiratory, intestinal and genitourinary tracts, tears, saliva, milk, cells (including but not limited to blood cells), tumors, organs, and also samples of in vitro cell culture constituents.

[00139] The term “biological sources” as used herein refers to the sources from which the target polynucleotides may be derived. The source can be of any form of “sample” as described above, including but not limited to, cell, tissue or fluid. “Different biological sources” can refer to different cells/tissues/organs of the same individual, or cells/tissues/organs from different individuals of the same species, or cells/tissues/organs from different species.

[00140] As used herein, the term “therapeutic” or “therapeutic agent” means an agent that can be used to treat, combat, ameliorate, prevent or improve an unwanted condition or disease of a patient. In part, embodiments of the present invention are directed to the treatment of cancer or the decrease in proliferation of cells. In some embodiments, the term “therapeutic” or “therapeutic agent” may refer to any molecule that associates with or affects the target marker, its expression or its function. In various embodiments, such therapeutics may include molecules such as, for example, a therapeutic cell, a therapeutic peptide, a therapeutic gene, a therapeutic compound, or the like, that associates with or affects the target marker, its expression or its function.

[00141] A “therapeutically effective amount” or “effective amount” of a composition is a predetermined amount calculated to achieve the desired effect, *i.e.*, to inhibit, block, or reverse the activation, migration, or proliferation of cells. In some embodiments, the effective amount is a prophylactic amount. In some embodiments, the effective amount is an amount used to medically treat the disease or condition. The specific dose of a composition administered according to this invention to obtain therapeutic and/or prophylactic effects will, of course, be determined by the particular circumstances surrounding the case, including, for example, the composition administered, the route of administration, and the condition being treated. It will be understood that the effective amount administered will be determined by the physician in the light of the relevant circumstances including the condition to be treated, the choice of composition to be administered, and the chosen route of administration. A therapeutically effective amount of composition of this invention is typically an amount such that when it is

administered in a physiologically tolerable composition, it is sufficient to achieve an effective systemic concentration or local concentration in the targeted tissue.

[00142] The terms “treat,” “treated,” or “treating” as used herein can refer to both therapeutic treatment or prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) an undesired physiological condition, disorder or disease, or to obtain beneficial or desired clinical results. In some embodiments, the term may refer to both treating and preventing. For the purposes of this disclosure, beneficial or desired clinical results include, but are not limited to, alleviation of symptoms; diminishment of the extent of the condition, disorder or disease; stabilization (*i.e.*, not worsening) of the state of the condition, disorder or disease; delay in onset or slowing of the progression of the condition, disorder or disease; amelioration of the condition, disorder or disease state; and remission (whether partial or total), whether detectable or undetectable, or enhancement or improvement of the condition, disorder or disease. Treatment includes eliciting a clinically significant response without excessive levels of side effects. Treatment also includes prolonging survival as compared to expected survival if not receiving treatment. Treat, treated, or treating may include inhibiting the growth a bladder cancer tumor and/or inhibiting the metastasis of a bladder cancer tumor.

[00143] Generally speaking, the term “tissue” refers to any aggregation of similarly specialized cells that are united in the performance of a particular function.

[00144] “Optional” or “optionally” means that the subsequently described structure, event or circumstance may or may not occur, and that the description includes instances where the event occurs and instances where it does not.

CANCER ASSOCIATED NUCLEIC ACID SEQUENCES AND CANCER DETECTION

[00145] Some embodiments herein are directed to one or more of sequences associated with cancers, such as, bladder cancer. A list of genes associated with bladder cancer is provided in Table 2 and the corresponding nucleic acid sequences are provided in Table 5.

[00146] In some embodiments, the cancer associated sequences are nucleic acids. As will be appreciated by those skilled in the art and is described herein, cancer associated sequences of embodiments herein may be useful in a variety of applications including diagnostic applications to detect nucleic acids or their expression levels in a subject, therapeutic applications or a combination thereof. Further, the cancer associated sequences of embodiments

herein may be used in screening applications; for example, generation of biochips comprising nucleic acid probes to the cancer associated sequences.

[00147] In some embodiments, cancer associated sequences may include nucleic acid and/or amino acid sequences. In some embodiments, the cancer associated sequences may include sequences having at least about 60% homology with the disclosed sequences. In some embodiments, the cancer associated sequences may have at least about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 99%, about 99.8% homology with the disclosed sequences. In some embodiments, the cancer associated sequences may be "mutant nucleic acids". As used herein, "mutant nucleic acids" refers to deletion mutants, insertions, point mutations, substitutions, translocations.

[00148] A nucleic acid of the present invention may include phosphodiester bonds, although in some cases, as outlined below (for example, in antisense applications or when a nucleic acid is a candidate drug agent), nucleic acid analogs 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); 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); and Pauwels et al., *Chemica Scripta* 26:141 91986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Pat. No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoroamidite 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. Pat. Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi 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. Pat. 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 included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp 169-176). Several nucleic acid analogs are described in Rawls, C & E News Jun. 2, 1997 page 35. 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 for use in anti-sense applications or as probes on a biochip.

[00149] As will be appreciated by those skilled in the art, such nucleic acid analogs can be used in some embodiments. 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.

[00150] In some embodiments, the nucleic acids may be single stranded or double stranded or may contain portions of both double stranded or single stranded sequence. As will be appreciated by those skilled in the art, the depiction of a single strand also defines the sequence of the other strand; 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 subject units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

[00151] In some embodiments, the cancer associated sequences may be recombinant nucleic acids. By the term "recombinant nucleic acid" herein refers to nucleic acid molecules, 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 a recombinant nucleic acid may also be an isolated nucleic acid, in a linear form, or cloned in a 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 can replicate 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 *in vivo*, are still considered recombinant or isolated for the purposes of the invention. As used herein, a "polynucleotide" or "nucleic acid" is a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term includes double- and single-stranded DNA and RNA. It also includes known types of modifications, for example, labels which are known in the art, methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications-such as, for example, those with uncharged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example proteins (including e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide.

[00152] In some embodiments, a method of identifying a target marker comprises the steps of: 1) obtaining a molecular profile of the mRNAs, miRNAs, proteins, or protein modifications of immortal pluripotent stem cells (such as embryonic stem ("ES") cells, induced pluripotent stem ("iPS") cells, and germ-line cells such as embryonal carcinoma ("EC") cells); 2) ES, iPS, or EC-derived clonal embryonic progenitor ("EP") cell lines malignant cancer cells including cultured cancer cell lines or human tumor tissues, and comparing those molecules to those present in mortal somatic cell types such as cultured clonal human embryonic progenitors, cultured somatic cells from fetal or adult sources, or normal tissue counterparts to malignant cancer cells. Target markers that are shared between pluripotent stem cells such as hES cells and malignant cancer cells, but are not present in a majority of somatic cell types may be candidate diagnostic markers and therapeutic targets.

[00153] Some embodiments are directed to a biochip comprising a nucleic acid segment which encodes a cancer associated protein, for example, but not limited to, selected from the sequences outlined in Table 2 (SEQ ID NOs: 1-55).

[00154] Also provided herein is a method for diagnosing or determining the propensity to cancers, e.g., bladder cancer. The method of diagnosing may comprise measuring the level of

expression of a cancer associated marker disclosed herein in a suitable sample and comparing the level of expression with a non-cancerous or normal sample.

[00155] In some embodiments, an isolated nucleic acid comprises at least 10, 12, 15, 20 or 30 contiguous nucleotides of a sequence selected from the group consisting of the cancer associated polynucleotide sequences disclosed in Table 2 (SEQ ID NOs: 1-55).

[00156] In some embodiments, the polynucleotide, or its complement or a fragment thereof, further comprises a detectable label, is attached to a solid support, is prepared at least in part by chemical synthesis, is an antisense fragment, is single stranded, is double stranded or comprises a microarray.

[00157] Cancer associated sequences associated with bladder cancer are disclosed in Table 2. These sequences were extracted from hotpop, fold-change and filter analysis KCKC110608.1. Once expression was determined, the gene sequence results were further filtered by considering fold-change in bladder cancer vs. normal bladder; general specificity; secreted or not, level of expression in bladder cancer; and signal to noise ratio. The cancer associated polynucleotide sequences include SEQ ID NOs: 1-55 shown in Table 2. In some embodiments, the polynucleotide sequences may be mRNA sequences selected from: Homo sapiens melanoma antigen family A, 10 (MAGEA10), transcript variant 2; Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 2; Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12); Homo sapiens chemokine (C-X-C motif) ligand 9 (CXCL9); Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 3; Homo sapiens keratin 81 (KRT81); Homo sapiens hypothetical protein LOC729826 (LOC729826); Homo sapiens parathyroid hormone-like hormone (PTH1H), transcript variant 3; Homo sapiens matrix metalloproteinase 11 (stromelysin 3) (MMP11); Homo sapiens S100 calcium binding protein A7 (S100A7); Homo sapiens WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1; Homo sapiens chemokine (C-X-C motif) ligand 10 (CXCL10); Homo sapiens neuromedin U (NMU); Homo sapiens guanylate binding protein 5 (GBP5); Homo sapiens topoisomerase (DNA) II alpha 170kDa (TOP2A); Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 4 (SERPINB4); Homo sapiens granulysin (GNLY), transcript variant 519; Homo sapiens gametocyte specific factor 1 (GTSF1); Homo sapiens peptidase inhibitor 3, skin-derived (SKALP) (PI3); Homo sapiens S100 calcium binding protein A7A (S100A7A); Homo sapiens indoleamine 2,3-dioxygenase 1 (IDO1); Homo sapiens

gap junction protein, beta 6 (GJB6); Homo sapiens calmodulin-like 3 (CALML3); Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 3 (SERPINB3); Homo sapiens chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6); Homo sapiens olfactomedin 4 (OLFM4); Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1); Homo sapiens visinin-like 1 (VSNL1); Homo sapiens ubiquitin D (UBD); Homo sapiens absent in melanoma 2 (AIM2); Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B; Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 13 (SERPINB13); Homo sapiens indoleamine-pyrrole 2,3 dioxygenase (INDO); Homo sapiens keratin 5 (KRT5); Homo sapiens hypothetical LOC100130897 (LOC100130897); Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner) (KRT14); Homo sapiens family with sequence similarity 83, member A (FAM83A), transcript variant 1; Homo sapiens family with sequence similarity 181, member B (FAM181B); RST24587 Athersys RAGE Library Homo sapiens cDNA mRNA sequence; Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB); Homo sapiens desmoglein 3 (pemphigus vulgaris antigen) (DSG3); Homo sapiens thymidine phosphorylase (TYMP), transcript variant 3; Homo sapiens keratin 6A (KRT6A); Homo sapiens keratin 6B (KRT6B); a polynucleotide derived therefrom or any combination thereof. In some embodiments, the bladder cancer associated sequences may be DNA sequences encoding the above mRNA or the cancer associated protein or cancer associated polypeptide expressed by the above mRNA. In some embodiments, the cancer associated sequence may be a mutant nucleic acid of the above disclosed sequences. In some embodiments, the cancer associated protein or polypeptide sequence may be selected from SEQ ID NOs: 56-110 or a homolog thereof. In some embodiments, the homolog may have at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5% identity with the disclosed polypeptide sequence.

[00158] In some embodiments, a method for diagnosing cancer comprises a) determining the expression of one or more genes comprising a nucleic acid sequence selected from the group consisting of the human genomic and mRNA sequences described in Table 2, in a first sample type (e.g. tissue) of a first individual; and b) comparing said expression of said gene(s) from a second normal sample type from said first individual or a second unaffected individual; wherein

a difference in said expression indicates that the first individual has cancer. In some embodiments, the expression is increased as compared to the normal sample. In some embodiments, the expression is decreased as compared to the normal sample.

[00159] In some embodiments, the present invention provides methods of diagnosing bladder cancer in a subject, the method comprising: a) determining the expression of one or more genes or gene products or homologs thereof; and b) comparing said expression of the one or more nucleic acid sequences from a second normal sample from said first subject or a second unaffected subject, wherein a difference in said expression indicates that the first subject has cancer, wherein the gene or the gene product is referred to as a gene selected from the group consisting of: MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, and GJB2.

[00160] In some embodiments, the present invention provides methods of detecting bladder cancer in a test sample, comprising: (i) detecting a level of activity of at least one polypeptide that is a gene product; and (ii) comparing the level of activity of the polypeptide in the test sample with a level of activity of polypeptide in a normal sample, wherein an altered level of activity of the polypeptide in the test sample relative to the level of polypeptide activity in the normal sample is indicative of the presence of bladder cancer in the test sample, wherein said gene product is a product of a gene selected from the group consisting of MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, and GJB2.

[00161] In certain embodiments the invention provides a panel of markers associated with bladder cancer comprising nucleic acid sequences, or fragments thereof of the genes:

MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 FCRLB, IL1A, KRT16, SLC1A6.

[00162] In other embodiments the invention provides a method of detecting bladder cancer in a subject comprising measuring the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 IL1A, KRT16, SLC1A6. in a sample, comparing the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in a non-cancerous sample such as normal bladder tissue, wherein elevated expression of at least one of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 relative to the non-cancerous sample indicates the subject has cancer. The method may also include comparing the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 to a known cancerous sample, e.g., a bladder cancer sample, wherein an expression level of at least one of the genes in the subject sample that is at least as high as the known cancer sample indicates the subject has cancer.

[00163] In still other embodiments the invention provides a method of detecting bladder cancer in a subject comprising measuring the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in sample, comparing the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in a non-cancerous sample such as normal bladder tissue, wherein elevated expression of a plurality of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 relative to the non-cancerous sample indicates the subject has cancer. The method may also include comparing the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 to a known cancerous sample, e.g., a bladder cancer sample, wherein an expression level of a plurality of the genes in the subject sample that is at least as high as the known cancer sample indicates the subject has cancer.

[00164] In still other embodiments the invention provides a method of detecting bladder cancer in a subject comprising measuring the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 in sample, comparing the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in a non-cancerous sample such as normal bladder tissue, wherein elevated

expression of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 relative to the non-cancerous sample indicates the subject has cancer. The method may also include comparing the expression level of the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 to a known cancerous sample, e.g., a bladder cancer sample, wherein an expression level of the genes in the subject sample that is at least as high as the known cancer sample indicates the subject has cancer.

CANCER ASSOCIATED PROTEINS AND CANCER DETECTION

[00165] Cancer associated sequences may also include proteins or peptides encoded by the nucleic acid sequences described above. A list of proteins or peptides associated with bladder cancer is provided in Table 3. The amino acid sequences encoding these proteins or peptides are provided in Table 6.

[00166] In some embodiments, the cancer associated sequence comprises a sequence of a naturally occurring protein. In some embodiments, the cancer associated sequence does not comprise a naturally occurring sequence. Thus in some embodiments the cancer associated sequence may encode a mutant protein or a fragment of a naturally occurring protein.

[00167] In some embodiments, the invention provides a method for detecting a cancer associated sequence with the expression of a polypeptide in a test sample, comprising detecting a level of expression of at least one polypeptide selected from the group consisting of SEQ ID NOs: 56-110 shown in Table 3, or a fragment thereof. In some embodiments, the method comprises comparing the level of expression of the polypeptide in the test sample with a level of expression of polypeptide in a normal sample, wherein an altered level of expression of the polypeptide, e.g. elevated expression, in the test sample relative to the level of polypeptide expression in the normal sample is indicative of the presence of cancer in the test sample. In some embodiments, the polypeptide expression is compared to a cancer sample, wherein the level of expression is at least the same as the cancer is indicative of the presence of cancer in the test sample. In some embodiments, the sample is a cell sample.

[00168] In some embodiments, the invention provides an isolated polypeptide, encoded within an open reading frame of a cancer associated sequence selected from the polynucleotide sequences of SEQ ID NOs: 56-110 shown in Table 3, or its complement. In some embodiments, the invention provides an isolated polypeptide, wherein said polypeptide comprises the amino

acid sequence encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 1-55. In some embodiments, the invention provides an isolated polypeptide, wherein said polypeptide comprises the amino acid sequence encoded by a polypeptide selected from the group consisting of SEQ ID NOs: 56-110, shown in Table 3.

[00169] In some embodiments, the invention further provides an isolated polypeptide, comprising the amino acid sequence of an epitope of the amino acid sequence of a cancer associated polypeptide selected from the group consisting of SEQ ID. NOs: 56-110 shown in Table 3, wherein the polypeptide or fragment thereof may be attached to a solid support. In some embodiments the invention provides an isolated antibody (monoclonal or polyclonal) or antigen binding fragment thereof, that binds to such a polypeptide. The isolated antibody or antigen binding fragment thereof may be attached to a solid support, or further comprises a detectable label.

[00170] In some embodiments, the invention provides a method for detecting cancer by detecting the presence of an antibody in a test serum sample. In some embodiments, the antibody recognizes a polypeptide or an epitope thereof disclosed herein. In some embodiments, the antibody recognizes a polypeptide or epitope thereof encoded by a nucleic acid sequence disclosed herein. In some embodiments, the method comprises detecting a level of an antibody against an antigenic polypeptide selected from the group consisting of SEQ ID NOs: 56-110 shown in Table 3, or antigenic fragment thereof. In some embodiments, the method comprises comparing the level of the antibody in the test sample with a level of the antibody in the control sample, wherein an altered level of antibody in said test sample relative to the level of antibody in the control sample is indicative of the presence of cancer in the test sample. In some embodiments, the control sample is a sample derived from a normal cell or non-cancerous sample. In some embodiments, the control is derived from a cancer sample, and, therefore, in some embodiments, the method comprises comparing the levels of binding and/or the amount of antibody in the sample, wherein when the levels or amount are the same as the cancer control sample is indicative of the presence of cancer in the test sample.

[00171] In some embodiments, the invention also provides a method for detecting presence or absence of cancer cells in a subject. In some embodiments, the method comprises contacting one or more cells from the subject with an antibody as described herein. In some embodiments, the method comprises detecting a complex of a cancer associated protein (CAP)

and the antibody, wherein detection of the complex indicates with the presence of cancer cells in the subject.

[00172] In still other embodiments the invention provides a method of detecting bladder cancer in a subject comprising measuring the protein expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in sample, comparing the expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in a non-cancerous sample such as normal bladder tissue, wherein elevated expression of at least one of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 relative to the non-cancerous sample indicates the subject has cancer. The method may also include comparing the expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 to a known cancerous sample, e.g., a bladder cancer sample, wherein an expression level of at least one of the proteins encoded for by the genes in the subject sample that is at least as high as the known cancer sample indicates the subject has cancer.

[00173] In still other embodiments the invention provides a method of detecting bladder cancer in a subject comprising measuring the protein expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in sample, comparing the expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in a non-cancerous sample such as normal bladder tissue, wherein elevated expression of a plurality of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 relative to the non-cancerous sample indicates the subject has cancer. The method may also include comparing the expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 to a known cancerous sample, e.g., a bladder cancer sample, wherein an expression level of a plurality of the proteins encoded for by the genes in the subject sample that is at least as high as the known cancer sample indicates the subject has cancer.

[00174] In still other embodiments the invention provides a method of detecting bladder cancer in a subject comprising measuring the protein expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in sample, comparing the expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 in a non-cancerous sample such as normal bladder tissue, wherein elevated expression of the proteins encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 relative to the non-cancerous sample indicates the subject has cancer. The method may also include comparing the expression level of the protein encoded for by the genes MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6 to a known cancerous sample, e.g., a bladder cancer sample, wherein an expression level of the proteins encoded for by the genes in the subject sample that is at least as high as the known cancer sample indicates the subject has cancer.

IMMUNE RESPONSE TO CANCER ASSOCIATED PROTEINS

[00175] Some embodiments are directed to the use of cancer associated polypeptides and polynucleotides encoding a cancer associated sequence, a fragment thereof, or a mutant thereof, and antigen presenting cells (such as, without limitation, dendritic cells), to elicit an immune response against cells expressing a cancer-associated polypeptide sequence, such as, without limitation, cancer cells, (in a subject, or in vitro) such as bladder cancer cells. In some embodiments, the method of eliciting an immune response against cells expressing a cancer associated sequence comprises (1) isolating a hematopoietic stem cell, (2) genetically modifying the cell to express a cancer associated sequence, (3) differentiating the cell into DCs; and (4) administering the DCs to the subject (e.g., human patient). In some embodiments, antigen presenting cells (APCs) may be used to activate T lymphocytes in vivo or ex vivo, to elicit an immune response against cells expressing a cancer associated sequence. APCs are highly specialized cells and may include, without limitation, macrophages, monocytes, and dendritic cells (DCs). APCs may process antigens and display their peptide fragments on the cell surface together with molecules required for lymphocyte activation. In some embodiments, the APCs may be dendritic cells. DCs may be classified into subgroups, including, e.g., follicular dendritic cells, Langerhans dendritic cells, and epidermal dendritic cells. In some embodiments, dendritic cell precursor cells are isolated for transduction with a cancer associated sequence, and induced

to differentiate into dendritic cells. The genetically modified DCs express the cancer associated sequence, and may display peptide fragments on the cell surface.

[00176] In some embodiments, the method of eliciting an immune response includes (1) isolating DCs (or isolation and differentiation of DC precursor cells), (2) pulsing the cells with a cancer associated sequence, and; (3) administering the DCs to the subject. These approaches are discussed in greater detail, *infra*. In some embodiments, the pulsed or expressing DCs may be used to activate T lymphocytes *ex vivo*. These general techniques and variations thereof may be within the skill of those in the art (see, e.g., WO97/29182; WO 97/04802; WO 97/22349; WO 96/23060; WO 98/01538; Hsu et al., 1996, *Nature Med.* 2:52-58), and that still other variations may be discovered in the future.

[00177] In some embodiments, the cancer associated sequence is contacted with a subject to stimulate an immune response. In some embodiments, the immune response is a therapeutic immune response. In some embodiments, the immune response is a prophylactic immune response. For example, the cancer associated sequence can be contacted with a subject under conditions effective to stimulate an immune response. The cancer associated sequence can be administered as, for example, a DNA molecule (*e.g.* DNA vaccine), RNA molecule, or polypeptide, or any combination thereof. Administering sequence to stimulate an immune responses are known, but the identity of which sequences to use was not known prior to the present disclosure. Any sequence or combination of sequences disclosed herein or a homolog thereof can be administered to a subject to stimulate an immune response.

[00178] In some embodiments, the cancer associated sequence comprises a sequence of a naturally occurring protein. In some embodiments, the cancer associate sequence does not comprise a naturally occurring sequence. As already noted, fragments of naturally occurring proteins may be used; in addition, the expressed polypeptide may comprise mutations such as deletions, insertions, or amino acid substitutions when compared to a naturally occurring polypeptide, so long as at least one peptide epitope can be processed by the DC and presented on a MHC class I or II surface molecule. In some embodiments, it may be desirable to use sequences other than "wild type," in order to, for example, increase antigenicity of the peptide or to increase peptide expression levels. In some embodiments, the introduced cancer associated sequences may encode variants such as polymorphic variants (*e.g.*, a variant expressed by a

particular human patient) or variants characteristic of a particular cancer (e.g., a cancer in a particular subject).

[00179] In some embodiments, a cancer associated expression sequence may be introduced (transduced) into DCs or stem cells in any of a variety of standard methods, including transfection, recombinant vaccinia viruses, adeno-associated viruses (AAVs), retroviruses, etc.

[00180] In some embodiments, the transformed DCs of the invention may be introduced into the subject (e.g., without limitation, a human patient) where the DCs may induce an immune response. Typically, the immune response includes a cytotoxic T-lymphocyte (CTL) response against target cells bearing antigenic peptides (e.g., in a MHC class I/peptide complex). These target cells are typically cancer cells.

[00181] In some embodiments, when the DCs of the invention are to be administered to a subject, they may preferably isolated from, or derived from precursor cells from, that subject (i.e., the DCs may administered to an autologous subject). However, the cells may be infused into HLA-matched allogeneic, or HLA-mismatched allogeneic subject. In the latter case, immunosuppressive drugs may be administered to the subject.

[00182] In some embodiments, the cells may be administered in any suitable manner. In some embodiments, the cell may be administered with a pharmaceutically acceptable carrier (e.g., saline). In some embodiments, the cells may be administered through intravenous, intra-articular, intramuscular, intradermal, intraperitoneal, or subcutaneous routes. Administration (i.e., immunization) may be repeated at time intervals. Infusions of DC may be combined with administration of cytokines that act to maintain DC number and activity (e.g., GM-CSF, IL-12).

[00183] In some embodiments, the dose administered to a subject may be a dose sufficient to induce an immune response as detected by assays which measure T cell proliferation, T lymphocyte cytotoxicity, and/or effect a beneficial therapeutic response in the patient over time, e.g., to inhibit growth of cancer cells or result in reduction in the number of cancer cells or the size of a tumor.

[00184] In some embodiments, DCs are obtained (either from a patient or by in vitro differentiation of precursor cells) and pulsed with antigenic peptides having a cancer associated sequence. The pulsing results in the presentation of peptides onto the surface MHC molecules of the cells. The peptide/MHC complexes displayed on the cell surface may be capable of inducing

a MHC-restricted cytotoxic T-lymphocyte response against target cells expressing cancer associated polypeptides (e.g., without limitations, cancer cells).

[00185] In some embodiments, cancer associated sequences used for pulsing may have at least about 6 or 8 amino acids and fewer than about 30 amino acids or fewer than about 50 amino acid residues in length. In some embodiments, an immunogenic peptide sequence may have from about 8 to about 12 amino acids. In some embodiments, a mixture of human protein fragments may be used; alternatively a particular peptide of defined sequence may be used. The peptide antigens may be produced by de novo peptide synthesis, enzymatic digestion of purified or recombinant human peptides, by purification of the peptide sequence from a natural source (e.g., a subject or tumor cells from a subject), or expression of a recombinant polynucleotide encoding a human peptide fragment.

[00186] In some embodiments, the amount of peptide used for pulsing DC may depend on the nature, size and purity of the peptide or polypeptide. In some embodiments, an amount of from about 0.05 ug/ml to about 1 mg/ml, from about 0.05 ug/ml to about 500 ug/ml, from about 0.05 ug/ml to about 250 ug/ml, from about 0.5 ug/ml to about 1 mg/ml, from about 0.5 ug/ml to about 500 ug/ml, from about 0.5 ug/ml to about 250 ug/ml, or from about 1 ug/ml to about 100 ug/ml of peptide may be used. After adding the peptide antigen(s) to the cultured DC, the cells may then be allowed sufficient time to take up and process the antigen and express antigen peptides on the cell surface in association with either class I or class II MHC. In some embodiments, the time to take up and process the antigen may be about 18 to about 30 hours, about 20 to about 30 hours, or about 24 hours.

[00187] Numerous examples of systems and methods for predicting peptide binding motifs for different MHC Class I and II molecules have been described. Such prediction could be used for predicting peptide motifs that will bind to the desired MHC Class I or II molecules. Examples of such methods, systems, and databases that those of ordinary skill in the art might consult for such purpose include NIH's Center for Information Technology and Peptide Binding Motifs for MHC Class I and II Molecules; William E. Biddison, Roland Martin, Current Protocols in Immunology, Unit 11 (DOI: 10.1002/0471142735.ima01is36; Online Posting Date: May, 2001), which provides an overview of the use of peptide-binding motifs to predict interaction with a specific MHC class I or II allele, and gives examples for the use of MHC binding motifs to predict T-cell recognition.

[00188] Table 1 provides an exemplary result for a HLA peptide motif search at the NIH Center for Information Technology website, BioInformatics and Molecular Analysis Section. The full length MAGEA10 peptide sequence (SEQ ID NO: 56 as shown in Table 3 and 5) was used as the search query.

[00189] In some embodiments, the present invention provides methods of eliciting an immune response against cells expressing a cancer associated sequence comprising contacting a subject with a a cancer associated sequence under conditions effective to elicit an immune response in the subject, wherein said cancer associated sequence comprises a sequence or fragment thereof a gene selected from the group consisting of MAGEA10, DSCR8, MMP12, CXCL9, DSCR8, KRT81, LOC729826, PTHLH, MMP11, S100A7, WISP3, CXCL10, NMU, GBP5, TOP2A, SERPINB4, GNLY, GTSF1, PI3, S100A7A, IDO1, GJB6, CALML3, SERPINB3, CXCL6, OLFM4, TCN1, VSNL1, UBD, AIM2, ABCC9, SERPINB13, INDO, KRT5, LOC100130897, KRT14, FAM83A, FAM181B, GZMB, DSG3, TYMP, KRT6A, KRT6B, HLA-DRB1, LCN2, KRT4, IFI30, LOC100134370, KIAA1618, S100A8, MMP7, MMP7, SPRR2A, and GJB2.

IMMUNOTHERAPY

[00190] In some embodiments, implementation of an immunotherapy strategy for treating, reducing the symptoms of, or preventing cancer or neoplasms, (e.g., a vaccine) may be achieved using many different techniques available to the skilled artisan.

[00191] Immunotherapy, or the use of antibodies for therapeutic purposes has been used in recent years to treat cancer. Passive immunotherapy involves the use of monoclonal antibodies in cancer treatments. See for example, Cancer: Principles and Practice of Oncology, 6th Edition (2001) Chapt. 20 pp. 495-508. Inherent therapeutic biological activity of these antibodies include direct inhibition of tumor cell growth or survival, and the ability to recruit the natural cell killing activity of the body's immune system. These agents may be administered alone or in conjunction with radiation or chemotherapeutic agents. Alternatively, antibodies may be used to make antibody conjugates where the antibody is linked to a toxic agent and directs that agent to the tumor by specifically binding to the tumor.

[00192] Some embodiments also provide for antigens (cancer-associated polypeptides) associated with a variety of cancers, including bladder cancer, as targets for diagnostic and/or

therapeutic antibodies. These antigens may also be useful for drug discovery (e.g., small molecules) and for further characterization of cellular regulation, growth, and differentiation.

TABLE 1

User Parameters and Scoring Information	
method selected to limit number of results	explicit number
number of results requested	20
HLA molecule type selected	A_0201
length selected for subsequences to be scored	9
echoing mode selected for input sequence	Y
echoing format	numbered lines
length of user's input peptide sequence	369
number of subsequence scores calculated	361
number of top-scoring subsequences reported back in scoring output table	20

Scoring Results			
Rank	Start Position	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1	310	SLLKFLAKV	2249.173
2	183	HLVFGIDV	1662.432
3	137	KVTDLVQFL	339.313
4	254	GLYDGMHL	315.870
5	228	ILILSIIFI	224.357
6	296	FLMGPRANA	189.678
7	245	VIWEALNMM	90.891
8	308	KMSLLKFLA	72.836
9	166	KNYEDHFPL	37.140
10	201	FVLVTSLGL	31.814
11	174	LLFSEASEC	31.249
12	213	GHLSDVQSH	30.534
13	226	ILILILSI	16.725
14	225	GILILILSI	12.208
15	251	NRMGLYDGH	9.758
16	88	QIACSSPSV	9.563
17	66	LIFSTFEV	7.966
18	220	SNERTGILI	7.535
19	233	IIFIEGYCT	6.445
20	247	WEALNMGGL	4.395

Rank 1-20 are assigned SEQ ID NOS: 198-217 respectively

TABLE 2

SEQ ID NO:	Symbol	Definition	mRNA Sequence
------------	--------	------------	---------------

1	MAGEA10	Homo sapiens melanoma antigen family A, 10 (MAGEA10), transcript variant 2, mRNA.	NM_021048.3
2	DSCR8	Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 2, mRNA.	NM_203428.1
3	MMP12	Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12), mRNA.	NM_002426.2
4	CXCL9	Homo sapiens chemokine (C-X-C motif) ligand 9 (CXCL9), mRNA.	NM_002416.1
5	DSCR8	Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 3, mRNA.	NM_203429.1
6	KRT81	Homo sapiens keratin 81 (KRT81), mRNA.	NM_002281.2
7	LOC729826	PREDICTED: Homo sapiens hypothetical protein LOC729826 (LOC729826), mRNA.	XM_001131447.1
8	PTH1H	Homo sapiens parathyroid hormone-like hormone (PTH1H), transcript variant 3, mRNA.	NM_198964.1
9	MMP11	Homo sapiens matrix metalloproteinase 11 (stromelysin 3) (MMP11), mRNA.	NM_005940.3
10	S100A7	Homo sapiens S100 calcium binding protein A7 (S100A7), mRNA.	NM_002963.3
11	WISP3	Homo sapiens WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1, mRNA.	NM_003880.2
12	CXCL10	Homo sapiens chemokine (C-X-C motif) ligand 10 (CXCL10), mRNA.	NM_001565.2
13	NMU	Homo sapiens neuromedin U (NMU), mRNA.	NM_006681.1
14	GBP5	Homo sapiens guanylate binding protein 5 (GBP5), mRNA.	NM_052942.2
15	TOP2A	Homo sapiens topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA.	NM_001067.2
16	SERPINB4	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), mRNA.	NM_002974.2
17	GNLY	Homo sapiens granulysin (GNLY), transcript variant 519, mRNA.	NM_012483.1
18	GTSF1	Homo sapiens gametocyte specific factor 1 (GTSF1), mRNA.	NM_144594.1
19	PI3	Homo sapiens peptidase inhibitor 3, skin-derived (SKALP) (PI3), mRNA.	NM_002638.2
20	S100A7A	Homo sapiens S100 calcium binding protein A7A (S100A7A), mRNA.	NM_176823.3
21	IDO1	Homo sapiens indoleamine 2,3-dioxygenase 1 (IDO1), mRNA.	NM_002164.4
22	GJB6	Homo sapiens gap junction protein, beta 6 (GJB6), mRNA.	NM_006783.2
23	CALML3	Homo sapiens calmodulin-like 3 (CALML3), mRNA.	NM_005185.2
24	SERPINB3	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 3 (SERPINB3), mRNA.	NM_006919.1

25	CXCL6	Homo sapiens chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6), mRNA.	NM_002993.2
26	OLFM4	Homo sapiens olfactomedin 4 (OLFM4), mRNA.	NM_006418.3
27	TCN1	Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1), mRNA.	NM_001062.3
28	VSNL1	Homo sapiens visinin-like 1 (VSNL1), mRNA.	NM_003385.4
29	UBD	Homo sapiens ubiquitin D (UBD), mRNA.	NM_006398.2
30	AIM2	Homo sapiens absent in melanoma 2 (AIM2), mRNA.	NM_004833.1
31	ABCC9	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B, mRNA.	NM_020297.1
32	SERPINB13	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), mRNA.	NM_012397.2
33	INDO	Homo sapiens indoleamine-pyrrole 2,3 dioxygenase (INDO), mRNA.	NM_002164.3
34	KRT5	Homo sapiens keratin 5 (KRT5), mRNA.	NM_000424.3
35	LOC100130897	PREDICTED: Homo sapiens hypothetical LOC100130897 (LOC100130897), mRNA.	XM_001718498.1
36	KRT14	Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner) (KRT14), mRNA.	NM_000526.3
37	FAM83A	Homo sapiens family with sequence similarity 83, member A (FAM83A), transcript variant 1, mRNA.	NM_032899.4
38	FAM181B	Homo sapiens family with sequence similarity 181, member B (FAM181B), mRNA.	NM_175885.3
39		RST24587 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence	BG205162
40	GZMB	Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA.	NM_004131.3
41	DSG3	Homo sapiens desmoglein 3 (pemphigus vulgaris antigen) (DSG3), mRNA.	NM_001944.2
42	TYMP	Homo sapiens thymidine phosphorylase (TYMP), transcript variant 3, mRNA.	NM_001113756.1
43	KRT6A	Homo sapiens keratin 6A (KRT6A), mRNA.	NM_005554.3
44	KRT6B	Homo sapiens keratin 6B (KRT6B), mRNA.	NM_005555.3
45	HLA-DRB1	Homo sapiens major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA.	NM_002124.1
46	LCN2	Homo sapiens lipocalin 2 (LCN2), mRNA.	NM_005564.3
47	KRT4	Homo sapiens keratin 4 (KRT4), mRNA.	NM_002272.2
48	IFI30	Homo sapiens interferon, gamma-inducible protein 30 (IFI30), mRNA.	NM_006332.3
49	LOC100134370	PREDICTED: Homo sapiens hypothetical protein LOC100134370 (LOC100134370), mRNA.	XM_001713687.1
50	KIAA1618	Homo sapiens KIAA1618 (KIAA1618), mRNA.	NM_020954.2

51	S100A8	Homo sapiens S100 calcium binding protein A8 (S100A8), mRNA.	NM_002964.3
52	MMP7	Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), mRNA.	NM_002423.3
53	MMP7	Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), mRNA.	NM_002423.3
54	SPRR2A	Homo sapiens small proline-rich protein 2A (SPRR2A), mRNA.	NM_005988.2
55	GJB2	Homo sapiens gap junction protein, beta 2, 26kDa (GJB2), mRNA.	NM_004004.4

TABLE 3

SEQ ID NO:	Symbol	Definition	Peptide Sequence
56	MAGEA10	Homo sapiens melanoma antigen family A, 10 (MAGEA10), transcript variant 2	NP_066386.1
57	DSCR8	Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 2	NP_982252.1
58	MMP12	Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12)	NP_002417.2
59	CXCL9	Homo sapiens chemokine (C-X-C motif) ligand 9 (CXCL9)	NP_002407.1
60	DSCR8	Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 3.	NP_982253.1
61	KRT81	Homo sapiens keratin 81 (KRT81).	NP_002272.1
62	LOC729826	PREDICTED: Homo sapiens hypothetical protein LOC729826 (LOC729826).	XP_001131447.1
63	PTHLH	Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 3	NP_945315.1
64	MMP11	Homo sapiens matrix metalloproteinase 11 (stromelysin 3) (MMP11)	NP_005931.2
65	S100A7	Homo sapiens S100 calcium binding protein A7 (S100A7)	NP_002954.2
66	WISP3	Homo sapiens WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1	NP_003871.1
67	CXCL10	Homo sapiens chemokine (C-X-C motif) ligand 10 (CXCL10)	NP_001556.2
68	NMU	Homo sapiens neuromedin U (NMU)	NP_006672.1
69	GBP5	Homo sapiens guanylate binding protein 5 (GBP5)	NP_443174.1
70	TOP2A	Homo sapiens topoisomerase (DNA) II alpha 170kDa (TOP2A)	
71	SERPINF4	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 4 (SERPINF4)	NP_002965.1

72	GNLY	Homo sapiens granulysin (GNLY), transcript variant 519	NP_036615.1
73	GTSF1	Homo sapiens gametocyte specific factor 1 (GTSF1)	NP_653195.1
74	PI3	Homo sapiens peptidase inhibitor 3, skin-derived (SKALP) (PI3)	NP_002629.1
75	S100A7A	Homo sapiens S100 calcium binding protein A7A (S100A7A)	NP_789793.1
76	IDO1	Homo sapiens indoleamine 2,3-dioxygenase 1 (IDO1)	NP_002155.1
77	GJB6	Homo sapiens gap junction protein, beta 6 (GJB6)	NP_006774.2
78	CALML3	Homo sapiens calmodulin-like 3 (CALML3)	NP_005176.1
79	SERPINB3	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 3 (SERPINB3)	NP_008850.1
80	CXCL6	Homo sapiens chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6)	NP_002984.1
81	OLFM4	Homo sapiens olfactomedin 4 (OLFM4)	NP_006409.3
82	TCN1	Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1)	NP_001053.2
83	VSNL1	Homo sapiens visinin-like 1 (VSNL1)	NP_003376.2
84	UBD	Homo sapiens ubiquitin D (UBD)	NP_006389.1
85	AIM2	Homo sapiens absent in melanoma 2 (AIM2)	NP_004824.1
86	ABCC9	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B	NP_064693.1
87	SERPINB13	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 13 (SERPINB13)	NP_036529.1
88	INDO	Homo sapiens indoleamine-pyrrole 2,3 dioxygenase (INDO)	NP_002155.1
89	KRT5	Homo sapiens keratin 5 (KRT5)	NP_000415.2
90	LOC100130897	PREDICTED: Homo sapiens hypothetical LOC100130897 (LOC100130897)	XP_001718550.1
91	KRT14	Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner) (KRT14)	NP_000517.2
92	FAM83A	Homo sapiens family with sequence similarity 83, member A (FAM83A), transcript variant 1	NP_116288.2
93	FAM181B	Homo sapiens family with sequence similarity 181, member B (FAM181B)	NP_787081.2
94		RST24587 Athersys RAGE Library Homo sapiens cDNA	

95	GZMB	Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB)	NP_004122.1
96	DSG3	Homo sapiens desmoglein 3 (pemphigus vulgaris antigen) (DSG3)	NP_001935.2
97	TYMP	Homo sapiens thymidine phosphorylase (TYMP), transcript variant 3	NP_001107228.1
98	KRT6A	Homo sapiens keratin 6A (KRT6A)	NP_005545.1
99	KRT6B	Homo sapiens keratin 6B (KRT6B)	NP_005546.2
100	HLA-DRB1	Homo sapiens major histocompatibility complex, class II, DR beta 1 (HLA-DRB1)	NP_002115.1
101	LCN2	Homo sapiens lipocalin 2 (LCN2)	NP_005555.2
102	KRT4	Homo sapiens keratin 4 (KRT4)	NP_002263.2
103	IFI30	Homo sapiens interferon, gamma-inducible protein 30 (IFI30)	NP_006323.2
104	LOC100134370	PREDICTED: Homo sapiens hypothetical protein LOC100134370 (LOC100134370)	XP_001713739.1
105	KIAA1618	Homo sapiens KIAA1618 (KIAA1618)	NP_066005.2
106	S100A8	Homo sapiens S100 calcium binding protein A8 (S100A8)	NP_002955.2
107	MMP7	Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7)	NP_002414.1
108	MMP7	Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7)	NP_002414.1
109	SPRR2A	Homo sapiens small proline-rich protein 2A (SPRR2A)	NP_005979.1
110	GJB2	Homo sapiens gap junction protein, beta 2, 26kDa (GJB2)	NP_003995.2

TABLE 4

SEQ ID No.	Probe Sequence	Symbol
111	GCCATGGCCAGTGCAAGTTCTAGCGCTACAGGTAGCTTCTCCTACCCTGA	MAGEA10
112	TCCCACTTGGCAGGGGCCGTCCTGTCCACTCGTTTCTGTAAACATGGGTG	DSCR8
113	TCTATTTGAAGCATGCTCTGTAAGTTGCTTCCTAACATCCTTGGACTGAG	MMP12
114	TGATTGGTGCCAGTTAGCCTCTGCAGGATGTGGAAACCTCCTCCAGGG	CXCL9
115	GAAGGCTGGCTCATAATTTCCAGACAGGAATTTGGCTGCCAACAGGG	DSCR8
116	CAGTGGGAAAGGCCACCTAGAAAGAAGTCCGCTGGCACCCATAGGAAGG	KRT81
117	CCTGCAGACACCGAGGCCTCTGCTGTGGCTGCCCACTGGCTGTGCTCAG	LOC729826
118	TGGTTAGACTCTGGAGTGAAGTGGGCTAGAAGGGGACCACCTGTC	PTHLH
119	CAGGTCTTGGTAGGTGCCTGCATCTGTCTGCCTTCTGGCTGACAATCCTG	MMP11
120	GCTGAGAGGTCCATAATAGCATGATCGACATGTTTCACAAATACACCAG	S100A7

121	GCTGTGGATTACATCTTGTGTGTGTCAGAGAACTGCAGAGAACCTGGAG	WISP3
122	GACTTCCACTGCCATCCTCCCAAGGGGCCCAAATTCTTTCAGTGGCTACC	CXCL10
123	GCTGCAGCTCGTTCCTCACCTGCATGAGAGAAGAATGAAGAGATTGAGAG	NMU
124	GCAGGAACAACAGATGCAGGAACAGGCTGCACAGCTCAGCACAACATTCC	GBP5
125		TOP2A
126	GCATGACCTGGAGCCACGGTCTCTCAGTATCTAAAGTCCTACACAAGGCC	SERPINB4
127	CTACAGGTCCCCTCTGAGCCCTCTCACCTTGTCTGTGGAAGAAGCACAG	GNLY
128	GGGGCACAACTCACTACTCTGACAACAACAGCCCTGCGAGCAACATAGTT	GTSF1
129	CTGACTGCCCAGGAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCC	PI3
130	AGAGTTCTGACCAGCACCAGATAAGCTTCAGTGCTCTCCTTTCTTTGGCC	S100A7A
131	CGCCTGTGTGAAAGCTCTGGTCTCCCTGAGGAGCTACCATCTGCAAATCG	IDO1
132	GCTGCGTCATAAGGAGACTTCTGTCTTCTCCAGAAGGCAATACCAACCTG	GJB6
133	AAAACAGCACTGCCCTTCCGCGCTGCCCCAGCTTGCCCCATTCTTGTCCG	CALML3
134	TGACCGGGAGCCGCGGTCTCGTGCTATCTGGAGTCCTACACAAGGCCTTT	SERPINB3
135	GTGTGCTGTTGAGGGAGGTATCCTGTTGTCTTACTCACTCTTCTCATAA	CXCL6
136	TGTTCAAGTCCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCC	OLFM4
137	TGAGTGGAGGCGAACCCTGAGCCAAGGAGCTGGTAGTTACGTTGTCCGC	TCN1
138	GAGGGACCCCTGGCTCCTGTGTCTGGTCCACACACCACAGAAGCTTGTAT	VSNL1
139	CCTCCTCCAGGTGCGAAGGTCCAGCTCAGTGGCACAAGTGAAAGCAATGA	UBD
140	GCTGGTGAAACCCCGAAGATCAACACGCTTCAAACCTCAGCCCCCTGGAAC	AIM2
141	CGAGTACACACTATTCTGACGGCAGACCTGGTTATTGTGATGAAGCGAGG	ABCC9
142	CTAGGTTACCAGTTGAGGGACATTTGGATTGTTCCCACTTCTTGGGCTG	SERPINB13
143	CTGATTCTGCAAGCCAGCAGCCAAAGGAGAATAAGACCTCTGAAGACCC	INDO
144	ACCACATTCTTTGGTTCCAGGAGAGCCCCATTCCCAGCCCCCTGGTCTCC	KRT5
145	TGCTGCTGGAAGCCTCCAAAGTACTTAGTGCTATTGTTTCCCCTGTGTG	LOC100130897
146	GTGGACACAGATCCCCTGGAAGATCCCCTCTCCTGCCCAAGCACTTCAC	KRT14
147	CAGCCTGGTCACCTCCTGAGGAATAAATGCTGAACCTCACAAGCCCCATC	FAM83A
148	GCTGGCTTCTGTAGCCACCTGTCCCTTCTATTTTTCAGCGAAGGTCAGTG	FAM181B
149	CCTGTGGCAAGCCAGCAAGATGGCCCTGGTGACAGCAAAAAGAACTGCAC	
150	ACAGGAAGCAAACCTAAGCCCCCGCTGTAATGAAACACCTTCTCTGGAGCC	GZMB
151	CAGAAAGGGTGATCTGTCCCATTTCCAGTGTTCTGGCAACCTAGCTGGC	DSG3
152	AGAACTCGTGGAGGGGCTGTCCGCTCTGGTGGTGACGTTAAGTTCGGA	TYMP
153	GTGTTGTGAACCCCCACCCAGGCAGTATCCATGAAAGCACAAGTGACTAG	KRT6A
154	CTCTTGCAGTGTCCCTGAATGGCAAGTGATGTACCTTCTGATGCAGTCTG	KRT6B
155	GGACTTCAGCCAACAGGATTCTGAGCTGAAATGCAGATGACCACATTCA	HLA-DRB1
156	CCACATCGTCTTCCCTGTCCCAATCGACCAGTGTATCGACGGCTGAGTGC	LCN2
157	CCAGGATGATCTTCTGTGCTGGGACAGGGACTCTGCCTCTTGGAGTTTGG	KRT4
158	TGGAAGATCAGACCCAGCTCCTTACCCTTGTCTGCCAGTTGTACCAGGGC	IFI30

159	CTACAGGCGCCTGCTGGAGGGCGAGGAGCATAGGCTGTGTGAAGGTGTTG	LOC100134370
160	CCCCGTTTATCCATGTGTCCATTGACGGCCATCTATGTTGCTTCTTCGGC	KIAA1618
161	TAACTTCCAGGAGTTCCTCATTCTGGTGATAAAGATGGGCGTGGCAGCCC	S100A8
162	GCTCACTTCGATGAGGATGAACGCTGGACGGATGGTAGCAGTCTAGGGAT	MMP7
163	GCAACTCATGAACTTGGCCATTCTTTGGGTATGGGACATTCTCTGATCC	MMP7
164	GCTCCACCTTCATCTTCTCATCAAAGCCTACCATGGATACACAGGGAGCT	SPRR2A
165	GATGAGCTTTGTCTACTTCAAAAGTTTGTGTTGCTTACCCCTTCAGCCTCC	GJB2

CANCER THERAPEUTICS

[00193] In some embodiments, the cancer cell may be targeted specifically with a therapeutic based upon the differentially expressed gene or gene product. For example, in some embodiments, the differentially expressed gene product is an enzyme, which can convert a anti-cancer prodrug into its active form. Therefore, in normal cells, where the differentially expressed gene product is not expressed or expressed at significantly lower levels, the prodrug is either not activated or activated in a lesser amount, and is, therefore less toxic to normal cells. Therefore, the cancer prodrug can, in some embodiments, be given in a higher dosage so that the cancer cells can metabolize the prodrug, which will, for example, kill the cancer cell, and the normal cells will not metabolize the prodrug or not as well, and, therefore, be less toxic to the patient. An example of this is where tumor cells overexpress a metalloprotease, which is described in Atkinson *et al.*, British Journal of Pharmacology (2008) 153, 1344–1352. Using proteases to target cancer cells is also described in Carl *et al.*, *PNAS*, Vol. 77, No. 4, pp. 2224–2228, April 1980. For example, doxorubicin or other type of chemotherapeutic can be linked to a peptide sequence that is specifically cleaved or recognized by the differentially expressed gene product. The doxorubicin or other type of chemotherapeutic is then cleaved from the peptide sequence and is activated such that it can kill or inhibit the growth of the cancer cell whereas in the normal cell the chemotherapeutic is never internalized into the cell or is not metabolized as efficiently, and is, therefore, less toxic.

[00194] In some embodiments, a method of treating cancer may comprise gene knockdown of one or more cancer associated sequences described herein. Gene knockdown refers to techniques by which the expression of one or more of an organism's genes is reduced, either through genetic modification (a change in the DNA of one of the organism's chromosomes such as, without limitation, chromosomes encoding cancer associated sequences) or by treatment with a reagent such as a short DNA or RNA oligonucleotide with a sequence complementary to

either an mRNA transcript or a gene. In some embodiments, the oligonucleotide used may be selected from RNase-H competent antisense, such as, without limitation, ssDNA oligonucleotides, ssRNA oligonucleotides, phosphorothioate oligonucleotides, or chimeric oligonucleotides; RNase-independent antisense, such as morpholino oligonucleotides, 2'-O-methyl phosphorothioate oligonucleotides, locked nucleic acid oligonucleotides, or peptide nucleic acid oligonucleotides; RNAi oligonucleotides, such as, without limitation, siRNA duplex oligonucleotides, or shRNA oligonucleotides; or any combination thereof. In some embodiments, a plasmid may be introduced into a cell, wherein the plasmid expresses either an antisense RNA transcript or an shRNA transcript. The oligo introduced or transcript expressed may interact with the target mRNA (ex. SEQ ID NOs. 1-55) by complementary base pairing (a sense-antisense interaction).

[00195] The specific mechanism of silencing may vary with the oligo chemistry. In some embodiments, the binding of a oligonucleotide described herein to the active gene or its transcripts may cause decreased expression through blocking of transcription, degradation of the mRNA transcript (e.g. by small interfering RNA (siRNA) or RNase-H dependent antisense) or blocking either mRNA translation, pre-mRNA splicing sites or nuclease cleavage sites used for maturation of other functional RNAs such as miRNA (e.g. by Morpholino oligonucleotides or other RNase-H independent antisense). For example, RNase-H competent antisense oligonucleotides (and antisense RNA transcripts) may form duplexes with RNA that are recognized by the enzyme RNase-H, which cleaves the RNA strand. As another example, RNase-independent oligonucleotides may bind to the mRNA and block the translation process. application In some embodiments, the oligonucleotides may bind in the 5'-UTR and halt the initiation complex as it travels from the 5'-cap to the start codon, preventing ribosome assembly. A single strand of RNAi oligonucleotides may be loaded into the RISC complex, which catalytically cleaves complementary sequences and inhibits translation of some mRNAs bearing partially-complementary sequences. The oligonucleotides may be introduced into a cell by any technique including, without limitation, electroporation, microinjection, salt-shock methods such as, for example, CaCl₂ shock; transfection of anionic oligo by cationic lipids such as, for example, Lipofectamine; transfection of uncharged oligonucleotides by endosomal release agents such as, for example, Endo-Porter; or any combination thereof. In some embodiments, the oligonucleotides may be delivered from the blood to the cytosol using techniques selected from

nanoparticle complexes, virally-mediated transfection, oligonucleotides linked to octaguanidinium dendrimers (Morpholino oligonucleotides), or any combination thereof.

[00196] In some embodiments, a method of treating bladder cancer may comprise treating cells to knockdown or inhibit expression of a gene encoding the mRNA disclosed in SEQ ID NOs. 1-55. The method may comprise culturing hES cell-derived clonal embryonic progenitor cell lines CM02 and EN13 (see U.S. Patent Publication 20080070303, entitled "Methods to accelerate the isolation of novel cell strains from pluripotent stem cells and cells obtained thereby"; and U.S. patent application Ser. No. 12/504,630 filed on July 16, 2009 and titled "Methods to Accelerate the Isolation of Novel Cell Strains from Pluripotent Stem Cells and Cells Obtained Thereby", each of which is incorporated by reference herein in its entirety) with a retrovirus expressing silencing RNA directed to a cancer-associated sequence. In some embodiments, the method may further comprise confirming down-regulation by qPCR. In some embodiments, the method further comprises cryopreserving the cells. In some embodiments, the method further comprises reprogramming the cells. In some embodiments, the method comprises cryopreserving or reprogramming the cells within two days by the exogenous administration of OCT4, MYC, KLF4, and SOX2 (see Takahashi and Yamanaka 2006 Aug 25;126(4):663-76; U.S. Patent Application Serial No. 12/086,479, published as US2009/0068742 and entitled "Nuclear Reprogramming Factor") and by the method described in PCT/US06/30632, published as WO/2007/019398 and entitled "Improved Methods of Reprogramming Animal Somatic Cells". In some embodiments, the method may comprise culturing mammalian differentiated cells under conditions that promote the propagation of ES cells. In some embodiments, any convenient ES cell propagation condition may be used, e.g., on feeders or in feeder free media capable of propagating ES cells. In some embodiments, the method comprises identifying cells from ES colonies in the culture. Cells from the identified ES colony may then be evaluated for ES markers, e.g., Oct4, TRA 1-60, TRA 1-81, SSEA4, etc., and those having ES cell phenotype may be expanded. Control lines that have not been preconditioned by the knockdown may be reprogrammed in parallel to demonstrate the effectiveness of the preconditioning.

[00197] In some embodiments, a method for treating bladder cancer comprises administering to a subject in need thereof a therapeutic agent modulating the activity of a cancer associated protein (CAP), wherein said CAP is encoded by a nucleic acid comprising a nucleic

acid sequence selected from the group consisting of the human nucleic acid sequences in Table 2 and further wherein the therapeutic agent binds to the cancer associated protein; wherein the cancer associated protein is selected from the group consisting of SEQ ID NOs: 56-110 shown in Table 3.

[00198] In some embodiments, a method of treating bladder cancer comprises administering an antibody (*e.g.* monoclonal antibody, human antibody, humanized antibody, chimeric antibody, and the like) that specifically binds to a cancer associated protein (CAP) that is expressed on a cell surface, wherein the cancer associated protein is selected from the group consisting of SEQ ID NOs: 56-110. In some embodiments, the antibody binds to an extracellular domain of the cancer associated protein. In some embodiments, the antibody binds to a cancer associated protein differentially expressed on a cancer cell surface relative to a normal cell surface, or, in some embodiments, to at least one human cancer cell line. In some embodiments, the antibody is linked to a therapeutic agent. Kits and pharmaceutical compositions for detecting a presence or an absence of cancer cells in a subject, and comprising such antibodies are also provided.

[00199] In some embodiments the invention provides a method for inhibiting growth of cancer cells in a subject. In some embodiments, the method comprises administering to the subject an effective amount of a pharmaceutical composition as described herein. In some embodiments the invention provides a method for delivering a therapeutic agent to cancer cells in a subject, the method comprising: administering to the subject an effective amount of a pharmaceutical composition according to the invention.

METHODS OF ANALYZING A SAMPLE

[00200] The pattern of gene expression in a particular living cell may be characteristic of its current state. Nearly all differences in the state or type of a cell are reflected in the differences in RNA levels of one or more genes. Comparing expression patterns of uncharacterized genes may provide clues to their function. High throughput analysis of expression of hundreds or thousands of genes can help in (a) identification of complex genetic diseases, (b) analysis of differential gene expression over time, between tissues and disease states, and (c) drug discovery and toxicology studies. Increase or decrease in the levels of expression of certain genes correlate with cancer biology. For example, oncogenes are positive regulators of tumorigenesis, while tumor suppressor genes are negative regulators of

tumorigenesis. (Marshall, Cell, 64: 313-326 (1991); Weinberg, Science, 254: 1138-1146 (1991)). Accordingly, some embodiments herein provide for polynucleotide and polypeptide sequences involved in cancer and, in particular, in oncogenesis.

[00201] Oncogenes are genes that can cause cancer. Carcinogenesis can occur by a wide variety of mechanisms, including infection of cells by viruses containing oncogenes, activation of protooncogenes in the host genome, and mutations of protooncogenes and tumor suppressor genes. Carcinogenesis is fundamentally driven by somatic cell evolution (i.e. mutation and natural selection of variants with progressive loss of growth control). The genes that serve as targets for these somatic mutations are classified as either protooncogenes or tumor suppressor genes, depending on whether their mutant phenotypes are dominant or recessive, respectively.

[00202] The detection of the expression level of the one or more markers disclosed infra may be by any means known in the art. For example where the marker is a protein associated with breast cancer an ELISA may be used to detect the expression level of the marker. Other suitable assays for detecting the presence of a protein marker include a radio-immunoassay, a western blot, an immunoprecipitation assay, such as a bead based assay, e.g. a magnetic bead based assay. In some embodiments the marker may be isolated from the sample before detection, but in other embodiments it is not isolated from the sample. In some embodiments the protein marker may be expressed in a cellular context (i.e. on the surface of the cell or within the cell). In these instances immunocytochemistry may be used to detect the marker. Alternatively, the flow cytometry can be used to detect the marker. Where the marker is contained within the cell, the cells may be treated with a detergent to make the marker accessible to a detection reagent. Suitable detection reagents would include any molecule that specifically binds the marker, such as an antibody that specifically binds to an epitope on the marker.

[00203] Suitable agents for detecting a protein marker as disclosed infra include any specific binding partner of the breast cancer marker. For example the specific binding partner may be a protein that binds the breast cancer marker, such as an antibody. Other suitable specific binding partners may include a receptor that binds the breast cancer marker or an enzyme that specifically binds the breast cancer marker.

[00204] The cancer can also be diagnosed to a specific tissue type as well by visualizing the labeled molecule. The molecule can be visualized or detected using any method, such as but not limited to, MRI, CAT scan, PET scan, and the like. In some embodiments, an antibody can

bind to the protein and then be detected. In some embodiments, the level of antibody binding can be quantified to determine whether the protein is overexpressed. Differential expression can also be determined by known methods. Accordingly, embodiments hereof provide a method for imaging structures in tissues and cells of a subject having cancer, is suspected of having cancer, or is undergoing a diagnostic procedure to determine if the person has cancer. If the imaging demonstrates that the cancer associated protein is overexpressed or differentially expressed then the patient is diagnosed as having cancer or suspected of having cancer. Other tests can also be done, such as but not limited to, a biopsy to confirm, or otherwise aid, the diagnosis.

[00205] The label molecules can also be labeled by, but not limited to, any radioisotopes that can be imaged with a PET or SPECT camera. For example, radiopharmaceuticals of various embodiments may be radiolabeled with radioisotopes such as, but not limited to, ^{76}Br , ^{123}I , ^{125}I , ^{131}I , $^{99\text{m}}\text{Tc}$, ^{11}C , ^{18}F , or other gamma- or positron-emitting radionuclides. In other embodiments, the label molecules may be radiolabeled with a combination of radioisotopes.

[00206] In some embodiments the marker associated with breast cancer may be a nucleic acid, e.g. an mRNA molecule. The nucleic acid may be isolated from the sample. Detection of the nucleic acid may be by any means known in the art. For example the nucleic acid molecule may be detected by Southern blot or northern blot mass spectroscopy, microarray and the like. The nucleic acid may be detected using PCR, for example where the nucleic acid is an RNA molecule, such as an mRNA molecule, rtPCR may be used. The PCR may be quantitative PCR (e.g. qPCT) or real time PCR. The nucleic acid may be detected by in situ hybridization where the sample includes breast cancer cells.

[00207] The assays described above may include the use of a probe to detect the nucleic acid marker. Probes are described infra. Briefly, the probe may be a nucleic acid molecule ranging from 5-40, 10-35, 15-30 nucleotides long. The probe may be about 5, about 10, about 20, about 25, about 30, about 35 nucleotides long. The probe may include a portion of a gene encoding the breast cancer marker, or a complement of a gene encoding a breast cancer marker.

[00208] It will be appreciated that there are various methods of obtaining expression data and uses of the expression data. For example, the expression data that can be used to detect or diagnose a subject with cancer can be obtained experimentally. In some embodiments, obtaining the expression data comprises obtaining the sample and processing the sample to experimentally determine the expression data. The expression data can comprise expression data for one or

more of the cancer associated sequences described herein. The expression data can be experimentally determined by, for example, using a microarray or quantitative amplification method such as, but not limited to, those described herein. In some embodiments, obtaining expression data associated with a sample comprises receiving the expression data from a third party that has processed the sample to experimentally determine the expression data.

[00209] The use of microarray analysis of gene expression allows the identification of sequences associated with cancer. These sequences may then be used in a number of different ways, including diagnosis, prognosis, screening for modulators (including both agonists and antagonists), antibody generation (for immunotherapy and imaging), etc. However, as will be appreciated by those skilled in the art, sequences that are identified in one type of cancer may have a strong likelihood of being involved in other types of cancers as well. Thus, while the sequences outlined herein are initially identified as correlated with bladder cancer, they may also be found in other types of cancers as well.

[00210] The comparison of gene expression on an mRNA level using Illumina gene expression microarrays hybridized to RNA probe sequences (SEQ ID NOs: 111-165, shown in Table 4) prepared from the diverse categories of cell types: 1) human embryonic stem ("ES") cells, or gonadal tissues 2) ES, iPS, or EC-derived clonal embryonic progenitor ("EP") cell lines, 3) nucleated blood cells including but not limited to CD34+ cells and CD133+ cells; 4) Normal mortal somatic adult-derived tissues and cultured cells including: skin fibroblasts, vascular endothelial cells, normal non-lymphoid and non-cancerous tissues, and the like, and 5) malignant cancer cells including cultured cancer cell lines or human tumor tissue and filters was performed to detect genes that are generally expressed (or not expressed) in categories 1, 3, and 5, or categories 1 and 5 but not expressed (or expressed) in categories 2 and 4. Therapies in these cancers based on this observation would be based on reducing the expression of the above referenced transcripts up-regulated in cancer, or otherwise reducing the expression of the gene products.

[00211] Gene Expression Assays: Measurement of the gene expression levels may be performed by any known methods in the art, including but not limited to quantitative PCR, or microarray gene expression analysis, bead array gene expression analysis and Northern analysis. The gene expression levels may be represented as relative expression normalized to the *ADPRT* (Accession number NM_001618.2), *GAPD* (Accession number NM_002046.2), or other

housekeeping genes known in the art. In the case of microarrayed probes of mRNA expression, the gene expression data may also be normalized by a median of medians method. In this method, each array gives a different total intensity. Using the median value is a robust way of comparing cell lines (arrays) in an experiment. As an example, the median was found for each cell line and then the median of those medians became the value for normalization. The signal from the each cell line was made relative to each of the other cell lines.

[00212] RNA extraction. Cells from a suitable subject may be incubated with 0.05% trypsin and 0.5 mM EDTA, followed by collecting in DMEM (Gibco, Gaithersburg, MD) with 0.5% BSA. Total RNA is purified from cells using the RNeasy Mini kit (Qiagen, Hilden, Germany).

[00213] Isolation of total and miRNA may be obtained from human embryonic stem cells and differentiated progeny cells. Total RNA or samples enriched for small RNA species were isolated from cell cultures that underwent serum starvation prior to harvesting RNA to approximate cellular growth arrest observed in many mature tissues. Cellular growth arrest was performed by changing to medium containing 0.5% serum for 5 days, with one medium change 2-3 days after the first addition of low serum medium. RNA were harvested according to the vendors instructions for Qiagen RNeasy kits to isolate total RNA or Ambion mirVana kits to isolate RNA enriched for small RNA species. The RNA concentrations were determined by spectrophotometry and RNA quality determined by denaturing agarose gel electrophoresis to visualize 28S and 18S RNA. Samples with clearly visible 28S and 18S bands without signs of degradation and at a ratio of approximately 2:1, 28S:18S, were used for subsequent miRNA analysis.

[00214] Assay for miRNA in samples isolated from human embryonic stem cells and differentiated progeny cells. The miRNAs were quantitated using a Human Panel TaqMan MicroRNA Assay from Applied Biosystems, Inc. This is a two-step assay that uses stem-loop primers for reverse transcription (RT) followed by real-time TaqMan®. A total of 330 miRNA assays were performed to quantitate the levels of miRNA in the H9 human embryonic stem cell line, a differentiated fibroblast cell line, and nine cell lines differentiated from human embryonic stem cells. The assay includes two steps, reverse transcription (RT) and quantitative PCR. Real-time PCR was performed on an Applied Biosystems 7500 Real-Time PCR System. The copy

number per cell was estimated based on the standard curve of synthetic mir-16 miRNA and assuming a total RNA mass of approximately 15pg/cell.

[00215] The reverse transcription reaction was performed using 1x cDNA archiving buffer, 3.35 units MMLV reverse transcriptase, 5mM each dNTP, 1.3 units AB RNase inhibitor, 2.5 nM 330-plex reverse primer (RP), 3 ng of cellular RNA in a final volume of 5 μ l. The reverse transcription reaction was performed on a BioRad or MJ thermocycler with a cycling profile of 20 °C for 30 sec; 42 °C for 30 sec; 50 °C for 1 sec, for 60 cycles followed by one cycle of 85 °C for 5 min.

[00216] Real-time PCR. Two microlitres of 1:400 diluted Pre-PCR product is used for a 20 μ l reaction. All reactions are duplicated. Because the method is very robust, duplicate samples are sufficient and accurate enough to obtain values for miRNA expression levels. TaqMan universal PCR master mix of ABI is used according to manufacturer's suggestion. Briefly, 1x TaqMan Universal Master Mix (ABI), 1 μ M Forward Primer, 1 μ M Universal Reverse Primer and 0.2 μ M TaqMan Probe is used for each real-time PCR. The conditions used are as follows: 95°C for 10 min, followed by 40 cycles at 95°C for 15 s, and 60°C for 1 min. All the reactions are run on ABI Prism 7000 Sequence Detection System.

[00217] Microarray hybridization and data processing. cDNA samples and cellular total RNA (5 μ g in each of eight individual tubes) are subjected to the One-Cycle Target Labeling procedure for biotin labeling by in vitro transcription (IVT) (Affymetrix, Santa Clara, CA) or using the Illumina Total Prep RNA Labelling kit. For analysis on Affymetrix gene chips, the cRNA is subsequently fragmented and hybridized to the Human Genome U133 Plus 2.0 Array (Affymetrix) according to the manufacturer's instructions. The microarray image data are processed with the GeneChip Scanner 3000 (Affymetrix) to generate CEL data. The CEL data are then subjected to analysis with dChip software, which has the advantage of normalizing and processing multiple datasets simultaneously. Data obtained from the eight nonamplified controls from cells, from the eight independently amplified samples from the diluted cellular RNA, and from the amplified cDNA samples from 20 single cells are normalized separately within the respective groups, according to the program's default setting. The model based expression indices (MBEI) are calculated using the PM/MM difference mode with log-2 transformation of signal intensity and truncation of low values to zero. The absolute calls (Present, Marginal and Absent) are calculated by the Affymetrix Microarray Software 5.0 (MAS 5.0) algorithm using

the dChip default setting. The expression levels of only the Present probes are considered for all quantitative analyses described below. The GEO accession number for the microarray data is GSE4309. For analysis on Illumina Human HT-12 v4 Expression Bead Chips, labeled cRNA are hybridized according to the manufacturer's instructions.

[00218] Calculation of coverage and accuracy. A true positive is defined as probes called Present in at least six of the eight nonamplified controls, and the true expression levels are defined as the log-averaged expression levels of the Present probes. The definition of coverage is (the number of truly positive probes detected in amplified samples)/(the number of truly positive probes). The definition of accuracy is (the number of truly positive probes detected in amplified samples)/(the number of probes detected in amplified samples). The expression levels of the amplified and nonamplified samples are divided by the class interval of 20.5 (20, 20.5, 21, 21.5...), where accuracy and coverage are calculated. These expression level bins are also used to analyze the frequency distribution of the detected probes.

[00219] Analysis of gene expression profiles of cells. The unsupervised clustering and class neighbor analyses of the microarray data from cells are performed using GenePattern software available online from MIT, which performs the signal-to-noise ratio analysis/T-test in conjunction with the permutation test to preclude the contribution of any sample variability, including those from methodology and/or biopsy, at high confidence. The analyses are conducted on the 14,128 probes for which at least 6 out of 20 single cells provided Present calls and at least 1 out of 20 samples provided expression levels >20 copies per cell. The expression levels calculated for probes with Absent/Marginal calls were truncated to zero. To calculate relative gene expression levels, the Ct values obtained with Q-PCR analyses are corrected using the efficiencies of the individual primer pairs quantified either with whole human genome (BD Biosciences) or plasmids that contain gene fragments. The relative expression levels are further transformed into copy numbers with a calibration line calculated using the spike RNAs included in the reaction mixture ($\log_{10}[\text{expression level}] = 1.05 \times \log_{10}[\text{copy number}] + 4.65$). The Chi-square test for independence is performed to evaluate the association of gene expressions with Gata4, which represents the difference between cluster 1 and cluster 2 determined by the unsupervised clustering and which is restricted to PE at later stages. The expression levels of individual genes measured with Q-PCR are classified into three categories: high (>100 copies per cell), middle (10–100 copies per cell), and low (<10 copies per cell). The Chi-square and P-

values for independence from Gata4 expression are calculated based on this classification. Chi squared is defined as follows: $\chi^2 = \sum \sum (n_{ij} - f_i f_j)^2 / n_{ij}$, where i and j represent expression level categories (high, middle or low) of the reference (Gata4) and the target gene, respectively; f_i , f_j , and f_{ij} represent the observed frequency of categories i , j and ij , respectively; and n represents the sample number ($n = 24$). The degrees of freedom are defined as $(r - 1) \times (c - 1)$, where r and c represent available numbers of expression level categories of Gata4 and of the target gene, respectively.

EXPRESSION OF CANCER ASSOCIATED SEQUENCES IN CELLS

[00220] Electroporation may be used to introduce the cancer associated nucleic acids described herein into mammalian cells (Neumann, E. et al. (1982) *EMBO J.* 1, 841-845), plant and bacterial cells, and may also be used to introduce proteins (Marrero, M.B. et al. (1995) *J. Biol. Chem.* 270, 15734-15738; Nolkrantz, K. et al. (2002) *Anal. Chem.* 74, 4300-4305; Rui, M. et al. (2002) *Life Sci.* 71, 1771-1778). Cells (such as the cells of this invention) suspended in a buffered solution of the purified protein of interest are placed in a pulsed electrical field. Briefly, high-voltage electric pulses result in the formation of small (nanometer-sized) pores in the cell membrane. Proteins enter the cell via these small pores or during the process of membrane reorganization as the pores close and the cell returns to its normal state. The efficiency of delivery may be dependent upon the strength of the applied electrical field, the length of the pulses, temperature and the composition of the buffered medium. Electroporation is successful with a variety of cell types, even some cell lines that are resistant to other delivery methods, although the overall efficiency is often quite low. Some cell lines may remain refractory even to electroporation unless partially activated.

[00221] Microinjection may be used to introduce femtoliter volumes of DNA directly into the nucleus of a cell (Capecchi, M.R. (1980) *Cell* 22, 470-488) where it can be integrated directly into the host cell genome, thus creating an established cell line bearing the sequence of interest. Proteins such as antibodies (Abarzua, P. et al. (1995) *Cancer Res.* 55, 3490-3494; Theiss, C. and Meller, K. (2002) *Exp. Cell Res.* 281, 197-204) and mutant proteins (Naryanan, A. et al. (2003) *J. Cell Sci.* 116, 177-186) can also be directly delivered into cells via microinjection to determine their effects on cellular processes firsthand. Microinjection has the advantage of introducing macromolecules directly into the cell, thereby bypassing exposure to potentially undesirable cellular compartments such as low-pH endosomes.

[00222] Several proteins and small peptides have the ability to transduce or travel through biological membranes independent of classical receptor-mediated or endocytosis-mediated pathways. Examples of these proteins include the HIV-1 TAT protein, the herpes simplex virus 1 (HSV-1) DNA-binding protein VP22, and the *Drosophila* Antennapedia (Antp) homeotic transcription factor. In some embodiments, protein transduction domains (PTDs) from these proteins may be fused to other macromolecules, peptides or proteins such as, without limitation, a cancer associated polypeptide to successfully transport the polypeptide into a cell (Schwarze, S.R. et al (2000) *Trends Cell Biol.* 10, 290-295). Exemplary advantages of using fusions of these transduction domains is that protein entry is rapid, concentration-dependent and appears to work with difficult cell types (Fenton, M. et al. (1998) *J. Immunol. Methods* 212, 41-48.).

[00223] In some embodiments, liposomes may be used as vehicles to deliver oligonucleotides, DNA (gene) constructs and small drug molecules into cells (Zabner, J. et al. (1995) *J. Biol. Chem.* 270, 18997-19007; Felgner, P.L. et al. (1987) *Proc. Natl. Acad. Sci. USA* 84, 7413-7417). Certain lipids, when placed in an aqueous solution and sonicated, form closed vesicles consisting of a circularized lipid bilayer surrounding an aqueous compartment. The vesicles or liposomes of embodiments herein may be formed in a solution containing the molecule to be delivered. In addition to encapsulating DNA in an aqueous solution, cationic liposomes may spontaneously and efficiently form complexes with DNA, with the positively charged head groups on the lipids interacting with the negatively charged backbone of the DNA. The exact composition and/or mixture of cationic lipids used can be altered, depending upon the macromolecule of interest and the cell type used (Felgner, J.H. et al. (1994) *J. Biol. Chem.* 269, 2550-2561). The cationic liposome strategy has also been applied successfully to protein delivery (Zelphati, O. et al. (2001) *J. Biol. Chem.* 276, 35103-35110). Because proteins are more heterogeneous than DNA, the physical characteristics of the protein, such as its charge and hydrophobicity, may influence the extent of its interaction with the cationic lipids.

SCREENING ASSAYS FOR CANCER DRUGS

[00224] In some embodiments, a method of screening drug candidates includes comparing the level of expression of the cancer-associated sequence in the absence of the drug candidate to the level of expression in the presence of the drug candidate.

[00225] Some embodiments are directed to a method of screening for a therapeutic agent capable of binding to a cancer-associated sequence (nucleic acid or protein), the method comprising combining the cancer-associated sequence and a candidate therapeutic agent, and determining the binding of the candidate agent to the cancer-associated sequence.

[00226] Further provided herein is a method for screening for a therapeutic agent capable of modulating the activity of a cancer-associated sequence. In some embodiments, the method comprises combining the cancer-associated sequence and a candidate therapeutic agent, and determining the effect of the candidate agent on the bioactivity of the cancer-associated sequence. An agent that modulates the bioactivity of the cancer associate sequence is said to be a therapeutic agent capable of modulating the activity of the cancer-associated sequence

[00227] A method of screening for anticancer activity, the method comprising: (a) contacting a cell that expresses a cancer associated gene which transcribes a cancer associated sequence selected from SEQ ID NOs: 1-55, homologs thereof, combinations thereof, or fragments thereof with an anticancer drug candidate; (b) detecting an effect of the anticancer drug candidate on an expression of the cancer associated polynucleotide in the cell; and (c) comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of the drug candidate; wherein an effect on the expression of the cancer associate polynucleotide indicates that the candidate has anticancer activity.

[00228] In some embodiments, a method of evaluating the effect of a candidate cancer drug may comprise administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. In some embodiments, the method may further comprise comparing the expression profile of the patient to an expression profile of a healthy individual. In some embodiments, the expression profile comprises measuring the expression of one or more or any combination thereof of the sequences disclosed herein. In some embodiments, where the expression profile of one or more or any combination thereof of the sequences disclosed herein is modified (increased or decreased) the candidate cancer drug is said to be effective.

[00229] In some embodiments, the invention provides a method of screening for anticancer activity comprising: (a) providing a cell that expresses a cancer associated gene encoded by a nucleic acid sequence selected from the group consisting of the cancer associated sequences shown in Table 2 (SEQ ID NOs: 1-55), or fragment thereof, (b) contacting the cell,

which can be derived from a cancer cell with an anticancer drug candidate; (c) monitoring an effect of the anticancer drug candidate on an expression of the cancer associated sequence in the cell sample, and optionally (d) comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of the drug candidate. The drug candidate may be an inhibitor of transcription, a G-protein coupled receptor antagonist, a growth factor antagonist, a serine-threonine kinase antagonist, a tyrosine kinase antagonist. In some embodiments, where the candidate modulates the expression of the cancer associated sequence the candidate is said to have anticancer activity. In some embodiments, the anticancer activity is determined by measuring cell growth. In some embodiments, the candidate inhibits or retards cell growth and is said to have anticancer activity. In some embodiments, the candidate causes the cell to die, and thus, the candidate is said to have anticancer activity.

[00230] In some embodiments, the invention provides a method for screening for a therapeutic agent capable of modulating the activity of a cancer associated sequence, wherein said sequence can be encoded by a nucleic acid comprising a nucleic acid sequence selected from the group consisting of the polynucleotide sequences SEQ ID NOs: 1-55 shown in Table 2, said method comprising: a) combining said cancer associated sequence and a candidate therapeutic agent; and b) determining the effect of the candidate agent on the bioactivity of said cancer associated sequence. According to the method the therapeutic agent: affects the expression of the cancer associated sequence; affects the activity of the cancer associated sequence, wherein such activity is selected from the activities listed in Table 21. In some embodiments, the cancer associated sequence is a cancer associate protein (CAP). In some embodiments, the cancer associated sequence is a cancer associate nucleic acid molecule.

PHARMACEUTICAL FORMULATIONS AND ADMINISTRATION

[00231] Modes of administration for a therapeutic (either alone or in combination with other pharmaceuticals) can be, but are not limited to, sublingual, injectable (including short-acting, depot, implant and pellet forms injected subcutaneously or intramuscularly), or by use of vaginal creams, suppositories, pessaries, vaginal rings, rectal suppositories, intrauterine devices, and transdermal forms such as patches and creams.

[00232] Specific modes of administration will depend on the indication. The selection of the specific route of administration and the dose regimen is to be adjusted or titrated by the clinician according to methods known to the clinician in order to obtain the optimal clinical

response. The amount of therapeutic to be administered is that amount which is therapeutically effective. The dosage to be administered will depend on the characteristics of the subject being treated, *e.g.*, the particular animal treated, age, weight, health, types of concurrent treatment, if any, and frequency of treatments, and can be easily determined by one of skill in the art (*e.g.*, by the clinician).

[00233] Pharmaceutical formulations containing the therapeutic of the present invention and a suitable carrier can be solid dosage forms which include, but are not limited to, tablets, capsules, cachets, pellets, pills, powders and granules; topical dosage forms which include, but are not limited to, solutions, powders, fluid emulsions, fluid suspensions, semi-solids, ointments, pastes, creams, gels and jellies, and foams; and parenteral dosage forms which include, but are not limited to, solutions, suspensions, emulsions, and dry powder; comprising an effective amount of a polymer or copolymer of the present invention. It is also known in the art that the active ingredients can be contained in such formulations with pharmaceutically acceptable diluents, fillers, disintegrants, binders, lubricants, surfactants, hydrophobic vehicles, water soluble vehicles, emulsifiers, buffers, humectants, moisturizers, solubilizers, preservatives and the like. The means and methods for administration are known in the art and an artisan can refer to various pharmacologic references for guidance. For example, *Modern Pharmaceutics*, Banker & Rhodes, Marcel Dekker, Inc. (1979); and *Goodman & Gilman's The Pharmaceutical Basis of Therapeutics*, 6th Edition, MacMillan Publishing Co., New York (1980) can be consulted.

[00234] The compositions of the present invention can be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. The compositions can be administered by continuous infusion subcutaneously over a period of about 15 minutes to about 24 hours. Formulations for injection can be presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers, with an added preservative. The compositions can take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and can contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

[00235] For oral administration, the compositions can be formulated readily by combining the therapeutic with pharmaceutically acceptable carriers well known in the art. Such carriers enable the therapeutic of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained by adding a solid excipient,

optionally grinding the resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients include, but are not limited to, fillers such as sugars, including, but not limited to, lactose, sucrose, mannitol, and sorbitol; cellulose preparations such as, but not limited to, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and polyvinylpyrrolidone (PVP). If desired, disintegrating agents can be added, such as, but not limited to, the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

[00236] Dragee cores can be provided with suitable coatings. For this purpose, concentrated sugar solutions can be used, which can optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments can be added to the tablets or dragee coatings for identification or to characterize different combinations of active therapeutic doses.

[00237] Pharmaceutical preparations which can be used orally include, but are not limited to, push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as, e.g., lactose, binders such as, e.g., starches, and/or lubricants such as, e.g., talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active therapeutic can be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers can be added. All formulations for oral administration should be in dosages suitable for such administration.

[00238] For buccal administration, the pharmaceutical compositions can take the form of, e.g., tablets or lozenges formulated in a conventional manner.

[00239] For administration by inhalation, the therapeutic for use according to the present invention is conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit can be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator can

be formulated containing a powder mix of the therapeutic and a suitable powder base such as lactose or starch.

[00240] The compositions can also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

[00241] In addition to the formulations described previously, the therapeutic of the present invention can also be formulated as a depot preparation. Such long acting formulations can be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection.

[00242] Depot injections can be administered at about 1 to about 6 months or longer intervals. Thus, for example, the compositions can be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

[00243] In transdermal administration, the compositions of the present invention, for example, can be applied to a plaster, or can be applied by transdermal, therapeutic systems that are consequently supplied to the organism.

[00244] Pharmaceutical compositions can include suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as, e.g., polyethylene glycols.

[00245] The compositions can also be administered in combination with other active ingredients, such as, for example, adjuvants, protease inhibitors, or other compatible drugs or compounds where such combination is seen to be desirable or advantageous in achieving the desired effects of the methods described herein.

[00246] In some embodiments, the disintegrant component comprises one or more of croscarmellose sodium, carmellose calcium, crospovidone, alginic acid, sodium alginate, potassium alginate, calcium alginate, an ion exchange resin, an effervescent system based on food acids and an alkaline carbonate component, clay, talc, starch, pregelatinized starch, sodium starch glycolate, cellulose floc, carboxymethylcellulose, hydroxypropylcellulose, calcium silicate, a metal carbonate, sodium bicarbonate, calcium citrate, or calcium phosphate.

[00247] In some embodiments, the diluent component may include one or more of mannitol, lactose, sucrose, maltodextrin, sorbitol, xylitol, powdered cellulose, microcrystalline cellulose, carboxymethylcellulose, carboxyethylcellulose, methylcellulose, ethylcellulose, hydroxyethylcellulose, methylhydroxyethylcellulose, starch, sodium starch glycolate, pregelatinized starch, a calcium phosphate, a metal carbonate, a metal oxide, or a metal aluminosilicate.

[00248] In some embodiments, the optional lubricant component, when present, comprises one or more of stearic acid, metallic stearate, sodium stearyl fumarate, fatty acid, fatty alcohol, fatty acid ester, glyceryl behenate, mineral oil, vegetable oil, paraffin, leucine, silica, silicic acid, talc, propylene glycol fatty acid ester, polyethoxylated castor oil, polyethylene glycol, polypropylene glycol, polyalkylene glycol, polyoxyethylene-glycerol fatty ester, polyoxyethylene fatty alcohol ether, polyethoxylated sterol, polyethoxylated castor oil, polyethoxylated vegetable oil, or sodium chloride.

KITS

[00249] In some embodiments, the invention provides a kit for diagnosing the presence of cancer in a test sample, said kit comprising at least one polynucleotide that selectively hybridizes to a cancer associated polynucleotide sequence shown in Table 2, or its complement. In another embodiment the invention provides an electronic library comprising a cancer associated polynucleotide, a cancer associated polypeptide, or fragment thereof, shown in Table 2. In other embodiments the invention provides a kit for diagnosing the presence of cancer in a test sample, said kit comprising at least one polypeptide or protein shown in Table 3. In further embodiments the invention provides at least one polynucleotide that selectively hybridizes to a cancer associated polynucleotide chosen from MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7. In still other embodiments the invention provides a plurality of polynucleotide that selectively hybridizes to a cancer associated polynucleotide chosen from MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7

[00250] The kits and systems for practicing the subject methods, as described above, may be configured to diagnose cancer in a subject, treat cancer in a subject, or perform basic research experiments on cancer cells (e.g., either derived directly from a subject, grown in vitro or ex vivo, or from an animal model of cancer. The various components of the kits may be

present in separate containers or certain compatible components may be precombined into a single container, as desired.

[00251] The subject systems and kits may also include one or more other reagents for performing any of the subject methods. The reagents may include one or more matrices, solvents, sample preparation reagents, buffers, desalting reagents, enzymatic reagents, denaturing reagents, probes, polynucleotides, vectors (e.g., plasmid or viral vectors), etc., where calibration standards such as positive and negative controls may be provided as well. As such, the kits may include one or more containers such as vials or bottles, with each container containing a separate component for carrying out a sample processing or preparing step and/or for carrying out one or more steps for producing a normalized sample according to the present invention.

[00252] In addition to above-mentioned components, the subject kits typically further include instructions for using the components of the kit to practice the subject methods. The instructions for practicing the subject methods are generally recorded on a suitable recording medium. For example, the instructions may be printed on a substrate, such as paper or plastic, etc. As such, the instructions may be present in the kits as a package insert, in the labeling of the container of the kit or components thereof (i.e., associated with the packaging or sub-packaging) etc. In other embodiments, the instructions are present as an electronic storage data file present on a suitable computer readable storage medium, e.g. CD-ROM, diskette, etc. In yet other embodiments, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source, e.g. via the internet, are provided. An example of this embodiment is a kit that includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded. As with the instructions, this means for obtaining the instructions is recorded on a suitable substrate.

[00253] In addition to the subject database, programming and instructions, the kits may also include one or more control samples and reagents, e.g., two or more control samples for use in testing the kit.

EXAMPLE 1

[00254] The Differential Expression of *SP100*--We utilized the screen of the present invention with a large gene expression microarray dataset performed on Illumina microarrays including >400 samples comprised of normal human cell lines including such cell types derived from all three embryonic germ layers as normal human astrocytes, normal human articular

chondrocytes, normal bronchial epithelial cells, adult-derived stem cells such as mesenchymal, adipocyte, and dental pulp stem cells, hES-derived clonal embryonic progenitor lines, pluripotent stem (hESCs), hESCs, iPS lines and an EC line. As shown in Figure 58, *SP100* is expressed in essentially all somatic cell types but is not expressed at all in hES cell lines or established iPS cell lines.

EXAMPLE 2

[00255] Knockdown/inhibition of *SP100* expression followed by transcriptional reprogramming accelerates reprogramming while reducing the accumulation of mutations. The hES cell-derived clonal embryonic progenitor cell lines CM02 and EN13 (see U.S. Patent Publication 20080070303, entitled “Methods to accelerate the isolation of novel cell strains from pluripotent stem cells and cells obtained thereby”; and U.S. patent application Ser. No. 12/504,630 filed on July 16, 2009 and titled “Methods to Accelerate the Isolation of Novel Cell Strains from Pluripotent Stem Cells and Cells Obtained Thereby”, each of which is incorporated by reference herein in its entirety) are first cultured with retrovirus expressing silencing RNA directed to *SP100* and the down-regulation is confirmed by qPCR. The cells are then cryopreserved or reprogrammed within two days by the exogenous administration of *OCT4*, *MYC*, *KLF4*, and *SOX2* (see Takahashi and Yamanaka 2006 Aug 25;126(4):663-76; U.S. Patent Application Serial No. 12/086,479, published as US2009/0068742 and entitled “Nuclear Reprogramming Factor”, each of which is incorporated herein by reference) and by the method described in PCT/US06/30632, published as WO/2007/019398 and entitled “Improved Methods of Reprogramming Animal Somatic Cells”, incorporated by reference herein in its entirety. The cells may also be conditioned to knockdown/inhibit the expression of the *LMNA* gene. Control lines that have not been preconditioned by the knockdown of *SP100* or *LMNA* or both *SP100* and *LMNA* are reprogrammed in parallel to demonstrate the shortened time to reprogramming to pluripotency and are sequenced to compare the accumulated mutations in the cells and the lower rate of mutations in the cells preconditioned to lower *SP100*, *LMNA*, or both gene products. *LMNA* expression has been shown previously to be low/absent from ES cells but present in many somatic cells.

EXAMPLE 3

[00256] Knockdown/inhibition of *SP100* expression followed by culturing under conditions for propagating ES cells.--Differentiated mammalian cells (e.g., human cells) are

treated to knockdown or inhibit *SP100* gene expression (e.g., as described above). The cells may also be treated to knockdown/inhibit the expression of *LMNA* gene. The cells are cultured under conditions that promote the propagation of ES cells. Any convenient ES cell propagation condition can be used, e.g., on feeders or in feeder free media capable of propagating ES cells. ES colonies are identified in the culture. Cells from the identified ES colony are then evaluated for ES markers, e.g., Oct4, TRA 1-60, TRA 1-81, SSEA4, etc., and those having ES cell phenotype are expanded. In certain embodiments, *LMNA*-negative cells are used in the above protocol, such as peripheral mononuclear cells (e.g., CD34+ or CD133+ cells). Control lines that have not been preconditioned by the knockdown of *SP100* or *LMNA* or both *SP100* and *LMNA* can be reprogrammed in parallel to demonstrate the effectiveness of the preconditioning.

EXAMPLE 4

[00257] Additional genes differentially expressed in normal versus diverse cancer types. RNA was obtained from cultured diverse cultured human cell types, normal human tissues, and malignant human tumors and analyzed on Illumina gene expression microarrays. As shown in Table VI, genes are easily identified that provide novel diagnostics for cancer and targets for cancer therapy.

EXAMPLE 5

[00258] *DSCR8* expression in diverse cancer types. RNA was obtained from cultured diverse cultured human cell types, normal human tissues, and malignant human tumors and analyzed on Illumina gene expression microarrays. The gene encoding the protein down syndrome critical region gene 8 *DSCR8* also known as *MMA-1a* (Illumina Probe ID 4280132, accession number NM_203428.1) was detected as a gene expressed in relatively higher levels in testis and diverse cancers compared to normal cultured somatic cell types and tissues. There are reports that *DSCR8* is expressed in testis and in melanoma (de Wit, N.J. et al Expression profiling of MMA-1a and splice variant MMA-1b: new cancer/testis antigens identified in human melanoma. *Int. J. Cancer* 98:547-553) and uterine (Risinger, J.I. et al (2007) Global expression analysis of cancer/testis genes in uterine cancers reveals a high incidence of BORIS expression. *Clin. Cancer Res.* 13:1713-1719) cancer. Measurements of *DSCR8* may be useful for screening or diagnosing a wide array of cancers. While these previous reports suggest *DSCR8* is expressed in relatively specifically in testis compared to other human tissues and report that it is expressed in uterine cancers and melanomas, they do not report that the relative expression of

DSCR8 is diagnostic of the malignant tumors described herein. Surprisingly, as shown in Figure 18, while diverse cultured normal somatic cell types such as brain microvascular endothelial cells, dermal fibroblasts, smooth muscle cells, esophageal epithelial cells, urothelial cells, pulmonary epithelial cells, prostate epithelial cells, hepatocytes, astrocytes, as well as others and normal tissues tested express relatively low levels of signal (i.e. either background signal of <100 RFU or in the case of eye-derived cells low (< 250 RFUs)), samples of normal testis, and diverse malignant tumors expressed the gene at relatively high levels (> 250 RFU). Examples of such tumors are: endometrial adenocarcinoma (as predicted based on the art), small cell lung cancer, bladder carcinoma, seminoma of the testis, adenocarcinoma of the stomach, the myelogenous leukemia cell line K562, the ovarian cancer cell line OVCAR3, and the melanoma cell line G361 (as expected in the art). Since sensitive technologies exist to express to detect genes such as *DSCR8*, said nucleotide probes such as PCR primers or the oligonucleotide probe used in the microarray described herein (TCCCACCTTGGCAGGGGCCGTCTTGTCCTCGTTTCTGTAAACATGGGTG), (SEQ ID NO:190) as well as other detection techniques described herein including but not limited to the detection of the protein in tissue samples or blood using monoclonal or polyclonal antibodies, may be used in the unexpected manner described herein to screen for or to otherwise stage the wide array of cancers described above.

[00259] In addition, the specific expression of *DSCR8* in varied malignancies may provide novel therapeutic strategies wherein the knockdown or inhibition of the activity of the protein encoded by *DSCR8* or down-regulating the expression or translation of the gene may be used in reducing tumor mass and treating cancer.

EXAMPLE 6

[00260] qPCR was performed on bladder tumor tissue, normal bladder tissue and normal bladder tissue that was located adjacent to a bladder tumor. Positive controls were bladder tumors previously assayed by microarray.

[00261] Total RNA was extracted with the RNeasy Mini Kit (Qiagen) and cDNA generated using the SuperScript III reverse transcriptase in combination with random hexamer primers alone or in combination with oligo-dT primers (all reverse transcription components from Invitrogen/Life Technologies). PCRs were carried out on a 7900HT Sequence Detection System or a 7500 Real Time PCR System (Applied Biosystems/Life Technologies) utilizing

SYBR Green or TaqMan chemistries. The primers used for the PCR reactions are listed in Tables 7 and 8. PCR parameters were: activation at 50°C for 2 minutes; denature at 95°C for 10 minutes; followed by 40-42 cycles of 95°C for 15 seconds and 60°C for 1 minute (72°C for amplicons > than 120bp) followed by dissociation at 95°C for 15 seconds; 60°C for 15 seconds, and 95°C for 15 seconds.

[00262] The results are provided in Figures 59-70 and showed that MMP-11, MMP-12, COL10A1, FCRLB, SERPINB5, SFN, KRT6A, FCRLB, IL1A, KRT16, SLC1A6, and S100A2 were all elevated relative to normal bladder tissue (normalized to β -actin expression). Moreover, the signal pattern seen for the positive controls previously analyzed by microarray, was the same obtained by microarray confirming that the PCR reaction worked.

Example 7

[00263] The UPL System contains a relatively small number of short hydrolysis probes that cover an extensive proportion of the human mRNA transcriptome. UPL probes contain locked nucleic acids (LNAs) lowering the probes' melting temperatures. This allowed the probe and the longer, unmodified, primers to anneal at the same temperature.

[00264] Quantitative reverse transcription-polymerase chain reaction (qRT-PCR) was performed as follows:

[00265] Total RNA was extracted with the RNeasy Mini Kit (Qiagen) and cDNA generated using the SuperScript III reverse transcriptase in combination with random hexamer primers alone or in combination with oligo-dT primers (all reverse transcription components from Invitrogen/Life Technologies). PCRs were carried out on a 7900HT Sequence Detection System or a 7500 Real Time PCR System (Applied Biosystems/Life Technologies) utilizing SYBR® Green I (Applied Biosystems/Life Technologies) or TaqMan chemistries. TaqMan PCR was conducted with probes from the Universal Probe Library (UPL) (Roche) in combination with correspondingly designed primers. Primers: AAGCCTGCTGACGATGATG (Forward) (SEQ ID NO:191) and GCGAGGTAATGTATGCCCTTT (Reverse) (SEQ ID NO:192) were used with UPL 60. The results were normalized to β -actin expression levels.

[00266] The result, indicating that S100A7A was elevated in bladder cancer, is shown in Figure 71.

EXAMPLE 8

[00267] Example 8 provides ELISA data for MMP12, ColX and MMP11 (Figs 71-73).

[00268] Levels of the three protein markers were assayed in serum using a USCN ELISA kit (USCN) according to the manufacturer's instructions. In brief, 100 μ L of the blank, standards, and samples with specified dilutions were added to the appropriate wells of a 96 well plate followed by 2 hours of incubation at 37°C. After removal of the liquid, 100 μ L of Detection Reagent A was added to each well and incubated for 1 hour at 37°C. After removal of Reagent A, each well was washed 3 times with 350 μ L of wash solution. 100 μ L of Detection Reagent B was added to each well and then incubated for 30 minutes at 37°C. After removal of Reagent B, each well was washed 5 times with 350 μ L of wash solution. 90 μ L of Substrate solution was added to each well and incubated for 15-25 minutes at 37°C. 50 μ L of Stop Solution was added to each well. The plate was read either on the Molecular Devices SpectraMax250 or the BioTek Synergy H1 plate reader at 450nm. A standard curve was derived from the standards supplied in the kit and the sample values were extrapolated from this curve.

[00269] The results are shown in Figures 72-74 that MMP12, ColX and MMP11 are all elevated in bladder cancer samples.

Example 9

[00270] Human urine samples from healthy subjects and cancer patients were analyzed by qPCR for expression of the markers COL10A1, MMP11, SFN, FCRLB, as described below.

[00271] RNA was extracted from cells in voided urine with the ZR Urine RNA Isolation KitTM (Zymo Research) then reverse-transcribed using SuperScript III reverse transcriptase in the presence of random hexamer and oligo-dT primers (Invitrogen/Life Technologies). Following PCR with 50 cycles, products were analyzed on pre-cast 4% Agarose (HR) gels containing ethidium bromide (E-Gel[®], Invitrogen/Life Technologies). Urine specimens: all from male individuals, three with bladder cancer (1-3), and three healthy controls (A-C). GAPDH served as loading and/or positive control. The following primers were used: **COL10A1**: ES577-COL10A1-F and ES578-COL10A1-R, **MMP11**: JK1178-MMP11-F and JK1179-MMP11-R, **SFN**: JK1206-SFN-F and JK1207-SFN-R, **FCRLB**: JK1200-FCRLB-F and JK1201-FCRLB-R, **GAPDH**: ES312-GAPD-F2 and ES313-GAPD-R2.

[00272] The results shown in Figure 75 indicate that elevated levels of the markers COL10A1, MMP11, SFN, FCRLB are seen in the urine of cancer patients relative to healthy patients.

EXAMPLE 10

[00273] qPCR was performed on bladder tumor tissue, normal bladder tissue and normal bladder tissue that was located adjacent to a bladder tumor. Positive controls were bladder tumors previously assayed by microarray.

[00274] Total RNA was extracted with the RNeasy Mini Kit (Qiagen) and cDNA generated using the SuperScript III reverse transcriptase in combination with random hexamer primers alone or in combination with oligo-dT primers (all reverse transcription components from Invitrogen/Life Technologies). PCRs were carried out on a 7900HT Sequence Detection System or a 7500 Real Time PCR System (Applied Biosystems/Life Technologies) utilizing SYBR Green or TaqMan chemistries. The primers used for the PCR reactions were: ACTGGTGGCAGGGGCTTCTAGC (SEQ ID NO:196) (Forward primer) and GCCATCTAAAGTAACTAAACCCATAGAC (SEQ ID NO: 197) (REVERSE PRIMER). PCR parameters were: activation at 50°C for 2 minutes; denature at 95°C for 10 minutes; followed by 40-42 cycles of 95°C for 15 seconds and 60°C for 1 minute (72°C for amplicons > than 120bp) followed by dissociation at 95°C for 15 seconds; 60°C for 15 seconds, and 95°C for 15 seconds.

[00275] The results are provided in Figure 76 and showed that SERPINB5 were all elevated relative to normal bladder tissue (normalized to β -actin expression). Moreover, the signal pattern seen for the positive controls previously analyzed by microarray, was the same obtained by microarray confirming that the PCR reaction worked.

[00276] Although the present invention has been described in considerable detail with reference to certain preferred embodiments thereof, other versions are possible. Therefore the spirit and scope of the appended claims should not be limited to the description and the preferred versions contained within this specification.

Claims:

1. A method of detecting bladder cancer in a subject comprising a) contacting a sample obtained from the subject with one or more agents that detect expression of a panel of markers comprising MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 IL1A, KRT16, SLC1A6 ; b) contacting a non-cancerous cell, with one or more agents that detect expression of a panel of markers comprising MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 IL1A, KRT16, SLC1A6 ; and c) comparing the expression level of the panel of markers comprising MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 IL1A, KRT16, SLC1A6 in the sample obtained from the subject with the expression level of the panel of markers comprising MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 IL1A, KRT16, SLC1A6 in the non-cancerous cell, wherein a higher level of expression of the panel of markers comprising MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 IL1A, KRT16, SLC1A6 in the sample compared to the non-cancerous cell indicates that the subject has bladder cancer.
2. The method of claim 1, wherein the subject is a human subject.
3. The method of claim 1, wherein the sample is a tissue sample.
4. The method of claim 1, wherein the sample is a bodily fluid.
5. The method of claim 4, wherein the bodily fluid is serum.
6. The method of claim 4, wherein the bodily fluid is urine.
7. The method of claim 1, wherein the agent is a nucleic acid.
8. The method of claim 1, wherein the agent is an antibody.
9. A kit comprising one or more agents that bind to the panel of markers MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7 IL1A, KRT16, SLC1A6.
10. The kit of claim 9, wherein the agent is a nucleic acid.
11. The kit of claim 10, wherein the nucleic acid is a DNA molecule.
12. The kit of claim 9, wherein the agent is a protein.
13. The kit of claim 12, wherein the protein is an antibody.

ProbeID	Symbol	[[135], Urinary bladder Within normal limits, MBA_2270_	[[185], Urinary bladder Carcinoma of bladder transitional cell, MBA_2271_	[[228], Urinary bladder Carcinoma of bladder small cell metastatic, MBA_2272_	[[030], HBdMEC t (Human Microvascula r Endothelial Cell), MBA_2150_	[[091], HBdSMC t (Human Bladder Smooth Muscle Cell), MBA_2151_	[[001], ESI 035 P49 mefs for P10, MBA_1622_	[[002], ESI 049 P21 matrigel P6, MBA_1654_	[[003], H1- GFP, MBA_1641_	[[004], H1- GFP (tech rep), MBA_1641_	[[005], Normal PB-B Cells (CD19+) Comprehensive RNA, MBA_2340_	[[006], Normal PB- Pan-T Cells Comprehensive RNA, MBA_2341_
2490541	MAGEA10	45	1338	84	70	59	86	66	84	74	140	92
4280132	DSCR8	45	917	145	55	59	53	48	49	51	58	54
4760626	MMP12	45	1027	1121	48	44	43	41	40	41	38	50
5570278	CXCL9	93	708	4172	37	41	47	39	39	44	48	52
4280504	DSCR8	46	502	196	47	46	44	40	51	50	52	49
430446	KRT81	46	13273	48	47	50	41	42	46	43	53	46
2750689	LOC729826	64	632	70	67	57	69	74	70	77	65	72
1980593	PTH1H	104	969	57	50	52	39	43	45	39	42	48
2370632	MMP11	93	1734	229	89	116	94	128	167	146	176	79
6550500	S100A7	78	1503	87	69	69	71	97	74	77	71	88
3310333	WISP3	49	505	54	76	56	80	64	58	74	57	73
6270553	CXCL10	132	2005	2120	77	57	54	47	55	55	55	58
7050220	NMU	64	791	76	107	39	534	318	315	339	61	55
1510364	GBP5	67	634	683	62	46	49	46	42	44	139	550
3990619	TOP2A	48	1246	1952	927	142	1722	1773	3520	3009	34	80
6860424	SERPINB4	49	4585	43	45	49	47	45	48	46	48	39
5360064	GNLY	55	321	765	48	44	47	45	48	43	50	3245
6290554	GTSF1	73	632	87	82	74	98	72	75	72	222	184
1050168	P13	54	13882	50	45	43	58	40	35	39	62	87
7550554	S100A7A	64	481	58	64	66	70	74	67	55	74	41
5570711	IDO1	90	4164	484	171	73	357	271	245	222	72	76
3120113	GJB6	135	2018	80	109	103	126	111	99	91	96	120
2320600	CALML3	63	2185	49	46	49	52	50	47	48	43	58
1470056	SERPINE3	85	6554	77	67	85	67	82	77	77	73	81
6620487	CXCL6	66	685	62	88	172	92	72	121	120	54	60
6770131	OLFML4	373	8377	40	38	45	41	43	42	47	37	40
1770603	TCN1	40	2366	39	37	36	39	37	39	34	42	51
6100239	VSNL1	70	788	76	73	66	263	597	1629	1429	53	78
6420605	UBD	92	1017	1074	153	76	65	92	71	72	70	70
1260270	AIM2	99	3435	374	86	67	86	145	89	107	1205	169
4490093	ABCC9	52	398	66	67	57	57	53	54	51	46	54
1580762	SERPINE13	64	1223	68	78	80	85	73	73	64	100	80
380259	INDO	69	2977	299	113	52	251	247	167	161	54	64
5860289	KRT5	149	2907	38	34	41	42	47	39	39	44	36
1580470	LOC1001308	57	283	66	51	53	54	56	57	53	61	53
4900458	KRT14	44	1015	41	47	52	46	46	48	41	52	48
2510605	FAM83A	156	918	41	46	42	48	43	41	42	43	44
4730242	FAM181B	77	329	52	43	50	59	53	54	47	46	53
6760286		50	371	93	64	62	73	61	60	60	70	68

FIGURE 1

ProbeID	Symbol	[[007], Normal PB-Monocytes (CD14+) Comprehensive RNA, MBA_2342	[[008], CD19+ B Cells, MBA_2343	[[009], CL Bone Marrow CD19+/CD5 + B Cells (Relapsed/Refractory), MBA_2344	[[010], CLL Peripheral Blood CD19+ B Cells Comprehensive RNA (Untreated), MBA_2345	[[011], Fetal Liver CD34+ Cells Comprehensive RNA, MBA_2346	[[012], Fetal Liver CD36+ Early Erythroid Progenitor Cells, MBA_2347	[[013], Mobilized PB-Stem/Progenitor cells (CD34+) Comprehensive RNA, MBA_2348	[[014], Normal BM Endothelial Cells (CD105+) Comprehensive RNA, MBA_2349	[[015], Normal BM Myeloid Cells (CD33+) Comprehensive RNA, MBA_2350	[[016], Normal BM Stem/Progenitor Cells (CD133+) Comprehensive RNA, MBA_2351	[[017], Normal BM Stem/Progenitor Cells (CD34+) Comprehensive RNA, MBA_2352
2490541	MAGEA10	77	79	58	73	67	86	51	63	63	70	61
4280132	DSCR8	54	63	54	48	41	48	47	47	55	54	46
4760626	MMP12	37	44	43	44	48	126	48	47	38	39	49
5570278	CXCL9	57	50	43	45	40	46	43	42	53	57	40
4280304	DSCR8	45	41	49	45	44	39	47	42	51	43	42
430446	KRT81	45	45	44	52	46	62	55	49	47	47	41
2750689	LOC729826	87	72	87	82	66	78	74	82	72	59	55
1980593	PTH1H	49	47	53	44	43	44	46	38	44	46	51
2370632	MMP11	69	126	250	200	92	86	89	75	71	92	77
6550500	S190A7	68	81	63	75	62	57	74	67	82	65	48
3310333	WISP3	52	62	67	71	60	68	65	73	69	82	71
6270553	CXCL10	492	53	59	62	84	57	178	81	177	93	55
7050220	NMU	51	59	48	56	84	1531	80	446	48	63	194
1510364	GBP5	316	111	75	124	66	187	332	78	138	150	100
3990619	TOP2A	44	74	58	57	2244	3281	102	3703	765	1417	1776
6860424	SERPINB4	40	42	40	41	45	46	40	41	40	46	42
5360064	GNYL	621	211	53	66	53	44	61	135	65	59	42
6290554	GTSF1	105	99	75	83	164	144	214	132	140	148	228
1050168	P13	40	36	38	40	45	40	66	41	48	38	36
7550554	S100A7A	71	76	59	57	61	78	58	64	75	54	71
5570711	IDO1	116	59	53	50	47	53	56	66	72	49	53
3120113	GBB6	103	131	84	86	86	74	107	86	127	93	92
2320600	CALML3	47	52	51	50	46	47	44	46	49	45	43
1470056	SERPINB3	69	107	88	63	75	64	60	94	68	68	73
6620487	CXCL6	55	60	56	67	56	84	70	58	51	43	66
6770131	OLFM4	40	40	41	50	52	43	82	388	1796	195	46
1770603	TCN1	40	35	34	33	44	948	44	152	1434	82	56
6100259	VSNL1	72	80	67	66	72	63	96	55	67	64	67
6420605	UBD	70	60	65	67	70	71	90	78	77	72	54
1260270	ATM2	355	1309	751	2195	80	84	73	69	151	79	100
4490093	ABCC9	56	62	59	53	53	77	59	54	57	51	59
1580762	SERPINB13	64	79	82	67	67	52	84	79	60	65	68
380259	INDO	98	44	48	45	49	48	48	46	56	50	49
5860289	KRT5	38	37	42	43	42	36	39	40	37	38	41
1580470	LOC1001308	58	54	70	53	63	44	44	47	53	54	57
4900458	KRT14	44	46	51	44	44	42	45	48	52	45	48
2510605	FAM83A	42	42	45	52	41	684	41	54	40	41	43
4730242	FAM181B	47	50	48	45	48	58	48	58	51	48	56
6760286		77	80	59	94	53	93	55	61	76	52	62

FIGURE 1-CONTINUED

ProbeID	Symbol	[[018], Normal PB- Immature Myeloid Dendritic Cells Comprehens ive RNA, MBA_2353	[[019], Relapsed/Ref ractory AML PBMC Comprehens ive RNA, MBA_2354	[[021], HMEC t (Human Brain Microvascula r Endothelial Cell), MBA_2100	[[022], HCEC t (Human Choroid Plexus Endothelial Cell), MBA_2103	[[023], HMEC t (Human Dermal Microvascula r Endothelial Cell), MBA_2112	[[024], HMEC t (Human Dermal Lymphatic Endothelial Cell), MBA_2113	[[025], HLEC t (Human Lymphatic Endothelial Cell), MBA_2124	[[026], HMEC t (Human Intestinal Microvascula r Endothelial Cell), MBA_2125	[[027], HMEC t (Human Pulmonary Microvascula r Endothelial Cell), MBA_2132	[[028], HPAEC t (Human Pulmonary Artery Endothelial Cell), MBA_2133	[[029], HMEC t (Human Renal Glomerular Endothelial Cell), MBA_2145
2490541	MAGEA10	49	70	89	78	52	63	73	66	73	57	57
4280132	DSCR8	51	44	55	54	53	64	48	55	55	53	59
4760626	MMP12	1178	43	45	46	41	56	44	37	46	41	44
5570278	CXCL9	35	40	37	42	41	38	47	44	40	41	48
4280504	DSCR8	50	48	44	42	43	43	51	43	45	44	49
430446	KRT81	41	39	51	42	41	41	42	49	49	54	46
2750689	LOC729826	64	56	64	81	62	54	68	83	69	80	72
1980593	PTHLH	45	51	52	55	55	49	51	52	600	51	57
2370632	MMP11	75	66	81	127	108	67	104	120	83	121	135
6550505	S100A7	72	64	80	101	67	77	64	63	120	52	86
3310333	WISP3	73	62	56	62	59	49	65	58	69	62	64
6270553	CXCL10	55	77	73	154	62	89	82	169	96	61	124
7050220	NMU	51	53	72	62	72	91	63	61	327	61	85
1510364	GBP5	154	1076	56	75	38	61	45	72	43	40	66
3990619	TOP2A	180	112	529	1319	649	829	1273	1822	953	737	680
6860424	SERPINE4	44	41	49	45	43	43	39	39	45	49	42
5360064	GNL1	45	4463	41	45	44	46	50	42	48	54	47
6290554	GTSF1	109	172	79	63	131	93	45	71	85	71	71
1050168	PTG	40	45	42	44	46	39	48	98	7405	40	41
7550554	S100A7A	77	65	69	63	77	53	68	65	58	65	62
5570711	IDO1	62	72	58	84	56	74	70	156	62	68	70
3120113	GBB6	80	121	78	92	81	78	79	102	1724	97	91
2320600	CALML3	46	51	47	46	46	54	56	44	204	41	40
1470056	SERPINE3	75	68	71	68	77	79	72	74	147	66	62
6620487	CXCL6	58	52	72	84	92	60	68	185	91	215	147
6770131	OLF4	52	148	39	43	44	41	46	43	44	43	45
1770603	TCN1	40	315	39	39	41	38	43	42	81	42	40
6100259	VSNL1	65	73	65	59	96	70	81	74	232	56	72
6420605	UBD	72	61	79	300	127	184	627	3553	312	75	71
1260270	AIM2	118	150	64	74	77	52	79	85	79	85	73
4490093	ABCC9	57	63	59	58	59	52	56	55	66	57	59
1580762	SERPINE3	63	58	65	79	57	85	65	77	528	84	73
380259	INDO	46	44	40	52	48	48	52	30	43	44	51
5860289	KRT5	36	39	41	38	37	40	37	41	8323	39	38
1580470	LOC1001308	45	59	53	51	52	74	39	61	54	65	49
4900458	KRT14	47	47	44	47	35	52	39	46	8572	50	47
2510605	FAM83A	45	206	46	41	47	37	46	41	578	44	41
4730242	FAM181B	44	46	45	44	52	51	47	48	73	37	44
6760286		68	82	57	67	64	57	56	64	101	66	66

FIGURE 1-CONTINUED

ProbeID	Symbol	[[031], (H)SEC t (Human Hepatic Sinusoidal Endothelial Cell), MBA_2159	[[032], (H)MEC t (Human Cardiac Microvascula r Endothelial Cell), MBA_2162	[[033], (H)AEC t (Human Aortic Endothelial Cell), MBA_2163	[[034], (H)VCEC t (Human Villus Capillary Endothelial Cell), MBA_2175	[[035], (H)OSEC t (Human Ovarian Microvascula r Endothelial Cell), MBA_2181	[[036], (H)UVEC t (Human Umbilical Vein Endothelial Cell), MBA_2190	[[037], (H)UAE t (Human Umbilical Artery Endothelial Cell), MBA_2191	[[038], (H)OPEC t (Human Choroid Plexus Epithelial Cell), MBA_2104	[[039], HEK t (Human Epidermal Keratinocyte adult), MBA_2114	[[040], HEK t (Human Epidermal Keratinocyte adult), MBA_2115	[[041], (H)HORSC t (Human Hair Outer Root Sheath Cell , MBA_2123
2490541	MAGEA10	56	55	82	56	60	69	58	56	53	62	61
4280132	DSOR8	56	51	58	52	56	58	56	50	52	57	56
4760626	MMP12	45	43	42	47	41	40	51	42	38	40	36
5570278	CXCL9	40	36	40	42	40	43	36	39	42	39	39
4280504	DSOR8	43	48	37	47	52	45	49	49	42	44	50
430446	KRT81	43	55	49	47	54	44	44	207	54	67	47
2750689	LOC729826	84	62	69	85	69	69	87	74	63	84	63
1980593	PTHLH	52	45	49	114	53	40	48	69	1235	159	58
2370632	MMP11	117	122	118	114	94	173	140	128	76	64	115
6550500	S100A7	77	77	66	84	63	73	84	68	65	118	77
3310333	WISP3	58	57	58	63	59	84	71	67	64	94	58
6270553	CXCL10	54	62	80	52	96	63	66	56	139	60	65
7050220	NMU	63	50	94	48	60	64	65	197	88	85	44
1510364	GBP5	47	42	50	48	70	39	70	51	48	42	55
3990619	TOP2A	822	807	1118	653	787	1951	618	429	1107	394	56
6860424	SERPINE4	51	46	38	40	43	45	48	49	184	61	49
5360064	GNYL	41	46	48	46	43	41	43	47	45	49	44
6290534	GTSE1	66	74	74	104	81	78	76	67	88	58	80
1050168	PI3	41	49	43	45	42	48	42	106	950	4682	40
7580554	S100A7A	75	75	61	63	68	61	74	72	73	60	75
5578711	IDO1	62	44	53	60	164	61	60	66	51	58	59
3120113	GIB6	102	87	89	106	100	92	75	89	1810	407	102
2320600	CALML3	55	57	46	60	46	53	53	45	133	204	47
1470056	SERPINE3	68	75	60	67	71	66	70	84	454	238	59
6620487	CXCL6	90	251	407	55	231	52	147	7383	67	70	195
6770131	OLFM4	42	43	47	39	48	46	45	46	46	45	36
1770603	TCN1	39	46	40	43	37	38	34	47	45	136	36
6100259	VSNU1	65	78	67	62	78	74	76	75	210	164	62
6420605	UBO	72	79	85	52	132	53	120	122	76	67	71
1260270	AIM2	84	63	76	91	70	90	91	73	111	78	82
4490093	ABCC9	62	54	58	50	50	56	75	60	62	53	54
1580762	SERPINE3	63	78	77	52	74	65	50	79	229	460	63
380259	INDO	46	58	45	47	116	36	44	42	48	53	49
5860289	KRT5	46	44	39	1201	40	42	37	45	10600	8457	40
1580470	LOC1001308	61	50	67	60	75	52	62	55	61	51	63
4900458	KRT14	46	39	42	299	47	41	48	39	10043	9810	42
2510605	FAM83A	44	46	44	504	47	41	47	44	814	426	49
4730242	FAM181B	45	47	55	49	44	47	45	44	73	61	51
6760286		61	63	66	64	69	71	69	64	70	113	61

FIGURE 1-CONTINUED

ProbeID	Symbol	[[042], HOK (Human Oral Keratinocyte)], MBA_2126	[[043], HEEPIC t (Human Esophageal Epithelial Cell), MBA_2128	[[044], HPAEPIC t (Human Pulmonary Alveolar Epithelial Cell), MBA_2136	[[045], HBSPIC t (Human Bronchial Epithelial Cell), MBA_2137	[[046], HTEPIC t (Human Tracheal Epithelial Cell), MBA_2138	[[049], HSAEPIC t(Human Small Airway Epithelial Cell), MBA_2139	[[050], HRPTEPIC t (Human Renal Proximal Tubular Epithelial Cell), MBA_2147	[[052], HREPIC t (Human Renal Epithelial Cell), MBA_2148	[[053], HUC t (Human Urothelial Cell), MBA_2152	[[054], HPTEPIC t (Human Prostate Epithelial Cells), MBA_2153	[[055], HH t (Human Hepatocyte)], MBA_2160
2490541	MAGEA10	53	56	72	75	70	65	61	78	87	55	70
4280132	DSCR8	65	64	52	66	59	54	61	59	53	69	55
4760626	MMP12	47	44	51	45	42	39	37	48	42	37	47
5570278	CXCL9	41	45	39	37	44	38	39	44	49	42	47
4280504	DSCR8	40	44	46	59	39	41	52	52	51	51	43
430446	KRT81	45	150	114	1684	105	2896	103	459	51	1534	328
2750689	LOC729826	58	72	72	90	81	97	74	64	72	70	60
1980593	PTH1H	1384	1164	43	931	1852	908	48	68	48	1400	52
2370632	MMP11	71	80	83	73	83	70	298	268	112	86	108
6550503	S100A7	75	83	72	54	104	63	62	78	67	87	69
3310333	WISP3	70	58	66	68	55	62	84	70	72	220	69
6270553	CXCL10	238	58	52	134	55	67	60	75	69	65	58
7050220	NMU	204	364	136	399	170	172	73	139	53	134	50
1510364	GBP5	47	38	45	46	44	48	45	40	49	43	51
3980619	TOP2A	115	747	553	972	235	93	41	836	939	279	83
6860424	SERPINA4	60	73	42	65	46	44	42	47	37	107	39
5360064	GNYL	48	48	61	42	47	54	46	48	43	46	44
6280594	GTSF1	73	91	81	69	75	87	74	66	92	88	86
1050168	P13	228	1050	52	2035	123	1846	42	49	45	4253	60
7550554	S100A7A	81	66	69	79	74	72	66	80	73	65	65
5570711	IDO1	47	65	67	55	66	50	55	78	54	58	60
3120113	GTB6	324	311	87	1628	211	118	79	94	68	632	80
2320600	CALML3	206	168	44	104	70	70	46	42	52	860	57
1470056	SERPINA3	179	707	70	525	196	368	73	81	86	704	80
6620487	CXCL6	65	73	53	70	69	62	61	818	68	63	158
6770131	OLFM4	46	45	37	53	66	44	41	48	39	39	39
1770803	TCN1	37	168	37	506	932	66	42	53	36	115	65
6100259	VSNN1	384	491	83	200	329	195	75	89	75	217	144
6420605	UBD	84	69	102	75	98	79	80	288	91	76	4585
1260270	AIM2	83	69	74	62	82	66	59	76	62	67	64
4490093	ABCC9	64	53	57	60	57	66	51	79	66	67	68
1580762	SERPINA3	240	782	75	712	839	591	74	71	78	356	76
380259	INDO	40	46	51	45	53	47	45	56	40	48	62
5860289	KRT5	10529	12094	43	10417	8323	8457	37	36	41	6992	41
1580470	LOC10013088	55	53	56	53	57	63	42	58	60	64	65
4900458	KRT14	9637	7033	43	8295	3250	9258	49	48	43	8572	40
2510605	FAM83A	394	220	303	666	1067	317	42	47	43	434	45
4730242	FAM181B	100	76	46	119	149	64	48	47	45	120	44
6760286		84	86	78	182	65	73	61	60	58	83	89

FIGURE 1 - CONTINUED

ProbeID	Symbol	[[1056], HCEpIC t (Human Corneal Epithelial Cell), MBA_2167	[[1057], HK t (Human Keratocyte), MBA_2168	[[1058], HREpIC t (Human Retinal Pigment Epithelial Cell), MBA_2169	[[1059], HLEpIC t (Human Lens Epithelial Cell), MBA_2170	[[1060], HPEpIC t (Human Iris Pigment Epithelial Cell), MBA_2171	[[1061], HNPCEpIC t (Human Non- Pigment Ciliary Epithelial Cell), MBA_2173	[[1062], HTMC t (Human Tubercular Meshwork Cell), MBA_2174	[[1063], HMEpIC t (Human Mammary Epithelial Cell), MBA_2188	[[1064], HN t (Human Neuron), MBA_2105	[[1065], HSC t (Human Schwann Cell), MBA_2107	[[1066], HPC t (Human Perineural Cell), MBA_2108
2490541	MAGEA10	82	61	69	59	106	66	63	65	69	75	73
4280132	DSCR8	59	49	61	192	131	209	60	52	57	55	51
4760626	MMP12	49	48	37	42	38	57	35	45	41	44	50
5570278	CXCL9	42	45	47	40	37	41	46	38	37	34	34
4280504	DSCR8	51	50	48	62	73	95	46	48	46	40	45
430446	KRT81	46	47	50	49	109	49	52	5557	46	49	325
2750689	LOC729826	71	87	73	75	80	66	60	59	68	63	76
1980593	PTHLH	639	61	54	80	54	61	51	1779	83	52	64
2370632	MMP11	69	293	582	312	153	383	318	84	117	103	156
6550500	S100A7	76	67	63	81	91	75	82	110	64	65	71
3310333	WISP3	67	65	59	52	67	57	57	254	62	50	60
6270553	CXCL10	107	51	61	118	53	77	53	80	58	52	54
7050220	NMU	389	59	82	177	182	157	60	61	100	56	67
1510364	GBP5	46	50	42	46	49	42	38	47	43	49	45
3990619	TOP2A	985	65	366	487	717	261	609	1114	691	876	135
6860424	SERPINB4	50	44	38	52	39	39	36	55	43	46	41
5360064	GNYL	54	43	48	42	41	47	52	39	50	43	41
6290554	GTSF1	63	73	70	66	94	70	61	76	66	64	83
1050168	PI3	7427	37	35	55	46	46	39	3536	50	39	46
7550554	S100A7A	86	64	76	66	75	68	85	52	61	63	60
5570711	IDO1	57	76	52	56	48	64	60	51	68	62	63
3120113	GJB6	1788	116	105	87	83	77	90	191	104	93	109
2320600	CALML3	241	46	50	63	44	51	57	1903	44	45	50
1470056	SERPINB3	168	79	45	66	73	74	72	406	67	65	58
6620487	CXCL6	82	765	73	225	173	99	438	73	177	416	333
6770131	OLFML4	43	42	42	43	54	41	46	89	46	52	41
1770603	TCN1	96	37	47	39	38	40	36	382	35	42	42
6100259	VSNL1	304	65	61	84	70	95	82	353	174	75	75
6420605	UBD	272	78	64	249	60	85	68	59	88	66	73
1260270	AIM2	98	80	71	81	61	66	71	73	107	96	81
4490093	ABCG9	52	59	47	47	66	46	65	60	63	70	63
1580762	SERPINB13	670	75	69	74	84	61	69	180	72	72	80
380259	INDO	45	48	43	45	48	42	45	45	48	43	38
5860289	KRT5	9194	50	41	38	39	41	34	9287	41	40	41
1580470	LOC1001308	53	66	36	68	64	50	67	57	49	54	62
4900458	KRT14	9469	43	56	38	51	39	43	12094	47	54	44
2510605	FAM83A	672	42	43	48	114	60	37	314	36	49	38
4730242	FAM181B	87	43	71	40	72	45	51	56	112	54	46
6760286		111	64	70	53	66	64	66	71	65	52	64

FIGURE 1-CONTINUED

ProbeID	Symbol	[[067], HA t (Human Astrocyte), MBA_2109	[[068], HA-c t (Human Astrocyte-cerebellar), MBA_2110	[[069], HA-h t (Human Astrocyte-hippocampal), MBA_2111	[[071], HBVSMC t (Human Brain Vascular Smooth Muscle Cell), MBA_2101	[[072], HBVP t (Human Brain Vascular Pericyte), MBA_2102	[[073], HOPF t (Human Choroid Plexus Fibroblast), MBA_2105	[[074], HDF- t (Human Dermal Fibroblast-fetal), MBA_2119	[[075], HDF- t (Human Dermal Fibroblast-neonate), MBA_2120	[[076], HDF- t (Human Dermal Fibroblast-adult), MBA_2121	[[077], "HHDPC t (Human Hair Papilla Cell), 10µg", MBA_2122	[[078], HLF t (Human Lymphatic Fibroblasts Cell), MBA_2125
2490541	MAGEA10	60	62	58	78	84	76	99	61	68	70	57
4280132	OSCR8	56	47	59	59	56	64	52	51	54	46	58
4760626	MMP12	44	41	37	48	43	48	42	44	48	46	43
5570278	CXCL9	35	43	39	42	42	36	42	39	41	39	36
4280504	OSCR8	50	46	46	35	49	47	50	49	45	41	38
430446	KRT81	84	196	57	46	43	167	49	43	40	49	40
2750689	LOC729826	67	72	76	80	60	84	76	51	67	66	68
1980593	PTH1H	90	57	126	44	44	75	49	49	54	52	50
2370632	MMP11	148	100	132	193	282	146	227	221	233	137	91
6550500	S100A7	71	82	61	58	86	65	370	84	69	76	61
3310333	WISP3	71	46	62	71	62	51	65	46	51	66	64
6270553	CXCL10	116	58	62	47	59	67	60	59	63	58	65
7050220	NMU	216	154	267	69	52	146	61	54	58	62	60
1510364	GRPS	162	55	61	43	45	46	334	47	36	109	42
3990619	TOP2A	277	999	2332	1285	1065	1977	2822	192	878	531	1295
6860424	SERPINE4	44	42	42	36	37	36	65	36	43	41	46
5360064	GNLY	38	43	41	43	54	47	44	53	51	49	43
6290554	GTSE1	70	73	66	75	75	75	65	71	72	73	76
1050168	PT3	44	34	39	43	36	58	263	39	38	38	38
7550554	S100A7A	69	59	63	58	68	70	108	73	60	71	58
5570711	IDO1	62	60	75	60	60	58	60	55	62	68	78
3120113	QSOX6	106	91	84	116	76	78	124	145	111	96	80
2320600	CALML3	43	53	53	50	49	49	54	32	51	44	49
1470056	SERPINE3	70	69	66	61	72	78	183	61	75	60	67
6620487	CXCL6	179	817	140	386	87	2031	1105	57	58	379	96
6770131	OLFM4	47	43	42	39	40	48	48	39	43	42	44
1770603	TCN1	35	42	37	38	39	40	47	31	42	39	37
6100259	VSNL1	83	113	163	104	73	63	78	75	62	76	78
6420605	UBO	97	84	61	67	80	101	67	84	60	68	70
1260270	AIM2	82	82	81	72	85	78	114	85	65	89	92
4490093	ABCC9	62	53	50	60	60	60	67	62	76	77	63
1580762	SERPINE13	78	67	72	85	71	69	82	71	65	60	65
380259	INDO	46	43	64	57	39	39	39	49	39	45	46
5860289	KRT5	39	39	36	43	38	43	351	40	45	36	39
1580470	LOC1001308	59	54	63	60	49	45	55	43	60	52	57
4900458	KRT14	47	42	46	47	47	42	477	47	47	45	44
2510605	FAM83A	45	48	44	46	42	45	54	47	45	41	49
4730242	FAM181B	88	51	56	45	54	68	52	42	54	50	45
6760286		55	55	65	60	65	75	64	69	56	68	61

FIGURE 1-CONTINUED

ProbeID	Symbol	[[079], HPLF t (Human Peridontal Ligament Fibroblast), MBA_2127	[[080], HISM t (Human Intestinal Smooth Muscle Cell), MBA_2130	[[081], HCoSM t (Human Colonic Smooth Muscle Cell), MBA_2131	[[082], HPA t (Human Pulmonary Artery Smooth Muscle Cell), MBA_2134	[[083], HPA t (Human Pulmonary Artery Fibroblast), MBA_2135	[[084], HP t (Human Pulmonary Fibroblast), MBA_2140	[[085], HBS t (Human Bronchial Smooth Muscle Cell), MBA_2141	[[086], HSM t (Human Tracheal Smooth Muscle Cell), MBA_2142	[[087], HSM t (Human Skeletal Muscle Satellite Cell), MBA_2143	[[088], HSM t (Human Skeletal Muscle Satellite Cell), MBA_2145	[[089], HSM t (Human Skeletal Muscle Myoblast), MBA_2145
2490541	MPGEA10	62	64	47	51	34	66	62	64	63	71	83
4280132	DSCR8	59	60	54	52	66	57	63	57	51	59	59
4760626	MMP12	35	47	43	49	45	39	48	43	30	44	45
5570278	OXCL9	38	43	51	38	40	43	39	37	40	51	38
4280504	DSCR8	50	46	49	45	52	48	57	41	48	39	45
430446	KRT81	48	45	49	165	56	57	49	41	42	47	53
2750689	LOC729826	88	59	64	61	88	55	64	64	71	65	82
1980593	PTH1H	50	58	43	54	55	47	45	50	49	46	50
2370632	MMP11	87	79	159	98	85	107	188	158	138	123	74
6550500	S100A7	68	73	54	71	75	72	74	67	81	65	65
3310333	WISP2	54	74	67	58	61	61	66	61	59	62	70
6270553	OXCL10	65	55	64	61	61	55	48	56	60	58	58
7050220	NMU	94	63	40	91	68	57	48	66	59	109	55
1510364	GBP5	41	44	46	43	44	34	46	43	42	44	47
3950619	TOP2A	1810	1101	72	458	1593	682	1756	1399	1802	1307	2222
6860424	SERPINB4	49	45	43	37	46	44	51	45	40	93	47
5360064	GNL1	44	36	54	44	47	44	50	46	43	40	45
6290554	GP1F1	72	64	79	82	81	79	61	83	63	71	71
1050168	P13	51	39	39	50	39	45	37	47	40	51	43
7550554	S100A7A	71	56	67	59	65	78	67	71	73	73	65
5570711	IDO1	63	55	55	69	67	63	74	68	64	52	57
3120113	GPB6	107	98	82	82	99	105	97	98	91	84	79
2320600	CALML3	51	56	53	56	48	48	54	48	44	39	51
1470056	SERPINB3	66	71	80	68	70	66	72	68	76	119	64
6620487	OXCL6	2624	231	188	345	892	67	69	72	128	748	353
6770131	OLF4	44	37	47	45	45	40	47	37	42	34	44
1770603	TCN1	42	39	44	44	38	40	34	36	32	40	39
6100259	VSNL1	65	63	65	78	79	69	74	57	82	77	67
6420605	UBD	79	67	69	58	57	77	78	68	71	68	67
1260270	AIM2	86	84	83	89	75	64	71	83	129	103	178
4490053	ABCC9	70	60	62	53	65	49	63	53	88	61	131
1580762	SERPINB13	69	87	65	75	77	64	72	58	60	76	70
380259	INDO	45	52	47	40	41	47	47	39	50	53	40
5860289	KRT5	36	43	40	38	40	37	44	43	39	48	42
1580470	LOC1001308	56	62	54	61	53	57	59	52	55	50	63
4900458	KRT14	46	45	55	56	38	50	44	40	47	50	45
2510605	FAM3A	44	52	40	49	39	40	47	47	41	46	43
4730242	FAM181B	49	50	49	46	47	39	45	41	47	44	48
6760286		55	71	51	55	60	55	67	68	70	65	59

FIGURE 1-CONTINUED

ProbeID	Symbol	[[1090], HRCMC t (Human Renal Mesangial Cell), MBA_2149	[[1021], HPF tDNA (Human Prostate Fibroblasts Cell), MBA_2154	[[1093], HCO t (Human Calvarial Osteoblasts Cell), MBA_2155	[[1096], HNPC.tDNA (Human Nucleus Pulposus Cells), MBA_2157	[[1097], HAF t (Human Annulus Fibrosus Cell , MBA_2158)	[[1098], H-HStEC t (Human Hepatic Stellate Cell , MBA_2161)	[[100], HCN a t (Human Cardiac Myocyte- adult), MBA_2165	[[101], HCF- a t (Human Cardiac Fibroblast- adult ventricle), MBA_2166	[[102], HConf t (Human Conjunctival Fibroblast), MBA_2172	[[103], HVMF t (Human Villous Mesenchyma (Fibroblast), MBA_2176	[[104], HAMMSC t (Human Amniotic Mesenchyma (Cell), MBA_2177
2490541	MAGEA10	78	88	65	61	64	70	64	74	69	73	94
4280132	DSR8	61	55	56	51	54	65	67	56	53	52	69
4760626	MMP12	39	46	42	39	41	41	42	47	40	40	36
5570278	CXCL9	43	40	38	42	38	41	48	40	43	44	40
4280504	DSR8	45	51	43	55	40	54	40	46	41	51	60
430446	KRT81	45	56	52	47	47	72	55	47	43	48	51
2750689	LOC729826	69	61	69	69	63	77	77	56	64	56	63
1980593	PTH1H	54	50	44	42	57	70	51	41	58	51	56
2370632	MMP11	240	104	96	127	128	118	114	136	202	98	133
6550500	S100A7	80	74	62	78	78	58	58	58	79	73	71
3310333	WISP3	75	70	52	193	140	59	63	64	72	67	74
6270553	CXCL10	62	65	71	56	57	66	58	56	59	52	65
7050220	NMU	87	56	49	57	61	107	74	50	53	53	52
1510364	GBP5	44	54	49	42	33	50	44	48	50	46	48
3990619	TOP2A	76	286	391	1575	1713	876	1847	121	421	335	462
6860424	SERPINE4	54	53	52	48	62	42	48	46	43	38	42
5360064	GNLY	44	44	41	45	49	51	45	47	49	43	45
6290534	GTSF1	67	73	79	70	73	70	89	74	79	136	133
1050168	P13	39	45	40	41	42	54	41	46	42	33	30
7550554	S100A7A	83	74	75	68	64	63	72	71	58	62	66
5570711	IDO1	61	63	68	66	58	64	70	59	52	80	56
3120113	GJB6	79	92	107	80	88	104	101	105	63	97	117
2320600	CALML3	43	43	57	46	50	55	55	52	53	46	59
1470056	SERPINE3	54	84	73	89	79	58	64	79	59	62	87
6620487	CXCL6	137	160	126	125	134	746	1072	759	231	130	148
6770131	OLFM4	42	36	38	43	40	51	34	46	43	38	39
1770603	TCN1	35	37	39	37	36	41	51	45	38	36	40
6100259	VSXN1	53	65	101	102	114	72	64	78	87	82	77
6420605	UBD	87	74	76	83	64	82	68	72	71	71	69
1260270	AIM2	98	75	78	85	79	89	84	65	79	71	71
4490093	ABCC9	63	68	55	48	70	68	54	58	57	49	69
1580762	SERPINE13	63	64	59	71	71	73	72	56	75	79	77
380259	INDO	47	39	48	48	48	45	45	40	43	48	39
5860289	KRT5	38	27	42	39	38	38	36	36	41	41	42
1580470	LOC1001308	72	57	57	67	50	62	64	57	51	68	68
4900458	KRT14	44	44	37	52	46	42	50	42	41	44	52
2510605	FAM83A	43	47	43	43	47	42	44	39	42	46	50
4730242	FAM181B	53	45	38	63	42	47	50	47	46	42	52
6760286		72	69	73	66	56	67	57	61	58	55	69

FIGURE 1-CONTINUED

ProbeID	Symbol	[[105], HCMSC t (Human Chorionic Mesenchyma Stromal Cell), MBA_2178	[[106], HPA- Preadipocyte- visceral), MBA_2179	[[107], HPA- Preadipocyte- subcutaneous (s), MBA_2180	[[108], HOF (Human Ovarian Fibroblast t), MBA_2182	[[109], HCMSC-bm t (Human Mesenchyma Stem Cell- bone marrow (adipose), MBA_2183	[[110], HCMSC-ad t (Human Mesenchyma Stem Cell- adipose), MBA_2184	[[111], HCMSC-he t (Human Mesenchyma Stem Cell- hepatic), MBA_2185	[[112], HCMSC t (Human Umbilical Mesenchyma Stem Cell), MBA_2186	[[113], HCMSC t (Human Vertebral Mesenchyma Stem Cell), MBA_2187	[[114], HMF (Human Mammary Fibroblast), MBA_2189	[[115], HUMSC t (Human Umbilical Vein Smooth Muscle Cell , 10 µg", MBA_2192
2490S41	MAGEA10	79	78	69	60	68	64	78	64	73	57	91
4280132	DSCR8	71	61	51	54	83	52	62	58	59	53	44
4760626	MMP12	57	50	43	38	46	46	43	39	45	45	45
5570278	CXCL9	44	43	30	47	41	34	43	38	36	38	42
4280504	DSCR8	42	40	45	51	50	35	47	43	44	47	59
430446	KRT81	48	55	44	45	47	49	54	66	47	71	44
2750689	LOC729826	70	60	54	83	74	66	63	71	62	67	64
1980593	PTH1H	52	40	46	83	50	43	71	50	41	47	49
2378632	MMP11	121	88	71	107	238	107	127	75	93	137	125
6550500	S100A7	60	79	90	62	54	75	68	56	69	64	56
3310333	WISP3	70	66	49	48	57	64	62	72	61	71	67
6270553	CXCL10	66	59	55	64	54	57	64	61	54	56	53
7050220	NMU	62	55	46	74	67	59	54	47	69	55	57
1510364	GBP5	45	43	48	42	52	47	37	48	51	39	40
3990619	TOP2A	346	1652	59	1190	328	58	701	250	176	800	2280
6860424	SERPINB4	46	92	45	50	45	42	43	45	38	43	51
5360064	GNL1	42	40	46	44	168	43	48	50	43	51	52
6290554	GTSF1	82	74	78	86	83	67	72	72	79	61	81
1050168	PI3	49	39	46	39	42	42	40	39	37	36	50
7550554	S100A7A	67	69	68	74	73	80	74	74	73	78	63
5570711	IDO1	54	63	64	66	51	74	51	55	60	81	72
3120113	GJB6	76	85	94	86	86	71	96	101	92	88	108
2320600	CALML3	43	41	48	56	48	40	55	53	44	44	50
1470056	SERPINB3	52	107	80	89	57	66	77	66	78	71	76
6620487	CXCL6	589	1177	100	1118	62	75	115	2668	77	67	224
6770131	OLFM4	38	46	41	46	43	46	41	42	40	40	39
1770603	TCN1	41	38	42	33	38	38	39	36	41	38	39
6100259	VSNL1	63	73	72	66	86	63	70	49	64	65	81
6420605	UBD	71	65	62	66	73	64	86	72	70	77	75
1260270	AIM2	92	82	166	83	90	76	76	81	79	82	70
4490093	ABCC9	60	48	83	52	79	77	77	51	57	55	67
1580762	SERPINB13	53	76	75	75	90	76	52	55	73	73	68
380259	INDO	42	47	42	55	45	46	42	52	50	50	45
5860289	KRT5	40	37	38	36	72	44	47	36	33	37	40
1580470	LOC1001308	59	55	58	52	55	61	64	54	52	71	56
4900458	KRT14	43	38	41	41	50	42	41	38	44	48	35
2510605	FAM83A	71	46	44	40	46	50	41	41	39	45	50
4730242	FAM181B	45	48	44	44	43	47	49	53	43	54	49
6760286		53	57	62	61	68	65	61	64	59	67	59

FIGURE 1-CONTINUED

ProbeID	Symbol	[[116], HUASMC t (Human Umbilical Artery Smooth Muscle Cell), MBA_2193]	[[117], HEM t (Human Epidermal Melanocyte), MBA_2116]	[[118], HEM- t (Human Epidermal Melanocyte/medium), MBA_2117]	[[119], HEM t (Human Epidermal Melanocyte dark), MBA_2118]	[[121], Breast Within normal limits, MBA_2252]	[[122], Breast Within normal limits, rep2, MBA_2253]	[[123], Colon: sigmoid Within normal limits, MBA_2258]	[[124], Cervix Within normal limits, MBA_2261]	[[125], Endometrium Within normal limits, MBA_2243]	[[126], Ovary Within normal limits, MBA_2246]	[[127], Bone: femur distal Within normal limits, MBA_2228]
2490541	MAGEA10	63	63	55	63	52	57	63	70	74	72	63
4280132	DSCR8	41	62	57	53	57	69	59	52	48	68	50
4760626	MMP12	44	46	45	40	45	42	139	39	39	46	50
5570278	CXCL9	41	38	42	49	49	51	150	77	74	51	135
4280504	DSCR8	49	44	53	51	40	43	49	47	41	52	37
430446	KRT81	41	36	43	41	206	66	46	51	121	42	46
2750689	LOC229826	75	68	75	71	81	76	55	59	75	72	68
1980593	PTH1H	46	50	57	53	441	335	59	85	74	88	46
2370632	MMP11	115	72	89	98	90	96	114	286	613	395	141
6550500	S100A7	76	68	71	61	68	71	84	70	70	55	58
3310332	WISP3	70	72	65	51	95	81	58	72	64	57	118
6270553	CXCL10	53	49	63	52	134	84	169	108	115	75	245
7050220	NMU	68	57	61	61	56	60	72	194	53	57	54
1510364	GBP5	49	46	45	53	51	44	81	71	59	56	71
3990619	TOP2A	415	1174	67	464	2752	1717	390	1291	1047	1162	712
6860424	SERPINE4	44	42	40	42	36	45	33	619	43	41	42
5360064	GNLY	48	47	38	42	74	79	75	71	6701	47	84
6290554	GTSE1	68	71	63	66	64	65	88	66	82	79	73
1050168	PI3	45	118	337	40	117	195	704	1005	53	49	35
7550554	S100A7A	63	54	70	71	62	62	82	60	49	58	68
5570711	IDO1	68	54	58	56	71	70	96	109	2515	59	70
3120113	GJB6	92	71	87	98	82	81	80	366	112	94	84
2320600	CAUML3	54	46	56	45	193	68	64	2106	45	59	57
1470056	SERPINE3	86	66	136	56	50	64	60	4227	65	64	64
6620487	CXCL6	282	107	73	65	80	76	69	68	57	63	48
6770131	OLFML4	40	40	43	44	818	52	1559	332	43	52	89
1770603	TCN1	40	47	115	58	104	77	34	830	1562	36	45
6100259	VSNL1	102	68	62	78	107	135	55	149	60	78	65
6420605	UBD	67	66	89	64	214	85	188	73	84	72	70
1260270	AIM2	72	77	86	81	83	77	170	72	72	68	84
4490093	ABCC9	66	62	57	57	59	63	53	69	58	89	69
1580762	SERPINE13	61	70	75	77	64	73	84	1324	69	79	69
380259	INDO	45	42	44	48	54	77	77	90	1997	43	50
5860289	KRT5	37	70	75	36	562	264	43	715	44	42	44
1580470	LOC1001308	62	61	55	50	51	52	61	57	51	54	46
4900458	KRT14	44	99	81	47	1135	276	48	331	41	47	48
2510605	FAM83A	43	43	66	38	58	43	47	210	38	41	44
4730242	FAM161B	43	51	80	54	81	129	74	151	83	85	66
6760286		70	63	65	66	72	64	44	68	63	64	58

FIGURE 1-CONTINUED

ProbeID	Symbol	[[128], Lung Within normal limits, MBA_2234	[[129], Lung Within normal limits rep2, MBA_2235	[[130], Kidney Within normal limits, MBA_2240	[[131], Esophagus Within normal limits, MBA_2249	[[132], Esophagus Within normal limits rep2, MBA_2264	[[133], Lymph node Within normal limits, MBA_2304	[[134], Thyroid gland Within normal limits, MBA_2273	[[136], Pancreas Within normal limits, MBA_2276	[[137], Prostate Within normal limits, MBA_2285	[[138], Prostate Within normal limits rep2, MBA_2286	[[139], Rectum Within normal limits, MBA_2289
2490541	IMAGER10	58	58	59	67	69	66	66	66	74	65	73
4280132	DSR8	50	44	59	63	56	50	59	59	56	58	60
4760626	NMP12	53	52	59	43	45	101	46	46	41	44	212
5570278	OXCL9	127	528	111	131	103	2055	52	51	88	49	158
4280504	DSR8	42	55	44	55	47	42	52	48	44	42	49
430446	KRT81	54	48	43	42	39	46	94	40	53	56	42
2750689	LOC729826	84	59	59	63	65	63	65	57	71	65	74
1980593	PTH1H	45	77	49	122	116	49	59	51	49	51	49
2370632	MMP11	69	90	88	73	89	93	67	71	83	84	92
6550500	S100A7	83	70	90	407	464	79	66	58	57	76	73
3310333	MTSP3	64	49	65	59	75	70	52	68	68	63	53
6270553	CXCL10	213	727	167	109	231	542	73	58	173	76	829
7050220	NMU	42	53	49	634	625	64	57	68	52	54	70
1510364	GBPS	133	278	100	133	75	67	47	52	59	57	75
3990619	TOP2A	1388	262	192	123	274	147	116	74	63	60	160
6860424	SERPINA4	39	41	52	1179	1781	51	81	45	41	44	40
5360064	GNL1	321	230	64	92	82	255	72	56	50	45	125
6290554	GT5F1	70	85	61	81	77	98	72	85	84	71	89
1050168	PI3	77	149	87	11523	6236	53	50	39	58	60	4877
7550554	S100A7A	73	64	68	68	69	69	61	62	82	79	61
5570711	IDO1	414	649	130	67	81	475	135	62	62	65	81
3120113	GLB6	98	94	95	1047	1309	106	157	183	103	76	82
2320600	CALML3	53	47	128	3435	4978	53	53	47	93	96	53
1470056	SERPINA8	74	83	91	8403	9227	70	74	68	66	59	67
6620487	OXCL6	83	86	173	66	73	62	61	66	64	86	71
6770131	OLFM4	41	40	91	55	405	49	307	455	677	122	2591
1770603	TCN1	40	47	43	421	182	40	42	364	45	38	45
6100259	VSNU1	89	77	72	383	471	75	66	471	97	102	77
6420605	UBD	137	202	262	81	107	1204	60	134	208	74	239
1260270	AIM2	83	126	214	105	110	906	71	85	81	73	109
4490093	ABCC9	77	89	77	83	76	60	56	59	62	82	46
1580762	SERPINA13	65	65	93	2668	3646	70	69	78	65	73	65
380259	INDO	247	558	81	57	68	332	98	56	56	48	64
5860289	KRT5	51	41	82	2095	4065	48	45	39	299	321	43
1580470	LOC10013083	67	65	54	48	50	67	58	68	51	51	48
4900458	KRT14	46	43	46	400	581	47	43	49	355	252	43
2510605	FAM83A	44	43	50	759	1208	44	57	44	48	47	41
4730242	FAM181B	55	43	85	75	58	56	94	77	77	94	54
6760266		63	80	72	52	68	70	61	57	71	69	76

FIGURE 1-CONTINUED

ProbeID	Symbol	[[140], Liver within normal limits, MBA_2294	[[141], Stomach within normal limits, MBA_2297	[[142], Brain within normal limits, MBA_2300	[[143], Brain total RNA, rep2, MBA_2338_2	[[144], Fetal Brain total RNA, rep2, MBA_2338_2	[[145], Testis Within normal limits, MBA_2280	[[146], Testes total RNA, MBA_2313	[[147], Thyroid total RNA, MBA_2312	[[148], Ovary total RNA, MBA_2314	[[149], Adrenal Cortex poly A RNA, MBA_2315	[[150], Prostate total RNA, MBA_2316
2490541	MAGEA10	72	82	68	72	76	175	169	94	63	62	69
4280132	DSCR8	62	57	54	48	45	992	1290	45	57	56	54
4760626	MMP12	39	153	40	40	38	39	40	38	43	43	42
5570278	CXCL9	32	115	38	38	41	83	82	162	90	84	81
4280504	DSCR8	43	47	46	46	41	170	175	44	45	45	48
430446	KRT18	50	35	56	41	52	44	43	76	46	48	53
2750689	LOC729826	67	59	47	57	63	83	86	57	54	60	70
1980593	PTHLH	56	55	57	51	45	54	61	69	43	56	58
2370632	MMP13	65	73	68	192	245	134	127	77	271	96	86
6550500	S100A7	64	73	71	71	55	68	69	75	63	62	90
3310333	WISP3	50	55	65	58	56	73	87	57	58	69	67
6270553	CXCL10	189	365	173	100	97	61	60	110	99	130	113
7050220	NMU	52	67	69	66	79	60	78	60	50	86	49
1510364	GBP5	68	61	48	38	44	55	55	57	55	75	49
3990619	TOP2A	78	255	332	585	56	52	49	54	494	54	274
6860424	SERPMB4	38	40	40	40	47	37	43	41	42	42	44
5360064	GNYL	65	87	73	44	47	47	49	95	133	77	67
6290554	GTSF1	89	74	75	80	82	3588	4012	77	61	70	61
1050168	PI3	47	288	39	41	44	44	47	176	41	44	92
7550554	S100A7A	89	74	56	78	65	66	53	56	61	61	73
5570711	IDO1	59	221	56	52	53	57	59	86	58	73	70
3120113	GJB6	92	88	311	153	154	87	84	134	96	76	76
2320600	CALML3	55	59	53	50	49	59	90	93	53	44	98
1470056	SERPMB3	65	69	63	60	55	79	71	74	58	56	84
6620487	CXCL6	126	66	74	66	66	63	61	68	52	57	94
6770131	OLFM4	44	2179	50	83	80	42	81	90	44	46	3265
1770603	TCN1	34	2304	38	39	49	50	49	860	32	33	51
6100259	VSNL1	182	68	6409	513	505	72	70	57	104	276	104
6420603	UBD	222	206	70	73	65	72	70	105	63	70	134
1260270	AIM2	90	74	71	113	117	88	86	95	78	87	96
4490093	ABCC9	104	58	69	68	55	60	69	65	59	90	80
1580762	SERPMB13	72	56	72	67	66	59	59	79	69	75	69
380259	INDO	52	113	47	40	49	46	45	79	50	46	54
5860289	KRT5	45	35	36	41	37	39	41	74	44	37	227
1580470	LOC1001308	55	45	53	59	55	378	717	50	59	48	52
4900458	KRT14	58	38	37	49	50	42	40	81	41	45	125
2510605	FAM83A	45	45	33	44	38	44	47	57	42	46	50
4730242	FAM181B	51	41	663	536	500	56	63	132	119	61	61
6760286		63	73	65	67	63	69	69	56	59	47	84

FIGURE 1 - CONTINUED

ProbeID	Symbol	[[151], Dorsal root ganglion total RNA, MBA_2317	[[152], Salivary Gland total RNA, MBA_2325	[[153], Salivary Gland total RNA, MBA_2326	[[154], MP Breast adjacent normal, MBA_2209	[[155], MP Colon adjacent normal, MBA_2211	[[156], MP Kidney adjacent normal, MBA_2213	[[157], MP Liver adjacent normal, MBA_2215	[[158], MP Lung adjacent normal, MBA_2217	[[159], MP Rectum adjacent normal, MBA_2219	[[160], MP Stomach adjacent normal, MBA_2221	[[161], Lymphoid tissue Lymphoma extranodal marginal zone B-cell, MBA_2268
2490541	MAGEA10	68	63	83	70	76	75	72	63	77	80	64
4280132	DSCR8	48	52	44	57	57	52	55	61	45	57	54
4760626	MMP12	43	44	50	151	92	58	42	59	419	50	58
5570278	CXCL9	53	97	71	258	170	98	231	584	222	72	244
4280504	DSCR8	42	48	46	46	50	44	51	46	47	50	44
430446	KRT81	45	106	101	1093	63	53	37	49	42	48	50
2750689	LOC729826	66	70	68	76	57	58	65	66	61	60	56
1980593	PTHLH	68	46	49	84	44	49	49	47	62	42	60
2370632	MMP11	79	60	125	400	92	504	58	70	96	72	133
6550500	S100A7	54	106	75	100	92	63	64	71	64	75	65
3310333	WISP3	72	67	79	86	76	85	51	67	57	59	84
6270553	CXCL10	121	72	72	423	314	179	781	1089	289	191	504
7050220	NMU	66	69	56	50	66	54	54	49	51	66	48
1510364	GBPS	49	46	50	72	68	65	74	278	99	64	315
3990619	TOP2A	45	94	100	1819	801	59	82	82	55	57	56
6860424	SERPINE4	38	50	45	44	43	44	41	34	40	41	42
5360064	GNLY	64	52	53	62	325	106	58	167	167	64	56
6290554	GTSE1	82	99	60	84	72	70	63	95	80	79	96
1050168	PF3	90	210	206	60	320	54	63	118	1604	65	37
7550554	S100A7A	60	56	84	72	63	58	70	60	61	90	64
5570711	DDI1	48	57	82	74	137	69	72	804	133	67	138
3120113	GJB6	110	86	109	72	120	75	133	93	103	90	79
2320600	CALML3	63	865	950	1158	52	53	58	53	51	45	55
1470056	SERPINE3	78	56	89	63	57	90	71	94	61	72	57
6620487	CXCL6	65	59	62	66	64	94	123	77	58	65	62
6770131	OLFML4	132	454	484	110	13882	607	44	39	963	51	44
1770603	TCN1	49	6104	5889	91	48	39	55	39	43	2836	40
6100259	VSNL1	668	85	73	135	78	86	219	98	84	57	81
6420605	UBD	106	159	93	215	1304	274	1049	266	196	216	1213
1260270	AIM2	154	68	100	87	98	74	137	123	154	102	1044
4490093	ABCC9	66	48	52	49	54	72	85	68	75	64	39
1580762	SERPINEB13	66	72	92	66	58	82	61	73	74	77	78
380259	INDO	49	50	44	69	83	56	56	622	70	54	92
5860289	KRT5	41	337	302	109	33	39	42	43	34	45	45
1580470	LOC1001308	52	74	66	51	61	57	53	55	72	57	55
4900438	KRT14	137	556	531	318	49	51	40	51	46	39	57
2510605	FAM83A	45	49	54	77	50	39	42	44	40	39	50
4730242	FAM181B	181	80	97	50	65	84	38	49	62	48	52
6760286		73	78	72	56	73	64	50	73	65	65	81

FIGURE 1-CONTINUED

ProbeID	Symbol	[[162], Lymphoid tissue Lymphoma follicular, MBA_2269	[[163], Uterus Tumor Adenocarcin oma, MBA_2318	[[164], Kidney Tumor renal cell carcinoma, MBA_2321	[[165], Breast Tumor invasive ductal carcinoma, MBA_2324	[[166], Breast Adenocarcin oma of breast, ductal, MBA_2255	[[167], Colon: right Adenocarcin oma of colon, MBA_2259	[[168], Colon Tumor invasive carcinoma, MBA_2323	[[169], Cervix cervix squamous cell, MBA_2263	[[170], Endometriu m Adenocarcin oma of endometriu m endometrioid, MBA_2244	[[171], Ovary Adenocarcin oma of ovary serous, MBA_2247	[[172], Ovary Tumor Carcinoma, MBA_2320
2490541	MAGEA10	54	62	74	62	74	66	71	76	71	56	58
4280132	DSR8	63	49	46	47	54	55	46	50	325	49	153
4760626	MMP12	62	339	59	52	51	324	474	373	181	46	217
5570278	OCL9	646	413	530	201	182	516	59	734	70	404	1060
4280504	DSR8	43	45	44	48	46	34	45	41	191	43	243
430446	KRT81	53	80	48	126	131	43	48	69	52	48	43
2750689	LOC729826	57	75	74	72	65	67	69	66	73	58	74
1980593	PTH1H	51	69	85	81	65	54	50	48	38	48	54
2370632	MMP11	85	2224	261	2551	317	1905	624	1111	691	470	773
6550500	S100A7	50	70	63	71	72	60	71	127	67	179	75
3310333	WISP3	59	103	65	75	86	58	79	61	71	275	166
6270553	CAC10	317	873	732	445	119	1588	204	2237	100	2527	1349
7050220	NMU	71	46	67	56	58	77	64	284	240	194	68
1510364	GBP5	210	685	174	79	54	109	67	245	51	198	206
3990619	TOP2A	45	736	622	138	94	104	375	93	474	452	127
6860424	SERPINB4	42	44	39	43	39	39	32	1140	45	34	45
5360064	GILY	164	450	238	97	67	60	69	261	114	115	206
6290554	GTSF1	349	83	74	84	69	103	69	82	59	74	88
1050168	PT3	58	545	103	65	222	335	2043	1682	44	904	111
7550554	S100A7A	63	60	74	79	55	48	65	85	66	117	56
5570711	IDO1	231	2724	216	76	53	253	66	1176	135	520	122
3120113	G386	90	93	87	88	96	83	83	83	83	86	89
2320600	CALML3	49	39	49	113	86	54	44	1271	60	53	51
1470856	SERPINB3	46	84	76	65	70	58	58	1713	48	74	60
6620487	CXCL6	75	248	54	68	62	79	66	193	77	66	146
6770131	OLFM4	37	622	42	97	251	3576	2104	60	58	35	42
1770603	TCN1	43	464	56	284	291	198	44	98	34	39	35
6100259	NSML1	66	77	78	87	81	248	71	487	70	60	84
6420603	UBD	1059	2065	2556	96	82	902	136	181	81	615	567
1260270	AIM2	1492	100	119	86	81	109	104	914	130	119	111
4490093	ABCC9	62	72	61	60	64	63	60	51	76	50	76
1580762	SERPINB13	72	61	62	70	73	59	77	1530	56	65	76
380259	INDO	157	2579	165	68	58	175	55	782	91	404	109
5860289	KRT5	39	69	40	138	187	35	37	5373	41	43	38
1580470	LOC1001308	59	52	65	44	58	53	50	57	71	50	50
4900458	KRT14	36	50	45	330	431	46	40	5685	48	58	49
2510605	FAM83A	52	287	43	41	45	42	42	64	49	82	45
4730242	FAM181B	53	114	44	57	56	44	77	56	719	91	56
6760286		73	67	89	69	60	70	62	354	67	68	72

FIGURE 1-CONTINUED

ProteinID	Symbol	[[173], Lung Carcinoma of lung squamous cell, MBA_2236	[[174], Lung Adenocarcin oma of lung, cell, MBA_2237	[[175], Lung Carcinoma of lung large cell, MBA_2238	[[177], Lung: left upper lobe Carcinoma of lung small cell, MBA_2239	[[178], Lung Tumor Squamous cell carcinoma, MBA_2232	[[179], Pleura Mesotheliom a of pleura, MBA_2256	[[180], Pleura Mesotheliom a of pleura mixed, MBA_2257	[[181], Kidney Carcinoma in situ of renal pelvis papillary transitional cell, MBA_2241	[[182], Gastroesoph ageal junction Adenocarcin oma of gastroesoph ageal junction, MBA_2251	[[184], Thyroid gland Carcinoma of thyroid follicular, MBA_2274	[[186], Pancreas oma of pancreas ductal, MBA_2277
2490541	MAGEA10	64	62	58	65	946	65	71	81	65	63	68
4280132	DSOR8	65	49	55	686	55	62	55	59	51	52	59
4760626	MMF12	1781	244	601	1965	137	66	44	130	811	50	801
5570278	CXCL9	189	1174	492	2054	61	245	91	57	100	43	71
4280504	DSOR8	38	46	43	585	49	46	47	56	44	46	41
430446	KRT81	79	73	46	167	57	50	45	49	49	50	52
2750689	LOC729825	63	65	60	72	70	70	55	56	70	78	67
1980593	PTH1H	206	102	69	52	1030	48	88	133	48	69	59
2370632	MMF11	442	848	1938	150	587	116	398	125	193	82	800
6550500	S100A7	85	62	73	74	131	61	64	83	77	57	85
3310333	WISP3	63	59	65	60	94	66	42	251	267	50	53
6270553	CXCL10	287	1775	1723	951	72	178	177	118	231	63	252
7050220	NMU	219	109	78	262	157	173	1798	71	196	962	168
1510364	GBP5	101	326	526	273	64	64	53	48	51	43	141
3980619	TOP2A	145	416	728	958	311	1595	1465	515	348	971	359
6860424	SERPINB4	293	34	59	41	53	50	39	432	39	48	53
5360064	GNYL	94	132	175	84	230	273	79	145	103	46	223
6290554	GTSF1	82	83	74	693	1257	68	67	200	76	78	84
1050163	PT3	264	92	66	55	644	339	87	3148	46	1405	61
7550554	S100A7A	98	68	67	71	71	58	65	59	59	67	117
5570711	IDO1	224	351	411	218	73	96	88	81	95	106	117
3120113	GJB6	73	87	83	92	459	96	86	1701	95	79	91
2320600	CALML3	1682	59	49	52	6189	44	54	1058	48	53	54
1470056	SERPINB3	269	67	74	73	97	87	69	4385	75	63	100
6630487	CXCL6	135	374	66	57	165	153	65	91	225	69	91
6770131	OLFML4	87	43	44	55	60	42	40	51	3536	46	2018
1770603	TCN1	56	149	58	37	47	40	43	5616	64	35	1355
6100259	VSNL1	443	70	87	64	236	74	75	56	62	61	72
6420605	URD	473	526	507	528	123	101	105	112	141	81	4591
1260270	AJM2	151	519	243	234	87	92	78	1409	78	55	128
4490093	ABCC9	73	62	60	71	55	59	48	45	61	76	58
1580762	SERPINB13	213	62	69	78	197	70	77	146	79	73	59
380259	INDO	158	202	235	136	58	69	53	63	62	98	75
5860289	KRT5	2261	39	40	37	6758	197	113	365	40	37	36
1580470	LOC1001308	61	55	52	60	58	46	49	55	60	57	60
4900458	KRT14	57	40	386	44	106	44	165	62	47	42	41
2510605	FAM83A	96	747	537	42	230	237	47	592	50	45	43
4730242	FAM181B	72	45	43	45	62	46	48	97	41	169	45
6760286		70	115	85	66	71	89	64	60	72	65	99

FIGURE 1-CONTINUED

ProbeID	Symbol	[[187], Pancreas Tumor of pancreas neuroendocrine, MBA_2278	[[188], Testis Seminoma of testis, MBA_2281	[[189], Testis Seminoma of testis rep2, MBA_2282	[[190], Prostate Adenocarcinoma of prostate, MBA_2287	[[191], Rectum Adenocarcinoma of colon, MBA_2290	[[192], Rectum Adenocarcinoma of rectum, MBA_2291	[[193], Liver: left lobe Carcinoma of liver hepatocellular, MBA_2295	[[194], Liver Cholangiocarcinoma of liver, MBA_2296	[[195], Bile duct Cholangiocarcinoma of bile duct, MBA_2283	[[196], Bile duct Cholangiocarcinoma of bile duct, MBA_2284	[[197], Stomach Tumor Adenocarcinoma, MBA_2319
2490541	MAGEA10	52	285	70	72	66	58	58	58	84	58	156
4280132	DSCR8	55	1033	525	57	53	57	51	53	54	50	457
4760626	MMP12	45	74	549	59	570	817	40	570	86	126	396
5570278	OXC19	31	1046	2185	190	676	94	136	408	100	148	312
4280504	DSCR8	46	538	364	43	45	42	45	48	38	51	240
430446	KRT81	45	40	43	46	45	49	42	53	51	218	49
2750689	LOC729826	71	62	70	69	80	55	67	65	64	64	77
1980593	PTHLH	45	130	45	48	59	52	53	78	54	54	57
2370632	MMP11	146	133	142	103	151	454	194	494	800	992	1332
6550500	S100A7	60	71	83	59	70	69	74	81	62	150	407
3310333	WISP3	50	45	48	68	58	89	72	64	65	144	70
6270553	OXC10	53	987	1443	268	436	299	211	3487	154	626	393
7050220	NMU	62	153	196	51	63	129	73	54	84	228	83
1510364	GBP5	43	175	422	74	162	78	76	153	67	128	130
3990619	TOP2A	295	2560	501	469	608	514	1494	128	321	159	929
6860424	SERPINE4	42	39	42	46	42	60	37	46	48	150	82
5360064	GNL1	57	316	125	67	128	131	56	300	86	85	94
6290354	GTSL1	63	1905	1730	61	89	102	85	73	89	59	293
1050168	P13	41	47	38	88	7712	1462	43	14093	1006	1979	14422
7550554	S100A7A	65	56	67	68	71	62	61	74	71	69	99
5570711	IDO1	63	112	214	112	264	162	85	87	81	378	119
3120113	GJB6	91	84	99	86	77	89	84	85	96	486	86
2320600	CALML3	47	55	44	83	70	46	57	44	53	52	60
1470056	SERPINE3	68	65	72	83	81	115	67	63	64	782	338
6620487	OXC15	73	56	56	87	154	129	170	4467	100	583	164
6770131	OLFML4	41	42	46	393	8403	4133	47	61	745	3157	897
1770603	TGNI	36	41	36	46	77	950	36	190	6644	1037	418
6100259	VSML1	274	62	78	96	148	258	219	68	66	94	130
6420605	URD	69	272	693	325	1079	379	2062	2584	427	1206	1400
1260270	AIM2	72	117	122	78	149	92	78	82	94	133	101
4450093	ABCC9	105	54	57	69	68	63	67	65	73	56	63
1580752	SERPINE13	65	66	50	71	64	62	62	65	73	56	63
380259	INDO	52	67	116	82	170	114	61	78	74	270	96
5860289	KRT15	36	39	42	145	43	46	45	42	40	124	55
1580470	LOC1001308	51	50	49	85	49	55	60	65	51	55	56
4900458	KRT14	46	46	43	81	41	38	44	54	43	239	47
2510605	FAM83A	42	51	43	39	40	41	43	49	59	2504	334
4730242	FAM181B	108	41	59	71	55	48	46	44	57	47	48
6750286		66	54	71	61	62	67	68	76	70	97	88

FIGURE 1-CONTINUED

ProbeID	Symbol	[[198], Stomach Adenocarcinoma of stomach, MBA_2298	[[199], Brain Glioblastoma multiforme, MBA_2301	[[200], Brain Oligodendro glioma anaplastic, MBA_2302	[[201], Brain Astrocytoma anaplastic, MBA_2303	[[202], MP Breast primary tumor, MBA_2208	[[203], MP2 Breast primary tumor, MBA_2194	[[204], MP Colon primary tumor, MBA_2230	[[205], MP2 Colon primary tumor, MBA_2196	[[206], MP Kidney primary tumor, MBA_2212	[[208], MP Liver primary tumor, MBA_2214	[[209], MP2 Liver primary tumor, MBA_2200
2490541	MAGEA10	50	64	74	74	72	76	68	57	70	72	64
4280132	DSCR8	53	58	49	49	49	44	58	55	56	62	48
4760626	MMP12	286	37	40	40	185	61	951	569	91	116	46
5570278	CXCL9	186	51	40	40	283	229	301	157	65	197	62
4280504	DSCR8	43	46	43	43	45	45	46	50	49	45	47
430446	KRT81	48	50	49	49	753	56	56	47	46	52	48
2750689	LOC729826	65	75	72	72	74	64	70	77	54	70	65
1980593	PTH14	51	87	51	51	87	48	59	48	50	56	45
2370632	MMP11	231	74	59	59	1582	291	473	1147	764	134	151
6350500	S100A7	60	59	82	69	65	81	59	86	77	69	79
3310333	WISP3	67	58	66	64	88	57	53	63	82	88	52
6270553	CXCL10	386	394	65	67	398	202	747	741	128	341	129
7050220	NMU	77	78	67	74	57	53	468	103	186	54	58
1510364	GBPS	119	56	45	49	73	71	135	65	68	70	77
3990619	TOP2A	1351	85	277	991	81	593	193	1483	833	278	826
6850424	SERPINE4	47	36	47	42	38	44	42	44	42	39	44
5360064	GNLY	130	50	57	59	62	44	95	51	98	64	41
6290554	GTSF1	66	71	69	78	101	89	87	87	72	336	69
1050168	PI3	1317	116	49	44	58	40	776	1517	53	81	54
7550554	S100A7A	57	65	65	90	61	64	62	64	65	59	67
5570711	IDO1	190	75	52	59	76	75	127	80	57	84	79
3120113	GJB6	102	102	103	338	87	95	100	94	86	132	91
2320500	CALML3	51	44	48	50	1727	51	58	54	48	47	51
1470056	SERPINE3	67	65	77	62	64	71	58	68	60	48	74
6620487	CXCL6	188	60	56	45	75	57	215	79	57	146	180
6270131	OLFEM4	4219	43	67	131	77	42	2613	4671	47	58	57
1770603	TCN1	861	33	40	68	438	37	60	141	41	68	149
6100259	VSNI1	82	825	70	6775	137	71	313	369	80	289	70
6420603	UBD	809	115	71	68	170	114	541	1282	65	1003	459
1260270	ATM2	107	75	196	196	88	96	94	135	68	120	2925
4490093	ABCC9	45	48	62	67	55	54	53	54	66	51	68
1580762	SERPINE13	68	65	59	70	78	63	58	72	63	78	90
380259	INDO	128	45	44	43	48	53	93	62	50	55	72
5860289	KRT5	34	38	50	43	95	49	52	34	40	40	35
1580470	LOC1001308	53	62	58	61	54	56	56	49	58	54	56
4900458	KRT14	46	38	53	39	244	57	47	48	44	43	45
2510605	FAM83A	55	39	46	49	81	43	46	45	51	48	38
4730242	FAM181B	62	1417	4537	693	49	43	52	47	336	48	48
6760286		69	71	57	61	64	64	61	69	53	65	57

FIGURE 1-CONTINUED

ProbeID	Symbol	[[210], MP Lung primary tumor, MBA_2216	[[211], MP2 Lung primary tumor, MBA_2202	[[212], MP Rectum primary tumor, MBA_2218	[[213], MP2 Rectum primary tumor, MBA_2204	[[214], MP Stomach primary tumor, MBA_2220	[[215], MP2 Stomach primary tumor, MBA_2206	[[216], Breast Adenocarcin oma of breast metastatic, MBA_2254	[[217], Colon Adenocarcin oma of colon metastatic, MBA_2262	[[218], Cervix Adenocarcin oma metastatic consistent with cervical primary, MBA_2262	[[219], Ovary Adenocarcin oma of ovary serous metastatic, MBA_2248	[[220], Skin Malignant melanoma metastatic, MBA_2231
2490541	IMAG8A10	80	50	70	65	80	61	68	68	57	70	73
4280132	DSOR8	51	57	51	54	64	58	59	66	59	55	152
4760626	MNP12	110	796	483	790	912	57	57	265	45	83	392
5570278	CXCL9	493	265	157	375	158	345	41	204	51	374	374
4280504	DSOR8	49	47	44	44	53	44	39	42	41	40	75
430446	KRT81	42	52	59	45	53	52	1378	52	40	92	41
2750689	LOC729826	74	64	60	67	83	61	62	53	72	73	59
1980593	PTH1	47	1108	41	59	47	46	38	72	60	61	55
2370632	MNP11	191	444	1115	669	330	248	248	377	263	1454	88
6550500	S100A7	48	163	73	70	62	67	79	69	68	65	75
3310333	WSP3	54	55	80	54	86	107	72	221	64	427	65
6270553	CXCL10	348	612	438	943	315	483	127	182	73	1235	608
7050220	NMU	878	69	282	63	220	258	78	79	53	236	62
1510364	GBP5	139	167	73	180	85	229	38	144	57	151	172
3990619	TOR2A	657	190	628	968	796	936	2356	60	225	163	681
6860424	SERPINE4	45	157	44	50	65	44	45	45	47	47	41
5360064	GNLY	163	115	101	178	89	97	43	293	46	109	70
6290554	GTSF1	72	76	94	70	74	76	78	99	77	75	204
1050168	P13	54	4805	5210	744	6291	120	36	597	40	863	50
7550554	S100A7A	51	151	72	76	67	74	75	65	60	80	63
5570711	IDO1	155	174	153	231	115	331	57	282	57	187	214
3120113	GJB6	91	1172	98	86	103	106	86	88	87	85	102
2320600	CALML3	47	3229	45	63	47	61	50	96	43	52	52
1470056	SERPINE3	51	828	65	56	150	71	63	70	57	68	52
6620487	CXCL6	74	58	72	126	181	63	55	55	54	75	58
6770131	OLFM4	39	47	12149	10673	4125	4095	54	1170	41	42	43
1770603	ICN1	43	52	63	49	2256	120	39	1032	42	42	240
6100259	VSX1	72	517	232	237	94	276	109	208	70	81	60
6420605	UBD	261	125	1162	4320	276	2691	73	1265	223	378	245
1260270	ATM2	197	466	117	98	123	200	88	185	84	131	110
4490093	ABC9	68	53	52	56	56	71	71	62	63	53	54
1580762	SERPINE13	64	548	73	62	57	58	60	75	58	46	72
380259	INDO	101	149	90	195	74	268	45	179	44	145	160
5860289	KRT5	52	4499	42	38	39	40	42	89	46	50	31
1580470	LOC10013088	49	66	55	61	51	52	56	54	78	56	51
4900458	KRT14	49	9194	44	55	41	41	48	91	49	59	35
2510605	FAM83A	380	1718	56	52	209	46	47	209	55	48	39
4730242	FAM181B	48	138	43	53	47	41	109	56	74	52	41
6760285		88	85	70	76	61	73	75	-69	58	63	57

FIGURE 1-CONTINUED

ProbeID	Symbol	[[221], Skin Malignant melanoma metastatic rep2, MBA_2232	[[222], Eye Malignant melanoma metastatic, MBA_2233	[[223], Kidney Carcinoma of kidney renal cell metastatic, MBA_2242	[[224], Gastroesoph ageal junction Adenocarcin oma of ageal junction metastatic, MBA_2250	[[225], Neck Carcinoma of neck squamous cell metastatic, MBA_2266	[[226], Tonsil Carcinoma of tonsil squamous cell metastatic, MBA_2267	[[227], Thyroid gland Carcinoma of thyroid papillary metastatic, MBA_2275	[[229], Pancreas Tumor of pancreas neuroendocr ine metastatic, MBA_2279	[[230], Prostate Adenocarcin oma of prostate metastatic, MBA_2288	[[231], MP2 Breast metastatic tumor, MBA_2195	[[232], MP2 Colon metastatic tumor, MBA_2197
2490541	MAGEA10	70	84	59	71	372	70	61	77	68	63	64
4280132	DSCR8	46	53	66	57	52	52	59	55	54	39	53
4760626	MMP12	51	43	325	619	520	187	76	48	65	41	478
5570278	CXCL9	437	345	235	492	695	226	454	50	277	196	359
4280504	DSCR8	47	45	47	45	47	42	41	45	51	47	43
430446	KRT81	50	41	46	45	51	49	76	44	39	44	41
2750689	LOC729826	93	58	66	71	65	73	75	47	69	89	82
1980593	PTH1H	46	46	2034	49	660	337	67	68	49	51	39
2370632	MMP11	151	245	1857	258	778	161	239	113	286	615	491
6550500	S100A7	63	75	74	81	373	72	78	75	68	74	70
3310333	WISP3	68	52	57	50	135	69	59	63	64	56	69
6270553	CXCL10	1063	411	249	397	753	271	416	90	346	168	649
7050220	NNU	48	70	86	76	78	637	458	91	192	51	89
1510364	GAP5	247	108	114	94	194	75	118	49	69	67	144
3990619	TOP2A	1392	1530	902	2353	1618	165	668	1818	536	560	397
6860424	SERP1NB4	47	44	38	43	53	43	39	45	39	42	43
5360084	GNLV	86	72	110	503	92	81	91	70	56	60	83
6290554	GTSE1	65	73	71	112	245	54	69	66	79	70	91
1050168	PTB	48	55	48	2452	165	448	45	41	63	44	356
7550554	S100A7A	69	68	66	62	222	62	56	62	50	70	58
5570711	IDO1	95	77	112	146	292	153	111	54	78	71	157
3120113	GJB6	86	101	99	99	314	97	79	78	92	93	86
2320608	CALML3	53	53	53	48	1349	2672	42	55	52	62	51
1470056	SERP1NB3	63	66	66	69	118	87	61	63	78	55	52
6620487	CXCL6	65	50	56	61	75	57	57	83	70	67	63
6770131	OLFML4	43	49	127	66	75	51	41	42	54	39	655
1770603	TCN1	62	66	153	96	43	109	35	43	36	39	120
6100259	VSN11	71	80	75	75	106	297	73	81	58	64	204
6420605	UBD	1047	286	567	384	374	443	182	136	299	75	571
1260270	AIN2	205	100	274	132	218	98	90	69	91	98	183
4490093	ABCC9	75	54	76	58	82	53	54	66	74	61	79
1580762	SERP1NB13	70	55	61	74	135	404	65	74	68	64	67
380259	INDO	74	59	63	85	176	92	88	46	70	60	120
5860289	KRT5	43	46	36	39	1192	907	44	42	42	48	35
1580470	LOC1001308	68	58	53	71	59	57	48	49	46	55	69
4900458	KRT14	54	55	42	41	2993	52	50	47	47	43	39
2510605	FAM83A	47	38	43	44	313	58	58	41	48	43	46
4730242	FAM181B	63	87	45	44	63	48	49	215	54	48	47
6760286		74	68	63	64	86	72	71	61	56	64	60

FIGURE 1-CONTINUED

ProbeID	Symbol	[[233], MP2 Kidney metastatic tumor, MBA_2199	[[234], MP2 Liver metastatic tumor, MBA_2201	[[235], MP2 Lung metastatic tumor, MBA_2203	[[236], MP2 Rectum metastatic tumor, MBA_2205	[[237], MP2 Stomach metastatic tumor, MBA_2207	[[238], Cartilage Chondrosar- coma, MBA_2292	[[239], Cartilage Chondrosar- coma, MBA_2293	[[240], Bone Osteosarcoma metastatic, MBA_2230	[[250], Smooth muscle Sarcoma metastatic consistent with leiomyosar- coma primary, MBA_2229	[[260], Endometriu- m Endometrial stromal Sarcinamet- astatic, MBA_2245	[[270], Human Tumor Cell Line: A431, MBA_2222
2490541	MAGEA10	781	92	66	69	70	75	68	70	134	63	58
4280132	OSCR8	52	51	59	52	52	55	47	52	61	61	61
4750626	MMP12	105	50	405	618	222	47	40	39	44	47	45
5570228	CXC19	68	107	530	445	539	47	47	77	105	58	45
4280504	OSCR8	53	44	45	51	52	45	44	45	50	48	49
430445	KRT81	45	50	51	45	51	49	51	48	46	46	12222
2750689	LOC729826	59	55	73	58	64	183	59	64	74	78	66
1980593	PTHLH	50	44	1477	51	54	51	51	62	62	61	57
2370632	MMP11	190	87	86	295	113	153	162	406	1212	458	99
6550500	S100A7	218	65	80	76	68	78	55	65	71	58	67
3210333	WISP3	262	52	61	54	149	58	65	58	70	58	85
6270553	CXCL10	112	135	444	449	555	96	77	220	562	90	73
7050220	NNU	76	63	114	41	274	269	220	170	55	61	2030
1510364	GBP5	54	165	116	151	156	53	54	88	131	51	44
3950619	TOP2A	171	261	940	309	1643	239	250	1013	1010	388	1546
6860424	SERPINA4	92	36	84	44	41	47	43	45	40	45	77
5360064	GNL1	50	68	98	129	156	44	46	79	156	76	37
6290554	GTSF1	78	62	74	87	80	79	65	85	88	81	77
1050168	PIS	526	73	5767	192	83	40	37	39	48	43	83
7550554	S100A7A	99	64	60	66	63	66	66	74	66	72	51
5570711	IDO1	58	195	148	228	310	49	51	71	97	52	325
3120113	GJB6	172	92	2073	91	76	93	115	96	83	87	258
2320600	CALML3	778	45	2458	52	88	49	43	49	51	46	1402
1470056	SERPINE3	387	70	570	78	70	81	74	80	59	59	316
6620487	CXCL6	61	74	58	51	72	55	58	46	67	48	65
6770131	OLFM4	55	173	44	7359	43	44	46	45	41	39	38
1770803	TGNI	5642	130	39	44	93	36	35	55	35	34	38
6100259	VSNI1	59	88	368	330	192	67	78	90	132	59	107
6420605	USD	169	156	132	3612	2188	82	72	80	81	79	83
1260270	ATM2	336	2993	447	283	205	84	127	140	814	76	292
4490093	ABCC9	58	74	57	63	56	50	51	51	75	46	55
1580762	SERPINE13	96	71	330	86	58	80	67	60	61	68	556
380259	INDO	61	162	99	128	213	49	46	61	75	49	230
5860289	KRT5	214	43	8060	41	44	36	35	39	43	43	825
1580470	LOC1001308	56	54	57	59	48	60	55	57	61	52	62
4900458	KRT14	52	43	12489	48	40	45	50	36	44	46	50
2510605	PAN83A	422	50	1191	39	49	45	41	43	46	46	956
4730242	FAM181B	74	43	104	50	52	70	58	153	48	47	170
6760286		77	65	84	71	69	61	58	62	77	60	65

FIGURE 1-CONTINUED

ProbeID	Symbol	[[280], Human Tumor Cell Line: Hela, MBA_2223	[[281], Human Tumor Cell Line: Jurkat, MBA_2224	[[282], Human Tumor Cell Line: K 562, MBA_2225	[[283], Human Tumor Cell Line: MCF 7, MBA_2226	[[284], Human Tumor Cell Line: Raji, MBA_2227	[[285], Breast: MB231: 1.3ug/ul 2.11 19.5 ug, MBA_2306	[[287], Ovarian: OVCAR3: 0.8ug/ul 2.12 12 ug, MBA_2307	[[288], Ovarian: OV90: 0.7ug/ul 2.11 10.5 ug, MBA_2308	[[289], Ovarian: TOV112D: 1.4ug/ul 2.11 21 ug, MBA_2309	[[290], Ovarian: SKOV3: 0.18ug/ul 2.17 2.7 ug, MBA_2310
2490541	IMAGEA10	65	73	68	66	69	53	128	80	52	56
4280132	DSQR8	54	53	1575	54	65	53	449	136	56	52
4760626	MMP12	48	48	40	46	44	53	47	42	47	46
5570278	CXCL5	39	43	42	38	45	34	35	40	40	39
4280504	DSQR8	43	40	772	51	47	46	325	59	43	47
430446	KRT81	130	45	46	100	42	362	87	47	45	55
2750689	LOC22826	77	63	77	61	74	75	65	83	75	63
1980593	PTHLH	52	46	53	43	45	45	71	120	83	69
2370632	MMP11	102	66	89	93	63	79	92	97	196	75
6550500	S100A7	76	65	68	60	83	74	64	72	74	63
3310333	WISP3	72	65	68	68	56	70	62	66	62	61
6270553	CXCL10	60	53	57	54	482	61	81	63	55	58
7050220	NMU	618	61	3154	158	950	64	231	136	63	280
1510364	G8P5	47	62	43	41	45	42	118	51	39	147
3990619	TOP2A	166	1910	743	2097	1452	544	1722	1141	2398	1943
6860424	SERPINE4	43	47	47	42	41	42	43	41	43	52
5360064	GNLY	45	50	38	36	44	47	47	42	44	46
6290554	G1SF1	75	307	2684	65	78	76	69	102	70	73
1050168	PT3	136	46	43	43	45	41	40	181	42	203
7550554	S100A7A	72	75	76	68	60	59	61	374	42	67
5570711	IDO1	53	64	65	53	58	60	58	55	72	67
3120113	GJ66	92	114	149	120	91	97	108	90	58	1539
2320600	CALML3	53	54	46	44	42	47	45	48	83	84
1470056	SERPINE3	64	66	66	55	74	73	78	61	53	40
6620487	CXCL6	59	66	58	55	64	56	80	391	52	66
6770131	OLF4	42	44	33	38	44	49	40	111	40	47
1770603	TCN1	64	38	60	55	40	39	188	40	38	39
6100259	MSN1	63	66	74	70	78	74	68	12680	66	72
6420605	UBD	72	69	71	69	69	79	84	68	67	72
1260270	AIM2	50	66	110	69	822	78	76	82	85	87
4490093	ABCC9	48	64	65	59	63	52	67	53	48	68
1580762	SERPINE13	73	81	69	65	109	68	71	65	78	59
380259	INDO	44	46	43	45	50	42	50	46	44	1072
5860289	KRT5	36	40	42	44	41	46	38	35	40	67
1580470	LOC1001308	57	52	54	63	62	51	52	64	51	51
4900458	KRT14	50	47	47	39	51	48	41	43	42	53
2510605	FAM83A	182	46	1095	46	42	110	51	42	48	97
4730242	FAM181B	48	41	52	52	53	36	56	46	48	70
6760286		81	61	59	67	52	55	69	66	57	91

FIGURE 1-CONTINUED

ProbeID	Symbol	[[291], Glioma: SF188: 1.1ug/dl 2.12 16.5 ug, MBA_2311	[[292], NIH OVCAR-3 (Ovary Adenocarcin oma) Poly A RNA, MBA_2334	[[293], Cell line HEP G2 (Hepatoblast oma) Poly A RNA, MBA_2335	[[294], Cell Line MCF7 (Breast Adenocarcino ma) Poly A RNA, MBA_2336	[[295], Cell Line ZR75-1 (Breast Carcinoma) Poly A RNA, MBA_2337
2490541	IMAGE10	54	57	53	72	65
4280132	DSCR8	56	614	60	64	58
4760626	MMP12	48	39	41	40	41
5570278	CXCL9	44	37	42	38	42
4280564	DSCR8	50	275	41	81	45
430446	KRT81	45	45	45	401	130
2750689	LOC729826	68	69	58	62	72
1980593	PTH1H	43	82	47	48	48
2370632	MMP11	131	111	552	72	87
6550500	S100A7	86	51	56	201	197
3310333	WISP3	68	60	65	70	58
6270553	CXCL10	56	84	62	69	109
7050220	TNFR	67	2449	56	71	359
1510364	GBPS	47	115	44	44	46
3990619	TOP2A	3635	2780	1470	1946	2665
6860424	SERPINE4	40	37	40	44	45
5360064	GNLY	49	46	47	49	48
6290554	GTSE1	67	68	69	65	81
1050168	PT3	43	111	43	191	144
7550554	S100A7A	74	69	56	78	58
5570711	IDO1	63	58	53	49	52
3120113	GJB6	85	101	84	78	73
2320600	CALML3	43	47	46	49	43
1470056	SERPINE3	65	61	66	67	61
6620487	CXCL6	62	85	64	62	59
6770131	OLPM4	42	39	45	41	41
1770603	TCN1	37	47	37	40	44
6100259	VSNI1	120	62	873	59	65
6420605	VED	65	67	315	66	70
1260270	AIM2	76	90	70	86	83
4490093	ABCC9	55	61	48	53	43
1580762	SERPINE13	74	65	68	66	69
3802591	INDO	44	56	41	41	40
5860289	KRT5	36	35	36	39	38
1580470	LOC1001308	59	44	58	57	50
4900458	KRT14	47	42	45	47	44
2510605	FAM83A	45	57	45	64	46
4730242	FAM181B	42	43	31	46	40
6760286		64	71	60	61	88

FIGURE 1-CONTINUED

ProbeID	Symbol	[[135], Urinary bladder Within normal limits, MBA_2270	[[185], Urinary bladder Carcinoma of bladder transitional cell, MBA_2271	[[128], Urinary bladder Carcinoma of bladder small cell metastatic, MBA_2272	[[1030], HBdMEC t (Human Microvascula r Endothelial Cell), MBA_2150	[[1091], HBdSMC t (Human Bladder Smooth Muscle Cell), MBA_2151	[[1081], ESI 035 P49 mefs for P10, MBA_1622	[[1002], ESI 049 P21 mabrigel P6, MBA_1654	[[1003], H1-GFP, MBA_1641	[[1004], H1-GFP (tech rep), MBA_1641_2	[[1005], Normal PB-B Cells (CD19+) Comprehensive RNA, MBA_2340	[[1006], Normal PB-Pan-T Cells Comprehensive RNA, MBA_2341
1850523	GZMB	74	358	732	40	37	38	36	46	38	46	1061
580376	DSG3	101	1089	70	57	67	64	69	66	66	71	85
20452	TYMP	83	902	424	71	92	61	58	57	63	85	66
3830681	KRT6A	110	21365	125	67	71	73	65	73	83	70	76
2350196	KRT6B	40	2622	52	48	49	37	48	46	47	55	46
5260484	HLA-DRB1	72	1757	3218	70	84	82	66	87	106	116	350
4390398	LCN2	138	3798	102	93	92	157	138	134	126	234	147
540546	KRT14	67	450	75	72	62	69	63	80	55	72	45
2000300	IFI30	111	570	1337	134	82	151	107	156	134	402	117
3370601	LOC1001343	59	294	61	53	63	52	55	47	51	58	52
7400743	KIAA1618	100	1374	222	251	166	52	53	58	66	166	248
6060468	S100A8	783	20548	621	64	81	101	89	80	66	752	446
2350537	MMP7	394	6518	251	67	65	71	75	58	55	73	58
3800088	MMP7	504	9810	329	34	45	40	39	29	40	35	42
6770187	SPRR2A	64	857	74	69	59	72	70	62	71	69	60
5260095	GJB2	577	10284	85	87	86	73	80	73	71	67	61

FIGURE 1-CONTINUED

ProbeID	Symbol	[[007], Normal PB-Monocytes (CD14+) Comprehensive ve RNA, MBA_2342	[[008], CD19+ B Cells, MBA_2343	[[009], CLL Bone Marrow/CD19+ B Cells + B Cells (Relapsed/Refractory), MBA_2344	[[010], CLL Peripheral Blood CD19+ B Cells Comprehensive ve RNA (Untreated), MBA_2345	[[011], Fetal Liver CD34+ Cells Comprehensive ve RNA, MBA_2346	[[012], Fetal Liver CD36+ Erythroid Progenitor Cells, MBA_2347	[[013], Mobilized PB-Stem/Progenitor cells (CD34+) Comprehensive ve RNA, MBA_2348	[[014], Normal BM Myeloid Cells (CD105+) Comprehensive ve RNA, MBA_2349	[[015], Normal BM Myeloid Cells (CD33+) Comprehensive ve RNA, MBA_2350	[[016], Normal BM Stem/Progenitor Cells (CD133+) Comprehensive ve RNA, MBA_2351	[[017], Normal BM Stem/Progenitor Cells (CD34+) Comprehensive ve RNA, MBA_2352
1850523	GZMB	280	85	49	53	308	290	40	75	55	47	107
580376	DSG3	83	82	87	52	62	71	47	64	61	61	70
20452	TYMP	673	79	60	71	73	115	61	75	343	77	62
2830681	KRT5A	59	83	53	79	65	79	62	69	63	76	60
2350196	KRT5B	52	52	46	42	44	47	44	44	50	46	47
5260484	HLA-DQB1	3798	2418	3935	2012	84	84	1182	428	3022	1375	702
4390398	RCN2	184	91	87	108	93	106	144	1310	8138	746	182
540546	KRT4	92	68	58	62	53	55	57	67	52	55	59
2000300	IFI30	2585	201	115	189	93	209	119	201	2045	150	82
3370601	LOC1001343	53	48	53	57	47	44	63	54	47	60	52
7400743	KIAA1618	270	117	109	159	108	64	98	58	157	92	90
6060468	SLC0A8	15088	126	75	81	217	3600	1444	4408	15152	4065	501
2350537	MMP7	67	54	66	72	67	58	89	57	49	102	67
3800088	MMP7	31	27	35	33	36	42	66	32	37	102	49
6770187	SPR2A	60	68	69	57	55	69	68	66	64	68	66
5260095	GJB2	90	82	76	73	65	82	93	87	92	76	92

FIGURE 1-CONTINUED

ProbeID	Symbol	[[1018], Normal PB- Immature Myeloid Dendritic Cells Comprehensive RNA, MBA_2353	[[1019], Relapsed/Ref actory AML PBMC Comprehensive RNA, MBA_2354	[[1021], HBMEC t (Human Brain Microvascula r Endothelial Cell), MBA_2100	[[1022], HCPEC t (Human Choroid Plexus Endothelial Cell), MBA_2103	[[1023], HDMEC t (Human Dermal Microvascula r Endothelial Cell), MBA_2112	[[1024], HDLEC t (Human Dermal Lymphatic Endothelial Cell), MBA_2113	[[1025], HLEC t (Human Lymphatic Endothelial Cell), MBA_2124	[[1026], HIMEC t (Human Intestinal Microvascula r Endothelial Cell), MBA_2129	[[1027], HPMEC t (Human Pulmonary Microvascula r Endothelial Cell), MBA_2132	[[1028], HPAEC t (Human Pulmonary Artery Endothelial Cell), MBA_2133	[[1029], HRGEC t (Human Renal Glomerular Endothelial Cell), MBA_2146
1850323	GZMB	46	2232	44	37	41	39	42	43	37	36	41
580376	DSG3	63	66	67	68	71	67	59	69	2515	66	67
20452	TYMP	192	190	61	72	58	56	67	84	136	59	52
3830681	KRT6A	82	71	75	62	61	70	73	67	18105	63	54
2350196	KRT6B	43	55	39	46	50	42	52	45	12533	43	43
5260484	HLA-DRB1	10600	64	107	72	72	81	93	73	93	69	67
4390398	LCN2	93	903	106	105	75	83	100	108	1024	89	79
540546	KRT14	65	55	57	53	61	60	60	51	82	63	61
2000300	IFI30	2762	1154	64	111	100	113	132	133	124	77	82
3370601	LOC1001343	61	54	53	55	59	57	47	58	57	61	46
7400743	KIAA1618	111	159	149	208	110	125	124	141	95	162	167
6060468	S100A8	810	11656	77	87	21	73	68	82	17563	70	77
2350537	TM97	82	57	67	61	77	77	77	74	65	73	92
3800088	MMP7	49	37	46	37	54	56	48	39	39	40	69
6770187	SPRR2A	58	57	77	96	75	44	71	65	2812	61	56
5260095	GJB2	546	73	82	80	74	110	85	76	10317	81	57

FIGURE 1-CONTINUED

ProbeID	Symbol	[[031], {Human Hepatic Sinusoidal Endothelial Cell }, MBA_2159	[[032], {Human Cardiac Microvascula r Endothelial Cell }, MBA_2162	[[033], {Human Aortic Endothelial Cell }, MBA_2163	[[034], {Human Villus Capillary Endothelial Cell }, MBA_2175	[[035], {Human Ovarian Microvascula r Endothelial Cell }, MBA_2181	[[036], {Human Umbilical Vein Endothelial Cell }, MBA_2190	[[037], {Human Umbilical Artery Endothelial Cell }, MBA_2191	[[038], {Human Choroid Plexus Epithelial Cell }, MBA_2104	[[039], {Human Epidermal Keratinocyte (adult), MBA_2114	[[040], {Human Epidermal Keratinocyte (adult), MBA_2115	[[041], {Human Hair Outer Root Sheath Cell , MBA_2123
1850523	GZMB	39	46	44	39	38	40	46	37	44	31	45
580376	DSG3	73	70	70	245	65	58	59	58	1762	3035	84
20452	TYMP	63	71	53	104	81	57	53	83	100	199	65
3830681	KRT6A	74	60	75	16671	72	54	79	82	20021	18459	68
2350196	KRT6B	38	45	43	43	51	50	45	101	8295	9603	53
5260484	HLA-DRA1	70	78	61	82	232	82	69	58	87	84	71
4390398	LGN2	127	88	99	180	96	81	98	306	245	2427	95
540546	KRT4	61	53	67	63	53	61	70	59	52	61	60
2000300	IFT130	88	88	77	93	105	78	94	91	194	118	118
3370601	LOC1001343	50	49	57	53	56	56	59	51	69	87	54
7400743	KOAA1618	116	146	138	161	305	156	64	90	164	80	181
6060468	S100A8	83	86	76	72	87	99	68	69	8685	2161	68
2350537	MMP7	52	73	75	61	62	58	122	263	60	59	77
3600088	MMP7	39	42	56	42	33	38	94	258	32	42	50
6770187	SPRR2A	63	61	72	75	80	63	68	66	897	117	63
5260095	GJB2	79	89	71	161	80	98	83	122	9975	3260	69

FIGURE 1-CONTINUED

ProbeID	Symbol	[[042], HOK (Human Keratinocyte) , MBA_2126	[[043], HEpIC t (Human Esophageal Epithelial Cell), MBA_2128	[[044], HPAEPIC t (Human Pulmonary Alveolar Epithelial Cell), MBA_2136	[[045], HBEPIC t (Human Bronchial Epithelial Cell), MBA_2137	[[046], HTEPIC t (Human Tracheal Epithelial Cell), MBA_2138	[[049], HSAEPIC (Human Small Airway Epithelial Cell), MBA_2139	[[050], HRPTEPIC t (Human Renal Proximal Tubular Epithelial Cell), MBA_2147	[[052], HREPIC t (Human Renal Epithelial Cell), MBA_2148	[[053], HUC (Human Urothelial Cell), MBA_2152	[[054], HP-EPIC r (Human Prostate Epithelial Cells), MBA_2153	[[055], HH t (Human Hepatocyte) , MBA_2160
1850323	GZMB	46	36	41	39	41	38	39	39	40	41	38
580376	DSG3	1199	1443	74	3105	1008	2263	60	63	62	2766	56
20452	TYMP	91	84	113	209	94	65	124	68	135	81	170
3830681	KRT6A	17490	20021	185	21365	13986	19626	74	66	74	19450	82
2350196	KRT6B	3281	4566	40	17725	1066	11919	43	57	50	5246	44
5260484	HLA-DRE1	87	80	74	81	101	63	76	77	91	73	80
4390398	LCN2	127	358	230	662	6013	362	638	470	104	1564	883
540546	KRT14	58	392	71	283	641	68	50	59	59	64	63
2000300	IFI30	196	155	279	89	150	116	177	119	78	131	240
3370601	LOC1001343	56	59	54	90	53	104	57	49	61	76	60
7400743	KIAA1618	150	63	131	118	63	78	192	135	94	74	78
6060468	S100A8	1429	5889	1225	7544	2185	4691	24	92	70	8084	94
2350537	NMP7	60	57	352	61	81	55	3134	6684	75	98	353
3800088	NMP7	47	40	464	41	84	40	3441	8241	54	80	387
6770187	SPRR2A	379	194	59	310	413	308	70	78	68	206	60
5260095	GJB2	7033	4436	120	8514	4773	1106	122	237	74	5272	406

FIGURE 1-CONTINUED

Probe ID	Symbol	[[056], HCEPIC t (Human Corneal Epithelial Cell), MBA_2167	[[057], HK t (Human Keratocyte), MBA_2168	[[058], HREPIC t (Human Retinal Pigment Epithelial Cell), MBA_2169	[[059], HLEPIC t (Human Lens Epithelial Cell), MBA_2170	[[060], HREPIC t (Human Iris Pigment Epithelial Cell), MBA_2171	[[061], HNPCEPIC t (Human Non-Pigment Ciliary Epithelial Cell), MBA_2173	[[062], HTMC t (Human Trabecular Meshwork Cell), MBA_2174	[[063], HMEPIC t (Human Mammary Epithelial Cell), MBA_2186	[[064], HN t (Human Neuron), MBA_2195	[[065], HSC t (Human Schwann Cell), MBA_2107	[[066], HPC t (Human Perineurial Cell), MBA_2108
1850523	GZMB	40	37	38	40	43	38	47	38	35	30	47
580376	D5G3	2848	57	69	62	66	57	68	1753	57	67	69
20452	TYMP	153	94	60	56	77	54	59	98	72	59	67
3830681	KRT6A	19450	54	76	74	103	76	66	21365	71	53	88
2350196	KRT6B	13119	52	44	41	50	51	48	17911	51	44	52
5260484	HLA-DRA1	84	103	80	98	89	112	68	81	87	85	83
4390398	LCN2	1211	102	87	96	109	107	94	693	75	94	90
540546	KRT4	91	54	56	73	62	66	56	62	67	61	63
2000300	IFI30	106	86	164	86	79	85	87	158	74	88	120
3370501	LOC1001343	58	63	57	55	53	60	56	165	65	59	59
7400743	KIAA1618	113	255	132	180	96	181	197	73	121	172	139
6060468	S100A8	17821	75	80	62	74	71	67	2073	84	82	78
2350537	MMP7	55	56	54	858	58	96	65	288	253	51	70
3800888	MMP7	41	44	43	1126	35	38	41	293	296	32	46
6770187	SPRR2A	3356	56	69	53	58	50	69	57	66	71	58
5260095	GJB2	9411	88	93	85	121	85	79	2993	92	103	145

FIGURE 1-CONTINUED

ProbeID	Symbol	[[067], HA t (Human Astrocyte), MBA_2109	[[068], HA-c (Human Astrocyte- cerebellar), MBA_2110	[[069], HA-h (Human Astrocyte- hippocampal), MBA_2111	[[071], HBVSMC t (Human Brain Vascular Smooth Muscle Cell), MBA_2101	[[072], HBVP t (Human Brain Vascular Pericyte), MBA_2102	[[073], HCPF t (Human Choroid Plexus Fibroblast), MBA_2105	[[074], HDF- ft (Human Dermal Fibroblast- fetal), MBA_2119	[[075], HDF- n t (Human Dermal Fibroblast- neonate), MBA_2120	[[076], HDF- a t (Human Dermal Fibroblast- adult), MBA_2121	[[077], HDFPC t (Human Hair Dermal Papilla Cell), MBA_2122	[[078], HLF t (Human Lymphatic Fibroblasts Cell), MBA_2125
1850523	GZNB	36	34	36	40	39	47	37	39	43	40	41
580376	DSG3	72	64	62	77	59	56	170	65	63	70	72
20452	TYMP	59	55	57	68	61	70	90	84	155	99	98
3830681	KRT8A	75	63	57	72	68	63	3859	84	89	69	64
2350196	KRT6B	49	45	39	50	47	58	2322	52	49	45	48
5260484	HLA-DRA	87	74	79	76	63	74	64	76	78	75	76
4390398	LCN2	71	75	97	82	80	175	630	101	111	90	102
540546	KRT4	54	67	65	71	58	62	68	68	62	58	59
2000300	IFI30	88	73	69	72	108	162	90	87	82	104	125
3370601	LOC1001343	49	55	61	60	61	66	52	52	62	54	49
7400743	KIAA1618	183	165	172	188	195	108	99	191	129	213	219
6060458	S100A8	75	70	56	84	81	151	1139	63	87	74	90
2350537	MMP7	1312	87	104	150	64	143	69	67	85	81	74
3800088	MMP7	1707	59	103	200	53	144	49	55	53	101	36
6770187	SPRR2A	58	64	75	60	62	56	101	59	65	78	59
5260095	GIB2	349	134	101	97	184	99	255	82	61	86	84

FIGURE 1-CONTINUED

ProbeID	Symbol	[[079], HPLF- (Human Periodontal Ligament Fibroblast), MBA_2127	[[080], HPLF- (Human Intestinal Smooth Muscle Cell), MBA_2130	[[081], HCoSMC t (Human Colonic Smooth Muscle Cell), MBA_2131	[[082], HPASMC t (Human Pulmonary Artery Smooth Muscle Cell), MBA_2134	[[083], HPAP (Human Pulmonary Artery Fibroblast), MBA_2135	[[084], HPF t (Human Pulmonary Fibroblast), MBA_2140	[[085], HBSM t (Human Bronchial Smooth Muscle Cell), MBA_2141	[[086], HTSMC t (Human Tracheal Smooth Muscle Cell), MBA_2142	[[087], HSKMC t (Human Skeletal Muscle Cell), MBA_2143	[[088], HSKMSC t (Human Skeletal Muscle Satellite Cell), MBA_2144	[[089], HSKMM t (Human Skeletal Muscle Myoblast), MBA_2145
1850523	GZNB	41	39	35	36	41	45	45	36	32	39	44
580376	DSG3	64	68	57	71	69	73	82	63	53	77	62
20452	ITMP	82	65	103	80	75	79	127	82	135	83	95
3830681	KRT16A	82	59	61	56	81	73	76	62	75	73	69
2350196	KRT16B	46	52	44	45	48	52	59	44	42	42	50
5260484	HLA-DQB1	61	72	66	71	67	83	78	72	83	109	80
4390398	LCN2	100	96	87	85	108	74	85	96	93	90	78
540546	KRT14	71	56	54	66	53	52	71	64	57	58	59
2000300	IFT30	102	81	90	112	91	83	98	135	216	130	135
3370601	LOC1001343	58	70	65	57	59	54	62	55	57	61	69
7400743	KIAA1618	244	190	107	257	182	201	152	248	175	178	122
6060489	S100A8	71	88	74	87	72	79	89	72	69	78	73
2350527	NMP7	72	73	55	68	68	63	72	73	64	79	60
3800088	NMP7	41	33	44	59	37	37	42	39	35	42	36
6770187	SPRR2A	73	66	46	75	60	68	55	62	66	81	63
5260095	GJB2	77	91	101	83	59	90	81	81	93	217	168

FIGURE 1-CONTINUED

ProbeID	Symbol	[[090], HRMC t {Human Renal Mesangial Cell }, MBA_2149	[[092], HPF- cDNA {Human Prostate Fibroblasts Cell }, MBA_2154	[[093], HCO {Human Calvarial Osteoblasts Cell }, MBA_2155	[[096], HNPC tDNA (Human Nucleus Pulposus Cells), MBA_2157	[[097], HAFc t (Human Annulus Fibrosus Cell , MBA_2158), MBA_2159	[[098], HHSStC t (Human Hepatic Stellate Cell , MBA_2161), MBA_2162	[[100], HCN- a t (Human Cardiac Myocyte- adult), MBA_2165	[[101], HCF- av t (Human Cardiac Fibroblast- adult ventricular), MBA_2166	[[102], HConf t (Human Conjunctival Fibroblast), MBA_2172	[[103], HVMF t (Human Villous Mesenchymal Fibroblast), MBA_2176	[[104], HAMMSC t (Human Amniotic Mesenchymal Stromal Cell), MBA_2177
1850523	GZMB	42	42	41	49	46	36	43	38	45	42	41
580376	DSG3	77	73	62	64	83	64	62	63	62	65	71
20452	TYMP	82	101	70	81	58	105	106	120	63	91	174
3830681	KRT6A	77	68	77	65	79	114	67	81	63	66	227
2350196	KRT6B	53	47	44	46	43	44	50	51	47	44	47
5260484	HLA-DRB1	74	83	83	65	69	80	64	64	91	67	64
4390398	LCN2	98	107	86	82	96	77	87	78	113	75	95
540546	KRT4	59	58	65	56	65	55	52	75	64	53	55
2000300	IFI30	97	95	130	107	122	68	214	122	107	112	79
3370601	LOC1001343	49	49	62	55	52	63	50	57	45	49	59
7400743	KJAA1618	121	162	147	234	376	133	236	174	259	236	254
6060468	SI00A8	58	68	64	71	72	95	79	94	84	64	75
2350537	MMP7	1294	67	58	57	58	74	60	71	57	63	88
3800088	MMP7	1548	46	42	36	37	32	38	38	41	40	75
6770187	SPRR2A	71	70	64	54	55	74	71	72	70	58	74
5260095	GJB2	293	100	112	68	95	102	74	96	91	80	76

FIGURE 1-CONTINUED

ProbeID	Symbol	[[105], HMSC t (Human Chorionic Mesenchyma Stromal Cell), MBA_2178	[[106], HPA- st (Human Preadipocyte Visceral), MBA_2179	[[107], HPA- st (Human Preadipocyte Subcutaneous), MBA_2180	[[108], HOF (Human Ovarian Fibroblast), MBA_2182	[[109], HMSC-bm t (Human Mesenchyma Stem Cell- bone marrow adipose), MBA_2183	[[110], HMSC-ad t (Human Mesenchyma Stem Cell- adipose), MBA_2184	[[111], HMSC-he t (Human Mesenchyma Stem Cell- hepatic), MBA_2185	[[112], HMSC t (Human Umbilical Mesenchyma Stem Cell), MBA_2186	[[113], HMSC t (Human Vertebral Mesenchyma Stem Cell), MBA_2187	[[114], HMF (Human Mammary Fibroblast), MBA_2189	[[115], HUSMC t (Human Umbilical Vein Smooth Muscle Cell , 10 μ g", MBA_2192
1850523	GZHB	37	40	50	44	39	39	36	38	45	45	44
580376	DSG3	69	76	64	63	68	63	57	69	63	66	78
20452	TYMP	176	99	70	68	73	105	119	119	61	164	66
3830681	KRT16A	82	78	91	74	81	67	66	66	62	66	89
2350196	KRT16B	49	58	56	51	54	44	42	47	45	52	49
5260484	HLA-DRA1	92	79	94	103	74	104	70	77	86	89	70
4390398	LCN2	96	101	83	122	80	102	109	99	103	143	77
540546	KRT14	73	61	55	58	56	59	56	65	70	68	72
2000300	IFI30	78	224	157	118	88	205	78	53	115	218	84
3370601	LOC1001343	51	69	59	58	66	67	65	59	58	48	52
7400743	KIAA1618	207	209	208	220	136	156	159	124	232	275	94
6060468	S100A8	94	87	74	62	99	92	84	69	78	80	79
2350537	MMP7	94	59	53	60	149	66	77	70	67	61	62
3800088	MMP7	64	46	45	41	130	43	36	35	29	39	40
6770187	SPRR2A	58	72	61	60	55	68	63	60	62	57	62
5260095	GB2	79	105	76	184	103	93	70	76	84	83	113

FIGURE 1-CONTINUED

ProbeID	Symbol	[[116], (Human Umbilical Artery Smooth Muscle Cell)], MBA_2193	[[117], HEM- t (Human Epidermal Melanocyte medium)], MBA_2116	[[118], HEM- t (Human Epidermal Melanocyte- medium)], MBA_2117	[[119], HEM- t (Human Epidermal Melanocyte dark)], MBA_2118	[[121], Breast Within normal limits], MBA_2252	[[122], Breast Within normal limits rep2], MBA_2253	[[123], Colon: sigmoid Within normal limits], MBA_2258	[[124], Cervix Within normal limits], MBA_2261	[[125], Endometriu m Within normal limits], MBA_2243	[[126], Ovary Within normal limits], MBA_2246	[[127], Bone: femur distal Within normal limits], MBA_2228
1850523	GZMB	38	57	33	41	53	52	65	48	1142	39	80
580376	DSG3	65	69	91	57	120	72	64	1570	75	64	49
20452	TYMP	85	75	90	75	103	79	115	83	122	59	117
3830681	KRT6A	71	397	1023	66	68	75	64	15967	68	70	62
2350196	KRT6B	44	271	423	46	758	101	47	1332	39	46	43
5260484	HLA-DQB1	68	73	92	94	844	579	72	76	468	80	754
4390398	LCN2	92	83	1690	102	213	141	1381	2997	370	86	137
540546	KRT4	52	62	56	79	69	58	64	4856	57	67	67
2000300	IFI30	98	93	83	109	114	110	212	85	150	79	285
3370601	LOC1001343	49	61	54	61	55	65	51	59	56	56	61
7400743	KIAA1618	119	189	169	166	124	102	87	178	131	109	133
6060468	S100A8	67	106	247	77	114	88	151	16268	175	155	548
2350537	MMP7	63	69	56	63	2542	389	63	83	1303	61	88
3800088	MMP7	36	40	34	35	3167	535	50	63	1546	36	85
6770187	SPRR2A	69	58	191	87	67	56	63	1958	71	66	56
5260095	GJB2	87	108	132	84	85	94	435	4490	102	72	103

FIGURE 1-CONTINUED

ProbeID	Symbol	[[128], Lung Within normal limits, MBA_2234	[[129], Lung Within normal limits, rep2, MBA_2235	[[130], Kidney Within normal limits, MBA_2240	[[131], Esophagus Within normal limits, MBA_2249	[[132], Esophagus Within normal limits, rep2, MBA_2264	[[133], Lymph node Within normal limits, MBA_2304	[[134], Thyroid Gland Within normal limits, MBA_2273	[[136], Pancreas Within normal limits, MBA_2276	[[137], Prostate Within normal limits, MBA_2285	[[138], Prostate Within normal limits, rep2, MBA_2286	[[139], Rectum Within normal limits, MBA_2289
1850523	GZMB	238	608	170	108	55	226	46	44	45	41	49
580376	DSG3	67	75	89	3845	5210	68	51	63	52	70	65
20452	TYMP	123	334	103	106	56	188	74	63	78	72	133
3830681	KRT6A	74	75	93	22156	20237	595	87	107	86	71	81
2350196	KRT6B	49	45	44	10348	11523	46	47	50	50	43	52
5260484	HLA-DRA1	84	4270	1298	98	84	70	89	99	67	444	817
4390398	LCN2	314	568	1552	6571	7687	83	89	714	574	255	2922
540546	KRT14	94	58	65	17067	16433	70	54	57	65	81	63
2000300	IFI30	762	886	241	103	117	912	102	189	129	93	244
3370601	LOC1001343	55	46	62	52	55	62	61	66	73	58	58
7400743	KIAA1618	109	185	258	96	102	171	142	59	101	127	119
6060468	SI00A8	1978	5573	1432	16830	16128	429	167	1205	146	150	105
2350537	MMP7	466	340	4157	108	70	75	66	905	1428	148	77
3800068	MMP7	533	388	5260	93	43	63	36	1237	1862	164	46
6770187	SPRR2A	55	63	76	16671	18459	72	52	78	61	56	67
5260095	GJB2	71	80	316	8216	6971	91	159	102	198	106	687

FIGURE 1-CONTINUED

ProbeID	Symbol	[[140], Liver Within normal limits, MBA_2294	[[141], Stomach Within normal limits, MBA_2297	[[142], Brain Within normal limits, MBA_2300	[[143], Fecal Brain total RNA, MBA_2338_2	[[144], Fecal Brain total RNA, MBA_2338_2	[[145], Testis Within normal limits, MBA_2260	[[146], Testes total RNA, MBA_2313	[[147], Thyroid total RNA, MBA_2312	[[148], Ovary total RNA, MBA_2314	[[149], Adrenal Cortex poly A RNA, MBA_2315	[[150], Prostate Total RNA, MBA_2316
1850523	GZMB	68	104	46	40	38	45	44	76	64	64	56
580376	DSG3	70	50	68	70	54	61	59	81	60	68	72
20452	TYMP	161	155	67	66	62	75	68	91	67	99	78
3830681	KRT16A	133	82	97	74	68	87	80	273	65	68	91
2350196	KRT6B	54	53	47	48	43	50	54	83	42	40	49
5260484	HLA-DRB1	74	94	271	91	93	85	108	395	248	312	291
4350398	LCN2	201	9942	98	88	83	78	80	281	87	96	899
540546	KRT4	59	59	62	64	60	59	51	158	68	52	80
200300	IFI30	354	261	125	64	68	77	65	130	113	233	84
3370601	LOC1001343	60	57	56	57	54	60	71	52	49	49	56
7400743	KIAA1618	84	88	149	101	105	79	95	159	179	167	128
6060468	S100A8	883	453	795	333	354	140	163	1100	358	196	287
2350537	MMP7	106	90	74	53	68	64	67	91	64	54	622
3800088	MMP7	72	77	34	36	35	43	61	81	41	45	794
6770187	SPRR2A	71	72	66	61	53	73	61	125	63	57	59
5260095	GJB2	529	393	132	111	101	83	85	170	78	81	98

FIGURE 1-CONTINUED

ProbeID	Symbol	[[151], Dorsal root ganglion total RNA, MBA_2317	[[152], Salivary Gland total RNA, MBA_2325	[[153], Salivary Gland total RNA, MBA_2326	[[154], MP Breast adjacent normal, MBA_2209	[[155], MP Colon adjacent normal, MBA_2211	[[156], MP Kidney adjacent normal, MBA_2213	[[157], MP Liver adjacent normal, MBA_2215	[[158], MP Lung adjacent normal, MBA_2217	[[159], MP Rectum adjacent normal, MBA_2219	[[160], MP Stomach adjacent normal, MBA_2221	[[161], Lymphoid tissue Lymphoma extranodal marginal zone B-cell, MBA_2268
1850523	GZMB	59	53	51	58	108	219	75	478	140	151	79
580376	DSG3	74	75	63	102	93	48	59	74	65	67	67
20452	TYMP	79	86	104	121	142	120	234	345	153	68	167
3830681	KRT16A	72	722	725	114	72	74	102	68	66	76	63
2350196	KRT16B	44	81	81	463	53	43	62	61	48	40	59
5260484	HLA-DRA	484	463	443	642	72	80	71	53	81	703	87
4390398	LCN2	160	2782	2646	117	1421	1754	349	465	1498	2356	95
540546	KRT4	67	327	345	52	52	58	58	92	60	80	63
2000300	IFI30	102	184	170	291	267	205	358	1051	344	302	580
3370601	LOC1001343	47	64	57	61	58	57	49	58	52	54	45
7400743	KIAA1618	212	68	76	184	90	265	77	203	105	68	172
6050468	S100A8	516	1174	845	307	769	186	439	1371	234	564	94
2350537	MMP7	48	416	359	399	44	10600	220	457	65	146	164
3850088	MMP7	42	478	423	474	40	11161	233	520	52	142	167
6770187	SPRR2A	66	233	154	67	65	50	64	84	59	64	80
5260095	GJB2	367	689	724	140	489	169	893	89	448	128	100

FIGURE 1-CONTINUED

ProbeID	Symbol	[[162], Lymphoid tissue Lymphoma follicular, MBA_2269	[[163], Uterus Tumor Adenocarcin oma, MBA_2318	[[164], Kidney Tumor renal cell carcinoma, MBA_2321	[[165], Breast Tumor invasive ductal carcinoma, MBA_2324	[[166], Breast Adenocarcin oma of breast ductal, MBA_2255	[[167], Colon: right Adenocarcin oma of colon, MBA_2259	[[168], Colon Tumor Invasive carcinoma, MBA_2323	[[169], Cervix Carcinoma of cervix squamous cell, MBA_2263	[[170], Endometriu m Adenocarcin oma of endometriu m endometrioid serous, MBA_2244	[[171], Ovary Adenocarcin oma of ovary serous, MBA_2247	[[172], Ovary Tumor Carcinoma, MBA_2320
1850523	GZMB	344	530	265	85	52	105	150	174	53	59	284
580376	DSG3	48	60	78	86	131	71	78	3076	53	63	70
20452	TYMP	124	531	856	221	88	116	124	623	64	245	252
3830681	KRT6A	74	964	83	76	279	77	88	14093	69	167	71
2350196	KRT6B	46	50	53	417	406	164	73	1449	40	76	49
5260484	HLA-DRB1	82	130	5602	2348	82	66	99	1830	71	2018	80
4390398	LCN2	81	14259	155	100	255	1250	1891	559	75	6929	75
540346	KRT4	66	98	59	57	70	66	68	2059	34	64	61
2000300	IFI30	370	758	876	366	214	335	307	443	96	315	769
3370601	LOC1001343	54	60	44	55	57	51	60	57	64	57	43
7400743	KJAA1618	168	332	399	107	157	102	101	138	82	280	163
6060468	S100A8	198	1072	192	153	541	329	516	10600	90	593	857
2350537	MMP7	74	7665	998	452	922	2896	66	314	65	961	398
3800088	MMP7	49	8601	1278	516	1122	3447	45	331	48	1168	534
6770187	SPRR2A	66	85	80	73	63	76	67	2270	61	58	68
5260095	GJB2	87	438	383	349	153	1328	456	696	96	178	1762

FIGURE 1 - CONTINUED

ProbeID	Symbol	[[173], Lung Carcinoma of lung squamous cell, MBA_2236	[[174], Lung Adenocarcin oma of lung, cell, MBA_2237	[[175], Lung Carcinoma of lung large cell, MBA_2238	[[177], Lung: left upper lobe Carcinoma of lung small cell, MBA_2239	[[176], Lung Tumor Squamous cell carcinoma, MBA_2322	[[179], Pleura Mesotheliom a of pleura, MBA_2256	[[180], Pleura Mesotheliom a of pleura mixed, MBA_2257	[[181], Kidney Carcinoma in situ of renal pelvis papillary transitional cell, MBA_2241	[[182], Gastroesoph ageal Adenocarcin oma of gastroesoph ageal junction, MBA_2251	[[184], Thyroid gland Carcinoma of thyroid follicular, MBA_2274_ TR	[[186], Pancreas oma of pancreas ductal, MBA_2277
1850523	GZM8	149	176	372	353	187	72	55	51	71	42	194
580376	D5G3	115	53	64	63	554	76	75	156	67	62	96
20452	TYMP	181	431	485	144	133	188	92	73	134	76	181
3830681	KRT6A	1218	174	162	77	19023	96	330	3811	57	86	314
2350196	KRT16B	377	54	55	51	6518	46	61	60	46	48	196
5260484	HLA-DQB1	71	2338	2918	1072	385	78	75	372	72	70	79
4390398	LON2	163	18433	257	101	681	82	155	650	15841	68	12967
540546	KRT4	69	57	63	61	65	72	72	519	61	52	66
2098300	IFI30	502	1123	834	424	408	273	196	114	530	160	350
3370601	LOC1001343	60	55	53	69	63	83	48	46	56	45	51
7400743	KIAA1618	207	174	316	173	165	297	421	103	149	145	189
6060468	S106A8	4227	680	599	223	2907	164	176	1338	450	103	597
2350537	MMP7	535	8572	921	127	218	59	74	302	65	66	10348
3808088	MMP7	587	9975	1170	119	278	48	51	332	43	42	11745
6770187	SPRR2A	652	61	65	60	1698	55	89	88	58	62	84
5260095	GIB2	361	542	1443	127	506	441	876	5002	1079	68	1187

FIGURE 1-CONTINUED

ProbeID	Symbol	[[187], Pancreas Tumor of pancreas neuroendocrine, MBA_2278	[[188], Testis Seminoma of testis, MBA_2281	[[169], Testis Seminoma of testis rep2, MBA_2282	[[190], Prostate Adenocarcinoma of prostate, MBA_2287	[[191], Rectum Adenocarcinoma of colon, MBA_2290	[[192], Rectum Adenocarcinoma of rectum, MBA_2291	[[193], Liver: left lobe Carcinoma of liver hepatocellular carcinoma, MBA_2295	[[194], Liver Cholangiocarcinoma of liver, MBA_2296	[[195], Bile duct Cholangiocarcinoma of bile duct, MBA_2283	[[196], Bile duct Cholangiocarcinoma of bile duct, MBA_2284	[[197], Stomach Tumor Adenocarcinoma, MBA_2319
1850523	G2MB	53	318	498	59	276	112	60	191	127	174	105
580376	DSG3	72	65	80	63	72	236	58	72	77	307	123
20452	TYMP	77	139	163	97	143	97	203	153	113	226	132
3830681	KRT6A	65	98	64	138	86	122	142	109	67	2802	1947
2350196	KRT6B	46	44	44	54	161	48	56	56	86	306	4480
5260484	HLA-DRB1	66	711	79	595	71	78	1233	1498	2263	75	79
4390398	LCN2	84	90	85	569	18012	8429	5116	3153	5360	10673	20021
540546	KRT4	63	61	57	65	61	49	68	62	59	50	77
2000300	IFI30	150	280	797	167	460	316	513	525	201	350	326
3370601	LOC1001343	65	56	52	44	51	50	49	53	64	71	45
7400743	KIAA1618	114	65	158	94	127	71	68	103	115	179	427
6060468	S100A8	68	115	195	141	806	536	258	1225	290	4877	2081
2350537	MMP7	68	54	59	2364	407	1615	214	1095	3265	7313	2659
3800088	MMP7	44	36	41	2652	427	2174	253	1252	4443	10709	3392
6770187	SPRR2A	62	56	74	61	58	82	69	55	65	78	169
5260095	G3B2	208	70	85	130	416	543	496	465	474	3026	906

FIGURE 1-CONTINUED

ProbeID	Symbol	[[198], Stomach Adenocarcin oma of stomach, MBA_2298	[[199], Brain Glioblastoma multiforme, MBA_2301	[[200], Brain Oligodendro glioma anaplastic, MBA_2302	[[201], Brain Astrocytoma anaplastic, MBA_2303	[[202], MP Breast primary tumor, MBA_2208	[[203], MP2 Breast primary tumor, MBA_2194	[[204], MP Colon primary tumor, MBA_2210	[[205], MP2 Colon primary tumor, MBA_2196	[[206], MP Kidney primary tumor, MBA_2212	[[208], MP Liver primary tumor, MBA_2214	[[209], MP2 Liver primary tumor, MBA_2200
1850523	GZMB	109	38	48	32	47	56	183	128	143	67	41
580376	DSG3	128	62	76	73	88	68	113	63	64	65	65
20452	TYMP	160	95	74	59	131	122	158	162	111	152	69
3830681	KRT6A	83	65	64	69	92	56	92	83	80	127	70
2350196	KRT6B	44	46	42	47	201	66	49	72	47	49	46
5260484	HLA-DRE1	76	74	68	266	613	420	72	81	76	77	125
4390398	LCN2	6071	100	122	120	105	107	3284	10348	126	192	419
540546	KRT4	66	59	62	63	52	44	55	68	63	59	75
2008300	IFT30	283	195	93	67	344	179	457	308	358	530	191
3370601	LOC1001343	55	51	53	52	63	56	50	49	67	62	58
7400743	KGA1618	89	105	65	103	196	247	114	154	211	79	54
6060468	S100A8	444	227	99	103	158	89	2197	124	250	243	1804
2350337	MMP7	1254	90	75	59	244	214	590	465	385	328	156
3800086	MMP7	1544	88	35	42	356	241	745	538	462	390	101
8770187	SPRR2A	59	66	55	60	55	57	72	71	67	65	59
5260095	GIB2	517	77	91	109	173	84	755	1812	78	317	129

FIGURE 1-CONTINUED

ProbeID	Symbol	[[210], MP Lung primary tumor, MBA_2216	[[211], MP2 Lung primary tumor, MBA_2202	[[212], MP Rectum primary tumor, MBA_2218	[[213], MP2 Rectum primary tumor, MBA_2204	[[214], MP Stomach primary tumor, MBA_2220	[[215], MP2 Stomach primary tumor, MBA_2206	[[216], Breast Adenocarcin oma of breast metastatic, MBA_2254	[[217], Colon Adenocarcin oma of colon metastatic, MBA_2260	[[218], Cervix Adenocarcin oma metastatic consistent with cervical primary, MBA_2262	[[219], Ovary Adenocarcin oma of ovary serous metastatic, MBA_2248	[[220], Skin Malignant melanoma metastatic, MBA_2231
1850523	GZMB	366	199	195	542	123	109	45	143	44	82	101
580376	DSG3	86	1882	78	61	85	152	64	329	67	64	59
20452	TYMP	327	271	90	125	150	282	84	150	75	128	178
3830681	KRT6A	291	20548	82	64	57	73	74	688	70	568	66
2350196	KRT6B	40	8323	53	63	145	3416	46	154	50	48	48
5260484	HLA-DRB1	90	270	71	648	871	76	293	85	111	927	78
4390398	LCN2	307	364	2738	7519	13986	14778	106	1828	81	5698	119
540546	KRT14	60	57	67	252	457	333	147	339	55	88	66
2000300	IFI30	1278	272	253	252	457	333	147	339	113	221	513
3370601	LOC1001343	61	50	50	41	53	58	76	51	52	56	52
7400743	KJAA1618	183	368	130	122	358	142	152	216	108	265	243
6060468	S100A8	794	7115	509	545	428	279	87	151	80	174	214
2350537	MMP7	2047	368	683	4286	658	308	70	402	78	439	71
3800088	MMP7	2483	447	941	5248	970	423	44	465	58	515	37
6770187	SPR2A	65	655	75	66	57	67	68	87	59	64	62
5260095	GIB2	171	4753	512	523	216	135	98	176	73	826	120

FIGURE 1-CONTINUED

ProbeID	Symbol	[[221], Skin Malignant melanoma metastatic rep2, MBA_2232	[[222], Eye Malignant melanoma metastatic, MBA_2233	[[223], Kidney Carcinoma of kidney renal cell metastatic, MBA_2242	[[224], Gastroesoph ageal junction adenocarcin oma of gastroesoph ageal junction metastatic, MBA_2250	[[225], Neck Carcinoma of neck squamous cell metastatic, MBA_2266	[[226], Tonsil Carcinoma of tonsil squamous cell metastatic, MBA_2267	[[227], Thyroid gland Carcinoma of thyroid papillary metastatic, MBA_2275	[[229], Pancreas Tumor of pancreas neuroendocri ne metastatic, MBA_2279	[[230], Prostate Adenocarcin oma of prostate metastatic, MBA_2288	[[231], MP2 Breast metastatic tumor, MBA_2195	[[232], MP2 Colon metastatic tumor, MBA_2197
1850523	GZMB	285	54	230	166	154	90	53	53	59	71	156
580376	DSG3	69	70	65	65	445	751	65	71	68	65	63
20452	TYMP	463	87	260	178	248	94	147	75	112	172	248
3830681	KRT6A	72	86	82	62	14663	12533	116	89	131	66	111
2350196	KRT68	42	50	43	45	2877	623	45	45	47	49	86
5260484	HLA-DRE1	95	89	992	84	74	67	2756	262	780	451	75
4390398	LCN2	109	93	282	121	840	315	633	129	109	79	1563
540346	KRT14	65	58	58	74	67	574	58	70	61	67	58
2000300	IFI30	1169	206	560	570	687	162	667	146	564	251	521
3370601	LOC1001343	58	60	48	56	58	45	51	64	54	48	54
7408743	KJAA1618	1080	102	186	72	132	99	156	79	128	320	147
6050468	S100A8	310	129	145	139	2218	2665	275	259	272	82	285
2350337	MMP7	78	100	1191	196	1540	58	250	107	1207	61	411
3800058	MMP7	41	75	1513	183	1802	42	248	96	1424	42	426
6770187	SPRR2A	57	67	62	69	138	300	61	59	80	62	66
5260095	GJB2	169	179	804	277	2714	1684	222	155	104	65	992

FIGURE 1-CONTINUED

ProbeID	Symbol	[[233], MP2 Kidney metastatic tumor, MBA_2199	[[234], MP2 Liver metastatic tumor, MBA_2201	[[235], MP2 Lung metastatic tumor, MBA_2203	[[236], MP2 Rectum metastatic tumor, MBA_2205	[[237], MP2 Stomach metastatic tumor, MBA_2207	[[238], Cartilage Chondrosar- coma, MBA_2292	[[239], Cartilage Chondrosar- coma, MBA_2293	[[240], Bone Osteosarcoma a metastatic, MBA_2230	[[250], Smooth muscle Sarcoma metastatic consistent with leiomyosarcoma primary, MBA_2229	[[260], Endometriu- m Endometrial stromal sarcoma metastatic, MBA_2245	[[270], Human Tumor Cell Line: A431, MBA_2222
1850523	GZMB	56	74	149	299	145	39	36	53	69	40	41
580376	DSG3	70	68	3148	80	114	65	60	71	75	68	212
20452	TYMP	87	152	281	144	440	68	69	121	119	85	104
3830681	KRT16A	3241	91	22156	81	74	78	79	68	63	66	1144
2350196	KRT16B	385	53	11443	50	3470	47	49	43	48	52	143
5260484	HLA-DRB1	150	98	368	1380	96	249	197	65	716	79	92
4390398	LON2	821	306	144	1381	20887	128	135	100	83	97	10214
540546	KRT14	56	76	75	60	62	68	70	75	49	72	92
2000300	IFI30	131	812	268	366	553	151	151	323	517	138	235
3370501	LOC1001343	54	60	50	46	60	65	61	48	64	56	247
7400743	KIAA1618	142	96	286	135	307	202	207	389	223	159	130
6060468	S100A8	1605	4603	10381	254	416	163	168	133	135	85	171
2350537	MMP7	75	93	186	293	201	60	78	108	85	73	141
3850088	MMP7	54	72	200	372	194	39	42	105	61	46	163
6770187	SPRR2A	81	67	281	70	61	52	81	56	65	65	72
5260095	GJB2	673	117	6738	415	121	79	79	136	1132	445	1669

FIGURE 1 - CONTINUED

ProbeID	Symbol	[[280], Human Tumor Cell Line: HeLa, MBA_2223	[[281], Human Tumor Cell Line: Jurkat, MBA_2224	[[282], Human Tumor Cell Line: K 562, MBA_2225	[[283], Human Tumor Cell Line: MCF 7, MBA_2226	[[384], Human Tumor Cell Line: Raji, MBA_2227	[[285], Breast: SKBR3: 1.2ug/ul 2.12 18 ug, MBA_2305	[[286], Breast: MB231: 1.3ug/ul 2.11 19.5 ug, MBA_2306	[[287], Ovarian: OVCAR3: 0.8ug/ul 2.12 12 ug, MBA_2307	[[288], Ovarian: OV90: 0.7ug/ul 2.11 10.5 ug, MBA_2308	[[289], Ovarian: TOV112D: 1.4ug/ul 2.11 21 ug, MBA_2309	[[290], Ovarian: SKOV3: 0.18ug/ul 2.17 2.7 ug, MBA_2310
1850523	GZMB	42	39	43	44	49	39	45	35	44	46	39
580376	DSG3	81	74	68	63	52	58	59	61	63	58	63
20452	TYMP	75	58	68	66	68	144	91	56	67	71	111
3830681	KRT16A	70	73	77	85	73	75	68	128	70	63	87
2350196	KRT16B	49	43	55	49	52	58	48	47	43	50	45
5260484	H1A-DRB1	104	84	95	135	89	76	74	69	73	78	80
4390398	LCN2	298	81	144	85	133	232	300	316	96	80	9701
540546	KRT14	69	65	60	75	83	484	65	315	64	88	48
2000300	IFI30	230	115	279	252	925	387	136	108	83	88	104
3370601	LOC1001343	82	56	55	69	54	155	57	63	48	49	58
7400743	KIAA1618	246	154	83	204	59	342	225	103	91	138	130
6060468	SI00A8	71	62	79	86	80	1731	77	88	91	72	71
2350537	MMP7	70	51	53	59	60	49	62	83	62	59	932
3800088	MMP7	44	44	46	44	38	33	45	61	35	38	1175
6770187	SPRR2A	63	69	55	62	70	56	59	67	56	68	58
5260095	GJB2	79	121	63	87	93	74	537	332	98	74	98

FIGURE 1-CONTINUED

ProbeID	Symbol	[[291], Glioma: SF188: 1.1ug/ul 2.12 16.5 ug, MBA_2311	[[292], NIH OVCAR-3 (Ovary Adenocarcinoma Poly A RNA, MBA_2334	[[293], Cell Line HEP G2 (Hepatoblastoma) Poly A RNA, MBA_2335	[[294], Cell Line MCF7 (Breast Adenocarcinoma) Poly A RNA, MBA_2336	[[295], Cell Line ZR75-1 (Breast Carcinoma) Poly A RNA, MBA_2337
1850523	GZMB	36	40	43	38	41
580376	DSG3	61	67	62	63	59
20452	TYMP	51	64	73	65	124
3830681	KRT6A	68	129	79	96	72
2350196	KRT16B	52	43	38	50	47
5260484	HLA-DRE1	60	62	84	126	77
4390398	LCN2	83	652	168	105	970
540545	KRT14	59	141	61	60	68
2000300	IFI30	126	97	113	218	129
3370601	LOC1001343	55	56	64	77	60
7400743	KIAA1618	164	84	106	124	239
6060468	S100A8	69	91	71	422	3001
2350537	MMP7	63	52	72	58	60
3800088	MMP7	35	47	55	42	33
6770187	SPRR2A	70	71	63	57	72
5260095	GJB2	142	432	80	99	87

FIGURE 1-CONTINUED

ProteinID	Symbol	Definition
6100259	VSNL1	Homo sapiens visinin-like 1 (VSNL1), mRNA.
1340176	C20orf197	Homo sapiens chromosome 20 open reading frame 197 (C20orf197), mRNA.
4900458	KRT14	Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Mearns, Koebner) (KRT14), mRNA.
7050220	NMU	Homo sapiens neuromedin U (NMU), mRNA.
1510364	GBPS	Homo sapiens guanylate binding protein 5 (GBPS), mRNA.
2490541	MAGEA10	Homo sapiens melanoma antigen family A, 10 (MAGEA10), transcript variant 2, mRNA.
5260484	HLA-DRB1	Homo sapiens major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA.
4280132	DSCR8	Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 2, mRNA.
2510605	FAM83A	Homo sapiens family with sequence similarity 83, member A (FAM83A), transcript variant 1, mRNA.
6860424	SERPINE4	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 4 (SERPINE4), mRNA.
2140707	SLPI	Homo sapiens secretory leukocyte peptidase inhibitor (SLPI), mRNA.
5360064	GNLY	Homo sapiens granulysin (GNLY), transcript variant 519, mRNA.
7400743	KIAA1618	Homo sapiens KIAA1618 (KIAA1618), mRNA.
6060468	S100A8	Homo sapiens S100 calcium binding protein A8 (S100A8), mRNA.
6290554	GTSF1	Homo sapiens gametocyte specific factor 1 (GTSF1), mRNA.
50689	C7orf288	Homo sapiens chromosome 7 open reading frame 288 (C7orf288), mRNA.
2190148	GBP1	Homo sapiens guanylate binding protein 1, interferon-inducible, 67kDa (GBP1), mRNA.
4760826	MMP12	Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12), mRNA.
6350189	MGC4677	Homo sapiens hypothetical protein MGC4677 (MGC4677), mRNA.
3830681	KRT6A	Homo sapiens keratin 6A (KRT6A), mRNA.
2350537	MMP7	Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), mRNA.
3800088	MMP7	Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), mRNA.
5570278	CXCL9	Homo sapiens chemokine (C-X-C motif) ligand 9 (CXCL9), mRNA.
4390398	LCN2	Homo sapiens lipocalin 2 (LCN2), mRNA.
540546	KRT4	Homo sapiens keratin 4 (KRT4), mRNA.
6420505	UBD	Homo sapiens ubiquitin D (UBD), mRNA.
3440754	IL32	Homo sapiens interleukin 32 (IL32), transcript variant 4, mRNA.
1980309	IL8	Homo sapiens interleukin 8 (IL8), mRNA.
4730196	TK1	Homo sapiens thymidine kinase 1, soluble (TK1), mRNA.
7550220	S100A2	Homo sapiens S100 calcium binding protein A2 (S100A2), mRNA.
1050168	PI3	Homo sapiens peptidase inhibitor 3, skin-derived (SKALP) (PI3), mRNA.
5390220	S100A9	Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA.
5960296	CLDN1	Homo sapiens claudin 1 (CLDN1), mRNA.
4280504	DSCR8	Homo sapiens Down syndrome critical region gene 8 (DSCR8), transcript variant 3, mRNA.
1010132	RARRES1	Homo sapiens retinoic acid receptor responder (tazarotene induced) 1 (RARRES1), transcript variant 2, mRNA.
1260270	AIM2	Homo sapiens absent in melanoma 2 (AIM2), mRNA.
2370632	MMP11	Homo sapiens matrix metalloproteinase 11 (stromelysin 3) (MMP11), mRNA.
4730242	FAM181B	Homo sapiens family with sequence similarity 181, member B (FAM181B), mRNA.
4490093	ABCC9	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR28, mRNA.
2750689	LOC729826	PREDICTED: Homo sapiens hypothetical protein LOC729826 (LOC729826), mRNA.
7550554	S100A7A	Homo sapiens S100 calcium binding protein A7A (S100A7A), mRNA.
6770187	SPRR2A	Homo sapiens small proline-rich protein 2A (SPRR2A), mRNA.
2000300	IFI30	Homo sapiens interferon, gamma-inducible protein 30 (IFI30), mRNA.
3840445	KRT17	Homo sapiens keratin 17 (KRT17), mRNA.
1500010	CDC20	Homo sapiens cell division cycle 20 homolog (S. cerevisiae) (CDC20), mRNA.
5420577	CLCA4	Homo sapiens chloride channel, calcium activated, family member 4 (CLCA4), mRNA.
3440204	FBN2	Homo sapiens fibrillin 2 (FBN2), mRNA.
3370601	LOC100134370	PREDICTED: Homo sapiens hypothetical protein LOC100134370 (LOC100134370), mRNA.
1580762	SERPINE13	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 13 (SERPINE13), mRNA.

FIGURE 2A

5760286	R5124587	Athersys RAGE Library Homo sapiens cDNA, mRNA sequence
5570711	IDO1	Homo sapiens indoleamine 2,3-dioxygenase 1 (IDO1), mRNA
3120113	GJB6	Homo sapiens gap junction protein, beta 6 (GJB6), mRNA
2260563	GJB6	Homo sapiens gap junction protein, beta 6 (GJB6), mRNA
2650379	GREM1	Homo sapiens gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis) (GREM1), mRNA
1850523	GZMB	Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA
6550500	S100A7	Homo sapiens S100 calcium binding protein A7 (S100A7), mRNA
380259	INDO	Homo sapiens indoleamine-pyrrole 2,3 dioxygenase (INDO), mRNA
5260095	GJB2	Homo sapiens gap junction protein, beta 2, 26kDa (GJB2), mRNA
2320600	CALML3	Homo sapiens calmodulin-like 3 (CALML3), mRNA
1470056	SERPINEB3	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 3 (SERPINEB3), mRNA
3310201	SERPINEB3	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 3 (SERPINEB3), mRNA
2630474	MLLT11	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (vitrothorax homolog, Drosophila); translocated to, 11 (MLLT11), mRNA
4070647	ALDH3B2	Homo sapiens aldehyde dehydrogenase 3 family, member B2 (ALDH3B2), transcript variant 2, mRNA
6620487	CXCL6	Homo sapiens chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6), mRNA
2510356	EMR1	Homo sapiens egr-like module containing, mucin-like, hormone receptor-like 1 (EMR1), mRNA
5860289	KRT5	Homo sapiens keratin 5 (KRT5), mRNA
2570079	STAT1	Homo sapiens signal transducer and activator of transcription 1, 91kDa (STAT1), transcript variant beta, mRNA
6770131	OLFML4	Homo sapiens olfactomedin 4 (OLFML4), mRNA
430446	KRT81	Homo sapiens keratin 81 (KRT81), mRNA
6370470	APOL1	Homo sapiens apolipoprotein L 1 (APOL1), transcript variant 2, mRNA
3990170	IFI27	Homo sapiens interferon, alpha-inducible protein 27 (IFI27), transcript variant 2, mRNA
3710068	WARS	Homo sapiens tryptophanyl-tRNA synthetase (WARS), transcript variant 2, mRNA
1770603	TCN1	Homo sapiens transcobalamin 1 (vitamin B12 binding protein, R binder family) (TCN1), mRNA
1580470	LOC100130897	PREDICTED: Homo sapiens hypothetical LOC100130897 (LOC100130897), mRNA
580376	D5G3	Homo sapiens desmoglein 3 (pemphigus vulgaris antigen) (D5G3), mRNA
2340681	RARRES1	Homo sapiens retinoic acid receptor responder (tazarotene induced) 1 (RARRES1), transcript variant 1, mRNA
3310333	WISP3	Homo sapiens WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1, mRNA
2350196	KRT68	Homo sapiens keratin 68 (KRT68), mRNA
6760341	KRT68	Homo sapiens keratin 68 (KRT68), mRNA
7610338	CDH3	Homo sapiens cadherin 3, type 1, P-cadherin (placental) (CDH3), mRNA
6270553	CXCL10	Homo sapiens chemokine (C-X-C motif) ligand 10 (CXCL10), mRNA
2350504	ECGF1	Homo sapiens endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA
2230500	SPRR2F	Homo sapiens small proline-rich protein 2F (SPRR2F), mRNA
6550356	SPRR2C	Homo sapiens small proline-rich protein 2C (pseudogene) (SPRR2C), non-coding RNA
1980593	PTH1H	Homo sapiens parathyroid hormone-like hormone (PTH1H), transcript variant 3, mRNA
20452	TYMP	Homo sapiens thymidine phosphorylase (TYMP), transcript variant 3, mRNA
6480364	LOC647460	PREDICTED: Homo sapiens similar to Ig kappa chain V-J region HK101 precursor (LOC647460), mRNA
2260731	ERAP2	Homo sapiens endoplasmic reticulum aminopeptidase 2 (ERAP2), mRNA
4490079	DHR59	Homo sapiens dehydrogenase/reductase (SDR family) member 9 (DHR59), transcript variant 1, mRNA
6900414	PTH1H	Homo sapiens parathyroid hormone-like hormone (PTH1H), transcript variant 1, mRNA
1690056	LYZ	Homo sapiens lysozyme (renal amyloidosis) (LYZ), mRNA

FIGURE 2B

ProteinID	Symbol	Accession	Chromosome End Index(Avadis)	Chromosome Start Index(Avadis)	Chromosome	Entrez_Gene_ID	GI
6100259	VSNI1	NM_003385.4	17700640	17700591	chr2	7447	63252921
1340176	C2orf197	NM_173644.1	58080663	58080614	chr20	284756	27735086
4900458	KRT14	NM_000526.3	36992173	36992124	chr17	3861	15431309
7050220	NMU	NM_006681.1	56166253	56166204	chr4	19874	5729946
1510364	GMP5	NM_052942.2	89500508	89499057	chr1	115352	31377630
2490541	MAGEA10	NM_021048.3	151303035	151302986	chrX	4109	25029613
5260484	HLA-DRB1	NM_002124.1	32656016	32654825	chr6	3123	4504410
4280132	DSCR8	NM_203428.1	38415518	38415469	chr21	84677	44680116
2510605	FAM83A	NM_032899.4	124220836	124220787	chr8	94985	46255015
6860424	SERPINA8	NM_002974.2	61305178	61305129	chr18	5318	115529480
2140707	SLPI	NM_003064.2	43882240	43881768	chr20	6590	15834632
5360064	GMLY	NM_012483.1	85779236	85778301	chr2	10578	7108345
7400743	KIAA1638	NM_020954.2	75909835	75909786	chr17	57714	66529202
6060468	S100A8	NM_002964.3	153362662	153362613	chr1	6279	21614543
6290354	GTSF1	NM_144594.1	531422166	53140480	chr12	121355	21389378
50689	C7orf288	NM_198097.1	68052274	6805225	chr7	221960	37674288
2190148	GBP1	NM_002053.1	89291084	89291035	chr1	2633	4503938
4760626	MMP12	NM_002426.2	102238796	102238747	chr11	4321	73858571
6350189	MGC4677	NM_052871.3	87602085	87602016	chr2	112597	62243377
3830681	KRT6A	NM_005554.3	52881097	52881048	chr12	3853	126273584
2350537	MMP7	NM_007423.3	102395711	102394128	chr11	4316	75709180
3800088	MMP7	NM_002423.3	102394111	102394062	chr11	4316	75709180
5570278	CXCL9	NM_002416.1	77142139	77142090	chr4	4283	4505186
4390398	LCN2	NM_005564.3	129955223	129954359	chr9	3934	108936958
540546	KRT4	NM_002272.2	53200708	53200659	chr12	3851	109255248
6420605	UBD	NM_006398.2	29631827	29631778	chr6	10537	50355987
3440754	IL32	NM_001012633.1	30582233	3058184	chr16	9235	61658632
1980309	IL6	NM_000584.2	74609174	74609125	chr4	3576	28610153
4730196	TK1	NM_003258.2	153533778	153533729	chr1	7083	142380763
7550220	S100A2	NM_005978.3	43238172	43238123	chr20	6273	45269153
1050168	P13	NM_002638.2	151599825	151599776	chr1	5266	31657130
5390220	S100A9	NM_002965.2	191506648	191506599	chr3	5280	9845520
5960296	CLDN1	NM_021101.3	38416555	38416506	chr21	9076	21536297
4280504	DSCR8	NM_203429.1	159914301	15991389	chr3	84677	44680116
1010132	RARRS1	NM_002888.2	159035779	159035730	chr1	5918	46255040
1260270	AIM2	NM_004833.1	22456250	22456201	chr22	9447	4757733
2370632	NMP11	NM_005940.3	82443187	82443138	chr11	4320	58331147
4730242	FAM1318	NM_175885.3	21845378	21845329	chr12	220382	54873601
4490093	ABCC9	NM_020297.1	25226807	25226758	chr5	10060	10947121
2750689	LOC729826	NM_001131447.1	151662225	151662176	chr1	729826	113416508
7550554	S100A7A	NM_176823.3	153028930	153028881	chr1	388324	126116577
6770187	SPRR2A	NM_005988.2	18149661	18149528	chr19	6700	45094054
2000300	IFB3	NM_006332.3	37029284	37029235	chr17	10437	29826337
3840445	KRT17	NM_000422.1	43601389	43601340	chr1	3872	4557700
1500010	CDC20	NM_001255.2	86818512	86818463	chr1	991	118402581
5420577	CLCA4	NM_012128.2	127669459	127669224	chr5	22802	12025666
3440204	FBN2	NM_001999.3	100134370	100134370		2201	66346694
3370601	LOC100134370	NM_001713687.1	59416917	59416868	chr18	100134370	169204720
1580762	SERPINA13	NM_012397.2				5275	19923400

FIGURE 2C

6760286	BG205162	49327863	49327814 chr22	13725849
5570711 IDO1	NM_002164.4	39785540	39785491 chr8	3620 156071492
3120113 GJB6	NM_006783.2	19694812	19694763 chr13	10804 40254836
2260563 GJB6	NM_006783.2	19694221	19694172 chr13	10804 40254836
2650379 GREM1	NM_013372.5	30813569	30813620 chr15	26585 71164890
1850523 GZMB	NM_004131.3	24170113	24170064 chr14	3002 32483414
6550500 S100A7	NM_002963.3	153431473	153431424 chr1	6278 115298656
380259 INDO	NM_002164.3	39904761	39904712 chr8	3620 38455405
5260095 GJB2	NM_004004.4	19659958	19659909 chr13	2706 118572604
2320600 CALML3	NM_005185.2	5558086	5558037 chr10	810 36031099
1470056 SERPINE3	NM_006919.1	59474093	59474044 chr18	6317 5902071
3310201 SERPINE3	NM_006919.1	59475605	59475556 chr18	6317 5902071
2630474 MLLT11	NM_006818.3	149307305	149307256 chr1	10962 55774979
4070647 ALDH3B2	NM_001031615.1	67429836	67429787 chr11	222 73695880
6620487 CXCL6	NM_002993.2	74922671	74922622 chr4	6372 52851409
2510356 EMR1	NM_001974.3	6891039	6890510 chr19	2015 40807488
5860289 KRT5	NM_000424.3	52908596	52908547 chr12	3852 119395753
2570079 STAT1	NM_139266.1	191548670	191548621 chr2	6772 21536300
6770131 OLPM4	NM_006418.3	52524157	52524108 chr13	10562 32313592
430446 KRT81	NM_002261.2	50966127	50966078 chr12	3887 15431319
6370470 APOL1	NM_145343.1	34979972	34979923 chr22	8542 21735615
3990170 IFIT2	NM_005532.3	93652605	93652556 chr14	3429 55925613
3710068 WARS	NM_173701.1	100800421	100800372 chr14	7453 47419915
1770603 TGN1	NM_001062.3	59620701	59620486 chr11	6947 133987572
1580470 LOC100130897	NM_001718498.1			100130897 169164782
580376 DSG3	NM_001944.2	27310155	27310106 chr18	1830 119964717
2340681 RARRES1	NM_206953.1	159897954	159897905 chr3	5918 46255042
3310333 WISP3	NM_003680.2	112497487	112497438 chr6	8838 18491002
2350196 KRT6B	NM_005555.3	52840556	52840507 chr12	3854 119703752
6760341 KRT6B	NM_005555.3	52845799	52845750 chr12	3854 119703752
7610338 CDH3	NM_001793.3	67290147	67290098 chr16	1001 45269142
6270553 CXCL10	NM_001565.2	77161676	77161627 chr4	3627 149999381
2350504 ECGF1	NM_001953.2	49311096	49311047 chr22	1890 7669488
2230500 SPRR2F	NM_001014456.1	153084829	153084780 chr1	6705 62945418
6550356 SPRR2C	NR_003062.1	153112855	153112804 chr1	6702 95113653
1980593 PTHLH	NM_198964.1	28116365	28116316 chr12	5744 39995068
20452 TYMP	NM_001113756.1	50965696	50965647 chr22	1890 166158924
6480364 LOC647460	NM_936525.1			647460 88956421
2260731 ERAP2	NM_022350.2	96274869	96274820 chr5	64167 141802345
4490079 DHR59	NM_005771.3	169637418	169637369 chr2	10170 40548399
6900414 PTHLH	NM_198965.1	28116534	28116485 chr12	5744 39995090
1690056 LYZ	NM_000239.1	68033213	68033210 chr12	4069 4557893

FIGURE 2D

ProbeID	Symbol	ILMN_Gene	Probe_Chromosome	Probe_Start	Probe_End	Probe_Sequence	Probe_Start
6100259	VSNL1	VSNL1	+	1676413	1676413	GAGGGACCTTGGCTCTGCTGTCACACACCAAGGCTTGTAT	1409
1340176	C20orf197	C20orf197	+	1691228	1691228	TGGGCTGGCTTCCAGTTTATGTTCCAAATGGTATGAGCTGTCCA	1513
4900458	KRT14	KRT14	-	1665035	1665035	GTGGACACAGATCCACTGGAAGATCCCTCTCTGCGCAAGCACTCAC	1519
7050220	NMU	NMU	-	162253	162253	GCTGACGCTGCTTCTCTCACTGATGAGAGAAATGAAGATTCAGAG	486
2490541	MAGEA10	MAGEA10	-	1741430	1741430	GCCATGGCAGTGCAGTTCTAGCGCTGAGCTGAGTGTCTCTACCTTGA	2153
5260484	HLA-DRB1	HLA-DRB1	-	1715189	1715189	GGACTTGGCAGGGGCGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1374
4280132	DSCR8	DSCR8	+	1763901	1763901	TCCACTTGGCAGGGGCGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	834
2510605	FAM83A	FAM83A	+	2239774	2239774	CAGCTTGGTCACTCTGAGGAAATGCTGAACTTCAAGCCCTTCA	33
6860424	SERPINB4	SERPINB4	+	1782716	1782716	GGATCTGGGACCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2309
2140707	SLP1	SLP1	-	1714720	1714720	GGATCTGGTGAACCCCAACCAAGGAGGAGCTGGGAGTGC	1033
5360054	GNYL	GNYL	+	1790692	1790692	CTACAGTCCCTCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	241
7400743	KIAA1618	KIAA1618	+	2289093	2289093	CCCGTTATCTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	654
6060468	S100A8	S100A8	-	1729801	1729801	TACTTCCAGGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	5246
6290554	GTSF1	GTSF1	-	2069632	2069632	GGGGCACACTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	253
50689	C7orf288	C7orf288	-	2246083	2246083	GCATATCTGCTTGAAGATCAGATTCGACTCGGCTGCTGCTGCTG	414
2190148	GBP1	GBP1	-	2148785	2148785	GTCTCCAGAGGAGTGGAGAACCTATGGGAGGAGTAGGAATTGAGT	1587
4760626	MMP12	MMP12	-	2073758	2073758	TCTATTGAAGCATGCTGTGAAGTTGCTCTCTCACTGCTGCTG	2388
6350189	MGC4677	MGC4677	+	2143795	2143795	GGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1701
3830681	KRT6A	KRT6A	-	2219002	2219002	GTGTTGTGAACCCCAACCAAGGAGTATCCATGAAGCACAAGTACTAG	360
2350337	MMP7	MMP7	-	1685403	1685403	ICTACTCTGATGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTG	2310
3800088	MMP7	MMP7	-	2190702	2190702	GCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	615
5570278	CXCL9	CXCL9	-	1745356	1745356	TGATTTGGTCCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	681
4390398	LCN2	LCN2	+	1692223	1692223	CCACATGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2052
540546	KRT4	KRT4	-	1744765	1744765	CCAGGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	625
6420605	UBD	UBD	-	1678841	1678841	CTCTCCAGGCTGGAAGTCCAGTCTGCTGCTGCTGCTGCTGCTG	2200
3440754	IL32	IL32	+	2368530	2368530	CGACTTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	530
1980309	IL8	IL8	+	2184373	2184373	CCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	355
4730196	TK1	TK1	+	1806037	1806037	TGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1345
7550220	S100A2	S100A2	-	1725852	1725852	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1071
1050168	PI3	PI3	+	1693192	1693192	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	768
5390220	S100A9	S100A9	+	1750974	1750974	CATCATGGAGGACTTGGACACAAATGCTGAGGCTCTTGGGAGTGGC	353
5960296	CLDN1	CLDN1	-	1724686	1724686	GTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	228
4280504	DSCR8	DSCR8	+	1758066	1758066	GAAGGCTGGCTATACATTTCCAGAGGAAATTTGGCTGCTGCTG	2967
1010132	RARRES1	RARRES1	-	1743620	1743620	GCACAGAGCGCTACACCCAGAGTCTTACTTCAAGAGGTTGAGGAGCT	368
1260270	AIM2	AIM2	-	1681301	1681301	GCTGGTGAACCCCGAAGATCAACACGCTTCAAGCTCAGCCCTTGAAC	388
2370632	MMP11	MMP11	+	1655915	1655915	CAGGCTGTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	981
4730342	FAM181B	FAM181B	-	1735502	1735502	GCTGGCTCTGTAGCCACTTCTCTCTCTCTCTCTCTCTCTCTCTCT	1719
4490093	ABCC9	ABCC9	-	1751453	1751453	CGAGTACACACTTCTGAGGAGAGCTGCTGCTGCTGCTGCTGCTG	4516
2750689	LOC729826	LOC729826	+	1750299	1750299	CCTGACACACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3168
7550554	S100A7A	S100A7A	+	1673191	1673191	AGAGTCTGACAGCAGCAGATTAAGCTTCAAGCTTCAAGCTTCAAG	4130
6770187	SPRR2A	SPRR2A	-	1795359	1795359	GCTCCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	342
2000300	IFB3	IFB3	+	1807277	1807277	TGGAAGATCAACCCAGCTCTTACTTCAAGCTTCAAGCTTCAAG	717
3840445	KRT17	KRT17	-	1666845	1666845	CCCTGCTTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1434
1500010	CDC20	CDC20	+	1683390	1683390	AAGCCAGTGCAGCCAAAGAGGCTCTCTCTCTCTCTCTCTCTCTCT	1554
5420577	CLCA4	CLCA4	+	1679176	1679176	AGCAATCTGATGACATTTGATCTCTCTCTCTCTCTCTCTCTCTCT	2649
3440204	FBN2	FBN2	-	1670895	1670895	GGCCAAAGCACATGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	30479
3370601	LOC100134370	LOC100134370	+	3239748	3239748	CTACAGGCGCTGCTGAGGGGAGGAGGCTGCTGCTGCTGCTGCTG	1282
1580762	SERPINB13	SERPINB13	+	1769759	1769759	CTAGGTCACAGTTGAGGGAGATTTGGATTTCTCCACTTCTTGGGCTG	2569

FIGURE 2E

6760286	HS.72010	-	ILMN_1910908	CCTGTGGCAAGCCAGCAAGATGGCCCTGGTGA	318
5570711 IDO1	+	ILMN_3239965	CGCTGTGTGAAAGCTCTGGTCTCCCTGAGGAGTACCATCTGCAATCG	1113	
3120113 GJB6	-	ILMN_1718671	GGTGGCTGATGAAGAGACTTCTGTCTCTCCAGAGGCAATACCACTCG	1053	
2260563 GJB6	-	ILMN_2262223	GTAGACGGAAACAGTGTGGAAGCAGAAAGCTTTTAACTCATCCGTTCG	1646	
2650379 GREM1	+	ILMN_1752965	GGGGAAACAAATCTTGACCCAGCTGAACATGTCTCTCTGAGTCACTGCC	3596	
1850523 GZMB	-	ILMN_2109489	JACAGGAAGCAAACTAAGCCCTGCTGTAATGAACACCTCTCTGAGGCC	813	
6550500 S100A7	-	ILMN_1757351	GCCTGAGAGTCCATAATAGGCAATGATGACATGTTTCAAAATACACAG	87	
380259 IND0	+	ILMN_1656310	CTGATCTCTGCAAGCAGCAGCAAGGAGGATAAGACCTCTGAGACCC	1177	
5260095 GJB2	-	ILMN_1769388	GATGAGCTTTGTCTACTTCAAAAGTTTGTTCCTTACCCCTTCAGCCTCC	1977	
2320600 CALML3	+	ILMN_1733333	AAACAGCACTGCTTCCGCGCTGCCAGCTTCCGCCCATCTCTCTGTCCG	1114	
1470056 SERPINB3	-	ILMN_1703855	TGACGGGAGCGGGGTCTGTGCTATCTGGAGTCTTACCAAGGGCTTT	1012	
3310201 SERPINB3	-	ILMN_2120222	CCTGAAGGTAATATTGGCAGCAATACCACTTGGTCTTAACTGTGGGTG	551	
2630474 MLT11	+	ILMN_1759097	CCCTCTTCCACCTACTTCACTTACAACTTGTCTTAACTGTGGGTG	1817	
4070647 ALDH3B2	-	ILMN_1763666	GGCGGTCTCCACAGAAACCATCGCAACTCTCTGCACTCTCTCTATAA	2290	
5620487 CXCL6	+	ILMN_1779234	GTGTGCTGTGAGGGAGGTATCTGTGTCTTACTCACTCTCTCTCTATAA	890	
2510356 EMR1	+	ILMN_1780601	TCTCAGCTTAACTGAAATGAGGATGCCACAGCCAGCAACCTCTCTGG	2781	
5860289 KRT5	-	ILMN_1801632	ACCACATCTTTGGTTCAGGAGAGCCCATGCCAGCCCTGGTCTCC	2065	
2570079 STAT1	-	ILMN_1691364	CGCCATCACAGCTGMACTTGTGAGATCCCGTGTACTGGCTATCAGCA	2595	
6770131 OLFM4	+	ILMN_2116877	TGTTCAAGTCTAGTCTATAGGATTTGGCAGTTTAAATGCTTACTCTCC	2734	
430446 KRT81	-	ILMN_1801442	CACTGGGAAAGCCACCTAGAAAGAGTCCGCTGGCAACCATAGGAGG	1746	
6370470 APO1	+	ILMN_1688631	GGTGGCTGTGGCATGATGCGACTTGAATGCAATGATGATGATGATGATG	236	
3990170 F127	+	ILMN_2058782	CCAAGTCACTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	422	
3710068 WARS	-	ILMN_1727271	AGTCTGGCTCCGAGATGCTTCAATTTGACCCCTTGGCTGCACTGGAAG	2363	
1770603 TON1	-	ILMN_1768469	TGAGTGGAGGGCAACCACTGAGCCAGGAGCTGTTAGTGTAGTGTCTCCG	1312	
1580478 LOC100130897	+	ILMN_3271398	TGCTGCTGGAGCTCTCAAGTACTTGTGTCTTGTGTCTTGTGTCTTGTGTG	1141	
580376 DSGB	+	ILMN_1655468	CAGAAAGGGTGTACTGTGCCCATTCGAGTGTCTCTGGCAACTTACTGTG	2994	
2340681 RARRES1	+	ILMN_1800091	CTCTGCTCAGTGTAAACAGTCAACAGCAGGTCTCTCAGGGTCTCAGCCC	1162	
3310333 WISP3	+	ILMN_1712360	GTCTGGATACATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1097	
2350196 KRT6B	-	ILMN_1721354	CTCTTGCAGTGTCTCTGAAATGGCAAGTGTACTCTTCTGATGCACTGTG	2160	
6760341 KRT6B	-	ILMN_1698772	CTCAGCCAGGCTCCTTGGGGTGAAGCTGCTGCTGCTGCTGCTGCTGCTG	111	
7610338 CDH3	-	ILMN_1704294	CTGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3291	
6270533 CXCL10	+	ILMN_1791759	GACTTCCACTGGCATCTCTCCAGGGGCTGAGGGGCTGAGGGGCTGAGGG	793	
2350504 ECGF1	-	ILMN_2109708	ITCCGAGAGCTGTCTTGGCGCGGCAAGCAATTAAGCTCTTCTTGGCGGAA	1550	
2230500 SPRR2F	-	ILMN_1674367	GGTTTCTTTTGGAGGCTGCCATCTGCCACTGTCCGAGTGGAGTGAAG	439	
6550356 SPRR2C	-	ILMN_2197577	CTTTCCTCTAGCTGTGATCTGCCATGATGATGATGATGATGATGATGATG	418	
1980593 PTHLH	-	ILMN_1785699	TGTTTAGACTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGG	742	
20452 TYMP	-	ILMN_3223126	AGAACTCTGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	782	
6480364 LOC647460	+	ILMN_1729198	CTGGATGACCCAGTCTCCATCTTACTCTTCTGCTGCTGCTGCTGCTGCTG	93	
2260731 ERAP2	+	ILMN_1743145	AACCTGGAGCTCTCTTCTGATGCAATGCGAGCTGCCAGAGCTCCAAAGGGCAGCA	2682	
4490079 DHRS9	+	ILMN_2281502	CAAGGAGAGGCTGGAGTGTGCAATATTTCTTCTGCTGCTGCTGCTGCTG	1373	
6900414 PTHLH	-	ILMN_2314169	CCACCCGTCCGATTTGGGTCTGATGATGAGGGGAGGAGTAACTACTCAGG	592	
1690056 LYZ	+	ILMN_1815205	GAGGGTGTCTCGTATCCAAAGGCAATAGAGCATGGGTGGCATGGAGAA	370	

FIGURE 2F

ProteinID	Symbol	Probe_Type	Protein_Product	RefSeq_ID	Search_Key	Source_Reference_ID
6100259	VSNL1	S	NP_003376.2	NM_003385.4	NM_003385.4	NM_003385.4
1340176	C20orf197	S	NP_775915.1	NM_173644.1	NM_173644.1	NM_173644.1
4900458	KRT14	S	NP_000517.2	NM_000526.3	NM_000526.3	NM_000526.3
7050220	NMU	S	NP_006672.1	NM_006681.1	NM_006681.1	NM_006681.1
1510364	GEP5	S	NP_443174.1	NM_052942.2	NM_052942.2	NM_052942.2
2490541	MAGEA10	A	NP_066386.1	NM_021048.3	NM_001011543.1	NM_021048.3
5260484	HLA-DRB1	S	NP_002115.1	NM_002124.1	NM_002124.1	NM_002124.1
4280132	OSCR8	A	NP_982252.1	NM_203428.1	NM_032899.4	NM_032899.4
2510605	FAM83A	I	NP_116288.2	NM_032899.4	NM_002974.1	NM_002974.2
6860424	SERPINB4	S	NP_002965.1	NM_002974.2	NM_003064.2	NM_003064.2
2140707	SLPI	S	NP_003055.1	NM_003064.2	NM_012483.1	NM_012483.1
5360064	GMYL	A	NP_036615.1	NM_012483.1	NM_020954.2	NM_020954.2
7400743	KIAA1618	I	NP_066005.2	NM_020954.2	NM_002964.3	NM_002964.3
6060468	S100A8	S	NP_002955.2	NM_002964.3	NM_144594.1	NM_144594.1
6290534	GTSF1	S	NP_653195.1	NM_144594.1	NM_198097.1	NM_198097.1
50689	C7orf288	I	NP_932765.1	NM_198097.1	NM_002053.1	NM_002053.1
2190148	GEP1	S	NP_002044.1	NM_002053.1	NM_002426.2	NM_002426.2
4760626	MMP12	S	NP_002417.2	NM_002426.2	NM_052871.3	NM_052871.3
6350189	MSC4677	S	NP_443103.1	NM_052871.3	NM_005554.3	NM_005554.3
3830881	KRT6A	S	NP_005545.1	NM_005554.3	NM_002423.3	NM_002423.3
2350537	MMP7	S	NP_002414.1	NM_002423.3	NM_002423.3	NM_002423.3
3800088	MMP7	S	NP_002414.1	NM_002423.3	NM_002416.1	NM_002416.1
5570278	CXCL9	S	NP_002407.1	NM_002416.1	NM_005564.3	NM_005564.3
4390398	LCN2	S	NP_005555.2	NM_005564.3	NM_002272.1	NM_002272.2
540546	KRT4	S	NP_002263.2	NM_002272.1	NM_006398.2	NM_006398.2
6420605	UBD	S	NP_006389.1	NM_006398.2	NM_001012633.1	NM_001012633.1
3440754	IL32	A	NP_001012651.1	NM_001012633.1	NM_000584.2	NM_000584.2
1980309	IL8	S	NP_000575.1	NM_000584.2	NM_003258.1	NM_003258.2
4730196	TK1	S	NP_003249.1	NM_003258.2	NM_005978.3	NM_005978.3
7550220	S100A2	S	NP_005969.1	NM_005978.3	NM_002638.2	NM_002638.2
1050168	PT3	S	NP_002629.1	NM_002638.2	NM_002965.2	NM_002965.2
5390220	S100A9	S	NP_002956.1	NM_002965.2	NM_021101.3	NM_021101.3
5960296	CLDN1	S	NP_066924.1	NM_021101.3	NM_203429.1	NM_203429.1
4280504	OSCR8	I	NP_982253.1	NM_203429.1	NM_002888.2	NM_002888.2
1010132	RARR51	A	NP_002879.2	NM_002888.2	NM_004833.1	NM_004833.1
1260270	AIM2	S	NP_004824.1	NM_004833.1	NM_005940.3	NM_005940.3
2370632	MMP11	S	NP_005931.2	NM_005940.3	NM_175885.3	NM_175885.3
4730242	FAM181B	S	NP_787081.2	NM_175885.3	NM_020297.1	NM_020297.1
4490093	ABCC9	I	NP_064693.1	NM_020297.1	NM_001131447.1	NM_001131447.1
2750689	LOC729826	A	XP_001131447.1	NM_001131447.1	NM_176823.2	NM_176823.2
7550554	S100A7A	S	NP_789793.1	NM_176823.2	NM_005988.2	NM_005988.2
6770187	SPRR2A	S	NP_005979.1	NM_005988.2	NM_006332.3	NM_006332.3
2000300	IFI30	S	NP_006323.2	NM_006332.3	NM_000422.1	NM_000422.1
3840445	KRT17	S	NP_000413.1	NM_000422.1	NM_001255.1	NM_001255.2
1500010	CDC20	S	NP_001246.2	NM_001255.2	NM_012128.2	NM_012128.2
5420577	CLCA4	S	NP_036260.1	NM_012128.2	NM_001999.3	NM_001999.3
3440204	FBN2	S	NP_001990.2	NM_001999.3	XP_001713687.1	XP_001713687.1
5370601	LOC100134370	S	XP_001713739.1	NM_001713687.1	NM_012397.2	NM_012397.2
1580762	SERPINS13	S	NP_036529.1	NM_012397.2	NM_012397.2	NM_012397.2

FIGURE 2G

	S		Hs. 72010	Hs. 72010	Hs. 72010
6760286	S				
5570711 IDO1	S	NP 002155.1	NM 002164.4	NM 002164.4	NM 002164.4
3120113 GIB6	S	NP 006774.2	NM 006783.2	NM 006783.2	NM 006783.2
2260563 GIB6	S	NP 006774.2	NM 006783.2	NM 006783.2	NM 006783.2
2650379 GREM1	S	NP 037504.1	NM 013372.5	NM 013372.5	NM 013372.5
1850523 GZM8	S	NP 004122.1	NM 004131.3	NM 004131.3	NM 004131.3
6550500 S100A7	S	NP 002954.2	NM 002963.3	NM 002963.3	NM 002963.3
380259 INDO	S	NP 002155.1	NM 002164.3	NM 002164.3	NM 002164.3
5260095 GJB2	S	NP 003995.2	NM 004004.4	NM 004004.4	NM 004004.4
2320600 CALML3	S	NP 005176.1	NM 005185.2	NM 005185.2	NM 005185.2
1470056 SERPINB3	S	NP 008850.1	NM 006919.1	NM 006919.1	NM 006919.1
3310201 SERPINB3	S	NP 008850.1	NM 006919.1	NM 006919.1	NM 006919.1
2630474 MLI113	S	NP 006809.1	NM 006818.3	NM 006818.3	NM 006818.3
4070647 ALDH3B2	A	NP 001026786.1	NM 001031615.1	NM 001031615.1	NM 001031615.1
6620487 CXCL6	S	NP 002984.1	NM 002993.2	NM 002993.2	NM 002993.2
2510356 EMR1	S	NP 001965.3	NM 001974.3	NM 001974.3	NM 001974.3
5860289 KRT5	S	NP 000415.2	NM 000424.3	NM 000424.3	NM 000424.3
2570079 STAT1	I	NP 644671.1	NM 139266.1	NM 139266.1	NM 139266.1
6770131 OLFM4	S	NP 006409.3	NM 006418.3	NM 006418.3	NM 006418.3
430446 KRT81	S	NP 002272.1	NM 002281.2	NM 002281.2	NM 002281.2
6370470 APOL1	I	NP 663318.1	NM 145343.1	NM 145343.1	NM 145343.1
3990170 IFI27	S	NP 005523.3	NM 005532.3	NM 005532.3	NM 005532.3
3710068 WARS	A	NP 776049.1	NM 173701.1	NM 173701.1	NM 173701.1
1770603 TCN1	S	NP 001053.2	NM 001062.3	NM 001062.3	NM 001062.3
1580470 LOC100130897	M	XP 001718550.1	NM 001718498.1	NM 001718498.1	NM 001718498.1
580376 DSG3	S	NP 001935.2	NM 001944.2	NM 001944.2	NM 001944.2
2340681 RARRES1	I	NP 996846.1	NM 206963.1	NM 206963.1	NM 206963.1
3310333 WISP3	A	NP 003871.1	NM 003880.2	NM 003880.2	NM 003880.2
2350196 KRT68	S	NP 005546.2	NM 005555.3	NM 005555.3	NM 005555.3
6760341 KRT68	S	NP 005546.2	NM 005555.3	NM 005555.3	NM 005555.3
7610338 CDH3	S	NP 001784.2	NM 001793.3	NM 001793.3	NM 001793.3
6270553 CXCL10	S	NP 001556.2	NM 001565.2	NM 001565.2	NM 001565.2
2350504 ECGF1	S	NP 001944.1	NM 001953.2	NM 001953.2	NM 001953.2
2230500 SPRR2F	S	NP 001014450.1	NM 001014450.1	NM 001014450.1	NM 001014450.1
6550356 SPRR2C	S		NR 003062.1	NR 003062.1	NR 003062.1
1980593 PTHLH	A	NP 945315.1	NM 198964.1	NM 198964.1	NM 198964.1
20452 TYMP	A	NP 00107228.1	NM 00113756.1	NM 00113756.1	NM 00113756.1
6480364 LOC647460	S	XP 941618.1	NM 936525.1	NM 936525.1	NM 936525.1
2260731 ERAP2	S	NP 071745.1	NM 022350.2	NM 022350.2	NM 022350.2
4490079 DHRS9	I	NP 005762.2	NM 005771.3	NM 005771.3	NM 005771.3
6900414 PTHLH	A	NP 945316.1	NM 198965.1	NM 198965.1	NM 198965.1
1690056 LYZ	S	NP 000230.1	NM 000239.1	NM 000239.1	NM 000239.1

FIGURE 2H

ProteinID	Symbol	Synonyms
6100259 VSNL1		HPCAL3; VILIP-1; HUVISL1; HUP3; VILIP
1340176 C20orf197		FLJ33860; MGC120496; RP5-1017F8.1
4900458 KRT14		NFI; CK14; EBS3; EBS4; K14
7050220 NMU		
1510364 GBP5		GBP-5
2490541 MAGEA10		MAGE10; MGC10599
5260484 HLA-DRB1		HLA-DRB1*; HLA-DRB1; HLA DRB1; DRB1
4280132 DSCR8		MTAG2; C21orf65; MNA-1
2510605 FAM83A		BI-TSA-9; MGC14128
6860424 SERPINB4		LEUPIN; SCCA-2; P111; SCCA1; SCCA2
2140707 SLPI		WFDC4; WAP4; MPI; ALK1; ALP; BLP; HUS1-I; HUS1
5360064 GNL1		D2569E; S19; LAG2; NK65; LAG-2; TLA519
7400743 KIAA1618		
6060468 S100A8		CFAG; 6068AG; MRP8; CGLA; LIAG; MIF; MA387; CAGA; CP-10; NIF; P8
6290554 GTSF1		FAM112B; FLJ32942
50689 C7orf288		H_NH0577018.2; MGC19819; DKFZP586I1023
2190148 GBP1		
4760626 MMP12		MGC138506; NME; HME
6350189 MGC4677		MGC17532; MGC88182
3830681 KRT6A		K6D; K6C; CK6C; K6A; KRT6C; KRT6D; CK6A; CK6D
2350537 MMP7		MMP-7; PUMP-1; MP5L1
3800988 MMP7		MMP-7; PUMP-1; MP5L1
5570278 CXCL9		MIG; c9-10; Humig; SCYB9; CMK
4390398 LCN2		NGAL
540546 KRT4		CK4; CYK4; K4; FLJ31692
6420605 UBD		UBD-3; FAT10
3440754 IL32		IL-32alpha; TAFD; IL-32beta; TAFc; TAFd; IL-32gamma; TAFb; TAFa; IL-32delta; NK4
1980309 IL8		GCP-1; MDNCF; NAPI; CXCL8; AMCF-1; TSG-1; LYNAP; NAP-1; MONAP; GCP1; SCYB8; LUCT; K60; LECT; 3-10C; b-ENAP; NAF
4730196 TK1		TK2
7550220 S100A2		S100L; CAN19; MGC111539
1050168 PI3		SKALP; ESI; WAP3; WFDC14; MGC13613
5390220 S100A9		CFAG; MAC387; 6068AG; MIF; MRP14; CGLB; CAGB; LIAG; NIF; P14; LIAG
5960296 CLDN1		SEMP1; ILVASC; CLD1
4280504 DSCR8		MTAG2; C21orf65; MNA-1
1010132 RARRES1		ITG1
1260270 AIM2		PYHIN4
2370632 MMP13		ST3; SL-3; STMY3
4730242 FAM181B		
4490093 ABCG9		ABCG7; FLJ36852; SUR2; CMD10
2750689 LOC729826		
7550554 S100A7A		S100A7; NICE-2; S100A7L1; S100A15
6770187 SPRR2A		
2000300 IFI30		MGC12056; IP30; GILT; IFI-30
3840445 KRT17		PCHC1; K17; PC2; PC
1500010 CDC20		CDC20A; BA276H19.3; MGC102824; p55CDC
5420577 CLCA4		CaCC3; MGC142249; CaCC; MGC142247
3440204 FBN2		CCA
3370601 LOC100134370		
1580762 SERPINB13		headpin; MGC126870; HUR7; P113

FIGURE 21

6760286	
5570711 ID01	CD107B; IDO
3120113 GJB6	HED; ED2; CX30; DFNA3; EDH
2260563 GJB6	HED; ED2; CX30; DFNA3; EDH
2650379 GREM1	DAND2; DRM; MGCL26660; GREMLIN; FIG2; IHG-2; CKTSFIB1
1850523 GZM8	CCPI; CGL1; CTSG11; CGL-1; CSP-8; CTU1; CSP8; SECT; HLP
6550500 S100A7	PSOR1; S100A7c
380259 INDO	CD107B; IDO
5260095 GJB2	DFNB1; NSRD1; HED; DFNA3; PPK; KID; CX26
2320600 CALML3	CLP
1470056 SERPINB3	SCCA-1; SCCA-PD; HST1196; SCCA1; SCC; T4-A
3310201 SERPINB3	SCCA-1; SCCA-PD; HST1196; SCCA1; SCC; T4-A
2630474 MLT11	AF1Q; RP11-316M1.10
4070647 ALDH8B2	ALDH8
6620487 CXCL5	GCP2; GCP-2; CXA-3; SCY86
2510356 EMR1	TM7LNS
5860289 KRT5	DDO; CK5; K5; EBS2; KRT5A
2570079 STAI1	ISGF-3; STAT91; DKFZp686804100
6770131 OLFM4	ba209J19.1; OIFD; KIAA4294; GW112; GCI
430446 KRT81	KRT81; HB-1; HB1; MLN157; THAKB2-1; qmHb1
6370470 APO1	APOL; APO1-1; APO-1
3990170 IFI27	FAM14D; P27; ISG12
3710068 WARS	IFI53; IFP53; GAMMA-2
1770603 TCN1	TCI; TCI
1580470 LOC100130897	
580376 DSG3	DKFZp686P231B4; CDHF6; PVA
2340681 RARRES1	TIG1
3310333 WISP3	PPD; CCN6; MGC125987; LBC; PPAC; MGC125989; MGC125988
2350196 KRT6B	PC2; K6B; CK6B; KRT11
5760341 KRT6B	PC2; K6B; CK6B; KRT11
7610338 CDH3	HJMD; PCAD; CDHP
6270553 CXCL10	IFI10; CT9-2; mob-1; INP10; gIP-10; C7; SCY810; IP-10
2350504 ECGF1	TP; PDECGF; hPD-ECGF; MNGIE
2230500 SPRR2F	
6550356 SPRR2C	
1980593 PTHLH	PTHRP; PLP; MGC14611; PTHR; HHM
20452 TYMP	TP; ECGF1; PDECGF; hPD-ECGF; MNGIE
6480364 LOC647460	
2260731 ERAP2	LRAP; FLJ23633; FLJ23807; FLJ23701; L-RAP; ERAP2
4490079 DHRS9	RDHL; 3alpha-HSD; RETSDR8; RDH15
6900414 PTHLH	PTHRP; PLP; MGC14611; PTHR; HHM
1690056 LYZ	

FIGURE 2J

ProbeID	Symbol	Transcript
6100259	VSNI1	ILMN_14853
1340176	C20orf197	ILMN_1118
4900458	KRT14	ILMN_9209
7050220	NMIU	ILMN_28975
1510364	GBP5	ILMN_24462
2490541	MAGEA10	ILMN_22178
5260484	HLA-DRA1	ILMN_20550
4280132	DSCR8	ILMN_22481
2510605	FAM83A	ILMN_14524
6860424	SERPINB4	ILMN_181898
2140707	SLPI	ILMN_28045
5360064	GNIY	ILMN_13145
7400743	KIAA1618	ILMN_176692
6060468	S100A8	ILMN_13072
6290554	GTSF1	ILMN_17221
50689	C7orf288	ILMN_8655
2190148	GBP1	ILMN_28413
4760626	MMP12	ILMN_176589
6350189	MGC4677	ILMN_18892
3830681	KRT6A	ILMN_20473
2350537	MMP7	ILMN_9188
3800088	MMP7	ILMN_9188
5570278	CXCL9	ILMN_12602
4390398	LON2	ILMN_20794
540546	KRT4	ILMN_14703
6420605	UBD	ILMN_161963
3440754	IL32	ILMN_17936
1980309	IL8	ILMN_179575
4730196	TK1	ILMN_50194
7550220	S100A2	ILMN_4973
1050168	P13	ILMN_13685
5390220	S100A9	ILMN_25646
5960296	CLDN1	ILMN_177119
4280504	DSCR8	ILMN_22589
1010132	RARRES1	ILMN_10965
1260270	AIM2	ILMN_10231
2370632	MMP11	ILMN_16214
4730242	FAM181B	ILMN_183956
4490093	ABCC9	ILMN_27550
2750689	LOC729826	ILMN_165087
7550554	S100A7A	ILMN_4534
6770187	SPRR2A	ILMN_4602
2000300	IFI30	ILMN_23180
3840445	KRT17	ILMN_5566
1500010	CDC20	ILMN_8354
5420577	CLCA4	ILMN_17695
3440204	FBN2	ILMN_22082
3370601	LOC100134370	ILMN_340180
1580762	SERPINB13	ILMN_9686

FIGURE 2K

6760286	ILMN_73498
5570711 IDO1	ILMN_7704
3120113 GJB6	ILMN_14068
2260563 GJB6	ILMN_14068
2650379 GREM1	ILMN_16591
1850523 GZMB	ILMN_23555
6550500 S100A7	ILMN_2266
380239 INDO	ILMN_7704
5260095 GJB2	ILMN_175314
2320600 CALM13	ILMN_20293
1470056 SERPINB3	ILMN_29229
3310201 SERPINB3	ILMN_29229
2630474 MLT11	ILMN_21397
4070647 ALDH3B2	ILMN_2557
6620487 CXCL6	ILMN_11101
2510336 EMR1	ILMN_12984
5860289 KRT5	ILMN_7654
2570079 STA11	ILMN_11054
6770131 OLFM4	ILMN_4558
430446 KRT81	ILMN_635
6370470 APOL1	ILMN_4231
3990170 IFI27	ILMN_17548
3710068 WARS	ILMN_26385
1770603 TCN1	ILMN_13727
1580470 LOC100130897	ILMN_350926
580376 DSG3	ILMN_174002
2340681 RARRES1	ILMN_12238
3310333 WISP3	ILMN_9986
2350196 KRT6B	ILMN_7664
6760341 KRT6B	ILMN_7664
7610338 CDH3	ILMN_12740
6270553 CXCL10	ILMN_5066
2350504 ECGF1	ILMN_18760
2230500 SPRR2F	ILMN_28582
6550356 SPRR2C	ILMN_179917
1980593 PTHLH	ILMN_14943
20452 TYMP	ILMN_338776
6480364 LOC647460	ILMN_38026
2260731 ERAP2	ILMN_22173
4490079 DHRS9	ILMN_184091
6900414 PTHLH	ILMN_4677
1690056 LYZ	ILMN_4879

FIGURE 2L

MAGEA10

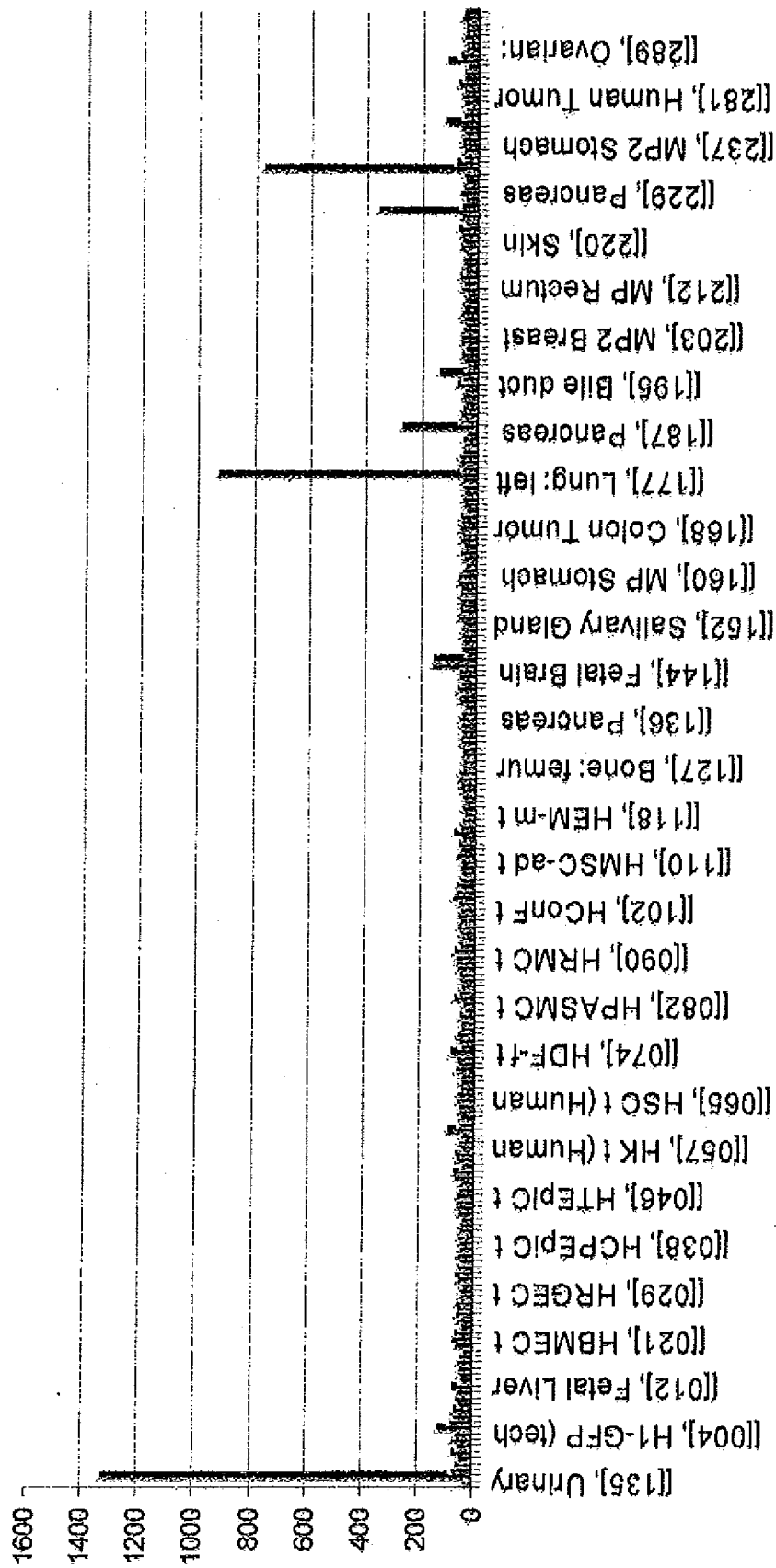


FIGURE 3

DSCR8

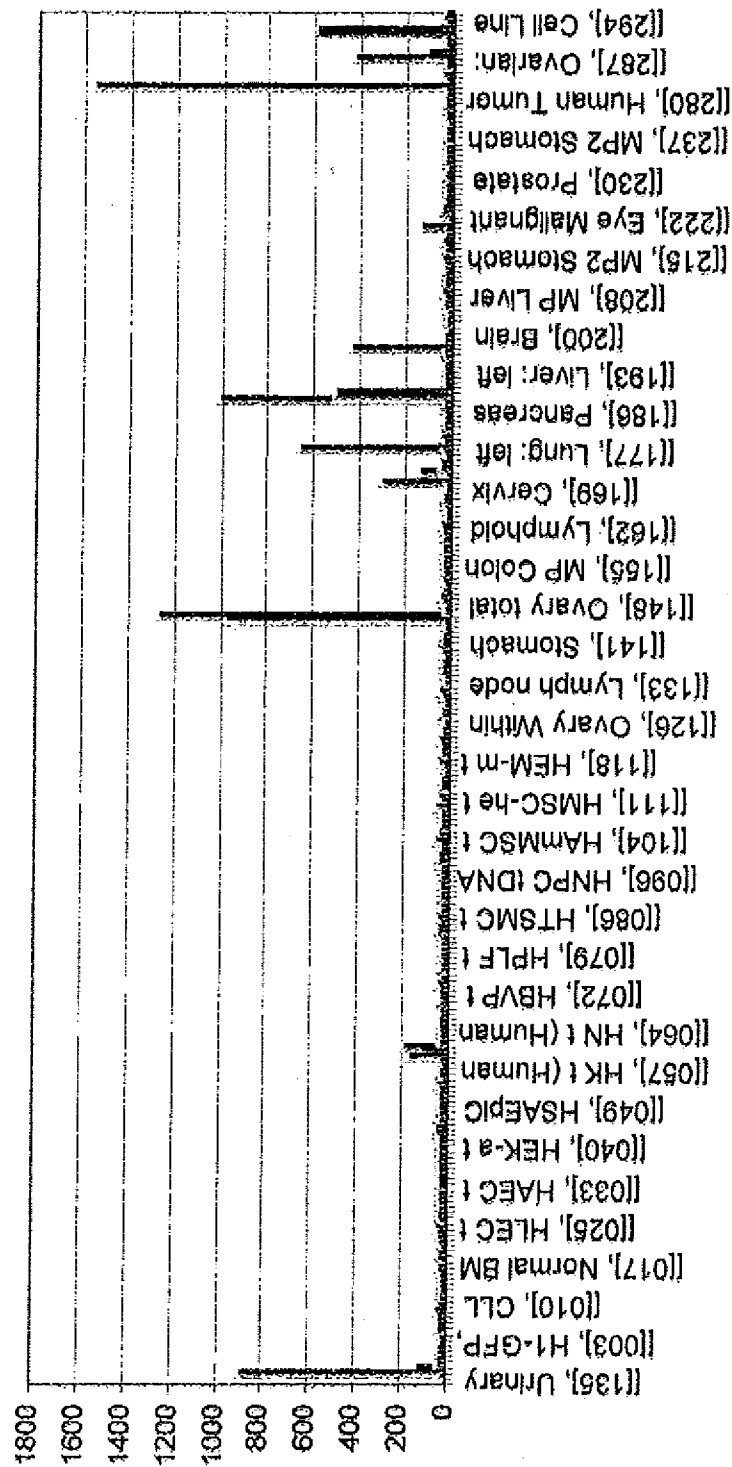


FIGURE 4

MMP12

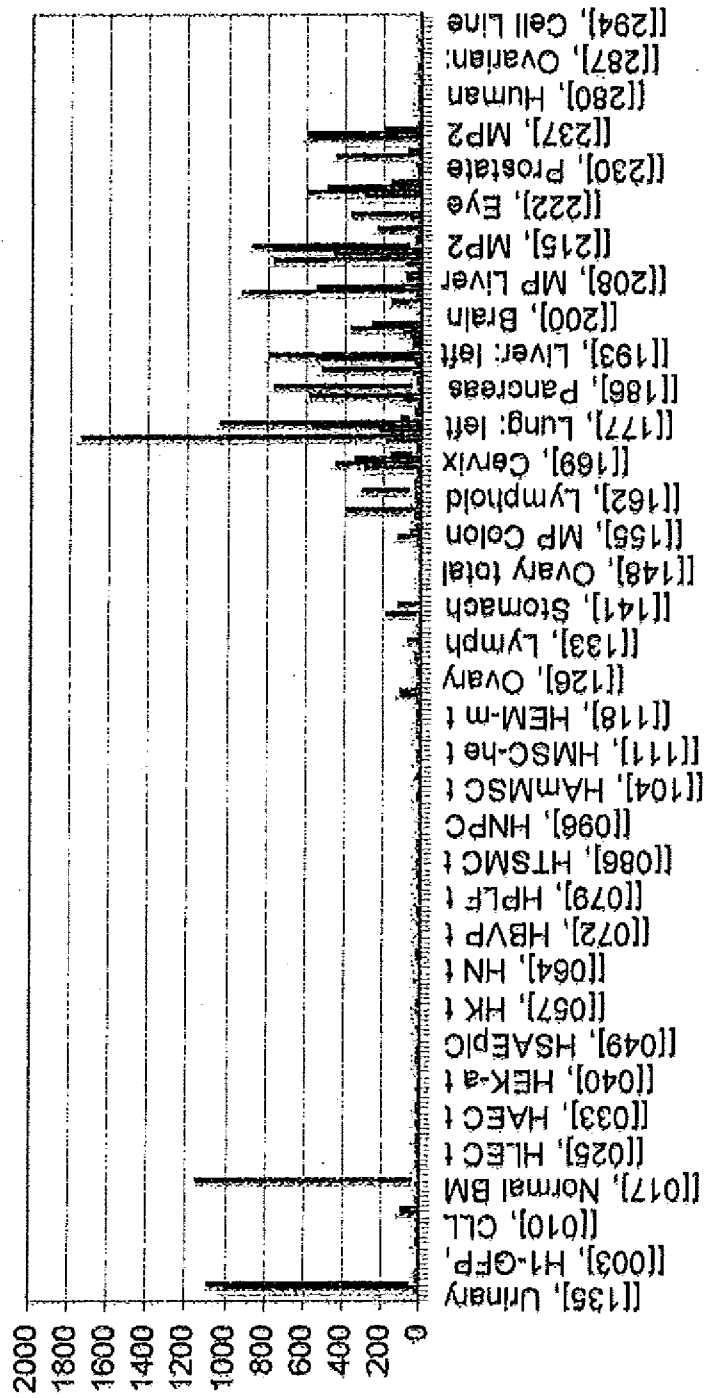


FIGURE 5

CXCL9

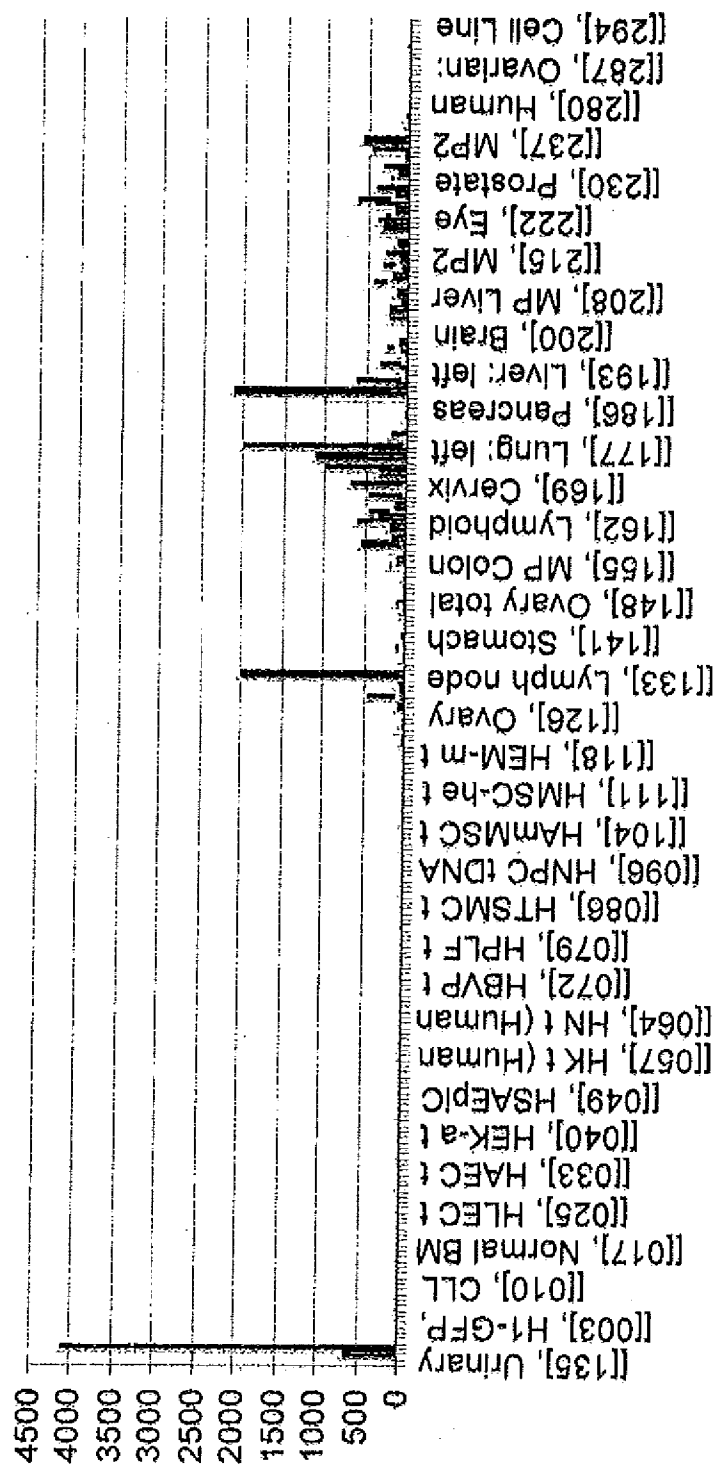


FIGURE 6

DSCR8

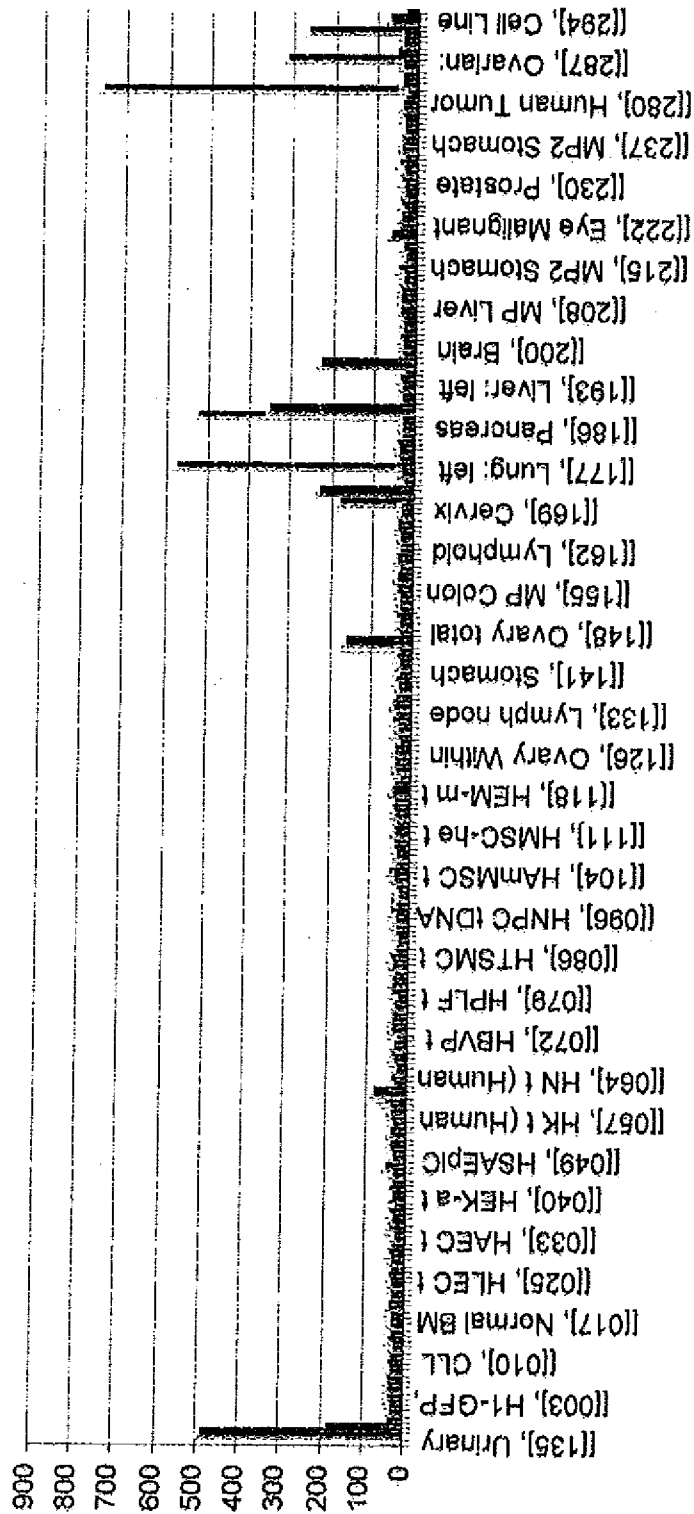


FIGURE 7

KRT81

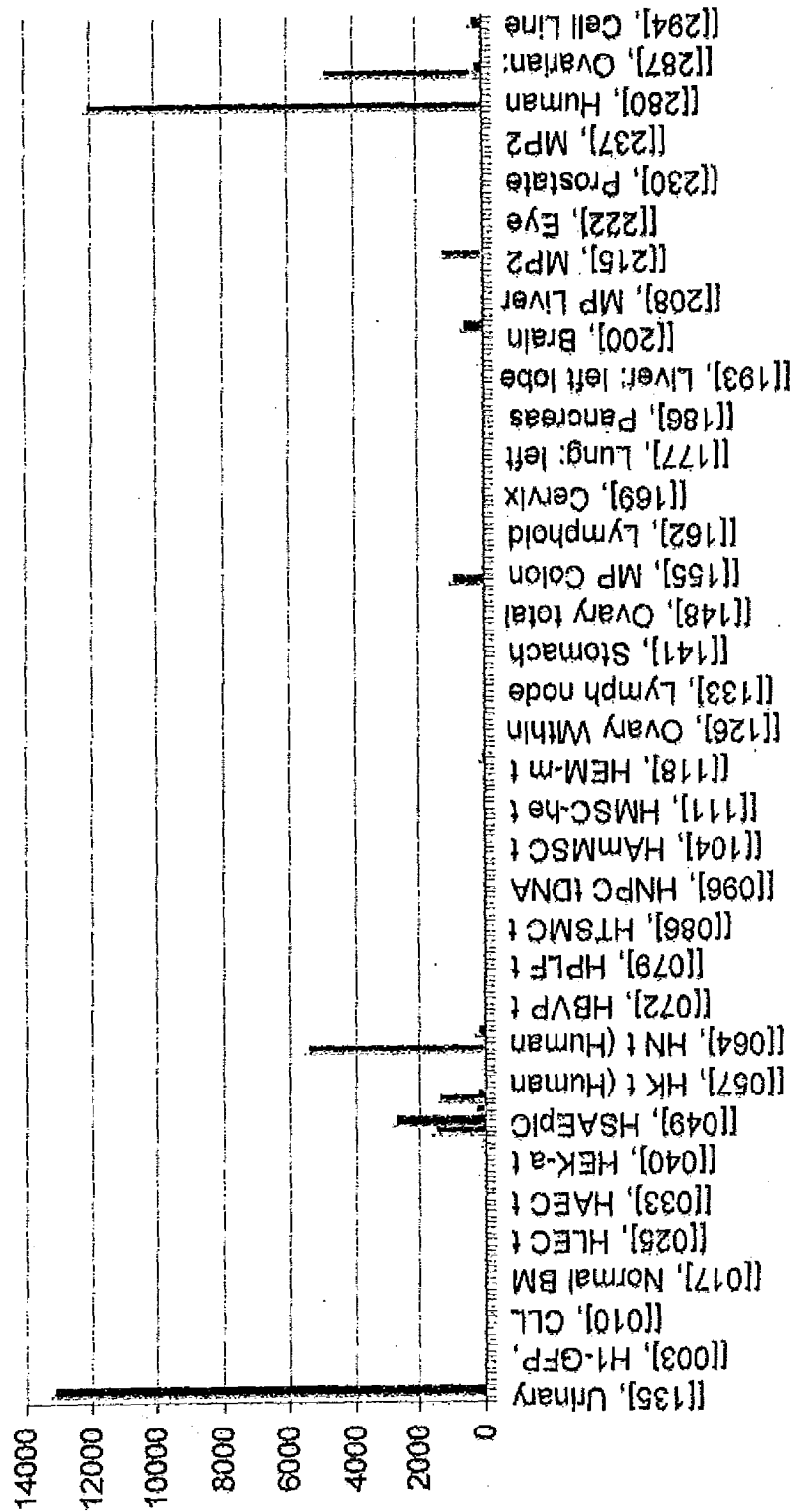


FIGURE 8

LOC729826

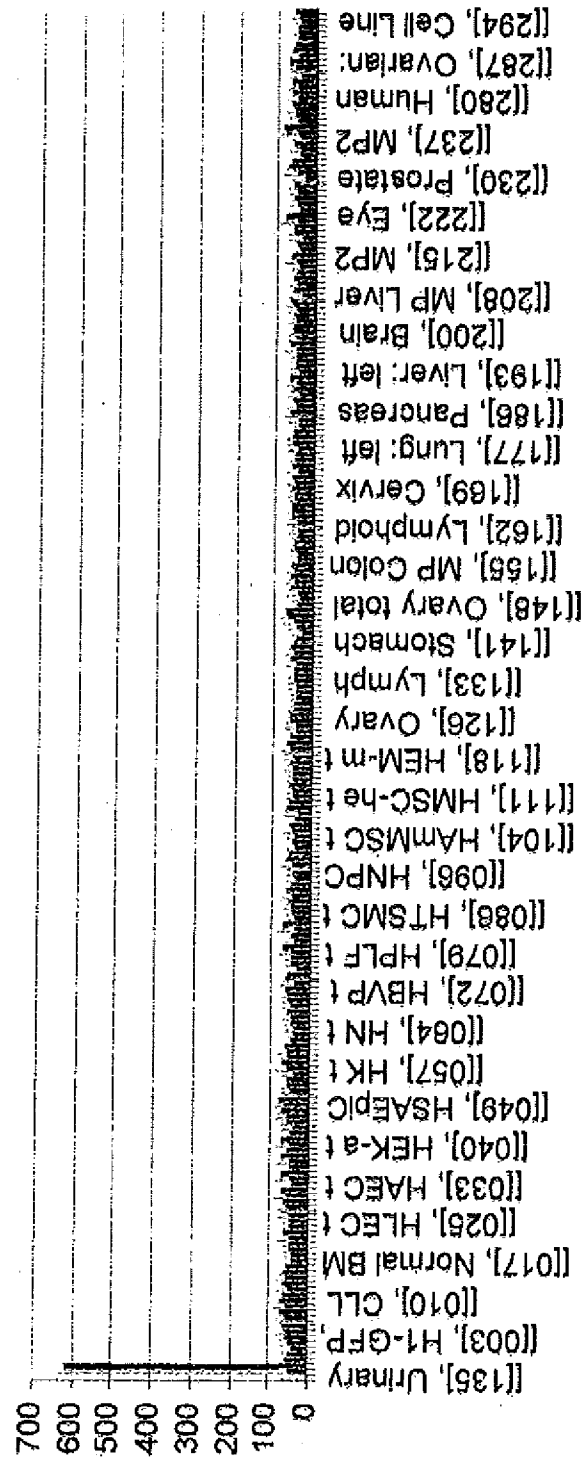


FIGURE 9

PTHLH

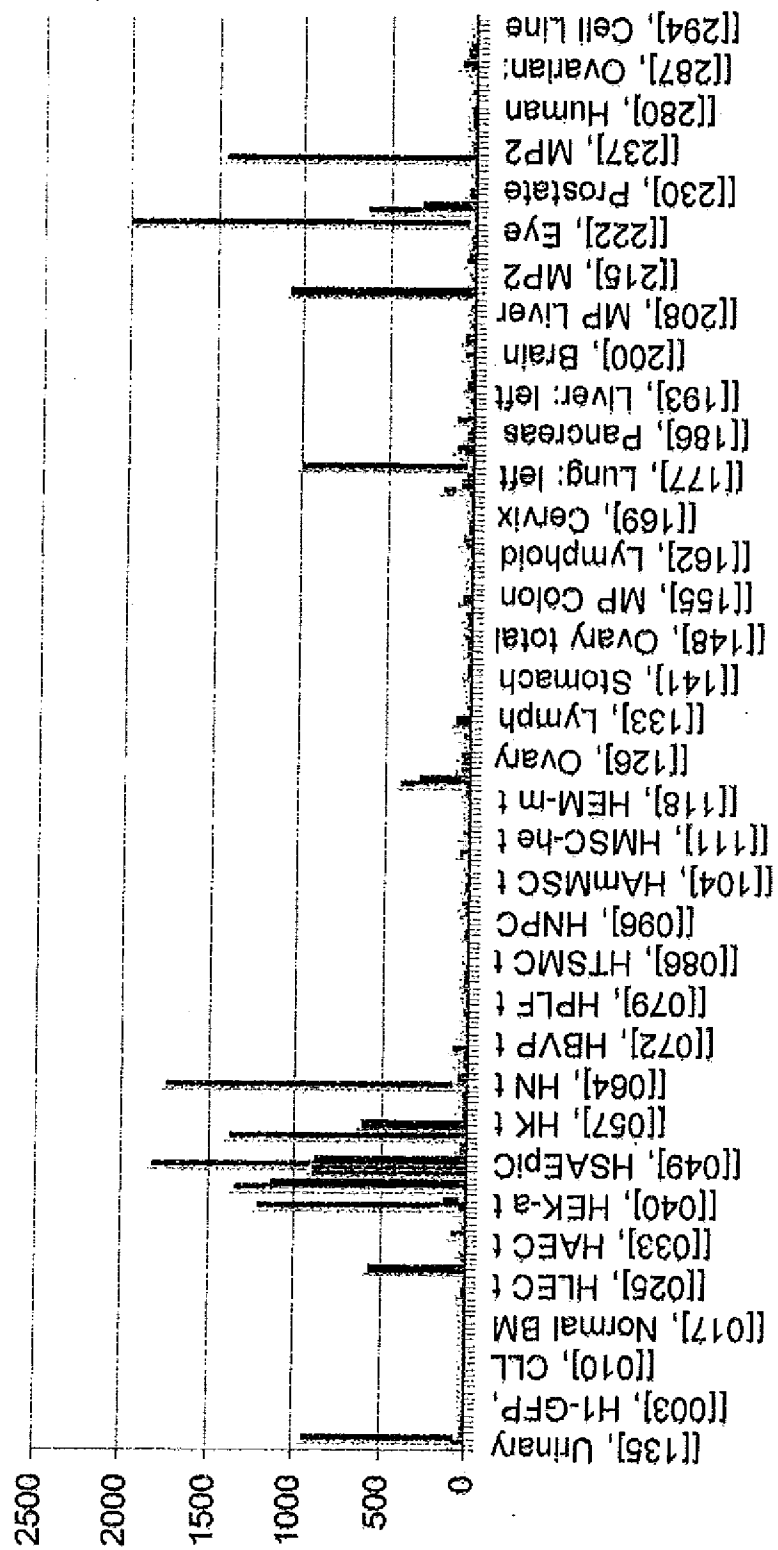


FIGURE 10

MMP11

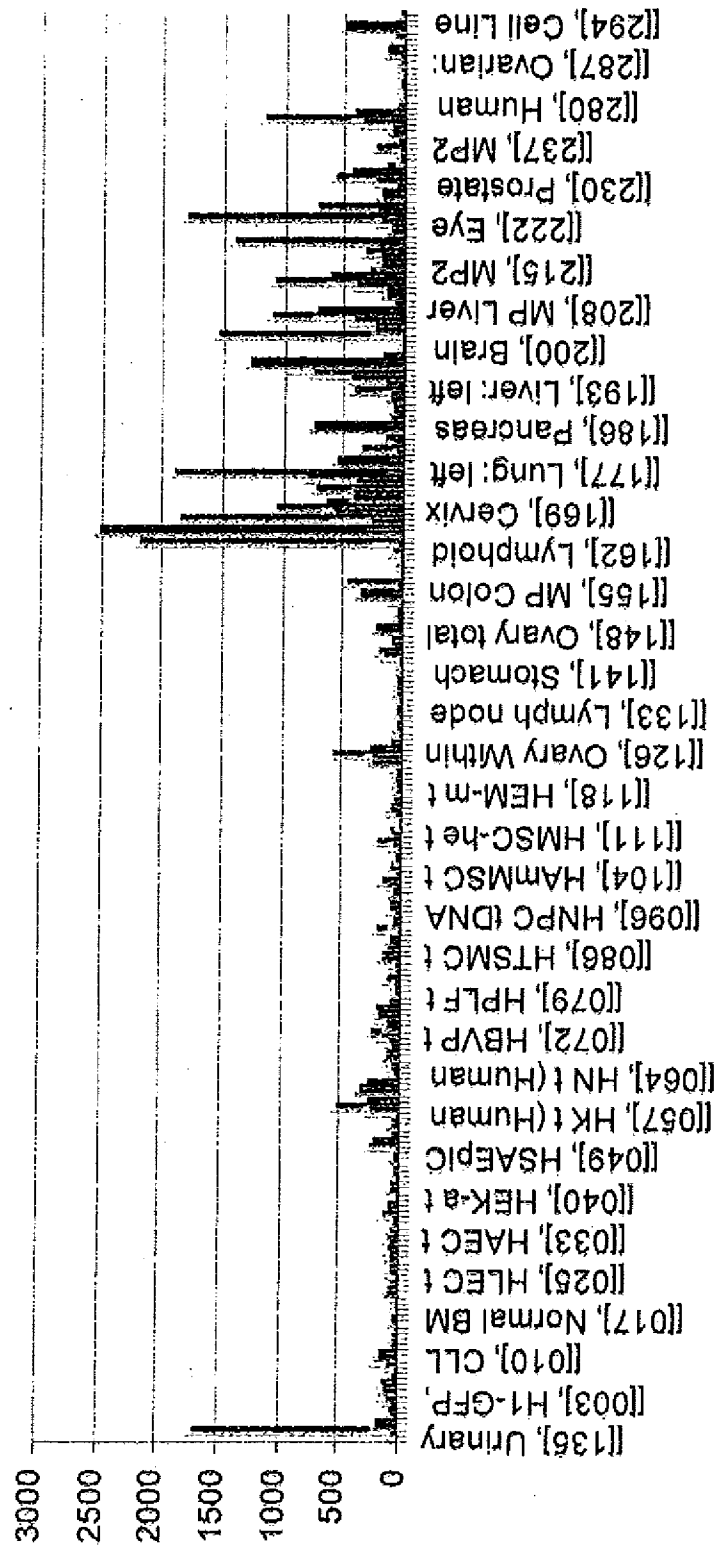


FIGURE 11

S100A7

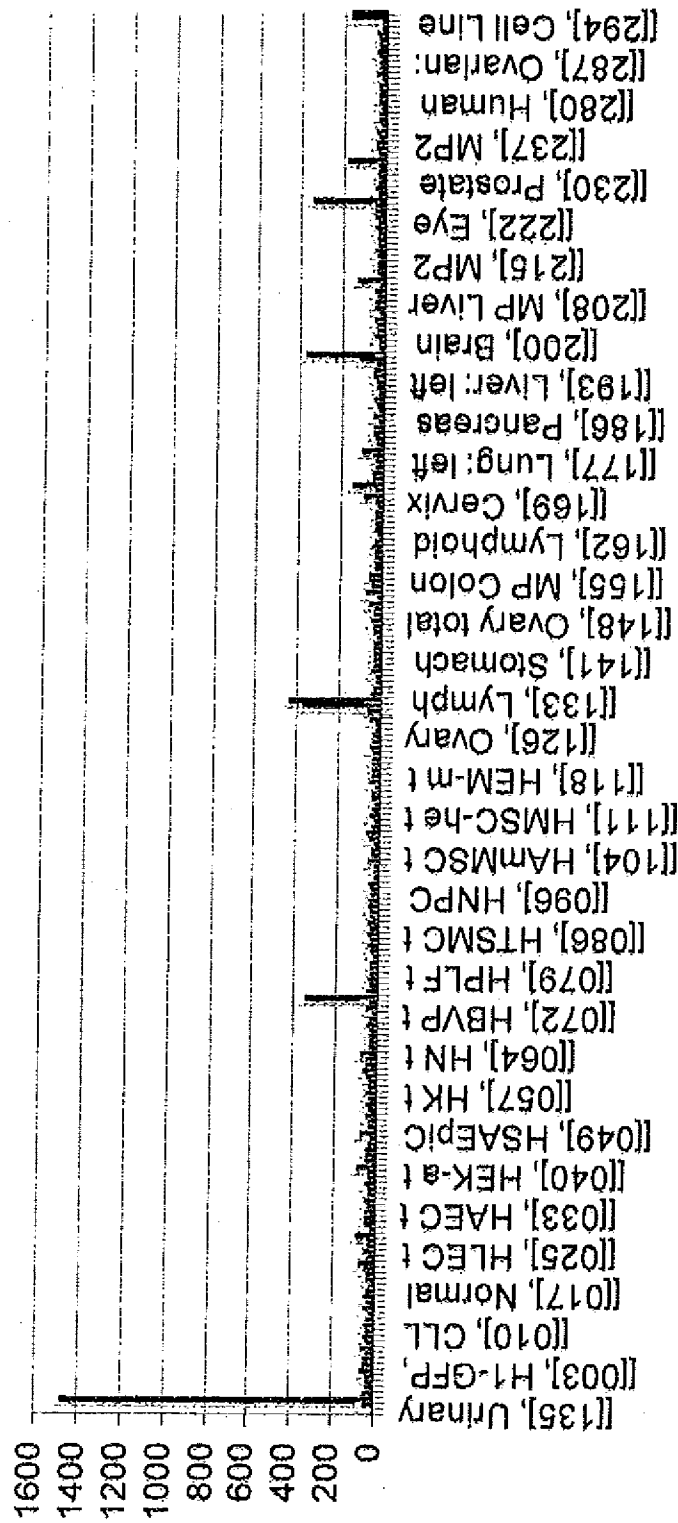


FIGURE 12

WISP3

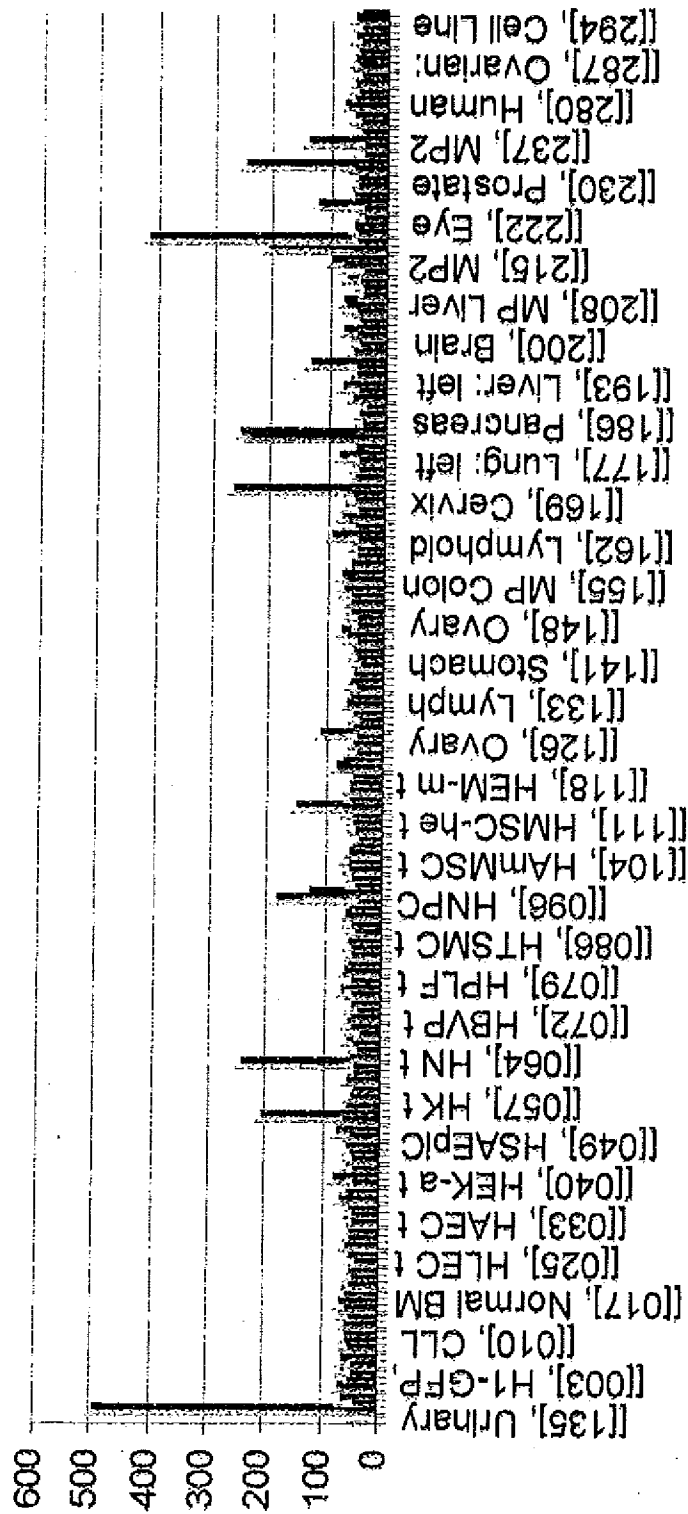


FIGURE 13

CXCL10

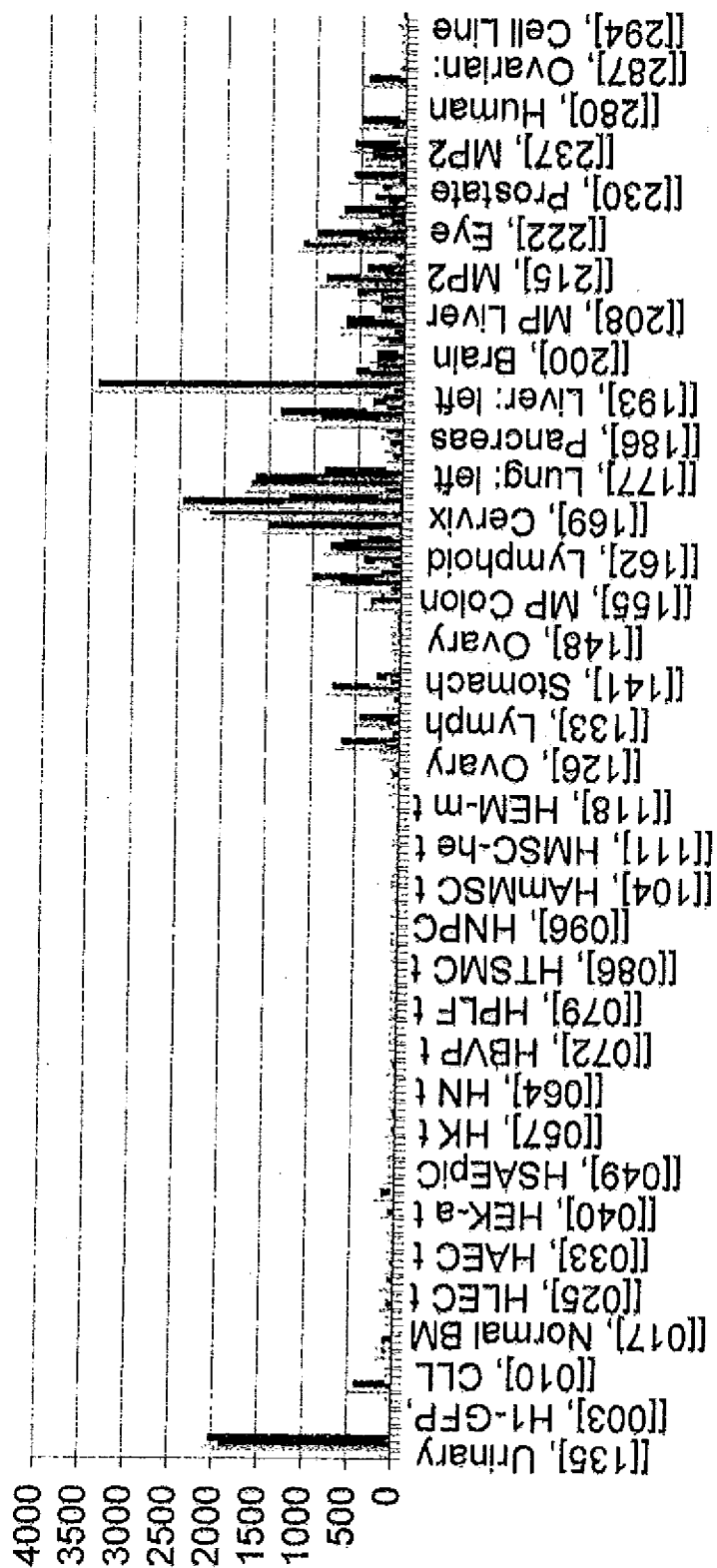


FIGURE 14

NMU

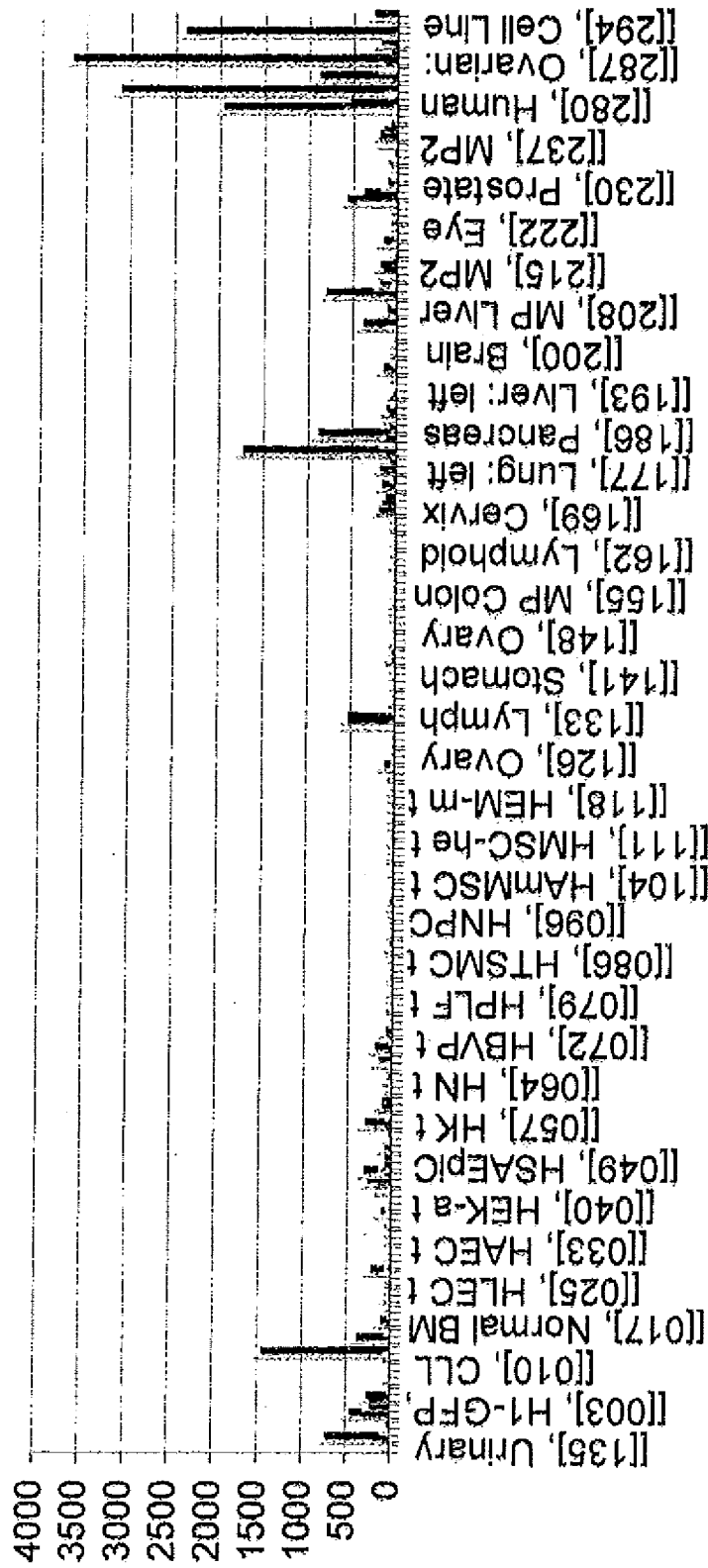


FIGURE 15

GBP5

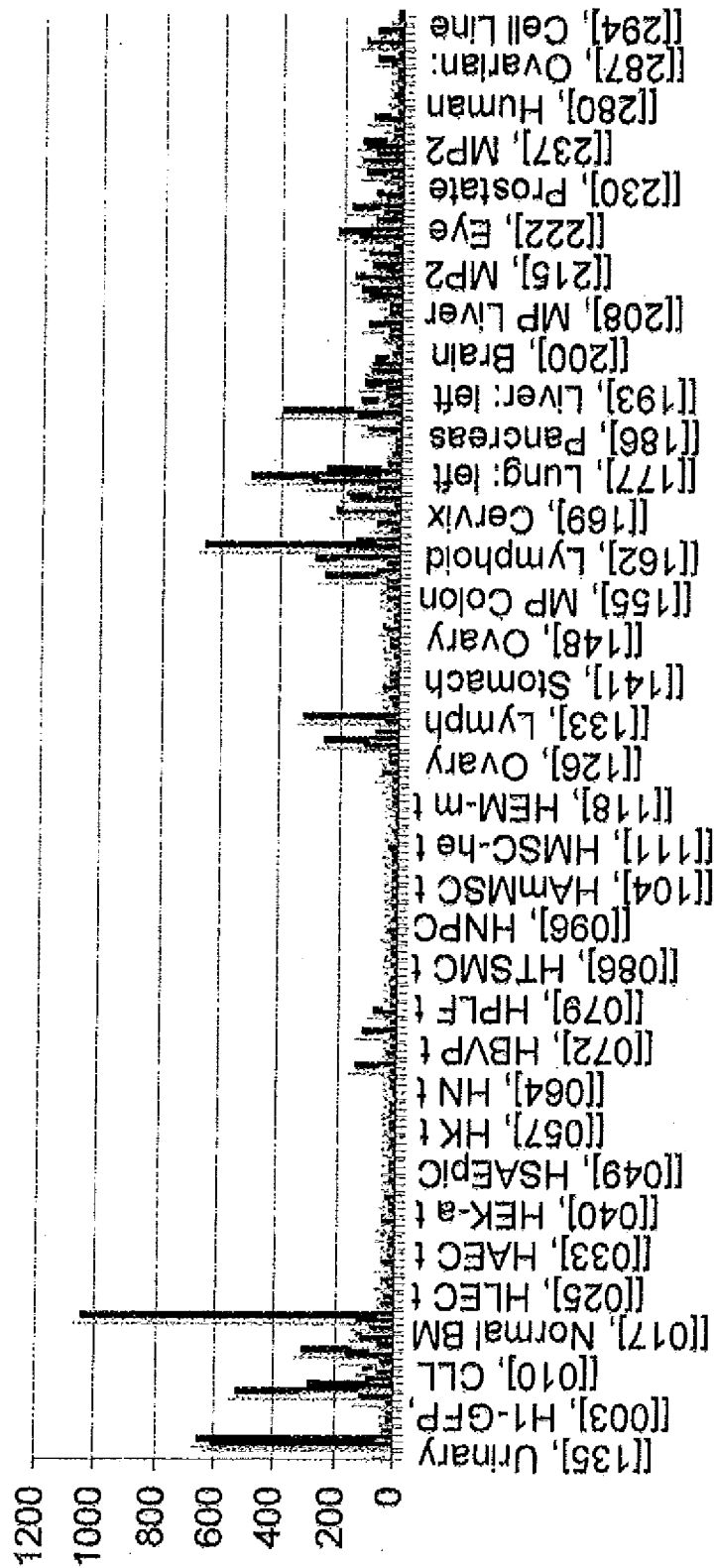


FIGURE 16

TOP2A

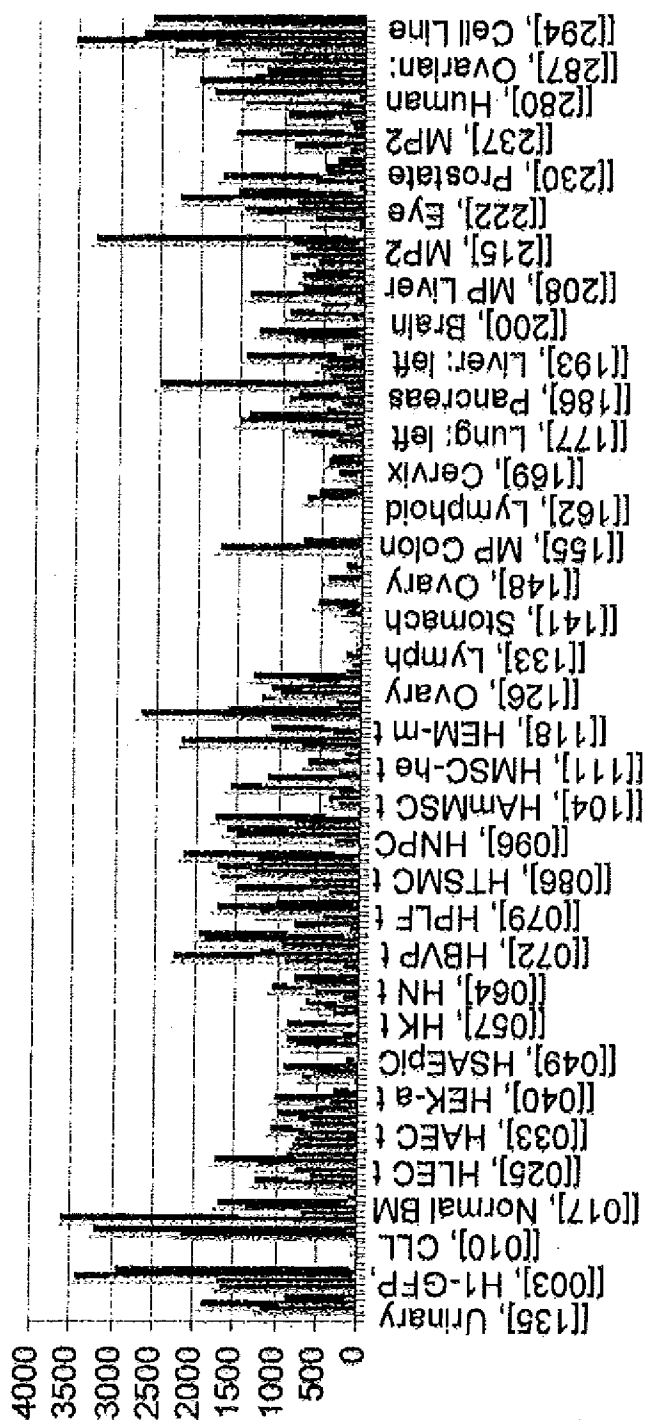


FIGURE 17

SERPINB4

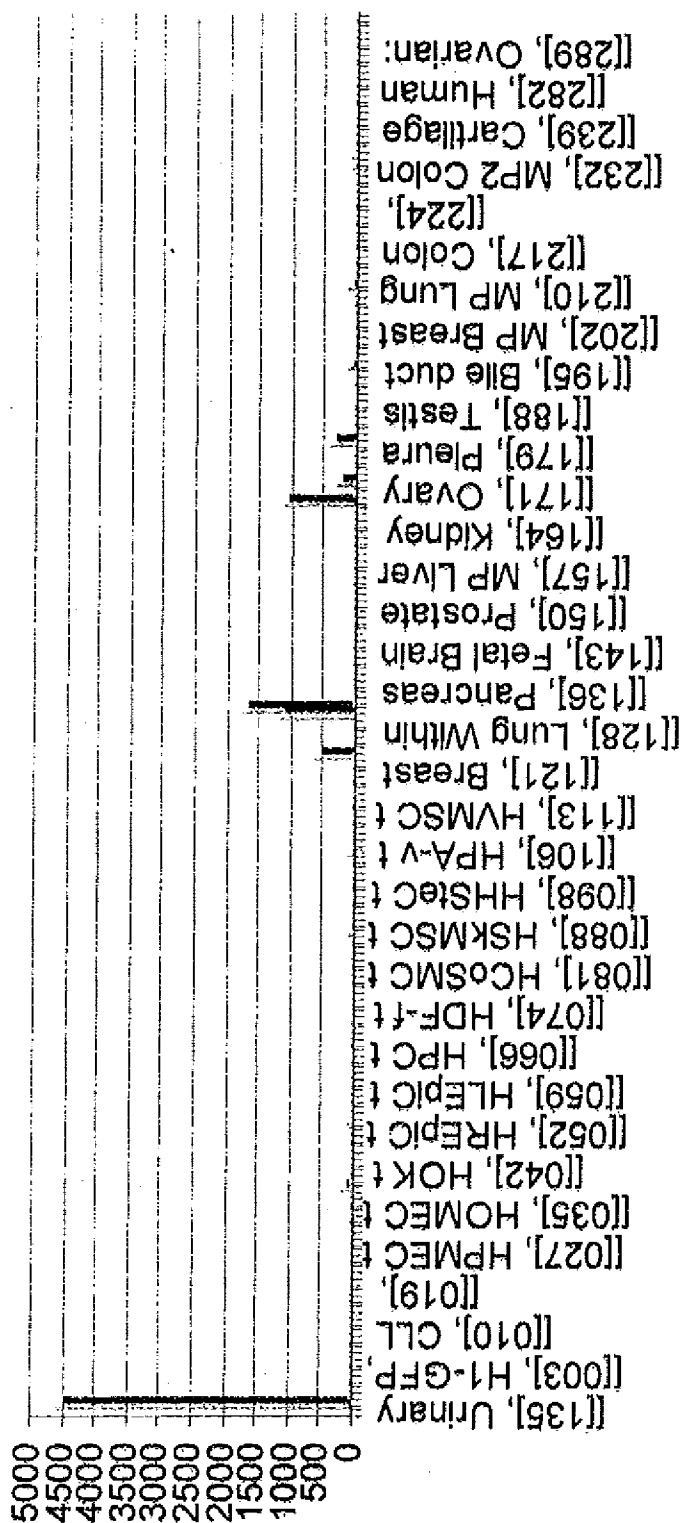


FIGURE 18

GONLY

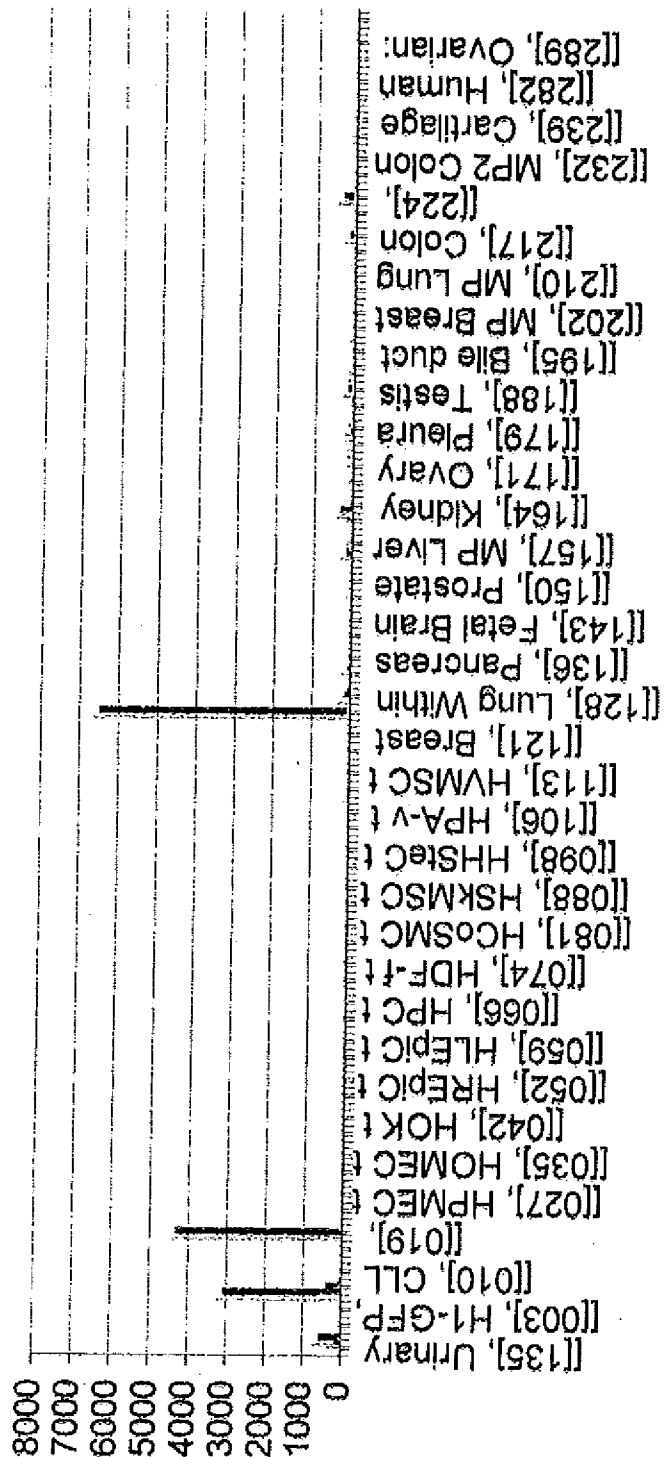


FIGURE 19

GTSF1

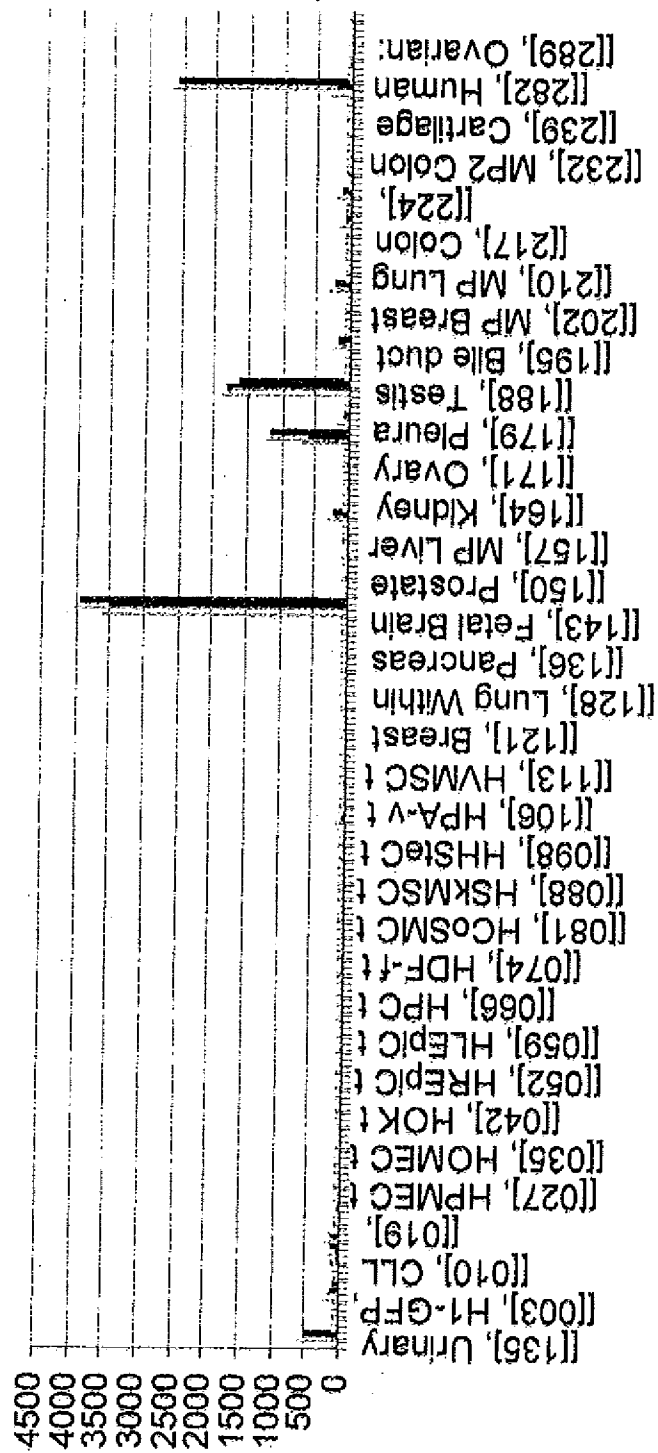


FIGURE 20

PI3

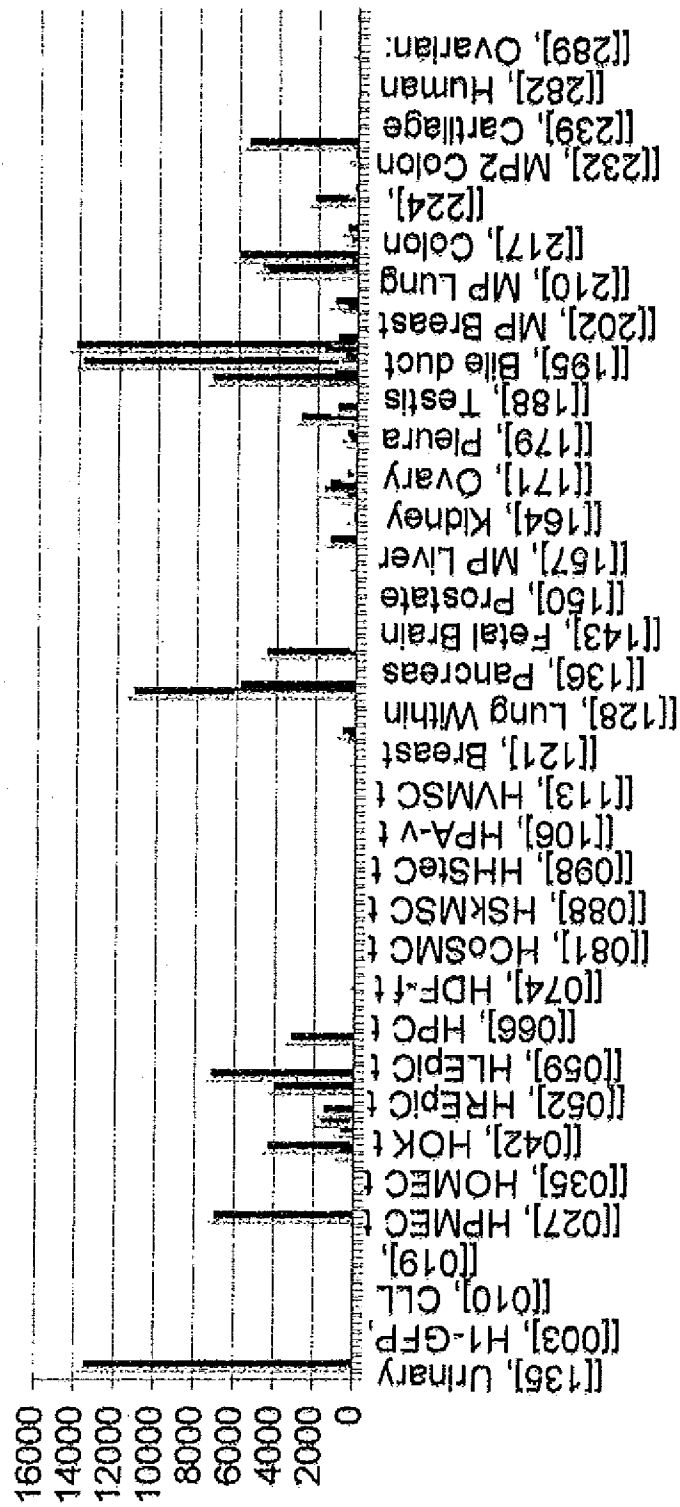


FIGURE 21

S100A7A

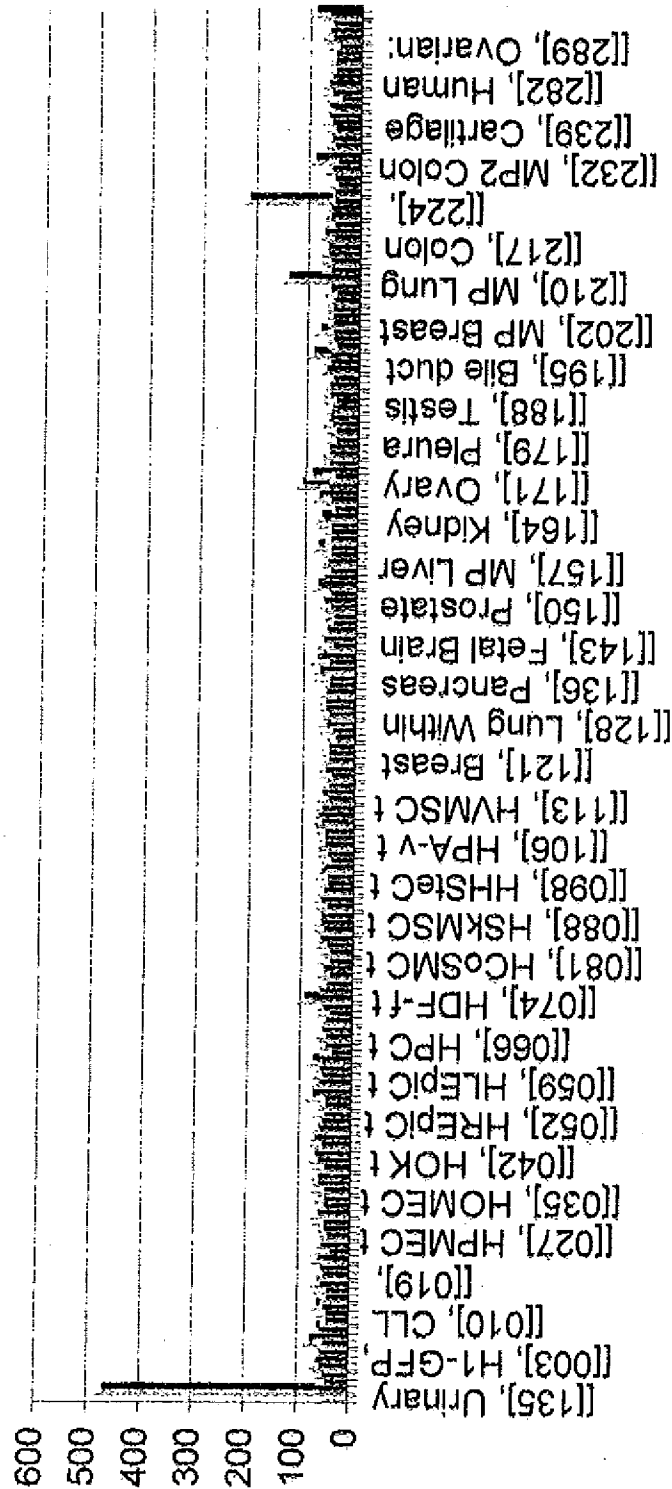


FIGURE 22

IDO1

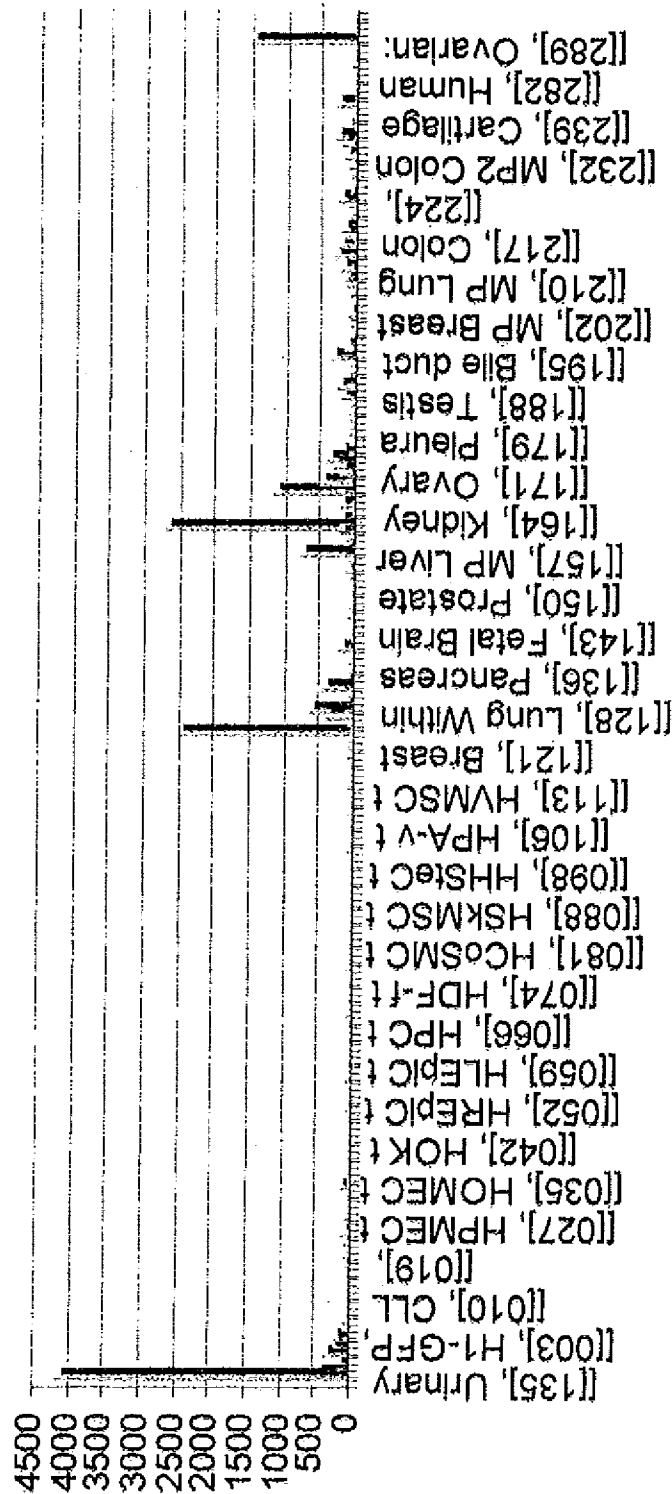


FIGURE 23

GJB6

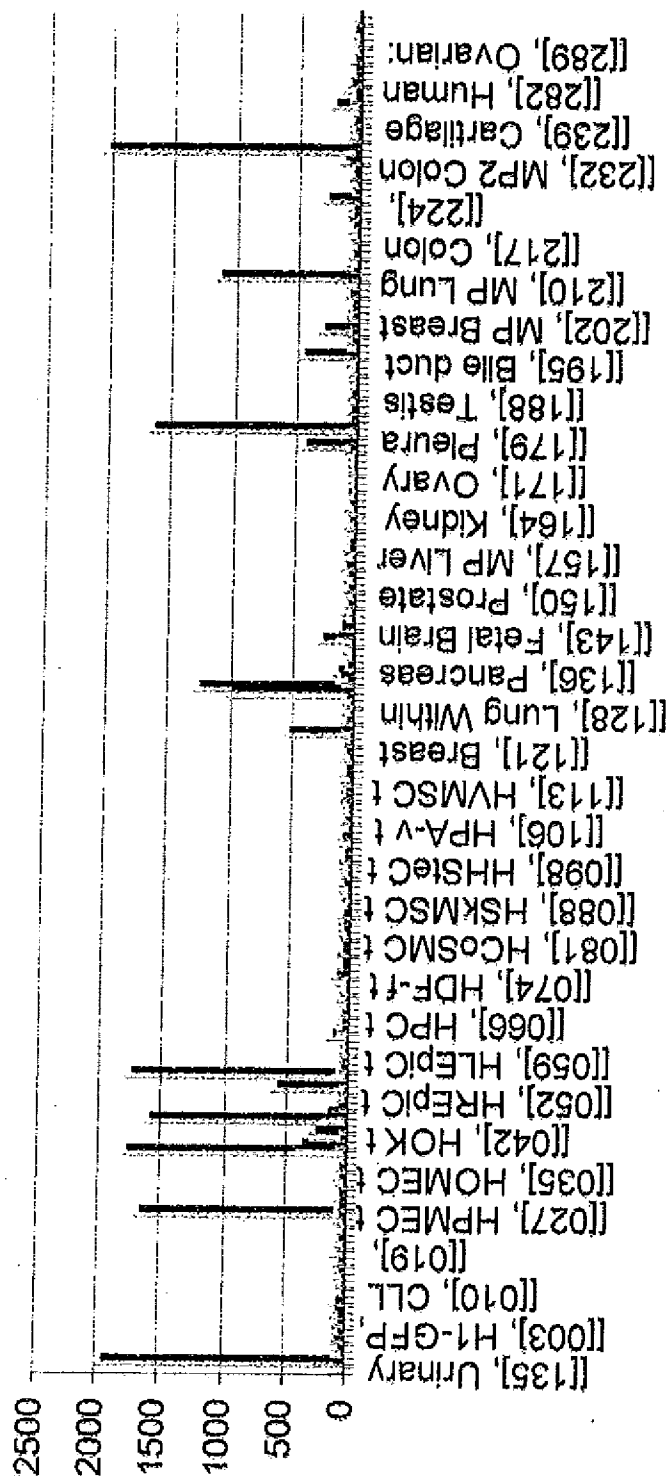


FIGURE 24

CALML3

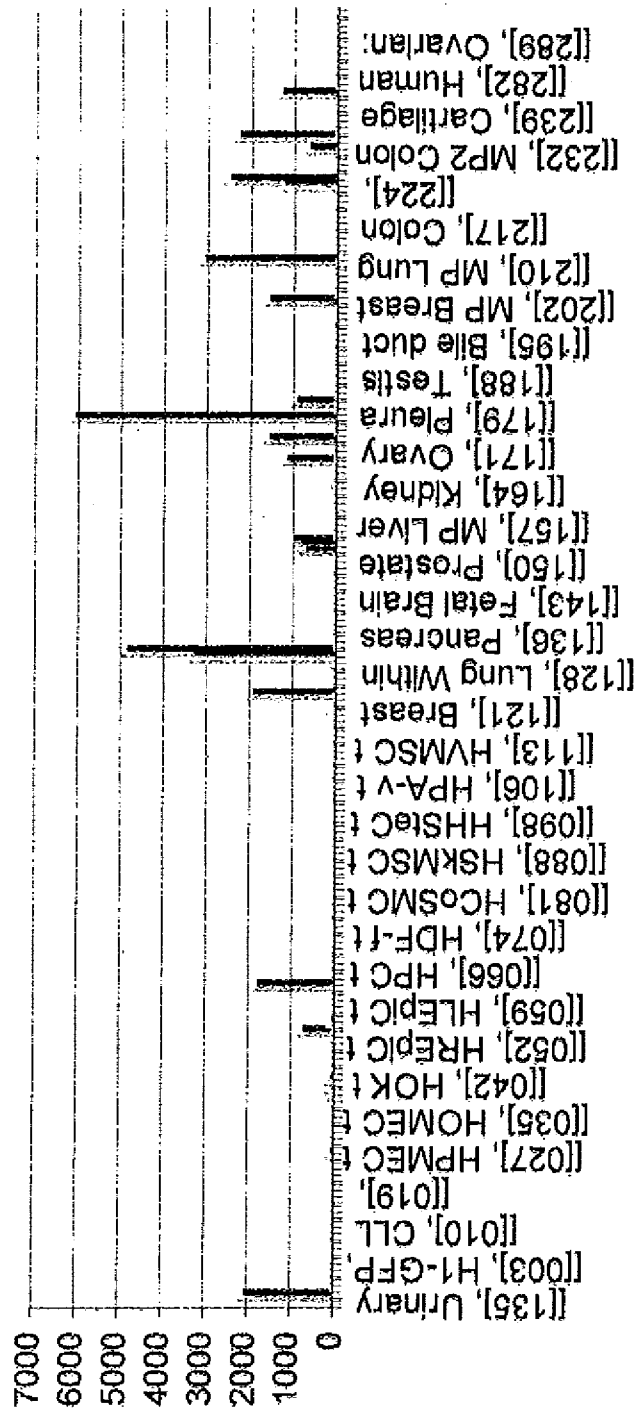


FIGURE 25

SERPINB3

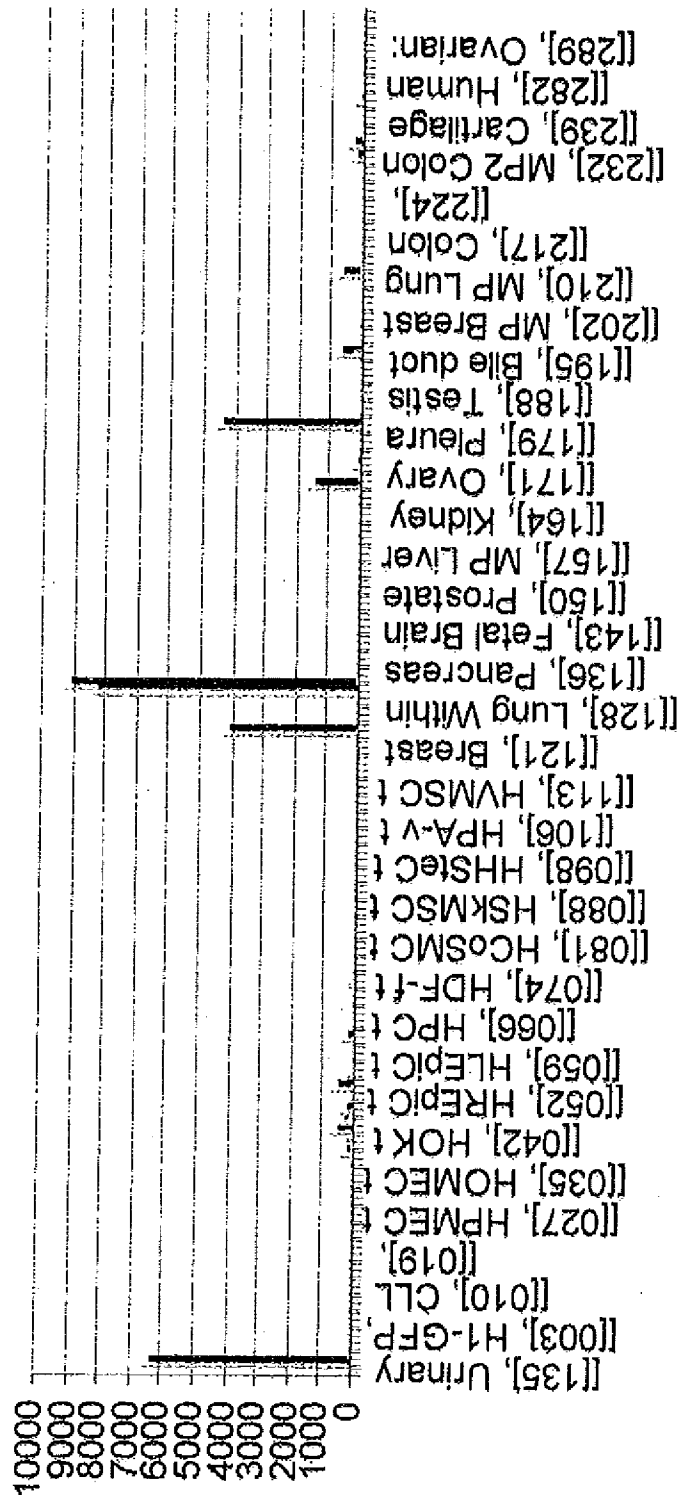


FIGURE 26

CXCL6

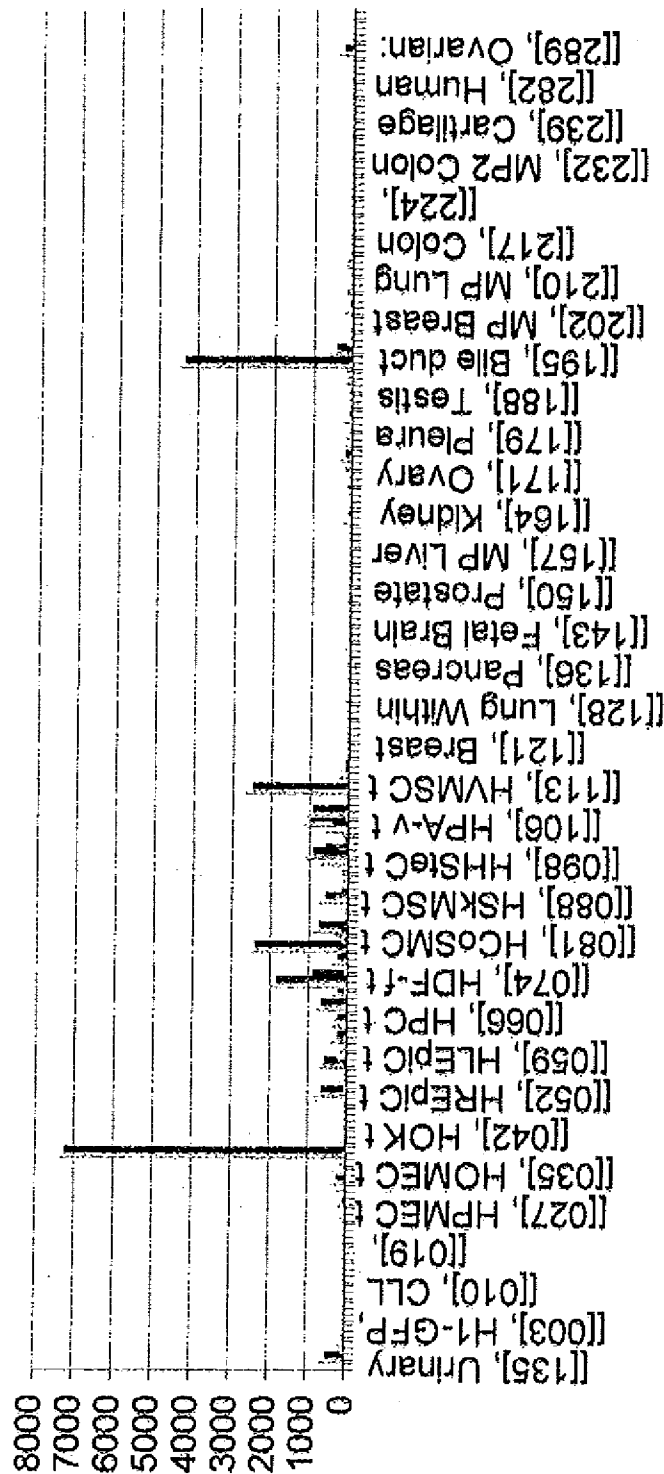


FIGURE 27

OLFM4

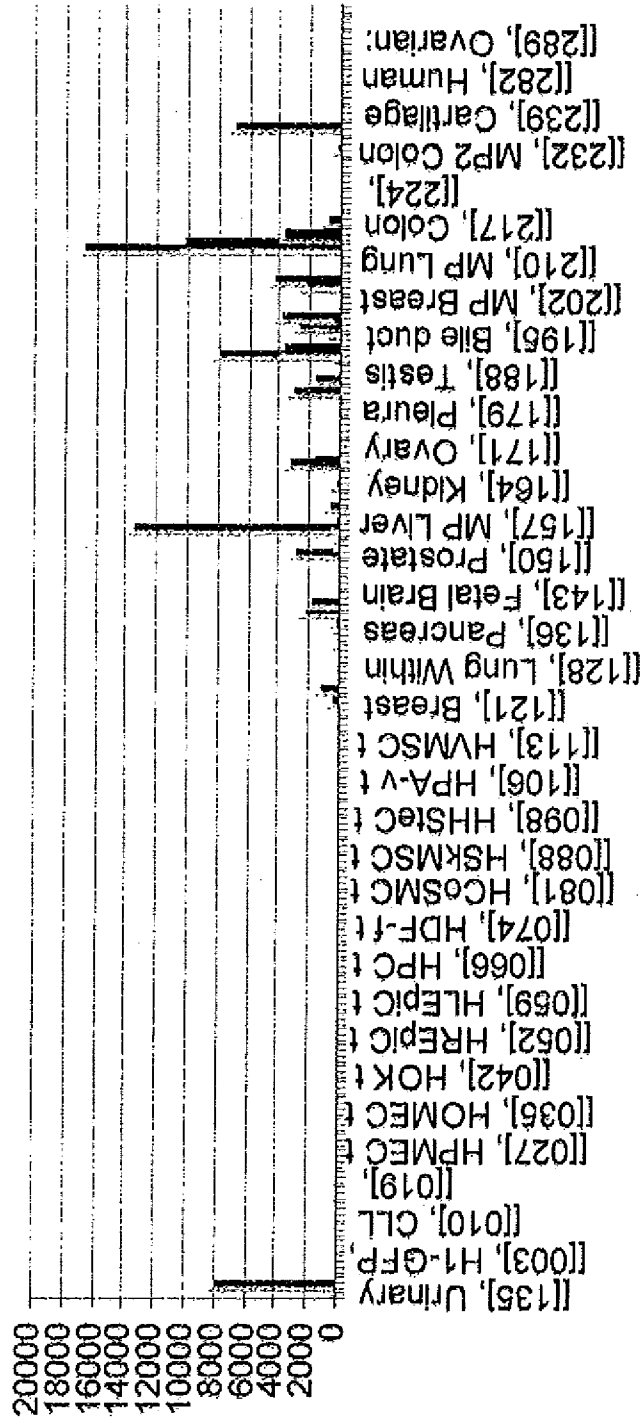


FIGURE 28

TCN1

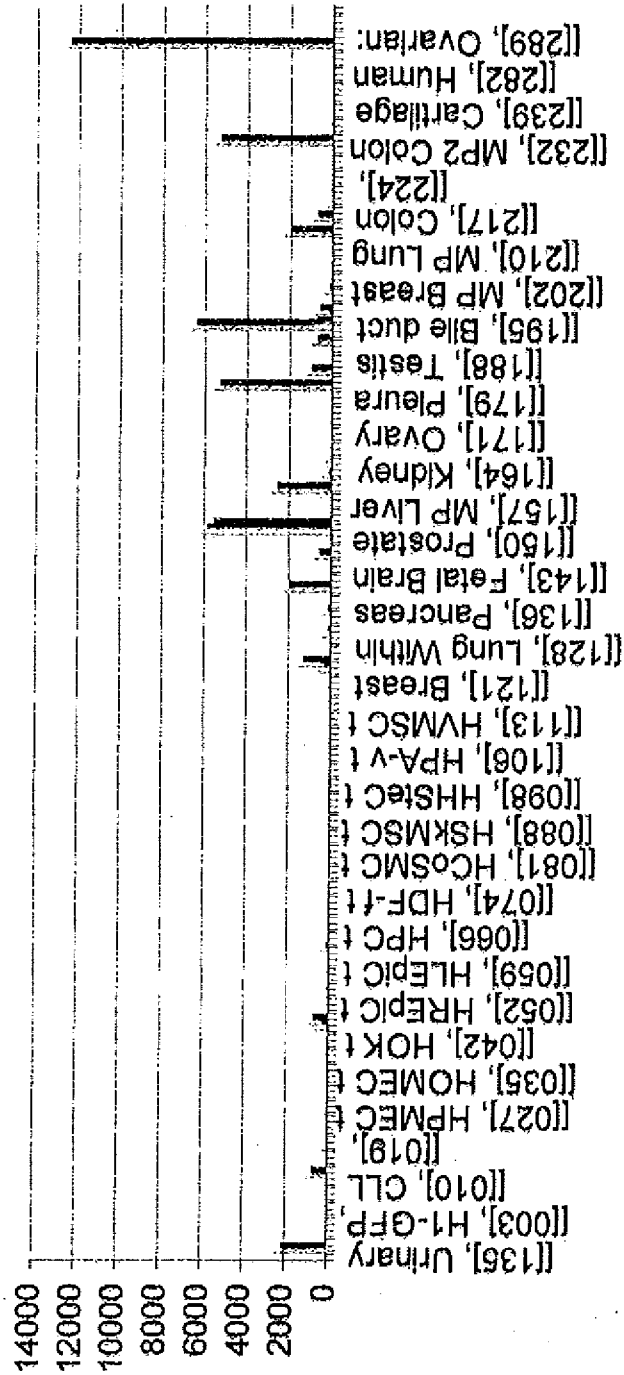


FIGURE 29

VSNL1

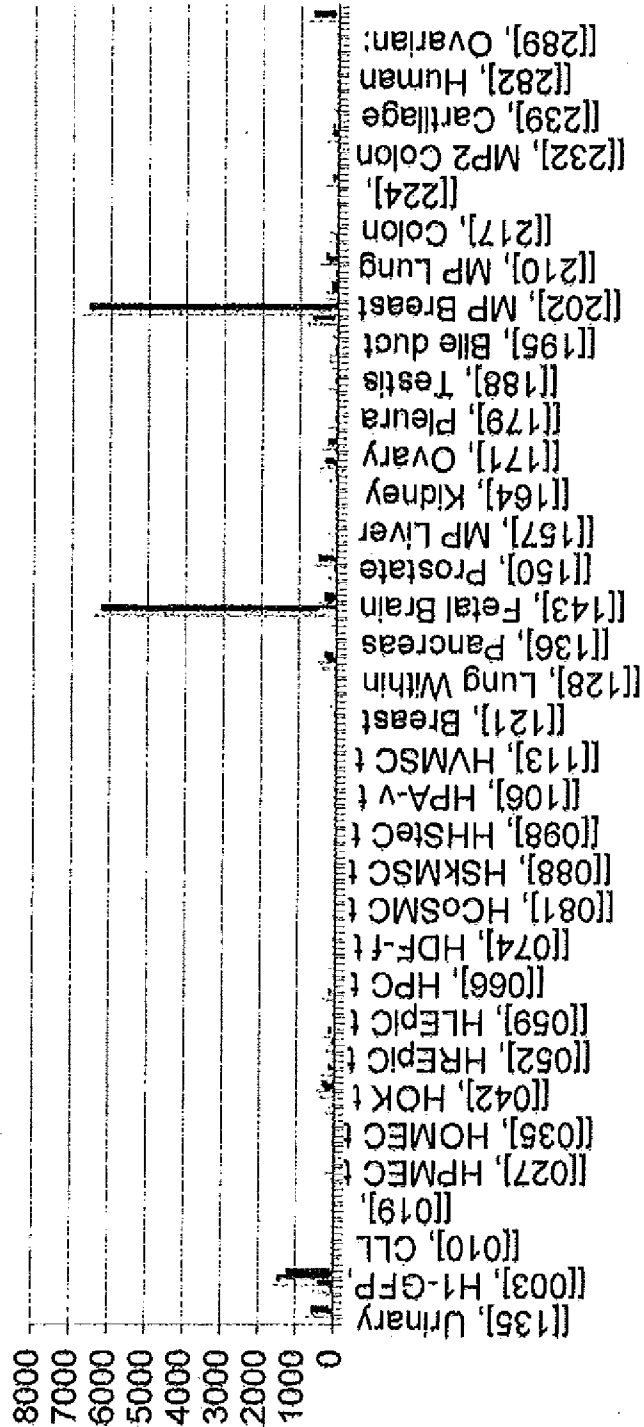


FIGURE 30

UBD

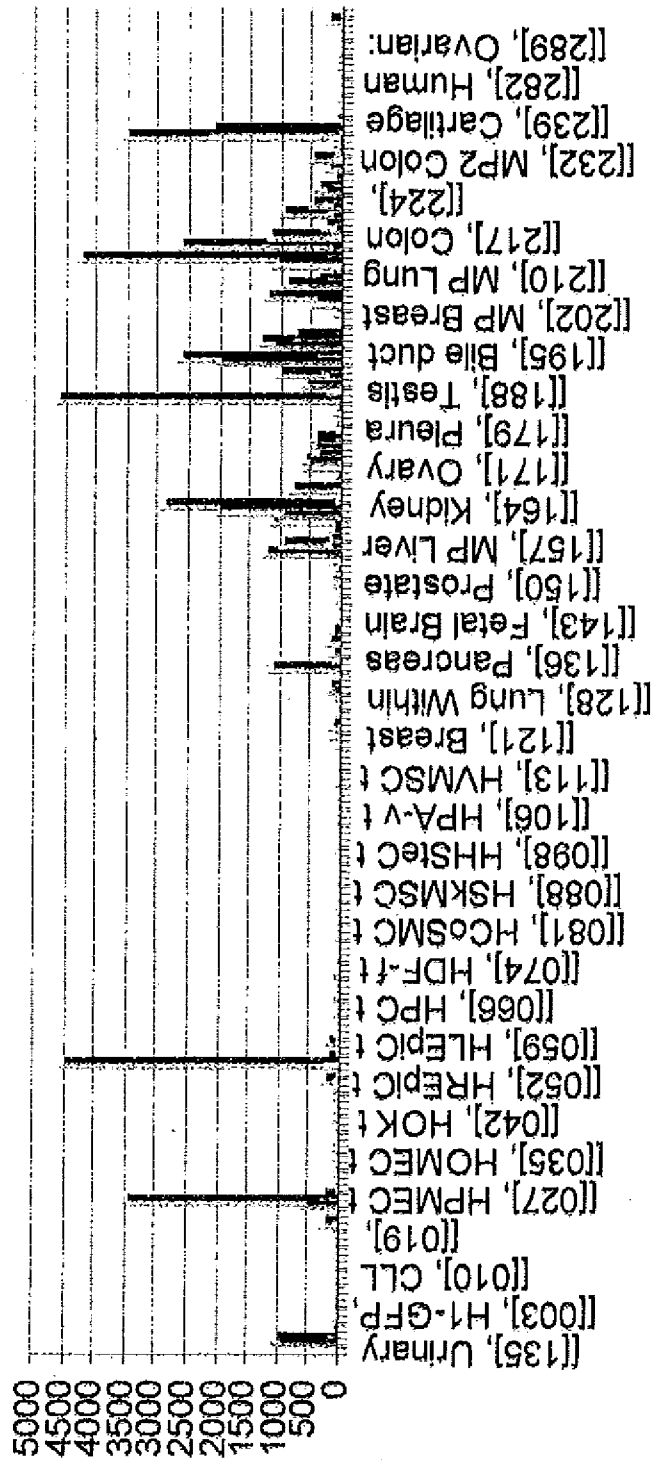


FIGURE 31

AIM2

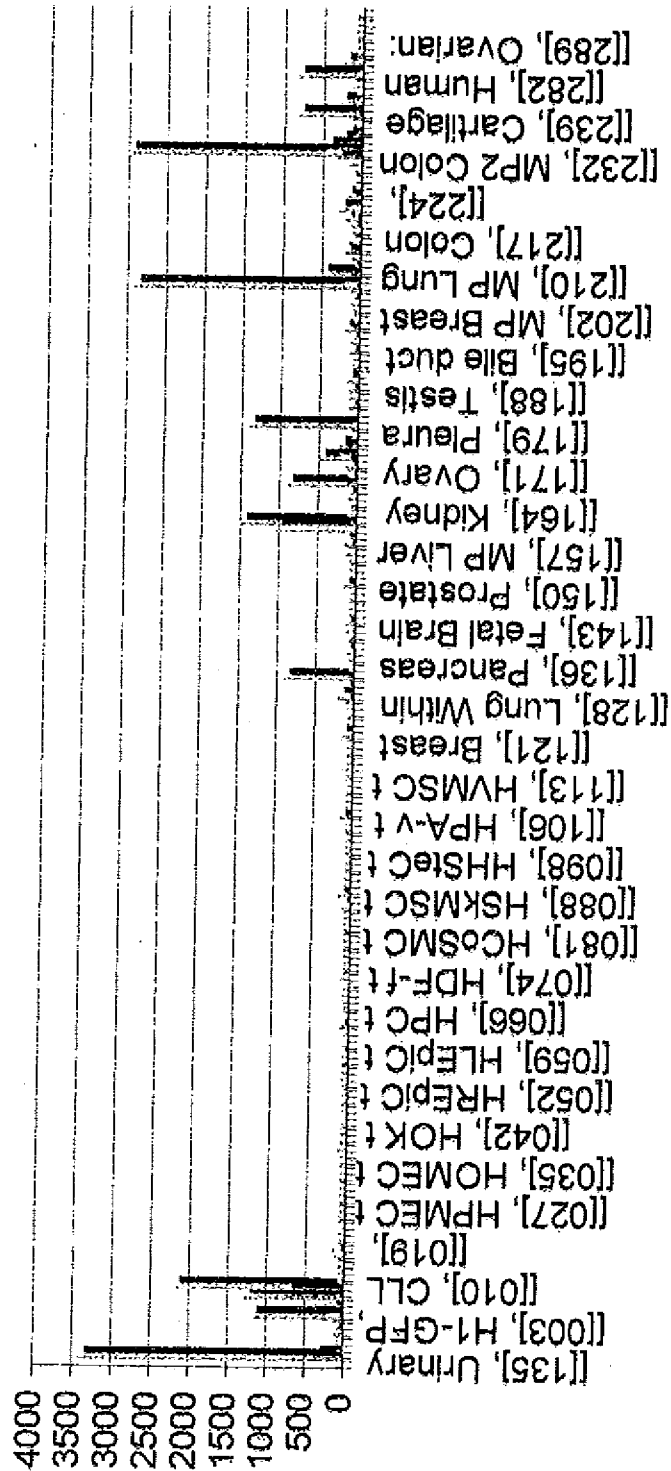


FIGURE 32

ABCC9

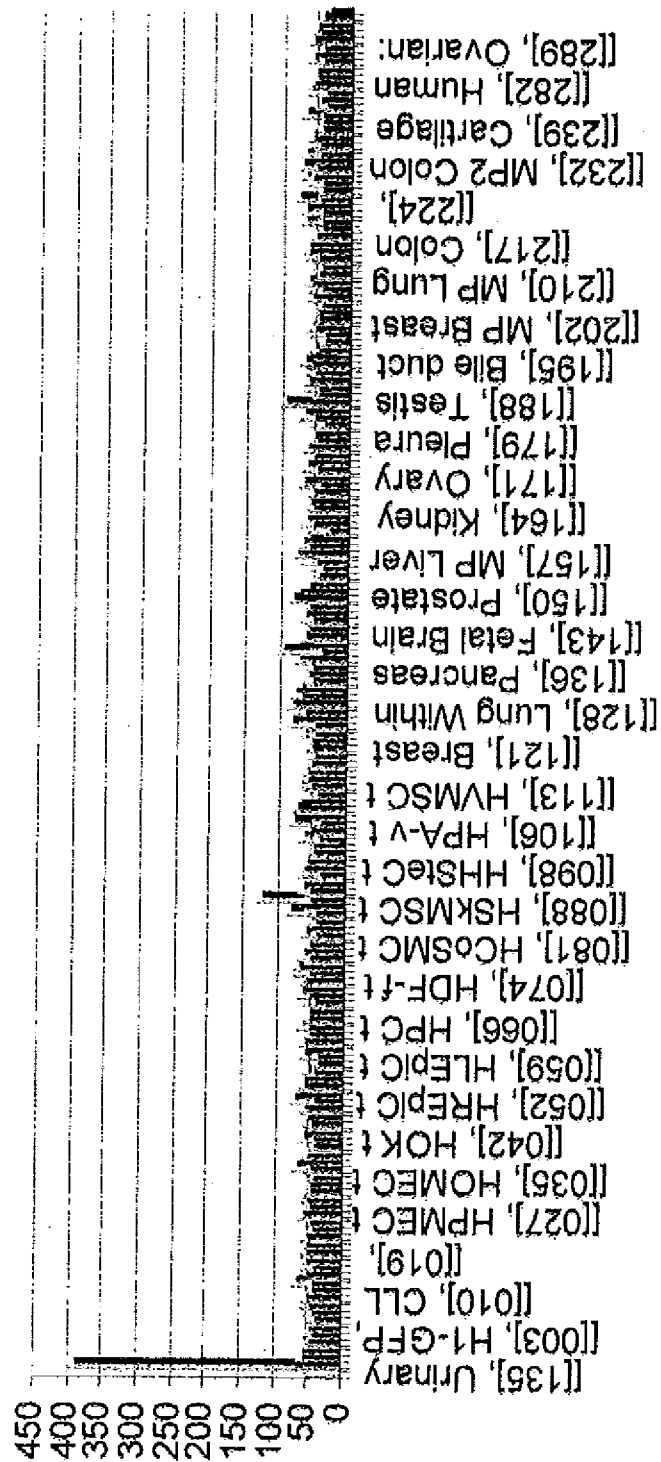


FIGURE 33

SERPINB13

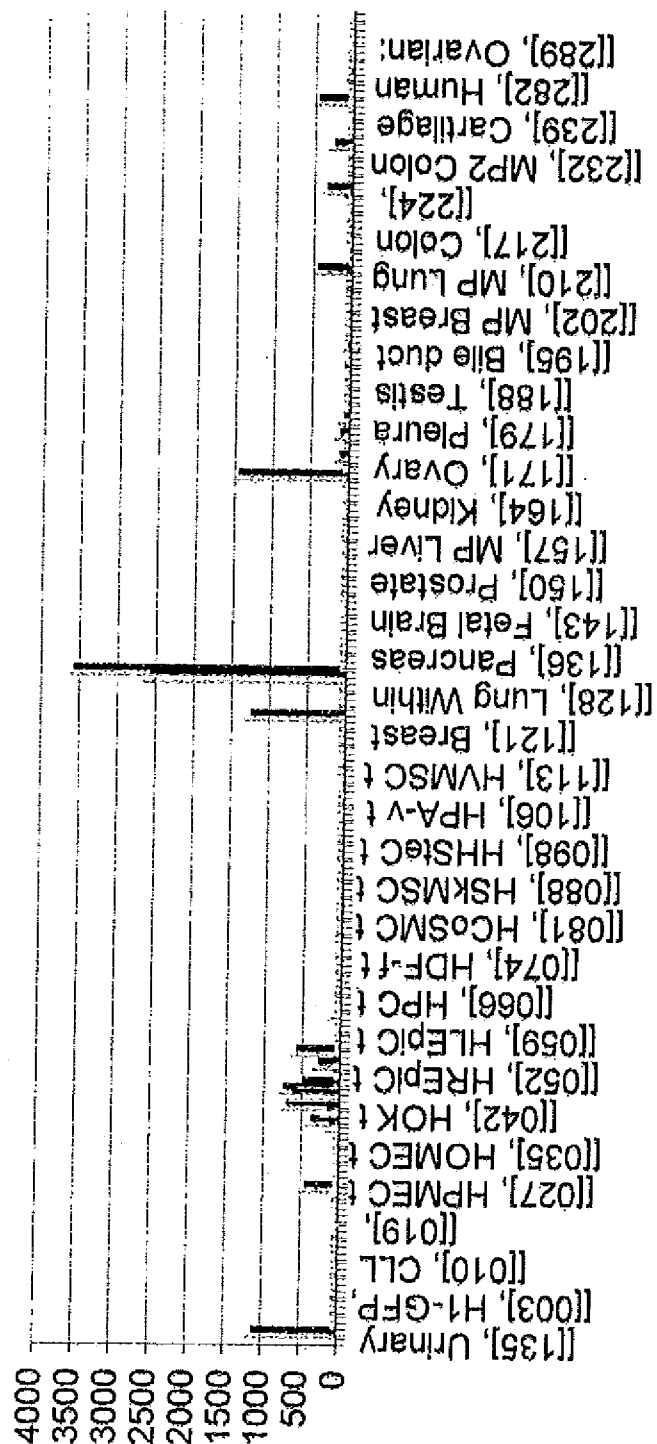


FIGURE 34

INDO

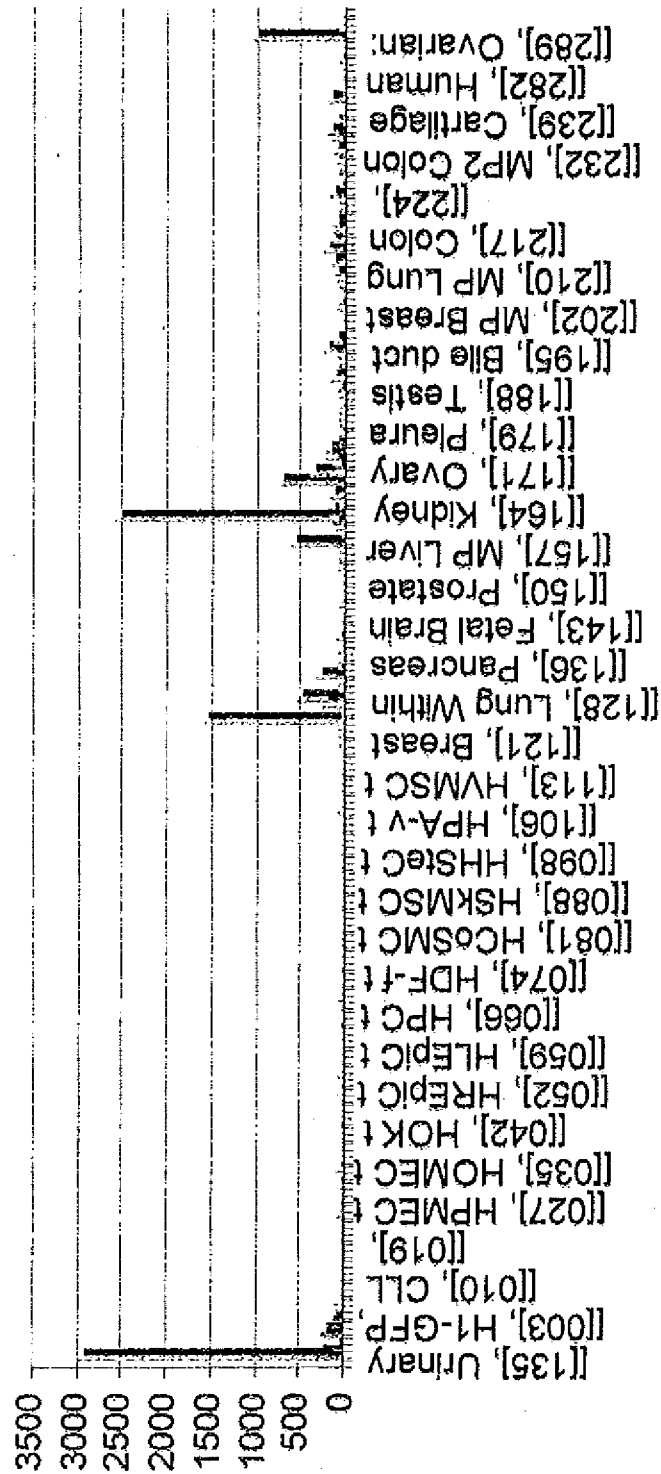


FIGURE 35

KRT5

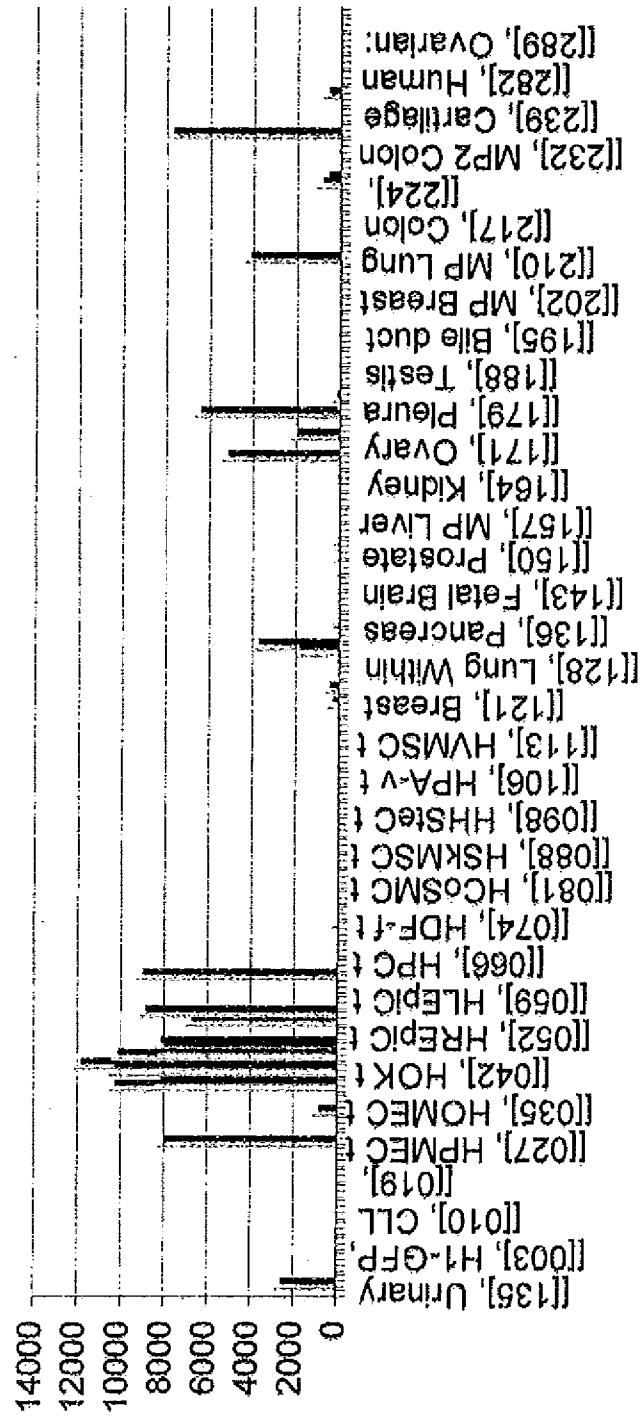


FIGURE 36

LOC100130897

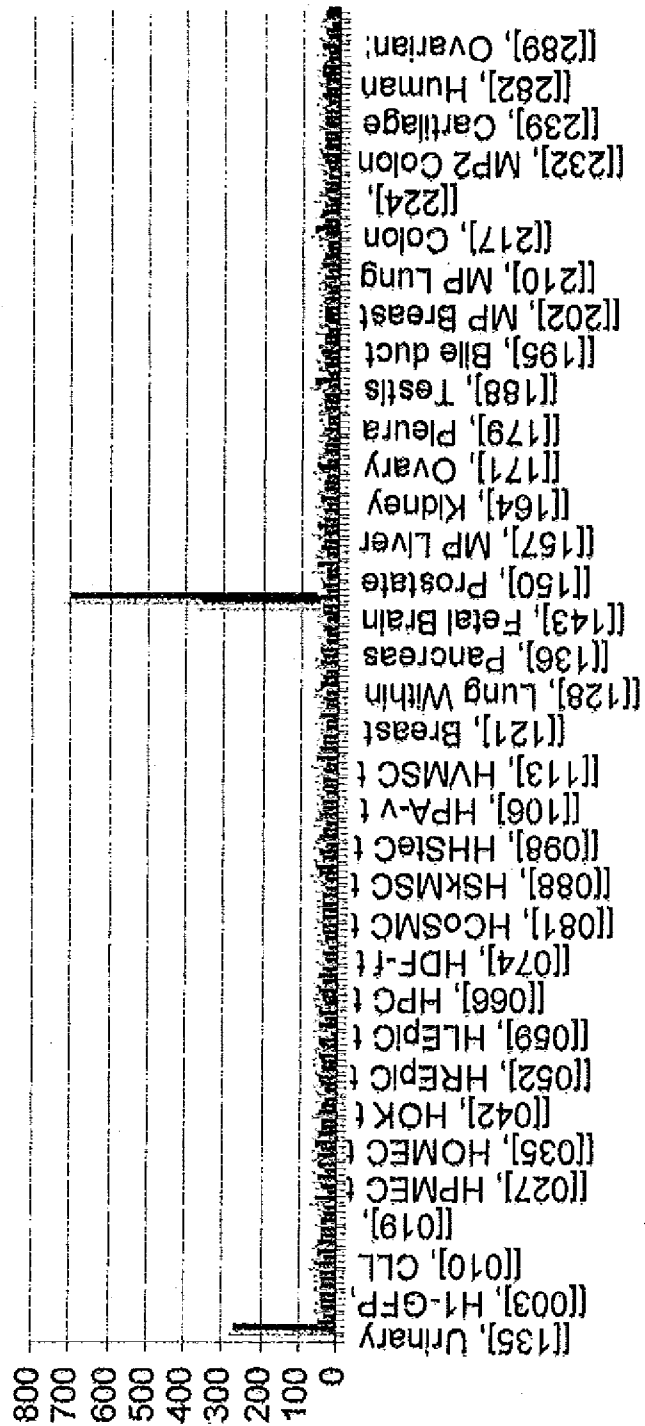


FIGURE 37

KRT14

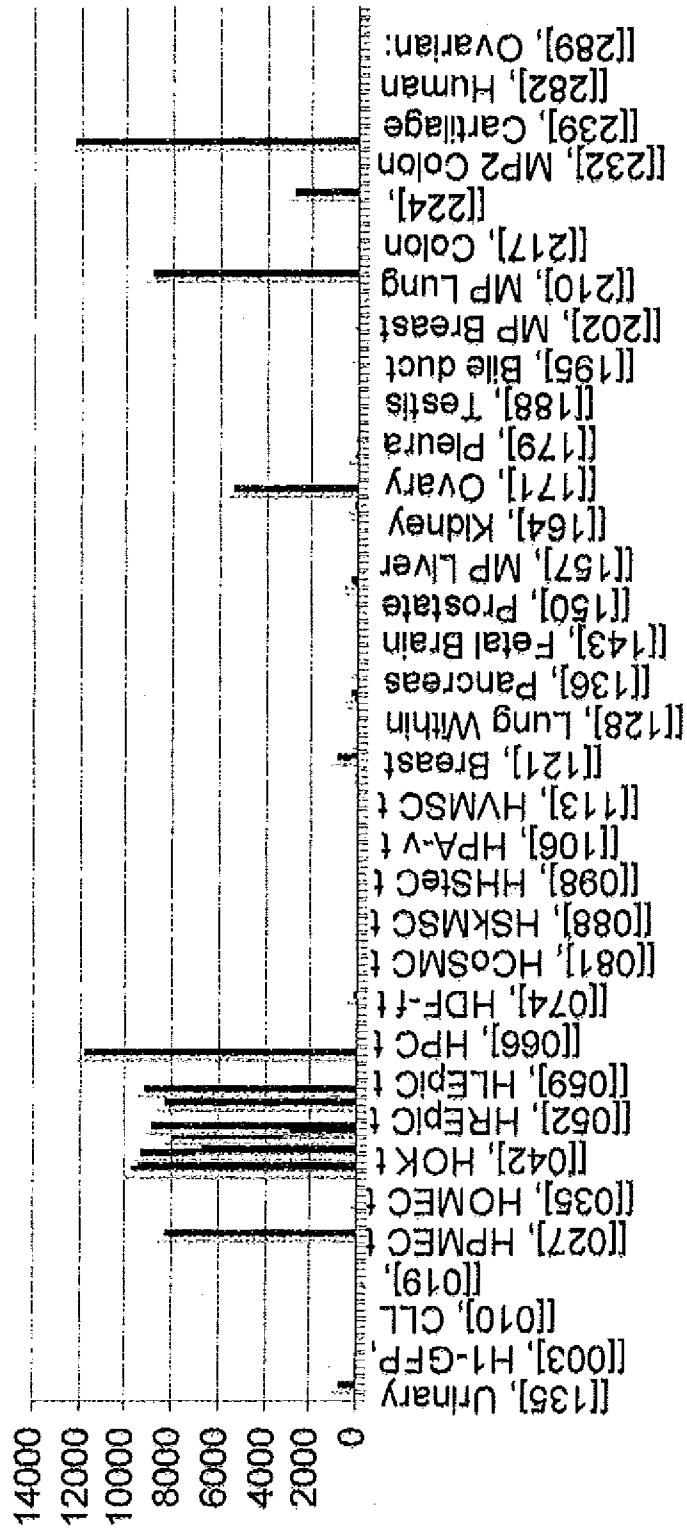


FIGURE 38

FAM83A

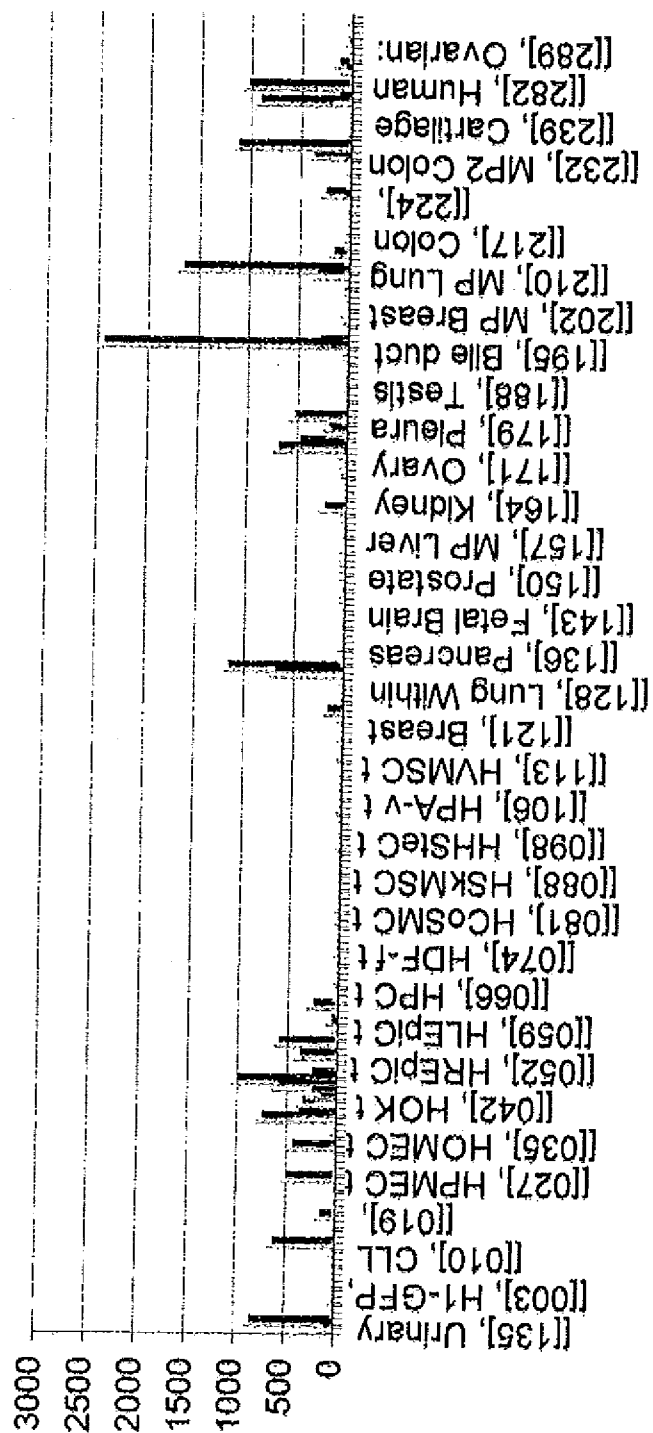


FIGURE 39

FAM181B

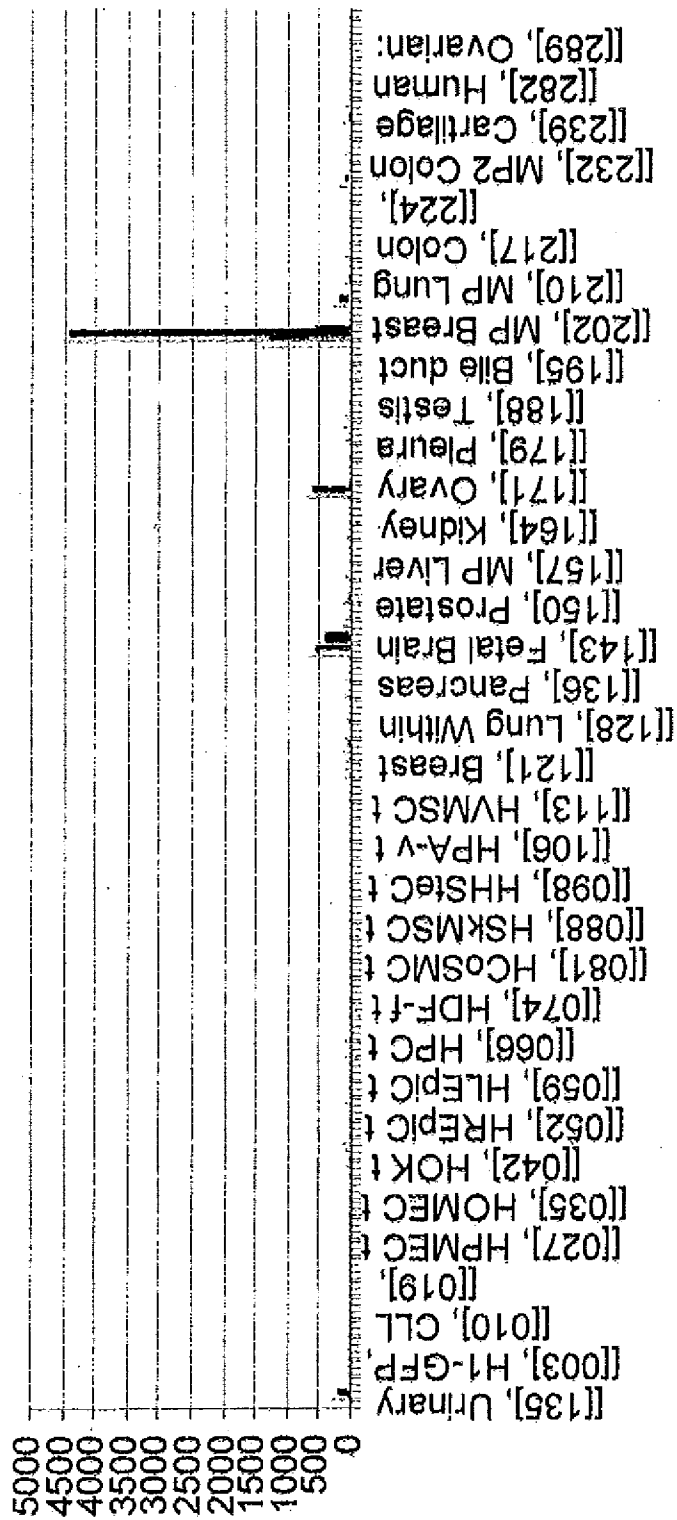


FIGURE 40

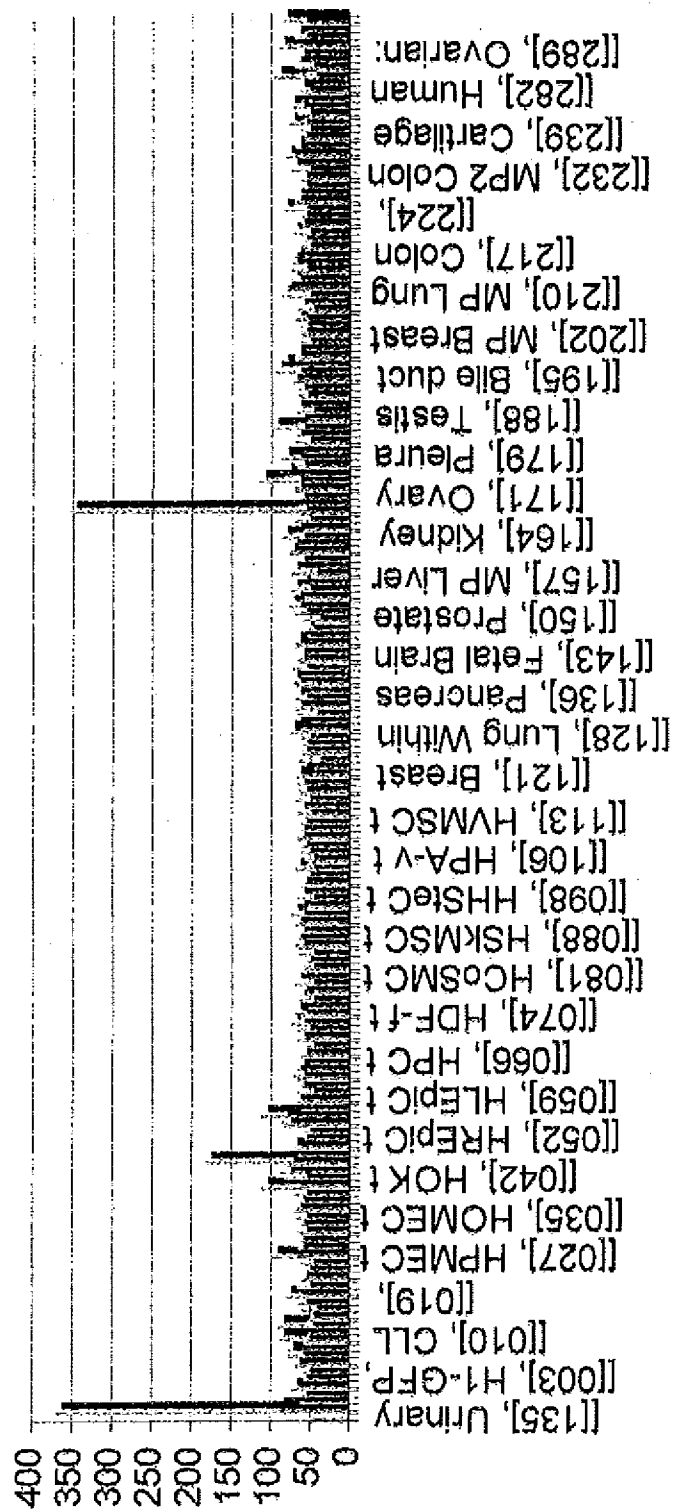


FIGURE 41

GZMB

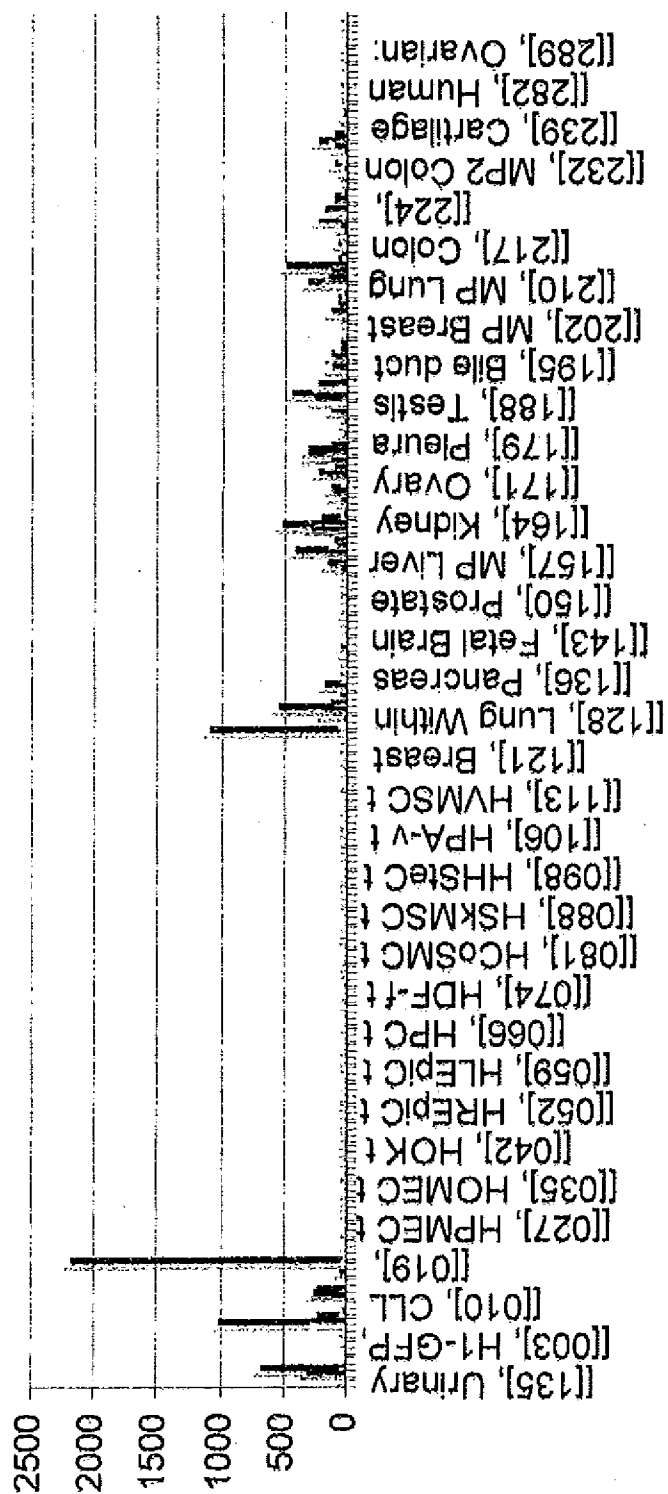


FIGURE 42

DSG3

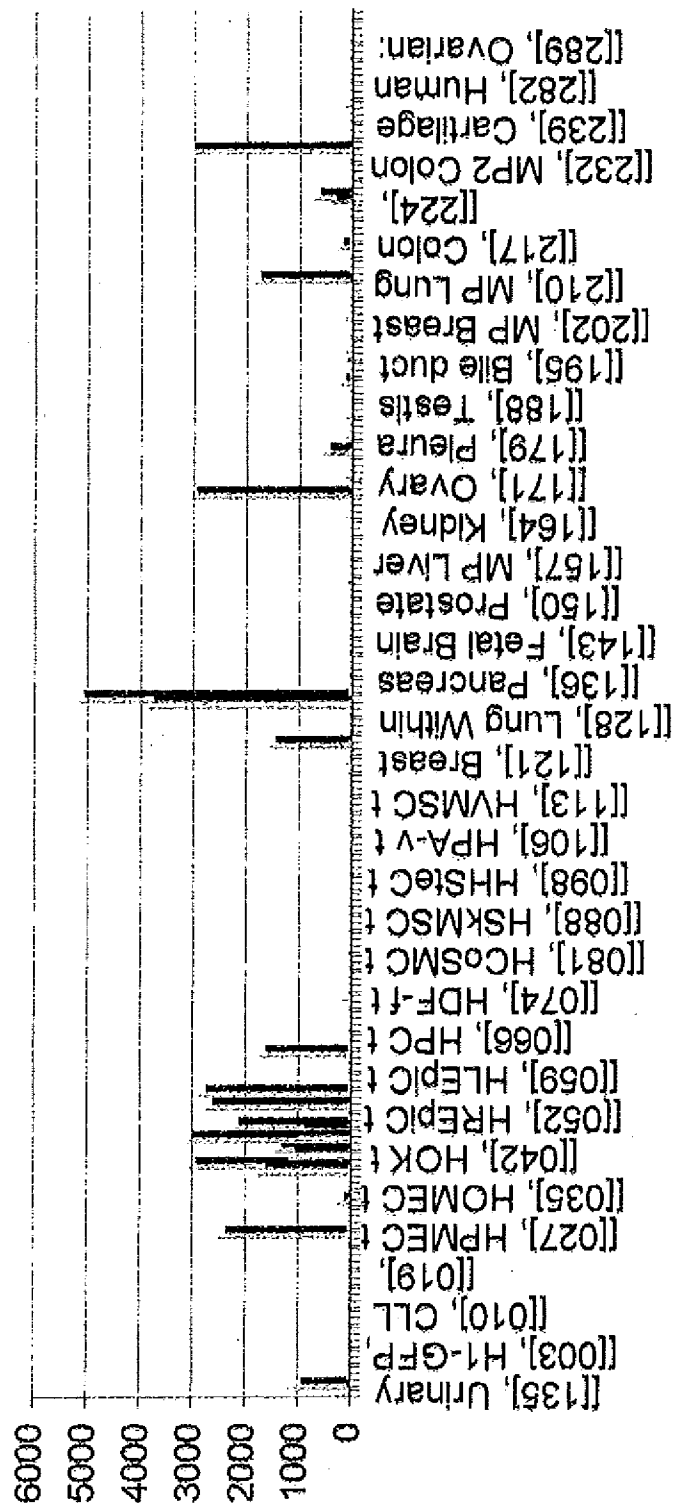


FIGURE 43

TYMP

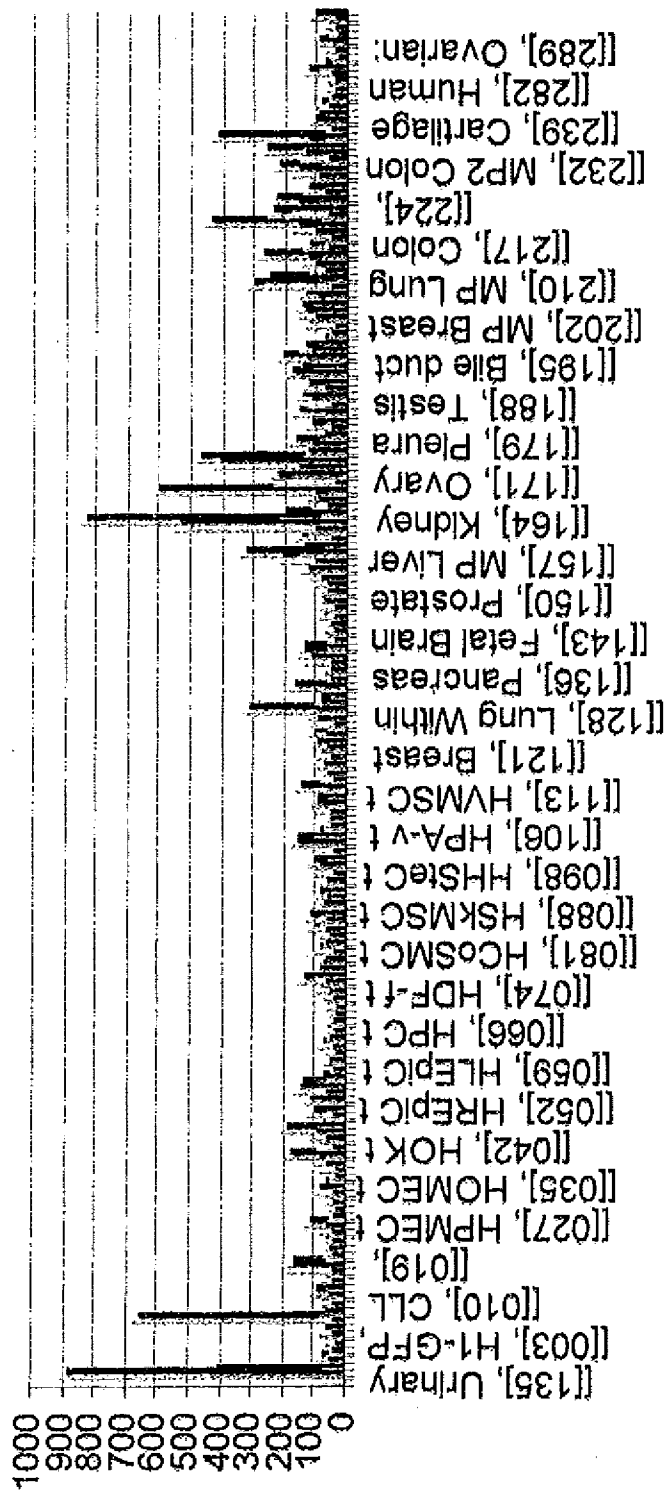


FIGURE 44

KRT6A

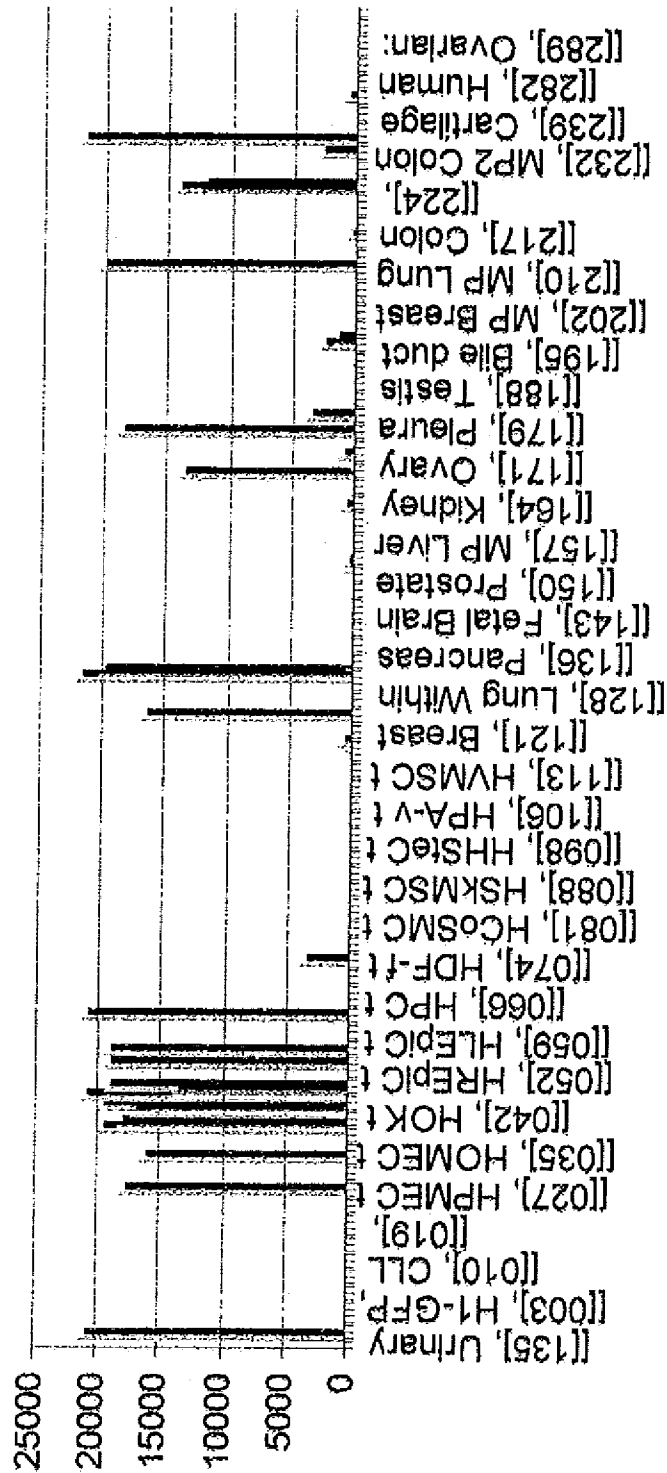


FIGURE 45

KRT6B

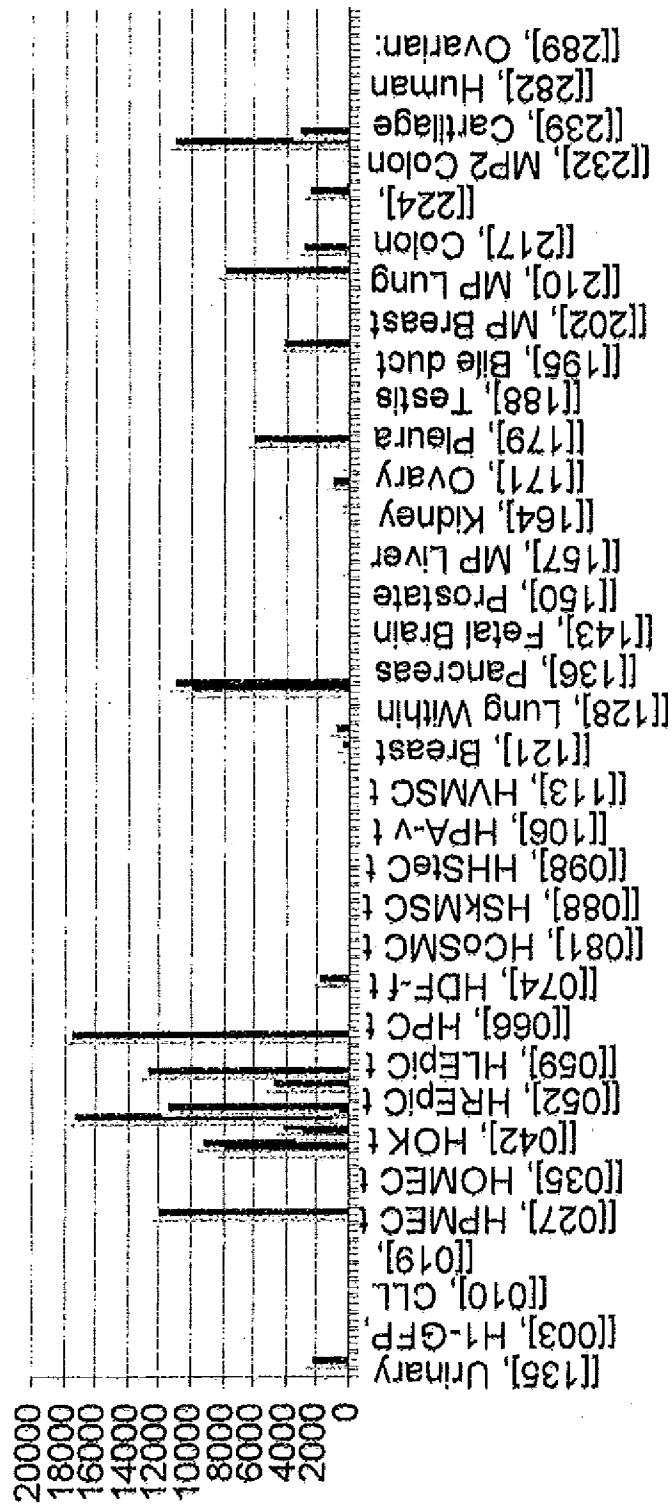


FIGURE 46

HLA-DRB1

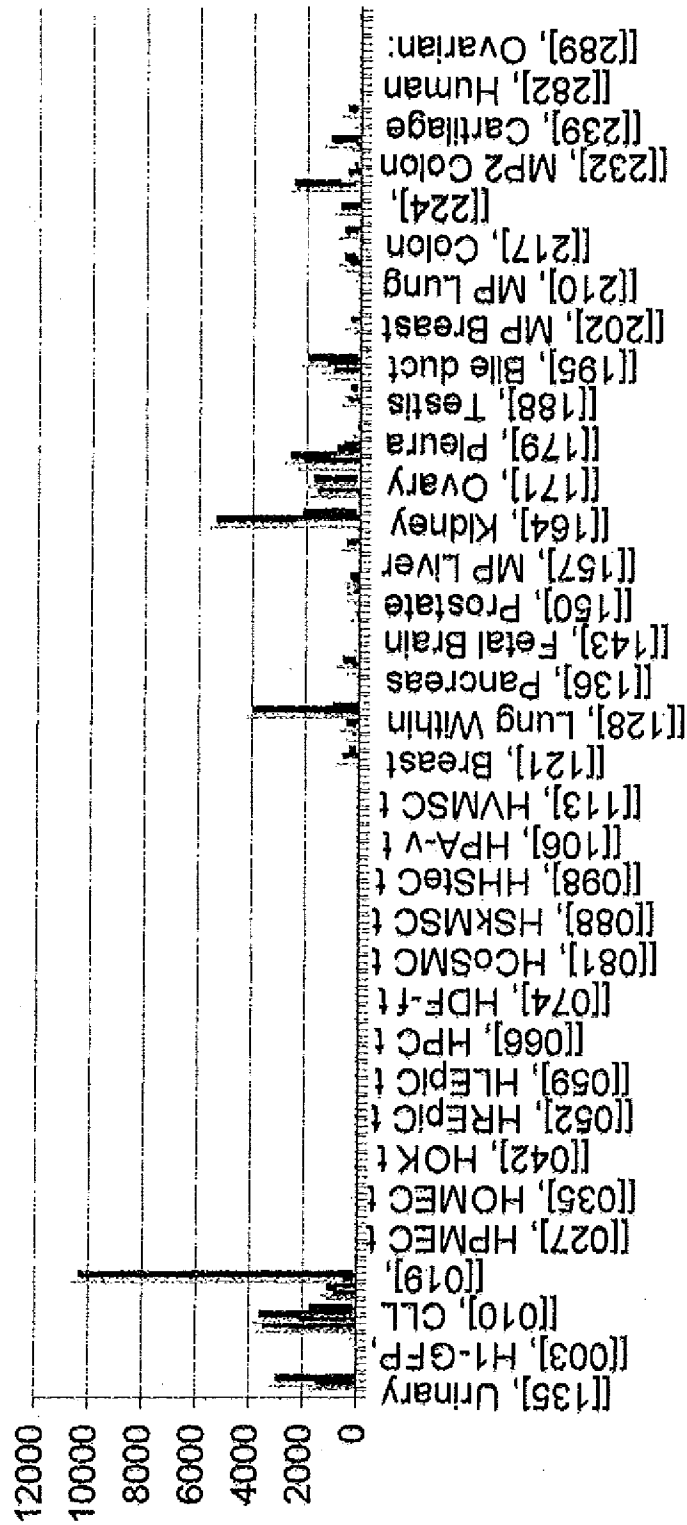


FIGURE 47

LCN2

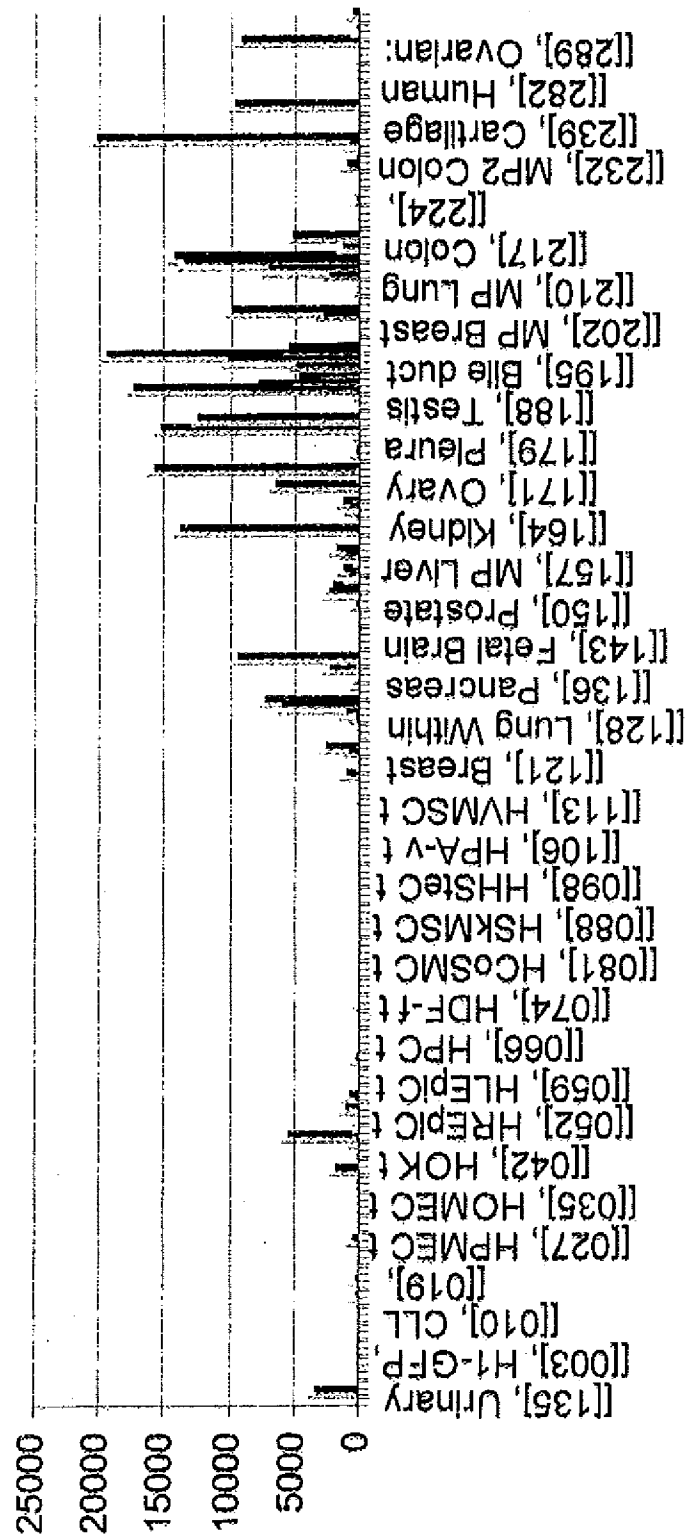


FIGURE 48

KRT4

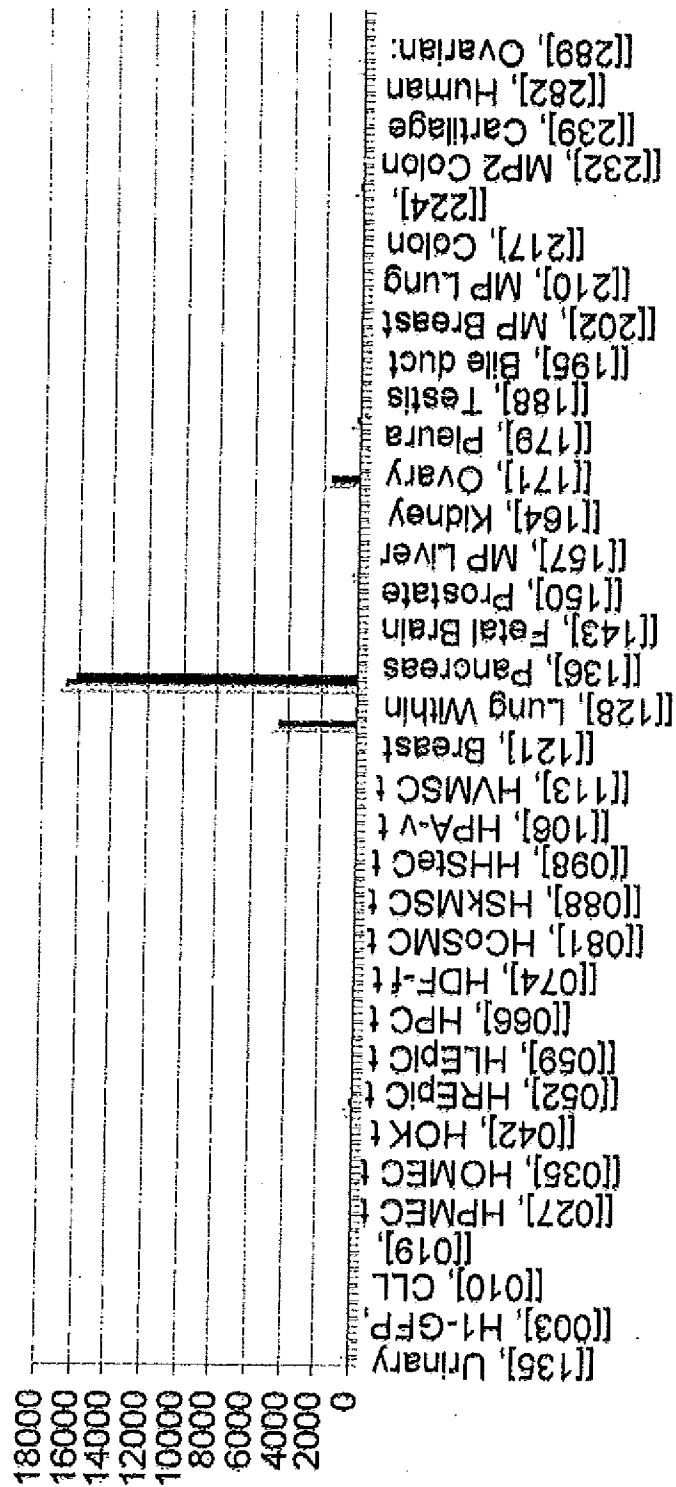


FIGURE 49

IFI30

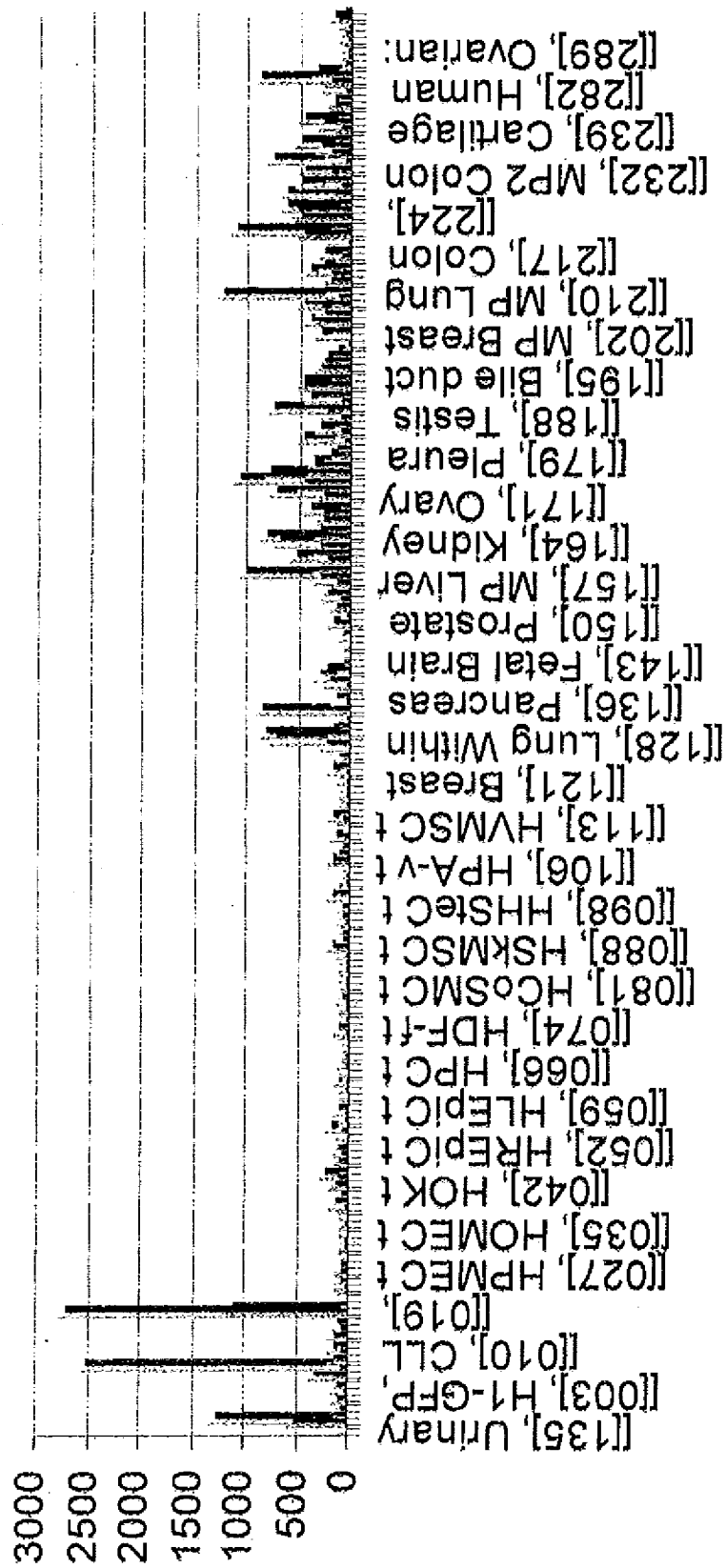


FIGURE 50

LOC100134370

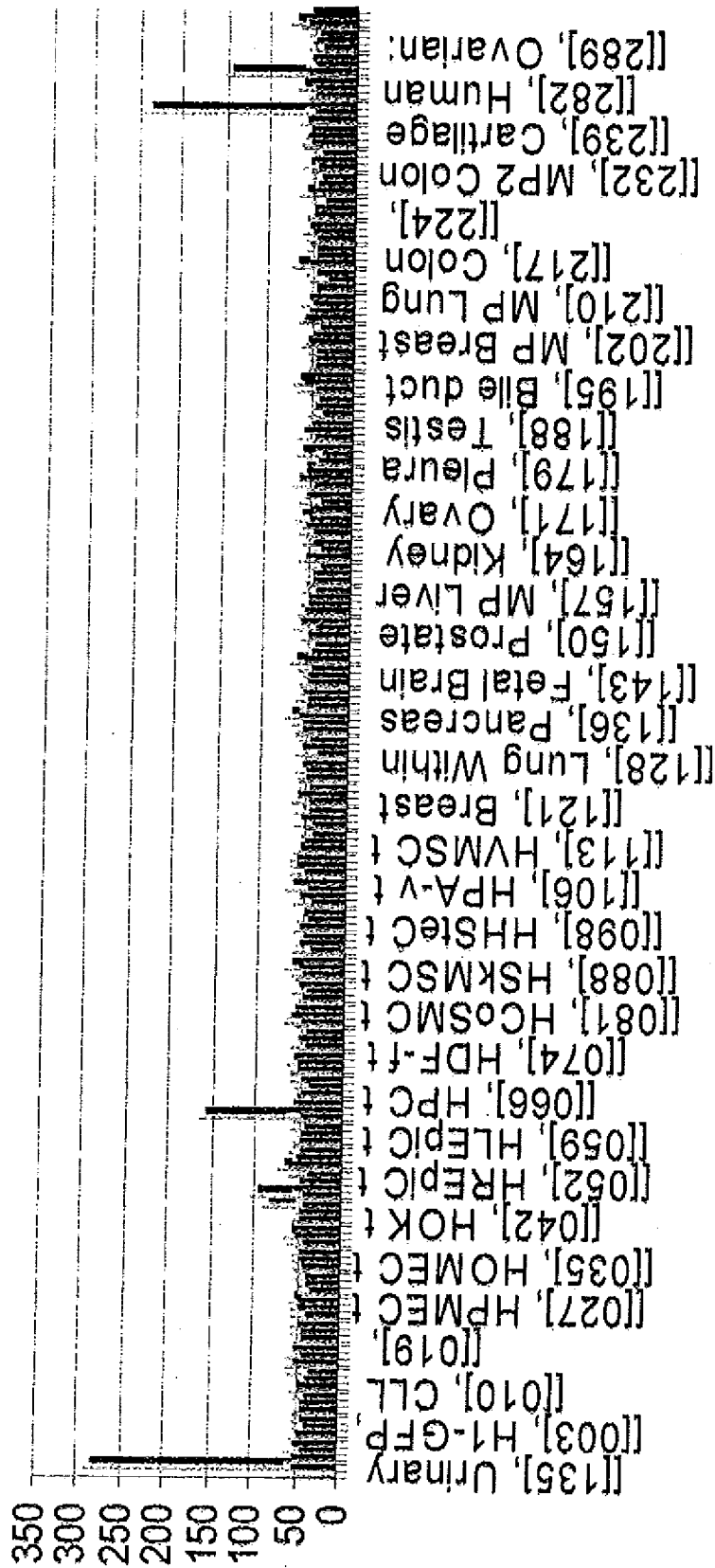


FIGURE 51

KIAA1618

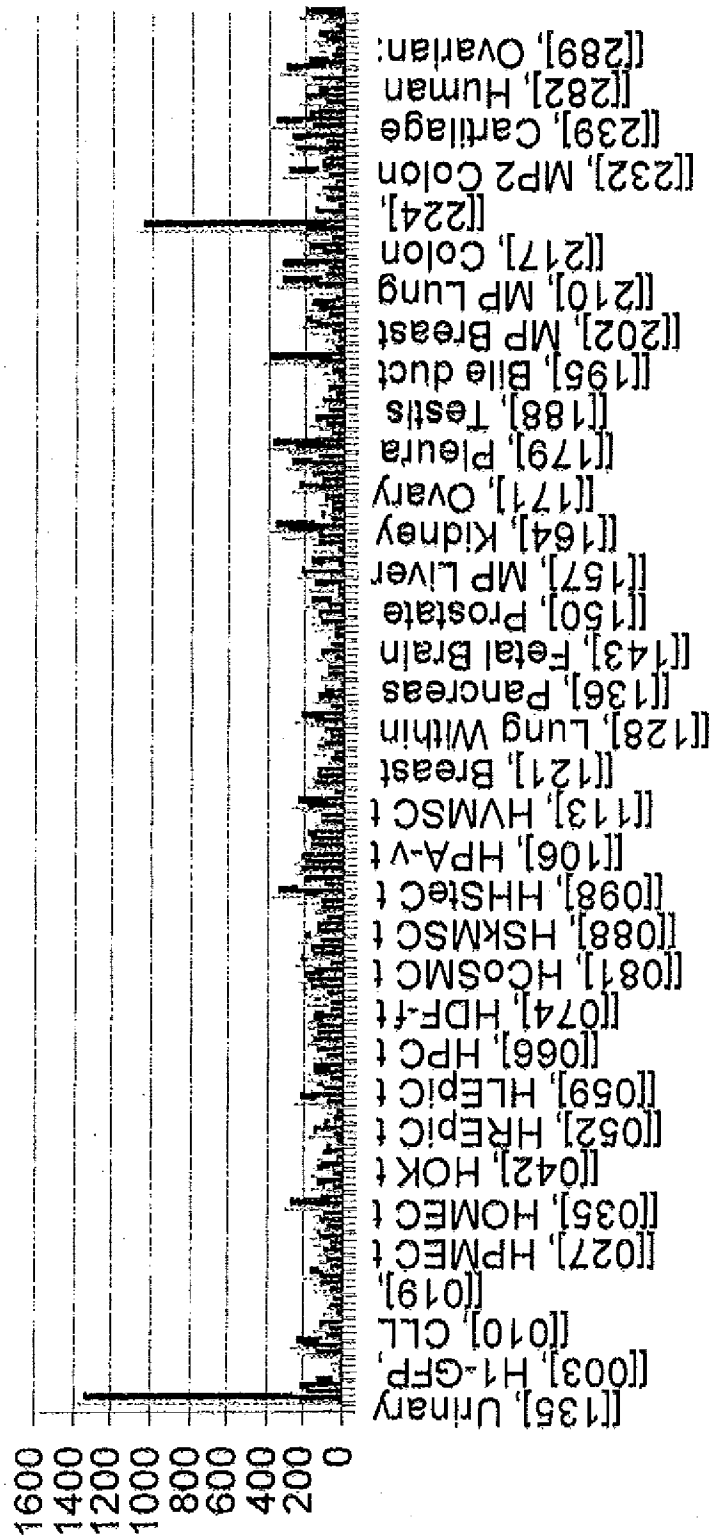


FIGURE 52

S100A8

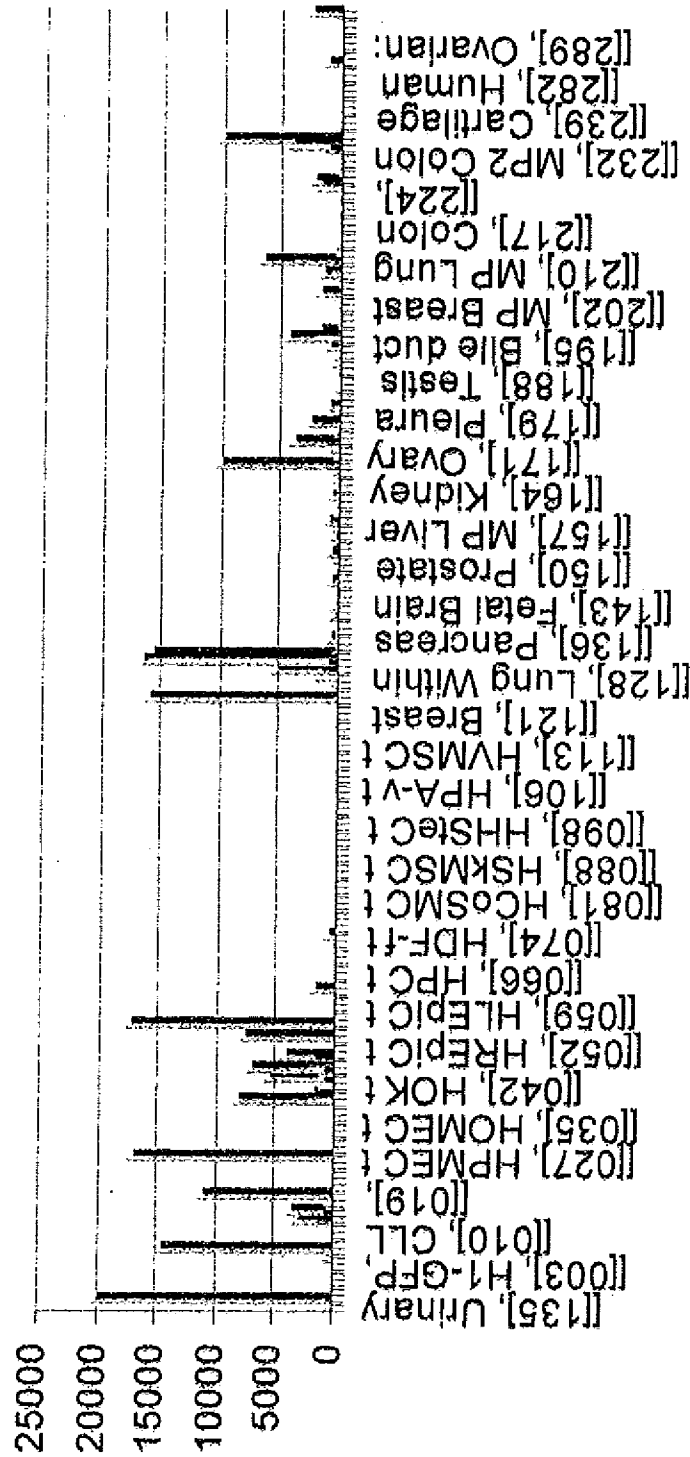


FIGURE 53

MMP7

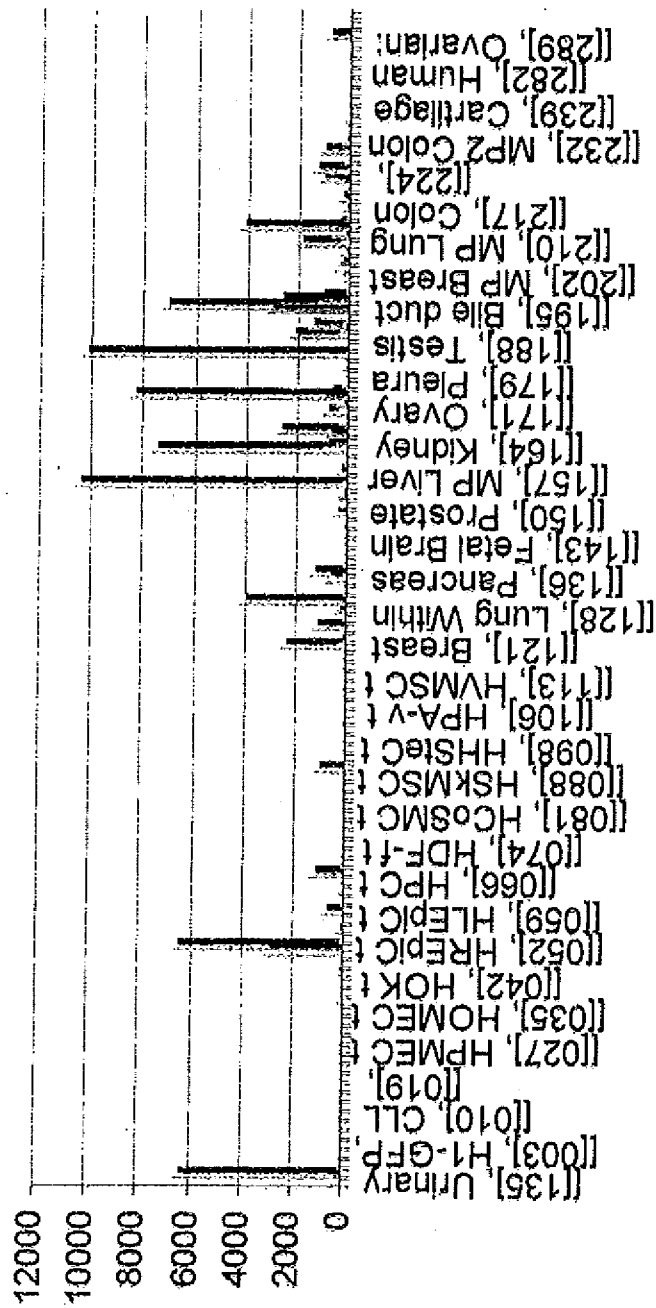


FIGURE 54

MMP7

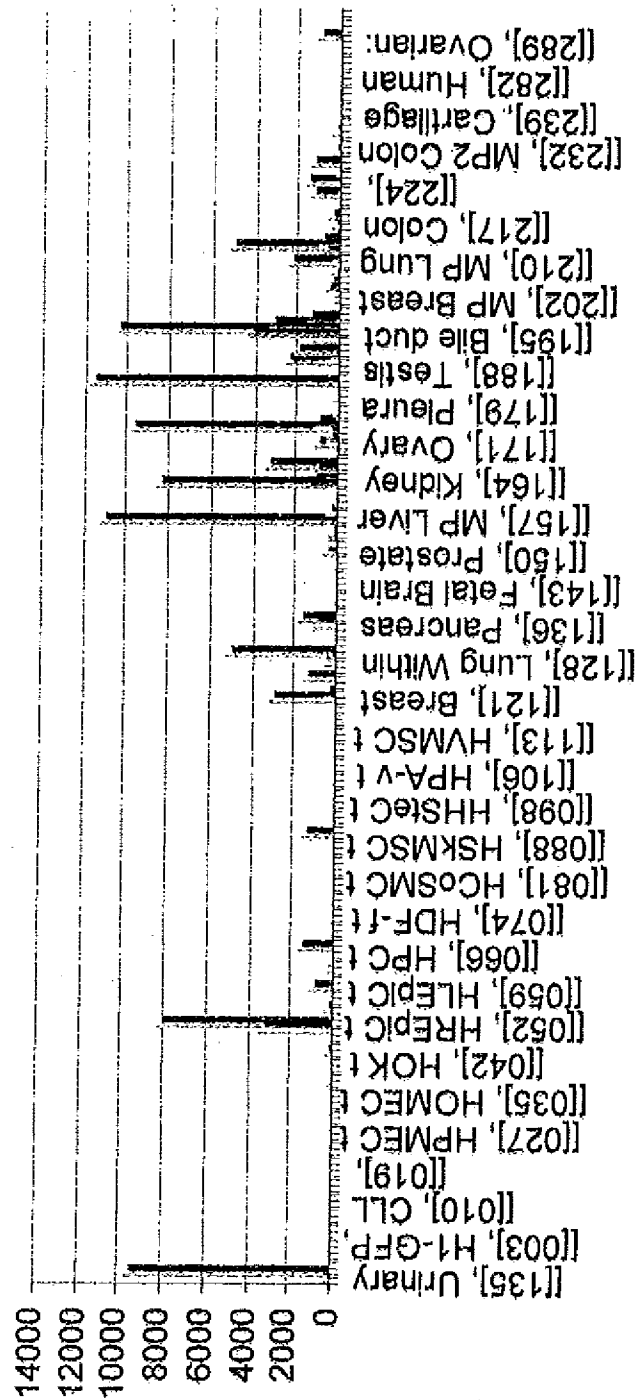


FIGURE 55

SPRR2A

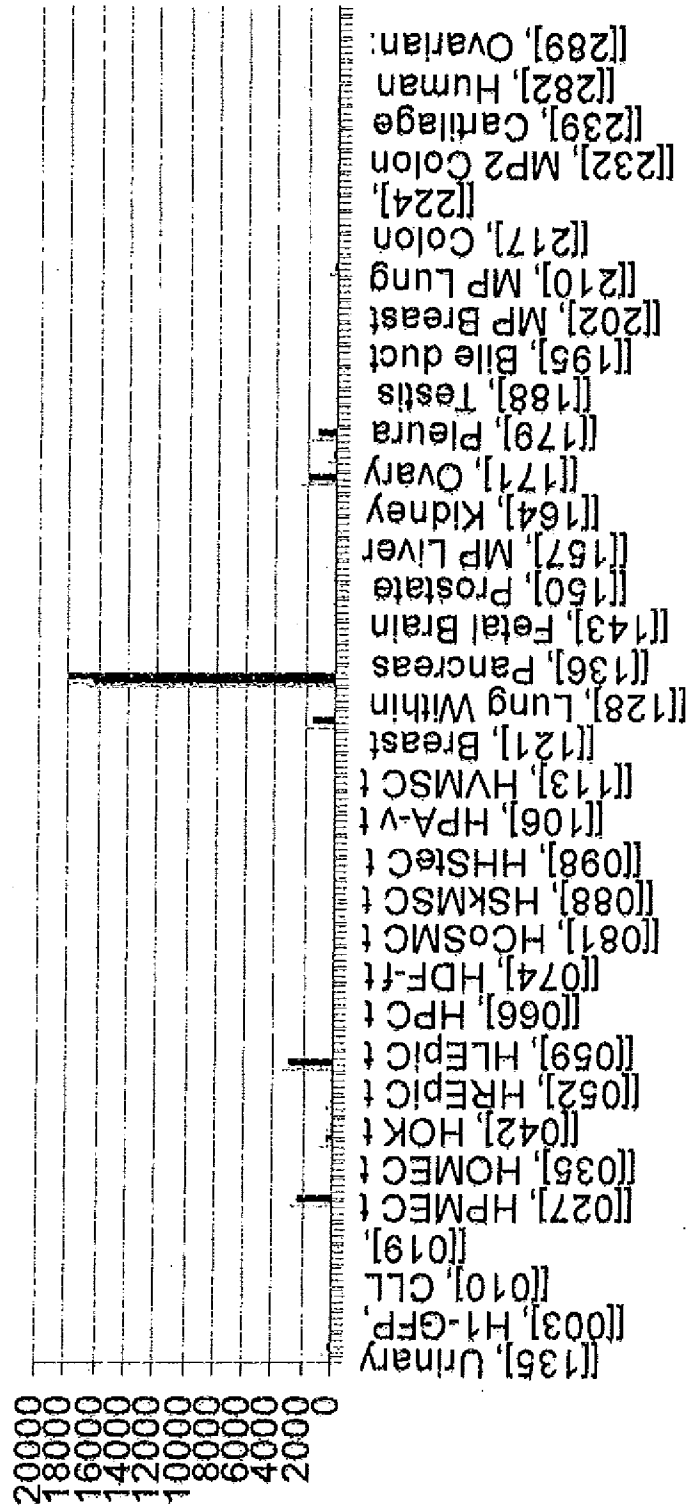


FIGURE 56

GJB2

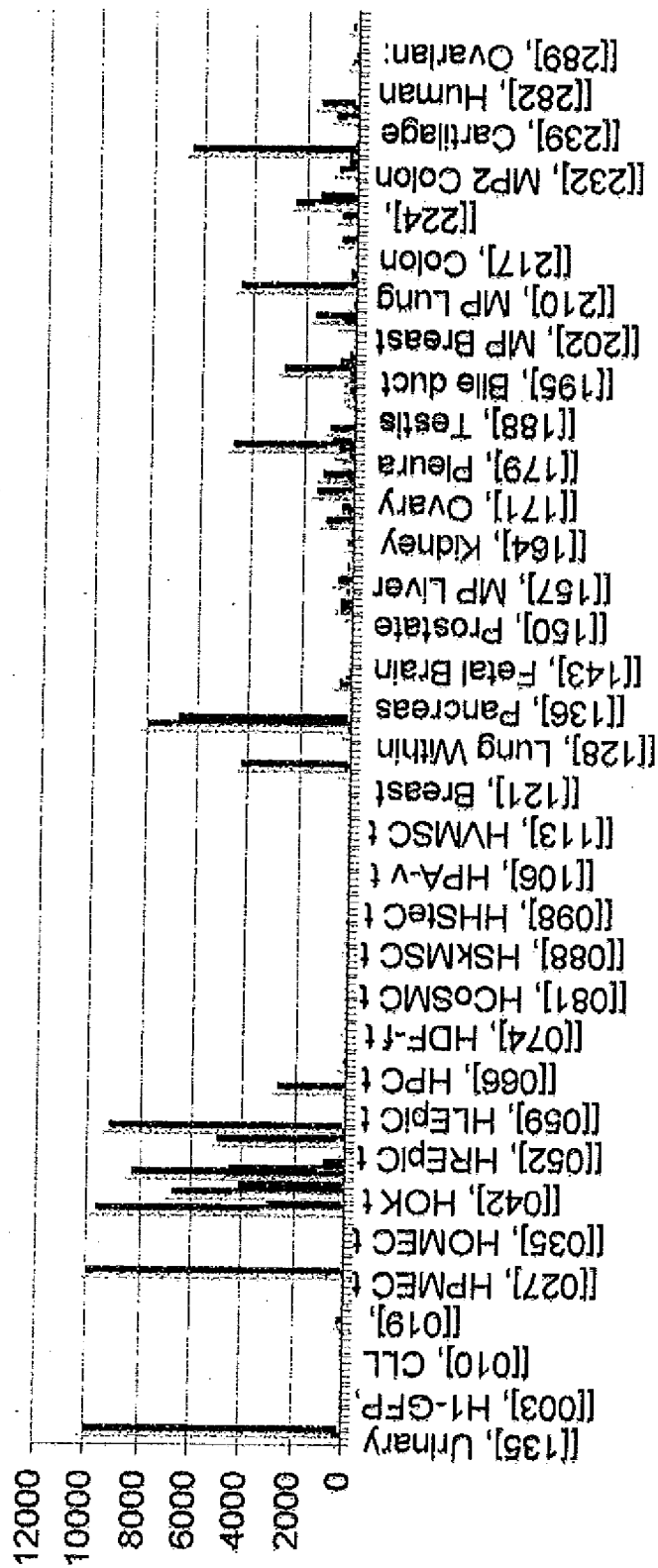
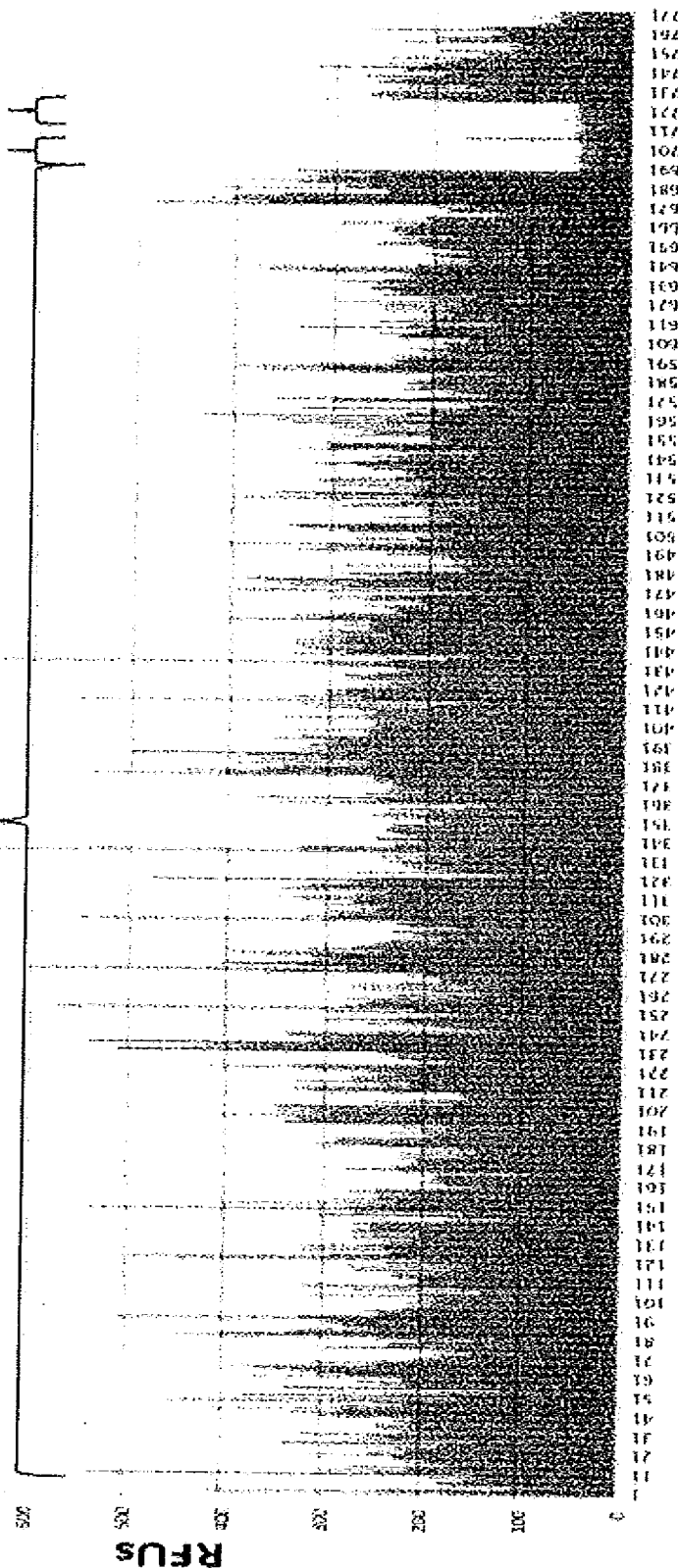


FIGURE 57

HES Cells

SP100 Transcript Var 1

Somatic Cell Types



Cell Lines

FIGURE 58

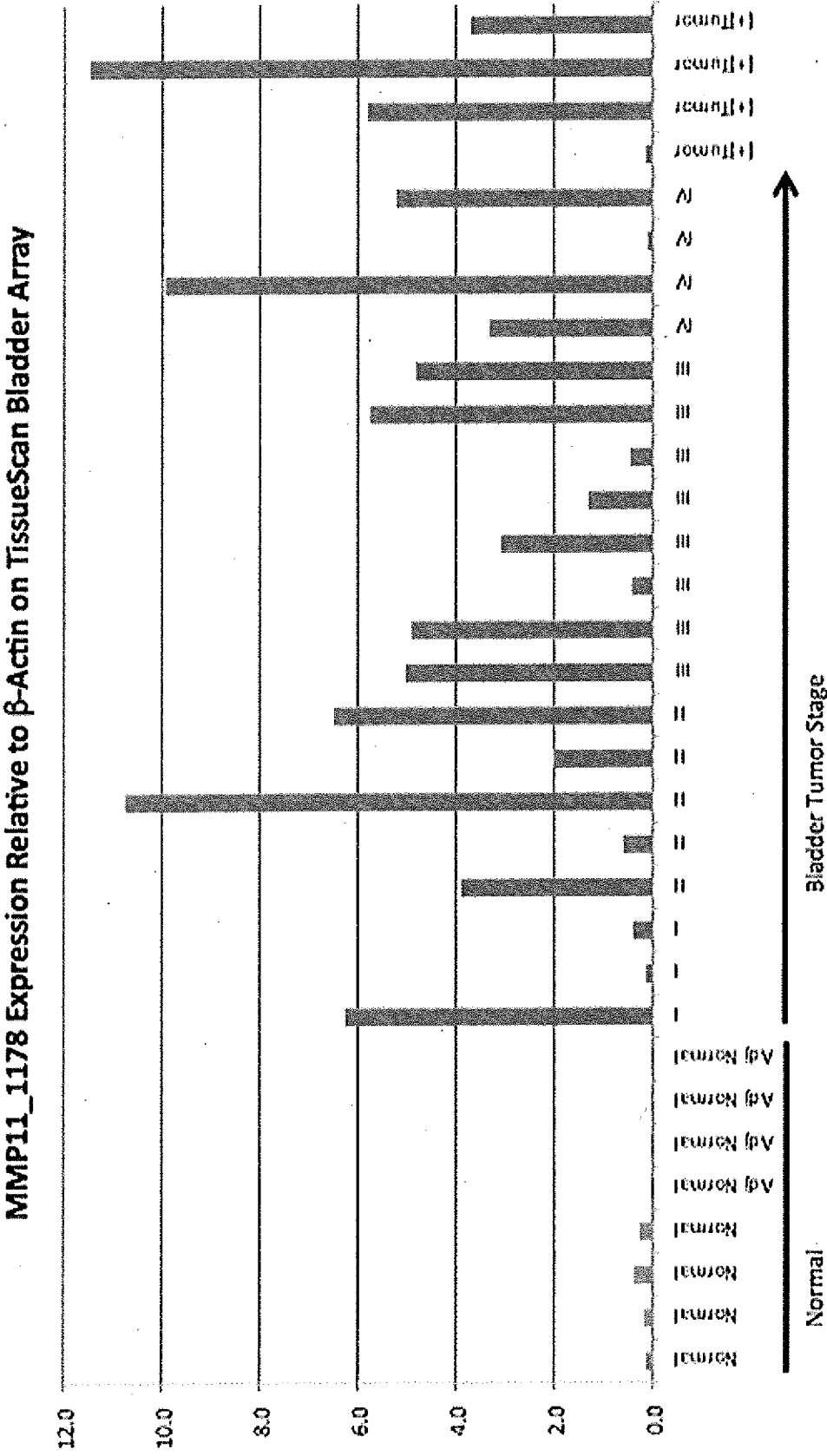


FIGURE 59

MMP12_1192 Expression Relative to β -Actin on TissueScan Bladder Array

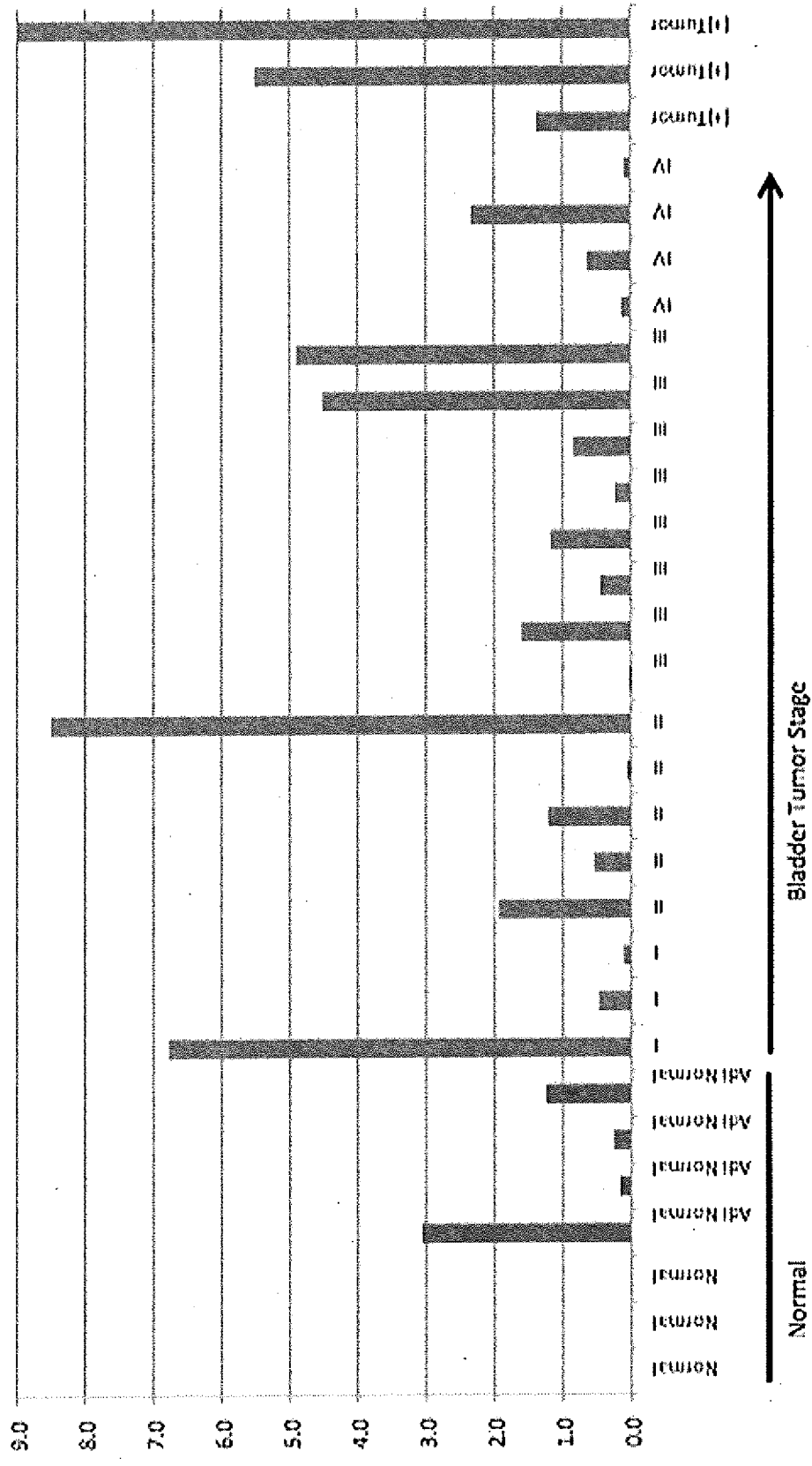


FIGURE 60

COL10A1_577 Expression Relative to β -Actin on TissueScan Bladder Array

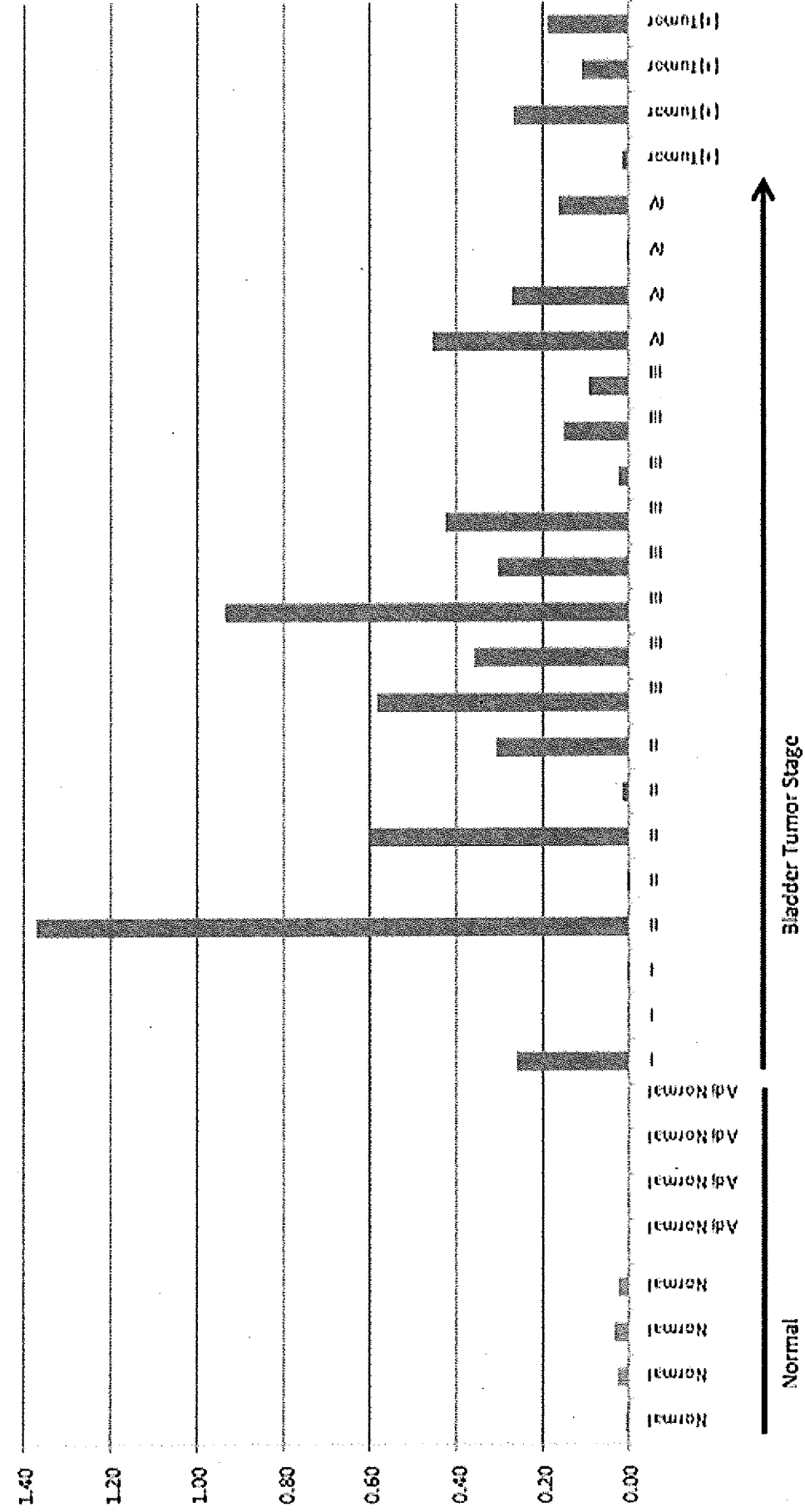


FIGURE 61

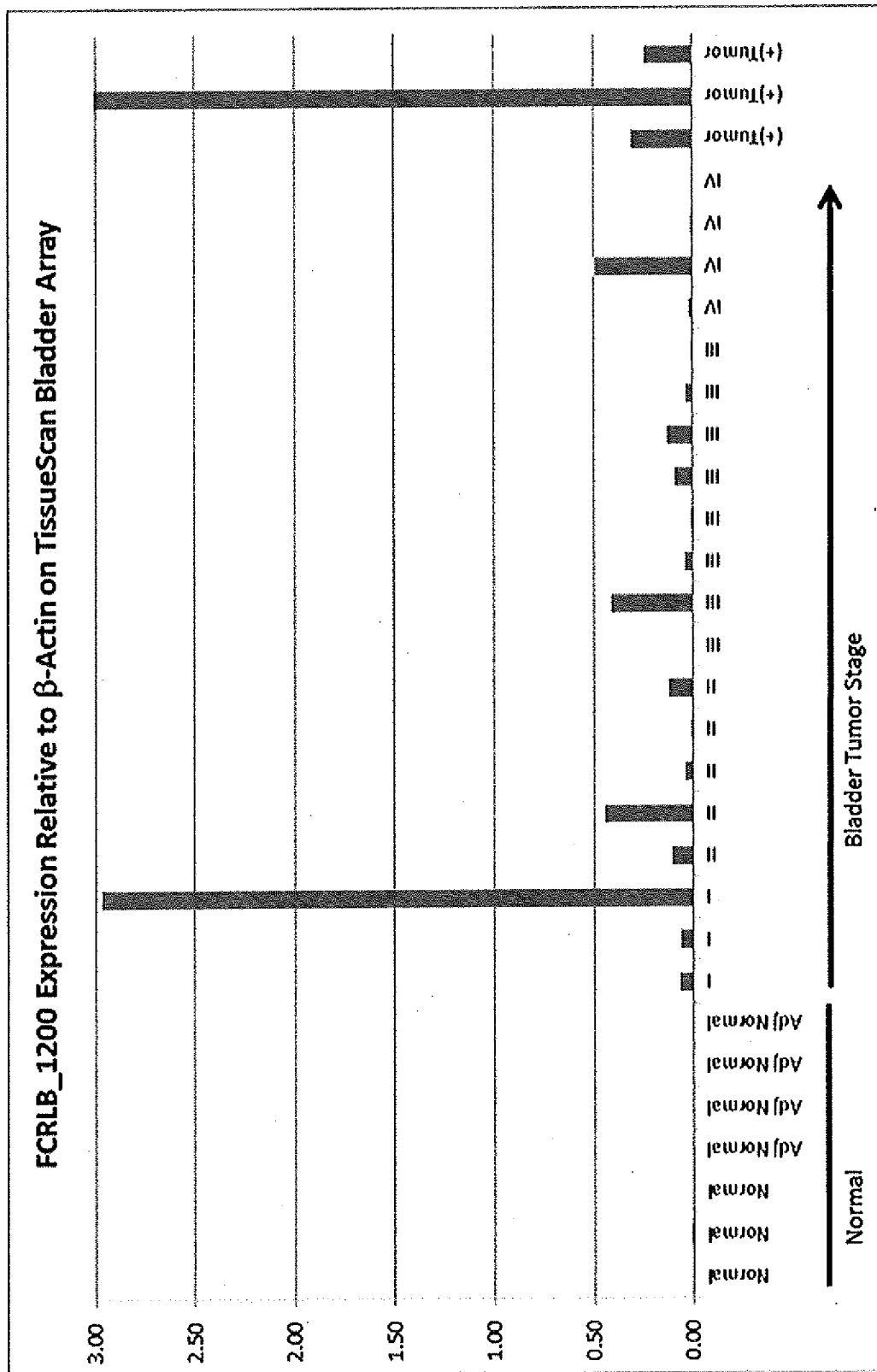


FIGURE 62

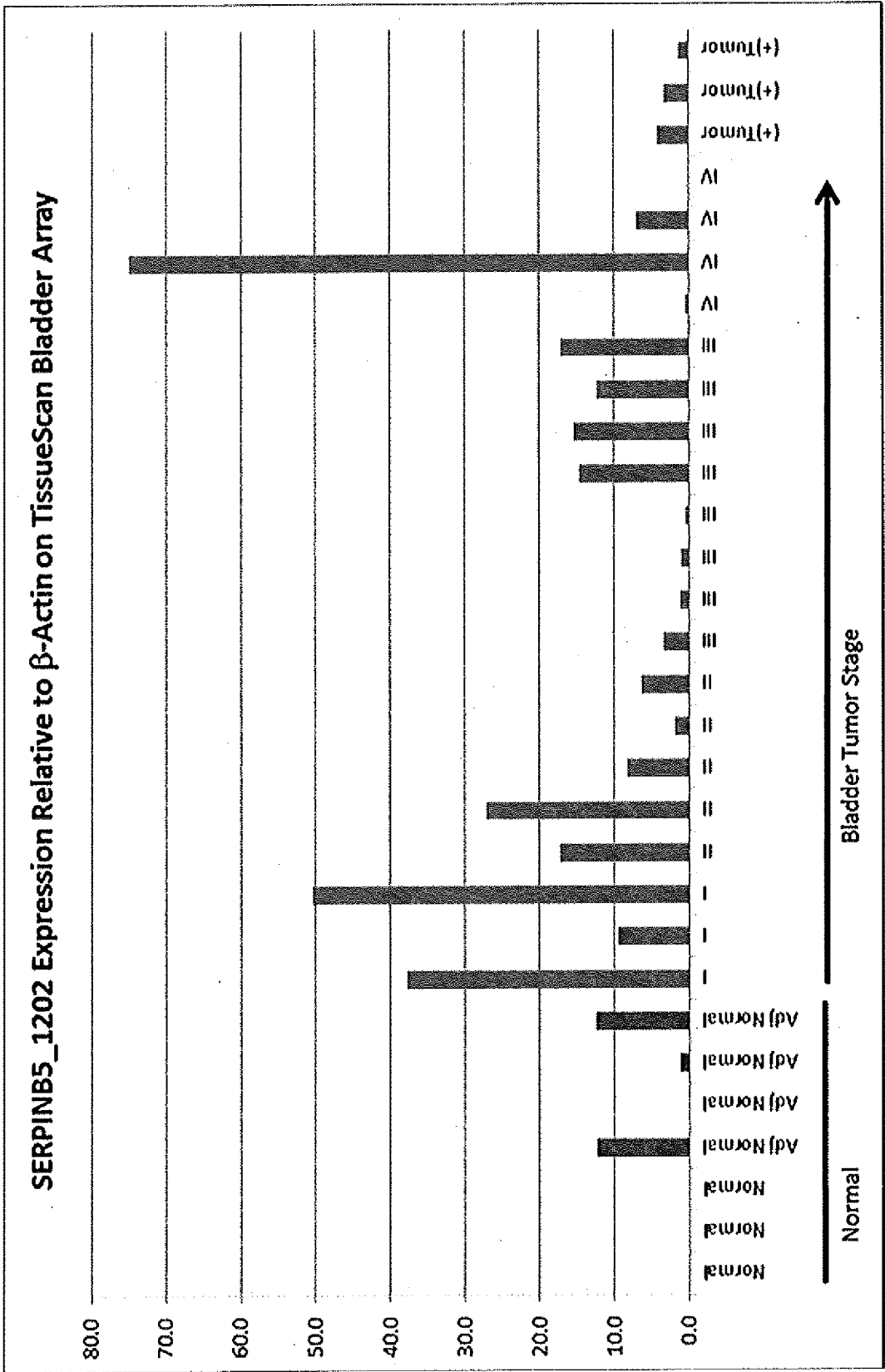


FIGURE 63

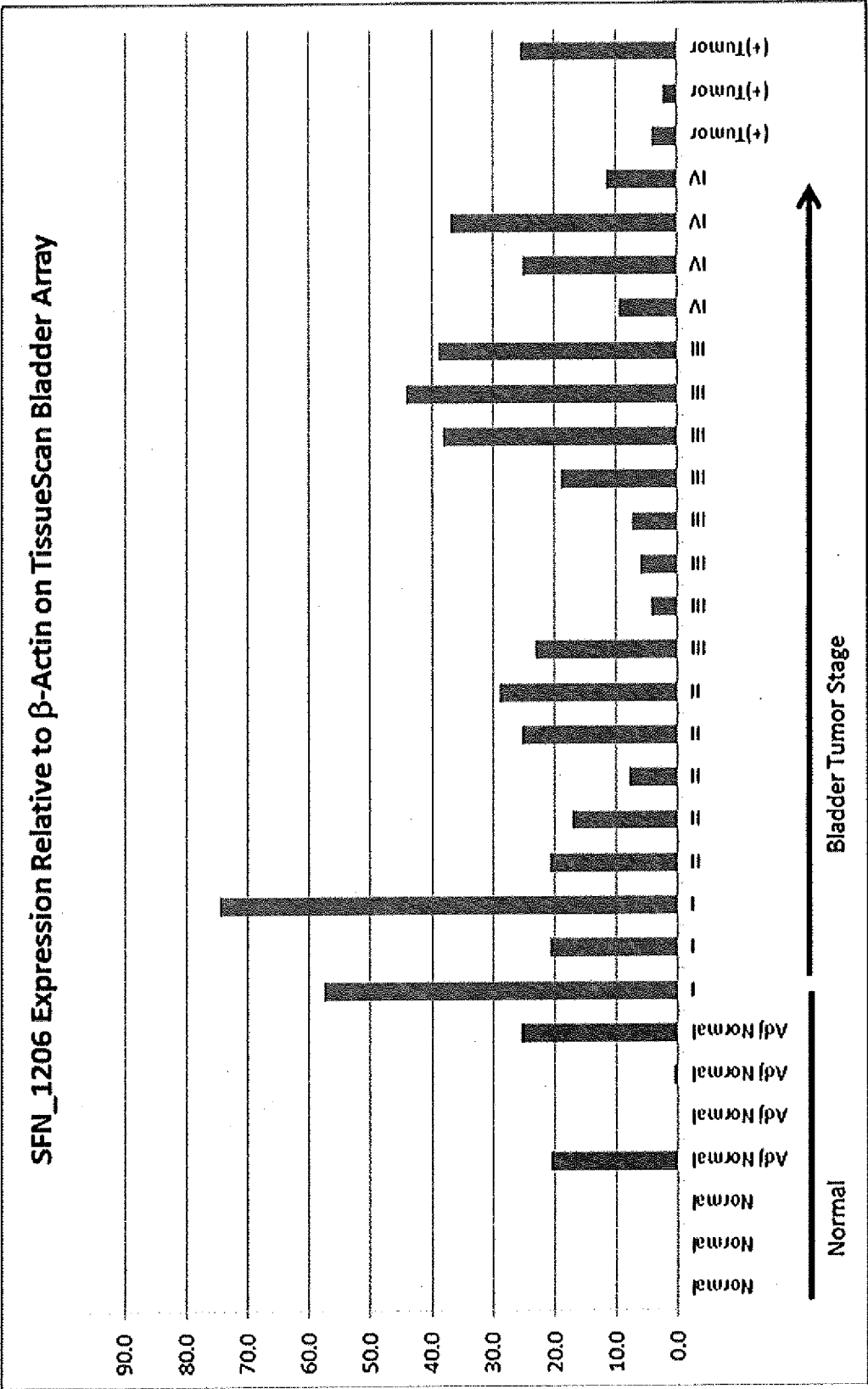


FIGURE 64

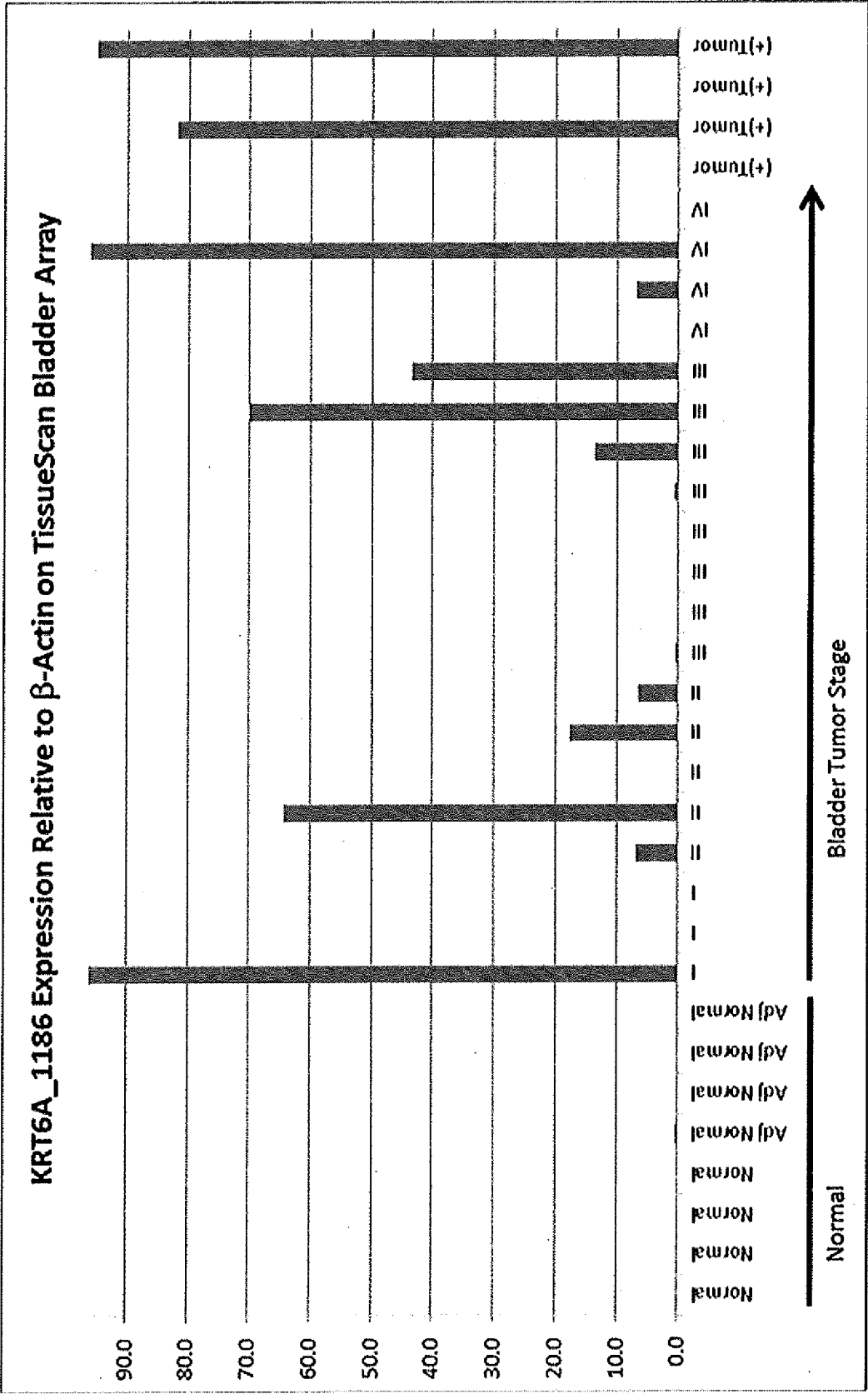


FIGURE 65

FCRLB Expression in Bladder Cancer

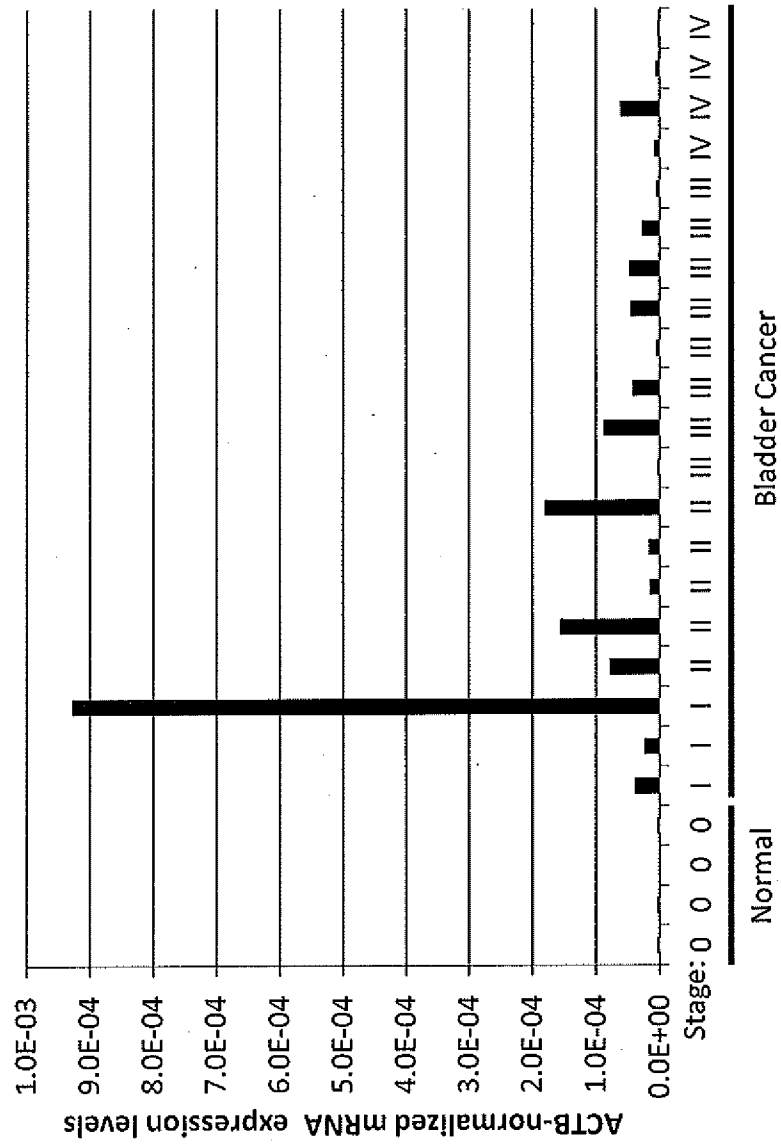


FIGURE 66

IL1A Expression in Bladder Cancer

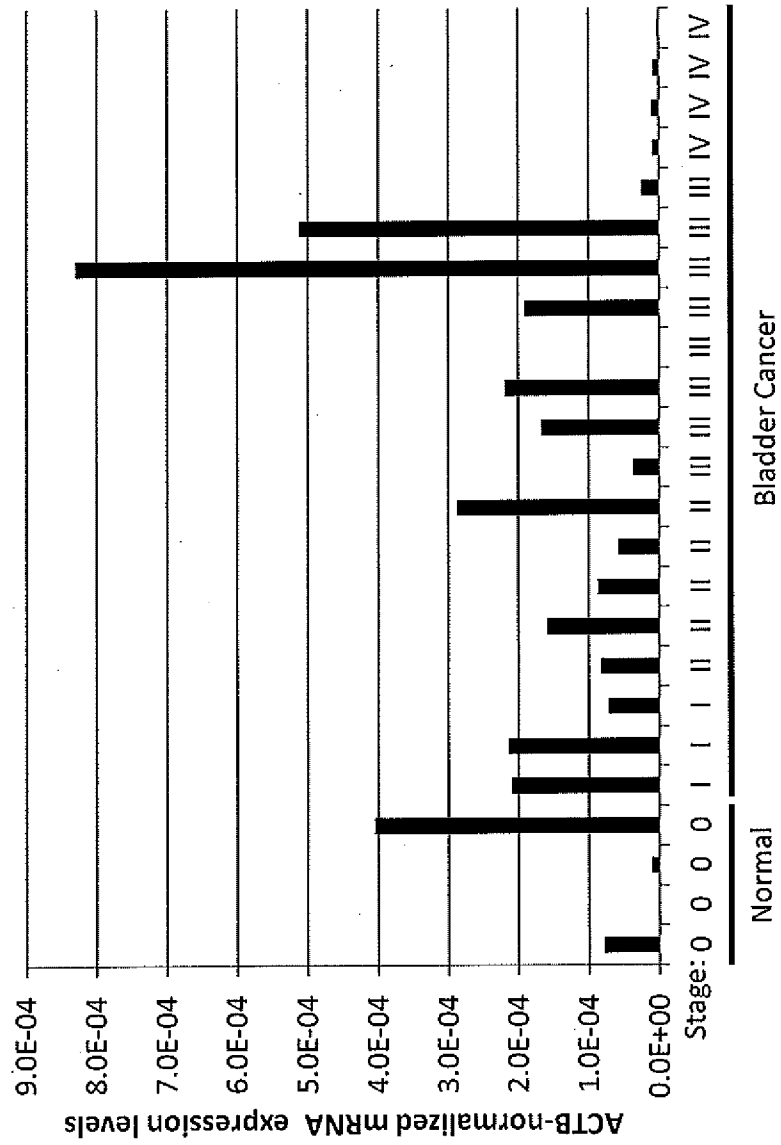


FIGURE 67

KRT16 Expression in Bladder Cancer

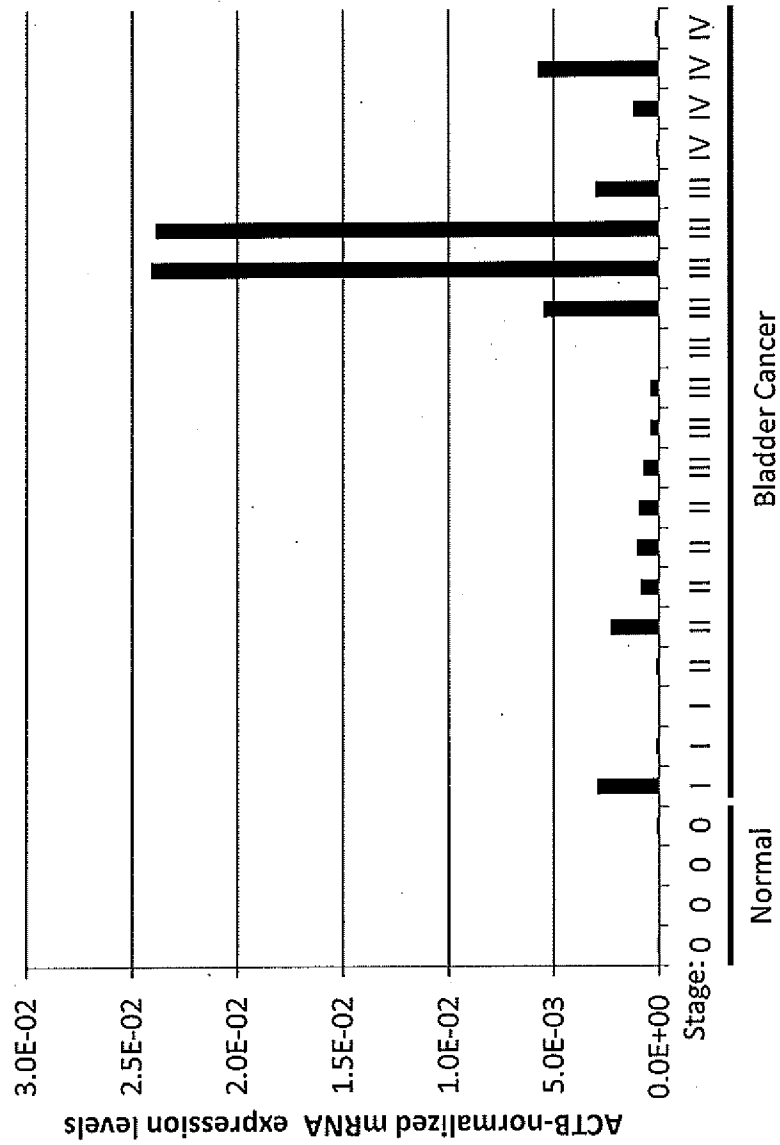


FIGURE 68

SLC1A6 Expression in Bladder Cancer

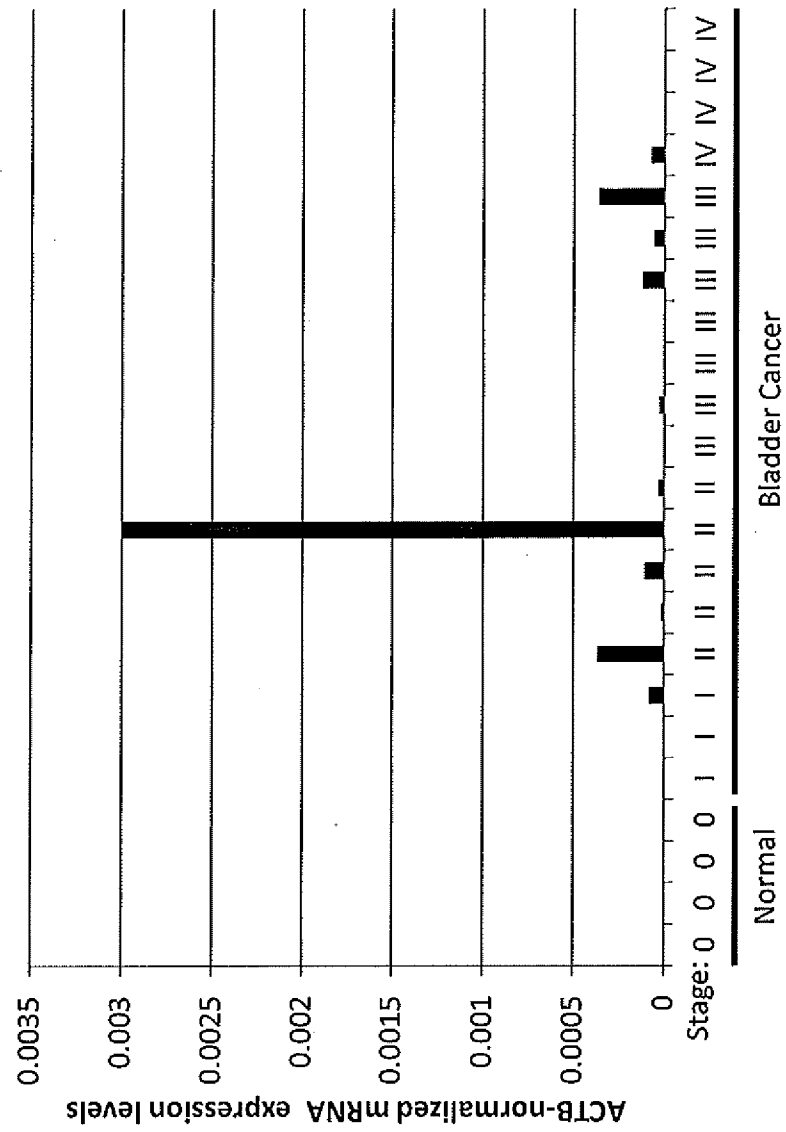


FIGURE 69

S100A2 Expression in Bladder Cancer

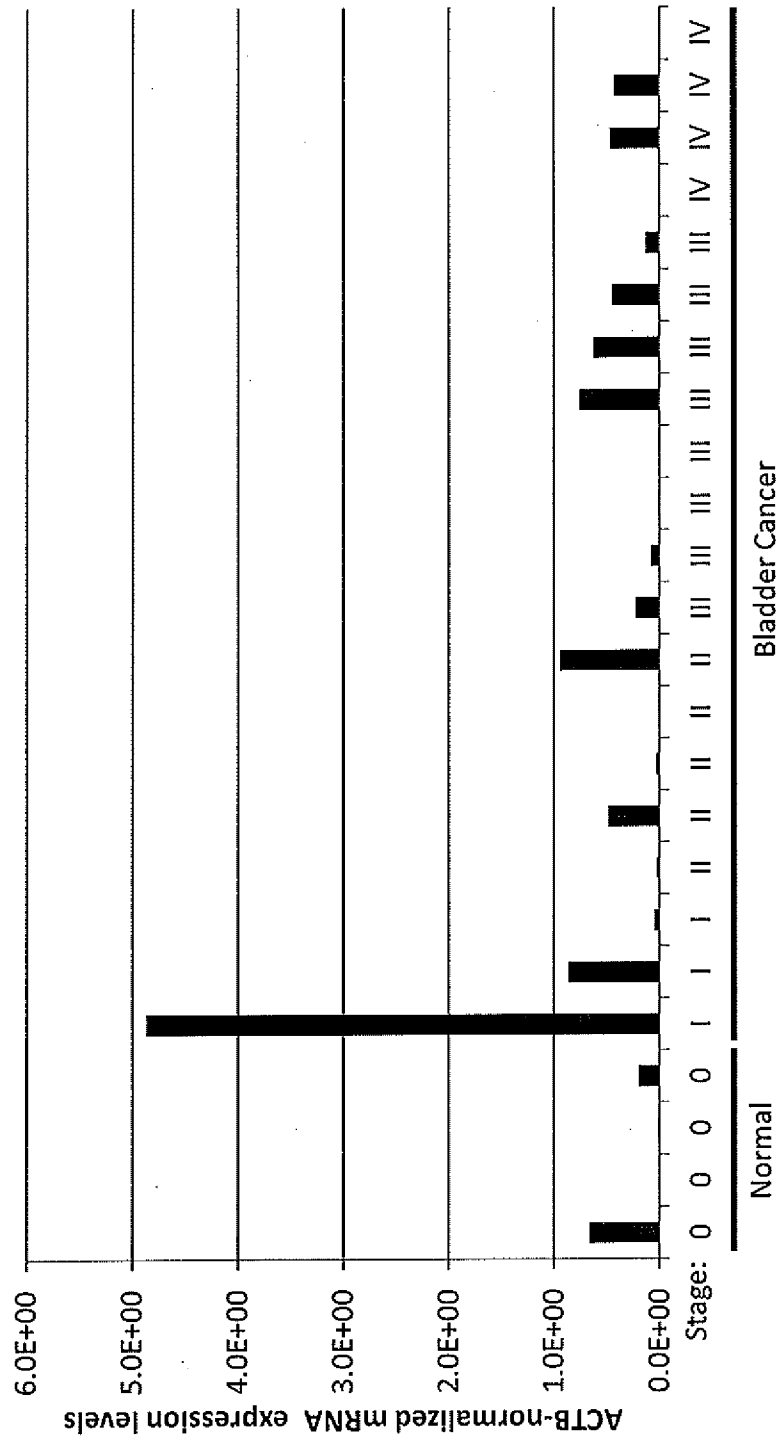


FIGURE 70

S100A7A Expression in Bladder Cancer

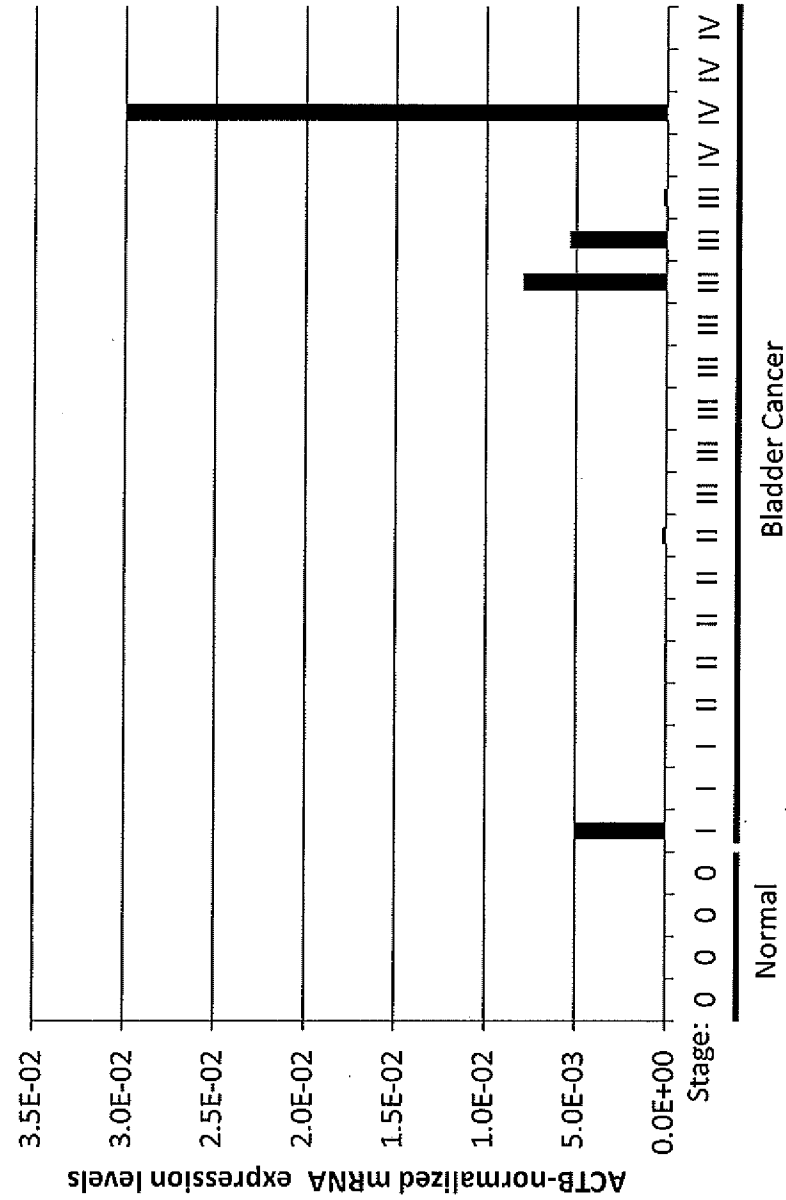


FIGURE 71

ppt slide #	slide 50
gene name	MMP12
assay type	ELISA
cancer type	bladder cancer

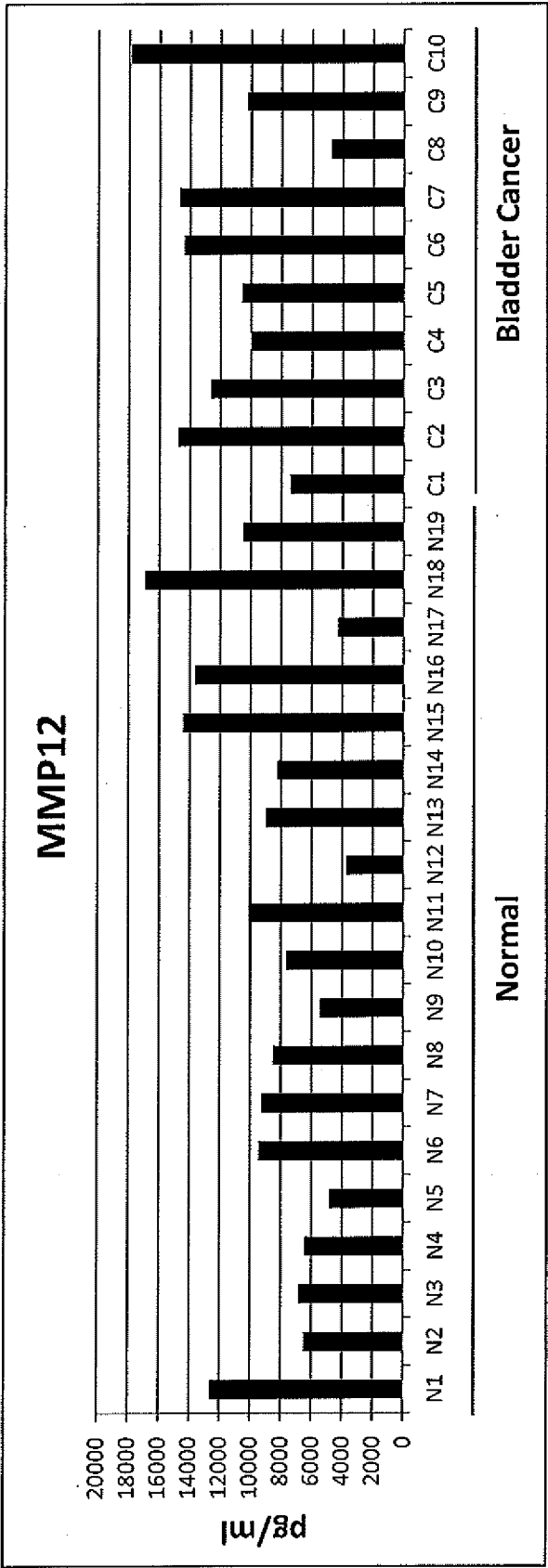


Figure 72

ppt slide #	slide 51
gene name	ColX
assay type	ELISA
cancer type	bladder cancer

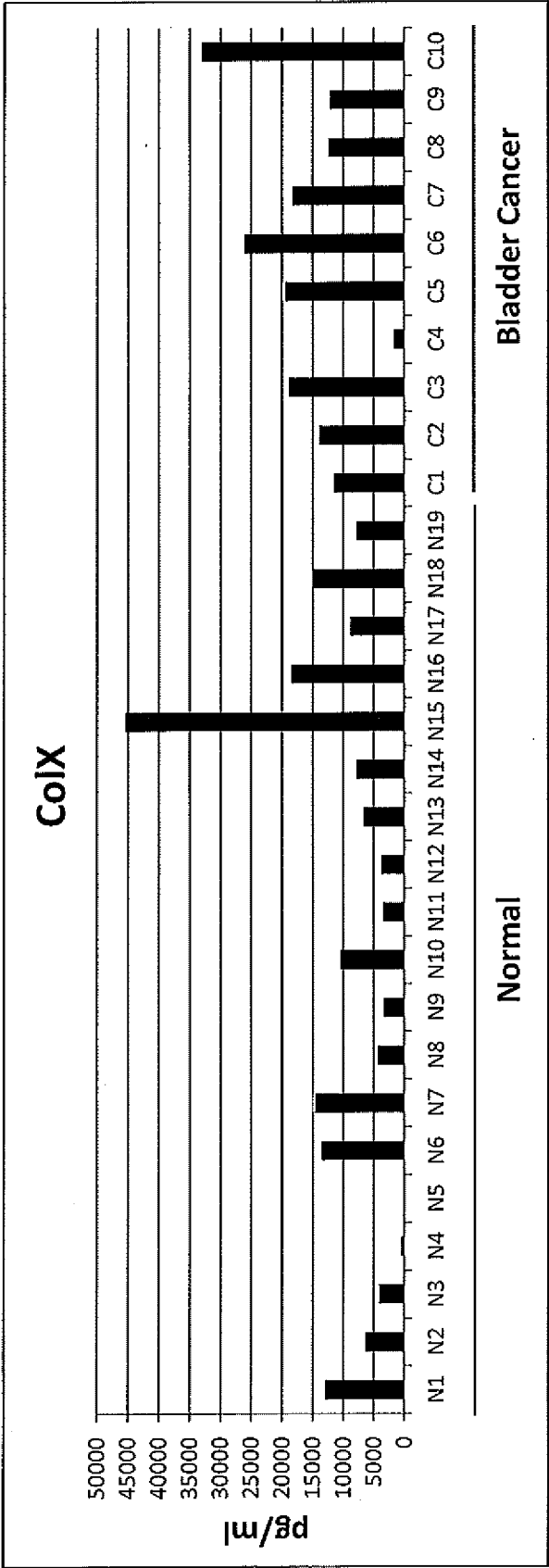


FIGURE 73

ppt slide #	Slide 30
gene name	MMP11
assay type	ELISA
cancer type	bladder cancer

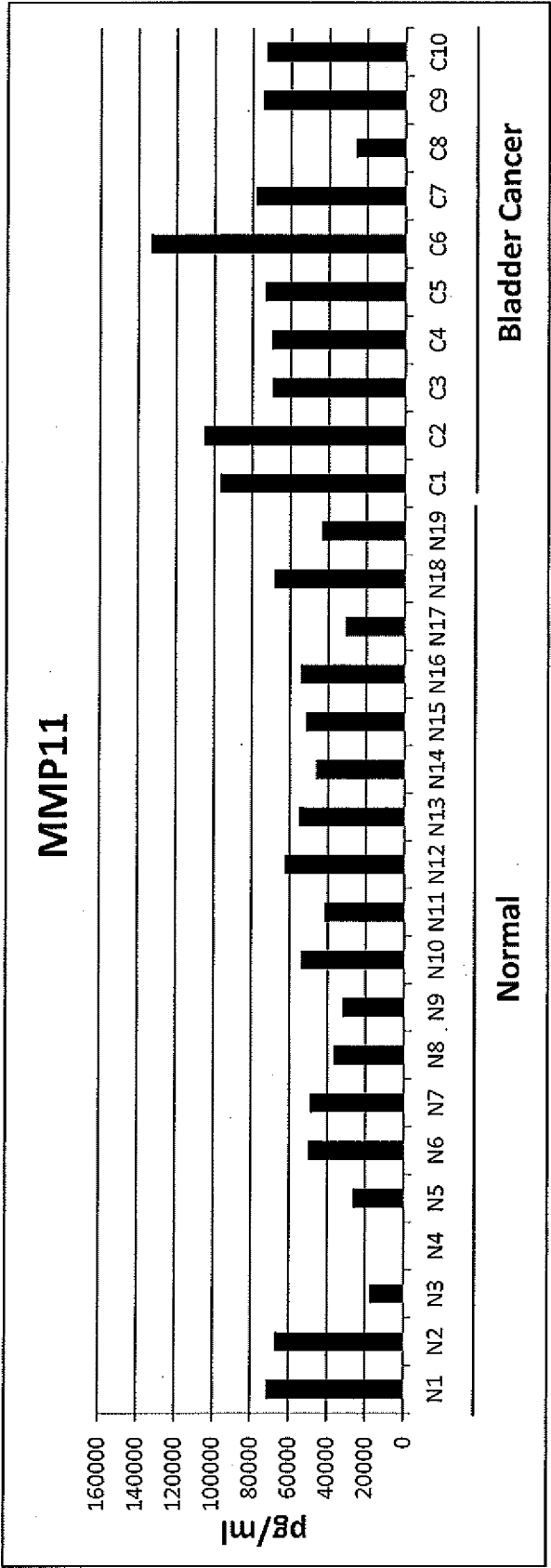


FIGURE 74

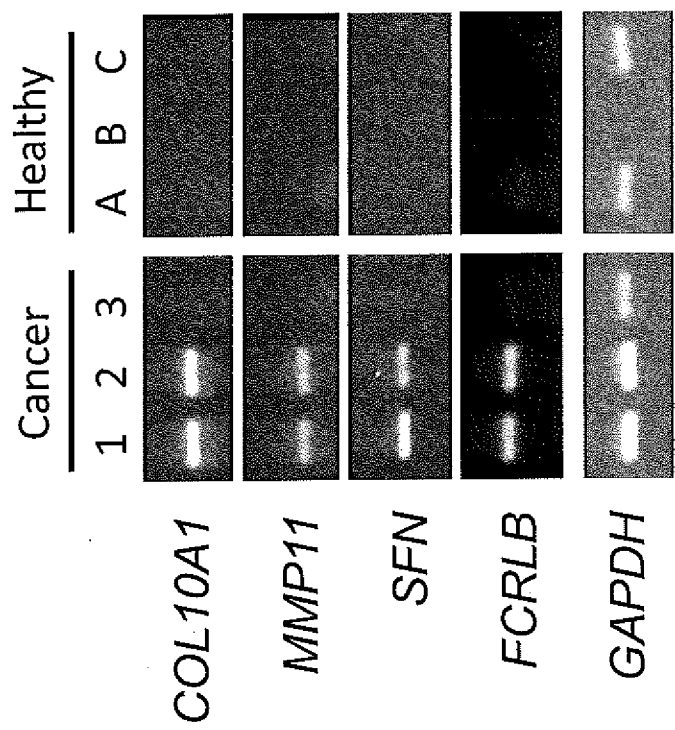


Fig. 75. Agarose gel analysis of markers of cells in voided urine.

SERPINB5
Bladder tumor marker
TissueScan Data

SERPINB5_1202 Expression Relative to β -Actin on TissueScan Bladder Array

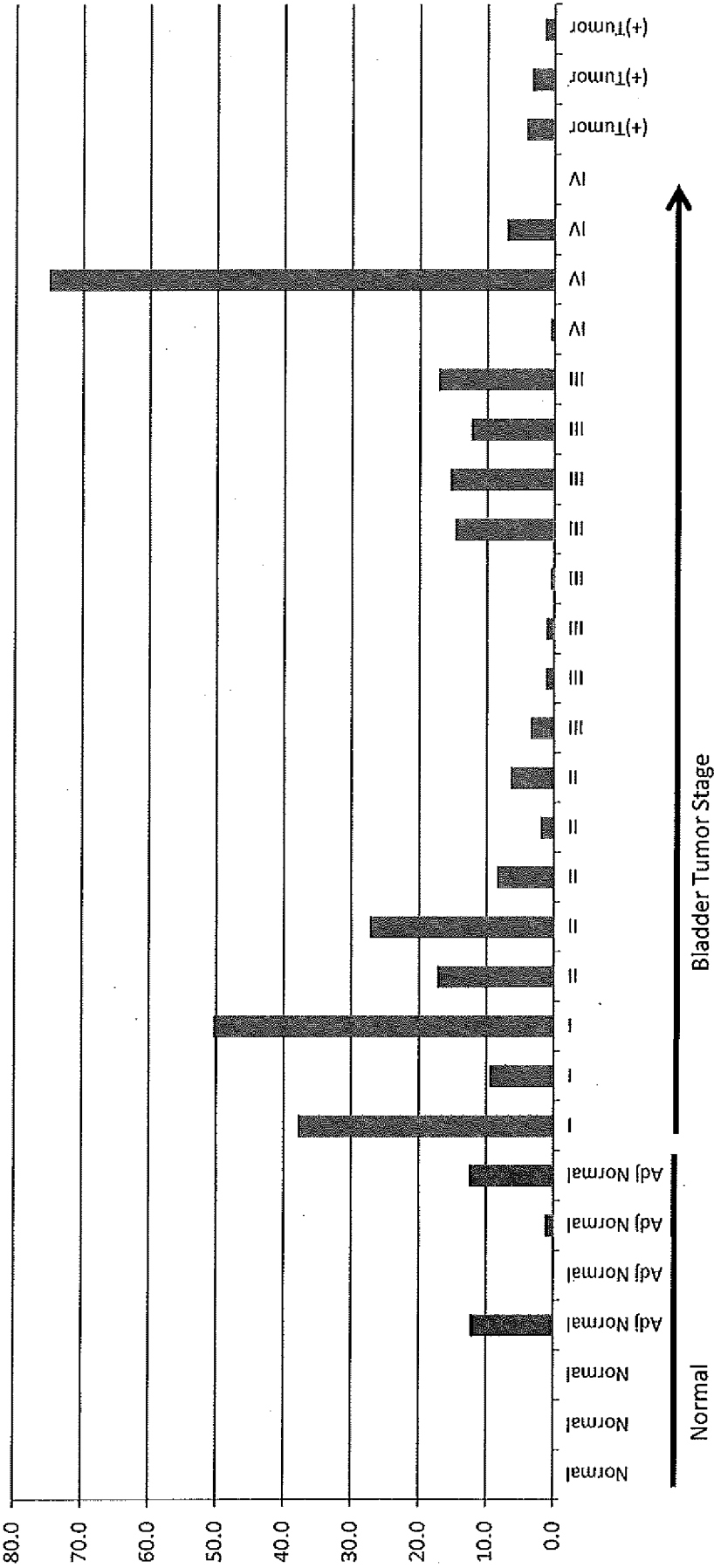


FIGURE 76

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 12/43852

A. CLASSIFICATION OF SUBJECT MATTER
 IPC(8) - C12Q 1/68; G01N 33/574 (2012.010)
 USPC - 435/6.14; 435/7.23

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(8): C12Q 1/68; G01N 33/574 (2012.010)

USPC: 435/6.14; 435/7.23

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC: 435/6.1; 435/7.2; 435/7.21

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

----- Please see continuation on attached additional sheet -----

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2009/0175844 A1 (NAKAMURA et al.) 9 July 2009 (09.07.2009), abstract; para [0018], [0019], [0020], [0021], [0029], [0047], [0048], [0057], [0058], [0059], [0176], [0183], pg 40, Table 4.	1-13
Y	US 2011/0123990 A1 (BAKER et al.) 26 May 2011 (26.05.2011), abstract; para [0044], pg 43, Table A; pg 47, Table A; pg 48, Table A.	1-13
Y	US 2004/0038207 A1 (ORNTTOFT) 26 February 2004 (26.02.2004), abstract; pg 14, Table 1; pg 108, Table; pg 207, Table.	1-13
Y	US 2010/0086932 A1 (ALCAREZ ASENSIO et al.) 8 April 2010 (08.04.2010), abstract; para [0085].	1-13
Y	US 2006/0019256 A1 (CLARKE et al.) 26 January 2006 (26.01.2006), abstract; para [0013], [0050], [0085].	1-13
Y	US 2008/0207483 A1 (VOLINIA) 28 August 2008 (28.08.2008), abstract; para [0029], pg 8, Table 1.	1-13
Y	WO 2010/074924 A1 (JONES et al.) 1 July 2010 (01.07.2010), abstract; pg 14, ln 19; pg 125, ln 15.	1-13

☐ Further documents are listed in the continuation of Box C.



* 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 application or patent 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 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

"&" document member of the same patent family

Date of the actual completion of the international search

28 August 2012 (28.08.2012)

Date of mailing of the international search report

19 SEP 2012

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents

P.O. Box 1450, Alexandria, Virginia 22313-1450

Facsimile No. 571-273-3201

Authorized officer:

Lee W. Young

PCT Helpdesk: 571-272-4300

PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 12/43852

Continuation of (B) Fields Searched - Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

PubWEST (PGPB,USPT,EPAB,JPAB); Google Scholar; NCBI, esp@cenet: bladder, cancer, biomarker, human, tissue, fluid, serum, urine, nucleic acid, antibody, MMP11, MMP12, COL10A1, FCRLB, SFN, KRT6A, S100A2, S100A7, IL1A, KRT16, SLC1A6, ST3, SL-3, STMY3, HME, MME, MMP-12, COL10A1, FcRY, FCRL2, FCRLY, FCRLM2, FREB-2, YWHAS, K6A, K6C, K6D, CK6A, CK6C, CK6D, KRT6C, KRT6D, CAN19, S100L, PSOR1, S100A7c, IL1, IL-1A, IL1F1, IL1-ALPHA, K16, CK16, K1CP, NEPPK, FNEPPK, KRT16A, EAAT4, Biotime, Oncocyte, Karen Chapman, Michael West, Joseph Wagner