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(54) Title: MOLECULAR PROFILING OF A LETHAL TUMOR MICROENVIRONMENT

(57) Abstract: Presented herein are useful biological markers related to cancers with stromal components. These newly identified biological markers are useful as prognostic signatures for assessing cancer prognosis in subject having cancer (e.g., risk of cancer recurrence, progression of a cancer in a cancer subject, overall survival of cancer by a cancer patient). They can also be implemented as a method of monitoring progression of breast cancer in subjects undergoing treatment for cancer or as a method of stratifying a subject or a group of subjects having a cancer tumor for a clinical trial.



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MOLECULAR PROFILING OF A LETHAL TUMOR MICROENVIRONMENT

FIELD OF THE INVENTION.

[0001] The present invention relates to the biological markers that are useful in the course of detection and/or treatment of cancer.

5 BACKGROUND OF THE INVENTION

[0002] Cancer is one of the most significant diseases confronting mankind, and even though progress has been made in cancer treatment, particularly in the medical therapy of cancer, many challenges remain. In medical therapy of cancer, for example, the various anticancer agents for suppressing the growth of cancer cells that have been developed suppress the growth of not only
10 cancer cells, but also normal cells, causing various side effects including nausea and vomiting, hair loss, myelosuppression, kidney damage, and nerve damage. Consequently, understanding the origins of these malignancies and their microenvironments will facilitate development of more precise diagnostic tools and more effective therapeutic strategies that minimize maximize therapeutic benefits and minimize toxicity for the patients undergoing treatment for cancer.

15 [0003] Some research suggests that the environment around a cancer, for example, interstitial tissue which includes blood vessels, extracellular matrix (ECM), and fibroblasts, may play a role in the onset and progression of cancer. For example, Camps et al. (Proc. Natl. Acad. Sci. USA 1990, 87(1), 75-79) reported that when an athymic nude mouse was inoculated with tumor cells that do not form a tumor on their own or for which the tumor formation rate is low, together with
20 tumorigenic fibroblasts, rapid and marked formation of a tumor was observed, and Olumi et al. (Cancer Res. 1999, 59(19), 5002-5011) reported that when peritumoral fibroblasts (i.e., cancer-associated fibroblasts or CAFs) from a prostate tumor patient were grafted on an athymic animal together with human prostate cells, neoplastic growth thereof was markedly accelerated. Furthermore, it has been clarified that a bioactive substance such as PDGF (platelet-derived
25 growth factor), TGF- β (transforming growth factor- β), HGF (hepatocyte growth factor), or SDF-1 (stromal cell-derived factor-1) produced in the interstitium is involved in such growth of a tumor (Micke et al., Expert Opin Ther Targets. 2005, 9(6), 1217-1233).

[0004] Despite these findings, many questions remain unanswered with respect to regulation of gene expression in the cancer microenvironment, innate and adaptive immunity in the cancer
30 microenvironment, inflammation and cancer, tumor-associated stroma and extracellular matrix, tumor-endothelium interactions (angiogenesis, extravasation), cancer stem cells, the metastatic

niche, and effective targeting of the tumor microenvironment both in preclinical and clinical trials. As a result, most treatments of cancers, including surgical and adjuvant therapies of patients with conventional chemotherapeutic agents, remain largely empirical, guided mostly by measured histological tumor parameters in the absence of specific mechanistic understanding.

5 [0005] Previously, it has been shown that a loss of stromal caveolin-1 can be a useful biomarker of a “lethal” tumor microenvironment. In triple negative breast cancers, for example, a loss of stromal Cav-1 was associated with a five-year survival rate of less than 10%. By contrast, triple negative patients from the same cohort, but having high stromal Cav-1 levels, had a twelve-year survival rate of greater than 75%. In ductal carcinoma in situ (DCIS) patients, a
10 loss of stromal Cav-1 was predictive of disease recurrence and progression to invasive breast cancer. In this particular study, all of the DCIS patients with a loss of stromal Cav-1 were reported to have undergone disease recurrence and 80% of them were reported to have progressed from DCIS to invasive disease. In prostate cancer, a loss of stromal Cav-1 was predictive of advanced prostate cancer, with a high Gleason score, and was also associated with
15 lymph-node or bone metastasis. (see: Sloan E.K. et al., “Stromal Cell Expression of Caveolin-1 Predicts Outcome in Breast Cancer” *Am J. Pathol.* 2009, 174, 2035-43; Witkiewicz A.K., “Towards a new “stromal-based” classification system for human breast cancer prognosis and therapy” *Cell Cycle* 2009, 8, 1654-8; Witkiewicz A.K., “Stromal caveolin-1 levels predict early DCIS progression to invasive breast cancer” *Cancer Biol. Ther.* 2009, 8, 1167-75; Witkiewicz
20 A.K., “Loss of Stromal Caveolin-1 Expression Predicts Poor Clinical Outcome in Triple Negative and Basal-like Breast Cancers” *Cancer Biology & Therapy* 2010, 10,135-43; and Witkiewicz A.K., “An Absence of Stromal Caveolin-1 Expression Predicts Early Tumor Recurrence and Poor Clinical Outcome in Human Breast Cancers” *Am. J. Pathol.* 2009, 174, 2023-34). Taken together, these reports suggest that a loss of stromal Cav-1 portends rapid
25 disease progression and death for a broad spectrum of epithelial tumor types. However, many questions remain as to why a loss of stromal Cav-1 should significantly influence patients’ prognosis and cancer progression.

[0006] Accordingly, there is an urgent need in the medical field for better diagnostic and prognostic indicators and better mechanistic understanding of tumor microenvironment to guide
30 the vigor and extent of surgical and adjuvant therapies of patients, especially those with early stage cancer.

[0007] In one aspect, the present disclosure provides a prognostic signature (also referred to herein as a biological marker or biomarker) for assessing cancer prognosis in a subject, comprising a set of one or more genes (or gene products) derived from a genome-wide transcriptional profiling of a cancer tumor stroma. In an embodiment, the prognostic signature is a Cav-1-deficient tumor stromal signature and comprises a set of at least one or more gene transcripts selected from the gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof. In another embodiment, the Cav-1-deficient tumor stromal signature comprises a first set of one or more gene transcripts that are up-regulated in the tumor stromal material and/or a second set of one or more gene transcripts that is down-regulated in the tumor stromal material. In another embodiment, said tumor stromal signature comprises a set of one or more gene transcripts that is up-regulated in the tumor stromal material, wherein said set of at least one or more up-regulated gene transcripts is selected from the up-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof. In another embodiment, said tumor stromal signature comprises a set of one or more gene transcripts that is down-regulated in the tumor stromal material, wherein said set of at least one or more down-regulated gene transcripts is selected from down-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof.

[0008] In another embodiment, said tumor stromal signature comprises a first set of one or more gene transcripts that is up-regulated in the tumor stromal material, wherein said first set of at least one or more up-regulated gene transcripts is selected from the up-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof; and a second set of one or more gene transcripts that is down-regulated in the tumor stromal material, wherein said second set of at least one or more down-regulated gene transcripts is selected from down-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof.

[0009] In another embodiment, the Cav-1-deficient tumor stromal signature is derived from a breast cancer tumor stroma. In another embodiment, the Cav-1-deficient tumor stromal signature is derived from a breast cancer stroma, wherein the breast cancer is of a subtype selected from the group consisting of ER positive (or ER(+)), ER negative (or ER(-)), and HER2 positive (or HER2(+)).

[0010] In another aspect, the present disclosure provides a method of assessing cancer prognosis, wherein the method comprises: (a) determining a genome-wide transcriptional profile of a first stromal material, wherein the first stromal material is derived from a biological sample obtained from a subject afflicted with cancer or suspected of having cancer; (b) comparing the genome-wide transcriptional profile (or a set of gene transcripts subgenome-transcriptional profile derived therefrom) to a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises a set of at least one or more gene transcripts selected from the gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof, whereby an overlap of from about 25% to about 75% between the genome-wide transcriptional profile (or a subgenome-transcriptional profile derived therefrom) and the Cav-1-deficient tumor stromal signature indicates a poor prognosis (e.g., risk of recurrence the cancer, decreased overall survival of the cancer, increased risk of progression of the cancer, increased risk of metastasis of the cancer).

[0011] In one embodiment, the method of assessing cancer prognosis, comprises: (a) determining a genome-wide transcriptional profile of a biological sample, wherein the biological sample is obtained from a subject afflicted with cancer or suspected of having cancer; (b) comparing the genome-wide transcriptional profile (or a set one or more gene transcripts comprising gene transcripts up-regulated and/or gene transcripts down-regulated or both gene transcripts up-regulated and gene transcripts down-regulated in the biological sample) to a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises at least a set of one or more gene transcripts selected from the gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof, whereby an overlap of from about 25% to about 75% between the genome-wide transcriptional profile and the Cav-1-deficient tumor stromal signature indicates a poor prognosis (e.g., risk of recurrence the cancer, decreased overall survival of the cancer, increased risk of progression of the cancer, increased risk of metastasis of the cancer).

[0012] In yet another aspect, the present disclosure provides a method of monitoring progression of cancer, including breast cancer, in a subject, the method comprising: (a) obtaining a first sample from a subject at a first time point and a second sample from said subject at a second time point; (b) determining a genome-wide transcriptional profile of said first and second samples; (c) comparing the genome-wide transcriptional profile of said first sample to the genome-wide transcriptional profile of said second sample; and (d) thereafter, comparing any difference in transcriptional profile between the genome-wide transcriptional profile of said first sample and the genome-wide transcriptional profile of said second sample to a Cav-1-deficient

tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises a set of at least one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof, whereby an overlap of from about 25% to about 75% is indicative of a poor clinical outcome (e.g., recurrence of the cancer in said subject, or decreased overall survival of the cancer by the subject, or is an indication that the cancer has progressed in said subject, or is an indication that the cancer has metastasized in said subject).

[0013] In another aspect, the present disclosure provides a method of stratifying a subject or a group of subjects having a cancer tumor for a clinical trial. In an embodiment, the method comprises: (a) providing a stromal material, wherein first stromal material is derived from a biological sample obtained from a subject having a cancer tumor; (b) determining a genome-wide transcriptional profile of the stromal material; (c) comparing the genome-wide transcriptional profile of said stromal material to a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises at least a set one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof; and (c) stratifying the subject for a clinical trial based on the results of the comparison step (c). In another embodiment an overlap of from about 25% to about 75% is indicative of stratification class of the subjects.

[0014] In one embodiment, the method of stratifying a subject or a group of subjects having a cancer tumor for a clinical trial comprises: (a) providing a biological sample, wherein biological sample is obtained from a subject having a cancer tumor; (b) determining a genome-wide transcriptional profile of the biological sample; (c) comparing the genome-wide transcriptional profile of said said biological sample to a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises at least one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof; and (c) stratifying the subject for a clinical trial based on the results of the comparison step (c). In one embodiment, overlap of from about 25% to about 75% is indicative of the stratification class of the subjects.

BRIEF DESCRIPTION OF THE DRAWINGS

[0015] **Figure 1** illustrates that stromal Cav-1 can be used to stratify human breast cancer patients into two transcriptionally distinct patient populations (comparison of the transcriptional profiles of Cav-1-positive (+) tumor stroma (N = 4) *versus* Cav-1-negative tumor stroma (N = 7));

[0016] **Figure 2** illustrates heatmaps of gene transcripts associated with myofibroblast differentiation, autophagy, lysosomal degradation, and glycolysis;

[0017] **Figure 3** illustrates heatmaps of gene transcripts associated with the response to hypoxia and mitochondria;

5 [0018] **Figure 4** illustrates heatmaps of gene transcripts associated with inflammation and redox/stress signaling;

[0019] **Figure 5** illustrates heatmaps of gene transcripts associated with dna damage and repair;

[0020] **Figure 6** illustrates heatmaps of gene transcripts associated with aging, apoptosis, and
10 brca1-mutation positive breast cancer patients;

[0021] **Figure 7** illustrates heatmaps of gene transcripts associated with ER-negative breast cancers;

[0022] **Figure 8** illustrates heatmaps of gene transcripts associated with neural stem cells;

[0023] **Figure 9** illustrates Venn diagrams for the intersection of the cav-1-deficient stromal
15 gene signature with other breast cancer tumor stromal gene sets;

[0024] **Figure 10** illustrates the Cav-1-deficient stromal gene signature is up-regulated in breast cancer and is associated with tumor recurrence;

[0025] **Figure 11** illustrates the Cav-1-deficient stromal gene signature is associated with tumor recurrence and poor survival in ER(+) and luminal A breast cancer patients; and

20 [0001] **Figure 12** illustrates understanding the hierarchy of the cellular processes associated with a Cav-1-deficient tumor microenvironment.

[0026] **LIST OF TABLES**

[0027] All tables referenced in this application and listed below are provided in Appendix A which is attached herewith.

25 [0028] **Table 1:** Cellular Processes that are Associated with a Lethal Tumor Micro-Environment in Human Breast Cancer (Cav-1 Deficient Stroma);

- [0029] **Supplemental Table 1:** Comparison of the transcriptional profiles of Cav-1-positive (+) tumor stroma (N = 4) *versus* Cav-1-negative tumor stroma (N = 7) revealed 238 gene transcripts that were up-regulated and 232 gene transcripts that were down-regulated in the stroma of tumors showing a loss of Cav-1 expression;
- 5 [0030] **Supplemental Table 4:** Intersection with Myofibroblast and Muscle-Related Proteins;
- [0031] **Supplemental Table 5:** Intersection with Autophagy and Lysosome Associated Gene Products;
- 10 [0032] **Supplemental Table 6:** Intersection with the Immune Response and TNF/NFkB Signaling;
- [0033] **Supplemental Table 7:** Intersection with Breast Tumors Derived from BRCA1-positive Patients;
- [0034] **Supplemental Table 7:** Intersection with Breast Tumors Derived from BRCA1-positive Patients;
- 15 [0035] **Supplemental Table 8:** Intersection with Breast Tumors Derived from ER-negative Patients;
- [0036] **Supplemental Table 9:** Intersection with Key Regulators of Apoptosis;
- [0037] **Supplemental Table 10:** Intersection with Glycolysis, Hypoxia, and Oxidative Stress;
- 20 [0038] **Supplemental Table 11:** Intersection with Genes Upregulated During DNA Damage and Repair;
- [0039] **Supplemental Table 12:** Intersection with Mitochondrial Associated Proteins;
- [0040] **Table 13:** Intersection with Neural Stem Cell Associated Genes;
- [0041] **Supplemental Table 14:** Intersection with Aging Associated Genes;
- 25 [0042] **Supplemental Table 15:** contains the 3,459 unique genes that were up-regulated in the stroma of tumors showing a loss of stromal Cav-1 expression; and

[0043] **Supplemental Table 16** contains the 1,297 unique genes that were up-regulated in the stroma of tumors showing a loss of stromal Cav-1 expression.

DETAILED DESCRIPTION OF THE INVENTION

[0044] Transcriptional profiling, among other things, includes analysis of the relative abundance of messenger RNA transcribed from different genes. Transcriptional profiling can be used to facilitate the understanding of patterns of gene expression that are associated with all biological processes, including development, differentiation, response to environmental stresses, and other cellular and organismal functions of interest. The ability to analyze patterns of gene expression can lead to discovery of new genes associated with biological processes. A detailed understanding of gene regulation at the transcriptional level is also a premier concern of the pharmaceutical industry, enabling identification of genetic targets for drug development and leading to the understanding of the well known heterogeneity in the way different individuals respond to pharmaceutical interventions. Transcriptional profiling may be conducted by the techniques of "differential display" (see, for example, Liang, P. and Pardee, A. B. *Science* 1992, 257, 967-971; Liang, *et al.*, *Nucl. Acids Res.* 1994, 22, 5763-5764; Prashar, Y. and Weissman, S. M. *Proc. Nat'l. Acad. Sci., U.S.A.* 1996, 93, 659-663.) and "representational difference analysis" (see, for example, Hubank, M. and Schatz, D. G. *Nucl. Acids Res.* 1994, 22, 5640-5648; Lisitsyn, N. A. *Trends Genet.* 1995, 11, 303-307), both of which involve PCR, and gel electrophoretic analysis of DNA fragments. However, it would be appreciated by those skill in the art that other techniques exist that enable quantitation of a very large number of gene transcripts.

[0045] Accordingly, in one aspect, the present disclosure provides new transcriptional gene signatures that can effectively be used for prognostic and therapeutic stratification of cancer tumors: According to exemplary embodiments of the present invention, said transcriptional gene signatures comprise at least a set of one or more gene transcripts, wherein the set of one or more gene transcripts is selected from the group consisting of gene transcripts having gene names and/or gene symbols listed in Table 1, or any one of Supplementary Tables 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 or combinations thereof. The sequence listings associated with the accession numbers, Entrez gene Id, Unigene Id, gene symbols, gene names, alias gene symbols, and Target Acc set forth in any one of Table 1 and Supplementary Tables 1-16 are hereby incorporated by reference as if set forth fully herein.

[0046] In one embodiment, transcriptional gene signatures are used to unambiguously stratify patients based on their stromal Cav-1 status, into Cav-1 (+) and Cav-1 (-) sub-groups, thus,

greatly facilitating prediction of their prognosis. In another embodiment, the transcriptional gene signatures of the present invention are used in therapeutic stratification of cancer patients. The present inventors have used transcriptional profiling of cancer patients to facilitate the understanding of patterns of gene expression that are associated with biological processes that are activated in cancer tumor cells in the presence and absence of Cav-1 in the cancer tumor stroma, thereby delineating novel mechanistic insights into how the the status of Cav-1 in the cancer tumor stroma modulates cancer tumor progression, recurrence of cancer tumor and/or metastasis of cancer. In one embodiment, mechanistic insights into how the status of Cav-1 in the breast cancer tumor stroma modulates the breast cancer tumor progression, recurrence of cancer tumor and/or metastasis of the breast cancer is provided.

[0047] The present inventors isolated tumor stroma from breast cancer patients with a loss of stromal Cav-1 and patients with high stromal Cav-1, for direct comparison and demonstrated that the Cav-1 deficient tumor stroma from human breast cancer patients shows transcriptional evidence for the same biological processes that have been implicated in the “Autophagic Tumor Stroma Model of Cancer”. These biological processes include oxidative stress/aging, hypoxia, a compensatory increase in mitochondria-associated genes, NFkB-activation, inflammation, DNA damage, aerobic glycolysis, autophagy/apoptosis, lysosomal degradation, and “stemness” (summarized in **Figure 12**). These same biological processes are also transcriptionally activated in mesenchymal stromal cells derived from the bone marrow of Cav-1 (-/-) null mice^{16, 31, 32}, and reflect oxidative stress and mitochondrial dys-function, leading to a glycolytic phenotype.

[0048] The present inventors also observed strong association between Cav-1 deficient tumor stroma and ER(-) breast cancer. In particular, gene profiles from Cav-1 deficient tumor stroma were elevated in all breast cancers, relative to normal healthy breast tissue. However, there was a stronger association with ER(-) negative breast cancers, that were identified either by ER IHC or via ESR1 transcriptional analysis (summarized in **Figure 10**). Furthermore, an association was observed with an ER(-) gene signature via gene set enrichment analysis (GSEA) (summarized in **Figure 7**), as well as hereditary breast cancer patients that harbor BRCA1-mutations (summarized in **Figure 6**). Importantly, these associations were all made with existing gene set data that were derived from whole breast tumors that were not laser-captured to isolate their stroma. Thus, these results demonstrate that the presently disclosed stromal signatures can be used effectively in conjunction with gene profiling data obtained from whole or portions of breast tumors.

[0049] Accordingly, one aspect of the present invention relates to use of the stromal Cav-1 deficient gene signature disclosed herein to predict clinical outcome in cancer patients, including breast cancer patients. In one embodiment, the stromal Cav-1 deficient gene signature in accordance with the present invention is used to predict recurrence of cancer, or progression of cancer and/or decreased overall survival in cancer patients, including ER(+) and luminal A breast cancer patients. In an exemplary embodiment, the present inventors have shown that the Cav-1-deficient stromal signature of the present invention is strongly associated with increased recurrence and decreased overall survival in ER(+) and luminal A breast cancer patients, despite the fact that these breast cancer-derived tumors were not subjected to laser capture microdissection prior to the transcriptional profiling. Thus, the tumor stromal signatures of the present invention can be used either alone or in conjunction with other diagnostic tests, including immuno-histochemical (IHC) staining.

[0050] Tumors with a “fibrotic focus” or “central scar” are reportedly associated with a poor prognosis^{36,37}. In accordance with this notion, it was observed that keloid fibroblasts (derived from non-tumorous “scarred skin”) show many of the same characteristics as Cav-1 deficient tumor stroma, with activation of HIF1-alpha and NFkB, as well as a shift towards aerobic glycolysis^{27,38,39}, thus, suggesting a mechanistic connection between loss of Cav-1 as a driver of tissue fibrosis, tumor progression, and metastasis⁴⁰. Consistent with this notion, a fibrotic focus in breast cancers is thought to be a surrogate marker for hypoxia^{36,37}. Similarly, a loss of Cav-1 drives activation of TGF-beta signaling in fibroblasts^{19,41-43}, and treatment of fibroblasts with the TGF-beta ligand is sufficient to induce autophagy⁴⁴ and aerobic glycolysis⁴⁵, possibly explaining the association of tumor fibrosis with a poor prognosis in cancer patients.

[0051] It has been discovered that gene set enrichment analysis (GSEA) of the tumor stroma of breast cancer patients with a loss of stromal Cav-1 showed the dramatic the up-regulation of gene transcripts normally associated with DNA damage and repair (summarized in **Figure 5**) and breast tumors with BRCA1-mutations (summarized in **Figure 6**). Thus, stromal reactive oxygen species (ROS) production, resulting in stromal DNA damage, may be an underestimated driver of tumor progression and metastasis. These findings may also have relevance for the guiding the use of DNA damaging agents and/or Poly(ADP-ribose) polymerase (PARP) inhibitors, as potential treatments for breast cancer patients with Cav-1-deficient stroma.

[0052] Accordingly, one aspect of the present invention provides a method of therapeutic stratification of cancer patients, said method comprising: (a) providing a stromal material, wherein first stromal material is derived from a biological sample obtained from patients having

a cancer tumor; (b) determining a genome-wide transcriptional profile of the stromal material, wherein the transcriptional profile comprises at least a set of one or more gene transcripts up-regulated and/or at least a set of one or more gene transcripts down-regulated in the stromal material; (c) comparing the genome-wide transcriptional profile (e.g., the set of at least one or more gene transcripts up-regulated and/or at least one or more gene transcripts down-regulated in the stromal material) of said stromal material with at least one or more Cav-1-deficient tumor stromal signatures, wherein the at least one or more Cav-1-deficient tumor stromal signatures comprise at least a set of one or more gene transcripts selected from the group consisting of gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof; and (d) stratifying the subject for a clinical trial based on the results of the comparison step (c). In one embodiment, the Cav-1-deficient tumor stromal signature comprises gene transcripts up-regulated in the Cav-1 deficient tumor stroma, wherein the gene transcripts up-regulated in the Cav-1 deficient stroma comprise a set of at least one or more up-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof. In one embodiment, the Cav-1-deficient tumor stromal signature comprises gene transcripts down-regulated in the Cav-1 deficient tumor stroma, wherein the gene transcripts down-regulated in the Cav-1 deficient stroma comprise a set of at least one or more down-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof.

[0053] . In yet another embodiment, the Cav-1-deficient tumor stromal signatures comprise gene transcripts up-regulated in the Cav-1 deficient tumor stroma and gene transcripts down-regulated in the Cav-1 deficient tumor stroma, wherein the gene transcripts up-regulated in the Cav-1 deficient stroma and the gene transcripts down-regulated in the Cav-1 deficient stroma comprise a set of at least one or more up-regulated gene transcripts and down-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof.

[0054] In another embodiment, the method of therapeutic stratification of cancer patients, comprises: (a) providing a biological sample obtained from patients having a cancer tumor; (b) determining a genome-wide transcriptional profile of the biological sample, wherein the transcriptional profile comprises at least a set of one or more gene transcripts up-regulated and/or at least a set of one or more gene transcripts down-regulated in the biological sample; (c) comparing the genome-wide transcriptional profile (e.g., the set of at least one or more gene transcripts up-regulated and/or at least one or more gene transcripts down-regulated in the

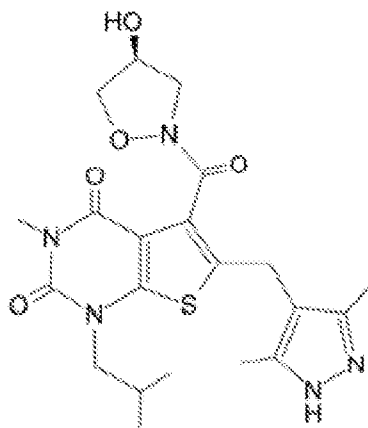
biological sample) of said biological sample with Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises at least a set of one or more sets of gene transcripts, wherein the at least one or more sets of gene transcripts comprise gene transcripts selected from the group consisting of gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof; and (d) stratifying the subject for a clinical trial based on the results of the comparison step (c).

[0055] In certain embodiments, the comparison of transcriptional profiles reveals stromal reactive oxygen species (ROS) production, as the driver of stromal DNA damage and tumor progression and metastasis. Accordingly, in further embodiments, the comparison results are used to identify cancer patients more likely to benefit from treatment with certain therapeutic agents, including DNA damaging agents and/or Poly(ADP-ribose) polymerase (PARP) inhibitors. In another embodiment, the comparison of the transcriptional profiles can be used to identify cancer patients more likely to benefit from treatment with Monocarboxylate Transporter (MCT1) inhibitors and/or a combination of PARP inhibitors and MCTI inhibitors.

[0056] Poly(ADP-ribose)polymerase-1 (PARP-1) is a nuclear enzyme that has been implicated in several mechanisms, including the mechanisms leading to postischemic neuronal death. Accordingly, PARP inhibitors have been proposed as potential therapeutic agents for treatment of various cancers as well as neuroprotective agents. PARP inhibitors are known in the art and may also be elucidated using various techniques. Non-limiting examples of PARP inhibitors include such as Iniparib (BSI-201), olaparib (AZD-2281), and veliparib (ABT-888), 3-aminobenzamide, 4-aminobenzamide, 3-aminophthalhydrazide, 1,5-dihydroxyisoquinoline. Preferred PARP inhibitors include benzamide, 3-aminophthalhydrazide, 1,5-dihydroxyisoquinoline, 6(5H)-Phenanthridinone, 4-Amino-1,8-naphthalimide, 1,5-Isoquinolinediol, 3-Aminobenzamide, and N-(6-oxo-5,6-dihydrophenanthridin-2-yl)-N,N-dimethylacetamide hydrochloride (PJ34). Inhibition of PARP may be effected by a number of approaches. A preferred method of the present invention is to employ specific inhibitors of PARP. For example, specific inhibitors of PARP, such as benzamide, 3-aminobenzamide, 4-aminobenzamide, 3-aminophthalhydrazide and 1,5-dihydroxyisoquinoline, may be used to inhibit apoptosis induced by PARP activity. U.S. Pat. No. 5,756, 510 (Griffin et al.) discloses benzamide analogs having PARP inhibitory efficacy and those compounds may be used in the present invention methods and compositions; the entire contents of which are incorporated herein by reference. U.S. Pat. No. Re. 36,397 (Zhang et al.) discloses PARP inhibitors useful for vascular stroke and neurodegenerative disorders and those compounds may be used in the present

invention methods and compositions. The PARP inhibitors for use in conjunction with the biological markers and methods of the present invention may also be determined by various assays described in the literature. The following publications teach various methods which may be employed to elucidate PARP inhibitors: (1) U.S. Pat. No. 5,756,510 (Griffin et al.); (2) Banasik et al. Specific inhibitors of poly(ADP-ribose) synthetase and mono(ADP-ribose) transferase., J Biol Chem, volume 267, pages 1569-1575 (1992); and (3) Schanraufstatter et al. Oxidant injury of cells. DNA strand-breaks activate polyadenosine diphosphate-ribose polymerase and lead to depletion of nicotinamide adenine dinucleotide, J Clin Invest, volume 77, pages 1312-1320 (1986); the entire contents of the foregoing literature references are incorporated herein by reference.

[0057] Other suitable therapeutic agents for use with the transcriptional gene signatures and methods of the present invention include metformin and Monocarboxylate Transporter (MCT1) inhibitors, including AR-C117977 and AR-C155858 and pharmaceutically acceptable salts thereof. AR-C155858 has the following structural formula.



[0058]

[0059] Examples of suitable MCT1 inhibitors are disclosed in WO 2010/089580 (published 12 August 2010).

[0060] In some embodiments, the comparison of a set of two or more transcriptional profiles derived from biological samples obtained from the same or different biological sources (e.g., individuals), as described herein, includes identification of relative changes in the levels of gene transcripts in the respective samples. In some embodiments, the comparison at least a set of two or more transcriptional profiles are used to identify a subject or a group of subjects with a significant probability of a poor clinical outcome. In another embodiment, comparisons of transcriptional gene profiles are used to identify cancer patients that are more likely to benefit from one or more therapeutic agents. In a further embodiment, the comparison of the set of two or

more transcriptional profiles is used to identify a subject or a group of subjects with a significant probability of benefiting from treatment with existing or new therapeutic agents, including PARP inhibitors and/or MCTI inhibitors. In another embodiment, the probability that a patient or a group of patients are expected to benefit from treatment with PARP inhibitors alone or

5 MCTI inhibitors alone or in combinations with PARP inhibitors is from about 25% to about 30%, from about 25% to about 35%, from about 25% to about 45%, from about 25% to about 50%, from about 25% to about 55%, from about 25% to about 60%, from about 25%, to about 65%, from about 25% to about 70%, from about 25%, to about 75%, from about 30% to about 35%, from about 30% to about 45%, from about 30% to about 50%, from about 30% to about 55%,
 10 from about 30% to about 60%, from about 30%, to about 65%, from about 30% to about 70%, from about 30%, to about 75%, from about 35% to about 45%, from about 35% to about 50%, from about 35% to about 55%, from about 35% to about 60%, from about 35%, to about 65%, from about 35% to about 70%, from about 35%, to about 75%, from about 40% to about 45%, from about 40% to about 50%, from about 40% to about 55%, from about 40% to about 60%,
 15 from about 40%, to about 65%, from about 40% to about 70%, from about 40%, to about 75%, from about 45% to about 50%, from about 45% to about 55%, from about 45% to about 60%, from about 45% to about 65%, from about 45% to about 70%, from about 45% to about 75%, from about 50% to about 55%, from about 50% to about 60%, from about 50% to about 65%, from about 50% to about 70%, from about 50% to about 75%, from about 55% to about 60%,
 20 from about 55% to about 65%, from about 55% to about 70%, from about 55% to about 75%, from about 60%, to about 65%, from about 60% to about 70%, from about 60% to about 75%, from about 65% to about 70%, from about 65% to about 75%, or from about 70% to about 75%.

[0061] In some embodiments, comparison of transcriptional profiles in accordance with the present invention identifies a cancer patients or a group of cancer patients having a probability of
 25 from about 25% to about 75% of a poor clinical outcome, wherein the poor clinical outcome is selected from the group consisting of cancer recurrence, progression of a cancer, overall survival of cancer, cancer metastasis and combinations thereof. In another embodiment, the probability of a poor clinical outcome is from about 25% to about 30%, from about 25% to about 35%, from about 25% to about 45%, from about 25% to about 50%, from about 25% to about 55%, from
 30 about 25% to about 60%, from about 25%, to about 65%, from about 25% to about 70%, from about 25%, to about 75%, from about 30% to about 35%, from about 30% to about 45%, from about 30% to about 50%, from about 30% to about 55%, from about 30% to about 60%, from about 30%, to about 65%, from about 30% to about 70%, from about 30%, to about 75%, from about 35% to about 45%, from about 35% to about 50%, from about 35% to about 55%, from

about 35% to about 60%, from about 35%, to about 65%, from about 35% to about 70%, from about 35%, to about 75%, from about 40% to about 45%, from about 40% to about 50%, from about 40% to about 55%, from about 40% to about 60%, from about 40%, to about 65%, from about 40% to about 70%, from about 40%, to about 75%, from about 45% to about 50%, from about 45% to about 55%, from about 45% to about 60%, from about 45% to about 65%, from about 45% to about 70%, from about 45% to about 75%, from about 50% to about 55%, from about 50% to about 60%, from about 50% to about 65%, from about 50% to about 70%, from about 50% to about 75%, from about 55% to about 60%, from about 55% to about 65%, from about 55% to about 70%, from about 55% to about 75%, from about 60%, to about 65%, from about 60% to about 70%, from about 60% to about 75%, from about 65% to about 70%, from about 65% to about 75%, or from about 70% to about 75%.

[0062] It has also been discovered that the over-expression of several different markers of autophagy or oxidative stress in the tumor stroma are associated with increased lympho-vascular invasion, increased lymph-node metastasis, or poor clinical outcome, in a variety of different epithelial cancer subtypes. These markers include ATG16L1 and the cathepsins (K and D) for autophagy, as well as carbonic anhydrase IX (CAIX) and HIF1-alpha for oxidative stress⁴⁹⁻⁵⁶.

[0063] Re-analysis of published transcriptional profiles¹⁵ of laser-captured tumor stroma, isolated from human breast cancers, by the present inventors revealed strong evidence for the enrichment of autophagy genes, lysosomal markers, as well as indicators of oxidative stress (such as peroxisomes), which were associated with tumor recurrence and metastasis^{16, 30}. These tumor stroma transcriptional profiles also showed significant overlap with transcriptional profiles of Cav-1 (-/-) null stromal cells^{16, 30, 31}, and Alzheimer's disease brain (known to be associated with oxidative stress)^{16, 31}. In fact the transcriptional profile of Alzheimer's disease brain was most closely related to the tumor stroma of human breast cancer patients that had undergone metastasis¹⁶, implicating stromal oxidative stress in promoting cancer cell metastasis.

[0064] In summary, the present inventors have shown that simple immuno-staining with antibodies directed against Cav-1 can be used effectively to detect two different populations of breast cancer patients (high-risk vs. low-risk), based on their stromal Cav-1 status. Genome-wide transcriptional profiling of these two different stromal populations shows that they are dramatically different, each with a unique transcriptional profile. The present inventors focused on the stromal Cav-1-deficient population, because they are associated with early tumor recurrence, and metastasis. Gene set enrichment analysis (GSEA) of this population provides *in vivo* human data to directly support the "Autophagic Tumor Stroma Model of Cancer", which is

largely focused on oxidative stress, hypoxia, autophagy, and DNA damage in the tumor microenvironment, as well as the pro-inflammatory response (summarized in **Figure 12**).

[0065] 1. TRANSCRIPTIONAL GENE SIGNATURES/BIOLOGICAL MARKERS

[0066] In one embodiment the transcriptional gene signatures of the present invention
 5 comprise a set of at least one or more gene transcripts up-regulated in cancer tumor stroma. In
 another embodiment the transcriptional gene signatures of the present invention comprise a set of
 at least one or more gene transcripts down-regulated in cancer tumor stroma. In another
 embodiment, the cancer tumor stroma is derived from derived from a Cav-1-deficient cancer
 tumor stromal material. In another embodiment, the cancer tumor stroma is derived from derived
 10 from a Cav-1-positive cancer tumor stromal material. As any type of cell in the body may be a
 source of cancer, any suitable types of cancer cells or cellular materials may be used in the
 present invention. A suitable cancer type includes carcinoma (cancer of the epithelial cells),
 sarcoma (cancer of the bone, muscle or other connective tissues), lymphoma (cancer of the
 lymphatic system), leukemia (cancer of blood cells or blood precursor cells) and melanoma
 15 (cancer of the pigment-providing cells). Examples of suitable types of cancer that may be useful
 in conjunction with the various exemplary embodiments of the present invention include, but are
 not limited to, leukemias, such as but not limited to, acute leukemia, acute lymphocytic leukemia,
 acute myelocytic leukemias, such as, myeloblastic, promyelocytic, myelomonocytic, monocytic,
 and erythroleukemia leukemias and myelodysplastic syndrome; chronic leukemias, such as but
 20 not limited to, chronic myelocytic (granulocytic) leukemia, chronic lymphocytic leukemia, hairy
 cell leukemia; polycythemia vera; lymphomas such as but not limited to Hodgkin's disease, non-
 Hodgkin's disease; multiple myelomas such as but not limited to smoldering multiple myeloma,
 nonsecretory myeloma, osteosclerotic myeloma, plasma cell leukemia, solitary plasmacytoma
 and extramedullary plasmacytoma; Waldenstrom's macroglobulinemia; monoclonal gammopathy
 25 of undetermined significance; benign monoclonal gammopathy; heavy chain disease; bone and
 connective tissue sarcomas such as but not limited to bone sarcoma, osteosarcoma,
 chondrosarcoma, Ewing's sarcoma, malignant giant cell tumor, fibrosarcoma of bone, chordoma,
 periosteal sarcoma, soft-tissue sarcomas, angiosarcoma (hemangiosarcoma), fibrosarcoma,
 Kaposi's sarcoma, leiomyosarcoma, liposarcoma, lymphangiosarcoma, neurilemmoma,
 30 rhabdomyosarcoma, synovial sarcoma; brain tumors such as but not limited to, glioma,
 astrocytoma, brain stem glioma, ependymoma, oligodendroglioma, nonglial tumor, acoustic
 neurinoma, craniopharyngioma, medulloblastoma, meningioma, pineocytoma, pineoblastoma,
 primary brain lymphoma; breast cancer including but not limited to ductal carcinoma,

adenocarcinoma, lobular (small cell) carcinoma, intraductal carcinoma, medullary breast cancer, mucinous breast cancer, tubular breast cancer, papillary breast cancer, Paget's disease, and inflammatory breast cancer; adrenal cancer such as but not limited to pheochromocytom and adrenocortical carcinoma; thyroid cancer such as but not limited to papillary or follicular thyroid cancer, medullary thyroid cancer and anaplastic thyroid cancer; pancreatic cancer such as but not limited to, insulinoma, gastrinoma, glucagonoma, vipoma, somatostatin-secreting tumor, and carcinoid or islet cell tumor; pituitary cancers such as but limited to Cushing's disease, prolactin-secreting tumor, acromegaly, and diabetes insipius; eye cancers such as but not limited to ocular melanoma such as iris melanoma, choroidal melanoma, and ciliary body melanoma, and retinoblastoma; vaginal cancers such as squamous cell carcinoma, adenocarcinoma, and melanoma; vulvar cancer such as squamous cell carcinoma, melanoma, adenocarcinoma, basal cell carcinoma, sarcoma, and Paget's disease; cervical cancers such as but not limited to, squamous cell carcinoma, and adenocarcinoma; uterine cancers such as but not limited to endometrial carcinoma and uterine sarcoma; ovarian cancers such as but not limited to, ovarian epithelial carcinoma, borderline tumor, germ cell tumor, and stromal tumor; esophageal cancers such as but not limited to, squamous cancer, adenocarcinoma, adenoid cystic carcinoma, mucoepidermoid carcinoma, adenosquamous carcinoma, sarcoma, melanoma, plasmacytoma, verrucous carcinoma, and oat cell (small cell) carcinoma; stomach cancers such as but not limited to, adenocarcinoma, fungating (polypoid), ulcerating, superficial spreading, diffusely spreading, malignant lymphoma, liposarcoma, fibrosarcoma, and carcinosarcoma; colon cancers; rectal cancers; liver cancers such as but not limited to hepatocellular carcinoma and hepatoblastoma; gallbladder cancers such as adenocarcinoma; cholangiocarcinomas such as but not limited to pappillary, nodular, and diffuse; lung cancers such as non-small cell lung cancer, squamous cell carcinoma (epidermoid carcinoma), adenocarcinoma, large-cell carcinoma and small-cell lung cancer; testicular cancers such as but not limited to germinal tumor, seminoma, anaplastic, classic (typical), spermatocytic, nonseminoma, embryonal carcinoma, teratoma carcinoma, choriocarcinoma (yolk-sac tumor), prostate cancers such as but not limited to, prostatic intraepithelial neoplasia, adenocarcinoma, leiomyosarcoma, and rhabdomyosarcoma; penial cancers; oral cancers such as but not limited to squamous cell carcinoma; basal cancers; salivary gland cancers such as but not limited to adenocarcinoma, mucoepidermoid carcinoma, and adenoidcystic carcinoma; pharynx cancers such as but not limited to squamous cell cancer, and verrucous; skin cancers such as but not limited to, basal cell carcinoma, squamous cell carcinoma and melanoma, superficial spreading melanoma, nodular melanoma, lentigo malignant melanoma, acral lentiginous melanoma; kidney cancers such as but not limited to renal cell carcinoma, adenocarcinoma, hypemephroma, fibrosarcoma, transitional cell cancer (renal pelvis

and/or uterine); Wilms' tumor; bladder cancers such as but not limited to transitional cell carcinoma, squamous cell cancer, adenocarcinoma, carcinosarcoma. In addition, cancers include myxosarcoma, osteogenic sarcoma, endotheliosarcoma, lymphangioendotheliosarcoma, mesothelioma, synovioma, hemangioblastoma, epithelial carcinoma, cystadenocarcinoma, bronchogenic carcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma and papillary adenocarcinomas (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J. B. Lippincott Co., Philadelphia and Murphy et al., 1997, Informed Decisions: The Complete Book of Cancer Diagnosis, Treatment, and Recovery, Viking Penguin, Penguin Books U.S.A., Inc., United States of America).

- 10 [0067] In one embodiment, the transcriptional gene signatures in accordance with the present invention are derived from a genome-wide transcriptional profiling of a tumor stromal material which is derived from a Cav-1-deficient breast cancer tumor stroma, wherein the tumor stromal signatures comprise (a) a first set of up-regulated gene transcripts, wherein the first set of up-regulated gene transcripts comprises at least a set of one or more up-regulated gene transcripts having gene symbols listed Supplemental Tables 1, 3, or combinations thereof; and (b) a second set of down-regulated gene transcripts, wherein the second set of down-regulated gene transcripts comprises at least a set of one or more gene transcripts having gene names and/or gene symbols listed Supplemental Tables 1, 3, or combinations thereof. In one embodiment, up-regulated gene transcripts having gene symbols listed Supplemental Tables 1, 3, or combinations thereof are selected from the group consisting of LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2, SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLC02B1, PTPN1, ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GFI1, AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17,

PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165, MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC, AMZ2, TYROBP, IFNGR2, RIOK2, C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.

[0068] In another embodiment, down-regulated gene transcripts having gene symbols listed Supplemental Tables 1, 3, or combinations thereof are selected from the group consisting of

HNRNPA0, ST3GAL3, LOC100288446, RGNEF, NTRK3, KIFAP3, FAM3A, FAM169A, PLAG1, RAB40A, GOT1, ZNF768, CYP20A1, ASTN2, REPS2, NOL3, SERPINA9, TRA2A, , GYPE, LOC729375, ZFAND2B, BRWD1, PTPRN, ZNF687, DYM, ARMC7, PNPLA8, LMOD1, MFSD11, SERF1B, C6orf130, TMEM138, UFSP1, SREBF2, KRT222, PIGM, C6orf26, FHL2, GLIS3, SLC7A14, ABCA10, DBT, ABLIM3, NOTCH3, PTPRN, DSG3, BACH1, LOC100131109, PLD1, , SIK3, FAM55B, PTGR1, UBE3B, PTPRS, DLG5, ZHX3, SOX5, LOC388152, KCNK1, ITIH5, RARG, ABHD3, IRAK1BP1, TRIM38, SLC19A3, XPO7, PDZD4, ESR1, LOC285147, ZNF193, MPP7, PKD1L2, PDZD4, , KCNQ1OT1, RAD1, KCMF1, LOC100293798, IGF1R, ZFP3, C21orf62, TLR6, CTBP2, , DDX46, FAM156B, RUNDC3B, TMEM138, LOC100131938, UNC13C, ZNF641, OBSCN, C18orf15, UBN2, MPHOSPH9, CRIM1, , SLC25A11, VWC2, DEAF1, DNAJC1, ADORA2B, PARK7, NCRNA00183, MAPK1, WDR34, RCOR3, VEZT, RPL7AP8, NLGN3, LOC100128288, RABL2A, GAB1, RSPH9, AUH, SLC18A2, VCPIP1, EAPP, BTN2A2, C17orf75, C1orf187, LOC643749, LOC100128288, RABL2A, CADPS, ZNF540, LRP2, CCDC96, SEC14L2, FBXO21, WDR78, ADCYAP1, LOC100128286, C6orf26, HRH1, ZNF764, ZNF823, LOC80154, NLK, SNORD20, THRA, XGPY2, SIGLEC6, DHCR24, LOC100129198, PTPN14, MAP7, LOC100128292, LOC646976, ZNF20, TMEM9B, IL17RB, TUBD1, TRIM66, SLC12A8, PDE4DIP, LOC92249, LOC100128651, RGS7, SIGLEC6, SH3BGR, RSPH9, MGC16121, SLC16A6, OAF, SETD4, C8orf84, ZFP90, C7orf63, GAB1, TRIM66, PCSK1N, SNORD121A, GFRA1, GAB1, MS4A2, NHEDC2, HPSE2, PGR, PGR, SLC18A2, AUTS2, AUTS2, KBTBD4, ERBB4, ADCYAP1, ADCYAP1, and combinations thereof.

[0069] In another embodiment, the tumor stromal signatures comprise (a) a first set of up-regulated gene transcripts, wherein the first set of up-regulated gene transcripts comprises at least a set of one or more up-regulated gene transcripts having gene names and/or gene symbols listed

in Supplemental Tables 1, 3, or combinations thereof, wherein the up-regulated gene transcripts are selected from the group consisting of LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6,

5 S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2, SERPINB8, CYP4F11, LOC728613, SNRK,

10 LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLC02B1, PTPN1, ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GFI1, AP4E1, ARHGAP5, C14orf106,

15 SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165, MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC, AMZ2, TYROBP, IFNGR2, RIOK2,

20 C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof; and

and (b) a second set of down-regulated gene transcripts, wherein the second set of down-regulated gene transcripts comprises at least a set of one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof, wherein the down-regulated gene transcripts are selected from the group consisting of HNRNPA0, ST3GAL3, LOC100288446, RGNEF, NTRK3, KIFAP3, FAM3A, FAM169A, PLAG1, RAB40A, GOT1, ZNF768, CYP20A1, ASTN2, REPS2, NOL3, SERPINA9, TRA2A, , GYPE,

30 LOC729375, ZFAND2B, BRWD1, PTPRN, ZNF687, DYM, ARMC7, PNPLA8, LMOD1, MFSD11, SERF1B, C6orf130, TMEM138, UFSP1, SREBF2, KRT222, PIGM, C6orf26, FHL2, GLIS3, SLC7A14, ABCA10, DBT, ABLIM3, NOTCH3, PTPRN, DSG3, BACH1, LOC100131109, PLD1, , SIK3, FAM55B, PTGR1, UBE3B, PTPRS, DLG5, ZHX3, SOX5, LOC388152, KCNK1, ITIH5, RARG, ABHD3, IRAK1BP1, TRIM38, SLC19A3, XPO7,

35 PDZD4, ESR1, LOC285147, ZNF193, MPP7, PKD1L2, PDZD4, , KCNQ1OT1, RAD1,

KCMF1, LOC100293798, IGF1R, ZFP3, C21orf62, TLR6, CTBP2, , DDX46, FAM156B, RUNDC3B, TMEM138, LOC100131938, UNC13C, ZNF641, OBSCN, C18orf15, UBN2, MPHOSPH9, CRIM1, , SLC25A11, VWC2, DEAF1, DNAJC1, ADORA2B, PARK7, NCRNA00183, MAPK1, WDR34, RCOR3, VEZT, RPL7AP8, NLGN3, LOC100128288, 5 RABL2A, GAB1, RSPH9, AUH, SLC18A2, VCIPI1, EAPP, BTN2A2, C17orf75, C1orf187, LOC643749, LOC100128288, RABL2A, CADPS, ZNF540, LRP2, CCDC96, SEC14L2, FBXO21, WDR78, ADCYAP1, LOC100128286, C6orf26, HRH1, ZNF764, ZNF823, LOC80154, NLK, SNORD20, THRA, XGPY2, SIGLEC6, DHCR24, LOC100129198, PTPN14, MAP7, LOC100128292, LOC646976, ZNF20, TMEM9B, IL17RB, TUBD1, TRIM66, 10 SLC12A8, PDE4DIP, LOC92249, LOC100128651, RGS7, SIGLEC6, SH3BGR, RSPH9, MGC16121, SLC16A6, OAF, SETD4, C8orf84, ZFP90, C7orf63, GAB1, TRIM66, PCSK1N, SNORD121A, GFRA1, GAB1, MS4A2, NHEDC2, HPSE2, PGR, PGR, SLC18A2, AUTS2, AUTS2, KBTBD4, ERBB4, ADCYAP1, ADCYAP1, and combinations thereof.

[0070] In another embodiment, the transcriptional gene signature in accordance with the 15 present invention is derived from a genome-wide transcriptional profiling of a tumor stromal material which is derived from a Cav-1-deficient breast cancer tumor stroma, and wherein the tumor stromal signature comprises at least a set of one or more gene transcripts up-regulated in the tumor stromal material, wherein the at least set of one or more gene transcripts comprise gene transcripts having gene names and/or gene symbols selected from the group consisting of: 20 LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, 25 HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2, SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLCO2B1, PTPN1, 30 ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GF11, AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165,

MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC, AMZ2, TYROBP, IFNGR2, RIOK2, C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, 5 BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.

[0071] In another embodiment, the transcriptional gene signature in accordance with the present invention is driven from a genome-wide transcriptional profiling of a tumor stromal 10 material which is derived from a Cav-1-deficient breast cancer tumor stroma, and wherein the tumor stromal signature comprises at least a set of one or more gene transcripts down-regulated in the tumor stromal material, wherein the at least set of one or more gene transcripts comprise gene transcripts having gene names and/or gene symbols selected from the group consisting of: at least a set of one or more genes having gene symbols selected from the group consisting of:

15 HNRNPA0, ST3GAL3, LOC100288446, RGNEF, NTRK3, KIFAP3, FAM3A, FAM169A, PLAG1, RAB40A, GOT1, ZNF768, CYP20A1, ASTN2, REPS2, NOL3, SERPINA9, TRA2A, , GYPE, LOC729375, ZFAND2B, BRWD1, PTPRN, ZNF687, DYM, ARMC7, PNPLA8, LMOD1, MFSD11, SERF1B, C6orf130, TMEM138, UFSP1, SREBF2, KRT222, PIGM, C6orf26, FHL2, GLIS3, SLC7A14, ABCA10, DBT, ABLIM3, NOTCH3, PTPRN, DSG3, 20 BACH1, LOC100131109, PLD1, , SIK3, FAM55B, PTGR1, UBE3B, PTPRS, DLG5, ZHX3, SOX5, LOC388152, KCNK1, ITIH5, RARG, ABHD3, IRAK1BP1, TRIM38, SLC19A3, XPO7, PDZD4, ESR1, LOC285147, ZNF193, MPP7, PKD1L2, PDZD4, , KCNQ1OT1, RAD1, KCMF1, LOC100293798, IGF1R, ZFP3, C21orf62, TLR6, CTBP2, , DDX46, FAM156B, RUNDC3B, TMEM138, LOC100131938, UNC13C, ZNF641, OBSCN, C18orf15, UBN2, 25 MPHOSPH9, CRIM1, , SLC25A11, VWC2, DEAF1, DNAJC1, ADORA2B, PARK7, NCRNA00183, MAPK1, WDR34, RCOR3, VEZT, RPL7AP8, NLGN3, LOC100128288, RABL2A, GAB1, RSPH9, AUH, SLC18A2, VCIPI1, EAPP, BTN2A2, C17orf75, C1orf187, LOC643749, LOC100128288, RABL2A, CADPS, ZNF540, LRP2, CCDC96, SEC14L2, FBXO21, WDR78, ADCYAP1, LOC100128286, C6orf26, HRH1, ZNF764, ZNF823, 30 LOC80154, NLK, SNORD20, THRA, XGPY2, SIGLEC6, DHCR24, LOC100129198, PTPN14, MAP7, LOC100128292, LOC646976, ZNF20, TMEM9B, IL17RB, TUBD1, TRIM66, SLC12A8, PDE4DIP, LOC92249, LOC100128651, RGS7, SIGLEC6, SH3BGR, RSPH9, MGC16121, SLC16A6, OAF, SETD4, C8orf84, ZFP90, C7orf63, GAB1, TRIM66, PCSK1N,

SNORD121A, GFRA1, GAB1, MS4A2, NHEDC2, HPSE2, PGR, PGR, SLC18A2, AUTS2, AUTS2, KBTBD4, ERBB4, ADCYAP1, ADCYAP1, and combinations thereof.

[0072] A. Transcriptional Profiling of a Cav-1 Deficient Tumor Microenvironment

[0073] Loss of stromal Cav-1 in human breast cancer(s) is associated with tumor recurrence, metastasis, and drug-resistance, conferring poor clinical outcome¹⁻⁵. However, until now nothing was known about the identity and the characteristics of the signaling pathways activated in Cav-1 negative tumor stroma. To mechanistically understand the “lethality” of a Cav-1 negative tumor micro-environment, the present inventors performed laser capture microdissection on the tumor stroma of patients that were pre-classified as stromal Cav-1-positive(+) (N = 4) and stromal Cav-1-negative(-) (N = 7), based on immuno-histochemical (IHC) staining. Then, the RNA extracted from these samples was subjected to genome-wide transcriptional profiling.

[0074] Based on this approach, the present inventors identified 238 gene transcripts that were specifically up-regulated and 232 gene transcripts that were down-regulated in the stroma of tumors showing a loss of Cav-1 expression ($p \leq 0.01$ and fold-change (f.c.) ≥ 1.5) (summarized in **Supplemental Table 1**). Using these stringent criteria, the present inventors were able to transcriptionally separate these two patient populations, in accordance with their IHC stromal Cav-1 status (negative *versus* positive). A HeatMap of the total patient cohort is shown in **Figure 1**, demonstrating that these two patient populations appear transcriptionally and “genetically” distinct.

[0075] B. Gene Set Enrichment Analysis (GSEA) of a Cav-1 Deficient Tumor Microenvironment

[0076] To understand what cellular processes are characteristic of a Cav-1-deficient tumor microenvironment, the present inventors next performed gene set enrichment analysis (GSEA), by comparison with other gene signatures available in various public databases. For this purpose, the present inventors focused on a wider list of gene transcripts that were up-regulated in Cav-1-deficient stroma (5,424 transcripts encoding 3,459 unique genes; $p \leq 0.1$ and fold-change (f.c.) ≥ 1.15) (summarized in **Supplemental Table 2**).

[0077] Results of the GSEA are summarized in **Table 1**. The GSEA results show up-regulation of cellular processes normally associated with “stemness”, inflammation, DNA

damage, oxidative stress, hypoxia, apoptotic signaling, autophagy, and mitochondrial dysfunction in the tumor stroma of patients lacking stromal Cav-1.

[0078] Individual HeatMaps (based on 1,819 transcripts encoding 1,297 unique genes; $p \leq 0.05$ and fold-change (f.c.) ≥ 1.15) (summarized in **Supplemental Table 3**) for key cellular

processes are shown in **Figures 2-8**. These HeatMaps illustrate the upregulation of gene transcripts associated with myofibroblast differentiation, autophagy, lysosomal degradation, glycolysis, hypoxia, mitochondria, inflammation and redox signaling, DNA damage and repair, aging, BRCA1-mutation positive and ER-negative breast cancer patients, apoptosis, and neural stem cells (summarized in **Supplemental Tables 4-14**).

[0079] The observed association between a Cav-1-deficient tumor stroma and neural stem cells may reflect increased stromal “neurogenesis”, which has previously been implicated in an aggressive reactive stromal phenotype in a subset of prostate cancers^{7,8}. Similarly, “neurogenesis” was associated with increased DNA damage in the tumor stroma^{7,8}.

[0080] In addition, the up-regulation of gene transcripts or gene sets associated with GOLPH3, NRF1 (nuclear respiratory factor 1), PRKDC (protein kinase, DNA-activated, catalytic polypeptide), or arsenic treatment is highly suggestive of mitochondrial dysfunction (**Table 1**). NRF1 is normally up-regulated during hypoxic-ischemic injury or oxidative stress, as an attempt to increase mitochondrial biogenesis^{9,10}. GOLPH3 (also known as MIDAS/GPP34) is a nuclear gene whose transcription is enhanced by the absence of mitochondrial DNA (mtDNA)¹¹.

MIDAS stands for mitochondrial DNA absence sensitive factor¹¹. PRKDC is a component of the machinery required for the proper repair and maintenance of the fidelity of mitochondrial DNA (mtDNA)¹², so its up-regulation is suggestive of increase mtDNA damage. Arsenic treatment is associated with increased ROS production, mtDNA damage, and mitochondrial dysfunction, with reduced ATP production, driving the onset of aerobic glycolysis^{13,14}.

[0081] C. Comparison with Other Breast Cancer Stromal Data Sets Obtained by Laser Capture Microdissection

[0082] The results of transcriptional profiling of a Cav-1 deficient tumor Microenvironment and GSEA were compared with an independent previously published transcriptional data set generated by Morag Park and colleagues¹⁵, via laser capture of the tumor stroma of human breast cancers. However, these previously published data were not stratified based on stromal Cav-1 status¹⁵. More specifically, the gene transcripts up-regulated in Cav-1-deficient tumor stroma (1,819 transcripts encoding 1,297 unique genes; $p \leq 0.05$ and fold-change (f.c.) ≥ 1.15)

(**Supplemental Table 3**) were compared with (1) tumor stroma and (2) recurrence stroma gene lists, as defined below:

(1) Tumor Stroma vs. Normal Stroma List: compares the transcriptional profiles of tumor stroma obtained from 53 patients to normal stroma obtained from 38 patients. Genes transcripts that were consistently upregulated in the tumor stroma were selected and assigned a p-value, with a cut-off of $p < 0.05$ (this set contains 6,777 unique genes)¹⁶.

(2) Recurrence Stroma List: compares the transcriptional profiles of tumor stroma obtained from 11 patients with tumor recurrence to the tumor stroma of 42 patients without tumor recurrence. Genes transcripts that were consistently upregulated in the tumor stroma of patients with recurrence were selected and assigned a p-value, with a cut-off of $p < 0.05$ (this set contains 3,354 unique genes)¹⁶.

[0083] **Figure 9** shows that the gene transcripts up-regulated in Cav-1-deficient tumor stroma show significant overlap with tumor stroma (a 440 transcript overlap; $p = 4.76 \times 10^{-9}$) and recurrence stroma (a 214 transcript overlap; $p < 0.001$). Thus, the gene transcripts up-regulated in Cav-1-deficient tumor stroma show a significant association with tumor recurrence, and are in accordance with the results of Morag Park and colleagues¹⁵.

[0084] D. Comparison with the Transcriptional Profiles of Breast Cancers that were Not Subjected to Laser Capture Microdissection

[0085] Most of the published and publicly available transcriptional profiles for breast cancer patients are derived from the analysis of whole tumors, which are not separated into stromal and epithelial compartments prior to analysis. Thus, a comparison of the gene transcripts up-regulated in Cav-1-deficient tumor stroma (summarized in **Supplemental Table 1**), with the transcriptional profiles of normal breast tissue and whole breast tumors was performed^{17, 18}.

[0086] **Figure 10A and B** show that the Cav-1-deficient tumor stromal signature is up-regulated in breast cancer(s), both ER(+) and ER(-) sub-types. However, a more significant association was observed with ER(-) breast cancers. In addition, the Cav-1-deficient stromal signature was also associated with increased recurrence in breast cancer patients (**Figure 10C**).

[0087] Similarly, the prognostic value of the Cav-1-deficient stromal signature was investigated in ER(+) and luminal A breast cancer patients, which account for nearly 60% of all breast cancer patients^{17, 18}. **Figure 11** shows that the Cav-1-deficient stromal signature is clearly

associated with increased recurrence and decreased overall survival, despite the fact that these breast cancer-derived tumors were not subjected to laser capture microdissection.

[0088] While not wishing to be bound by a particular theory, it is believed that cancer cells induce oxidative stress (pseudo-hypoxia) in adjacent fibroblasts, which activate certain key transcription factors (namely HIF1-alpha and NFkB), that then drive the onset of autophagy, leading to the cancer-associated fibroblast phenotype.^{20, 21} HIF1-alpha and NFkB are the master regulator(s) of aerobic glycolysis (the response to hypoxia and oxidative stress) and inflammation, respectively²⁵⁻²⁷. In turn, these autophagic fibroblasts undergo mitophagy, forcing them to use glycolysis as their main energy source.^{20, 21} These autophagic stromal fibroblasts produced high-energy nutrients (lactate, ketones, and glutamine) that could then be used as “fuel” for oxidative mitochondrial metabolism in epithelial breast cancer cells²⁸⁻³⁰. Also, the reactive oxygen species (ROS) that is generated in cancer-associated fibroblasts is associated with DNA-damage (double-strand breaks) in both cancer cells and fibroblasts¹⁹⁻²¹.

[0089] In certain embodiments, proteomics can be used to discover suitable biomarkers for use in accordance with the present invention. Proteomics is the study of proteome, the protein complement of the genome. The term proteome also used to refer to the totality of the proteins present in a sample (e.g. tissue, organism, or cell culture) at a certain point of time. Proteomics includes, among other things, study of the global changes of protein expression in a sample (also referred to as “expression proteomics”). Proteomics typically includes the following steps: (1) separation of individual proteins in a sample by 2-D gel electrophoresis (2-D PAGE); (2) identification of the individual proteins recovered from the gel, e.g. by mass spectrometry and/or N-terminal sequencing, and (3) analysis of the data using bioinformatics. Proteomics methods are valuable supplements to other methods of gene expression profiling, and can be used, alone or in combination with other methods of the present invention, to detect the biomarkers of the present invention.

II. Method of Use of the Biomarkers

[0090] Thus, one aspect of the present invention is to provide a prognostic method for and/or treatment of cancer. In certain embodiments particular cancers having a stromal component/cells can be diagnosed and/or treated.

[0091] Stromal cells are connective tissue cells of an organ found in the loose connective tissue, including uterine mucosa (endometrium), prostate, bone marrow, bone marrow precursor cells, and the ovary and the hematopoietic system. The most common types of stromal cells

include fibroblasts, immune cells, pericytes, endothelial cells, and inflammatory cells. Thus, cancers having a stromal component can occur in any organ or tissue with stromal component, including uterine mucosa (endometrium), prostate, bone marrow, the ovary and the hematopoietic system.

- 5 [0092] In one embodiment, the present invention provides a method of stratifying a subject or a group of subjects having a cancer tumor for a clinical trial. In an embodiment, the method comprises: (a) providing a stromal material, wherein first stromal material is derived from a biological sample obtained from a subject having a cancer tumor; (b) determining a genome-wide transcriptional profile of the stromal material; (c) comparing the genome-wide transcriptional
10 profile (or a subgenome transcriptional profile derived therefrom) of said stromal material a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises a set of at least one or more genes selected from the genes in Supplemental Table 1; and (d) stratifying the subject for a clinical trial based on the results of the comparison step (c).

III. EXAMPLES

15 Experimental Procedures

[0093] Example 1: Laser Capture Microdissection and Genome-Wide Expression Profiling

- [0094] Tumor stroma was laser capture microdissected using a Leica LCM system from 4 cases showing high stromal Cav-1 expression and 7 cases with loss of stromal Cav-1. Total RNA
20 was amplified using the NuGEN™ WT-Ovation™ FFPE RNA Amplification System V2 and cDNA was hybridized to Affymetrix GeneChip® arrays. One-way ANOVA was setup to extract differentially expressed genes between Cav-1 positive and negative stromal samples. Stromal tissue was laser capture microdissected (LCM) from fresh frozen (FF) tumor tissue samples collected from the patients pre-treatment, and samples included were closely matched for age,
25 race, stage and grade.

- [0095] All eukaryotic target preparations (ALMAC Diagnostics, Inc.) using the project-appropriate NuGEN™ RNA Amplification System in combination with the Encore™ Biotin Module were performed in accordance with the guidelines detailed in the corresponding NuGEN™ technical manual. Total RNA was amplified using the NuGEN™ Ovation™ Pico
30 WTA System. First-strand synthesis of cDNA was performed using a unique first-strand DNA/RNA chimeric primer mix, resulting in cDNA/mRNA hybrid molecules. Following

fragmentation of the mRNA component of the cDNA/mRNA molecules, second-strand synthesis was performed and double-stranded cDNA was formed with a unique DNA/RNA heteroduplex at one end. In the final amplification step, RNA within the heteroduplex was degraded using RNaseH, and replication of the resultant single-stranded cDNA was achieved through DNA/RNA chimeric primer binding and DNA polymerase enzymatic activity. The amplified single-stranded cDNA was purified for accurate quantitation of the cDNA and to ensure optimal performance during the fragmentation and labeling process. The single stranded cDNA was assessed using spectrophotometric methods in combination with the Agilent Bioanalyzer. The appropriate amount of amplified single-stranded cDNA was fragmented and labeled using the Encore™ Biotin Module. The enzymatically and chemically fragmented product (50-100 nt) was labeled via the attachment of biotinylated nucleotides onto the 3'-end of the fragmented cDNA. The resultant fragmented and labeled cDNA was added to the hybridization cocktail in accordance with the NuGEN™ guidelines for hybridization onto Affymetrix GeneChip® arrays. Following the hybridization for 18 hours at 45°C in an Affymetrix GeneChip® Hybridization Oven 640, the array was washed and stained on the GeneChip® Fluidics Station 450 using the appropriate fluidics script, before being inserted into the Affymetrix autoloader carousel and scanned using the GeneChip® Scanner 3000.

[0096] Example 2: Gene set enrichment analysis (GSEA)

[0097] For the list of genes that are up-regulated in Cav-1-negative patients compared to Cav-1 positive patients (fold change ≥ 1.15 and p-value ≤ 0.1) (**Supplemental Table 2**), we computed enrichments in gene sets contained in the latest release of Molecular Signatures Database (MSigDB v2.5, April 2008, ⁶⁸). MSigDB is a database of gene sets:

- collected from various sources, such as online pathway databases, publications, and knowledge of domain experts,
- comprising genes that share a conserved cis-regulatory motif across the human, mouse, rat, and dog genomes,
- identified as co-regulated gene clusters by mining large collections of cancer-oriented microarray data, and
- annotated by a common Gene Ontology (GO) term.

[0098] The enrichment analysis consisted of computing p-values for the intersections between a gene list of interest X and each gene set Y in MSigDB. First, we computed the overlap between X and Y. Then, we computed the probability (p-value) that the observed overlap

between sets X and Y is less than or equal to the overlap between set X and a randomly-chosen set of size equal to the size of set Y. This probability was calculated by applying the cumulative density function of the hypergeometric distribution on the size of set X, the size of set Y, the observed overlap between X and Y, and the total number of available genes. In order to account for multiple hypothesis testing, we used randomly selected gene lists of the same size as the list under consideration to estimate the false discovery rate at a given p-value threshold. The final list of significant MSigDB gene sets was determined by setting a p-value threshold which ensures that the false discovery rate does not exceed 5%.

[0099] Example 3: Analysis of Clinical Outcome in Human Breast Cancer Patients

[00100] A microarray dataset that was previously compiled from the public repositories Gene Expression Omnibus (<http://www.ncbi.nlm.nih.gov/geo/>)⁶⁹ and ArrayExpress (<http://www.ebi.ac.uk/arrayexpress/>)⁷⁰ was used to evaluate the stromal Cav-1 deficient gene signature in the context of clinical samples^{17, 18}. Samples were first analyzed in subsets based on their ER status. Additional subsets were defined by classifying samples among five canonical breast cancer subtypes, including luminal A, luminal B, normal-like, basal, and Her-2-overexpressing disease. Samples were classified by computing their correlation against five expression profile centroids representing these breast cancer subtypes and assigning them to the subtype with the highest corresponding correlation coefficient⁷¹. Samples with a maximum correlation coefficient below 0.3 were considered unclassified. Differential expression of the averaged gene signature magnitude among these sample subsets was evaluated using a two-tailed t-test. Kaplan-meier analysis was used to evaluate survival trends within sample subsets. The Log-rank test was used to evaluate differences in survival curves for high vs. low signature-expressing populations. In the BoxPlots (**Figure 10, panel A**), samples with ER immunohistochemistry (IHC) data were selected for analysis, including 959 ER-positive and 323 ER-negative, for a total of 1,282 samples; in addition, 102 normal healthy breast tissue controls were used for comparison purposes. In the BoxPlots (**Figure 10, panel B**), samples with information on ESR1 mRNA transcript levels were selected for analysis, including 1,674 ESR1-positive and 478 ESR1-negative, for a total of 2,152 samples; in addition, 102 normal healthy breast tissue controls were used for comparison purposes. The ESR1 high/low expression cutoff was defined at the RMA-normalized expression value of 7.5. This was determined from the bimodal expression transcript profile of ESR1, previously described in the Ertel et al. 2010^{17, 18}.

[00101] Additional Information

[00102] In Supplemental Tables 1-14, the fold-change data are represented as stromal Cav-1 (negative/positive), resulting in a positive fold-change for the transcripts that are up-regulated in Cav-1 negative stromal patients.

[00103] **Supplemental Table 1** contains 238 gene transcripts that were specifically up-regulated and 232 gene transcripts that were down-regulated in the stroma of tumors showing a loss of stromal Cav-1 expression ($p \leq 0.01$ and fold-change (f.c.) ≥ 1.5). Comparison of the transcriptional profiles of Cav-1-positive (+) tumor stroma (N = 4) *versus* Cav-1-negative tumor stroma (N = 7) revealed 238 gene transcripts that were up-regulated and 232 gene transcripts that were down-regulated in the stroma of tumors showing a loss of Cav-1 expression. The two patient populations are transcriptionally different. One-way ANOVA was setup to extract differentially expressed genes between Cav-1 positive and Cav-1 negative samples. The resultant p-values were further adjusted by multi-test correction (MTC) method of FDR step-up. The standardized intensity data from the stringent gene list ($p\text{-value} \leq 0.01$ and fold change ≥ 1.5) were used in generating the hierarchical clustering HeatMap.

[00104] As provided in **Figure 11**, the Cav-1-deficient stromal gene signature is associated with tumor recurrence and poor survival in ER(+) and luminal A breast cancer patients. Here the Cav-1-deficient stromal signature (238 transcripts that were specifically up-regulated; $p \leq 0.01$ and fold-change (f.c.) ≥ 1.5 ; **Supplemental Table 1**) is clearly associated with increased recurrence (**panels A and C**) and decreased overall survival (**panels B and D**), despite the fact that these breast cancer-derived tumors were not subjected to laser capture microdissection. **Panels A and B** are ER(+) breast cancer patients, while **panels C and D** are the luminal A subset of ER(+) breast cancer patients. Qualitatively similar results were also obtained with the longer signature included in **Supplemental Table 3**.

[00105] **Supplemental Table 2** contains 5,424 transcripts encoding 3,459 unique genes ($p \leq 0.1$ and fold-change (f.c.) ≥ 1.15) that were up-regulated in the stroma of tumors showing a loss of stromal Cav-1 expression.

[00106] **Supplemental Table 3** contains 1,819 transcripts encoding 1,297 unique genes ($p \leq 0.05$ and fold-change (f.c.) ≥ 1.15) that were up-regulated in the stroma of tumors showing a loss of stromal Cav-1 expression.

[00107] In **Supplemental Tables 4, 5, and 10** Cav-1-deficient stroma showed the up-regulation of myofibroblast differentiation (15 transcripts), autophagy (22 transcripts), lysosomal proteases

(5 transcripts), lysosomal proteins (29 transcripts), and glycolysis/pyruvate metabolism (15 transcripts).

[00108] **Supplemental Tables 4-14** contain the data shown in HeatMaps, as **Figures 2-8**.

[00109] As provided in **Supplemental Tables 10, and 12** Cav-1-deficient stroma showed the up-regulation of hypoxia target genes (65 transcripts) and mitochondrial-associated proteins (41 transcripts).

[00110] As provided in **Supplemental Tables 6, and 10** Cav-1-deficient stroma showed the up-regulation of the TNF/NFkB signaling (11 transcripts), the immune response (31 transcripts), and redox/stress signaling (19 transcripts).

[00111] As provided in **Supplemental Table 11**: Cav-1-deficient stroma showed the up-regulation of the DNA damage response (67 transcripts).

[00112] **Supplemental Tables 7, 9 and 14**: Cav-1-deficient stroma showed the up-regulation of aging (73 transcripts), apoptosis (51 transcripts), and BRCA1-mutation associated genes (20 transcripts).

[00113] As provided in **Supplemental Table 3**, the inventors compared the gene transcripts up-regulated in Cav-1-deficient tumor stroma (1,819 transcripts encoding 1,297 unique genes; $p \leq 0.05$ and fold-change (f.c.) ≥ 1.15 ; **Supplemental Table 3**) with (*Upper*) tumor stromal and (*Lower*) recurrence stromal gene lists, as defined in the text of the manuscript. The gene transcripts up-regulated in Cav-1-deficient tumor stroma showed significant overlap with tumor stroma (a 440 transcript overlap; $p = 4.76 \times 10^{-9}$) and recurrence stroma (a 214 transcript overlap; $p < 0.001$).

[00114] As provided in **Figure 10**, the Cav-1-deficient stromal gene signature is up-regulated in breast cancer and is associated with tumor recurrence. In **panels A and B**, box-plots show that the Cav-1-deficient stromal signature is up-regulated in all breast cancers, both ER(+) and ER(-) sub-types, relative to normal healthy breast tissue. In panel A, ER status was determined by immuno-histochemistry, while in panel B, ER status was inferred from ESR1 transcript expression. In **panel C**, the Cav-1-deficient stromal signature was associated with increased recurrence in breast cancer patients. In **panels A-C**, we used the Cav-1-deficient stromal signature included in **Supplemental Table 1** (238 transcripts that were specifically up-regulated;

$p \leq 0.01$ and fold-change (f.c.) ≥ 1.5) Qualitatively similar results were also obtained with the longer signature included in **Supplemental Table 3**.

Figure 9 illustrates Venn diagrams for the intersection of the cav-1-deficient stromal gene signature with other breast cancer tumor stromal gene sets. **Figure 9** shows that the gene

transcripts up-regulated in Cav-1-deficient tumor stroma show significant overlap with tumor stroma (a 440 transcript overlap; $p = 4.76 \times 10^{-9}$) and recurrence stroma (a 214 transcript overlap; $p < 0.001$). Thus, the gene transcripts up-regulated in Cav-1-deficient tumor stroma show a significant association with tumor recurrence, and are in accordance with the results of Morag Park and colleagues¹⁵. The present inventors, compared the gene transcripts up-regulated in Cav-1-deficient tumor stroma (1,819 transcripts encoding 1,297 unique genes; $p \leq 0.05$ and fold-change (f.c.) ≥ 1.15 ; **Supplemental Table 3**) with (*Upper*) tumor stromal and (*Lower*) recurrence stromal gene lists, as defined in the text of the manuscript. Note that the gene transcripts up-regulated in Cav-1-deficient tumor stroma show significant overlap with tumor stroma (a 440 transcript overlap; $p = 4.76 \times 10^{-9}$) and recurrence stroma (a 214 transcript overlap; $p < 0.001$).

[00115] Supplemental Table 15 contains the 3,459 unique genes that were up-regulated in the stroma of tumors showing a loss of stromal Cav-1 expression.

[00116] Supplemental Table 16 contains the 1,297 unique genes that were up-regulated in the stroma of tumors showing a loss of stromal Cav-1 expression.

[00117] Figure 12 illustrates understanding of the hierarchy of the cellular processes associated with a Cav-1-deficient tumor microenvironment. Oxidative stress in fibroblasts is known to be sufficient to induce 1) myo-fibroblast differentiation, 2) DNA damage, and 3) a pseudo-hypoxic state^{16, 19-21, 31, 32}. This pseudo-hypoxic state in fibroblasts then leads to the activation of NFkB and HIF1-alpha, which are master regulators of the immune response, and mitochondrial function, as well as autophagy¹⁹⁻²¹. The autophagic destruction of mitochondria then drives aerobic glycolysis²². We have previously shown that transient knock-down of Cav-1 in fibroblasts, using a targeted siRNA-approach, is sufficient to induce myo-fibroblast differentiation, DNA damage, and ROS production, leading to a pseudo-hypoxic state¹⁹⁻²¹. Similarly, knock down of Cav-1 in fibroblasts is sufficient to drive NFkB-, and HIF1-activation, as well as mitochondrial dys-function, autophagy, and the induction of glycolytic enzymes¹⁹⁻²¹. Interestingly, transcriptional profiling of a Cav-1-deficient tumor microenvironment provides direct evidence to support the involvement of all of these biological processes (See HeatMaps in

Figures 2-6). The **red arrow** denotes that NFkB-activation is known to augment HIF1-activation, and visa versa, indicating that they act synergistically²⁸.

[00118] The Examples that follow are illustrative of specific embodiments of the invention, and various uses thereof. They set forth for explanatory purposes only, and are not to be taken as
5 limiting the invention.

[00119] **Example 1: Transcriptional Profiling of a Cav-1 Deficient Tumor Microenvironment**

[00120] Loss of stromal Cav-1 in human breast cancer(s) is associated with tumor recurrence, metastasis, and drug-resistance, conferring poor clinical outcome¹⁻⁵. To mechanistically
10 understand the “lethality” of a Cav-1 negative tumor micro-environment, we performed laser capture microdissection on the tumor stroma of patients that were pre-classified as stromal Cav-1-positive(+) (N = 4) and stromal Cav-1-negative(-) (N = 7), based on immuno-histochemical (IHC) staining. Then, the RNA extracted from these samples was subjected to genome-wide transcriptional profiling.

[00121] Based on this approach, we identified 238 gene transcripts that were specifically up-regulated and 232 gene transcripts that were down-regulated in the stroma of tumors showing a loss of Cav-1 expression ($p \leq 0.01$ and fold-change (f.c.) ≥ 1.5) (**Supplemental Table 1**). Using these stringent criteria, we were able to transcriptionally separate these two patient populations, in accordance with their IHC stromal Cav-1 status (negative *versus* positive). A HeatMap of the
20 total patient cohort is shown in **Figure 1**, demonstrating that these two patient populations appear transcriptionally and “genetically” distinct.

[00122] **Example 2: Gene Set Enrichment Analysis (GSEA) of a Cav-1 Deficient Tumor Microenvironment**

[00123] To understand what cellular processes that are characteristic of a Cav-1-deficient tumor
25 microenvironment, we next performed gene set enrichment analysis (GSEA), by comparison with other gene signatures available in various public databases. For this purpose, we focused on a wider list of gene transcripts that were up-regulated in Cav-1-deficient stroma (5,424 transcripts encoding 3,459 unique genes; $p \leq 0.1$ and fold-change (f.c.) ≥ 1.15) (**Supplemental Table 2**), as is normally recommended for GSEA.

[00124] **Table 1:** shows the results of this detailed analysis. Note that we see the up-regulation of cellular processes normally associated with “stemness”, inflammation, DNA damage, oxidative stress, hypoxia, apoptotic signaling, autophagy, and mitochondrial dysfunction in the tumor stroma of patients lacking stromal Cav-1.

5 [00125] Individual HeatMaps (based on 1,819 transcripts encoding 1,297 unique genes; $p \leq 0.05$ and fold-change (f.c.) ≥ 1.15) (**Supplemental Table 3**) for key cellular processes are shown in **Figures 2-8**. These HeatMaps illustrate the upregulation of gene transcripts associated with myofibroblast differentiation, autophagy, lysosomal degradation, glycolysis, hypoxia, mitochondria, inflammation and redox signaling, DNA damage and repair, aging, BRCA1-
10 mutation positive and ER-negative breast cancer patients, apoptosis, and neural stem cells (See **Supplemental Tables 4-14**).

[00126] The observed association between a Cav-1-deficient tumor stroma and neural stem cells may reflect increased stromal “neurogenesis”, which has previously been implicated in an aggressive reactive stromal phenotype in a subset of prostate cancers ^{7,8}. Similarly,
15 “neurogenesis” was associated with increased DNA damage in the tumor stroma ^{7,8}.

[00127] In addition, the up-regulation of gene transcripts or gene sets associated with GOLPH3, NRF1 (nuclear respiratory factor 1), PRKDC (protein kinase, DNA-activated, catalytic polypeptide), or arsenic treatment is highly suggestive of mitochondrial dysfunction (**Table 1**). NRF1 is normally up-regulated during hypoxic-ischemic injury or oxidative stress, as an attempt
20 to increase mitochondrial biogenesis ^{9,10}. GOLPH3 (also known as MIDAS/GPP34) is a nuclear gene whose transcription is enhanced by the absence of mitochondrial DNA (mtDNA) ¹¹. MIDAS stands for mitochondrial DNA absence sensitive factor ¹¹. PRKDC is a component of the machinery required for the proper repair and maintenance of the fidelity of mitochondrial DNA (mtDNA) ¹², so its up-regulation is suggestive of increase mtDNA damage. Arsenic
25 treatment is associated with increased ROS production, mtDNA damage, and mitochondrial dysfunction, with reduced ATP production, driving the onset of aerobic glycolysis ^{13,14}.

[00128] **Example 3: Comparison with Other Breast Cancer Stromal Data Sets Obtained by Laser Capture Microdissection**

[00129] Next, we compared our new results with an independent previously published
30 transcriptional data set generated by Morag Park and colleagues ¹⁵, via laser capture of the tumor stroma of human breast cancers. However, these previously published data were not stratified based on stromal Cav-1 status ¹⁵.

[00130] More specifically, we compared the gene transcripts up-regulated in Cav-1-deficient tumor stroma (1,819 transcripts encoding 1,297 unique genes; $p \leq 0.05$ and fold-change (f.c.) ≥ 1.15) (**Supplemental Table 3**) with 1) tumor stroma and 2) recurrence stroma gene lists, as defined below:

5 [00131] (1) Tumor Stroma vs. Normal Stroma List - Compares the transcriptional profiles of tumor stroma obtained from 53 patients to normal stroma obtained from 38 patients. Genes transcripts that were consistently upregulated in the tumor stroma were selected and assigned a p-value, with a cut-off of $p < 0.05$ (this set contains 6,777 unique genes)¹⁶.

10 [00132] (2) Recurrence Stroma List - Compares the transcriptional profiles of tumor stroma obtained from 11 patients with tumor recurrence to the tumor stroma of 42 patients without tumor recurrence. Genes transcripts that were consistently upregulated in the tumor stroma of patients with recurrence were selected and assigned a p-value, with a cut-off of $p < 0.05$ (this set contains 3,354 unique genes)¹⁶.

15 [00133] **Figure 9:** shows that the gene transcripts up-regulated in Cav-1-deficient tumor stroma show significant overlap with tumor stroma (a 440 transcript overlap; $p = 4.76 \times 10^{-9}$) and recurrence stroma (a 214 transcript overlap; $p < 0.001$). Thus, the gene transcripts up-regulated in Cav-1-deficient tumor stroma show a significant association with tumor recurrence, and are in accordance with the results of Morag Park and colleagues¹⁵.

20 [00134] **Example 4: Comparison with the Transcriptional Profiles of Breast Cancers that were Not Subjected to Laser Capture Microdissection**

[00135] Most of the published and publicly available transcriptional profiles for breast cancer patients are derived from the analysis of whole tumors, which are not separated into stromal and epithelial compartments prior to analysis. Thus, we compared the gene transcripts up-regulated in Cav-1-deficient tumor stroma (**Supplemental Table 1**), with the transcriptional profiles of
25 normal breast tissue and whole breast tumors^{17, 18}.

[00136] **Figure 10A,B:** shows that the Cav-1-deficient tumor stromal signature is up-regulated in breast cancer(s), both ER(+) and ER(-) sub-types. However, a more significant association was observed with ER(-) breast cancers. In addition, the Cav-1-deficient stromal signature was also associated with increased recurrence in breast cancer patients (**Figure 10C**).

[00137] Similarly, we also looked at the prognostic value of the Cav-1-deficient stromal signature in ER(+) and luminal A breast cancer patients, which account for nearly 60% of all breast cancer patients^{17, 18}. Interestingly, **Figure 11** shows that the Cav-1-deficient stromal signature is clearly associated with increased recurrence and decreased overall survival, despite the fact that these breast cancer-derived tumors were not subjected to laser capture microdissection.

[00138] STATISTICAL ANALYSIS

[00139] The conventional statistical analysis method for gene expression microarray experiments is to examine one gene at a time, determine a p-value that the gene is differentially expressed in different phenotypes, and then to apply a correction (penalty) to the p-value for having tested multiple genes. In contrast, Gene set enrichment analysis (“GSEA”) is a statistical method to determine if predefined sets of genes are differentially expressed in different phenotypes. Predefined gene sets may be genes in a known metabolic pathway, located in the same cytogenetic band, sharing the same Gene Ontology category, or any user-defined set. In microarray experiments where no single gene shows statistically significant differential expression between phenotypes, GSEA has identified significant differentially expressed sets of genes, even where the average difference in expression between two phenotypes is only 20% for genes in the gene set. The gene set identified in the first GSEA analysis (oxidative phosphorylation genes differentially expressed in diabetic versus non-diabetic patients) was subsequently confirmed by independent laboratory studies published in the New England Journal of Medicine. Since the first paper on GSEA was published, many extensions and alternative methods have been described in the literature. GSEA has becoming more widely used because predictions of GSEA have been validated in independent laboratory experiments (see, for example, Patti M.E. et al., “Coordinated reduction of genes of oxidative metabolism in humans with insulin resistance and diabetes: Potential role of PGC1 and NRF1” Proc. Natl. Acad. Sci. USA 2003, 100, 8466-8471; and Petersen K.F. et al. “ Impaired mitochondrial activity in the insulin-resistant offspring of patients with type 2 diabetes” N. Engl. J. Med. 2004, 350, 664-671).

[00140] All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.

[00141] The use of the terms “a” and “an” and “the” and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The terms “comprising,” “having,” “including,” and “containing” are to be construed as open-ended terms (i.e., meaning “including, but not limited to,”) unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., “such as”) provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

[00142] Preferred embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Variations of those preferred embodiments may become apparent to those of ordinary skill in the art upon reading the foregoing description. The inventors expect skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context

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Supplemental Table 1 (page 46 through page 81)

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
1	ADXEC.19900.C1_at	Homo sapiens hypothetical protein LOC100293390	LOC100293390	0.0100	7.14329	100293390	XM_002346092	
2	ADXEC.32873.C1_x_at	Ring finger protein 217	RNF217	0.0052	4.7904	154214	CA436239	Hs.368639
3	ADXEC.26338.C1-a_s_at	Homo sapiens piggyBac transposable element derived 2 (PGBD2)	PGBD2	0.0075	4.68558	267002	NM_001017434	Hs.602037
4	ADXEC.30057.C1_s_at	Homo sapiens lactamase beta (LACTB) nuclear gene encoding	LACTB	0.0016	4.61882	114294	NM_171846	Hs.410388
5	ADXECNTD1.1029_s_at	Homo sapiens tRNA isopentenyltransferase 1 (TRIT1) mRNA.	TRIT1	0.0051	4.38491	54802	NM_017646	Hs.356554
6	ADXEC.32873.C1_at	Ring finger protein 217	RNF217	0.0074	4.34579	154214	CA436239	Hs.368639
7	ADXEC.12395.C1_at	Homo sapiens hypothetical LOC654433 (LOC654433) non-coding RNA.	LOC654433	0.0011	3.99819	654433	NR_015377	Hs.656660
8	ADXEC.4008.C2_s_at	Homo sapiens DNA fragmentation factor 45kDa alpha polypeptide	DFFA	0.0085	3.93961	1676	NM_213566	Hs.484782
9	ADXEC.16346.C1_at	Homo sapiens mRNA for FLJ00095 protein.	DNAIC5	0.0049	3.82963	80331	AK074041	Hs.164419
10	ADXECRS.38829_at	Homo sapiens zinc finger protein 365 (ZNF365) transcript variant	ZNF365	0.0085	3.76299	22891	NM_014951	Hs.22653
11	ADXECADA.18213_at	Transcribed locus		0.0013	3.69733		BF447243	Hs.673464
12	ADXECRS.38829_x_at	Homo sapiens zinc finger protein 365 (ZNF365) transcript variant	ZNF365	0.0056	3.67241	22891	NM_014951	Hs.22653
13	ADXEC.17269.C1_s_at	MDN1 midasin homolog (yeast)	MDN1	0.0078	3.5888	23195	AI424987	Hs.529948

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
14	ADXECEMUTR.3609_at	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog	ERG	0.0061	3.56429	2078	NM_004449	Hs.473819
15	ADXEC.686.C6_s_at	Homo sapiens cathepsin B (CTSB) transcript variant 4 mRNA.	CTSB	0.0089	3.50595	1508	NM_147782	Hs.520898
16	ADXEC.26095.C1_at	Human DNA sequence from clone RP5-1042K10 on chromosome 22q13.1-13.2 Contains the	SGSM3	0.0032	3.44465	57591	AL022238	Hs.654688
17	ADXEC.2002.C2_at	Homo sapiens myosin light chain 5 regulatory (MYL5) mRNA.	MYL5	0.0090	3.41779	4636	NM_002477	Hs.410970
18	ADXEC.17526.C1-a_s_at	Transcribed locus		0.0064	3.39122		BE551905	Hs.594106
19	ADXEC.19477.C1_at	H.sapiens DMA DMB HLA-Z1 IPP2 LMP2 TAP1 LMP7 TAP2 DOB DQB2 and RING8 9 13 and 14	HLA-Z	0.0004	3.34464	267017	X87344	
20	ADXEC.11663.C1_s_at	Homo sapiens IKAROS family zinc finger 1 (Ikaros) (IKZF1) mRNA.	IKZF1	0.0035	3.34422	10320	NM_006060	Hs.488251
21	ADXECRS.20577_at	Homo sapiens chromosome 15 open reading frame 23 (C15orf23)	C15orf23	0.0098	3.31524	90417	NM_001142761	Hs.525796
22	ADXECEMUTR.3721_at	Homo sapiens CD84 mRNA alternatively spliced complete cds.	CD84	0.0013	3.26785	8832	U96627	Hs.398093
23	ADXECADA.8726_at	Homo sapiens chromosome 21 segment HS21C049.	C21orf7	0.0012	3.23755	56911	AL163249	Hs.222802
24	ADXEC.13002.C1_s_at	Homo sapiens vacuolar protein sorting 26 homolog B (S. pombe)	VPS26B	0.0030	3.22935	112936	NM_052875	Hs.334684
25	ADXECAD.11893_at	Transcribed locus		0.0044	3.18985		AW838616	Hs.716898
26	ADXECEMUTR.467_s_at	Homo sapiens suppressor of fused homolog (Drosophila) (SUFU)	SUFU	0.0002	3.18841	51684	NM_001178133	Hs.404089

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
27	ADXEC.31324.C1_at	Homo sapiens mutS homolog 6 (E. coli) (MSH6) gene complete cds.	MSH6	0.0073	3.17394	2956	AY082894	Hs.445052
28	ADXEC.8734.C1_s_at	Homo sapiens sphingosine-1-phosphate receptor 3 (S1PR3) mRNA.	S1PR3	0.0017	3.15236	1903	NM_005226	Hs.585118
29	ADXEC.29904.C1_at	Transcribed locus		0.0079	3.11861		AI799887	Hs.541432
30	ADXOCEC.4815.C3_x_at	Homo sapiens Fc fragment of IgG low affinity IIb receptor (CD32)	FCGR2B	0.0078	3.09923	2213	NM_001002275	Hs.654395
31	ADXECAD.15182_at	Homo sapiens BCL2-like 11 (apoptosis facilitator) (BCL2L11)	BCL2L11	0.0009	3.09625	10018	NM_138621	Hs.469658
32	ADXEC.652.C3-a_s_at	Homo sapiens replication factor C (activator 1) 536.5kDa (RFC5)	RFC5	0.0022	3.02581	5985	NM_181578	Hs.506985
33	ADXEC.2091.C1-a_s_at	Homo sapiens RAB3D member RAS oncogene family (RAB3D) mRNA.	RAB3D	0.0089	2.99798	9545	NM_004283	Hs.723925
34	ADXEC.17437.C1_at	Transcribed locus		0.0015	2.99074		AW572564	Hs.444645
35	ADXEC.23718.C1_s_at	Similar to hCG2038853	LOC100128943	0.0022	2.98874	284926	AK091355	Hs.615175
36	ADXECRS.22704_s_at	Homo sapiens proteasome (prosome macropain) subunit beta type 9	PSMB9	0.0026	2.98409	5698	NM_002800	Hs.721140
37	ADXEC.19258.C1_at	polypeptide N-acetylglucosaminyltransferase 11 (GalNAc-T11)	GALNT11	0.0079	2.97644	63917	DC361567	Hs.647109
38	ADXECAD.7829_s_at	Homo sapiens apolipoprotein C-II (APOC2) mRNA.	APOC2	0.0002	2.97326	344	NM_000483	Hs.75615
39	ADXECAD.12843_at	Transcribed locus		0.0005	2.96145		BF336130	Hs.606876
40	ADXECAD.13677_at	Homo sapiens serine palmitoyl transferase subunit II gene complete cds	ISM2	0.0005	2.95115	145501	AF1111168	Hs.29742

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
41	ADXEC.15135.C1_at	Homo sapiens PMS2 C-terminal like pseudogene (PMS2CL) non-coding	PMS2CL	0.0013	2.94774	441194	NR_002217	Hs.73105
42	ADXECADA.18686_s_at	Transcribed locus		0.0072	2.94636		AI053629	Hs.666899
43	ADXEC.7572.C1_at	Homo sapiens RD RNA binding protein (RDBP) mRNA.	RDBP	0.0014	2.94532	7936	NM_002904	Hs.423935
44	ADXEC.4499.C2-a_s_at	Homo sapiens G1 to S phase transition 2 (GSPT2) mRNA.	GSPT2	0.0078	2.9043	23708	NM_018094	Hs.59523
45	ADXEC.12456.C1_at	Homo sapiens NOD2 gene for LRR- containing protein exons 1-11	NOD2	0.0064	2.90397	64127	AJ303140	Hs.592072
46	ADXEC.31099.C1_at	Homo sapiens USP6 N-terminal like (USP6NL) transcript variant 1	USP6NL	0.0052	2.89555	9712	NM_014688	Hs.498661
47	ADXECEMUTR.8031_at	TAF13 RNA polymerase II TATA box binding protein (TBP)-associated factor 18kDa	TAF13	0.0084	2.89332	6884	BG675152	Hs.632426
48	ADXEC.7176.C1_s_at	Transcribed locus		0.0098	2.88848		AI932879	Hs.123362
49	ADXEC.32186.C1_at	Homo sapiens H2A histone family member X (H2AFX) mRNA.	H2AFX	0.0061	2.8756	3014	NM_002105	Hs.477879
50	ADXECNTDJ.7829_s_at	Homo sapiens CD53 molecule (CD53) transcript variant 2 mRNA.	CD53	0.0035	2.86627	963	NM_000560	Hs.443057
51	ADXEC.21508.C1_at	Homo sapiens truncated cytochrome P450 family 3 subfamily A polypeptide5 (CYP3A5)	CYP3A5	0.0080	2.85013	1577	DQ680079	Hs.695915
52	ADXEC.19477.C1_x_at	H.sapiens DMA DMB HLA-Z1 IPP2 LMP2 TAP1 LMP7 TAP2 DOB DQB2 andRING8 9 13 and 14	HLA-Z	0.0005	2.83976	267017	X87344	
53	ADXEC.34784.C1_at	DDB1 and CUL4 associated factor 8	DCAF8	0.0015	2.83794	50717	AI208342	Hs.632447

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
54	ADXEC.3104.C1_at	CTTNBP2 N-terminal like	CTTNBP2NL	0.0056	2.81995	55917	AI140499	Hs.724560
55	ADXEC.8565.C2_s_at	Transcribed locus		0.0037	2.81679		BE502790	Hs.713963
56	ADXEC.17933.C1_s_at	Transcribed locus		0.0032	2.7749		BQ184524	Hs.656062
57	ADXECAD.13677_x_at	Homo sapiens serine palmitoyl transferase subunit II gene complete cds	ISM2	0.0086	2.76101	145501	AF111168	Hs.29742
58	ADXECAD.18570_at	Homo sapiens potassium channel tetramerisation domain containing 20	KCTD20	0.0006	2.75012	222658	NM_173562	Hs.188757
59	ADXEC.16191.C1_at	Homo sapiens hyaluronan-mediated motility receptor (RHAMM) (HMMR)	HMMR	0.0097	2.74856	3161	NM_012485	Hs.723889
60	ADXEC.18082.C1_at	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1) transcript	RYR1	0.0040	2.72668	6261	NM_001042723	Hs.466664
61	ADXPCEC.473.C1-a_s_at	FLJ21028 fis clone CAE07155		0.0006	2.70392		AI677880	Hs.723898
62	ADXEC.29808.C1_at	Transcribed locus		0.0064	2.6787		AA317107	Hs.599025
63	ADXEC.9262.C1_at	Homo sapiens methyltransferase like 3 (METTL3) mRNA.	METTL3	0.0002	2.67088	56339	NM_019852	Hs.168799
64	ADXEC.18142.C1_at	Transcribed locus		0.0080	2.66583		AW511786	Hs.664153
65	ADXECAD.10111_s_at	Homo sapiens branched chain amino-acid transaminase 1 cytosolic	BCAT1	0.0028	2.63313	586	NM_001178092	Hs.438993
66	ADXPCEC.11099.C1_at	Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.	GSPT1	0.0034	2.62229	2935	U95742	Hs.528780
67	ADXECADA.12202_at	Transcribed locus		0.0086	2.61789		BG427399	Hs.687173
68	ADXEC.24661.C1_at	PREDICTED: Homo sapiens hypothetical protein MGC27345	MGC27345	0.0093	2.60984	157247	XR_079036	Hs.552129

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
69	ADXECNTDJ.5644_s_at	(MGC27345) Homo sapiens pyroglutamyl- peptidase I (PGPEP1) mRNA.	PGPEP1	0.0082	2.60186	54858	NM_017712	Hs.131776
70	ADXEC.3742.C2_s_at	Homo sapiens transcription factor EB (TFEB) transcript variant 2	TFEB	0.0090	2.59866	7942	NM_001167827	Hs.715310
71	ADXEC.20400.C1_s_at	Homo sapiens polymerase (DNA directed) gamma 2 accessory subunit	POLG2	0.0033	2.59701	11232	NM_007215	Hs.437009
72	ADXECAD.17510_at	Homo sapiens RNA binding motif protein 33 (RBM33) mRNA.	RBM33	0.0070	2.59057	155435	NM_053043	Hs.591815
73	ADXEC.26110.C1_x_at	Homo sapiens hypothetical LOC80054 (LOC80054) non-coding RNA.	LOC80054	0.0054	2.58678	80054	NR_026887	Hs.287521
74	ADXEC.1471.C1_at	fatty acid binding protein 3 muscle and heart (mammary-derived growth inhibitor)	FABP3	0.0005	2.56886	2170	NM_004102	Hs.657242
75	ADXEC.12232.C1_at	Homo sapiens grancalcin EF-hand calcium binding protein (GCA)	GCA	0.0030	2.56633	25801	NM_012198	Hs.377894
76	ADXEC.54.C1_s_at	Transcribed locus		0.0098	2.5551		AW271797	Hs.673771
77	ADXEC.35016.C1_at	Homo sapiens Fanconi anemia complementation group C (FANCC) mRNA.	FANCC	0.0031	2.55016	2176	NM_000136	Hs.494529
78	ADXEC.6333.C1_at	Homo sapiens RNA pseudouridylate synthase domain containing 4	RPUSD4	0.0012	2.53332	84881	NM_032795	Hs.150458
79	ADXECADA.8726_x_at	Homo sapiens chromosome 21 segment HS21C049.	C21orf7	0.0013	2.53074	56911	AL163249	Hs.222802
80	ADXEC.9351.C1_s_at	Homo sapiens zinc finger protein 609 (ZNF609) mRNA.	ZNF609	0.0005	2.52807	23060	NM_015042	Hs.696256

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
81	ADXECEMUTR.3960_at	Homo sapiens SAM domain and HD domain 1 (SAMHD1) mRNA.	SAMHD1	0.0031	2.52216	25939	NM_015474	Hs.580681
82	ADXECCRS.21006_s_at	Homo sapiens nuclear factor of activated T-cells cytoplasmic	NFATC2	0.0045	2.5121	4773	NM_173091	Hs.713650
83	ADXECC.23013.C2_s_at	Homo sapiens serpin peptidase inhibitor clade B (ovalbumin)	SERPINB8	0.0040	2.50071	5271	NM_198833	Hs.368077
84	ADXECCAD.18147_at	Transcribed locus		0.0094	2.49423		AI248951	Hs.659882
85	ADXECCRS.27925_at	Homo sapiens cytochrome P450 family 4 subfamily F polypeptide 11	CYP4F11	0.0020	2.49189	57834	NM_001128932	Hs.187393
86	ADXECCRS.15653_at	Programmed cell death 6 pseudogene	LOC728613	0.0091	2.47704	728613	CN280876	Hs.720393
87	ADXECC.22555.C1_at	Homo sapiens SNF related kinase (SNRK) transcript variant 2 mRNA.	SNRK	0.0025	2.46669	54861	NM_001100594	Hs.476052
88	ADXECC.26110.C1_at	Homo sapiens hypothetical LOC80054 (LOC80054) non-coding RNA.	LOC80054	0.0039	2.44843	80054	NR_026887	Hs.287521
89	ADXECC.6937.C1_s_at	Homo sapiens solute carrier family 8 (sodium/calcium exchanger)	SLC8A1	0.0066	2.43008	6546	NM_021097	Hs.468274
90	ADXECC.13165.C1_s_at	Homo sapiens vitelline membrane outer layer 1 homolog (chicken)	VMO1	0.0051	2.40436	284013	NM_001144940	Hs.122561
91	ADXECC.13172.C1_at	Homo sapiens interleukin 28 receptor alpha (interferon lambda receptor)	IL28RA	0.0018	2.40394	163702	NM_173065	Hs.221375
92	ADXECCADA.461_s_at	PREDICTED: Homo sapiens hypothetical protein LOC100288109	LOC100288109	0.0003	2.38099	100288109	XM_002342922	Hs.634705
93	ADXECC.7744.C3_s_at	Homo sapiens apoptosis-inducing TAF9-like domain 1 (APITD1)	APITD1	0.0020	2.37715	378708	NM_199295	Hs.412311

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
94	ADXEC.12903.C1_s_at	Homo sapiens thyroid hormone receptor interactor 6 (TRIP6) mRNA.	TRIP6	0.0047	2.37513	7205	NM_003302	Hs.534360
95	ADXECNTDJ.3859_at	Transmembrane protein 165	TMEM165	0.0097	2.37289	55858	BG230486	Hs.479766
96	ADXEC.30470.C1_at	Transcribed locus		0.0079	2.35396		BX112681	Hs.624324
97	ADXEC.3788.C1_s_at	Homo sapiens thromboxane A synthase 1 (platelet) (TBXAS1)	TBXAS1	0.0066	2.35355	6916	NR_029394	Hs.520757
98	ADXECADA.12963_at	Homo sapiens class II major histocompatibility complex transactivator(CIITA) gen		0.0031	2.35092		EF064747	
99	ADXECNTDJ.4256_at	Homo sapiens kelch-like 12 (Drosophila) (KLHL12) mRNA.	KLHL12	0.0027	2.33733	59349	NM_021633	Hs.706793
100	ADXEC.1893.C2_s_at	Homo sapiens lymphocyte antigen 86 (LY86) mRNA.	LY86	0.0096	2.33313	9450	NM_004271	Hs.653138
101	ADXEC.25579.C1_s_at	Kruppel-like factor 3 (basic)	KLF3	0.0041	2.32838	51274	BM988294	Hs.298658
102	ADXECRS.43632_s_at	Homo sapiens Wolf-Hirschhorn syndrome candidate 1 (WHSC1)	WHSC1	0.0060	2.32218	7468	NM_007331	Hs.113876
103	ADXEC.9417.C1_at	Zinc finger and BTB domain containing 46	ZBTB46	0.0046	2.32036	140685	AI670887	Hs.585028
104	ADXECNTDJ.9418_at	Homo sapiens SNF related kinase (SNRK) transcript variant 2 mRNA.	SNRK	0.0061	2.31106	54861	NM_001100594	Hs.476052
105	ADXEC.14388.C1_at	Myeloid/lymphoid or mixed-lineage leukemia 2	MLL2	0.0086	2.30441	8085	AW269020	Hs.724368
106	ADXOCEC.13491.C1_x_at	CDNA FLJ36844 fis clone ASTRO2012601		0.0001	2.28983		CN398621	Hs.272234
107	ADXEC.30928.C1_x_at	Homo sapiens inwardly rectifying potassium channel Kir7.1 gene	KCNJ13	0.0010	2.28651	3769	AF082182	Hs.467338

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
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108	ADXEC.31342.C1_s_at	Homo sapiens tRNA-histidine guanylyltransferase 1-like (S.	THG1L	0.0077	2.28154	54974	NM_017872	Hs.353090
109	ADXECAD.9792_s_at	Homo sapiens cytochrome P450 family 4 subfamily V polypeptide 2 (CYP4V2)gene com	CYP4V2	0.0088	2.25771	285440	FJ440682	Hs.720053
110	ADXECADA.21347_at	Homo sapiens solute carrier family 23 (nucleobase transporters)	SLC23A2	0.0099	2.25009	9962	NM_203327	Hs.516866
111	ADXEC.14823.C1-a_s_at	Homo sapiens opioid growth factor receptor-like 1 (OGFRL1) mRNA.	OGFRL1	0.0068	2.23826	79627	NM_024576	Hs.648434
112	ADXEC.17023.C1_s_at	Homo sapiens solute carrier organic anion transporter family	SLCO2B1	0.0055	2.23301	11309	NM_001145212	Hs.7884
113	ADXEC.29413.C1_at	Transcribed locus		0.0099	2.21379		R82458	Hs.657793
114	ADXECAD.17716_x_at	Protein tyrosine phosphatase non- receptor type 1	PTPN1	0.0087	2.2079	5770	BF938981	Hs.417549
115	ADXEC.29413.C1_x_at	Transcribed locus		0.0038	2.1951		R82458	Hs.657793
116	ADXEC.16192.C2-a_s_at	Homo sapiens arachidonate 5- lipoxigenase-activating protein	ALOX5AP	0.0031	2.19415	241	NM_001629	Hs.507658
117	ADXECAD.17469_s_at	Homo sapiens MORC family CW-type zinc finger 2 (MORC2) mRNA.	MORC2	0.0057	2.19385	22880	NM_014941	Hs.555918
118	ADXECNTDJ.10553_at	ATP-binding cassette sub-family D (ALD) member 1 pseudogene 4	ABCD1P4	0.0046	2.18503	26957	AP000543	
119	ADXECADA.8743_at	Full length insert cDNA clone ZB81B12		0.0083	2.18057		AW663510	Hs.102941
120	ADXEC.21162.C2_s_at	Homo sapiens uridine-cytidine kinase 2 (UCK2) mRNA.	UCK2	0.0075	2.17387	7371	NM_012474	Hs.458360

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
121	ADXEC.2484.C1_at	Homo sapiens transmembrane emp24 protein transport domain	TMED5	0.0089	2.17356	50999	NM_016040	Hs.482873
122	ADXECAD.24150_at	Homo sapiens cell-type natural killer cells Fc gamma receptor RIIc4(Fc- gammaRIIC	FCGR2C	0.0098	2.16444	9103	U90941	Hs.352642
123	ADXOCEC.13491.C1_at	CDNA FLJ36844 fis clone ASTRO2012601		0.0004	2.16357		AI244126	Hs.272234
124	ADXECRS.15490_s_at	Homo sapiens family with sequence similarity 185 member A	FAM185A	0.0081	2.16008	222234	NM_001145268	Hs.202543
125	ADXEC.28650.C1_at	PHD finger protein 20-like 1	PHF20L1	0.0060	2.15688	51105	AW173534	Hs.304362
126	ADXECADA.23430_s_at	Homo sapiens erythrocyte membrane protein band 4.1-like 3	EPB41L3	0.0043	2.15319	23136	NM_012307	Hs.213394
127	ADXECAD.10006_s_at	Homo sapiens La ribonucleoprotein domain family member 4B	LARP4B	0.0011	2.15226	23185	NM_015155	Hs.713649
128	ADXEC.27188.C1_s_at	Homo sapiens dehydrogenase/reductase (SDR family) X-linked (DHRSX)	DHRSX	0.0080	2.15042	207063	NM_145177	Hs.131452
129	ADXEC.5821.C1-a_s_at	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1)	PDPK1	0.0069	2.14947	5170	NM_031268	Hs.459691
130	ADXEC.19905.C1_s_at	CDNA FLJ20196 fis clone COLF0944		0.0046	2.13871		DB551313	Hs.664322
131	ADXEC.6968.C1_at	Homo sapiens APEX nuclease (apurinic/aprimidinic endonuclease) 2	APEX2	0.0007	2.12913	27301	NM_014481	Hs.659558
132	ADXOCEC.14095.C1_at	Transcribed locus		0.0063	2.12609		AI637589	Hs.671681
133	ADXECNTDJ.8315_s_at	Homo sapiens cathepsin B (CTSB) transcript variant 3 mRNA.	CTSB	0.0037	2.12056	1508	NM_147781	Hs.520898

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
134	ADXECAD.16766_x_at	Homo sapiens mitochondrial ribosomal protein L9 (MRPL9) nuclear	MRPL9	0.0034	2.11287	65005	NM_031420	Hs.288936
135	ADXECAD.8352_at	PREDICTED: Homo sapiens similar to hCG2006901 (LOC100293165) mRNA.	LOC100293165	0.0005	2.11169	100293165	XM_002344820	
136	ADXECEMUTR.3274_at	Homo sapiens chromosome 1 open reading frame 104 mRNA (cDNA cloneMGC:149516 IMAG	C1orf104	0.0099	2.06592	284618	BC131614	Hs.650801
137	ADXECRS.27012_at	Homo sapiens syntaxin 7 (STX7) mRNA.	STX7	0.0073	2.0653	8417	NM_003569	Hs.593148
138	ADXECADA.20351_at	Homo sapiens growth factor independent 1 transcription repressor	GFI1	0.0096	2.06269	2672	NM_005263	Hs.73172
139	ADXECAD.27315_at	Homo sapiens adaptor-related protein complex 4 epsilon 1 subunit	AP4E1	0.0023	2.06022	23431	NM_007347	Hs.413366
140	ADXECAD.158_s_at	Homo sapiens Rho GTPase activating protein 5 (ARHGAP5) transcript	ARHGAP5	0.0095	2.05846	394	NM_001030055	Hs.592313
141	ADXEC.28173.C1-a_s_at	Homo sapiens chromosome 14 open reading frame 106 (C14orf106)	C14orf106	0.0089	2.04924	55320	NM_018353	Hs.437941
142	ADXEC.79.C10_at	Transcribed locus		0.0082	2.04875		AA112373	Hs.666931
143	ADXEC.5096.C1-a_s_at	Homo sapiens suppressor of defective silencing 3 homolog (S.	SUDS3	0.0088	2.0456	64426	NM_022491	Hs.602312
144	ADXEC.12654.C1_at	Transcribed locus		0.0082	2.03686		AA938573	Hs.724034
145	ADXEC.17001.C1-a_s_at	Homo sapiens HLA-B associated transcript 2-like 1 (BAT2L1) mRNA.	BAT2L1	0.0025	2.03672	84726	NM_013318	Hs.495349
146	ADXEC.17718.C1_at	Homo sapiens breast carcinoma	BCAS3	0.0066	2.03366	54828	NM_001099432	Hs.655028

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
147	ADXEC.2453.C1_s_at	amplified sequence 3 (BCAS3)						
		Homo sapiens lipase maturation factor 2 (LMF2) mRNA.	LMF2	0.0032	2.02986	91289	NM_033200	Hs.150540
148	ADXEC.8778.C2_s_at	Homo sapiens integrator complex subunit 4 (INTS4) mRNA.	INTS4	0.0058	2.02783	92105	NM_033547	Hs.533723
149	ADXEC.3341.C3_at	Homo sapiens Fc fragment of IgG low affinity IIa receptor (CD32)	FCGR2A	0.0032	2.01126	2212	NM_001136219	Hs.352642
150	ADXECAD.20979_s_at	Homo sapiens ADAM metalloproteinase domain 10 (ADAM10) mRNA.	ADAM10	0.0011	2.00123	102	NM_001110	Hs.578508
151	ADXECEMUTR.3430_s_at	CCZ1 vacuolar protein trafficking and biogenesis associated homolog (S. cerevisi)	CCZ1	0.0093	1.99995	51622	NM_015622	Hs.530000
152	ADXECAD.11485_s_at	Homo sapiens RAN binding protein 9 (RANBP9) mRNA.	RANBP9	0.0053	1.98261	10048	NM_005493	Hs.708182
153	ADXEC.692.C2_at	Matrin 3	MATR3	0.0090	1.97767	9782	BM662841	Hs.268939
154	ADXEC.731.C2_at	Homo sapiens SUMO1/sentrin specific peptidase 5 (SEN5) mRNA.	SEN5	0.0047	1.96993	205564	NM_152699	Hs.240770
155	ADXECADA.6912_s_at	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2)	PPIL2	0.0094	1.96377	23759	NM_148176	Hs.438587
156	ADXEC.34450.C1_x_at	Homo sapiens threonine synthase-like 1 (S. cerevisiae) (THNSL1)	THNSL1	0.0055	1.95649	79896	NM_024838	Hs.645274
157	ADXECCRS.19463_at	Homo sapiens dynein heavy chain domain 1 (DNHD1) transcript	DNHD1	0.0029	1.93872	144132	NM_173589	Hs.720080
158	ADXECADA.24831_s_at	Homo sapiens RNA binding motif single stranded interacting protein	RBMS2	0.0041	1.92689	5939	NM_002898	Hs.683360

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159	ADXEC.15087.C2_x_at	Homo sapiens symplekin (SYMPK) mRNA.	SYMPK	0.0068	1.91819	8189	NM_004819	Hs.515475
160	ADXEC.15730.C1_at	Deoxyribonuclease I	DNASE1	0.0090	1.91679	1773	AA653004	Hs.629638
161	ADXECAD.24015_s_at	Homo sapiens Fc fragment of IgG low affinity IIa receptor (CD32)	FCGR2A	0.0091	1.9162	2212	NM_001136219	Hs.352642
162	ADXEC.7799.C1_s_at	Homo sapiens kinesin family member C2 (KIFC2) mRNA.	KIFC2	0.0069	1.91104	90990	NM_145754	Hs.528713
163	ADXECAD.15346_at	Tetratricopeptide repeat domain 17	TTC17	0.0077	1.91076	55761	BE074507	Hs.191186
164	ADXECADA.22455_at	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1)	PDPK1	0.0004	1.90373	5170	NM_031268	Hs.459691
165	ADXEC.9451.C1_s_at	Homo sapiens BCL2-like 13 (apoptosis facilitator) (BCL2L13)	BCL2L13	0.0005	1.9034	23786	NM_015367	Hs.631672
166	ADXEC.2002.C6_s_at	Homo sapiens major facilitator superfamily domain containing 7	MFSD7	0.0083	1.90316	84179	NM_032219	Hs.567612
167	ADXECAD.5956_at	Transcribed locus		0.0088	1.89342		AW959948	Hs.595186
168	ADXEC.1909.C1_at	Homo sapiens eukaryotic translation termination factor 1 (ETF1)	ETF1	0.0027	1.88352	2107	NM_004730	Hs.483494
169	ADXEC.6036.C1_s_at	Homo sapiens receptor accessory protein 4 (REEP4) mRNA.	REEP4	0.0060	1.87637	80346	NM_025232	Hs.289063
170	ADXPCEC.11965.C1_at	Transmembrane protein 165	TMEM165	0.0092	1.87133	55858	DA407774	Hs.479766
171	ADXECAD.16766_at	Homo sapiens mitochondrial ribosomal protein L9 (MRPL9) nuclear	MRPL9	0.0051	1.86882	65005	NM_031420	Hs.288936
172	ADXEC.944.C1_s_at	Homo sapiens HAUS augmin-like complex subunit 2 (HAUS2)	HAUS2	0.0097	1.86387	55142	NM_001130447	Hs.14347
173	ADXECNTDJ.5584_at	Homo sapiens ArfGAP with dual PH	ADAP2	0.0067	1.86047	55803	NM_018404	Hs.514063

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174	ADXECNTDJ.2829_at	domains 2 (ADAP2) mRNA. Homo sapiens interleukin 1 receptor accessory protein (IL1RAP)	IL1RAP	0.0009	1.85359	3556	NM_001167928	Hs.478673
175	ADXEC.8949.C1_s_at	Homo sapiens parvin gamma (PARVG) transcript variant 2 mRNA.	PARVG	0.0053	1.8518	64098	NM_001137605	Hs.658995
176	ADXLCEC.5249.C1_x_at	Homo sapiens mRNA for KIAA1152 protein partial cds.	C14orf118	0.0078	1.84839	55668	AB032978	Hs.410231
177	ADXEC.20561.C1_at	Genomic sequence from Human 6 complete sequence.	ATXN1	0.0025	1.84648	6310	AC002112	Hs.434961
178	ADXECEMUTR.6197_at	Transcribed locus		0.0003	1.83876		BQ446348	Hs.683515
179	ADXECCRS.5224_s_at	Homo sapiens phosphodiesterase 7A (PDE7A) transcript variant 1	PDE7A	0.0021	1.83715	5150	NM_002603	Hs.584788
180	ADXEC.6409.C1-a_s_at	Homo sapiens DENN/MADD domain containing 4B (DENND4B) mRNA.	DENND4B	0.0060	1.83702	9909	NM_014856	Hs.632480
181	ADXECAD.16270_at	Homo sapiens zinc finger protein 502 (ZNF502) transcript variant	ZNF502	0.0038	1.83388	91392	NM_001134440	Hs.224843
182	ADXEC.4862.C4_s_at	Homo sapiens chromosome 1 open reading frame 77 (C1orf77) mRNA.	C1orf77	0.0004	1.83096	26097	NM_015607	Hs.723142
183	ADXECEMUTR.5611_x_at	Homo sapiens chromosome 19 cosmid R32889 complete sequence.	OPA3	0.0053	1.8241	80207	AC006261	Hs.466945
184	ADXEC.25318.C1_at	Transcribed locus		0.0088	1.81634		BM979839	Hs.614573
185	ADXEC.4541.C1_s_at	Homo sapiens transportin 3 (TNPO3) mRNA.	TNPO3	0.0002	1.8081	23534	NM_012470	Hs.193613
186	ADXECAD.2809_x_at	Homo sapiens kinesin family member 1B (KIF1B) transcript variant	KIF1B	0.0080	1.80183	23095	NM_015074	Hs.97858
187	ADXECEMUTR.7014_at	Homo sapiens mRNA for PAP		0.0040	1.80104		AK225159	

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		associated domain containing 1 variant						
188	ADXEC.2201.C2_s_at	Homo sapiens ribonuclease RNase A family 1 (pancreatic) (RNASE1)	RNASE1	0.0021	1.79477	6035	NM_198235	Hs.623499
189	ADXEC.5655.C1_s_at	Homo sapiens annexin A11 (ANXA11) transcript variant a mRNA.	ANXA11	0.0009	1.78654	311	NM_001157	Hs.530291
190	ADXEC.22516.C1-a_s_at	Homo sapiens family with sequence similarity 84 member A (FAM84A)	FAM84A	0.0068	1.77958	151354	NM_145175	Hs.260855
191	ADXEC.26956.C1_x_at	Homo sapiens genomic DNA chromosome 6p21.3 HLA Class I region.	C6orf26	0.0088	1.77282	401251	BA000025	Hs.371225
192	ADXEC.EMUTR.419_at	Clathrin heavy chain (Hc)	CLTC	0.0089	1.7687	1213	AF130062	Hs.491351
193	ADXEC.6844.C1_s_at	Homo sapiens archaealysin family metallopeptidase 2 (AMZ2)	AMZ2	0.0019	1.75982	51321	NM_001033574	Hs.293560
194	ADXEC.1926.C1_s_at	Homo sapiens TYRO protein tyrosine kinase binding protein (TYROBP)	TYROBP	0.0008	1.74685	7305	NM_001173514	Hs.515369
195	ADXEC.2802.C2_s_at	Homo sapiens interferon gamma receptor 2 (interferon gamma receptor 2)	IFNGR2	0.0060	1.74342	3460	NM_005534	Hs.634632
196	ADXEC.18446.C1_at	Homo sapiens RIO kinase 2 (yeast) (RIOK2) transcript variant 1	RIOK2	0.0098	1.74302	55781	NM_018343	Hs.27021
197	ADXECADA.21635_s_at	Homo sapiens chromosome 17 open reading frame 63 (C17orf63)	C17orf63	0.0003	1.73835	55731	NM_018182	Hs.564533
198	ADXECADA.8638_at	FLJ21358 fis clone COL02842		0.0077	1.73601		AK025011	Hs.677312
199	ADXECADA.12751_at	Transcribed locus		0.0015	1.72888		AW204422	Hs.673398
200	ADXEC.23053.C1_at	Homo sapiens G protein-coupled bile acid receptor 1 (GPBAR1)	GPBAR1	0.0000	1.72158	151306	NM_001077191	Hs.160954

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201	ADXEC.7383.C1_x_at	Homo sapiens zinc finger protein 639 (ZNF639) mRNA.	ZNF639	0.0033	1.70966	51193	NM_016331	Hs.632578
202	ADXEC.33954.C1_x_at	Homo sapiens mRNA for KIAA0948 protein partial cds.	TBRG4	0.0078	1.70599	9238	AB023165	Hs.231411
203	ADXECRS.14355_s_at	Homo sapiens S-phase kinase-associated protein 2 (p45) (SKP2)	SKP2	0.0077	1.70535	6502	NM_005983	Hs.23348
204	ADXEC.1093.C1-a_s_at	Homo sapiens phosphorylase kinase alpha 2 (liver) (PHKA2) mRNA.	PHKA2	0.0060	1.70021	5256	NM_000292	Hs.54941
205	ADXEC.2954.C1_at	Homo sapiens stress-associated endoplasmic reticulum protein 1	SERP1	0.0081	1.68367	27230	NM_014445	Hs.518326
206	ADXEC.24170.C1_s_at	Homo sapiens centromere protein C 1 (CENPC1) mRNA.	CENPC1	0.0021	1.67955	1060	NM_001812	Hs.479867
207	ADXECAD.18174_s_at	Homo sapiens MICAL C-terminal like (MICALCL) mRNA.	MICALCL	0.0077	1.67808	84953	NM_032867	Hs.128196
208	ADXEC.2751.C1_at	Homo sapiens ras homolog gene family member G (rho G) (RHOG)	RHOG	0.0047	1.67338	391	NM_001665	Hs.501728
209	ADXEC.24741.C1_at	CDNA FLJ42263 fis clone TKIDN2014570		0.0099	1.66998		AA676397	Hs.600998
210	ADXECRS.42976_s_at	Homo sapiens phosphodiesterase 4D interacting protein (PDE4DIP)	PDE4DIP	0.0067	1.66335	9659	NM_001002812	Hs.657490
211	ADXEC.5123.C1_s_at	Homo sapiens KIAA1147 (KIAA1147) mRNA.	KIAA1147	0.0034	1.66176	57189	NM_001080392	Hs.521240
212	ADXEC.21785.C1_s_at	Ubiquitin associated protein 1	UBAP1	0.0098	1.65288	51271	R67923	Hs.268963
213	ADXEC.12026.C2_at	Homo sapiens chromosome 20 open reading frame 7 (C20orf7)	C20orf7	0.0084	1.65208	79133	NR_029377	Hs.472165
214	ADXECAD.9950_at	Homo sapiens serrate RNA effector	SRRT	0.0071	1.64834	51593	NM_001128854	Hs.111801

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215	ADXEC.1477.C1_s_at	molecule homolog (Arabidopsis)	BTN3A2	0.0026	1.63816	11118	NM_007047	Hs.376046
216	ADXEC.13413.C1_s_at	Homo sapiens butyrophilin subfamily 3 member A2 (BTN3A2) mRNA.	DCP2	0.0050	1.62892	167227	NM_152624	Hs.443875
217	ADXEC.24853.C1_s_at	Transcribed locus		0.0064	1.62622		CA416633	Hs.639165
218	ADXEC.11516.C3_at	Human DNA sequence from clone RP11-395L14 on chromosome 2 Contains the 3end of t	MIR1302-3	0.0082	1.61923	100302128	AL078621	
219	ADXECAD.14311_at	Ubiquitin-fold modifier 1	UFM1	0.0084	1.61393	51569	AA715013	Hs.643655
220	ADXEC.23135.C1-a_s_at	Homo sapiens pyruvate dehydrogenase phosphatase regulatory subunit	PDPR	0.0084	1.60409	55066	NM_017990	Hs.461183
221	ADXEC.1.C3_s_at	Homo sapiens DNA (cytosine-5-)-methyltransferase 1 (DNMT1)	DNMT1	0.0061	1.60018	1786	NM_001130823	Hs.202672
222	ADXEC.7681.C1_s_at	Homo sapiens structural maintenance of chromosomes 2 (SMC2)	SMC2	0.0051	1.59987	10592	NM_006444	Hs.119023
223	ADXECEMUTR.5434_s_at	Homo sapiens galactose-1-phosphate uridyl transferase (GALT) gene completecds.	GALT	0.0041	1.56621	2592	M96264	Hs.522090
224	ADXECCRS.6935_x_at	PREDICTED: Homo sapiens hypothetical LOC730235 (LOC730235)	LOC730235	0.0063	1.56614	730235	XR_079018	Hs.535032
225	ADXEC.23256.C1_at	Homo sapiens syntaxin 8 (STX8) transcript variant 1 mRNA.	STX8	0.0039	1.5645	9482	NM_004853	Hs.431109

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226	ADXEC.1690.C5_s_at	Homo sapiens guanine nucleotide binding protein (G protein) beta	GNB1	0.0021	1.56308	2782	NM_002074	Hs.721030
227	ADXEC.25945.C1_at	Homo sapiens hypothetical LOC283267 (LOC283267) non-coding RNA.	LOC283267	0.0056	1.55804	283267	NR_015451	Hs.723242
228	ADXEC.633.C1_x_at	Homo sapiens WD repeat domain 1 (WDR1) transcript variant 1 mRNA.	WDR1	0.0084	1.55745	9948	NM_017491	Hs.128548
229	ADXECAD.23957_s_at	Homo sapiens BTB and CNC homology 1 basic leucine zipper	BACH1	0.0088	1.54438	571	NM_206866	Hs.721915
230	ADXECAD.9802_s_at	Homo sapiens ArfGAP with FG repeats 1 (AGFG1) transcript variant	AGFG1	0.0006	1.54207	3267	NM_001135187	Hs.352962
231	ADXECAD.8397_at	CDNA FLJ11364 fis clone HEMBA1000264		0.0083	1.54143		BX093323	Hs.657693
232	ADXEC.6408.C1_s_at	Homo sapiens protein inhibitor of activated STAT 1 (PIAS1) mRNA.	PIAS1	0.0082	1.53813	8554	NM_016166	Hs.162458
233	ADXEC.7350.C1_s_at	Homo sapiens sorting nexin 6 (SNX6) transcript variant 2 mRNA.	SNX6	0.0077	1.53481	58533	NM_152233	Hs.356647
234	ADXECAD.9888_at	Homo sapiens Rho-associated coiled-coil containing protein kinase	ROCK1	0.0043	1.52771	6093	NM_005406	Hs.306307
235	ADXEC.971.C3-a_s_at	Homo sapiens eukaryotic translation initiation factor 2-alpha	EIF2AK1	0.0078	1.52122	27102	NM_001134335	Hs.724455
236	ADXECEMUTR.5334_at	UBX domain protein 11	UBXN11	0.0059	1.52001	91544	AK094198	Hs.145061
237	ADXEC.11953.C2_s_at	Homo sapiens apoptotic peptidase activating factor 1 (APAF1)	APAF1	0.0069	1.50699	317	NM_181869	Hs.552567
238	ADXEC.34450.C1_at	Homo sapiens threonine synthase-like 1 (S. cerevisiae) (THNSL1)	THNSL1	0.0089	1.50693	79896	NM_024838	Hs.645274

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239	ADXEC.4151.C3_s_at	Homo sapiens heterogeneous nuclear ribonucleoprotein A0 (HNRNPA0)	HNRNPA0	0.0035	-1.50264	10949	NM_006805	Hs.96996
240	ADXECAD.1455_at	Homo sapiens ST3 beta-galactoside alpha-23-sialyltransferase 3	ST3GAL3	0.0061	-1.52297	6487	NM_174966	Hs.597915
241	ADXEC.22374.C1_x_at	Homo sapiens chromosome 19 CIT- HSP-444n24 complete sequence.	LOC100288446	0.0066	-1.52357	100288446	AC005261	Hs.722347
242	ADXEC.25270.C2_s_at	Homo sapiens 190 kDa guanine nucleotide exchange factor (RGNEF)	RGNEF	0.0031	-1.52816	64283	NM_001177693	Hs.482521
243	ADXECEMUTR.7452_x_at	Homo sapiens truncated receptor tyrosine kinase TrkC mRNA partial cds.	NTRK3	0.0027	-1.53021	4916	AY065844	Hs.410969
244	ADXEC.13119.C2_at	Kinesin-associated protein 3	KIFAP3	0.0027	-1.53686	22920	N63216	Hs.433442
245	ADXEC.30160.C1_at	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6- phosphate d	FAM3A	0.0063	-1.54231	60343	L44140	Hs.289108
246	ADXEC.12766.C1_x_at	Homo sapiens family with sequence similarity 169 member A	FAM169A	0.0064	-1.55343	26049	NM_015566	Hs.91662
247	ADXOCEC.2.C2_x_at			0.0042	-1.56832		NC_000001	
248	ADXECENTDJ.6322_s_at	Homo sapiens pleiomorphic adenoma gene 1 (PLAG1) transcript	PLAG1	0.0033	-1.5686	5324	NM_001114635	Hs.14968
249	ADXECADA.17298_at	Homo sapiens RAB40A member RAS oncogene family (RAB40A) mRNA.	RAB40A	0.0014	-1.57663	142684	NM_080879	Hs.27453
250	ADXEC.4038.C1_x_at	Transcribed locus		0.0011	-1.5779		AW974968	Hs.721720
251	ADXEC.9677.C1_s_at	glutamic-oxaloacetic transaminase 1 soluble (aspartate aminotransferase 1)	GOT1	0.0063	-1.58595	2805	NM_002079	Hs.500756

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
252	ADXEC.11286.C1_s_at	Homo sapiens zinc finger protein 768 (ZNF768) mRNA.	ZNF768	0.0012	-1.5868	79724	NM_024671	Hs.85658
253	ADXECRS.20566_at	Homo sapiens cytochrome P450 family 20 subfamily A polypeptide 1	CYP20A1	0.0044	-1.59256	57404	NM_177538	Hs.446065
254	ADXECNTDJ.10141_at	Homo sapiens mRNA	ASTN2	0.0034	-1.59546	23245	BX648673	Hs.601562
255	ADXEC.5953.C2_at	Homo sapiens RALBP1 associated Eps domain containing 2 (REPS2)	REPS2	0.0049	-1.60098	9185	NM_001080975	Hs.186810
256	ADXECAD.25435_s_at	Homo sapiens nucleolar protein 3 (apoptosis repressor with CARD	NOL3	0.0054	-1.60369	8996	NM_001185057	Hs.513667
257	ADXECAD.673_s_at	serpin peptidase inhibitor clade A (alpha-1 antitrypsinase antitrypsin) member 9	SERPINA9	0.0075	-1.60603	327657	NM_175739	Hs.317970
258	ADXEC.2530.C1_s_at	Homo sapiens transformer 2 alpha homolog (Drosophila) (TRA2A)	TRA2A	0.0032	-1.60983	29896	NM_013293	Hs.445652
259	ADXECADA.16176_at	Homo sapiens clones 24611 and 24705 mRNA sequence.		0.0016	-1.61239		AF070566	
260	ADXECADA.1194_s_at	4826441		0.0074	-1.62019		BC033543	Hs.666740
261	ADXECRS.14691_at	Homo sapiens glycophorin E (MNS blood group) (GYPE) transcript	GYPE	0.0052	-1.6243	2996	NM_002102	Hs.709199
262	ADXEC.1620.C8-a_x_at	Homo sapiens family with sequence similarity 86 member A	LOC729375	0.0062	-1.62456	729375	NR_024252	Hs.123633
263	ADXEC.21020.C1_at	Transcribed locus		0.0029	-1.63014		DN949639	Hs.690641
264	ADXECEMUTR.975_at	Homo sapiens cDNA FLJ60439 complete cds highly similar to AN1-type zincfinger pr	ZFAND2B	0.0028	-1.63042	130617	AK293714	Hs.534540
265	ADXEC.27790.C1-a_s_at	Homo sapiens bromodomain and WD	BRWD1	0.0046	-1.63445	54014	NM_033656	Hs.654740

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
		repeat domain containing 1 (BRWD1)						
266	ADXEC.10226.C1_at	Homo sapiens protein tyrosine phosphatase receptor type N	PTPRN	0.0072	-1.63535	5798	NM_002846	Hs.89655
267	ADXECRS.4257_at	Homo sapiens zinc finger protein 687 (ZNF687) mRNA.	ZNF687	0.0042	-1.63646	57592	NM_020832	Hs.186756
268	ADXPCEC.16625.C1_x_at	Homo sapiens chromosome 18 clone RP11-30L3 complete sequence.	DYM	0.0049	-1.63678	54808	AC044840	Hs.162996
269	ADXECNTDJ.1697_s_at	Homo sapiens armadillo repeat containing 7 (ARMC7) mRNA.	ARMC7	0.0035	-1.64018	79637	NM_024585	Hs.413047
270	ADXEC.6625.C1_x_at	Patatin-like phospholipase domain containing 8	PNPLA8	0.0077	-1.65972	50640	AL834147	Hs.617340
271	ADXEC.8619.C2_at	Homo sapiens leiomodlin 1 (smooth muscle) (LMOD1) mRNA.	LMOD1	0.0063	-1.66455	25802	NM_012134	Hs.519075
272	ADXEC.23460.C1_at	Homo sapiens chromosome 17 clone CTD1-2246P4 complete sequence.	MFSD11	0.0089	-1.66714	79157	AC027694	Hs.73965
273	ADXEC.7543.C2_s_at	Small EDRK-rich factor 1B (centromeric)	SERF1B	0.0008	-1.66933	728492	W51889	Hs.658079
274	ADXEC.16796.C1_x_at	Chromosome 6 open reading frame 130	C6orf130	0.0006	-1.67356	221443	BU688723	Hs.227457
275	ADXEC.10824.C1_x_at	Transmembrane protein 138	TMEM138	0.0062	-1.68482	51524	CA313117	Hs.406530
276	ADXECAD.12820_s_at	Homo sapiens acetylcholinesterase (ACHE) gene partial cds	UFSP1	0.0076	-1.68637	402682	AF312032	Hs.534845
277	ADXEC.2570.C1-a_s_at	sterol regulatory element binding transcription factor 2	SREBF2	0.0051	-1.71164	6721	BC051799	Hs.443258
278	ADXECAD.15190_at	Homo sapiens keratin 222 (KRT222) mRNA.	KRT222	0.0087	-1.71791	125113	NM_152349	Hs.6920

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
279	ADXCADA.10902_at	Homo sapiens phosphatidylinositol glycan anchor biosynthesis class	PIGM	0.0087	-1.71802	93183	NM_145167	Hs.552810
280	ADXEC.10310.C1_x_at	Homo sapiens genomic DNA chromosome 6p21.3 HLA Class I region.	C6orf26	0.0080	-1.71884	401251	BA000025	Hs.371225
281	ADXCAD.17787_at	Homo sapiens mRNA for RAR-related orphan receptor A isoform d variant protein.		0.0020	-1.71888		AB209916	
282	ADXEC.17571.C1_at	Four and a half LIM domains 2	FHL2	0.0046	-1.73684	2274	DA080655	Hs.443687
283	ADXEC.25286.C1_at	Homo sapiens GLIS family zinc finger 3 (GLIS3) transcript variant	GLIS3	0.0065	-1.73949	169792	NM_152629	Hs.162125
284	ADXCAD.8354_s_at	solute carrier family 7 (cationic amino acid transporter y system) member 14	SLC7A14	0.0062	-1.74006	57709	NM_020949	Hs.596660
285	ADXECRS.5002_at	Homo sapiens ATP-binding cassette sub-family A (ABC1) member 10	ABCA10	0.0014	-1.74691	10349	NM_080282	Hs.25377
286	ADXEC.20660.C1_at	Homo sapiens dihydrolipoamide branched chain transacylase E2 (DBT)	DBT	0.0007	-1.75013	1629	NM_001918	Hs.709187
287	ADXEC.12064.C1_at	Homo sapiens actin binding LIM protein family member 3 (ABLIM3)	ABLIM3	0.0004	-1.7509	22885	NM_014945	Hs.49688
288	ADXCAD.14565_at	Homo sapiens chromosome 19 cosmid R29783 complete sequence.	NOTCH3	0.0017	-1.75243	4854	AC004663	Hs.8546
289	ADXEC.10226.C1_x_at	Homo sapiens protein tyrosine phosphatase receptor type N	PTPRN	0.0031	-1.75644	5798	NM_002846	Hs.89655
290	ADXEC.21091.C1_x_at	Human Chromosome 11 Overlapping Cosmids cSRL125c1 and cSRL135f4 complete sequence		0.0063	-1.76079		U73630	

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
291	ADXECAD.26040_at	Homo sapiens desmoglein 3 (pemphigus vulgaris antigen) (DSG3)	DSG3	0.0048	-1.77118	1830	NM_001944	Hs.1925
292	ADXECRS.20172_at	Homo sapiens BTB and CNC homology 1 basic leucine zipper	BACH1	0.0084	-1.77492	571	NR_027655	Hs.721915
293	ADXECADA.19694_s_at	PREDICTED: Homo sapiens hypothetical LOC100131109 (LOC100131109)	LOC100131109	0.0038	-1.78502	100131109	XM_001725288	Hs.597458
294	ADXLCEC.9420.C1_at	5311269		0.0090	-1.78584		DB343445	Hs.497287
295	ADXEC.30311.C1_at	Homo sapiens phospholipase D1 phosphatidylcholine-specific (PLD1)	PLD1	0.0085	-1.7861	5337	NM_002662	Hs.382865
296	ADXEC.14592.C1_s_at	5206490) partial cds.		0.0010	-1.79081		BC048809	
297	ADXEC.30415.C1_at	Transcribed locus		0.0055	-1.80323		BF939077	Hs.175569
298	ADXECAD.6206_s_at	Homo sapiens SIK family kinase 3 (SIK3) mRNA.	SIK3	0.0092	-1.80674	23387	NM_025164	Hs.167451
299	ADXECRS.13153_s_at	Homo sapiens family with sequence similarity 55 member B (FAM55B)	FAM55B	0.0016	-1.8077	120406	NM_182495	Hs.446760
300	ADXEC.21260.C1_x_at	Prostaglandin reductase 1	PTGR1	0.0081	-1.80774	22949	BQ647750	Hs.584864
301	ADXECAD.6712_at	Homo sapiens ubiquitin protein ligase E3B (UBE3B) transcript	UBE3B	0.0090	-1.8114	89910	NM_130466	Hs.374067
302	ADXEC.24476.C1_x_at	Homo sapiens chromosome 19 cosmid R31646 complete sequence.	PTPRS	0.0038	-1.81409	5802	AC005338	Hs.724512
303	ADXECADA.7277_at	Homo sapiens discs large homolog 5 (Drosophila) (DLG5) mRNA.	DLG5	0.0056	-1.81814	9231	NM_004747	Hs.652690
304	ADXECAD.17255_s_at	Human DNA sequence from clone RP4-796111 on chromosome 20q12 Contains the5' end o	ZHX3	0.0046	-1.82116	23051	AL031257	Hs.380133

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
305	ADXCADA.3939_at	SRY (sex determining region Y)-box 5	SOX5	0.0071	-1.82239	6660	BC014929	Hs.657542
306	ADXCADA.2499_at	MRNA		0.0029	-1.82775		AL512742	Hs.684541
307	ADXCERS.34203_x_at	Homo sapiens hypothetical LOC388152 (LOC388152) non-coding RNA.	LOC388152	0.0081	-1.83192	388152	NR_027001	Hs.710289
308	ADXCOC.13628.C1_s_at	Transcribed locus		0.0079	-1.83225		AA658840	Hs.655920
309	ADXCADA.3412_at	Potassium channel subfamily K member 1	KCNK1	0.0042	-1.83526	3775	AL833343	Hs.208544
310	ADXC.31937.C1_at	3934974 mRNA		0.0073	-1.8359		BJ997426	Hs.667050
311	ADXC.23391.C1_at	Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5)	ITIH5	0.0065	-1.84259	80760	NM_001001851	Hs.498586
312	ADXCNTD1.8255_s_at	Homo sapiens retinoic acid receptor gamma (RARG) transcript	RARG	0.0021	-1.84923	5916	NM_001042728	Hs.1497
313	ADXC.26583.C1_x_at	Homo sapiens alpha/beta hydrolase domain containing protein 3 (ABHD3) genecomple	ABHD3	0.0025	-1.85061	171586	EF444943	Hs.397978
314	ADXC.3491.C1_at	Transcribed locus		0.0090	-1.85194		AI700036	Hs.666770
315	ADXC.30157.C1_at	Interleukin-1 receptor-associated kinase 1 binding protein 1	IRAK1BP1	0.0051	-1.85461	134728	BX107880	Hs.656212
316	ADXCOC.14963.C1_at	Human hereditary haemochromatosis region histone 2A-like protein genehereditary	TRIM38	0.0096	-1.86693	10475	U91328	Hs.584851
317	ADXC.32881.C1_s_at	Transcribed locus		0.0059	-1.86729		H10992	Hs.438869
318	ADXC.5588.C1_x_at	Homo sapiens solute carrier family 19 member 3 (SLC19A3) mRNA.	SLC19A3	0.0006	-1.87636	80704	NM_025243	Hs.221597
319	ADXC.11831.C1_x_at	CDNA FLJ33355 fis clone		0.0033	-1.87879		AI720040	Hs.655691

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
		BRACE2005151						
320	ADXEC.5956.C1_at	Homo sapiens exportin 7 (XPO7) transcript variant 2 mRNA.	XPO7	0.0068	-1.88558	23039	NM_015024	Hs.172685
321	ADXEC.13307.C1_at	Homo sapiens PDZ domain containing 4 (PDZD4) mRNA.	PDZD4	0.0002	-1.88903	57595	NM_032512	Hs.92732
322	ADXECAD.24092_s_at	Homo sapiens estrogen receptor 1 (ESR1) transcript variant 4	ESR1	0.0020	-1.90647	2099	NM_001122742	Hs.208124
323	ADXEC.22612.C1_at	Hypothetical protein LOC285147	LOC285147	0.0070	-1.91779	285147	H89554	Hs.467627
324	ADXEC.28916.C1_at	Transcribed locus		0.0024	-1.91963		AI479578	Hs.573319
325	ADXEC.12637.C1_s_at	Homo sapiens zinc finger protein 193 (ZNF193) mRNA.	ZNF193	0.0097	-1.92208	7746	NM_006299	Hs.100921
326	ADXEC.28033.C1_s_at	Homo sapiens membrane protein palmitoylated 7 (MAGUK p55 subfamily	MPP7	0.0007	-1.92654	143098	NM_173496	Hs.499159
327	ADXECNTD1.6579_at	Polycystic kidney disease 1-like 2	PKD1L2	0.0003	-1.92944	114780	CR627341	Hs.413525
328	ADXEC.13307.C1_x_at	Homo sapiens PDZ domain containing 4 (PDZD4) mRNA.	PDZD4	0.0010	-1.93553	57595	NM_032512	Hs.92732
329	ADXEC.34080.C1_x_at	Human Chromosome 11 Cosmid cSRL187d6 complete sequence.		0.0017	-1.9368		U73641	
330	ADXECADA.12864_at	Transcribed locus		0.0081	-1.94573		BE327701	Hs.676086
331	ADXEC.3492.C1_s_at	Homo sapiens KCNQ1 overlapping transcript 1 (non-protein coding)	KCNQ1OT1	0.0063	-1.94778	10984	NR_002728	Hs.604823
332	ADXECEMUTR.5853_at	RAD1 homolog (S. pombe)	RAD1	0.0067	-1.95437	5810	AK125316	Hs.38114
333	ADXEC.14697.C1_s_at	Homo sapiens potassium channel modulatory factor 1 (KCMF1) mRNA.	KCMF1	0.0068	-1.96184	56888	NM_020122	Hs.654968
334	ADXECNTD1.7445_s_at	PREDICTED: Homo sapiens	LOC100293798	0.0096	-1.97542	100293798	XM_002344714	

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
335	ADXEC.32091.C1_x_at	hypothetical protein LOC100293798 Homo sapiens insulin-like growth factor 1 receptor (IGF1R) gene completecds.	IGF1R	0.0023	-1.98259	3480	AY332722	Hs.643120
336	ADXEC.19828.C1-a_s_at	Transcribed locus		0.0074	-1.99065		W73590	Hs.597523
337	ADXEC.12482.C1_at	Homo sapiens zinc finger protein 3 homolog (mouse) (ZFP3) mRNA.	ZFP3	0.0045	-1.99302	124961	NM_153018	Hs.48832
338	ADXEC.34304.C1_x_at	Homo sapiens chromosome 21 open reading frame 62 (C21orf62)	C21orf62	0.0063	-1.99529	56245	NM_019596	Hs.517235
339	ADXECAD.12441_at	Homo sapiens toll-like receptor 6 (TLR6) mRNA.	TLR6	0.0008	-2.00244	10333	NM_006068	Hs.575090
340	ADXECADA.15293_at	128781 mRNA sequence		0.0064	-2.03482		R16848	Hs.679511
341	ADXECRS.35760_s_at	Homo sapiens C-terminal binding protein 2 (CTBP2) transcript	CTBP2	0.0082	-2.03536	1488	NM_001329	Hs.501345
342	ADXECEMUTR.7290_at	Transcribed locus		0.0023	-2.04768		N51903	Hs.597033
343	ADXPCEC.6839.C1_at	Transcribed locus		0.0001	-2.05005		AW242613	Hs.87384
344	ADXEC.14129.C1_s_at	Homo sapiens DEAD (Asp-Glu-Ala- Asp) box polypeptide 46 (DDX46)	DDX46	0.0031	-2.05587	9879	NM_014829	Hs.406549
345	ADXOCEC.10667.C1_at	Family with sequence similarity 156 member B	FAM156B	0.0037	-2.06186	727866	AI357038	Hs.6451
346	ADXEC.30771.C1_at	Homo sapiens RUN domain containing 3B (RUNDC3B) transcript variant	RUNDC3B	0.0043	-2.0718	154661	NM_001134405	Hs.411488
347	ADXEC.10824.C1_at	Transmembrane protein 138	TMEM138	0.0019	-2.07393	51524	CA313117	Hs.406530
348	ADXECEMUTR.5313_at	Hypothetical LOC100131938	LOC100131938	0.0019	-2.07465	100131938	AK093508	Hs.720898
349	ADXECADA.892_s_at	Homo sapiens unc-13 homolog C (C.	UNC13C	0.0034	-2.08233	440279	NM_001080534	Hs.657273

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
		elegans) (UNC13C) mRNA.						
350	ADXEC.8432.C1_at	Transcribed locus		0.0035	-2.08475		AI537355	Hs.562927
351	ADXEC.14866.C1_at	Homo sapiens zinc finger protein 641 (ZNF641) transcript variant	ZNF641	0.0005	-2.08944	121274	NM_001172682	Hs.23492
352	ADXECEMUTR.6377_at	Homo sapiens partial OBSCN gene for obscurin exons C-22	OBSCN	0.0000	-2.09704	84033	AJ314903	Hs.650039
353	ADXECEMUTR.4945_at	Chromosome 18 open reading frame 15	C18orf15	0.0067	-2.11225	147276	DB321566	Hs.675872
354	ADXECNTDJ.9279_s_at	Homo sapiens ubinuclein 2 (UBN2) mRNA.	UBN2	0.0006	-2.11825	254048	NM_173569	Hs.511486
355	ADXEC.167.C1_x_at	M-phase phosphoprotein 9	MPHOSPH9	0.0036	-2.12343	10198	CV571561	Hs.577404
356	ADXECAD.2204_at	Homo sapiens CRIM1 protein gene partial cds	CRIM1	0.0054	-2.1243	51232	AF168681	Hs.699247
357	ADXEC.10030.C1_at	Transcribed locus		0.0051	-2.1381		AL110177	Hs.724264
358	ADXEC.32853.C1_at	Transcribed locus		0.0066	-2.14741		AI610602	Hs.635523
359	ADXECADA.12169_x_at	Transcribed locus		0.0055	-2.15107		AI033391	Hs.594230
360	ADXEC.1517.C1_at	Homo sapiens solute carrier family 25 (mitochondrial carrier;	SLC25A11	0.0033	-2.15665	8402	NM_001165418	Hs.184877
361	ADXECCRS.6583_at	Homo sapiens von Willebrand factor C domain containing 2 (VWFC2)	VWFC2	0.0000	-2.15752	375567	NM_198570	Hs.629302
362	ADXEC.9824.C2_x_at	Homo sapiens deformed epidermal autoregulatory factor 1	DEAF1	0.0034	-2.15971	10522	NM_021008	Hs.243994
363	ADXEC.32767.C1_x_at	Homo sapiens Dnal homolog subfamily C member 1 (DNAJC1) gene complete cdsalterna	DNAJC1	0.0038	-2.16692	64215	EF444973	Hs.499000
364	ADXECADA.8411_x_at	MRNA		0.0073	-2.1735		N45998	Hs.594784

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
365	ADXECNTD1.6536_s_at	Homo sapiens adenosine A2b receptor (ADORA2B) mRNA.	ADORA2B	0.0090	-2.17455	136	NM_000676	Hs.167046
366	ADXEC.1386.C1_at	Parkinson disease (autosomal recessive early onset) 7	PARK7	0.0078	-2.17997	11315	BU682926	Hs.419640
367	ADXOCEC.13054.C1_at	Transcribed locus		0.0076	-2.18365		BU587510	Hs.587209
368	ADXECRS.7178_s_at	Non-protein coding RNA 183	NCRNA00183	0.0076	-2.19536	554203	CR601050	Hs.648316
369	ADXECRS.5126_s_at	Homo sapiens mitogen-activated protein kinase 1 (MAPK1) transcript	MAPK1	0.0081	-2.21044	5594	NM_002745	Hs.431850
370	ADXEC.33397.C1_at	Human DNA sequence from clone RP11-216B9 on chromosome 9 Contains the 3end of th	WDR34	0.0041	-2.21138	89891	AL356481	Hs.495240
371	ADXECADA.21596_s_at	Homo sapiens REST corepressor 3 (RCOR3) transcript variant 1	RCOR3	0.0013	-2.21817	55758	NM_001136223	Hs.356399
372	ADXEC.29005.C1_at	Homo sapiens vezatin adherens junctions transmembrane protein	VEZT	0.0035	-2.24273	55591	NM_017599	Hs.24135
373	ADXECADA.2172_at	Full length insert cDNA clone YU66F07		0.0045	-2.25166		H66282	Hs.690159
374	ADXEC.33482.C1-a_s_at	Homo sapiens chromosome 10 clone RP11-359E3 complete sequence.	RPL7AP8	0.0073	-2.2527	340749	AC067750	
375	ADXECAD.9160_x_at	Homo sapiens neuroligin 3 (NLGN3) transcript variant 3 mRNA.	NLGN3	0.0088	-2.25739	54413	NM_001166660	Hs.438877
376	ADXOCEC.10697.C1_x_at	Homo sapiens hypothetical protein LOC100128288 (LOC100128288)	LOC100128288	0.0091	-2.2574	100128288	NR_024447	Hs.549913
377	ADXECRS.18590_x_at	RAB member of RAS oncogene family-like 2A	RABL2A	0.0055	-2.27273	11159	BX494089	Hs.446425
378	ADXEC.16188.C1-a_s_at	Homo sapiens GRB2-associated	GAB1	0.0073	-2.28355	2549	NM_002039	Hs.80720

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
379	ADXEC.10617.C3_x_at	binding protein 1 (GAB1) transcript Radial spoke head 9 homolog (Chlamydomonas)	RSPH9	0.0015	-2.29694	221421	AI004786	Hs.534585
380	ADXECADA.12087_at	4791597		0.0045	-2.33355		AI343000	Hs.481342
381	ADXECAD.13693_at	Human DNA sequence from clone RP11-309N12 on chromosome 9 Contains part of the AU	AUH	0.0069	-2.33562	549	AL513353	Hs.175905
382	ADXEC.13258.C1_s_at	Homo sapiens solute carrier family 18 (vesicular monoamine) member	SLC18A2	0.0065	-2.34834	6571	NM_003054	Hs.596992
383	ADXEC.24828.C1_at	Valosin containing protein (p97)/p47 complex interacting protein 1	VCPIP1	0.0041	-2.35912	80124	AI624715	Hs.632066
384	ADXOCEC.12047.C1_at	Transcribed locus		0.0075	-2.36163		AA416764	Hs.483104
385	ADXEC.5079.C1_at	Homo sapiens E2F-associated phosphoprotein (EAPP) mRNA.	EAPP	0.0006	-2.36604	55837	NM_018453	Hs.433269
386	ADXECADA.6204_s_at	Homo sapiens butyrophilin subfamily 2 member A2 (BTN2A2)	BTN2A2	0.0001	-2.36605	10385	NM_181531	Hs.373938
387	ADXECRS.17454_s_at	CDNA FLJ26160 fis clone ADG02164		0.0003	-2.37699		CV330853	Hs.664886
388	ADXECRS.8137_at	Homo sapiens chromosome 17 open reading frame 75 (C17orf75) mRNA.	C17orf75	0.0078	-2.40411	64149	NM_022344	Hs.655257
389	ADXEC.10371.C1_s_at	Chromosome 1 open reading frame 187	C1orf187	0.0012	-2.42572	374946	AA974305	Hs.371716
390	ADXECEMUTR.6658_at	CDNA FLJ23933 fis clone COL07392		0.0001	-2.44134		BU732672	Hs.685751
391	ADXECADA.10862_at	Hypothetical LOC643749	LOC643749	0.0059	-2.47263	643749	AI500417	Hs.657289
392	ADXOCEC.13054.C1_x_at	Transcribed locus		0.0011	-2.47296		BU587510	Hs.587209
393	ADXOCEC.10697.C1_at	Homo sapiens hypothetical protein LOC100128288 (LOC100128288)	LOC100128288	0.0030	-2.47859	100128288	NR_024447	Hs.549913

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
394	ADXECRS.18590_at	RAB member of RAS oncogene family-like 2A	RABL2A	0.0021	-2.48401	11159	BX494089	Hs.446425
395	ADXECAD.13080_at	Transcribed locus		0.0052	-2.49977		BE929797	Hs.500245
396	ADXEC.13407.C1_at	Homo sapiens Cadependent secretion activator (CADPS) transcript	CADPS	0.0000	-2.53695	8618	NM_183393	Hs.654933
397	ADXEC.3342.C2_at	Homo sapiens zinc finger protein 540 (ZNF540) transcript variant	ZNF540	0.0050	-2.54341	163255	NM_001172226	Hs.121283
398	ADXECADA.20191_at	Homo sapiens low density lipoprotein receptor-related protein 2	LRP2	0.0042	-2.56904	4036	NM_004525	Hs.657729
399	ADXEC.17252.C1_at	Homo sapiens coiled-coil domain containing 96 (CCDC96) mRNA.	CCDC96	0.0085	-2.60712	257236	NM_153376	Hs.656757
400	ADXEC.14740.C1_at	Homo sapiens SEC14-like 2 (S. cerevisiae) (SEC14L2) transcript	SEC14L2	0.0024	-2.61311	23541	NM_012429	Hs.335614
401	ADXEC.34002.C1_s_at	F-box protein 21	FBXO21	0.0016	-2.6373	23014	AI394612	Hs.159699
402	ADXECADA.11185_at	Transcribed locus		0.0036	-2.68931		AI310380	Hs.635296
403	ADXEC.24507.C1_at	Homo sapiens WD repeat domain 78 (WDR78) transcript variant 1	WDR78	0.0010	-2.69279	79819	NM_024763	Hs.49421
404	ADXEC.28876.C1_at	Homo sapiens adenylylate cyclase activating polypeptide 1 (pituitary)	ADCYAP1	0.0000	-2.69536	116	NM_001099733	Hs.531719
405	ADXECNTD1.9467_s_at	Transcribed locus	LOC100128286	0.0010	-2.70026	100128286	AF130086	Hs.673135
406	ADXECEMUTR.7371_at	Homo sapiens genomic DNA chromosome 6p21.3 HLA Class I region.	C6orf26	0.0016	-2.70141	401251	BA000025	Hs.371225
407	ADXEC.7229.C1_s_at	Transcribed locus		0.0023	-2.7111		AA983959	Hs.666355

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
408	ADXEC.20881.C1_s_at	Homo sapiens histamine receptor H1 (HRH1) transcript variant 4	HRH1	0.0012	-2.71552	3269	NM_000861	Hs.1570
409	ADXEC.11669.C2-a_s_at	Homo sapiens zinc finger protein 764 (ZNF764) transcript variant	ZNF764	0.0012	-2.72248	92595	NM_001172679	Hs.132227
410	ADXEC.3448.C1_at	Homo sapiens zinc finger protein 823 (ZNF823) mRNA.	ZNF823	0.0052	-2.75746	55552	NM_001080493	Hs.142167
411	ADXEC.28948.C1_at	Transcribed locus		0.0091	-2.762		AI554062	Hs.710583
412	ADXECRS.6398_x_at	Homo sapiens hypothetical LOC80154 (LOC80154) non-coding RNA.	LOC80154	0.0018	-2.78038	80154	NR_026811	Hs.546614
413	ADXECAD.1982_at	Homo sapiens nemo like kinase (NLK) gene complete cds.	NLK	0.0019	-2.83233	51701	DQ316259	Hs.208759
414	ADXECRS.15353_x_at	Homo sapiens small nucleolar RNA C/D box 20 (SNORD20) small	SNORD20	0.0002	-2.85052	6082	NR_002908	
415	ADXECAD.18628_at	Homo sapiens thyroid hormone receptor alpha (erythroblastic	THRA	0.0097	-2.85501	7067	NM_199334	Hs.724
416	ADXECRS.30138_s_at	Homo sapiens Xg pseudogene Y- linked 2 (XGPY2) non-coding RNA.	XGPY2	0.0091	-2.87613	100132596	NR_003254	Hs.179675
417	ADXECAD.13807_at	CDNA FLJ12293 fis clone MAMMA1001815		0.0041	-2.88042		AI800518	Hs.659765
418	ADXECRS.7568_s_at	Homo sapiens sialic acid binding Ig- like lectin 6 (SIGLEC6)	SIGLEC6	0.0009	-2.89033	946	NM_001177549	Hs.720304
419	ADXEC.534.C1_s_at	Homo sapiens 24-dehydrocholesterol reductase (DHCR24) mRNA.	DHCR24	0.0063	-2.90224	1718	NM_014762	Hs.498727
420	ADXECADA.19311_at	Transcribed locus	LOC100129198	0.0083	-2.90526	100129198	AI207511	Hs.661697
421	ADXECADA.13175_x_at	Homo sapiens protein tyrosine	PTPN14	0.0068	-2.91863	5784	NM_005401	Hs.696573

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
422	ADXEC.2693.C2-a_s_at	phosphatase non-receptor type 14 Homo sapiens microtubule-associated protein 7 (MAP7) mRNA.	MAP7	0.0087	-2.93849	9053	NM_003980	Hs.486548
423	ADXECEMUTR.5340_s_at	Homo sapiens hypothetical LOC100128292 (LOC100128292) non-coding	LOC100128292	0.0048	-2.96232	100128292	NR_024585	Hs.547908
424	ADXECCRS.5978_s_at	PREDICTED: Homo sapiens hypothetical LOC646976 (LOC646976)	LOC646976	0.0082	-2.96731	646976	XR_079360	Hs.632485
425	ADXECCRS.23657_s_at	Homo sapiens zinc finger protein 20 (ZNF20) mRNA.	ZNF20	0.0081	-3.01692	7568	NM_021143	Hs.709334
426	ADXEC.17940.C1_at	Transcribed locus		0.0007	-3.01715		BQ184563	Hs.647834
427	ADXPCEC.758.C1_x_at	Homo sapiens ASCL3 gene CEGP1 gene C11orf14 gene C11orf15 gene C11orf16 gene and	TMEM9B	0.0016	-3.05994	57758	AJ400877	Hs.523468
428	ADXECAD.28669_s_at	Homo sapiens interleukin 17 receptor B (IL17RB) mRNA.	IL17RB	0.0042	-3.12914	55540	NM_018725	Hs.654970
429	ADXECADA.11360_at	Clone 23618 mRNA sequence		0.0071	-3.15505		BX090254	Hs.656681
430	ADXECAD.19257_s_at	Homo sapiens tubulin delta 1 (TUBD1) mRNA.	TUBD1	0.0036	-3.17201	51174	NM_016261	Hs.463638
431	ADXEC.34890.C1_x_at	Homo sapiens ST5 gene for suppression of tumorigenicity 5 L27a gene forribosomal	TRIM66	0.0018	-3.19213	9866	AJ400879	Hs.130836
432	ADXEC.19089.C1_at	Homo sapiens 3 BAC RP11-775J23 (Roswell Park Cancer Institute Human BAClibrary)	SLC12A8	0.0000	-3.21259	84561	AC108688	Hs.658514
433	ADXEC.14049.C2_at	Homo sapiens phosphodiesterase 4D	PDE4DIP	0.0045	-3.22454	9659	NM_022359	Hs.657490

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
434	ADXECAD.18824_s_at	interacting protein (PDE4DIP) Homo sapiens hypothetical LOC922249 (LOC922249) non-coding RNA.	LOC922249	0.0010	-3.2704	92249	NR_015353	Hs.708316
435	ADXEC.10714.C1_at	Homo sapiens BAC clone RP11- 69D13 from 4 complete sequence.	LOC100128651	0.0021	-3.27393	100128651	AC105915	Hs.536770
436	ADXECAD.12161_at	Homo sapiens regulator of G-protein signaling 7 (RGS7) mRNA.	RGS7	0.0073	-3.27528	6000	NM_002924	Hs.655739
437	ADXECEMUTR.3428_at	Homo sapiens mRNA for CD33L1 complete cds.	SIGLEC6	0.0081	-3.31061	946	D86358	Hs.720304
438	ADXEC.13696.C1_at	Homo sapiens SH3 domain binding glutamic acid-rich protein	SH3BGR	0.0058	-3.35004	6450	NM_001001713	Hs.473847
439	ADXEC.10617.C3_at	Radial spoke head 9 homolog (Chlamydomonas)	RSPH9	0.0001	-3.42022	221421	AI004786	Hs.534585
440	ADXOCEC.12679.C1_at	Homo sapiens hypothetical protein MGC16121 (MGC16121) non-coding	MGC16121	0.0034	-3.492	84848	NR_024607	Hs.416379
441	ADXEC.15328.C1_at	Homo sapiens solute carrier family 16 member 6 (monocarboxylic	SLC16A6	0.0086	-3.50693	9120	NM_001174166	Hs.42645
442	ADXEC.27369.C1_at	hypothetical protein [Macaca mulatta]		0.0092	-3.53224		AW236366	Hs.661256
443	ADXEC.8250.C1_s_at	OAF homolog (Drosophila)	OAF	0.0085	-3.56477	220323	AA902624	Hs.445081
444	ADXEC.14562.C1_at	Homo sapiens SET domain containing 4 (SETD4) transcript variant 1	SETD4	0.0028	-3.58437	54093	NM_017438	Hs.606200
445	ADXEC.9034.C1-a_s_at	Homo sapiens chromosome 8 open reading frame 84 (C8orf84) mRNA.	C8orf84	0.0087	-3.6202	157869	NM_153225	Hs.439040
446	ADXECADA.13201_at	Zinc finger protein 90 homolog	ZFP90	0.0012	-3.6792	146198	AW135652	Hs.461074

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
447	ADXEC.25324.C3_s_at	(mouse) Homo sapiens chromosome 7 open reading frame 63 (C7orf63)	C7orf63	0.0009	-3.72594	79846	NM_001160138	Hs.657403
448	ADXECAD.7070_at	Homo sapiens GRB2-associated binding protein 1 (GAB1) transcript	GAB1	0.0075	-3.80155	2549	NM_002039	Hs.80720
449	ADXEC.34890.C1_at	Homo sapiens ST5 gene for suppression of tumorigenicity 5 L27a gene forribosomal	TRIM66	0.0010	-3.84621	9866	AJ400879	Hs.130836
450	ADXECADA.21374_s_at	Homo sapiens chromosome X multiple clones map p11.23 complete sequence.	PCSK1N	0.0016	-3.86859	27344	AF196971	Hs.522640
451	ADXECRS.45122_x_at	Homo sapiens small nucleolar RNA C/D box 121A (SNORD121A) small	SNORD121A	0.0035	-3.97126	100113379	NR_003685	
452	ADXEC.28475.C1_at	Transcribed locus		0.0077	-3.98044		BQ686844	Hs.683694
453	ADXECADA.7446_at	Homo sapiens GDNF family receptor alpha 1 (GFRA1) transcript	GFRA1	0.0085	-3.9827	2674	NM_001145453	Hs.388347
454	ADXEC.26460.C1_at	Transcribed locus		0.0008	-4.11222		AI916068	Hs.671496
455	ADXECAD.7070_x_at	Homo sapiens GRB2-associated binding protein 1 (GAB1) transcript	GAB1	0.0061	-4.13368	2549	NM_002039	Hs.80720
456	ADXECAD.22862_s_at	Homo sapiens membrane-spanning 4-domains subfamily A member 2 (Fc	MS4A2	0.0080	-4.25536	2206	NM_000139	Hs.386748
457	ADXEC.13979.C1_at	Homo sapiens Na ⁺ /K ⁺ exchanger domain containing 2 (NHEDC2) nuclear	NHEDC2	0.0033	-4.26094	133308	NM_178833	Hs.546482
458	ADXECRS.22100_at	Homo sapiens heparanase 2 (HPSE2) transcript variant 4 mRNA.	HPSE2	0.0099	-4.2979	60495	NM_001166246	Hs.689544

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)	Entrez gene Id	Target Acc	Unigene Id
459	ADXEC.27569.C1_at	Homo sapiens progesterone receptor (PGR) mRNA.	PGR	0.0027	-4.75422	5241	NM_000926	Hs.32405
460	ADXEC.27569.C1_x_at	Homo sapiens progesterone receptor (PGR) mRNA.	PGR	0.0070	-4.95331	5241	NM_000926	Hs.32405
461	ADXECRS.14720_s_at	Homo sapiens solute carrier family 18 (vesicular monoamine) member	SLC18A2	0.0071	-4.9696	6571	NM_003054	Hs.596992
462	ADXECAD.14333_at	Homo sapiens PAC clone RP5-837C9 from 7 complete sequence.	AUTS2	0.0096	-5.62883	26053	AC006319	Hs.21631
463	ADXEC.29654.C1_at	Transcribed locus		0.0000	-5.75429		AA888671	Hs.667931
464	ADXECAD.14333_x_at	Homo sapiens PAC clone RP5-837C9 from 7 complete sequence.	AUTS2	0.0096	-5.78117	26053	AC006319	Hs.21631
465	ADXECAD.28655_s_at	Homo sapiens kelch repeat and BTB (POZ) domain containing 4	KBTBD4	0.0018	-5.79232	55709	NM_018095	Hs.718483
466	ADXEC.17947.C1_at	Homo sapiens cDNA FLJ14142 fis clone MAMMA1002880.	ERBB4	0.0089	-5.96387	2066	AK024204	Hs.390729
467	ADXEC.28164.C1_at	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary)	ADCYAP1	0.0010	-6.19958	116	NM_001099733	Hs.531719
468	ADXEC.34080.C1_s_at	Transcribed locus		0.0002	-6.85193		AU155091	Hs.685245
469	ADXEC.23926.C1_at	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary)	ADCYAP1	0.0017	-7.72128	116	NM_001099733	Hs.531719
470	ADXECEMUTR.4370_at	Homo sapiens pregnancy-induced hypertension syndrome-related protein 4(PIH4) mRNA		0.0012	-9.56948		AF361250	

Supplemental Table 3: Cav1 Negative vs. Cav1 Positive (page 81 through page 158)

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1	ADXEC.522.C17_x_at	PREDICTED: Homo sapiens similar to major histocompatibility	LOC100290966	0.0281	8.25
2	ADXEC.9453.C1_x_at	Homo sapiens paternally expressed 10 (PEG10) transcript variant 2	PEG10	0.0269	7.6
3	ADXEC.19900.C1_at	Homo sapiens hypothetical protein LOC100293390	LOC100293390	0.01	7.14
4	ADXEC.9453.C1_at	Homo sapiens paternally expressed 10 (PEG10) transcript variant 2	PEG10	0.0307	6.95
5	ADXECRS.12320_at	Homo sapiens paternally expressed 3 (PEG3) transcript variant 5	PEG3	0.0285	5.25
6	ADXEC.4213.C1_s_at	Homo sapiens hypothetical LOC404266 (LOC404266) non-coding RNA.	LOC404266	0.0316	5.18
7	ADXECRS.32128_at	Homo sapiens RFT1 homolog (S. cerevisiae) (RFT1) mRNA.	RFT1	0.0237	5.13
8	ADXEC.31458.C1_at	Homo sapiens polymerase (DNA directed) nu (POLN) gene complete cds.	POLN	0.0244	4.91
9	ADXEC.32873.C1_x_at	Ring finger protein 217	RNF217	0.0052	4.79
10	ADXEC.28330.C1_s_at	hypothetical protein [Pan troglodytes]		0.026	4.7
11	ADXEC.26338.C1-a_s_at	Homo sapiens piggyBac transposable element derived 2 (PGBD2)	PGBD2	0.0075	4.69
12	ADXEC.30057.C1_s_at	Homo sapiens lactamase beta (LACTB) nuclear gene encoding	LACTB	0.0016	4.62
13	ADXECNTDJ.1029_s_at	Homo sapiens tRNA isopentenyltransferase 1 (TRIT1) mRNA.	TRIT1	0.0051	4.38
14	ADXEC.32873.C1_at	Ring finger protein 217	RNF217	0.0074	4.35
15	ADXECRS.3766_s_at	Homo sapiens pyruvate dehydrogenase phosphatase regulatory subunit	PDPR	0.0131	4.15
16	ADXEC.2392.C8_at	Homo sapiens chromosome 8 clone XX-72A2 map 8p23 complete sequence.		0.0211	4.12
17	ADXECNTDJ.3411_s_at	H. sapiens mRNA for T cell receptor alpha chain variable region (cloneP3_15)		0.0366	4.08
18	ADXECRS.10328_s_at	Homo sapiens similar to major histocompatibility	LOC731682	0.0389	4.02
19	ADXEC.12395.C1_at	Homo sapiens hypothetical LOC654433 (LOC654433) non-coding RNA.	LOC654433	0.0011	4
20	ADXEC.2392.C8_x_at	Homo sapiens chromosome 8 clone XX-72A2 map 8p23 complete sequence.		0.0146	3.98
21	ADXEC.4008.C2_s_at	Homo sapiens DNA fragmentation factor 45kDa alpha polypeptide	DFFA	0.0085	3.94
22	3470276_at			0.035	3.87
23	ADXECNTDJ.4382_s_at	Homo sapiens neural precursor cell expressed developmentally	NEDD4L	0.0464	3.87

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
24	ADXPCEC.12489.C1_at	Homo sapiens T-cell gamma receptor locus complete sequence.	TRGVB	0.0153	3.86
25	ADXEC.491.C15_x_at	Homo sapiens RPS16 gene for ribosomal protein S16 complete cds and sequence.	RPS16	0.0232	3.86
26	ADXEC.22568.C1_s_at	Homo sapiens hypothetical LOC220906 (LOC220906) non-coding RNA.	LOC220906	0.0184	3.85
27	ADXEC.16346.C1_at	Homo sapiens mRNA for FLJ00095 protein.	DNAJC5	0.0049	3.83
28	ADXECRS.32128_x_at	Homo sapiens RFT1 homolog (S. cerevisiae) (RFT1) mRNA.	RFT1	0.0214	3.83
29	ADXECRS.38829_at	Homo sapiens zinc finger protein 365 (ZNF365) transcript variant	ZNF365	0.0085	3.76
30	ADXECNTD1.1583_s_at	Homo sapiens C2 calcium-dependent domain containing 4C (C2CD4C)	C2CD4C	0.0204	3.74
31	ADXECAD.26784_s_at	Homo sapiens killer cell lectin-like receptor subfamily D member 1	KLRD1	0.0324	3.74
32	ADXECADA.18213_at	Transcribed locus		0.0013	3.7
33	ADXECRS.38829_x_at	Homo sapiens zinc finger protein 365 (ZNF365) transcript variant	ZNF365	0.0056	3.67
34	ADXEC.23287.C1_s_at	CD300e molecule	CD300E	0.0384	3.67
35	ADXEC.11581.C1_at	Homo sapiens DAZ associated protein 2 (DAZAP2) transcript variant	DAZAP2	0.0393	3.65
36	ADXEC.31458.C1_x_at	Homo sapiens polymerase (DNA directed) nu (POLN) gene complete cds.	POLN	0.0268	3.63
37	ADXECAD.12789_s_at	Homo sapiens chromosome 19 BC335474 (CIT-HSPC_482H14) complete sequence.	LOC100128439	0.0245	3.61
38	ADXEC.19873.C1_at	Homo sapiens cDNA FLJ56914 complete cds highly similar to Rattus norvegicus rcd1	RQCD1	0.0514	3.6
39	ADXEC.17269.C1_s_at	MDN1 midasin homolog (yeast)	MDN1	0.0078	3.59
40	ADXEC.27761.C1_at	Transcribed locus		0.0127	3.59
41	ADXECRS.29962_s_at	Homo sapiens neutrophil cytosolic factor 1 (NCF1) mRNA.	NCF1	0.0367	3.57
42	ADXEC.22550.C1_at	Transcribed locus		0.0451	3.57
43	ADXECMUTR.3609_at	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog	ERG	0.0061	3.56
44	ADXECADA.4604_s_at	Homo sapiens RNA binding motif single stranded interacting protein	RBMS2	0.0186	3.56
45	ADXECADA.24499_s_at	Homo sapiens phosphodiesterase 6B cGMP-specific rod beta	PDE6B	0.047	3.54

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
46	ADXEC.6133.C2_s_at	leukocyte immunoglobulin-like receptor subfamily B (with TM and ITIM domains) me	LILRB3	0.0265	3.52
47	ADXECRS.10595_s_at	Homo sapiens transmembrane and coiled-coil domain family 1 (TMCC1)	TMCC1	0.0297	3.52
48	ADXEC.686.C6_s_at	Homo sapiens cathepsin B (CTSB) transcript variant 4 mRNA.	CTSB	0.0089	3.51
49	ADXEC.7503.C1_s_at	Homo sapiens dipeptidyl-peptidase 3 (DPP3) transcript variant 1	DPP3	0.0214	3.5
50	ADXECNTDJ.7965_at	Homo sapiens IL2RG mRNA for IL2RG nirs variant 1 complete cds.	IL2RG	0.0228	3.5
51	ADXEC.2081.C1_s_at	Interferon stimulated exonuclease gene 20kDa	ISG20	0.0255	3.5
52	ADXECNTDJ.7322_s_at	Homo sapiens GINS complex subunit 1 (Psf1 homolog) (GINS1) mRNA.	GINS1	0.0104	3.48
53	ADXEC.26095.C1_at	Human DNA sequence from clone RP5-1042K10 on chromosome 22q13.1-13.2Contains the	SGSM3	0.0032	3.44
54	ADXEC.2002.C2_at	Homo sapiens myosin light chain 5 regulatory (MYL5) mRNA.	MYL5	0.009	3.42
55	ADXPCEC.12489.C2_s_at	Homo sapiens T-cell gamma receptor locus complete sequence.	TRGVB	0.018	3.42
56	ADXEC.17526.C1-a_s_at	Transcribed locus		0.0064	3.39
57	ADXEC.4533.C4_at	Transcribed locus		0.0388	3.38
58	ADXEC.4766.C1-a_s_at	Homo sapiens LAS1-like (<i>S. cerevisiae</i>) (LAS1L) transcript variant	LAS1L	0.0233	3.37
59	ADXEC.19017.C1_at	Homo sapiens CD84 molecule (CD84) transcript variant 4 mRNA.	CD84	0.0267	3.35
60	ADXEC.19477.C1_at	H.sapiens DMA DMB HLA-Z1 IPP2 LMP2 TAP1 LMP7 TAP2 DOB DQB2 andRING8 9 13 and 14	HLA-Z	0.0004	3.34
61	ADXEC.11663.C1_s_at	Homo sapiens IKAROS family zinc finger 1 (Ikaros) (IKZF1) mRNA.	IKZF1	0.0035	3.34
62	ADXEC.1082.C15_s_at	Homo sapiens tropomyosin 3 (TPM3) transcript variant 1 mRNA.	TPM3	0.0218	3.34
63	ADXEC.1862.C1_s_at	Homo sapiens peroxisomal biogenesis factor 19 (PEX19) transcript	PEX19	0.0528	3.34
64	ADXECNTDJ.7787_s_at	Homo sapiens complement component 5a receptor 1 (C5AR1) mRNA.	C5AR1	0.0118	3.33
65	ADXECADA.12961_at	Transcribed locus		0.0368	3.33
66	ADXECRS.20577_at	Homo sapiens chromosome 15 open reading frame 23 (C15orf23)	C15orf23	0.0098	3.32
67	2599909_at			0.0114	3.28

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
68	ADXEC.14486.C1_at	CDNA FLJ42497 fis clone BRACE2035278		0.0164	3.28
69	ADXEC.25005.C1_s_at	Homo sapiens mannosyl (alpha-13-)-glycoprotein	MGAT4A	0.0243	3.28
70	ADXECEMUTR.3721_at	Homo sapiens CD84 mRNA alternatively spliced complete cds.	CD84	0.0013	3.27
71	ADXEC.3341.C2_x_at	Homo sapiens Fc fragment of IgG low affinity IIb receptor (CD32)	FCGR2B	0.0187	3.27
72	ADXPCEC.16710.C1_at	Homo sapiens zinc finger and SCAN domain containing 18 mRNA (cdna cloneIMAGE:461	ZSCAN18	0.051	3.27
73	ADXEC.29785.C1_s_at	Human MLL-AF4 der(11) fusion protein mRNA complete cds.	AFF1	0.0121	3.25
74	ADXECADA.8726_at	Homo sapiens chromosome 21 segment HS21C049.	C21orf7	0.0012	3.24
75	ADXECNTDJ.3576_s_at	Homo sapiens valosin-containing protein (VCP) mRNA.	VCP	0.0118	3.24
76	ADXEC.15047.C2-a_s_at	Homo sapiens Sin3A-associated protein 130kDa (SAP130) transcript	SAP130	0.0322	3.24
77	ADXEC.13002.C1_s_at	Homo sapiens vacuolar protein sorting 26 homolog B (S. pombe)	VPS26B	0.003	3.23
78	ADXECRS.42581_at	Homo sapiens small nucleolar RNA C/D box 2 (SNORD2) small	SNORD2	0.0276	3.23
79	ADXECAD.8596_s_at	Homo sapiens parvin gamma (PARVG) transcript variant 2 mRNA.	PARVG	0.0258	3.21
80	ADXECRS.3112_at	Chromosome 10 open reading frame 18	C10orf18	0.0179	3.2
81	ADXECEMUTR.467_s_at	Homo sapiens suppressor of fused homolog (Drosophila) (SUFU)	SUFU	0.0002	3.19
82	ADXECAD.11893_at	Transcribed locus		0.0044	3.19
83	ADXEC.491.C13_s_at	Homo sapiens RPS16 gene for ribosomal protein S16 complete cds andsequence.	RPS16	0.0486	3.19
84	ADXEC.31324.C1_at	Homo sapiens mutS homolog 6 (E. coli) (MSH6) gene complete cds.	MSH6	0.0073	3.17
85	ADXEC.11813.C1-a_s_at	F-box and leucine-rich repeat protein 4	FBXL4	0.0336	3.16
86	ADXEC.8734.C1_s_at	Homo sapiens sphingosine-1-phosphate receptor 3 (S1PR3) mRNA.	S1PR3	0.0017	3.15
87	ADXECAD.23267_s_at	Homo sapiens macrophage scavenger receptor 1 (MSR1) transcript	MSR1	0.0105	3.15
88	ADXEC.7415.C3_at	Homo sapiens TATA box binding protein (TBP)-associated factor RNA	TAF1D	0.0168	3.15
89	ADXEC.29904.C1_at	Transcribed locus		0.0079	3.12
90	3570087_at			0.0217	3.12

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91	ADXEC.23065.C1_at	Transcribed locus strongly similar to NP_001129295.1 sarcospan isoform 2 [Homo s		0.0395	3.12
92	ADXECAD.15182_at	Homo sapiens BCL2-like 11 (apoptosis facilitator) (BCL2L11)	BCL2L11	0.0009	3.1
93	ADXOCEC.4815.C3_x_at	Homo sapiens Fc fragment of IgG low affinity IIb receptor (CD32)	FCGR2B	0.0078	3.1
94	ADXEC.23335.C1_at	Transcribed locus strongly similar to NP_065605.2 negative elongation factor D [		0.0299	3.08
95	ADXEC.261.CB3_s_at	Homo sapiens triosephosphate isomerase 1 (TPI1) transcript variant	TPI1	0.0106	3.07
96	ADXEC.33560.C1_at	Human chromosome 14 DNA sequence BAC R-873E2 of library RPCI-11 from chromosome 1	C14orf183	0.0424	3.07
97	ADXECADA.12329_at	Transcribed locus		0.017	3.04
98	ADXEC.652.C3-a_s_at	Homo sapiens replication factor C (activator 1) 5 36.5kDa (RFC5)	RFC5	0.0022	3.03
99	ADXECRS.28664_s_at	Homo sapiens caspase recruitment domain family member 16 (CARD16)	CARD16	0.0239	3.03
100	ADXOCEC.13389.C1-a_s_at	Homo sapiens branched chain amino-acid transaminase 1 cytosolic	BCAT1	0.0256	3.02
101	ADXEC.3854.C1_s_at	Homo sapiens diacylglycerol kinase alpha 80kDa (DGKA) transcript	DGKA	0.0387	3.02
102	3725819_at			0.0161	3.01
103	ADXEC.15068.C1-a_s_at	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide F 39	POLR3F	0.0226	3.01
104	ADXECAD.13017_s_at	Homo sapiens nuclear transcription factor Y beta (NFYB) mRNA.	NFYB	0.0411	3.01
105	ADXEC.5487.C2_s_at	Homo sapiens paroxysmal nonkinetic dyskinesia (PNKD) nuclear	PNKD	0.0474	3.01
106	ADXECAD.24396_s_at	Homo sapiens YKT6 v-SNARE homolog (S. cerevisiae) (YKT6) mRNA.	YKT6	0.0482	3.01
107	ADXEC.2091.C1-a_s_at	Homo sapiens RAB3D member RAS oncogene family (RAB3D) mRNA.	RAB3D	0.0089	3
108	ADXECADA.11237_at	Homo sapiens PP2A B56 gamma gene complete cds alternative spliceproducts.	PPP2R5C	0.0242	3
109	ADXECNTDJ.5475_s_at	Homo sapiens fibronectin type III domain containing 3B (FNDC3B)	FNDC3B	0.0398	3
110	ADXECADA.4265_at	Human DNA sequence from clone RP5-886K2 on chromosome 1p35.1-36.12 Containsa neu	C1orf128	0.0452	3
111	ADXEC.17437.C1_at	Transcribed locus		0.0015	2.99
112	ADXEC.23718.C1_s_at	Similar to hCG2038853	LOC100128943	0.0022	2.99

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113	ADXECADA.13253_at	Transcribed locus		0.0278	2.99
114	ADXECAD.14621_at	Transcribed locus		0.0505	2.99
115	ADXECRS.22704_s_at	Homo sapiens proteasome (prosome macropain) subunit beta type 9	PSMB9	0.0026	2.98
116	ADXEC.19258.C1_at	polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)	GALNT11	0.0079	2.98
117	ADXEC.31403.C1_at	CDNA FLJ12399 fis clone MAMMA1002780		0.0245	2.98
118	ADXECAD.7829_s_at	Homo sapiens apolipoprotein C-II (APOC2) mRNA.	APOC2	0.0002	2.97
119	ADXEC.18483.C2_at	Homo sapiens TRAF3 interacting protein 3 (TRAF3IP3) mRNA.	TRAF3IP3	0.0124	2.97
120	ADXECRS.31469_s_at	Homo sapiens consoritin connexin sorting protein (CNST) transcript	CNST	0.0211	2.97
121	ADXEC.14896.C1_at	Transcribed locus		0.0349	2.97
122	ADXECAD.2438_s_at	Homo sapiens F-box protein 10 (FBXO10) mRNA.	FBXO10	0.0491	2.97
123	ADXECAD.12843_at	Transcribed locus		0.0005	2.96
124	ADXECAD.8877_at	Homo sapiens protocadherin 11 X-linked (PCDH11X) transcript	PCDH11X	0.0133	2.96
125	ADXECNTDJ.9365_s_at	pleckstrin homology domain containing family A (phosphoinositide binding specific)	PLEKHA2	0.0141	2.96
126	ADXECRS.14061_at	Homo sapiens tumor necrosis factor (ligand) superfamily member 8	TNFSF8	0.0276	2.96
127	ADXEC.12576.C1_at	Homo sapiens kinesin family member 5C (KIF5C) mRNA.	KIF5C	0.0345	2.96
128	ADXECAD.13677_at	Homo sapiens serine palmitoyl transferase subunit II gene complete cds	ISM2	0.0005	2.95
129	ADXEC.15135.C1_at	Homo sapiens PMS2 C-terminal like pseudogene (PMS2CL) non-coding	PMS2CL	0.0013	2.95
130	ADXEC.7572.C1_at	Homo sapiens RD RNA binding protein (RDBP) mRNA.	RDBP	0.0014	2.95
131	ADXECADA.18686_s_at	Transcribed locus		0.0072	2.95
132	ADXEC.13587.C1_s_at	Homo sapiens solute carrier family 12 (potassium/chloride)	SLC12A6	0.0208	2.95
133	ADXEC.34747.C1_s_at	Serine racemase	SRR	0.0247	2.91
134	ADXEC.31099.C1_at	Homo sapiens USP6 N-terminal like (USP6NL) transcript variant 1	USP6NL	0.0052	2.9
135	ADXEC.12456.C1_at	Homo sapiens NOD2 gene for LRR-containing protein exons 1-11	NOD2	0.0064	2.9
136	ADXEC.4499.C2-a_s_at	Homo sapiens G1 to S phase transition 2 (GSPT2) mRNA.	GSPT2	0.0078	2.9

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137	ADXEC.4933.C1_s_at	Homo sapiens ER degradation enhancer mannosidase alpha-like 2	EDEM2	0.0109	2.9
138	ADXECAD.11953_s_at	Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA.	MTAP	0.0396	2.9
139	ADXECEMUTR.8031_at	TAF13 RNA polymerase II TATA box binding protein (TBP)-associated factor 18kDa	TAF13	0.0084	2.89
140	ADXEC.7176.C1_s_at	Transcribed locus		0.0098	2.89
141	ADXEC.9076.C1_s_at	Homo sapiens pyruvate kinase muscle (PKM2) gene complete cds.	PKM2	0.0431	2.89
142	ADXEC.32186.C1_at	Homo sapiens H2A histone family member X (H2AFX) mRNA.	H2AFX	0.0061	2.88
143	ADXEC.31712.C1_s_at	Homo sapiens PTPRF interacting protein binding protein 1 (liprin	PPFIBP1	0.0121	2.88
144	ADXLCEC.3953.C1_at	Homo sapiens CD86 molecule (CD86) transcript variant 2 mRNA.	CD86	0.0173	2.88
145	ADXECNTDJ.7829_s_at	Homo sapiens CD53 molecule (CD53) transcript variant 2 mRNA.	CD53	0.0035	2.87
146	ADXEC.4933.C2_s_at	Homo sapiens ER degradation enhancer mannosidase alpha-like 2	EDEM2	0.0125	2.86
147	ADXEC.554.C4_at	Homo sapiens isocitrate dehydrogenase 3 (NAD) beta (IDH3B)	IDH3B	0.0155	2.86
148	ADXECAD.7889_at	Homo sapiens glycine amidinotransferase (L-arginine:glycine	GATM	0.0227	2.86
149	ADXEC.21508.C1_at	Homo sapiens truncated cytochrome P450 family 3 subfamily A polypeptide5 (CYP3A5	CYP3A5	0.008	2.85
150	ADXECADA.13951_at	Transcribed locus		0.017	2.85
151	ADXECAD.16976_at	Hypothetical protein LOC100129884	LOC100129884	0.0211	2.85
152	ADXEC.19477.C1_x_at	H.sapiens DMA DMB HLA-Z1 IPP2 LMP2 TAP1 LMP7 TAP2 DOB DQB2 andRING8 9 13 and 14	HLA-Z	0.0005	2.84
153	ADXEC.34784.C1_at	DDB1 and CUL4 associated factor 8	DCAF8	0.0015	2.84
154	ADXECAD.22944_s_at	Homo sapiens neutrophil cytosolic factor 4 40kDa (NCF4)	NCF4	0.0262	2.84
155	ADXECADA.18263_at	Transcribed locus		0.0134	2.83
156	ADXEC.22235.C1_x_at	Homo sapiens poliovirus receptor related immunoglobulin domain	PVRIG	0.0407	2.83
157	ADXEC.34663.C1_at	CDNA FLJ27105 fis clone SPL05019		0.0472	2.83
158	ADXEC.8565.C2_s_at	Transcribed locus		0.0037	2.82

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159	ADXEC.3104.C1_at	CTTNBP2 N-terminal like	CTTNBP2NL	0.0056	2.82
160	ADXECAD.10405_at	Homo sapiens TWIST neighbor (TWISTNB) mRNA.	TWISTNB	0.0211	2.82
161	ADXEC.972.C1_x_at	Homo sapiens TYRO3 protein tyrosine kinase (TYRO3) mRNA.	TYRO3	0.0254	2.82
162	ADXECAD.19874_at	Transcribed locus		0.039	2.82
163	ADXECAD.18329_at	Transcribed locus		0.0153	2.81
164	ADXEC.27214.C1_at	Nucleoporin 214kDa	NUP214	0.0261	2.8
165	ADXECAD.28637_s_at	Homo sapiens blood vessel epicardial substance (BVES) transcript	BVES	0.0395	2.78
166	ADXECNTDJ.3978_at	Homo sapiens protein kinase C substrate 80K-H (PRKCSH) transcript	PRKCSH	0.0521	2.78
167	ADXEC.17933.C1_s_at	Transcribed locus		0.0032	2.77
168	ADXEC.16064.C1_s_at	Homo sapiens SLAM family member 8 (SLAMF8) mRNA.	SLAMF8	0.0122	2.77
169	ADXECRS.18114_s_at	Similar to Quinone oxidoreductase-like protein 2	LOC100131700	0.0143	2.77
170	ADXECNTDJ.6816_at	Homo sapiens solute carrier family 10 (sodium/bile acid	SLC10A7	0.0164	2.77
171	ADXEC.23283.C1_s_at	Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2)	EZH2	0.0213	2.77
172	ADXECADA.1090_at	Full length insert cDNA clone YR23G01		0.0284	2.77
173	ADXEC.5772.C1_at	Homo sapiens chromosome 3 open reading frame 23 (C3orf23)	C3orf23	0.0328	2.77
174	ADXECRS.12931_at	Homo sapiens protein phosphatase Mg2? dependent 1K (PPM1K)	PPM1K	0.0349	2.77
175	ADXECRS.3727_s_at	Homo sapiens homeobox A4 (HOXA4) mRNA.	HOXA4	0.0436	2.77
176	ADXECAD.13677_x_at	Homo sapiens serine palmitoyl transferase subunit II gene complete cds	ISM2	0.0086	2.76
177	ADXECAD.16692_s_at	Antigen MMSA-2 mRNA sequence		0.0241	2.76
178	ADXECAD.18570_at	Homo sapiens potassium channel tetramerisation domain containing 20	KCTD20	0.0006	2.75
179	ADXEC.16191.C1_at	Homo sapiens hyaluronan-mediated motility receptor (RHAMM) (HMMR)	HMMR	0.0097	2.75
180	ADXECADA.18168_at	Homo sapiens SH3-containing protein EEN (EEN) and chromatin assemblyfactor-I p15	CHAF1A	0.0114	2.75
181	ADXECADA.24429_at	Homo sapiens microfibillar-associated protein 3-like (MFAP3L)	MFAP3L	0.0435	2.75
182	3740562_at			0.049	2.74

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183	ADXEC.18082.C1_at	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1) transcript	RYR1	0.004	2.73
184	ADXECAD.16653_s_at	Homo sapiens bromodomain adjacent to zinc finger domain 1B	BAZ1B	0.0236	2.73
185	ADXEC.6363.C1_at	Homo sapiens glycosyltransferase 25 domain containing 1 (GLT25D1)	GLT25D1	0.0432	2.73
186	ADXEC.9513.C1_x_at	Homo sapiens interferon regulatory factor 5 (IRF5) transcript	IRF5	0.0473	2.73
187	ADXEC.30999.C1_at	Homo sapiens genomic DNA chromosome 21q section 57/105.		0.0275	2.72
188	ADXEC.2585.C3_s_at	Homo sapiens bromodomain containing 2 (BRD2) transcript variant 2	BRD2	0.0534	2.72
189	ADXECAD.9207_s_at	Homo sapiens MDN1 midasin homolog (yeast) (MDN1) mRNA.	MDN1	0.0284	2.71
190	ADXEC.29992.C1_s_at	Transcribed locus		0.0398	2.71
191	ADXEC.1467.C1_at	UTP18 small subunit (SSU) processome component homolog (yeast)	UTP18	0.0421	2.71
192	ADXPCEC.473.C1-a_s_at	FLJ21028 fis clone CAE07155		0.0006	2.7
193	ADXECAD.20904_s_at	Homo sapiens death effector domain containing (DEDD) transcript	DEDD	0.0353	2.7
194	ADXECAD.14082_at	Transcribed locus		0.0126	2.69
195	ADXEC.13261.C1_s_at	Homo sapiens Down syndrome critical region gene 3 (DSCR3) mRNA.	DSCR3	0.0214	2.69
196	ADXECAD.371_s_at	Homo sapiens serologically defined colon cancer antigen 8	SDCCAG8	0.0256	2.69
197	ADXEC.28432.C1_s_at	Homo sapiens Hermansky-Pudlak syndrome 1 (HPS1) transcript variant	HPS1	0.0297	2.69
198	ADXECAD.18616_s_at	Homo sapiens T cell receptor gamma variable 3 mRNA (cDNA clone IMAGE:5229127).	TRGV3	0.0338	2.69
199	ADXPCEC.14412.C2_at	Homo sapiens protein kinase C beta (PRKCB1) gene complete cds.		0.044	2.69
200	ADXEC.29808.C1_at	Transcribed locus		0.0064	2.68
201	Adx-200070-up_s_at	Homo sapiens chromosome 2 open reading frame 24 (C2orf24) mRNA.	C2orf24	0.0165	2.68
202	ADXECEMUTR.2840_x_at	Homo sapiens T cell receptor gamma variable 3 mRNA (cDNA clone IMAGE:5229127).	TRGV3	0.0217	2.68
203	ADXECAD.12447_s_at	Homo sapiens transmembrane and coiled-coil domain family 1 (TMCC1)	TMCC1	0.0277	2.68
204	ADXECADA.18527_at	Transcribed locus		0.0367	2.68
205	ADXEC.6350.C1_s_at	Homo sapiens dishevelled dsh homolog 3 (Drosophila) (DVL3) mRNA.	DVL3	0.038	2.68

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206	ADXEC.29014.C1_at	Homo sapiens chromosome 14 clones CTD-3211F8 and RP11-173A8 containing KIAA0317 g	YIPM1	0.0483	2.68
207	ADXPCEC.15695.C1-a_s_at	CDNA FLJ141419 fis clone BRHIP2002339		0.0544	2.68
208	ADXEC.9262.C1_at	Homo sapiens methyltransferase like 3 (METTL3) mRNA.	METTL3	0.0002	2.67
209	ADXEC.18142.C1_at	Transcribed locus		0.008	2.67
210	ADXECAD.4629_at	Clone 23712 mRNA sequence		0.0284	2.67
211	ADXEC.472.C3_s_at	Homo sapiens Mov10 Moloney leukemia virus 10 homolog (mouse)	MOV10	0.0529	2.67
212	ADXEC.4927.C1_at	Homo sapiens complement component 1 r subcomponent-like (C1RL)	C1RL	0.016	2.66
213	ADXEC.972.C1_at	Homo sapiens TYRO3 protein tyrosine kinase (TYRO3) mRNA.	TYRO3	0.0181	2.66
214	ADXLCEC.816.C1_s_at	Homo sapiens fukutin related protein (FKRP) transcript variant 2	FKRP	0.0202	2.66
215	ADXEC.10083.C2_s_at	Homo sapiens NFKB inhibitor interacting Ras-like 2 (NKIRAS2)	NKIRAS2	0.0138	2.65
216	ADXEC.9513.C1_at	Homo sapiens interferon regulatory factor 5 (IRF5) transcript	IRF5	0.0388	2.65
217	ADXECADA.18562_at	Transcribed locus		0.0497	2.65
218	ADXEC.4246.C1_at	Homo sapiens chromosome 16 open reading frame 75 (C16orf75) mRNA.	C16orf75	0.0503	2.65
219	ADXEC.27951.C1_at	Homo sapiens cAMP responsive element modulator (CREM) transcript	CREM	0.0517	2.65
220	ADXEC.16051.C2_s_at	Homo sapiens protein tyrosine phosphatase receptor type J	PTPRJ	0.02	2.64
221	ADXEC.9342.C1_s_at	Ring finger protein 34	RNF34	0.0539	2.64
222	ADXECAD.10111_s_at	Homo sapiens branched chain amino-acid transaminase 1 cytosolic	BCAT1	0.0028	2.63
223	ADXEC.27079.C1_at	Homo sapiens RAD1 homolog (S. pombe) (RAD1) transcript variant 1	RAD1	0.0102	2.63
224	ADXEC.583.C2_s_at	Homo sapiens complement component 1 q subcomponent B chain	C1QB	0.0416	2.63
225	ADXEC.6850.C1-a_s_at	Homo sapiens DnaJ (Hsp40) homolog subfamily B member 6 (DNAJB6)	DNAJB6	0.0423	2.63
226	ADXEC.6170.C3_s_at	Homo sapiens F11 receptor (F11R) mRNA.	F11R	0.0436	2.63
227	ADXECRS.33227_at	Homo sapiens zinc finger protein 831 (ZNF831) mRNA.	ZNF831	0.0529	2.63
228	ADXECNTDJ.9852_at	Human beta-galactoside alpha26-sialyltransferase (SIAT1) mRNA exon U.		0.0537	2.63

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
229	ADXPCEC.11099.C1_at	Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.	GSPT1	0.0034	2.62
230	ADXECADA.12202_at	Transcribed locus		0.0086	2.62
231	ADXECADA.9928_at	Homo sapiens membrane-associated ring finger (C3HC4) 3 (MARCH3)	2-Mar	0.0191	2.62
232	ADXECNTDJ.7311_s_at	Homo sapiens HSPB (heat shock 27kDa) associated protein 1	HSPBAP1	0.0197	2.62
233	ADXEC.15363.C3_at	Transcribed locus		0.0198	2.62
234	ADXECRS.26106_at	Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein)	AKT3	0.0271	2.62
235	ADXECADA.24660_x_at	Homo sapiens minichromosome maintenance complex component 10	MCM10	0.0475	2.62
236	ADXEC.25435.C1_s_at	Homo sapiens cAMP-regulated phosphoprotein 19kDa (ARPP19) mRNA.	ARPP19	0.0507	2.62
237	ADXEC.24661.C1_at	PREDICTED: Homo sapiens hypothetical protein MGC27345 (MGC27345)	MGC27345	0.0093	2.61
238	ADXEC.11606.C3_s_at	Homo sapiens histone cluster 1 H2bk (HIST1H2BK) mRNA.	HIST1H2BK	0.017	2.61
239	ADXEC.9485.C1_at	Homo sapiens DnaI homolog subfamily C member 1 (DNAJC1) gene complete cds alterna	DNAJC1	0.0195	2.61
240	ADXEC.17902.C1_s_at	PREDICTED: Homo sapiens similar to PNAS-119 (LOC100287552) mRNA.	LOC100287552	0.0241	2.61
241	ADXECAD.6885_at	Ankyrin repeat domain 44	ANKRD44	0.0423	2.61
242	ADXEC.22119.C1_x_at	Homo sapiens high-mobility group box 3 (HMGB3) mRNA.	HMGB3	0.0489	2.61
243	ADXEC.20400.C1_s_at	Homo sapiens polymerase (DNA directed) gamma 2 accessory subunit	POLG2	0.0033	2.6
244	ADXECNTDJ.5644_s_at	Homo sapiens pyroglutamyl-peptidase I (PGPEP1) mRNA.	PGPEP1	0.0082	2.6
245	ADXEC.3742.C2_s_at	Homo sapiens transcription factor EB (TFEB) transcript variant 2	TFEB	0.009	2.6
246	ADXECAD.14211_x_at	Homo sapiens FYVE RhoGEF and PH domain containing 4 (FGD4) mRNA.	FGD4	0.0328	2.6
247	ADXEC.14057.C1_at	Homo sapiens nurim (nuclear envelope membrane protein) (NRM) mRNA.	NRM	0.0378	2.6
248	ADXEC.26110.C1_x_at	Homo sapiens hypothetical LOC80054 (LOC80054) non-coding RNA.	LOC80054	0.0054	2.59
249	ADXECAD.17510_at	Homo sapiens RNA binding motif protein 33 (RBM33) mRNA.	RBM33	0.007	2.59
250	ADXEC.21936.C1-a_s_at	Homo sapiens dephospho-CoA kinase domain containing (DCAKD)	DCAKD	0.0203	2.59
251	ADXEC.8252.C1_x_at	Homo sapiens C2 calcium-dependent domain containing 3 mRNA (cDNA clone IMAGE:3871	C2CD3	0.0418	2.59

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
252	ADXECAD.14211_at	Homo sapiens FYVE RhoGEF and PH domain containing 4 (FGD4) mRNA.	FGD4	0.0522	2.59
253	ADXEC.522.C5_x_at	similar to HLA class II histocompatibility antigen DRB1-7 beta chain [Homo sapiens]		0.0188	2.58
254	ADXEC.23214.C3_s_at	Homo sapiens chemokine (C-C motif) ligand 28 (CCL28) gene complete cds.		0.0385	2.58
255	ADXECADA.18979_s_at	Homo sapiens ubiquitin specific peptidase 38 (USP38) mRNA.	USP38	0.0465	2.58
256	ADXEC.1471.C1_at	fatty acid binding protein 3 muscle and heart (mammary-derived growth inhibitor)	FABP3	0.0005	2.57
257	ADXEC.12232.C1_at	Homo sapiens grancalcin EF-hand calcium binding protein (GCA)	GCA	0.003	2.57
258	ADXEC.216.C5_at	Homo sapiens RPS27 gene for ribosomal protein S27 complete cds and sequence.	RPS27	0.0104	2.57
259	ADXEC.17138.C1_at	Homo sapiens nucleolar and coiled-body phosphoprotein 1 (NOLC1)	NOLC1	0.0258	2.57
260	ADXEC.54.C1_s_at	Transcribed locus		0.0098	2.56
261	ADXEC.32358.C1_s_at	Homo sapiens male-specific lethal 1 homolog (Drosophila) (MSL1)	MSL1	0.021	2.56
262	ADXECRS.42780_x_at	Homo sapiens similar to HLA class II histocompatibility	LOC100133811	0.04	2.56
263	ADXEC.1131.C12_s_at	Transcribed locus		0.044	2.56
264	ADXEC.35016.C1_at	Homo sapiens Fanconi anemia complementation group C (FANCC) mRNA.	FANCC	0.0031	2.55
265	ADXEC.17381.C1_at	Transcribed locus		0.0341	2.55
266	ADXEC.3501.C1_at	Homo sapiens solute carrier family 39 (zinc transporter) member 13	SLC39A13	0.0404	2.55
267	ADXEC.5538.C1_at	Nucleoporin 214kDa	NUP214	0.0457	2.55
268	ADXEC.5597.C1_s_at	Ral guanine nucleotide dissociation stimulator-like 2	RGL2	0.0523	2.55
269	ADXECAD.25618_s_at	Homo sapiens potassium voltage-gated channel KQT-like subfamily	KCNQ5	0.0173	2.54
270	ADXEC.989.C2_at	Homo sapiens B-cell translocation gene 1 anti-proliferative	BTG1	0.0236	2.54
271	ADXECNTDJ.9184_at	Dermatan sulfate epimerase	DSE	0.0312	2.54
272	ADXEC.488.C4_s_at	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA.	THOP1	0.0348	2.54
273	ADXECAD.18048_at	Transcribed locus		0.0407	2.54
274	ADXEC.9351.C1_s_at	Homo sapiens zinc finger protein 609 (ZNF609) mRNA.	ZNF609	0.0005	2.53

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
275	ADXEC.6333.C1_at	Homo sapiens RNA pseudouridylation synthase domain containing 4	RPUSD4	0.0012	2.53
276	ADXECADA.8726_x_at	Homo sapiens chromosome 21 segment HS21C049.	C21orf7	0.0013	2.53
277	ADXEC.8712.C1-a_s_at	Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4) transcript	CXCR4	0.013	2.53
278	ADXECAD.1752_at	Homo sapiens 5-3 exoribonuclease 1 (XRN1) transcript variant 2	XRN1	0.025	2.53
279	ADXEC.1178.C1_s_at	Homo sapiens eukaryotic translation initiation factor 4H (EIF4H)	EIF4H	0.0358	2.53
280	ADXECEMUTR.3960_at	Homo sapiens SAM domain and HD domain 1 (SAMHD1) mRNA.	SAMHD1	0.0031	2.52
281	ADXECRS.12752_x_at	Homo sapiens centromere protein L (CENPL) transcript variant 1	CENPL	0.0218	2.52
282	ADXEC.98.C2_x_at	Homo sapiens tubulin beta (TUBB) mRNA.	TUBB	0.0268	2.52
283	ADXEC.34926.C1_at	Human Xq28 cosmid U126G1 U142F2 U69B6 U145C10 U169A5 U84H1 U24D12U80A7 U153E6 L	CXorf40A	0.0475	2.52
284	ADXECNTDJ.1013_at	Homo sapiens chromosome 1 open reading frame 123 (C1orf123) mRNA.	C1orf123	0.0524	2.52
285	ADXECRS.21006_s_at	Homo sapiens nuclear factor of activated T-cells cytoplasmic	NFATC2	0.0045	2.51
286	ADXECNTDJ.2647_at	Homo sapiens myosin heavy chain 11 smooth muscle isoform 2 (MYH11) gene complete		0.0155	2.51
287	ADXEC.34398.C1_at	Human DNA sequence from clone RP11-732M18 on chromosome 6 Contains the 5' end of t	TULP4	0.0223	2.51
288	ADXEC.12679.C2_s_at	Homo sapiens phosphatidylinositol 4-kinase type 2 alpha (PI4K2A)	PI4K2A	0.0224	2.51
289	ADXECRS.6774_s_at	Homo sapiens small nucleolar RNA H/ACA box 8 (SNORA8) small	SNORA8	0.0255	2.51
290	ADXECAD.15438_s_at	Homo sapiens Mdm2 p53 binding protein homolog (mouse) (MDM2)	MDM2	0.0264	2.51
291	ADXECEMUTR.278_s_at	Homo sapiens solute carrier family 25 member 37 (SLC25A37)	SLC25A37	0.031	2.51
292	ADXEC.21358.C1_at	Transcribed locus		0.0494	2.51
293	ADXECADA.13411_at	Transcribed locus		0.0516	2.51
294	ADXEC.23013.C2_s_at	Homo sapiens serpin peptidase inhibitor clade B (ovalbumin)	SERPINF8	0.004	2.5
295	ADXECADA.18434_at	Homo sapiens glutathione peroxidase 2 (gastrintestinal) (GPX2) gene complete cds	GPX2	0.0157	2.5
296	ADXEC.15587.C1_at	Homo sapiens adenosine A3 receptor (ADORA3) transcript variant 2	ADORA3	0.034	2.5

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
297	ADXEC.21764.C1_at	Hypothetical gene supported by AK124295	LOC389641	0.0351	2.5
298	ADXEC.22509.C1_at	Homo sapiens 2-5-oligoadenylate synthetase 2 69/71kDa (OAS2)	OAS2	0.0392	2.5
299	ADXECEMUTR.7992_at	Homo sapiens CDGSH iron sulfur domain 2 (CISD2) mRNA.	CISD2	0.0446	2.5
300	ADXEC.18098.C1-a_s_at	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	DDX60L	0.0523	2.5
301	ADXECRS.27925_at	Homo sapiens cytochrome P450 family 4 subfamily F polypeptide 11	CYP4F11	0.002	2.49
302	ADXECAD.18147_at	Transcribed locus		0.0094	2.49
303	ADXECADA.2632_at	Synaptotagmin-like 3	SYTL3	0.0368	2.49
304	ADXEC.15742.C5_at	Suppressor of zeste 12 homolog pseudogene	SUZ12P	0.039	2.49
305	ADXECRS.15653_at	Programmed cell death 6 pseudogene	LOC728613	0.0091	2.48
306	ADXEC.6509.C2_s_at	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 3	AGPAT3	0.0163	2.48
307	ADXEC.31398.C1_at	Homo sapiens PRO2822 mRNA complete cds.		0.0233	2.48
308	ADXEC.14462.C1_at	Homo sapiens phosphate cytidylyltransferase 1 choline alpha	PCYT1A	0.0445	2.48
309	ADXEC.22555.C1_at	Homo sapiens SNF related kinase (SNRK) transcript variant 2 mRNA.	SNRK	0.0025	2.47
310	ADXEC.27856.C1_s_at	PREDICTED: Homo sapiens hypothetical LOC400099 (LOC400099)	LOC400099	0.0268	2.47
311	ADXECNTDJ.5606_at	Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD)	CYLD	0.029	2.47
312	ADXECAD.6693_s_at	Transcribed locus		0.0445	2.47
313	ADXECAD.11971_at	Homo sapiens TAF1 RNA polymerase II TATA box binding protein	TAF1	0.0159	2.46
314	ADXEC.24620.C1_at	Homo sapiens calcium binding tyrosine-(Y)-phosphorylation regulated	CABYR	0.0294	2.46
315	ADXEC.26110.C1_at	Homo sapiens hypothetical LOC80054 (LOC80054) non-coding RNA.	LOC80054	0.0039	2.45
316	ADXEC.8845.C1-a_s_at	Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1) mRNA.	TRIB1	0.0184	2.45
317	ADXECNTDJ.3801_at	Homo sapiens myotubularin related protein 9 (MTMR9) mRNA.	MTMR9	0.0328	2.45
318	ADXEC.12297.C1_s_at	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 8 (HSD17B8)	HSD17B8	0.0513	2.45
319	ADXECNTDJ.2810_at	Homo sapiens cDNA FLJ54219 complete cds highly similar to Probableglutamyl-tRNA(	PET112L	0.023	2.44
320	ADXECAD.4816_s_at	Homo sapiens protein phosphatase 1 regulatory (inhibitor) subunit	PPP1R11	0.0249	2.44

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
321	ADXECAD.18269.s_at	Homo sapiens protein phosphatase Mg2? dependent 1K (PPM1K)	PPM1K	0.029	2.44
322	ADXEC.5689.C1_s_at	Homo sapiens adaptor-related protein complex 4 beta 1 subunit	AP4B1	0.0331	2.44
323	ADXEC.12118.C1_s_at	Homo sapiens BCL2-like 13 (apoptosis facilitator) (BCL2L13)	BCL2L13	0.0417	2.44
324	ADXEC.6937.C1_s_at	Homo sapiens solute carrier family 8 (sodium/calcium exchanger)	SLC8A1	0.0066	2.43
325	ADXEC.16866.C1_at	Homo sapiens adenosine A1 receptor (ADORA1) transcript variant 2	ADORA1	0.0304	2.43
326	ADXEC.24462.C1_at	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuramin	CMAH	0.0359	2.43
327	ADXECRS.8194.x_at	Homo sapiens zinc finger protein 91 pseudogene (LOC441666)	LOC441666	0.0379	2.43
328	ADXECEMUTR.2994_at	Homo sapiens mRNA for KIAA1652 protein partial cds.	KIAA1652	0.0389	2.43
329	ADXEC.21693.C1_s_at	Human DNA sequence from clone RP11-364F8 on chromosome 13 Contains part of the PC	PCCA	0.0199	2.42
330	ADXECAD.9613.s_at	Homo sapiens tet oncogene family member 2 (TET2) transcript	TET2	0.0214	2.42
331	ADXEC.25521.C1_s_at	Homo sapiens cytidine monophosphate-N-acetylneuraminic acid	CMAH	0.0273	2.42
332	ADXEC.6876.C1_at	Homo sapiens signal recognition particle receptor B subunit	SRPRB	0.0531	2.42
333	ADXEC.11334.C1-a_s_at	Homo sapiens target of EGR1 member 1 (nuclear) (TOE1) mRNA.	TOE1	0.0195	2.41
334	ADXEC.30575.C1_x_at	Homo sapiens prenylcysteine oxidase 1 (PCYOX1) mRNA.	PCYOX1	0.0238	2.41
335	ADXEC.1248.C1_at	Homo sapiens dehydrogenase E1 and transketolase domain containing 1	DHTKD1	0.0381	2.41
336	ADXEC.25229.C1_at	Homo sapiens SH2 domain containing 4A (SH2D4A) transcript variant	SH2D4A	0.0405	2.41
337	ADXEC.23249.C1_at	Homo sapiens cDNA FLJ52198 complete cds.	C17orf87	0.0418	2.41
338	ADXEC.13172.C1_at	Homo sapiens interleukin 28 receptor alpha (interferon lambda	IL28RA	0.0018	2.4
339	ADXEC.13165.C1_s_at	Homo sapiens vitelline membrane outer layer 1 homolog (chicken)	VMO1	0.0051	2.4
340	ADXEC.342.C1_at	Homo sapiens deoxyribonuclease II lysosomal (DNASE2) mRNA.	DNASE2	0.0184	2.4
341	ADXEC.27761.C1_s_at	Transcribed locus		0.0204	2.4
342	ADXEC.409.C92_at	Ribosomal protein S15a	RPS15A	0.0225	2.4
343	ADXECRS.9851_at	Homo sapiens oculomedin (OCLM) mRNA.	OCLM	0.0233	2.4

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
344	ADXECAD.21656_at	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 1	RAPGEF1	0.0294	2.4
345	ADXECADA.12887_at	Transcribed locus		0.0303	2.4
346	ADXEC.8586.C1_s_at	Homo sapiens paired immunoglobulin-like type 2 receptor alpha	PILRA	0.0342	2.4
347	ADXECRS.8469_s_at	Homo sapiens small nucleolar RNA C/D box 105B (SNORD105B) small	SNORD105B	0.0346	2.4
348	ADXEC.34764.C1_at	Homo sapiens baculoviral IAP repeat-containing 4 (BIRC4) gene completecds.	XIAP	0.0442	2.4
349	ADXEC.2003.C1_at	Homo sapiens septin 6 (SEPT6) transcript variant II mRNA.	5-Sep	0.0466	2.4
350	ADXEC.7826.C1_s_at	Homo sapiens zinc finger MYND-type containing 8 (ZMYND8)	ZMYND8	0.0534	2.4
351	ADXECADA.461_s_at	PREDICTED: Homo sapiens hypothetical protein LOC100288109	LOC100288109	0.0003	2.38
352	ADXEC.7744.C3_s_at	Homo sapiens apoptosis-inducing TAF9-like domain 1 (APITD1)	APITD1	0.002	2.38
353	ADXEC.12903.C1_s_at	Homo sapiens thyroid hormone receptor interactor 6 (TRIP6) mRNA.	TRIP6	0.0047	2.38
354	ADXECEMUTR.6360_at	Transcribed locus		0.0154	2.38
355	ADXEC.30575.C1_at	Homo sapiens prenylcysteine oxidase 1 (PCYOX1) mRNA.	PCYOX1	0.0262	2.38
356	ADXEC.28434.C1_x_at	Transcribed locus		0.0385	2.38
357	ADXECNTDJ.3859_at	Transmembrane protein 165	TMEM165	0.0097	2.37
358	ADXEC.32186.C1_x_at	Homo sapiens H2A histone family member X (H2AFX) mRNA.	H2AFX	0.0229	2.36
359	ADXECADA.18520_x_at	Homo sapiens BAC clone RP11-568N6 from 2 complete sequence.	LOC100128607	0.0333	2.36
360	ADXEC.7415.C3_x_at	Homo sapiens TATA box binding protein (TBP)-associated factor RNA	TAF1D	0.0371	2.36
361	ADXEC.2738.C1_s_at	Homo sapiens plasminogen activator urokinase receptor (PLAUR)	PLAUR	0.0511	2.36
362	ADXECADA.12963_at	Homo sapiens class II major histocompatibility complex transactivator(CIITA) gen		0.0031	2.35
363	ADXEC.3788.C1_s_at	Homo sapiens thromboxane A synthase 1 (platelet) (TBXAS1)	TBXAS1	0.0066	2.35
364	ADXEC.30470.C1_at	Transcribed locus		0.0079	2.35
365	ADXECADA.9979_at	Homo sapiens vesicle-associated membrane protein 1 (synaptobrevin	VAMP1	0.0204	2.35
366	ADXECEMUTR.4649_at	Homo sapiens cDNA FLJ11824 fis clone HEMBA1006492.	TANC2	0.0261	2.35
367	ADXPCEC.16852.C1_at	Coiled-coil domain containing 45	CCDC45	0.0368	2.35

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
368	ADXECMG.11_at	Homo sapiens mitochondrial DNA complete genome	ND4L	0.0457	2.35
369	ADXECNTDJ.3106_at	Homo sapiens tenascin C (TNC) mRNA.	TNC	0.0492	2.35
370	ADXECAD.7010_at	Homo sapiens presenilin associated rhomboid-like (PARL) nuclear	PARL	0.0542	2.35
371	ADXECNTDJ.4256_at	Homo sapiens kelch-like 12 (Drosophila) (KLHL12) mRNA.	KLHL12	0.0027	2.34
372	ADXECAD.15438_x_at	Homo sapiens Mdm2 p53 binding protein homolog (mouse) (MDM2)	MDM2	0.01	2.34
373	ADXPCEC.8291.C1_s_at	Homo sapiens schlafen family member 5 (SLFN5) mRNA.	SLFN5	0.0133	2.34
374	ADXPCEC.16375.C1_at	Transcribed locus		0.0182	2.34
375	ADXECNTDJ.2565_x_at	Homo sapiens hypothetical protein LOC100293970	LOC100293970	0.0228	2.34
376	ADXECADA.18529_at	Homo sapiens interleukin 4 receptor (IL4R) gene complete cds.	IL4R	0.0292	2.34
377	ADXEC.6133.C7_x_at	Homo sapiens leukocyte immunoglobulin-like receptor subfamily B	LILRB2	0.0401	2.34
378	ADXEC.14462.C1_x_at	Homo sapiens phosphate cytidylyltransferase 1 choline alpha	PCYT1A	0.0416	2.34
379	ADXEC.7240.C1-a_s_at	Homo sapiens elongation factor RNA polymerase II 2 (ELL2) mRNA.	ELL2	0.0443	2.34
380	ADXEC.25579.C1_s_at	Kruppel-like factor 3 (basic)	KLF3	0.0041	2.33
381	ADXEC.1893.C2_s_at	Homo sapiens lymphocyte antigen 86 (LY86) mRNA.	LY86	0.0096	2.33
382	ADXEC.6557.C2_s_at	Homo sapiens HIV-1 Tat interactive protein 2 30kDa (HTATIP2)	HTATIP2	0.0231	2.33
383	ADXECAD.12804_x_at	Protein tyrosine phosphatase non-receptor type 1	PTPN1	0.0279	2.33
384	ADXEC.2240.C2-a_s_at	Homo sapiens dual specificity phosphatase 3 (DUSP3) mRNA.	DUSP3	0.0327	2.33
385	ADXEC.11748.C2_s_at	Homo sapiens inositol hexakisphosphate kinase 2 (IP6K2) transcript	IP6K2	0.0542	2.33
386	ADXEC.9417.C1_at	Zinc finger and BTB domain containing 46	ZBTB46	0.0046	2.32
387	ADXECRS.43632_s_at	Homo sapiens Wolf-Hirschhorn syndrome candidate 1 (WHSC1)	WHSC1	0.006	2.32
388	ADXECNTDJ.9418_at	Homo sapiens SNF related kinase (SNRK) transcript variant 2 mRNA.	SNRK	0.0061	2.31
389	ADXEC.19774.C1_at	Homo sapiens dihydrouridine synthase 4-like (S. cerevisiae)	DUS4L	0.0197	2.31
390	ADXEC.12396.C1_at	Homo sapiens chemokine (C-X3-C motif) ligand 1 (CX3CL1) mRNA.	CX3CL1	0.0257	2.31
391	ADXEC.4317.C1_at	Homo sapiens BEN domain containing 3 (BEND3) mRNA.	BEND3	0.0397	2.31
392	ADXEC.14388.C1_at	Myeloid/lymphoid or mixed-lineage leukemia 2	MLL2	0.0086	2.3

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
393	ADXEC.487.C1-a_s_at	Homo sapiens ring finger protein 14 (RNF14) transcript variant 2	RNF14	0.0152	2.3
394	ADXEC.8369.C1_s_at	Homo sapiens ArfGAP with RhoGAP domain ankyrin repeat and PH	ARAP2	0.0162	2.3
395	ADXECADA.15939_at	CDNA FLJ37319 fis clone BRAMY2018027		0.0167	2.3
396	ADXECNTDJ.2647_x_at	Homo sapiens myosin heavy chain 11 smooth muscle isoform 2 (MYH11) genecomplete		0.0298	2.3
397	ADXECRS.26750_s_at	PREDICTED: Homo sapiens family with sequence similarity 22 member	FAM22E	0.0407	2.3
398	ADXECNTDJ.1003_s_at	Homo sapiens alkB alkylation repair homolog 4 (E. coli) (ALKBH4)	ALKBH4	0.0425	2.3
399	ADXEC.34601.C1_at	Human DNA sequence from clone RP11-467D18 on chromosome 1 Contains the 5end of t	MECR	0.0431	2.3
400	ADXECRS.6560_s_at	Homo sapiens chromosome 3 subtelomeric region.		0.0507	2.3
401	ADXOCEC.13491.C1_x_at	CDNA FLJ36844 fis clone ASTRO2012601		0.0001	2.29
402	ADXEC.30928.C1_x_at	Homo sapiens inwardly rectifying potassium channel Kir7.1 gene completeintron an	KCNJ13	0.001	2.29
403	ADXECAD.15320_at	AVL9 homolog (S. cerevisiae)	AVL9	0.0333	2.29
404	ADXEC.5419.C1_s_at	Homo sapiens leukocyte-associated immunoglobulin-like receptor 1	LAIR1	0.0437	2.29
405	ADXEC.31342.C1_s_at	Homo sapiens tRNA-histidine guanylyltransferase 1-like (S.	THG1L	0.0077	2.28
406	ADXEC.16192.C1_at	Homo sapiens arachidonate 5-lipoxygenase-activating protein	ALOX5AP	0.0207	2.28
407	ADXEC.22766.C1_at	Homo sapiens HEAT repeat containing 5A (HEATR5A) mRNA.	HEATR5A	0.0237	2.28
408	ADXEC.18352.C1_at	Radical S-adenosyl methionine domain containing 1	RSAD1	0.0281	2.28
409	ADXEC.10647.C1-a_s_at	Homo sapiens zinc finger protein 644 (ZNF644) transcript variant	ZNF644	0.0355	2.28
410	ADXECNTDJ.1237_at	Homo sapiens karyopherin alpha 1 (importin alpha 5) (KPNA1)	KPNA1	0.0478	2.28
411	ADXECAD.23141_at	Homo sapiens dystrophin (DMD) transcript variant Dp71ab mRNA.	DMD	0.0482	2.28
412	ADXEC.1226.C2_x_at	Homo sapiens gene for thymidylate synthase complete cds.	TYMS	0.017	2.27
413	ADXECEMUTR.8089_at	Homo sapiens nuclear autoantigen mRNA partial cds	SP100	0.0247	2.27
414	ADXEC.6801.C5_s_at	Homo sapiens tubulin folding cofactor D (TBCD) mRNA.	TBCD	0.0275	2.27

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
415	ADXEC.15864.C2_s_at	Homo sapiens myosin heavy chain 11 smooth muscle isoform 2 (MYH11) genecomplete		0.0288	2.27
416	ADXECAD.2413_s_at	Homo sapiens Smith-Magenis syndrome chromosome region candidate 8	SMCR8	0.0311	2.27
417	ADXEC.15547.C1_x_at	Zinc finger protein 789	ZNF789	0.0408	2.27
418	ADXEC.2003.C1_x_at	Homo sapiens septin 6 (SEPT6) transcript variant II mRNA.	5-Sep	0.0434	2.27
419	ADXEC.21689.C1_s_at	Transcribed locus		0.054	2.27
420	ADXECAD.9792_s_at	Homo sapiens cytochrome P450 family 4 subfamily V polypeptide 2 (CYP4V2)gene com	CYP4V2	0.0088	2.26
421	ADXEC.28842.C1_s_at	Ets2 repressor factor	ERF	0.0107	2.26
422	ADXECNTDJ.6285_s_at	Homo sapiens mitogen-activated protein kinase kinase kinase 3	MAP3K3	0.0212	2.26
423	ADXECADA.605_s_at	Homo sapiens IKAROS family zinc finger 2 (Helios) (IKZF2)	IKZF2	0.0215	2.26
424	ADXECAD.22624_at	Homo sapiens ST8 alpha-N-acetyl-neuraminide	ST8SIA4	0.0249	2.26
425	ADXECADA.16846_at	Homo sapiens cell division cycle 42 (GTP binding protein 25kDa)	CDC42	0.0332	2.26
426	ADXECNTDJ.9195_s_at	Homo sapiens KIAA0240 (KIAA0240) mRNA.	KIAA0240	0.0385	2.26
427	ADXEC.4983.C1_s_at	Homo sapiens ring finger protein 213 (RNF213) transcript variant	RNF213	0.039	2.26
428	ADXECADA.21347_at	Homo sapiens solute carrier family 23 (nucleobase transporters)	SLC23A2	0.0099	2.25
429	ADXEC.14533.C1-a_s_at	Homo sapiens transcription factor 1 hepatic	HNF1A	0.0231	2.25
430	ADXEC.16157.C1_s_at	Homo sapiens arachidonate 5-lipoxygenase (ALOX5) mRNA.	ALOX5	0.0329	2.25
431	ADXECADA.5893_s_at	Homo sapiens transmembrane and coiled-coil domain family 3 (TMCC3)	TMCC3	0.0335	2.25
432	ADXECEMUTR.2647_at	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia 5	MLL5	0.0456	2.25
433	ADXEC.3299.C1-a_s_at	TAF4 RNA polymerase II TATA box binding protein (TBP)-associated factor 135kDa	TAF4	0.0531	2.25
434	ADXEC.14823.C1-a_s_at	Homo sapiens opioid growth factor receptor-like 1 (OGFRL1) mRNA.	OGFRL1	0.0068	2.24
435	ADXEC.1226.C2_at	Homo sapiens gene for thymidylate synthase complete cds.	TYMS	0.0134	2.24
436	ADXEC.16192.C1_s_at	Homo sapiens arachidonate 5-lipoxygenase-activating protein	ALOX5AP	0.0147	2.24

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437	ADXEC.33764.C1_s_at	Homo sapiens mitogen-activated protein kinase kinase kinase 8 (MAP3K8) gene compl	MAP3K8	0.0265	2.24
438	ADXEC.20945.C1_at	Homo sapiens BRCA1 associated RING domain 1 (BARD1) mRNA.	BARD1	0.0293	2.24
439	ADXEC.13816.C2_at	Homo sapiens FAST kinase domains 1 (FASTKD1) mRNA.	FASTKD1	0.0367	2.24
440	ADXPCEC.13599.C1_at	Transcribed locus		0.0396	2.24
441	ADXEC.4833.C1_at	Homo sapiens ras homolog gene family member H (RHOH) mRNA.	RHOH	0.0422	2.24
442	ADXEC.16473.C1-a_s_at	Homo sapiens transcription factor CP2 (TFCP2) transcript variant	TFCP2	0.0476	2.24
443	ADXEC.5973.C1_at	Homo sapiens RMI1 RecQ mediated genome instability 1 homolog (S.	RMI1	0.0542	2.24
444	ADXEC.17023.C1_s_at	Homo sapiens solute carrier organic anion transporter family	SLCO2B1	0.0055	2.23
445	ADXEC.686.C3_s_at	Homo sapiens cathepsin B (CTSB) transcript variant 4 mRNA.	CTSB	0.0119	2.23
446	2436410_at			0.0155	2.23
447	ADXEC.3267.C1-a_s_at	Homo sapiens protein kinase AMP-activated gamma 2 non-catalytic	PRKAG2	0.0168	2.23
448	ADXECNTDJ.8978_at	Homo sapiens GDNF-inducible zinc finger protein 1 (GZF1) mRNA.	GZF1	0.022	2.23
449	ADXEC.17138.C1_x_at	Homo sapiens nucleolar and coiled-body phosphoprotein 1 (NOLC1)	NOLC1	0.0221	2.23
450	ADXECADA.13445_at	Transcribed locus		0.0229	2.23
451	ADXEC.11220.C1_at	Homo sapiens immunoglobulin superfamily member 4D (IGSF4) gene completecds alter		0.0272	2.23
452	ADXEC.13304.C1_s_at	General transcription factor IIIC polypeptide 3 102kDa	GTF3C3	0.0292	2.23
453	ADXECEMUTR.4384_at	Homo sapiens Fc-gamma receptor 1lc5 mRNA partial cds.	FCGR2A	0.0395	2.23
454	ADXECNTDJ.6286_s_at	Homo sapiens mitogen-activated protein kinase kinase kinase 3	MAP3K3	0.0403	2.23
455	ADXEC.7578.C2_s_at	Homo sapiens zinc finger protein 511 (ZNF511) mRNA.	ZNF511	0.0456	2.23
456	ADXECADA.671_s_at	Homo sapiens DIP2 disco-interacting protein 2 homolog A	DIP2A	0.0529	2.23
457	ADXEC.3159.C2_s_at	Homo sapiens poly (ADP-ribose) polymerase family member 12	PARP12	0.0537	2.23
458	ADXECAD.20993_s_at	Homo sapiens poly(A) polymerase gamma (PAPOLG) mRNA.	PAPOLG	0.0165	2.22
459	ADXEC.6420.C1-a_s_at	Homo sapiens additional sex combs like 1 (Drosophila) (ASXL1)	ASXL1	0.0225	2.22

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460	ADXECADA.209_at	Homo sapiens ankyrin repeat and SOCS box-containing 14 (ASB14)	ASB14	0.0228	2.22
461	ADXEC.16712.C1_at	Transcribed locus		0.0301	2.22
462	ADXEC.926.C1-a_s_at	Homo sapiens transmembrane protein 106C (TMEM106C) transcript	TMEM106C	0.0413	2.22
463	ADXECAD.17716_x_at	Protein tyrosine phosphatase non-receptor type 1	PTPN1	0.0087	2.21
464	ADXEC.29413.C1_at	Transcribed locus		0.0099	2.21
465	ADXEC.8387.C1_at	FLJ21028 fis clone CAE07155		0.0117	2.21
466	ADXEC.2672.C1_s_at	Homo sapiens MORC family CW-type zinc finger 2 (MORC2) mRNA.	MORC2	0.0142	2.21
467	ADXEC.15363.C3_x_at	Transcribed locus		0.0331	2.21
468	ADXECADA.990_x_at	Homo sapiens neuroplasma apoptosis-related RNA-binding protein (CUGBP2) gene ex	CELF2	0.0352	2.21
469	ADXEC.23032.C1_at	Homo sapiens CD68 molecule (CD68) transcript variant 2 mRNA.	CD68	0.0395	2.21
470	Adx-200054-up_s_at	Homo sapiens zinc finger protein 259 (ZNF259) mRNA.	ZNF259	0.0413	2.21
471	ADXEC.29413.C1_x_at	Transcribed locus		0.0038	2.2
472	2328487_at			0.0084	2.2
473	ADXEC.34398.C1_x_at	Homo sapiens peroxisome proliferative activated receptor alpha (PPARA) gene compl	PPARA	0.0213	2.2
474	ADXECNTDJ.5307_at	Homo sapiens tripartite motif-containing 35 (TRIM35) transcript	TRIM35	0.0237	2.2
475	ADXEC.14809.C1_at	F-box and leucine-rich repeat protein 14	FBXL14	0.0328	2.2
476	ADXEC.869.C1_x_at	Homo sapiens chromosome 17 open reading frame 106 (C17orf106)	C17orf106	0.0354	2.2
477	ADXECAD.20607_s_at	Homo sapiens serglycin (SRGN) mRNA.	SRGN	0.0377	2.2
478	ADXEC.3819.C2-a_s_at	Homo sapiens family with sequence similarity 131 member A	FAM131A	0.0431	2.2
479	ADXEC.22813.C1-a_s_at	Homo sapiens sialophorin (SPN) transcript variant 1 mRNA.	SPN	0.0519	2.2
480	ADXECADA.23331_s_at	Homo sapiens high-mobility group 20B (HMG20B) mRNA.	HMG20B	0.0543	2.2
481	ADXEC.16192.C2-a_s_at	Homo sapiens arachidonate 5-lipoxygenase-activating protein	ALOX5AP	0.0031	2.19
482	ADXECNTDJ.10553_at	ATP-binding cassette sub-family D (ALD) member 1 pseudogene 4	ABCD1P4	0.0046	2.19

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483	ADXECAD.17469_s_at	Homo sapiens MORC family CW-type zinc finger 2 (MORC2) mRNA.	MORC2	0.0057	2.19
484	ADXEC.14388.C1_x_at	Myeloid/lymphoid or mixed-lineage leukemia 2	MLL2	0.011	2.19
485	ADXECAD.28846_s_at	Homo sapiens caspase 2 apoptosis-related cysteine peptidase	CASP2	0.0117	2.19
486	ADXEC.4103.C1_at	Homo sapiens casein kinase 2 alpha prime polypeptide (CSNK2A2)	CSNK2A2	0.0122	2.19
487	ADXEC.30036.C1_at	Homo sapiens SEPN1 gene for selenoprotein N exons 1-13	SEPN1	0.0246	2.19
488	ADXECNTDJ.3778_at	Estrogen receptor 1	ESR1	0.0349	2.19
489	ADXEC.15673.C1_s_at	Homo sapiens RAB8B member RAS oncogene family (RAB8B) mRNA.	RAB8B	0.0389	2.19
490	ADXECNTDJ.5144_at	Homo sapiens toll-like receptor 2 (TLR2) mRNA 5 untranslated regions splice variant		0.0413	2.19
491	3096458_at			0.0076	2.18
492	ADXECADA.8743_at	Full length insert cDNA clone ZB81B12		0.0083	2.18
493	ADXEC.17943.C1_s_at	Homo sapiens trafficking protein particle complex 10 (TRAPPC10)	TRAPPC10	0.0155	2.18
494	ADXECAD.14786_at	FGFR1 oncogene partner 2	FGFR1OP2	0.0241	2.18
495	ADXEC.22145.C1_at	Ets variant 5	ETV5	0.037	2.18
496	ADXEC.23032.C1_x_at	Homo sapiens CD68 molecule (CD68) transcript variant 2 mRNA.	CD68	0.0414	2.18
497	ADXEC.19598.C1_at	Homo sapiens cDNA FLJ60178 complete cds moderately similar to Membrane-spanning 4	MS4A6A	0.0466	2.18
498	ADXEC.15722.C1_at	Homo sapiens zinc finger protein 671 (ZNF671) mRNA.	ZNF671	0.0504	2.18
499	ADXEC.21162.C2_s_at	Homo sapiens uridine-cytidine kinase 2 (UCK2) mRNA.	UCK2	0.0075	2.17
500	ADXEC.2484.C1_at	Homo sapiens transmembrane emp24 protein transport domain	TMED5	0.0089	2.17
501	ADXEC.31107.C1_at	Homo sapiens Rho GTPase activating protein 5 (ARHGAP5) transcript	ARHGAP5	0.0324	2.17
502	ADXOCEC.13491.C1_at	CDNA FLJ36844 fis clone ASTRO2012601		0.0004	2.16
503	ADXEC.28650.C1_at	PHD finger protein 20-like 1	PHF20L1	0.006	2.16
504	ADXECRS.15490_s_at	Homo sapiens family with sequence similarity 185 member A	FAM185A	0.0081	2.16
505	ADXECAD.24150_at	Homo sapiens cell-type natural killer cells Fc gamma receptor RIIc4(Fc-	FCGR2C	0.0098	2.16

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
		gammaRIIC			
506	ADXECAD.8834_s_at	Homo sapiens KIAA1632 (KIAA1632) mRNA.	KIAA1632	0.0186	2.16
507	ADXECAD.7698_s_at	Homo sapiens LSM14B SCD6 homolog B (S. cerevisiae) (LSM14B) mRNA.	LSM14B	0.0238	2.16
508	ADXECNTDJ.2692_s_at	Homo sapiens kinesin family member 3C (KIF3C) mRNA.	KIF3C	0.0273	2.16
509	ADXECADA.10671_at	tumor protein p53 binding protein 2 [Macaca mulatta]		0.0296	2.16
510	ADXECRS.39826_at	Homo sapiens phosphoglycerate kinase 1 (PGK1) mRNA.	PGK1	0.0513	2.16
511	ADXECAD.11923_at	tumor protein p53 binding protein 2 [Macaca mulatta]		0.0521	2.16
512	ADXEC.34337.C1_at	Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene	XRCC3	0.0528	2.16
513	ADXECAD.10006_s_at	Homo sapiens La ribonucleoprotein domain family member 4B	LARP4B	0.0011	2.15
514	ADXECADA.23430_s_at	Homo sapiens erythrocyte membrane protein band 4.1-like 3	EPB41L3	0.0043	2.15
515	ADXEC.5821.C1-a_s_at	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1)	PDPK1	0.0069	2.15
516	ADXEC.27188.C1_s_at	Homo sapiens dehydrogenase/reductase (SDR family) X-linked (DHRX)	DHRX	0.008	2.15
517	ADXEC.10875.C1_at	Homo sapiens nucleoporin 210kDa (NUP210) mRNA.	NUP210	0.0104	2.15
518	ADXECAD.16644_at	Peroxisomal biogenesis factor 26	PEX26	0.012	2.15
519	ADXECADA.18518_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	PCMTD1	0.0195	2.15
520	ADXEC.3168.C2_s_at	Transcribed locus		0.0208	2.15
521	ADXECEMUTR.5659_at	Zinc finger protein 292	ZNF292	0.0224	2.15
522	ADXEC.5484.C1_at	Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1) mRNA.	TRIB1	0.0302	2.15
523	ADXEC.27117.C1-a_s_at	Homo sapiens signal transducer and activator of transcription 6	STAT6	0.0325	2.15
524	ADXEC.20111.C1_x_at	Homo sapiens sideroflexin 1 (SFXN1) mRNA.	SFXN1	0.0338	2.15
525	ADXEC.30999.C1_x_at	Homo sapiens genomic DNA chromosome 21q section 57/105.		0.0445	2.15
526	ADXECRS.25801_s_at	Homo sapiens zinc finger protein 45 (ZNF45) mRNA.	ZNF45	0.048	2.15
527	ADXEC.9246.C1_at	Homo sapiens neuropilin 1 (NRP1) transcript variant 2 mRNA.	NRP1	0.0522	2.15
528	ADXEC.19905.C1_s_at	CDNA FLJ20196 fis clone COLF0944		0.0046	2.14

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
529	ADXEC.28650.C1_x_at	PHD finger protein 20-like 1	PHF20L1	0.0106	2.14
530	ADXEC.5947.C1_s_at	Homo sapiens solute carrier family 39 (zinc transporter) member 4	SLC39A4	0.0131	2.14
531	ADXECRS.6440_s_at	Homo sapiens spermatid perinuclear RNA binding protein (STRBP)	STRBP	0.0132	2.14
532	ADXEC.31137.C1_at	Homo sapiens dual adaptor of phosphotyrosine and	DAPP1	0.0248	2.14
533	ADXEC.32664.C1_s_at	CDNA FLJ36325 fis clone THYMU2005574		0.0258	2.14
534	ADXEC.32661.C1_x_at	Transcribed locus		0.0275	2.14
535	3676673_at			0.0346	2.14
536	ADXECAD.8526_at	Homo sapiens tousled-like kinase 2 (TLK2) transcript variant B	TLK2	0.0349	2.14
537	ADXEC.20635.C2_s_at	Homo sapiens zinc finger MYM-type 3 (ZMYM3) transcript variant 4	ZMYM3	0.0354	2.14
538	ADXECNTDJ.2873_s_at	Homo sapiens cathepsin Z (CTSZ) mRNA.	CTSZ	0.0404	2.14
539	ADXEC.3299.C1_s_at	TAF4 RNA polymerase II TATA box binding protein (TBP)-associated factor 135kDa	TAF4	0.0476	2.14
540	ADXECAD.5686_x_at	Homo sapiens interleukin 17 receptor B (IL17RB) gene complete cds.	IL17RB	0.0531	2.14
541	ADXEC.6968.C1_at	Homo sapiens APEX nuclease (apurinic/aprimidinic endonuclease) 2	APEX2	0.0007	2.13
542	ADXOCEC.14095.C1_at	Transcribed locus		0.0063	2.13
543	ADXECAD.23079_s_at	Homo sapiens myocyte enhancer factor 2C (MEF2C) transcript variant	MEF2C	0.0336	2.13
544	ADXECNTDJ.8048_at	Homo sapiens dihydropyrimidinase-like 3 (DPYSL3) mRNA.	DPYSL3	0.0338	2.13
545	ADXEC.31502.C1_at	PREDICTED: Homo sapiens hypothetical LOC728650 (LOC728650) mRNA.	LOC728650	0.0339	2.13
546	ADXECADA.13879_at	Homo sapiens chromosome 5 clone CTC-37017 complete sequence.	LSM11	0.0391	2.13
547	ADXECNTDJ.8315_s_at	Homo sapiens cathepsin B (CTSB) transcript variant 3 mRNA.	CTSB	0.0037	2.12
548	ADXEC.24458.C1-a_s_at	Deoxythymidylate kinase (thymidylate kinase)	DTYMK	0.0154	2.12
549	ADXECADA.7487_at	Homo sapiens chromosome 1 open reading frame 104 mRNA (cDNA cloneMGC:149516 IMAG	C1orf104	0.0266	2.12
550	ADXEC.28034.C1_s_at	4800262		0.0267	2.12
551	ADXECRS.820_s_at	Homo sapiens hypothetical protein LOC202181 (LOC202181) non-coding	LOC202181	0.0345	2.12

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
552	ADXEC.17825.C2_at	Homo sapiens chromosome 2 open reading frame 77 (C2orf77) mRNA.	C2orf77	0.0369	2.12
553	ADXECNTDJ.2995_s_at	PREDICTED: Homo sapiens similar to hCG1686079 (LOC100290084) mRNA.	LOC100290084	0.038	2.12
554	ADXEC.8915.C1-a_s_at	Homo sapiens protein tyrosine phosphatase receptor type C	PTPRC	0.0402	2.12
555	ADXEC.22295.C1_at	hypothetical protein [Pan troglodytes]		0.0422	2.12
556	ADXECAD.8352_at	PREDICTED: Homo sapiens similar to hCG2006901 (LOC100293165) mRNA.	LOC100293165	0.0005	2.11
557	ADXECAD.16766_x_at	Homo sapiens mitochondrial ribosomal protein L9 (MRPL9) nuclear	MRPL9	0.0034	2.11
558	ADXEC.14575.C2-a_s_at	Homo sapiens SUMO1/sentrin/SMT3 specific peptidase 3 (SEN3) mRNA.	SEN3	0.0109	2.11
559	ADXEC.22252.C1-a_s_at	Homo sapiens Ras-like without CAAX 1 (RIT1) mRNA.	RIT1	0.011	2.11
560	ADXEC.2250.C1_at	Homo sapiens proteasome (prosome macropain) subunit beta type 7	PSMB7	0.0116	2.11
561	ADXEC.2002.C8_s_at	Homo sapiens major facilitator superfamily domain containing 7	MFSD7	0.0148	2.11
562	ADXEC.3100.C2_at	Homo sapiens trinucleotide repeat containing 6C (TNRC6C)	TNRC6C	0.0158	2.11
563	ADXEC.31190.C1_s_at	Homo sapiens zinc finger protein 609 (ZNF609) mRNA.	ZNF609	0.0187	2.11
564	ADXEC.24984.C1_at	Homo sapiens BMP2 inducible kinase (BMP2K) transcript variant 2	BMP2K	0.0275	2.11
565	ADXEC.17916.C1_at	Homo sapiens RAB14 member RAS oncogene family (RAB14) mRNA.	RAB14	0.0418	2.11
566	ADXECNTDJ.2671_at	potassium voltage-gated channel shaker-related subfamily beta member 3	KCNAB3	0.0445	2.11
567	ADXECAD.24402_s_at	Homo sapiens selenoprotein T (SELT) mRNA.	SELT	0.0494	2.11
568	ADXEC.18185.C1_at	Homo sapiens SCAN domain containing 2 pseudogene (SCAND2)	SCAND2	0.0515	2.11
569	ADXEC.14239.C1-a_s_at	Homo sapiens myotubularin related protein 4 (MTMR4) mRNA.	MTMR4	0.018	2.1
570	ADXECNTDJ.6300_at	Homo sapiens adaptor-related protein complex 1 gamma 1 subunit	AP1G1	0.029	2.1
571	ADXEC.21429.C1_s_at	Full length insert cDNA clone YP77A07		0.0326	2.1
572	ADXECAD.2402_s_at	Homo sapiens serologically defined colon cancer antigen 1	SDCCAG1	0.0354	2.1
573	ADXECNTDJ.4196_s_at	Homo sapiens CD274 molecule (CD274) mRNA.	CD274	0.0485	2.1
574	ADXEC.12903.C3_s_at	Homo sapiens thyroid hormone receptor interactor 6 (TRIP6) mRNA.	TRIP6	0.0138	2.09
575	3959645_at			0.016	2.09
576	ADXEC.23124.C1_x_at	Homo sapiens NLR family pyrin domain containing 1 (NLRP1)	NLRP1	0.0311	2.09

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
577	ADXECADA.5884_at	Homo sapiens suppressor of IKBKE 1 (SIKE1) transcript variant 2	SIKE1	0.0213	2.08
578	ADXEC.28434.C1_at	Transcribed locus		0.0485	2.08
579	ADXEC.19985.C1-a_s_at	Homo sapiens calcineurin-like phosphoesterase domain containing 1	CPPED1	0.054	2.08
580	ADXECRS.27012_at	Homo sapiens syntaxin 7 (STX7) mRNA.	STX7	0.0073	2.07
581	ADXECEMUTR.3274_at	Homo sapiens chromosome 1 open reading frame 104 mRNA (cDNA cloneMGC:149516 IMAG	C1orf104	0.0099	2.07
582	ADXEC.16747.C1-a_s_at	Homo sapiens sorting nexin 11 (SNX11) transcript variant 2 mRNA.	SNX11	0.0359	2.07
583	ADXECNTDJ.5332_at	Homo sapiens zinc finger protein 618 (ZNF618) mRNA.	ZNF618	0.038	2.07
584	ADXECEMUTR.8064_at	Homo sapiens lysyl oxidase-like protein 3 variant (LOXL3) mRNA completecds.	LOXL3	0.0439	2.07
585	ADXEC.12879.C1_s_at	Homo sapiens chromosome 14 open reading frame 21 mRNA (cDNA cloneIMAGE:3884657).	C14orf21	0.0496	2.07
586	ADXECAD.27315_at	Homo sapiens adaptor-related protein complex 4 epsilon 1 subunit	AP4E1	0.0023	2.06
587	ADXECAD.158_s_at	Homo sapiens Rho GTPase activating protein 5 (ARHGAP5) transcript	ARHGAP5	0.0095	2.06
588	ADXECADA.20351_at	Homo sapiens growth factor independent 1 transcription repressor	GFI1	0.0096	2.06
589	ADXEC.22845.C1_s_at	ATPase H transporting lysosomal accessory protein 1-like	ATP6AP1L	0.0314	2.06
590	ADXEC.16702.C1_at	Transcribed locus		0.032	2.06
591	ADXEC.10361.C1_at	Homo sapiens transforming growth factor beta regulator 1 mRNA (cDNA cloneIMAGE:5	TBRG1	0.0388	2.06
592	ADXEC.11629.C2_s_at	Hypothetical LOC100133660	LOC100133660	0.0521	2.06
593	ADXEC.79.C10_at	Transcribed locus		0.0082	2.05
594	ADXEC.5096.C1-a_s_at	Homo sapiens suppressor of defective silencing 3 homolog (S.	SUDS3	0.0088	2.05
595	ADXEC.28173.C1-a_s_at	Homo sapiens chromosome 14 open reading frame 106 (C14orf106)	C14orf106	0.0089	2.05
596	ADXECAD.9863_at	Homo sapiens twinfilin actin-binding protein homolog 1	TWF1	0.0226	2.05
597	ADXEC.7891.C1_at	Mediator complex subunit 6	MED6	0.0251	2.05
598	ADXECAD.1657_at	Homo sapiens SUMO1 activating enzyme subunit 1 (SAE1) transcript	SAE1	0.0375	2.05

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
599	ADXEC.2358.C2_s_at	Homo sapiens synaptogyrin 2 (SYNGR2) mRNA.	SYNGR2	0.0464	2.05
600	ADXECEMUTR.6831_at	Transcribed locus		0.0464	2.05
601	ADXEC.20828.C1_at	Homo sapiens genomic DNA chromosome 21q section 61/105.	RPS5P3	0.0485	2.05
602	ADXEC.7150.C1_at	Homo sapiens N-acetylglucosamine-1-phosphodiester	NAGPA	0.0491	2.05
603	ADXEC.981.C3_s_at	Transcribed locus		0.0512	2.05
604	ADXEC.7491.C1_at	DnaI (Hsp40) homolog subfamily C member 9	DNAJC9	0.0525	2.05
605	ADXEC.1472.C1_at	Homo sapiens family with sequence similarity 82 member A2	FAM82A2	0.0534	2.05
606	ADXEC.17001.C1-a_s_at	Homo sapiens HLA-B associated transcript 2-like 1 (BAT2L1) mRNA.	BAT2L1	0.0025	2.04
607	ADXEC.12654.C1_at	Transcribed locus		0.0082	2.04
608	ADXECADA.1912_at	3910609		0.0146	2.04
609	ADXEC.1986.C1_s_at	Homo sapiens nuclear prelamin A recognition factor (NARF)	NARF	0.0276	2.04
610	ADXEC.111.C71_at	Human elongation factor EF-1-alpha gene complete cds.	EEF1A1	0.0491	2.04
611	ADXEC.2453.C1_s_at	Homo sapiens lipase maturation factor 2 (LMF2) mRNA.	LMF2	0.0032	2.03
612	ADXEC.8778.C2_s_at	Homo sapiens integrator complex subunit 4 (INTS4) mRNA.	INTS4	0.0058	2.03
613	ADXEC.17718.C1_at	Homo sapiens breast carcinoma amplified sequence 3 (BCAS3)	BCAS3	0.0066	2.03
614	ADXECADA.6303_at	Homo sapiens tetraspanin 18 (TSPAN18) mRNA.	TSPAN18	0.0321	2.03
615	ADXEC.14775.C1-a_s_at	Homo sapiens leucine rich repeat (in FLII) interacting protein 2	LRRFIP2	0.0333	2.03
616	ADXECRS.20577_s_at	Homo sapiens chromosome 15 open reading frame 23 (C15orf23)	C15orf23	0.0396	2.03
617	ADXEC.13671.C1_at	Homo sapiens branched chain amino-acid transaminase 1 cytosolic	BCAT1	0.0404	2.03
618	ADXEC.13555.C1_at	Homo sapiens Src-like-adaptor (SLA) transcript variant 3 mRNA.	SLA	0.0412	2.03
619	ADXECRS.42385_at	Homo sapiens small nucleolar RNA H/ACA box 80 (SNORA80) small	SNORA80	0.0465	2.03
620	ADXEC.6107.C3-a_s_at	Homo sapiens ATPase H transporting lysosomal 38kDa V0 subunit	ATP6V0D1	0.0497	2.03
621	ADXECAD.11579_x_at	Homo sapiens sphingomyelin phosphodiesterase 1 acid lysosomal	SMPD1	0.0155	2.02
622	ADXEC.13922.C1_s_at	Transcribed locus		0.0338	2.02
623	ADXEC.15864.C1_s_at	Homo sapiens myosin heavy chain 11 smooth muscle isoform 2 (MYH11)		0.0397	2.02

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
		genecomplete			
624	ADXEC.2392.C9_x_at	Homo sapiens SH3-containing protein EEN (EEN) and chromatin assembly factor-1 p15	CHAF1A	0.0446	2.02
625	ADXEC.8484.C1_s_at	Homo sapiens serpin peptidase inhibitor clade E (nexin)	SERPINE1	0.045	2.02
626	ADXEC.3341.C3_at	Homo sapiens Fc fragment of IgG low affinity IIa receptor (CD32)	FCGR2A	0.0032	2.01
627	ADXECAD.23427_s_at	Homo sapiens alpha thalassemia/mental retardation syndrome X-linked	ATRX	0.0101	2.01
628	ADXEC.31455.C1_x_at	Zinc finger protein 582	ZNF582	0.0107	2.01
629	ADXECAD.12645_at	Transcribed locus		0.0224	2.01
630	ADXECRS.33_s_at	Homo sapiens chromosome 6 open reading frame 114 (C6orf114) mRNA.	C6orf114	0.0259	2.01
631	ADXECRS.35893_x_at	Homo sapiens CD3g molecule gamma (CD3-TCR complex) (CD3G) mRNA.	CD3G	0.026	2.01
632	ADXECNTDJ.8942_s_at	Homo sapiens C2 calcium-dependent domain containing 4C (C2CD4C)	C2CD4C	0.0296	2.01
633	ADXECRS.11163_s_at	Hypothetical protein LOC100133089	LOC100133089	0.0385	2.01
634	ADXECAD.7088_at	Homo sapiens RUN and FYVE domain containing 1 (RUFY1) transcript	RUFY1	0.0413	2.01
635	ADXEC.32494.C1_at	Transcribed locus		0.0434	2.01
636	ADXECAD.20979_s_at	Homo sapiens ADAM metalloproteinase domain 10 (ADAM10) mRNA.	ADAM10	0.0011	2
637	ADXECEMUTR.3430_s_at	CCZ1 vacuolar protein trafficking and biogenesis associated homolog (S. cerevisiae)	CCZ1	0.0093	2
638	ADXEC.17029.C1_s_at	Homo sapiens sialic acid binding Ig-like lectin 1 sialoadhesin	SIGLEC1	0.0151	2
639	ADXEC.23279.C1_x_at	Homo sapiens hyaluronan and proteoglycan link protein 3 (HAPLN3)	HAPLN3	0.0322	2
640	ADXECAD.28808_s_at	Homo sapiens WD repeat domain 48 (WDR48) mRNA.	WDR48	0.0364	2
641	ADXEC.25682.C1_at	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily	SMARCE1	0.044	2
642	ADXECAD.7356_s_at	excision repair cross-complementing rodent repair deficiency complementation group	ERCC6	0.0111	1.99
643	ADXECNTDJ.5985_s_at	Homo sapiens YLP motif containing 1 (YLP1) mRNA.	YLP1	0.0174	1.99
644	ADXEC.14089.C2_at	Homo sapiens diaphanous homolog 1 (Drosophila) (DIAPH1) transcript	DIAPH1	0.0204	1.99

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645	ADXECNTDJ.7831_s_at	Homo sapiens TATA box binding protein (TBP) transcript variant 2	TBP	0.0205	1.99
646	ADXEC.11266.C1_at	Pellino homolog 1 (Drosophila)	PELI1	0.0226	1.99
647	ADXEC.14653.C1_x_at	Tetratricopeptide repeat domain 17	TTC17	0.0347	1.99
648	ADXEC.8047.C1_s_at	Homo sapiens nucleolar protein with MIF4G domain 1 (NOM1) mRNA.	NOM1	0.0377	1.99
649	ADXEC.9580.C1-a_s_at	Homo sapiens small VCP/p97-interacting protein (SVIP) mRNA.	SVIP	0.0406	1.99
650	ADXEC.6547.C1-a_s_at	Homo sapiens RCSD domain containing 1 (RCSD1) mRNA.	RCSD1	0.046	1.99
651	ADXEC.12717.C1_at	Homo sapiens SAM and SH3 domain containing 3 (SASH3) mRNA.	SASH3	0.0514	1.99
652	ADXECAD.11485_s_at	Homo sapiens RAN binding protein 9 (RANBP9) mRNA.	RANBP9	0.0053	1.98
653	ADXEC.692.C2_at	Matrin 3	MATR3	0.009	1.98
654	ADXECNTDJ.1543_at	Homo sapiens solute carrier family 35 member F2 (SLC35F2) mRNA.	SLC35F2	0.0115	1.98
655	ADXEC.5070.C1_s_at	Homo sapiens U2 small nuclear RNA auxiliary factor 1-like 4	U2AF1L4	0.0153	1.98
656	ADXECAD.20947_at	Homo sapiens membrane-spanning 4-domains subfamily A member 7	MS4A7	0.0224	1.98
657	ADXECEMUTR.2170_s_at	Tetratricopeptide repeat domain 17	TTC17	0.0226	1.98
658	ADXECADA.16003_x_at	Homo sapiens hypothetical CG030 (CG030) non-coding RNA.	CG030	0.0275	1.98
659	ADXECADA.13904_at	Transcribed locus		0.0382	1.98
660	ADXEC.111.C99_s_at	Homo sapiens ubiquitin specific peptidase 22 (USP22) mRNA.	USP22	0.04	1.98
661	ADXECAD.13209_at	Tetratricopeptide repeat domain 7A	TTC7A	0.0432	1.98
662	ADXECCRS.8168_s_at	Homo sapiens colony stimulating factor 1 receptor (CSF1R) mRNA.	CSF1R	0.0518	1.98
663	ADXEC.19326.C1_at	Homo sapiens zinc finger protein 407 (ZNF407) transcript variant	ZNF407	0.0535	1.98
664	ADXEC.24209.C1_at	Transcribed locus		0.0544	1.98
665	ADXEC.731.C2_at	Homo sapiens SUMO1/sentrin specific peptidase 5 (SEN5) mRNA.	SEN5	0.0047	1.97
666	ADXECCRS.3185_s_at	Homo sapiens UBX domain protein 2B (UBXN2B) mRNA.	UBXN2B	0.0137	1.97
667	ADXEC.28724.C1_x_at	Homo sapiens PNAS-128 mRNA partial sequence.	SETDB2	0.0157	1.97
668	ADXECAD.17716_at	Protein tyrosine phosphatase non-receptor type 1	PTPN1	0.0163	1.97
669	ADXEC.237.C1_s_at	Homo sapiens myotubularin related protein 14 (MTMR14) transcript	MTMR14	0.0184	1.97

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
670	ADXEC.15321.C1_s_at	Homo sapiens zinc finger protein 618 (ZNF618) mRNA.	ZNF618	0.0269	1.97
671	ADXEC.34699.C1_s_at	Transcribed locus		0.0323	1.97
672	ADXEC.32742.C1_s_at	Homo sapiens N-myc downstream regulated 1 (NDRG1) transcript	NDRG1	0.0391	1.97
673	ADXEC.15773.C1_x_at	Homo sapiens membrane-spanning 4-domains subfamily A member 4	MS4A4A	0.0395	1.97
674	ADXEC.2920.C1_at	Chromodomain helicase DNA binding protein 7	CHD7	0.0493	1.97
675	ADXEC.34450.C1_x_at	Homo sapiens threonine synthase-like 1 (S. cerevisiae) (THNSL1)	THNSL1	0.0055	1.96
676	ADXECADA.6912_s_at	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2)	PPIL2	0.0094	1.96
677	ADXECADA.20527_s_at	Homo sapiens ATP-binding cassette sub-family F (GCM20) member 2	ABCF2	0.0135	1.96
678	ADXEC.10359.C1_at	CDNA FLJ27231 fis clone SYN06240		0.0168	1.96
679	ADXECAD.14318_at	Ral GEF with PH domain and SH3 binding motif 1	RALGPS1	0.0217	1.96
680	ADXEC.13314.C1_at	Homo sapiens Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ARHGEF6	0.0245	1.96
681	ADXEC.20469.C1_at	SFT2 domain containing 2	SFT2D2	0.0376	1.96
682	ADXECAD.11894_at	Transcribed locus		0.0412	1.96
683	ADXEC.14397.C2-a_s_at	Homo sapiens tumor necrosis factor (ligand) superfamily member 13	TNFSF13	0.0416	1.96
684	ADXEC.31875.C1_at	Homo sapiens family with sequence similarity 22 member A (FAM22A)	FAM22A	0.0421	1.96
685	ADXECNTDJ.1492_at	Homo sapiens TAF15 RNA polymerase II TATA box binding protein(TBP)-associated fa	TAF15	0.0465	1.96
686	ADXEC.1043.C1-a_s_at	Homo sapiens bystin-like (BYSL) mRNA.	BYSL	0.0474	1.96
687	ADXEC.1987.C1_at	Homo sapiens chromosome 12 open reading frame 44 (C12orf44)	C12orf44	0.0535	1.96
688	ADXEC.1728.C2_at	Homo sapiens solute carrier family 12 (potassium/chloride	SLC12A8	0.0155	1.95
689	ADXEC.5070.C2_s_at	Homo sapiens U2 small nuclear RNA auxiliary factor 1-like 4	U2AF1L4	0.0182	1.95
690	ADXEC.10862.C2_s_at	Homo sapiens galactose-1-phosphate uridylyltransferase (GALT)	GALT	0.0212	1.95
691	ADXEC.21971.C1_at	Homo sapiens ring finger protein 41 (RNF41) transcript variant 1	RNF41	0.024	1.95
692	ADXEC.30725.C1_at	Homo sapiens protein tyrosine phosphatase receptor type K	PTPRK	0.0266	1.95
693	ADXECADA.16682_at	CDNA FLJ26437 fis clone KDN02067		0.0365	1.95

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
694	ADXECAD.9122_s_at	Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene	XRCC3	0.0398	1.95
695	ADXECRS.19463_at	Homo sapiens dynein heavy chain domain 1 (DNHD1) transcript	DNHD1	0.0029	1.94
696	ADXECRS.24883_s_at	Homo sapiens transmembrane protein 86A (TMEM86A) mRNA.	TMEM86A	0.012	1.94
697	ADXEC.28457.C1_s_at	Homo sapiens p21 protein (Cdc42/Rac)-activated kinase 2 (PAK2)	PAK2	0.018	1.94
698	ADXEC.33002.C1_at	Homo sapiens chromosome 8 clone RP11-1007J8 complete sequence.	SLC20A2	0.0252	1.94
699	ADXECRS.15653_x_at	Programmed cell death 6 pseudogene	LOC728613	0.0262	1.94
700	ADXECAD.4571_at	Homo sapiens mRNA containing U19H snoRNA	SNHG4	0.0288	1.94
701	ADXEC.256.C5_at	Homo sapiens coiled-coil domain containing 137 (CCDC137) mRNA.	CCDC137	0.0339	1.94
702	ADXEC.33559.C1_x_at	Homo sapiens stromal antigen 3 opposite strand mRNA (cDNA clone IMAGE:6156265) pa	GATS	0.0375	1.94
703	ADXEC.28633.C1_s_at	Hypothetical protein LOC256021	LOC256021	0.0376	1.94
704	ADXEC.725.C4_s_at	Transcribed locus		0.041	1.94
705	ADXECADA.20351_x_at	Homo sapiens growth factor independent 1 transcription repressor	GFI1	0.0455	1.94
706	ADXEC.22905.C1_at	Transcribed locus		0.0474	1.94
707	ADXECNTDJ.9516_at	Homo sapiens chromosome 12 open reading frame 51 (C12orf51) mRNA.	C12orf51	0.048	1.94
708	ADXEC.12290.C1_s_at	PREDICTED: Homo sapiens hypothetical LOC728836 (LOC728836) mRNA.	LOC728836	0.0484	1.94
709	ADXEC.34156.C1_at	Homo sapiens PAC clone RP5-991G20 from 16 complete sequence.	RNU7-71P	0.0495	1.94
710	ADXECADA.24831_s_at	Homo sapiens RNA binding motif single stranded interacting protein	RBMS2	0.0041	1.93
711	3740525_at			0.0098	1.93
712	ADXEC.23874.C1_s_at	Homo sapiens endoplasmic reticulum protein 44 (ERP44) mRNA.	ERP44	0.01	1.93
713	ADXECAD.3802_at	Homo sapiens hypothetical LOC285965 (LOC285965) non-coding RNA.	LOC285965	0.0114	1.93
714	ADXECEMUTR.2405_at	Homo sapiens progesterone immunomodulatory binding factor 1 mRNA (cDNA clone MGC:	PIBF1	0.0134	1.93
715	ADXECADA.13185_at	HECT domain containing 1	HECTD1	0.0205	1.93

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
716	ADXECMUTR.2604_at	Homo sapiens chromosome 14 open reading frame 118 mRNA (cDNA cloneMGC:61896 IMAG	C14orf118	0.0227	1.93
717	ADXECADA.22330_s_at	Homo sapiens kin of IRRE like (Drosophila) (KIRREL) mRNA.	KIRREL	0.0241	1.93
718	ADXECAD.17994_at	Human DNA sequence from clone RP11-505P4 on chromosome 6 Contains the 5end of th	LOC100129409	0.0369	1.93
719	ADXECS.13593_at	Homo sapiens PDGFA associated protein 1 (PDAP1) mRNA.	PDAP1	0.038	1.93
720	ADXECS.36764_at	Homo sapiens lin-52 homolog (C. elegans) (LIN52) mRNA.	LIN52	0.0394	1.93
721	ADXECEMUTR.5725_s_at	Transcribed locus		0.0411	1.93
722	ADXEC.4049.C6_at	Homo sapiens KH type splicing regulatory protein (KHSRP) gene exons andpartial c	KHSRP	0.0438	1.93
723	ADXECAD.17506_s_at	Homo sapiens chromosome 10 open reading frame 18 (C10orf18) mRNA.	C10orf18	0.0516	1.93
724	ADXEC.1443.C2-a_s_at	Homo sapiens G protein-coupled receptor 160 (GPR160) mRNA.	GPR160	0.052	1.93
725	ADXEC.15087.C2_x_at	Homo sapiens symplekin (SYMPK) mRNA.	SYMPK	0.0068	1.92
726	ADXEC.15730.C1_at	Deoxyribonuclease I	DNASE1	0.009	1.92
727	ADXECAD.24015_s_at	Homo sapiens Fc fragment of IgG low affinity IIa receptor (CD32)	FCGR2A	0.0091	1.92
728	ADXECAD.26276_s_at	Homo sapiens guanine nucleotide binding protein (G protein) alpha	GNA13	0.0102	1.92
729	ADXEC.13922.C1_at	Transcribed locus		0.0117	1.92
730	ADXEC.33954.C1_at	Homo sapiens mRNA for KIAA0948 protein partial cds.	TBRG4	0.0221	1.92
731	ADXEC.19299.C1_at	Homo sapiens zinc finger and BTB domain containing 44 (ZBTB44)	ZBTB44	0.0272	1.92
732	ADXEC.3840.C1_at	Homo sapiens mitofusin 1 (MFN1) nuclear gene encoding	MFN1	0.028	1.92
733	ADXEC.26350.C1_at	Homo sapiens ADP-dependent glucokinase (ADPGK) transcript variant	ADPGK	0.0321	1.92
734	ADXEC.20776.C1_x_at	Homo sapiens hypothetical protein mRNA complete cds.	HEATR3	0.034	1.92
735	ADXECAD.18989_at	Homo sapiens chromodomain helicase DNA binding protein 7 (CHD7)	CHD7	0.0346	1.92
736	ADXEC.8794.C1_at	Homo sapiens CD53 molecule (CD53) transcript variant 2 mRNA.	CD53	0.0377	1.92
737	ADXEC.3720.C1_at	Homo sapiens Fc fragment of IgA receptor (FCAR) gene complete cds.	FCAR	0.0393	1.92

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
738	ADXEC.20792.C1_at	Homo sapiens G protein-coupled receptor 65 (GPR65) mRNA.	GPR65	0.0414	1.92
739	ADXECEMUTR.5845_at	Calcium homeostasis modulator 2	CALHM2	0.0424	1.92
740	ADXEC.22819.C1-a_s_at	Homo sapiens NLR family apoptosis inhibitory protein (NAIP)	NAIP	0.0438	1.92
741	3275388_at			0.0468	1.92
742	ADXEC.7799.C1_s_at	Homo sapiens kinesin family member C2 (KIFC2) mRNA.	KIFC2	0.0069	1.91
743	ADXECAD.15346_at	Tetratricopeptide repeat domain 17	TTC17	0.0077	1.91
744	ADXEC.31742.C1_at	Transcribed locus		0.0193	1.91
745	ADXECNTDJ.4097_s_at	Homo sapiens REST corepressor 1 (RCOR1) mRNA.	RCOR1	0.0231	1.91
746	ADXEC.7799.C2_s_at	Homo sapiens kinesin family member C2 (KIFC2) mRNA.	KIFC2	0.0238	1.91
747	ADXEC.17365.C1_at	Homo sapiens cAMP responsive element modulator (CREM) transcript	CREM	0.0244	1.91
748	ADXECNTDJ.8881_s_at	Homo sapiens zinc finger DHHC-type containing 2 (ZDHHC2) mRNA.	ZDHHC2	0.0288	1.91
749	ADXECNTDJ.7782_at	Homo sapiens retinoid X receptor beta (RXRB) mRNA.	RXRB	0.03	1.91
750	ADXEC.10295.C2-a_s_at	Homo sapiens KIAA0892 (KIAA0892) mRNA.	KIAA0892	0.0432	1.91
751	ADXEC.1230.C1_at	Homo sapiens activating transcription factor 5 (ATF5) mRNA.	ATF5	0.044	1.91
752	ADXECADA.22455_at	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1)	PDPK1	0.0004	1.9
753	ADXEC.9451.C1_s_at	Homo sapiens BCL2-like 13 (apoptosis facilitator) (BCL2L13)	BCL2L13	0.0005	1.9
754	ADXEC.2002.C6_s_at	Homo sapiens major facilitator superfamily domain containing 7	MFSD7	0.0083	1.9
755	ADXECRS.38063_s_at	Homo sapiens TBC1 domain family member 5 (TBC1D5) transcript	TBC1D5	0.0141	1.9
756	ADXEC.11294.C2_at	Homo sapiens ribosomal protein S6 kinase 90kDa polypeptide 3	RPS6KA3	0.0144	1.9
757	ADXEC.8760.C1-a_s_at	Homo sapiens WD repeat domain 37 (WDR37) mRNA.	WDR37	0.0152	1.9
758	ADXECADA.12739_x_at	CAP-GLY domain containing linker protein 1	CLIP1	0.0242	1.9
759	ADXEC.7957.C1_at	Homo sapiens potassium inwardly-rectifying channel subfamily J	KCNJ16	0.0274	1.9
760	ADXECRS.7301_s_at	Lysine (K)-specific demethylase 2A	KDM2A	0.0321	1.9
761	3740522_at			0.0387	1.9
762	ADXEC.26485.C1_at	Homo sapiens tetratricopeptide repeat protein 12 (TTC12) gene completecds	TTC12	0.0415	1.9

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
		altern			
763	ADXEC.3284.C1_s_at	Homo sapiens seryl-tRNA synthetase 2 mitochondrial (SARS2)	SARS2	0.0417	1.9
764	ADXEC.4619.C1-a_s_at	Homo sapiens Fanconi anemia complementation group A (FANCA)	FANCA	0.0439	1.9
765	ADXEC.3074.C1_s_at	Homo sapiens cyclin-dependent kinase 3 (CDK3) mRNA.	CDK3	0.0445	1.9
766	ADXEC.23200.C1_s_at	Homo sapiens metal-regulatory transcription factor 1 (MTF1) mRNA.	MTF1	0.045	1.9
767	ADXEC.21981.C1_at	Homo sapiens Fas apoptotic inhibitory molecule 3 (FAIM3)	FAIM3	0.0503	1.9
768	ADXEC.25832.C1_s_at	Inositol 145-trisphosphate 3-kinase B	ITPKB	0.051	1.9
769	ADXECAD.5956_at	Transcribed locus		0.0088	1.89
770	ADXEC.6304.C1_at	Homo sapiens endothelin converting enzyme 1 (ECE1) transcript	ECE1	0.0103	1.89
771	ADXEC.17266.C2_at	hypothetical protein isoform 1 [Pan troglodytes]		0.0153	1.89
772	ADXEC.11501.C1_s_at	Homo sapiens nucleoporin 93kDa (NUP93) mRNA.	NUP93	0.0166	1.89
773	ADXEC.256.C6_x_at	Homo sapiens transmembrane protein 69 (TMEM69) mRNA.	TMEM69	0.0313	1.89
774	ADXECRS.18611_at	Homo sapiens mastermind-like 2 (Drosophila) (MAML2) mRNA.	MAML2	0.0331	1.89
775	ADXEC.11294.C2-a_s_at	Homo sapiens ribosomal protein S6 kinase 90kDa polypeptide 3	RPS6KA3	0.0357	1.89
776	ADXECADA.22882_s_at	Homo sapiens programmed cell death 2 (PDCD2) transcript variant 1	PDCD2	0.0375	1.89
777	ADXECRS.35356_s_at	Homo sapiens dedicator of cytokinesis 9 (DOCK9) transcript variant	DOCK9	0.0436	1.89
778	ADXECRS.33044_s_at	Homo sapiens H2A histone family member V (H2AFV) transcript	H2AFV	0.0451	1.89
779	ADXECNTDJ.4526_s_at	Homo sapiens solute carrier family 38 member 1 (SLC38A1)	SLC38A1	0.0463	1.89
780	ADXEC.1909.C1_at	Homo sapiens eukaryotic translation termination factor 1 (ETF1)	ETF1	0.0027	1.88
781	2901705_at			0.0043	1.88
782	ADXEC.6036.C1_s_at	Homo sapiens receptor accessory protein 4 (REEP4) mRNA.	REEP4	0.006	1.88
783	ADXECRS.25428_s_at	Homo sapiens opiate receptor-like 1 (OPRL1) transcript variant 2	OPRL1	0.0105	1.88
784	ADXECAD.18815_at	Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1) and SNAPprotei	NIPSNAP3B	0.0259	1.88
785	ADXECAD.13671_x_at	Human DNA sequence from clone XX-HW2 on chromosome 4	MXD4	0.0301	1.88

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
786	ADXECADA.22236_at	Hypothetical protein MGC5566	MGC5566	0.0322	1.88
787	ADXECEMUTR.6744_at	KIAA0090	KIAA0090	0.0346	1.88
788	ADXEC.24053.C1_s_at	Homo sapiens congenital dyserythropoietic anemia type I (CDAN1)	CDAN1	0.0376	1.88
789	ADXECNTDJ.4966_s_at	Homo sapiens spermatogenesis associated 5 (SPATA5) mRNA.	SPATA5	0.0411	1.88
790	ADXEC.1710.C3_at	Transcribed locus		0.0435	1.88
791	ADXEC.31379.C1_s_at	Homo sapiens mRNA for KIAA1433 protein partial cds.	CTTNBP2NL	0.0454	1.88
792	ADXECADA.12739_at	CAP-GLY domain containing linker protein 1	CLIP1	0.046	1.88
793	ADXECNTDJ.5628_s_at	Homo sapiens stabilin 1 (STAB1) mRNA.	STAB1	0.0461	1.88
794	ADXECAD.19332_s_at	Homo sapiens cofilin 2 (muscle) (CFL2) transcript variant 1 mRNA.	CFL2	0.052	1.88
795	ADXECAD.16766_at	Homo sapiens mitochondrial ribosomal protein L9 (MRPL9) nuclear	MRPL9	0.0051	1.87
796	ADXPCEC.11965.C1_at	Transmembrane protein 165	TMEM165	0.0092	1.87
797	ADXECS.22932_at	PREDICTED: Homo sapiens hypothetical LOC100134170 (LOC100134170)	LOC100134170	0.0121	1.87
798	ADXECADA.22175_s_at	Transmembrane and coiled-coil domains 3	TMCO3	0.0133	1.87
799	ADXECAD.4973_at	Human cell line Ad-312/SV40 ectopic sequence from HMGI-C fusion mRNA 3sequence.		0.0169	1.87
800	ADXEC.3918.C1_s_at	Homo sapiens cAMP responsive element binding protein 3-like 2 mRNA (cDNAclone IM	CREB3L2	0.0301	1.87
801	ADXEC.16224.C1_at	Serine carboxypeptidase 1	SCPEP1	0.0347	1.87
802	ADXEC.30838.C1_at	Hypothetical LOC100216546	LOC100216546	0.0371	1.87
803	ADXEC.2718.C1_s_at	Homo sapiens nucleoporin 98kDa (NUP98) transcript variant 1 mRNA.	NUP98	0.0376	1.87
804	ADXECNTDJ.5669_at	Human T-cell membrane glycoprotein CD28 mRNA exon 2.		0.0384	1.87
805	ADXECEMUTR.5341_at	Homo sapiens alpha/beta hydrolase domain containing protein 3 (ABHD3) genecomple	ABHD3	0.0393	1.87
806	ADXEC.23611.C1_at	Transcribed locus		0.0426	1.87
807	ADXEC.619.C3_x_at	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia 2 (MLL2)	MLL2	0.0428	1.87

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808	ADXECMUTR.3915_at	Aftiphilin	AFTPH	0.0469	1.87
809	ADXCAD.18727_s_at	Homo sapiens PR domain containing 1 with ZNF domain (PRDM1)	PRDM1	0.0472	1.87
810	ADXC.22203.C1_at	Transcribed locus weakly similar to XP_001788090.1 PREDICTED: similar to endonuc	FP6628	0.0497	1.87
811	ADXCNTDJ.5584_at	Homo sapiens ArfGAP with dual PH domains 2 (ADAP2) mRNA.	ADAP2	0.0067	1.86
812	ADXC.944.C1_s_at	Homo sapiens HAUS augmin-like complex subunit 2 (HAUS2)	HAUS2	0.0097	1.86
813	ADXC.8213_at	Human mRNA 3 untranslated region for rapid chromosome assignment		0.0182	1.86
814	ADXC.3279.C1-a_s_at	Homo sapiens AT rich interactive domain 1A (SWI-like) (ARID1A)	ARID1A	0.0213	1.86
815	ADXC.18212.C1_at	Transcribed locus		0.0401	1.86
816	ADXC.1637.C1_s_at	pleckstrin homology domain containing family M (with RUN domain) member 2	PLEKHM2	0.0406	1.86
817	ADXCNTDJ.2829_at	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP)	IL1RAP	0.0009	1.85
818	ADXC.20561.C1_at	Genomic sequence from Human 6 complete sequence.	ATXN1	0.0025	1.85
819	ADXC.8949.C1_s_at	Homo sapiens parvin gamma (PARVG) transcript variant 2 mRNA.	PARVG	0.0053	1.85
820	ADXLCEC.5249.C1_x_at	Homo sapiens mRNA for KIAA1152 protein partial cds.	C14orf118	0.0078	1.85
821	ADXC.4434.C1_at	Homo sapiens solute carrier family 41 member 1 (SLC41A1) mRNA.	SLC41A1	0.0211	1.85
822	ADXC.399.C22_x_at	Homo sapiens low density lipoprotein receptor-related protein 1	LRP1	0.0228	1.85
823	ADXLCEC.6502.C1_x_at	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 3	AGPAT3	0.0236	1.85
824	ADXCAD.2689_s_at	CDNA FLJ37336 fis clone BRAMY2020412		0.0286	1.85
825	ADXC.3341.C1_x_at	Homo sapiens Fc fragment of IgG low affinity IIb receptor (CD32)	FCGR2B	0.0307	1.85
826	ADXCADA.9560_at	FLJ20914 fis clone ADSE00646		0.0312	1.85
827	ADXC.6.C11_at	Homo sapiens isolate MMAB-VI-T cob (MMAB) gene complete cds.	MMAB	0.047	1.85
828	ADXC.16609.C1_at	G protein-coupled receptor kinase interacting ArfGAP 2	GIT2	0.0485	1.85
829	ADXCAD.11689_at	Transcribed locus		0.0486	1.85
830	ADXC.18617.C1_s_at	Transcribed locus		0.05	1.85
831	ADXC.6197_at	Transcribed locus		0.0003	1.84

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
832	ADXECRS.5224_s_at	Homo sapiens phosphodiesterase 7A (PDE7A) transcript variant 1	PDE7A	0.0021	1.84
833	ADXEC.6409.C1-a_s_at	Homo sapiens DENN/MADD domain containing 4B (DENND4B) mRNA.	DENND4B	0.006	1.84
834	ADXEC.224.C27_at	Homo sapiens mediator of DNA-damage checkpoint 1 (MDC1) mRNA.	MDC1	0.0119	1.84
835	ADXEC.169.C9_x_at	Homo sapiens (N6-adenosine)-methyltransferase gene complete cds.	METTL3	0.0126	1.84
836	ADXECADA.3305_at	Full length insert cDNA clone ZB94A08		0.0136	1.84
837	ADXEC.194.C2_at	Homo sapiens family with sequence similarity 107 member B	FAM107B	0.0165	1.84
838	ADXEC.15087.C2_s_at	Homo sapiens symplekin (SYMPK) mRNA.	SYMPK	0.0181	1.84
839	ADXEC.16630.C1_s_at	Homo sapiens outer dense fiber of sperm tails 2 (ODF2) transcript	ODF2	0.0222	1.84
840	ADXEC.30911.C1_x_at	Transcribed locus		0.0377	1.84
841	ADXEC.16104.C2_s_at	Homo sapiens nucleotide binding protein 1 (MinD homolog E. coli)	NUBP1	0.0384	1.84
842	ADXEC.1293.C1_s_at	Homo sapiens KIAA1967 (KIAA1967) transcript variant 2 non-coding	KIAA1967	0.0401	1.84
843	ADXEC.16910.C1_s_at	Homo sapiens RAS protein activator like 3 (RASAL3) mRNA.	RASAL3	0.0427	1.84
844	ADXECNTDJ.780_s_at	Homo sapiens mitochondrial ribosomal protein L49 (MRPL49) nuclear	MRPL49	0.0444	1.84
845	ADXEC.19032.C1_at	PREDICTED: Homo sapiens hypothetical LOC727804 (LOC727804) mRNA.	LOC727804	0.0492	1.84
846	ADXEC.4862.C4_s_at	Homo sapiens chromosome 1 open reading frame 77 (C1orf77) mRNA.	C1orf77	0.0004	1.83
847	ADXECAD.16270_at	Homo sapiens zinc finger protein 502 (ZNF502) transcript variant	ZNF502	0.0038	1.83
848	ADXEC.8778.C1_s_at	Homo sapiens integrator complex subunit 4 (INTS4) mRNA.	INTS4	0.0107	1.83
849	ADXECAD.2058_s_at	2337111 mRNA sequence		0.0117	1.83
850	ADXECAD.11938_s_at	Homo sapiens zinc finger CCH-type containing 18 (ZC3H18) mRNA.	ZC3H18	0.0179	1.83
851	ADXOCEC.10681.C1_at	Homo sapiens tubulin tyrosine ligase-like family member 4 (TTL4)	TTL4	0.0187	1.83
852	ADXEC.20776.C1_at	Homo sapiens hypothetical protein mRNA complete cds.	HEATR3	0.0188	1.83
853	ADXEC.1473.C1_s_at	Homo sapiens coiled-coil and C2 domain containing 1B (CC2D1B)	CC2D1B	0.0278	1.83
854	ADXEC.6913.C1-a_s_at	Homo sapiens tripartite motif-containing 25 (TRIM25) mRNA.	TRIM25	0.031	1.83
855	ADXEC.23124.C1_at	Homo sapiens NLR family pyrin domain containing 1 (NLRP1)	NLRP1	0.042	1.83
856	ADXEC.26657.C1_at	Homo sapiens zinc finger protein 577 (ZNF577) transcript variant	ZNF577	0.0461	1.83

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857	ADXEC.26121.C2_s_at	Homo sapiens acyl-CoA synthetase medium-chain family member 3	ACSM3	0.0467	1.83
858	ADXEC.20884.C1_s_at	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 1	ARHGEF1	0.0492	1.83
859	ADXECADA.13198_x_at	Transcribed locus		0.0492	1.83
860	ADXEC.8622.C1_at	Homo sapiens IKAROS family zinc finger 1 (Ikaros) (IKZF1) mRNA.	IKZF1	0.0512	1.83
861	ADXEC.23062.C1_at	Homo sapiens chromosome 18 open reading frame 25 (C18orf25)	C18orf25	0.0518	1.83
862	ADXECNTDJ.5398_s_at	Dual specificity phosphatase 16	DUSP16	0.0521	1.83
863	ADXECEMUTR.5611_x_at	Homo sapiens chromosome 19 cosmid R32889 complete sequence.	OPA3	0.0053	1.82
864	ADXEC.25318.C1_at	Transcribed locus		0.0088	1.82
865	ADXECAD.19997_at	Solute carrier family 4 (anion exchanger) member 1 adaptor protein	SLC4A1AP	0.0167	1.82
866	ADXECNTDJ.7039_at	Homo sapiens Rho GTPase activating protein 18 (ARHGAP18) mRNA.	ARHGAP18	0.0185	1.82
867	ADXEC.5920.C1_s_at	Homo sapiens SH3 domain binding glutamic acid-rich protein like 3	SH3BGRL3	0.0196	1.82
868	ADXECAD.18742_x_at	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	LOC100288009	0.0232	1.82
869	ADXECCRS.8012_at	Homo sapiens diacylglycerol O-acyltransferase homolog 1 (mouse) mRNA (cDNA clone)	DGAT1	0.0424	1.82
870	ADXECAD.22713_s_at	Homo sapiens GRB2-associated binding protein 1 (GAB1) transcript	GAB1	0.0427	1.82
871	ADXECNTDJ.7720_at	Homo sapiens dihydropyrimidine dehydrogenase (DPYD) transcript	DPYD	0.0427	1.82
872	ADXEC.29114.C1_x_at	Homo sapiens chemokine (C-X-C motif) receptor 3 (CXCR3) transcript	CXCR3	0.0516	1.82
873	ADXEC.4541.C1_s_at	Homo sapiens transportin 3 (TNPO3) mRNA.	TNPO3	0.0002	1.81
874	ADXEC.10626.C1_s_at	Homo sapiens zinc finger protein 611 (ZNF611) transcript variant	ZNF611	0.0114	1.81
875	ADXEC.33841.C1_at	Homo sapiens chromosome 19 clone CTB-14D10 complete sequence.	NANOS2	0.0132	1.81
876	ADXEC.31978.C1_at	KB1588E7 complete sequence.		0.0145	1.81
877	ADXEC.3751.C2_at	Homo sapiens TBC1 (tre-2/USP6 BUB2 cdc16) domain family member 1	TBC1D1	0.0157	1.81
878	ADXEC.5304.C2_at	Homo sapiens metastasis associated in colon cancer 1 (MACC1) mRNA.	MACC1	0.0191	1.81
879	ADXLCEC.4623.C1_at	Homo sapiens macrophage scavenger receptor 1 (MSR1) gene complete cds.	MSR1	0.02	1.81

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
880	ADXEC.20725.C1_at	Homo sapiens cell division cycle 42 (GTP binding protein 25kDa)	CDC42	0.0268	1.81
881	ADXECEMUTR.913_s_at	Homo sapiens hypothetical LOC652276 (LOC652276) non-coding RNA.	LOC652276	0.0312	1.81
882	ADXECADA.13436_at	Coiled-coil domain containing 93	CCDC93	0.0317	1.81
883	ADXECAD.17086_x_at	Peptidylprolyl isomerase domain and WD repeat containing 1	PPWD1	0.033	1.81
884	ADXECNTDJ.6431_s_at	Homo sapiens CD8a molecule (CD8A) transcript variant 1 mRNA.	CD8A	0.0417	1.81
885	ADXECEMUTR.7777_s_at	Homo sapiens ZNF01 and HUMORFKG1B genes partial sequence complete sequence.		0.047	1.81
886	ADXEC.15623.C1_at	Homo sapiens SET domain containing 1B (SETD1B) mRNA.	SETD1B	0.0513	1.81
887	ADXECAD.2934_at	Homo sapiens metastasis associated in colon cancer 1 (MACC1) mRNA.	MACC1	0.0523	1.81
888	ADXECEMUTR.7014_at	Homo sapiens mRNA for PAP associated domain containing 1 variant		0.004	1.8
889	ADXECAD.2809_x_at	Homo sapiens kinesin family member 1B (KIF1B) transcript variant	KIF1B	0.008	1.8
890	ADXECRS.10658_s_at	Homo sapiens myocyte enhancer factor 2A (MEF2A) transcript variant	MEF2A	0.0174	1.8
891	ADXECRS.16999_at	Homo sapiens POU class 3 homeobox 1 (POU3F1) mRNA.	POU3F1	0.0189	1.8
892	ADXEC.522.C5_at	Human mRNA for HLA class II DR-beta 1 (Dw14)	HLA-DRB1	0.027	1.8
893	ADXEC.7821.C1-a_s_at	Homo sapiens phosphatase and actin regulator 4 (PHACTR4)	PHACTR4	0.0303	1.8
894	ADXEC.14444.C1_s_at	Homo sapiens chloride channel CLIC-like 1 (CLCC1) transcript	CLCC1	0.0306	1.8
895	ADXECAD.16298_at	Homo sapiens isolate 495CLS7 haplotype HLA-B3801/HLA-Cw120301 genomic sequence.		0.0345	1.8
896	ADXEC.409.C32_at	Transcribed locus	PTP4A2	0.0357	1.8
897	ADXEC.30057.C1_x_at	Lactamase beta	LACTB	0.0409	1.8
898	ADXECEMUTR.4612_s_at	Homo sapiens RNA binding motif protein 41 (RBM41) transcript	RBM41	0.0437	1.8
899	ADXECAD.6907_s_at	Homo sapiens single stranded DNA binding protein 4 (SSBP4)	SSBP4	0.0444	1.8
900	ADXECRS.27967_s_at	Homo sapiens grancalcin EF-hand calcium binding protein (GCA)	GCA	0.0488	1.8
901	ADXECAD.4974_at	Human cell line Ad-312/SV40 ectopic sequence from HMGI-C fusion mRNA 3sequence.		0.0524	1.8

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
902	ADXEC.25687.C1-a_s_at	Homo sapiens methionyl aminopeptidase 1 (METAP1) mRNA.	METAP1	0.0534	1.8
903	ADXEC.5655.C1_s_at	Homo sapiens annexin A11 (ANXA11) transcript variant a mRNA.	ANXA11	0.0009	1.79
904	ADXEC.2201.C2_s_at	Homo sapiens ribonuclease RNase A family 1 (pancreatic) (RNASE1)	RNASE1	0.0021	1.79
905	ADXEC.20904.C1_at	Transcribed locus		0.0122	1.79
906	ADXECAD.19475_at	Homo sapiens KIAA2026 (KIAA2026) mRNA.	KIAA2026	0.0141	1.79
907	ADXECADA.1579_at	CDNA FLJ90641 fis clone PLACE1004028		0.017	1.79
908	ADXEC.11161.C1-a_s_at	Homo sapiens kinesin family member 5B (KIF5B) mRNA.	KIF5B	0.0217	1.79
909	ADXOCEC.14417.C1_at	Ral GTPase activating protein alpha subunit 2 (catalytic)	RALGAPA2	0.0229	1.79
910	ADXECAD.806_at	Homo sapiens potassium channel tetramerisation domain containing 7	KCTD7	0.0233	1.79
911	ADXEC.224.C27_x_at	Homo sapiens mediator of DNA-damage checkpoint 1 (MDC1) mRNA.	MDC1	0.0295	1.79
912	ADXECAD.22145_s_at	Homo sapiens glutathione reductase (GSR) mRNA.	GSR	0.0363	1.79
913	ADXEC.3211.C2_s_at	RNA binding motif protein 39	RBM39	0.0417	1.79
914	ADXEC.2026.C1_s_at	Homo sapiens phosphoinositide-3-kinase adaptor protein 1 (PIK3AP1)	PIK3AP1	0.045	1.79
915	ADXEC.25928.C1_at	CDNA FLJ13554 fis clone PLACE1007478		0.05	1.79
916	ADXEC.12104.C1-a_s_at	Homo sapiens chromosome 4 open reading frame 19 (C4orf19)	C4orf19	0.0542	1.79
917	ADXEC.22516.C1-a_s_at	Homo sapiens family with sequence similarity 84 member A (FAM84A)	FAM84A	0.0068	1.78
918	ADXEC.194.C1_at	Homo sapiens family with sequence similarity 107 member B	FAM107B	0.0195	1.78
919	ADXECAD.19560_at	Homo sapiens membrane-associated ring finger (C3HC4) 1 (MARCH1)	28-Feb	0.0215	1.78
920	ADXEC.1230.C1_x_at	Homo sapiens activating transcription factor 5 (ATF5) mRNA.	ATF5	0.0258	1.78
921	ADXEC.9707.C1_at	Homo sapiens lysosomal protein transmembrane 5 (LAPTM5) mRNA.	LAPTM5	0.0307	1.78
922	ADXECAD.15849_s_at	guanine nucleotide binding protein (G protein) alpha activating activity polypep	GNAL	0.0322	1.78
923	ADXECADA.8947_at	Human immunodeficiency virus type I enhancer binding protein 3	HIVEP3	0.0368	1.78
924	ADXECRS.6844_at	Homo sapiens ADAM metalloproteinase domain 10 (ADAM10) mRNA.	ADAM10	0.037	1.78
925	ADXECNTDJ.1274_at	Homo sapiens leukocyte receptor cluster (LRC) member 8 (LENG8)	LENG8	0.0372	1.78
926	ADXECAD.27910_s_at	Homo sapiens solute carrier family 12 (potassium/chloride	SLC12A6	0.0377	1.78

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
927	ADXECAD.3337_at	Homo sapiens ATP binding domain 4 (ATPBD4) transcript variant 2	ATPBD4	0.0396	1.78
928	ADXECNTDJ.4629_at	Homo sapiens CNDP dipeptidase 2 (metallopeptidase M20 family)	CNDP2	0.0458	1.78
929	ADXEC.3103.C1_s_at	Transcribed locus strongly similar to NP_006592.3 prostaglandin E synthase 3 [Ho]		0.049	1.78
930	ADXECRS.13926_s_at	Homo sapiens similar to SAPS domain family member 2	LOC652875	0.0514	1.78
931	ADXEC.26956.C1_x_at	Homo sapiens genomic DNA chromosome 6p21.3 HLA Class I region.	C6orf26	0.0088	1.77
932	ADXECEMUTR.419_at	Clathrin heavy chain (Hc)	CLTC	0.0089	1.77
933	ADXEC.20643.C1_x_at	Homo sapiens genomic DNA chromosome 21q section 15/105.	RPL37P3	0.0126	1.77
934	ADXECADA.21291_at	Homo sapiens death-associated protein kinase 1 (DAPK1) mRNA.	DAPK1	0.0256	1.77
935	ADXEC.4815.C1_at	Transcribed locus		0.0262	1.77
936	ADXEC.13239.C1_s_at	Homo sapiens membrane protein palmitoylated 1 55kDa (MPP1)	MPP1	0.0264	1.77
937	ADXEC.3302.C1_s_at	Homo sapiens calpain 5 (CAPN5) mRNA.	CAPN5	0.0307	1.77
938	ADXEC.24147.C1-a_s_at	Homo sapiens muscleblind-like 3 (Drosophila) (MBNL3) transcript	MBNL3	0.0344	1.77
939	ADXEC.409.C56_s_at	Transcribed locus	PTP4A2	0.0398	1.77
940	ADXEC.20402.C1_s_at	Homo sapiens coronin actin binding protein 1C (CORO1C)	CORO1C	0.0418	1.77
941	ADXEC.11553.C1_s_at	Homo sapiens solute carrier family 25 (mitochondrial carrier	SLC25A14	0.0452	1.77
942	ADXECAD.11309_at	Homo sapiens ADP-ribosylation factor guanine nucleotide-exchange	ARFGEF2	0.0507	1.77
943	ADXEC.6844.C1_s_at	Homo sapiens archaelysin family metallopeptidase 2 (AMZ2)	AMZ2	0.0019	1.76
944	ADXEC.9777.C1_at	Homo sapiens vesicle-associated membrane protein 7 (VAMP7)	VAMP7	0.0138	1.76
945	ADXECAD.10244_s_at	Homo sapiens quaking homolog KH domain RNA binding (mouse) (QKI)	QKI	0.0147	1.76
946	ADXEC.29628.C1_at	Homo sapiens NF2 gene	NF2	0.016	1.76
947	ADXECRS.113_s_at	Transcribed locus		0.0163	1.76
948	ADXEC.19080.C2_s_at	Homo sapiens male-specific lethal 3 homolog (Drosophila) (MSL3)	MSL3	0.0361	1.76
949	ADXEC.30071.C1_x_at	Human Chromosome 16 BAC clone CIT987SK-A-735G6 complete sequence.	LOC100288661	0.041	1.76
950	ADXEC.8794.C1_x_at	Homo sapiens CD53 molecule (CD53) transcript variant 2 mRNA.	CD53	0.0418	1.76

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
951	ADXECAD.9133_at	Homo sapiens HERV-H LTR-associating 3 (HHLA3) transcript variant	HHLA3	0.0483	1.76
952	ADXEC.4634.C3_at	inhibitor of DNA binding 2 dominant negative helix-loop-helix protein	ID2	0.0502	1.76
953	ADXEC.1926.C1_s_at	Homo sapiens TYRO protein tyrosine kinase binding protein (TYROBP)	TYROBP	0.0008	1.75
954	ADXEC.3333.C2_s_at	Homo sapiens erythrocyte membrane protein band 4.1 (elliptocytosis	EPB41	0.0101	1.75
955	ADXEC.23835.C1_at	Transcribed locus strongly similar to NP_002694.3 phosphoribosyl pyrophosphate a		0.0158	1.75
956	ADXECEMUTR.3274_x_at	Homo sapiens chromosome 1 open reading frame 104 mRNA (cDNA cloneMGC:149516 IMAG	C1orf104	0.0211	1.75
957	ADXECAD.6865_at	Homo sapiens EGF-containing fibulin-like extracellular matrix	EFEMP1	0.0247	1.75
958	ADXEC.23003.C1_at	Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT)	RNGTT	0.0254	1.75
959	ADXECNTDJ.3226_at	Homo sapiens CD200 molecule (CD200) transcript variant 1 mRNA.	CD200	0.0262	1.75
960	ADXEC.32437.C1_at	Human DNA sequence from clone RP11-452J13 on chromosome 1 Contains a novelgene.		0.0272	1.75
961	ADXEC.11842.C1_at	Homo sapiens SERTA domain containing 2 (SERTAD2) mRNA.	SERTAD2	0.0332	1.75
962	ADXEC.20528.C1_s_at	Transcribed locus		0.0361	1.75
963	ADXEC.6728.C2_at	Homo sapiens protein tyrosine phosphatase type IVA member 1	PTP4A1	0.0382	1.75
964	ADXEC.9302.C1_s_at	Zinc finger protein 397 opposite strand	ZNF397OS	0.0447	1.75
965	ADXECADA.19246_s_at	Homo sapiens RAB7A member RAS oncogene family (RAB7A) mRNA.	RAB7A	0.0534	1.75
966	ADXECADA.21635_s_at	Homo sapiens chromosome 17 open reading frame 63 (C17orf63)	C17orf63	0.0003	1.74
967	ADXEC.2802.C2_s_at	Homo sapiens interferon gamma receptor 2 (interferon gamma	IFNGR2	0.006	1.74
968	ADXECADA.8638_at	FLJ21358 fis clone COL02842		0.0077	1.74
969	3362760_at			0.008	1.74
970	ADXEC.18446.C1_at	Homo sapiens RIO kinase 2 (yeast) (RIOK2) transcript variant 1	RIOK2	0.0098	1.74
971	ADXEC.862.C1_s_at	Homo sapiens ganglioside induced differentiation associated protein	GDAP2	0.0104	1.74
972	ADXEC.32407.C1_x_at	Homo sapiens AXL receptor tyrosine kinase (AXL) transcript variant	AXL	0.0136	1.74

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
973	ADXCADA.20237_at	Homo sapiens fasciculation and elongation protein zeta 1 (zyglin I)	FEZ1	0.0161	1.74
974	ADXEC.19393.C1_s_at	Transcribed locus		0.0235	1.74
975	ADXEC.22969.C1_at	Homo sapiens tripartite motif-containing 22 (TRIM22) mRNA.	TRIM22	0.0243	1.74
976	ADXEC.3642.C2_s_at	Homo sapiens myeloid leukemia factor 2 (MLF2) transcript variant	MLF2	0.032	1.74
977	ADXEC.4627.C3_s_at	Homo sapiens solute carrier family 15 member 3 (SLC15A3)	SLC15A3	0.0337	1.74
978	ADXEC.7693.C1_x_at	Homo sapiens mbt domain containing 1 (MBTD1) mRNA.	MBTD1	0.0341	1.74
979	ADXECRS.39842_s_at	Homo sapiens SET domain bifurcated 2 (SETDB2) transcript variant	SETDB2	0.0369	1.74
980	ADXEC.32870.C1_x_at	Homo sapiens chromosome 19 cosmid R31973 complete sequence.	CASP14	0.0417	1.74
981	ADXEC.19299.C1_x_at	Homo sapiens zinc finger and BTB domain containing 44 (ZBTB44)	ZBTB44	0.0423	1.74
982	ADXEC.3550.C1_s_at	Homo sapiens protein kinase C delta binding protein (PRKCDBP)	PRKCDBP	0.0426	1.74
983	ADXEC.20290.C1_at	Homo sapiens oxidoreductase NAD-binding domain containing 1	OXNAD1	0.0499	1.74
984	ADXCADA.12751_at	Transcribed locus		0.0015	1.73
985	ADXEC.14337.C2_at	Homo sapiens protein phosphatase 1 regulatory (inhibitor) subunit	PPP1R15B	0.0107	1.73
986	ADXEC.22249.C1_at	Homo sapiens mediator complex subunit 6 (MED6) mRNA.	MED6	0.0188	1.73
987	ADXEC.3547.C2-a_s_at	Homo sapiens poly (ADP-ribose) polymerase 1 (PARP1) mRNA.	PARP1	0.0205	1.73
988	ADXEC.2514.C1_at	Homo sapiens sulfide quinone reductase-like (yeast) (SQRD1)	SQRDL	0.0252	1.73
989	ADXEC.9209.C1_at	Homo sapiens cardiophillin 1 (CTF1) transcript variant 1 mRNA.	CTF1	0.0301	1.73
990	ADXEC.2932.C3_s_at	Homo sapiens thymocyte nuclear protein 1 (THYN1) transcript	THYN1	0.0304	1.73
991	ADXECRS.325_s_at	Homo sapiens sema domain immunoglobulin domain (Ig) transmembrane	SEMA4D	0.0305	1.73
992	ADXEC.34320.C1_x_at	Transcribed locus		0.0361	1.73
993	ADXECNTDJ.4573_at	Homo sapiens hepatitis A virus cellular receptor 2 (HAVCR2) mRNA.	HAVCR2	0.0377	1.73
994	ADXEC.20525.C1_s_at	Homo sapiens leukocyte specific transcript 1 (LST1) transcript	LST1	0.0386	1.73
995	ADXEC.23136.C1_s_at	Hypothetical protein LOC150166	LOC150166	0.0387	1.73
996	ADXEC.20508.C1_s_at	Glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	GPCPD1	0.0442	1.73
997	ADXEC.19219.C1_s_at	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation	DYRK2	0.0442	1.73

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
998	ADXECADA.3274_x_at	5278245		0.0485	1.73
999	ADXECADA.11176_at	Transcribed locus		0.054	1.73
1000	ADXEC.23053.C1_at	Homo sapiens G protein-coupled bile acid receptor 1 (GPBAR1)	GPBAR1	0	1.72
1001	ADXEC.3377.C1_s_at	Homo sapiens cathepsin S (CTSS) mRNA.	CTSS	0.0143	1.72
1002	ADXEC.13875.C1-a_s_at	Homo sapiens guanine nucleotide binding protein (G protein) alpha	GNA12	0.0146	1.72
1003	ADXEC.2514.C1_x_at	Homo sapiens sulfide quinone reductase-like (yeast) (SQORDL)	SQORDL	0.0147	1.72
1004	ADXEC.14780.C2_s_at	Homo sapiens cDNA FLJ58787 complete cds highly similar to Cleavagestimulaion fa	CSTF2	0.0214	1.72
1005	ADXEC.1048.C1_x_at	Homo sapiens polymerase (DNA directed) epsilon 3 (p17 subunit)	POLE3	0.0238	1.72
1006	ADXEC.18416.C1_s_at	Clone 23728 mRNA sequence		0.0263	1.72
1007	ADXECADA.7794_at	Transcribed locus		0.0264	1.72
1008	ADXECAD.16674_at	Homo sapiens establishment of cohesion 1 homolog 1 (S. cerevisiae)	ESCO1	0.0351	1.72
1009	ADXEC.29259.C1_at	Homo sapiens toll-like receptor 5 (TLR5) mRNA.	TLR5	0.0382	1.72
1010	ADXECNTDJ.1667_x_at	Homo sapiens non-protein coding RNA 256B (NCRNA00256B) non-coding	NCRNA00256B	0.0438	1.72
1011	ADXEC.8189.C1-a_s_at	Homo sapiens origin recognition complex subunit 3-like (yeast)	ORC3L	0.0485	1.72
1012	ADXEC.9082.C1-a_s_at	Homo sapiens signal recognition particle 68kDa (SRP68) mRNA.	SRP68	0.0518	1.72
1013	ADXEC.7383.C1_x_at	Homo sapiens zinc finger protein 639 (ZNF639) mRNA.	ZNF639	0.0033	1.71
1014	ADXECRS.14355_s_at	Homo sapiens S-phase kinase-associated protein 2 (p45) (SKP2)	SKP2	0.0077	1.71
1015	ADXEC.33954.C1_x_at	Homo sapiens mRNA for KIAA0948 protein partial cds.	TBRG4	0.0078	1.71
1016	ADXECNTDJ.5115_at	small glutamine-rich tetratricopeptide repeat (TPR)-containing alpha	SGTA	0.0137	1.71
1017	ADXEC.4115.C1-a_s_at	LUC7-like 2 (S. cerevisiae)	LUC7L2	0.0149	1.71
1018	ADXECNTDJ.9072_at	Homo sapiens claudin 12 (CLDN12) transcript variant 2 mRNA.	CLDN12	0.0162	1.71
1019	ADXEC.3331.C1_s_at	amyloid beta (A4) precursor protein-binding family B member 1 interacting protei	APBB1IP	0.0175	1.71
1020	ADXEC.30120.C1_at	Homo sapiens adaptor-related protein complex 1 sigma 3 subunit	AP1S3	0.0352	1.71

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1021	ADXECAD.6255_at	Homo sapiens TRAF-interacting protein with forkhead-associated	TIFA	0.0422	1.71
1022	ADXEC.15023.C1_at	Homo sapiens v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1) genecomplet	RAF1	0.0461	1.71
1023	ADXEC.33165.C1_at	Transcribed locus		0.0532	1.71
1024	ADXEC.1093.C1-a_s_at	Homo sapiens phosphotyrase kinase alpha 2 (liver) (PHKA2) mRNA.	PHKA2	0.006	1.7
1025	ADXECADA.24681_s_at	Homo sapiens single stranded DNA binding protein 3 (SSBP3)	SSBP3	0.016	1.7
1026	ADXEC.7383.C1_at	Homo sapiens zinc finger protein 639 (ZNF639) mRNA.	ZNF639	0.0264	1.7
1027	ADXEC.14583.C1_at	Homo sapiens paired box 8 (PAX8) transcript variant PAX8D mRNA.	PAX8	0.0288	1.7
1028	ADXEC.12925.C1_at	Homo sapiens sarcoglycan alpha (50kDa dystrophin-associated	SGCA	0.0344	1.7
1029	ADXEC.17232.C1-a_s_at	Homo sapiens trafficking protein particle complex 10 mRNA (cDNA cloneIMAGE:59256	TRAPPC10	0.0442	1.7
1030	ADXEC.20957.C1-a_s_at	Homo sapiens Rho GTPase activating protein 18 (ARHGAP18) mRNA.	ARHGAP18	0.0462	1.7
1031	ADXEC.9347.C1_s_at	Ubiquitin-fold modifier conjugating enzyme 1	UFC1	0.0508	1.7
1032	ADXCNTDJ.198_at	Leukocyte-associated immunoglobulin-like receptor 2	LAIR2	0.052	1.7
1033	ADXEC.318.CB3_s_at	Homo sapiens arrestin beta 2 (ARRB2) transcript variant 1 mRNA.	ARRB2	0.0115	1.69
1034	ADXEC.20828.C1-a_s_at	Homo sapiens genomic DNA chromosome 21q section 61/105.	RPS5P3	0.0158	1.69
1035	ADXECAD.11135_at	Splicing factor arginine/serine-rich 3	SFRS3	0.0168	1.69
1036	ADXECAD.13897_at	Homo sapiens solute carrier family 8 (sodium/calcium exchanger)	SLC8A1	0.0184	1.69
1037	ADXEC.7354.C1_at	Small VCP/p97-interacting protein	SVIP	0.0192	1.69
1038	ADXECADA.1371_x_at	Homo sapiens KVLQT1 gene	KCNQ1	0.0265	1.69
1039	ADXEC.22459.C1_at	Transcribed locus		0.0267	1.69
1040	ADXECADA.634_s_at	Homo sapiens pyroglutamyl-peptidase I (PGPEP1) mRNA.	PGPEP1	0.033	1.69
1041	ADXEC.20525.C2_s_at	Homo sapiens leukocyte specific transcript 1 (LST1) transcript	LST1	0.0362	1.69
1042	2840670_at			0.037	1.69
1043	ADXCERS.7423_s_at	PREDICTED: Homo sapiens similar to ribosomal protein S7	LOC100129381	0.0443	1.69

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1044	ADXEC.29028.C1_x_at	Homo sapiens nasal embryonic LHRH factor (NELF) transcript variant	NELF	0.0494	1.69
1045	ADXEC.718.C1_x_at	Homo sapiens ethanolamine kinase 1 (ETNK1) transcript variant 1	ETNK1	0.0495	1.69
1046	ADXEC.14372.C2_s_at	Homo sapiens WEE1 homolog (S. pombe) (WEE1) transcript variant 1	WEE1	0.0516	1.69
1047	ADXEC.24170.C1_s_at	Homo sapiens centromere protein C 1 (CENPC1) mRNA.	CENPC1	0.0021	1.68
1048	ADXECAD.18174_s_at	Homo sapiens MICAL C-terminal like (MICALCL) mRNA.	MICALCL	0.0077	1.68
1049	ADXEC.2954.C1_at	Homo sapiens stress-associated endoplasmic reticulum protein 1	SERP1	0.0081	1.68
1050	ADXECADA.24803_s_at	Homo sapiens GTP binding protein 2 (GTPBP2) mRNA.	GTPBP2	0.0132	1.68
1051	ADXECRS.27469_s_at	PREDICTED: Homo sapiens similar to synaptophysin-like 1	LOC100132972	0.0132	1.68
1052	ADXEC.21098.C1_at	Homo sapiens heat shock 70kDa protein 5 (glucose-regulated protein	HSPA5	0.0184	1.68
1053	ADXEC.731.C2-a_s_at	Homo sapiens SUMO1/sentrin specific peptidase 5 (SENPS) mRNA.	SENPS	0.0246	1.68
1054	ADXEC.22969.C1_s_at	Homo sapiens tripartite motif-containing 22 (TRIM22) mRNA.	TRIM22	0.0323	1.68
1055	ADXEC.15955.C1-a_s_at	Homo sapiens coiled-coil domain containing 82 (CCDC82) mRNA.	CCDC82	0.0373	1.68
1056	ADXEC.23381.C1_at	Acyl-CoA synthetase family member 2	ACSF2	0.0386	1.68
1057	ADXECAD.14017_at	Transcribed locus		0.0528	1.68
1058	ADXEC.2751.C1_at	Homo sapiens ras homolog gene family member G (rho G) (RHOG)	RHOG	0.0047	1.67
1059	ADXEC.24741.C1_at	CDNA FLJ42263 fis clone TKIDN2014570		0.0099	1.67
1060	ADXEC.23021.C2_at	PARK2 co-regulated-like	PACRGL	0.014	1.67
1061	ADXEC.22249.C1_x_at	Homo sapiens mediator complex subunit 6 (MED6) mRNA.	MED6	0.0179	1.67
1062	ADXEC.8815.C1_s_at	Homo sapiens LIM domain containing preferred translocation partner	LPP	0.0228	1.67
1063	ADXEC.3268.C1_at	Homo sapiens ASF1 anti-silencing function 1 homolog B (S.	ASF1B	0.0233	1.67
1064	ADXEC.29681.C1_at	Human DNA sequence from clone RP1-65J11 on chromosome 1 Contains the 5 endof the	LOC100288670	0.0245	1.67
1065	ADXEC.2002.C8_x_at	Homo sapiens major facilitator superfamily domain containing 7	MFSD7	0.0268	1.67
1066	ADXECNTDJ.3207_at	Homo sapiens genomic DNA chromosome 11 clone:RP11-856B14.	PCNXL3	0.0289	1.67
1067	ADXEC.1852.C1-a_s_at	Homo sapiens CCR4-NOT transcription complex subunit 6 (CNOT6)	CNOT6	0.0292	1.67

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1068	ADXECADA.24456_s_at	Homo sapiens nuclear transport factor 2-like export factor 2	NXT2	0.0316	1.67
1069	ADXEC.21314.C2_s_at	Homo sapiens TAO kinase 3 (TAOK3) mRNA.	TAOK3	0.0327	1.67
1070	ADXEC.32169.C1_at	Apolipoprotein B mRNA editing enzyme catalytic polypeptide-like 2	APOBEC2	0.0432	1.67
1071	ADXECAD.17857_at	Transcribed locus		0.044	1.67
1072	ADXEC.7693.C1_at	Homo sapiens mbt domain containing 1 (MBTD1) mRNA.	MBTD1	0.05	1.67
1073	ADXEC.5123.C1_s_at	Homo sapiens KIAA1147 (KIAA1147) mRNA.	KIAA1147	0.0034	1.66
1074	ADXECRS.42976_s_at	Homo sapiens phosphodiesterase 4D interacting protein (PDE4DIP)	PDE4DIP	0.0067	1.66
1075	ADXEC.564.C1_at	Homo sapiens Hermansky-Pudlak syndrome 5 (HPS5) transcript variant	HPS5	0.0117	1.66
1076	ADXECAD.25947_s_at	Homo sapiens ATG12 autophagy related 12 homolog (S. cerevisiae)	ATG12	0.0119	1.66
1077	ADXEC.1013.C2_s_at	Homo sapiens tetratricopeptide repeat domain 9C (TTC9C) mRNA.	TTC9C	0.0122	1.66
1078	ADXEC.22227.C1_s_at	Formin binding protein 1	FNBP1	0.0132	1.66
1079	ADXEC.18223.C1_at	Similar to hCG1987955	LOC100288939	0.0232	1.66
1080	ADXEC.15802.C1_at	Homo sapiens triggering receptor expressed on myeloid cells 2	TREM2	0.0236	1.66
1081	ADXECNTDJ.546_s_at	Homo sapiens solute carrier family 15 member 3 (SLC15A3)	SLC15A3	0.0248	1.66
1082	ADXEC.39.C1_s_at	Homo sapiens lamin B1 (LMNB1) mRNA.	LMNB1	0.026	1.66
1083	ADXECADA.18591_at	Transcribed locus		0.0284	1.66
1084	ADXECAD.7717_at	Transcribed locus		0.0353	1.66
1085	ADXECAD.10026_at	Human ribosomal protein S14 gene complete cds.	RPS14	0.0412	1.66
1086	ADXEC.17920.C1_at	Homo sapiens dispatched homolog 1 (Drosophila) (DISP1) mRNA.	DISP1	0.0414	1.66
1087	ADXEC.6073.C1-a_s_at	Homo sapiens high mobility group nucleosomal binding domain 4	HMGN4	0.047	1.66
1088	ADXECADA.14018_at	UDP-glucose glycoprotein glucosyltransferase 1	UGGT1	0.048	1.66
1089	ADXEC.11581.C2_at	Homo sapiens spleen focus forming virus (SFFV) proviral integration	SPI1	0.05	1.66
1090	ADXEC.24943.C2_s_at	Homo sapiens genomic DNA chromosome 6p21.3 HLA Class I region.	C6orf26	0.051	1.66
1091	ADXECAD.9950_at	Homo sapiens serrate RNA effector molecule homolog (Arabidopsis)	SRRT	0.0071	1.65
1092	ADXEC.12026.C2_at	Homo sapiens chromosome 20 open reading frame 7 (C20orf7)	C20orf7	0.0084	1.65

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1093	ADXEC.21785.C1_s_at	Ubiquitin associated protein 1	UBAP1	0.0098	1.65
1094	ADXEC.11364.C1_s_at	TAF7 RNA polymerase II TATA box binding protein (TBP)-associated factor 55kDa	TAF7	0.011	1.65
1095	ADXEC.3703.C2-a_s_at	Homo sapiens protein-O-mannosyltransferase 1 (POMT1) transcript	POMT1	0.016	1.65
1096	ADXEC.30276.C1_s_at	Homo sapiens myocyte enhancer factor 2C (MEF2C) transcript variant	MEF2C	0.0163	1.65
1097	ADXEC.6.C13_at	Homo sapiens leucine rich repeat containing 37B (LRRC37B) mRNA.	LRRC37B	0.0202	1.65
1098	ADXEC.760.C2_at	Homo sapiens centrosomal protein 250kDa (CEP250) mRNA.	CEP250	0.0231	1.65
1099	ADXEC.26888.C1_at	Zinc finger CCHC domain containing 2	ZCCHC2	0.0266	1.65
1100	ADXECAD.6357_at	Tetratricopeptide repeat domain 5	TTC5	0.0271	1.65
1101	ADXEC.14221.C1-a_s_at	Homo sapiens speckle-type POZ protein-like (SPOPL) mRNA.	SPOPL	0.0283	1.65
1102	ADXECEMUTR.2627_at	Homo sapiens smad-interacting protein-1 gene partial cds.	ZEB2	0.0302	1.65
1103	ADXECADA.20454_at	Homo sapiens regulatory factor X 3 (influences HLA class II	RFX3	0.0369	1.65
1104	ADXEC.2675.C1_at	Homo sapiens metal response element binding transcription factor 2	MTF2	0.0421	1.65
1105	ADXEC.30118.C1_s_at	Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming	CBLL1	0.0445	1.65
1106	ADXEC.17504.C1_at	Homo sapiens genomic DNA chromosome 8p11.2 senescence gene regionsection 2/19.		0.0486	1.65
1107	ADXEC.9171.C1_at	Ubiquitin specific peptidase 34	USP34	0.0504	1.65
1108	ADXEC.1477.C1_s_at	Homo sapiens butyrophilin subfamily 3 member A2 (BTN3A2) mRNA.	BTN3A2	0.0026	1.64
1109	ADXPCEC.2046.C2_s_at	Homo sapiens nucleobindin 1 (NUCB1) mRNA.	NUCB1	0.0121	1.64
1110	ADXEC.10195.C1_at	Homo sapiens coiled-coil domain containing 106 (CCDC106) mRNA.	CCDC106	0.013	1.64
1111	ADXEC.9890.C2_s_at	Homo sapiens endoglin (ENG) transcript variant 1 mRNA.	ENG	0.0142	1.64
1112	ADXECADA.8020_at	Coiled-coil domain containing 88C	CCDC88C	0.016	1.64
1113	ADXEC.26956.C1_at	Homo sapiens genomic DNA chromosome 6p21.3 HLA Class I region.	C6orf26	0.0172	1.64
1114	ADXEC.15811.C1_at	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6) mRNA.	KPNA6	0.0173	1.64
1115	ADXECAD.18070_at	Homo sapiens isolate 541CLS41 haplotype HLA-B5001/HLA-Cw0602 genomicsequence.		0.0196	1.64

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1116	ADXPEC.6710.C1_s_at	Homo sapiens quaking homolog KH domain RNA binding (mouse) (QKI)	QKI	0.0203	1.64
1117	ADXECRS.19560_s_at	Homo sapiens basic leucine zipper and W2 domains 1 (BZW1) mRNA.	BZW1	0.0221	1.64
1118	ADXEC.6014.C1_at	Cullin-associated and neddylation-dissociated 1	CAND1	0.0317	1.64
1119	ADXEC.14865.C2_s_at	Homo sapiens synovial sarcoma translocation chromosome 18 (SS18)	SS18	0.0327	1.64
1120	ADXOCEC.6210.C1_at	Transcribed locus		0.036	1.64
1121	ADXECADA.18789_at	Homo sapiens centromere protein K (CENPK) mRNA.	CENPK	0.0365	1.64
1122	ADXEC.29585.C1_at	Chromosome 11 open reading frame 58	C11orf58	0.0424	1.64
1123	ADXEC.22516.C2-a_s_at	Homo sapiens family with sequence similarity 84 member A (FAM84A)	FAM84A	0.0452	1.64
1124	ADXOCEC.4106.C1_s_at	Homo sapiens calcium/calmodulin-dependent protein kinase type 1D (CAMK1D) gene co	CAMK1D	0.0524	1.64
1125	ADXEC.13413.C1_s_at	Homo sapiens DCP2 decapping enzyme homolog (S. cerevisiae) (DCP2)	DCP2	0.005	1.63
1126	ADXEC.24853.C1_s_at	Transcribed locus		0.0064	1.63
1127	ADXEC.23048.C1_s_at	Homo sapiens arachidonate 12-lipoxygenase (ALOX12) gene complete cds.	ALOX12	0.014	1.63
1128	ADXEC.11414.C1_s_at	Homo sapiens mRNA for KIAA1229 protein partial cds.	ODF2L	0.0173	1.63
1129	ADXEC.703.C2_s_at	Homo sapiens RAD23 homolog A (S. cerevisiae) (RAD23A) mRNA.	RAD23A	0.0179	1.63
1130	ADXECAD.8079_at	Human DNA sequence from clone RP11-122G18 on chromosome 1 Contains the 3end of a	TRNAE23	0.025	1.63
1131	ADXECADA.19420_s_at	Homo sapiens SDA1 domain containing 1 (SDAD1) mRNA.	SDAD1	0.0337	1.63
1132	ADXEC.20554.C1-a_s_at	Homo sapiens WAS/WASL interacting protein family member 1 (WIPF1)	WIPF1	0.0339	1.63
1133	ADXEC.8345.C2_s_at	Homo sapiens G-rich RNA sequence binding factor 1 (GRSF1)	GRSF1	0.035	1.63
1134	ADXEC.25133.C1_at	Vacuolar protein sorting 13 homolog A (S. cerevisiae)	VPS13A	0.0356	1.63
1135	ADXEC.9967.C1_s_at	Transcribed locus weakly similar to NP_078982.2 zinc finger protein 668 [Homo sa	FOXO6	0.0368	1.63
1136	ADXEC.8269.C1_s_at	Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin	PTGS1	0.0372	1.63
1137	ADXEC.29813.C1_at	Homo sapiens GRAM domain containing 4 (GRAMD4) mRNA.	GRAMD4	0.0384	1.63

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1138	ADXECADA.13106_at	ArfGAP with RhoGAP domain ankyrin repeat and PH domain 1	ARAP1	0.0421	1.63
1139	ADXPCEC.16122.C1_at	Human DNA sequence from clone RP11-533K9 on chromosome 9 Contains the 3end of a	HIATL1	0.0496	1.63
1140	ADXEC.11516.C3_at	Human DNA sequence from clone RP11-395L14 on chromosome 2 Contains the 3end of t	MIR1302-3	0.0082	1.62
1141	ADXEC.760.C2_s_at	Homo sapiens centrosomal protein 250kDa (CEP250) mRNA.	CEP250	0.0127	1.62
1142	ADXEC.4547.C1_at	Homo sapiens ornithine decarboxylase antizyme 2 (OAZ2) mRNA.	OAZ2	0.0167	1.62
1143	ADXECADA.22793_s_at	Homo sapiens ferritin light polypeptide (FTL) mRNA.	FTL	0.0199	1.62
1144	ADXEC.1998.C1_at	Homo sapiens galactokinase 1 (GALK1) mRNA.	GALK1	0.0224	1.62
1145	ADXECRS.37364_s_at	PREDICTED: Homo sapiens hypothetical LOC653631 (LOC653631) mRNA.	LOC653631	0.0243	1.62
1146	ADXEC.27983.C1_s_at	Transcribed locus		0.0273	1.62
1147	ADXECAD.22627_s_at	Homo sapiens hexose-6-phosphate dehydrogenase (glucose	H6PD	0.0292	1.62
1148	ADXECADA.4502_s_at	Homo sapiens secernin 3 (SCRN3) mRNA.	SCRN3	0.0327	1.62
1149	ADXEC.4272.C1_at	5-azacytidine induced 2	AZ12	0.0327	1.62
1150	ADXECNTD1.2697_at	H.sapiens mRNA for an acute myeloid leukaemia protein (346bp)	RUNX1	0.0349	1.62
1151	ADXECAD.6384_at	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene partial cdsneural	SMN1	0.0372	1.62
1152	ADXEC.8507.C1-a_s_at	Homo sapiens serine incorporator 3 (SERINC3) transcript variant 1	SERINC3	0.0402	1.62
1153	ADXECADA.1199_at	Homo sapiens full length insert cDNA YH97G12.		0.0403	1.62
1154	ADXGood8_at			0.0459	1.62
1155	ADXEC.30118.C1_at	Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming	CBLL1	0.047	1.62
1156	ADXOCEC.1467.C1_x_at	Homo sapiens thyroid hormone receptor interactor 10 (TRIP10) mRNA.	TRIP10	0.0504	1.62
1157	ADXEC.1324.C1_s_at	Homo sapiens ubiquitin associated protein 2-like (UBAP2L)	UBAP2L	0.0527	1.62
1158	ADXECAD.14311_at	Ubiquitin-fold modifier 1	UFM1	0.0084	1.61
1159	ADXECAD.10084_at	Transcribed locus		0.0112	1.61

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1160	ADXEC.14571.C1_s_at	Homo sapiens PVR gene intron 6.		0.0184	1.61
1161	ADXEC.16204.C1_at	AE binding protein 2	AEBP2	0.0254	1.61
1162	ADXGood80_at			0.0277	1.61
1163	ADXLCEC.3004.C1_at	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuramin	CMAH	0.0332	1.61
1164	ADXPCEC.11965.C1_x_at	Transmembrane protein 165	TMEM165	0.0363	1.61
1165	ADXEC.2512.C1_at	Homo sapiens lysophosphatidylglycerol acyltransferase 1 (LPGAT1)	LPGAT1	0.0466	1.61
1166	ADXEC.8549.C1_at	Homo sapiens NudC domain containing 3 (NUDCD3) mRNA.	NUDCD3	0.0473	1.61
1167	ADXECAD.20490_s_at	Homo sapiens inhibitor of DNA binding 2 dominant negative	ID2	0.0494	1.61
1168	ADXEC.7681.C1_s_at	Homo sapiens structural maintenance of chromosomes 2 (SMC2)	SMC2	0.0051	1.6
1169	ADXEC.1.C3_s_at	Homo sapiens DNA (cytosine-5-)methyltransferase 1 (DNMT1)	DNMT1	0.0061	1.6
1170	ADXEC.23135.C1-a_s_at	Homo sapiens pyruvate dehydrogenase phosphatase regulatory subunit	PDPR	0.0084	1.6
1171	ADXEC.8712.C1_at	Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4) transcript	CXCR4	0.0179	1.6
1172	ADXEC.23157.C1_s_at	guanine nucleotide binding protein (G protein) alpha inhibiting activity polypep	GNAI3	0.0316	1.6
1173	ADXEC.182.C1-a_s_at	Homo sapiens sirtuin (silent mating type information regulation 2	SIRT5	0.0334	1.6
1174	ADXEC.999.C18_s_at	Homo sapiens golgi to ER traffic protein 4 homolog (S. cerevisiae)	GET4	0.0348	1.6
1175	ADXECAD.9496_at	Homo sapiens cyclin-dependent kinase 6 (CDK6) transcript variant	CDK6	0.0363	1.6
1176	ADXEC.10003.C2_s_at	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	YWHAZ	0.0376	1.6
1177	ADXEC.32392.C1-a_s_at	Transcribed locus		0.0381	1.6
1178	ADXEC.5134.C1_s_at	Homo sapiens N(alpha)-acetyltransferase 38 NatC auxiliary subunit	NAA38	0.0432	1.6
1179	ADXEC.4544.C1_at	Homo sapiens regulator of G-protein signaling 19 (RGS19)	RGS19	0.0436	1.6
1180	ADXECNTDJ.82_s_at	Homo sapiens FYN binding protein (FYB) transcript variant 2 mRNA.	FYB	0.0517	1.6
1181	ADXEC.881.C2_s_at	Homo sapiens proteolipid protein 2 (colonic epithelium-enriched)	PLP2	0.0122	1.59
1182	ADXEC.7567.C1_s_at	Homo sapiens coiled-coil domain containing 23 (CCDC23) mRNA.	CCDC23	0.0127	1.59
1183	ADXEC.9265.C1_at	Homo sapiens eukaryotic translation initiation factor 4A2 (EIF4A2)	EIF4A2	0.0133	1.59

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1184	ADXEC.6317.C1_at	Homo sapiens thioredoxin-related transmembrane protein 4 (TMX4)	TMX4	0.0203	1.59
1185	ADXEC.13567.C1_s_at	Homo sapiens choline kinase beta (CHKB) mRNA.	CHKB	0.0246	1.59
1186	ADXECRS.1245_s_at	Homo sapiens zinc finger protein 805 (ZNF805) transcript variant	ZNF805	0.0265	1.59
1187	ADXECAD.28179_s_at	Homo sapiens TGF-beta activated kinase 1/MAP3K7 binding protein 2	TAB2	0.0287	1.59
1188	ADXEC.5808.C1_s_at	Homo sapiens p21 protein (Cdc42/Rac)-activated kinase 2 (PAK2)	PAK2	0.0331	1.59
1189	ADXEC.1890.C1_at	Transcribed locus		0.0467	1.59
1190	ADXEC.30931.C1_x_at	Human chromosome 14 DNA sequence BAC R-639F2 of library RPCI-11 from chromosome 1		0.0511	1.59
1191	ADXECRS.10622_s_at	PREDICTED: Homo sapiens hypothetical LOC100128994 (LOC100128994)	LOC100128994	0.0511	1.59
1192	ADXECAD.14508_at	Chromosome 2 open reading frame 49	C2orf49	0.0539	1.59
1193	3362762_at			0.0024	1.58
1194	ADXEC.4957.C1_s_at	Homo sapiens GM2 ganglioside activator (GM2A) transcript variant	GM2A	0.0149	1.58
1195	ADXECADA.1623_s_at	SMG1 homolog phosphatidylinositol 3-kinase-related kinase pseudogene	LOC100271836	0.0226	1.58
1196	ADXEC.33122.C1-a_s_at	Zinc finger CCHC domain containing 6	ZCCHC6	0.0255	1.58
1197	ADXEC.1517.C2_s_at	Homo sapiens solute carrier family 25 (mitochondrial carrier;	SLC25A11	0.0308	1.58
1198	ADXECAD.19905_at	Homo sapiens chromosome 8 clone XX-36G5 map 8p23 complete sequence.		0.0335	1.58
1199	ADXEC.2481.C1_at	Homo sapiens RNA binding motif protein 28 (RBM28) transcript	RBM28	0.0518	1.58
1200	ADXECEMUTR.5434_s_at	Homo sapiens galactose-1-phosphate uridyl transferase (GALT) gene completecds.	GALT	0.0041	1.57
1201	ADXECRS.6935_x_at	PREDICTED: Homo sapiens hypothetical LOC730235 (LOC730235)	LOC730235	0.0063	1.57
1202	ADXECNTDJ.789_s_at	Homo sapiens sulfatase modifying factor 2 (SUMF2) transcript	SUMF2	0.0263	1.57
1203	ADXECADA.7794_x_at	Transcribed locus		0.0289	1.57
1204	ADXEC.14840.C1_at	Homo sapiens phospholipase C beta 2 (PLCB2) mRNA.	PLCB2	0.0347	1.57
1205	ADXEC.9701.C1_at	Transcribed locus		0.0393	1.57
1206	ADXEC.19638.C1_at	Homo sapiens osteopetrosis associated transmembrane protein 1	OSTM1	0.0462	1.57

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1207	ADXECAD.16985_s_at	Homo sapiens proliferation-associated 2G4 38kDa (PA2G4) mRNA.	PA2G4	0.048	1.57
1208	ADXECAD.6191_x_at	Homo sapiens NFKB inhibitor interacting Ras-like 1 (NKIRAS1) gene completecds.	NKIRAS1	0.0488	1.57
1209	ADXECEMUTR.1246_at	SeI-1 suppressor of lin-12-like (C. elegans)	SEL1L	0.0492	1.57
1210	ADXEC.7696.C1-a_s_at	Homo sapiens syntaxin 12 (STX12) mRNA.	STX12	0.0506	1.57
1211	ADXEC.15989.C1_x_at	Homo sapiens mRNA for KIAA1652 protein partial cds.	KIAA1652	0.0542	1.57
1212	ADXEC.1690.C5_s_at	Homo sapiens guanine nucleotide binding protein (G protein) beta	GNB1	0.0021	1.56
1213	ADXEC.23256.C1_at	Homo sapiens syntaxin 8 (STX8) transcript variant 1 mRNA.	STX8	0.0039	1.56
1214	ADXEC.25945.C1_at	Homo sapiens hypothetical LOC283267 (LOC283267) non-coding RNA.	LOC283267	0.0056	1.56
1215	ADXEC.633.C1_x_at	Homo sapiens WD repeat domain 1 (WDR1) transcript variant 1 mRNA.	WDR1	0.0084	1.56
1216	ADXEC.5841.C2_x_at	Similar to Serine/threonine-protein kinase PRKX (Protein kinase PKX1)	LOC389906	0.0157	1.56
1217	ADXECAD.3273_x_at	5247201 mRNA		0.0186	1.56
1218	ADXECEMUTR.898_at	Homo sapiens anterior pharynx defective 1 homolog B (C. elegans)	APH1B	0.0195	1.56
1219	ADXECADA.18476_x_at	Homo sapiens chromosome 3 clone RP11-949J7 complete sequence.	LOC100289156	0.0196	1.56
1220	ADXEC.8002.C1_x_at	Homo sapiens scavenger receptor class F member 1 (SCARF1)	SCARF1	0.023	1.56
1221	ADXEC.20154.C2_x_at	Transcribed locus		0.0264	1.56
1222	ADXEC.10033.C1-a_s_at	Homo sapiens ankyrin repeat domain 36 (ANKRD36) mRNA.	ANKRD36	0.0264	1.56
1223	ADXECS.4234_s_at	Homo sapiens CAP adenylate cyclase-associated protein 1 (yeast)	CAP1	0.0265	1.56
1224	ADXECAD.18258_at	Human DNA sequence from clone RP11-61K9 on chromosome 13 Contains the ZNF237 gene	LOC400099	0.0366	1.56
1225	ADXEC.2435.C10_s_at	Homo sapiens FK506 binding protein 1A 12kDa (FKBP1A) transcript	FKBP1A	0.0377	1.56
1226	ADXECADA.22533_at	Homo sapiens trafficking protein particle complex 9 (TRAPPC9)	TRAPPC9	0.0386	1.56
1227	ADXEC.13730.C1_at	5-nucleotidase cytosolic II	NT5C2	0.0415	1.56
1228	ADXECAD.9888_x_at	Homo sapiens Rho-associated coiled-coil containing protein kinase	ROCK1	0.042	1.56
1229	ADXEC.13354.C1-a_s_at	Homo sapiens SDA1 domain containing 1 (SDAD1) mRNA.	SDAD1	0.0442	1.56

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1230	ADXEC.1821_s_at	Homo sapiens poliovirus receptor-related 3 mRNA (cDNA clone IMAGE:4066485) complete	PVRL3	0.0492	1.56
1231	ADXEC.5445.C1_x_at	Homo sapiens embigin homolog (mouse) (EMB) mRNA.	EMB	0.0125	1.55
1232	ADXEC.2886.C2-a_s_at	Homo sapiens golgi phosphoprotein 3 (coat-protein) (GOLPH3) mRNA.	GOLPH3	0.0146	1.55
1233	ADXEC.32536.C1_at	Homo sapiens ATP-binding cassette sub-family C (CFTR/MRP) member 1 (ABCC1) gene c	ABCC1	0.0235	1.55
1234	ADXEC.6047_s_at	Homo sapiens zinc finger MYND-type containing 8 (ZMYND8)	ZMYND8	0.0263	1.55
1235	ADXEC.926.C1_s_at	Homo sapiens transmembrane protein 106C (TMEM106C) transcript	TMEM106C	0.0303	1.55
1236	ADXEC.20738.C1_at	Homo sapiens docking protein 1 62kDa (downstream of tyrosine	DOK1	0.0307	1.55
1237	ADXEC.13729.C1_s_at	Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38)	DHX38	0.0393	1.55
1238	ADXEC.24548.C1_at	Homo sapiens vesicle transport through interaction with t-SNAREs	VT1A	0.0469	1.55
1239	ADXEC.5134_s_at	Homo sapiens phosphoinositide-3-kinase class 2 alpha polypeptide	PIK3C2A	0.051	1.55
1240	ADXEC.5984.C1_at	Homo sapiens ADP-ribosylation factor 4 (ARF4) mRNA.	ARF4	0.0536	1.55
1241	ADXEC.9802_s_at	Homo sapiens ArfGAP with FG repeats 1 (AGFG1) transcript variant	AGFG1	0.0006	1.54
1242	ADXEC.6408.C1_s_at	Homo sapiens protein inhibitor of activated STAT 1 (PIAS1) mRNA.	PIAS1	0.0082	1.54
1243	ADXEC.8397_at	CDNA FLJ11364 fis clone HEMBA1000264		0.0083	1.54
1244	ADXEC.23957_s_at	Homo sapiens BTB and CNC homology 1 basic leucine zipper	BACH1	0.0088	1.54
1245	ADXEC.16562.C1_s_at	Homo sapiens cyclin J (CCNJ) transcript variant 3 mRNA.	CCNJ	0.0251	1.54
1246	ADXEC.13350.C1_at	Homo sapiens chromosome 18 open reading frame 25 (C18orf25)	C18orf25	0.029	1.54
1247	ADXEC.37780_s_at	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP) transcript	LNPEP	0.0308	1.54
1248	ADXEC.8020.C5_x_at	Homo sapiens zinc finger protein 43 (ZNF43) mRNA.	ZNF43	0.0328	1.54
1249	ADXEC.23765_s_at	Homo sapiens cyclin-dependent kinase inhibitor 2D (p19 inhibits	CDKN2D	0.0363	1.54
1250	ADXEC.2959.C3_s_at	Homo sapiens coatomer protein complex subunit gamma (COPG) mRNA.	COPG	0.0507	1.54
1251	ADXEC.6599.C1_s_at	Homo sapiens family with sequence similarity 50 member A (FAM50A)	FAM50A	0.052	1.54
1252	ADXEC.319.C10_at	Homo sapiens cDNA FLJ50834 complete cds highly similar to Homo	SHISA5	0.0525	1.54

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
		sapiensscotin [SC			
1253	ADXECAD.9888_at	Homo sapiens Rho-associated coiled-coil containing protein kinase	ROCK1	0.0043	1.53
1254	ADXEC.7350.C1_s_at	Homo sapiens sorting nexin 6 (SNX6) transcript variant 2 mRNA.	SNX6	0.0077	1.53
1255	ADXECNTDJ.3602_at	Homo sapiens discoidin CUB and LCCL domain containing 2 (DCBLD2)	DCBLD2	0.0134	1.53
1256	ADXEC.20199.C1_at	Homo sapiens WD repeat domain 12 (WDR12) mRNA.	WDR12	0.0172	1.53
1257	ADXEC.2032.C1_at	Homo sapiens discs large (Drosophila) homolog-associated protein 4	DLGAP4	0.0198	1.53
1258	ADXECAD.9650_at	Homo sapiens methionine adenosyltransferase II alpha (MAT2A)	MAT2A	0.0263	1.53
1259	ADXECADA.13461_at	Peptidylprolyl isomerase E (cyclophilin E)	PPIE	0.0285	1.53
1260	ADXEC.169.C9_at	Homo sapiens (N6-adenosine)-methyltransferase gene complete cds.	METTL3	0.0303	1.53
1261	ADXEC.16616.C1_x_at	Homo sapiens chromosome 1 open reading frame 109 (C1orf109) mRNA.	C1orf109	0.0307	1.53
1262	ADXEC.5437.C2_x_at	Nuclear receptor subfamily 1 group H member 3	NR1H3	0.0377	1.53
1263	ADXEC.2744.C2_s_at	Homo sapiens cortactin (CTTN) transcript variant 1 mRNA.	CTTN	0.0451	1.53
1264	ADXECAD.23132_s_at	Homo sapiens leukocyte-associated immunoglobulin-like receptor 1	LAIR1	0.0493	1.53
1265	ADXEC.6728.C2_x_at	Homo sapiens protein tyrosine phosphatase type IVA member 1	PTP4A1	0.0496	1.53
1266	ADXEC.33375.C1_at	Human DNA sequence from clone RP1-65J11 on chromosome 1 Contains the 5' end of the	LOC100288670	0.0516	1.53
1267	ADXECEMUTR.5334_at	UBX domain protein 11	UBXN11	0.0059	1.52
1268	ADXEC.971.C3-a_s_at	Homo sapiens eukaryotic translation initiation factor 2-alpha	EIF2AK1	0.0078	1.52
1269	ADXEC.23286.C1_at	G patch domain containing 2	GPATCH2	0.0152	1.52
1270	ADXECADA.1744_s_at	Homo sapiens v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (KRAS) gene complete cds.	KRAS	0.0169	1.52
1271	ADXEC.1114.C2-a_s_at	Homo sapiens capping protein (actin filament) muscle Z-line alpha	CAPZA1	0.0212	1.52
1272	ADXECNTDJ.6218_at	Homo sapiens poly (ADP-ribose) polymerase family member 8 (PARP8)	PARP8	0.0236	1.52
1273	ADXEC.29514.C1_at	Homo sapiens mitogen-activated protein kinase 1 (MAPK1) gene complete cds.		0.0301	1.52
1274	ADXECADA.961_s_at	Hypothetical gene supported by AK057627	FLJ33065	0.0304	1.52

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1275	ADXEC.20369.C1_at	Homo sapiens zinc finger protein 296 (ZNF296) mRNA.	ZNF296	0.031	1.52
1276	ADXEC.2206.C2_at	NADH dehydrogenase (ubiquinone) 1 subcomplex unknown 1 6kDa	NDUFC1	0.032	1.52
1277	ADXECADA.16206_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibit	ARFGEF1	0.0338	1.52
1278	ADXEC.719.C1_s_at	Homo sapiens lamin B2 (LMNB2) mRNA.	LMNB2	0.0343	1.52
1279	ADXEC.11795.C1_at	Homo sapiens TMC3 protein (TMC3) mRNA complete cds.	TMC3	0.0349	1.52
1280	ADXECAD.5359_at	Transcribed locus		0.0359	1.52
1281	ADXEC.6260.C2_at	Transmembrane protein 219	TMEM219	0.036	1.52
1282	ADXECAD.1571_s_at	Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1	ASAH1	0.037	1.52
1283	ADXEC.8002.C1_at	Homo sapiens scavenger receptor class F member 1 (SCARF1)	SCARF1	0.0406	1.52
1284	ADXECNTDJ.5877_at	Homo sapiens ubiquitin specific peptidase 8 (USP8) transcript	USP8	0.0434	1.52
1285	ADXEC.8260.C2_s_at	Homo sapiens casein kinase 1 delta (CSNK1D) transcript variant 2	CSNK1D	0.0474	1.52
1286	ADXEC.34486.C1_at	Transcribed locus		0.0507	1.52
1287	ADXECADA.24708_s_at	Homo sapiens tankyrase TRF1-interacting ankyrin-related ADP-ribose	TNKS2	0.0512	1.52
1288	ADXEC.2401.C5-a_s_at	Homo sapiens cell division cycle 37 homolog (S. cerevisiae)	CDC37	0.0529	1.52
1289	ADXEC.11953.C2_s_at	Homo sapiens apoptotic peptidase activating factor 1 (APAF1)	APAF1	0.0069	1.51
1290	ADXEC.34450.C1_at	Homo sapiens threonine synthase-like 1 (S. cerevisiae) (THNSL1)	THNSL1	0.0089	1.51
1291	ADXEC.633.C1_at	Homo sapiens WD repeat domain 1 (WDR1) transcript variant 1 mRNA.	WDR1	0.0119	1.51
1292	ADXOCEC.2903.C1_s_at	Homo sapiens ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog	UBE2D2	0.0138	1.51
1293	ADXEC.18224.C1-a_s_at	Homo sapiens caspase recruitment domain family member 8 (CARD8)	CARD8	0.0153	1.51
1294	ADXEC.7671.C1_at	Homo sapiens chromosome 12 open reading frame 32 (C12orf32)	C12orf32	0.0166	1.51
1295	ADXEC.30837.C2_s_at	Claudin 15	CLDN15	0.018	1.51
1296	ADXEC.2291.C1_x_at	Homo sapiens NDUFB2 gene for 24-kDa subunit of complex I partial cds.	NDUFV2	0.0189	1.51
1297	ADXPCEC.15490.C1_s_at	Homo sapiens SMAD family member 2 (SMAD2) transcript variant 1	SMAD2	0.0206	1.51
1298	ADXECADA.633_at	citb_338_f_24 complete sequence.		0.0209	1.51

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1299	ADXECAD.6713_s_at	Homo sapiens chromosome 19 cosmid R26420 complete sequence.	LOC729645	0.0273	1.51
1300	ADXECAD.26276_at	Homo sapiens guanine nucleotide binding protein (G protein) alpha	GNA13	0.0273	1.51
1301	ADXEC.1260.C8_s_at	Proteasome (prosome macropain) subunit beta type 4	PSMB4	0.0297	1.51
1302	ADXEC.34320.C1_at	Transcribed locus		0.0378	1.51
1303	ADXEC.1164.C1_at	Homo sapiens ring finger protein 44 (RNF44) mRNA.	RNF44	0.0399	1.51
1304	ADXEC.5437.C2_at	Nuclear receptor subfamily 1 group H member 3	NR1H3	0.0434	1.51
1305	ADXEC.5483.C1_at	Homo sapiens NF-E2-related factor 3 gene complete cds.	NFE2L3	0.0448	1.51
1306	ADXEC.26415.C1-a_s_at	Transcribed locus		0.0471	1.51
1307	ADXEC.27866.C2_x_at	Homo sapiens cDNA FLJ14272 fis clone PLACE1004793.		0.0506	1.51
1308	ADXECAD.8551_at	CDNA FLJ13333 fis clone OVARC1001828		0.0517	1.51
1309	ADXPCEC.17181.C1_at	Transcribed locus		0.0532	1.51
1310	ADXECADA.253_s_at	Homo sapiens KIAA1524 (KIAA1524) mRNA.	KIAA1524	0.0123	1.5
1311	ADXECADA.15426_at	FLJ23200 fis clone KAIA38871		0.0241	1.5
1312	ADXPCEC.205.C2_x_at	Homo sapiens myosin heavy chain 11 smooth muscle isoform 2 (MYH11) gene complete		0.032	1.5
1313	ADXECADA.12824_at	Homo sapiens BAC clone CH17-260O16 from chromosome 17 complete sequence.		0.0364	1.5
1314	ADXEC.2311.C2-a_s_at	Homo sapiens microtubule-associated protein 1 light chain 3 beta	MAP1LC3B	0.0452	1.5
1315	ADXEC.3966.C2_x_at	Homo sapiens glucosidase alpha	GAA	0.0482	1.5
1316	ADXECNTDJ.4604_at	Homo sapiens butyrophilin subfamily 3 member A3 (BTN3A3)	BTN3A3	0.0485	1.5
1317	ADXECEMUTR.4869_x_at	Cytochrome b5 reductase 1	CYB5R1	0.0494	1.5
1318	ADXEC.8646.C1-a_s_at	Homo sapiens survival motor neuron domain containing 1 (SMNDC1)	SMNDC1	0.0525	1.5
1319	ADXECADA.4192_at	Zinc finger protein 746	ZNF746	0.0014	1.49
1320	ADXECAD.19976_at	Transcribed locus		0.0017	1.49
1321	ADXEC.16636.C2_at	Human chromosome 12p13 sequence complete sequence.	GPR162	0.0037	1.49

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1322	ADXECAD.12250_at	Transcribed locus		0.01	1.49
1323	ADXEC.5508.C1_at	Ankyrin repeat and sterile alpha motif domain containing 6	ANKS6	0.013	1.49
1324	ADXEC.8810.C1_s_at	Homo sapiens tRNA splicing endonuclease 34 homolog (S. cerevisiae)	TSEN34	0.0165	1.49
1325	ADXEC.9282.C1_at	Transcribed locus		0.0169	1.49
1326	ADXECRS.30524_s_at	Homo sapiens family with sequence similarity 115 member A	FAM115A	0.0178	1.49
1327	ADXEC.29299.C1_s_at	Transcribed locus		0.0252	1.49
1328	ADXECADA.18698_s_at	Homo sapiens WD repeat domain 1 (WDR1) transcript variant 1 mRNA.	WDR1	0.0263	1.49
1329	ADXECRS.34598_x_at	Homo sapiens pyruvate dehydrogenase kinase isozyme 3 (PDK3)	PDK3	0.0289	1.49
1330	ADXEC.34889.C1_s_at	Homo sapiens N(alpha)-acetyltransferase 15 NatA auxiliary subunit	NAA15	0.0295	1.49
1331	ADXEC.8228.C2_s_at	Homo sapiens endo-beta-N-acetylglucosaminidase (ENGASE) mRNA.	ENGASE	0.0307	1.49
1332	ADXLCEC.7884.C1_s_at	Homo sapiens protein tyrosine phosphatase receptor type E	PTPRE	0.0315	1.49
1333	ADXECNTDJ.1716_s_at	citb_54_o_2 complete sequence.		0.0344	1.49
1334	ADXEC.607.C1_x_at	Homo sapiens TOX high mobility group box family member 4 (TOX4)	TOX4	0.0412	1.49
1335	ADXEC.20035.C2_x_at	Homo sapiens schlafen family member 13 (SLFN13) mRNA.	SLFN13	0.0419	1.49
1336	ADXEC.23968.C1_s_at	Homo sapiens Ral GEF with PH domain and SH3 binding motif 1	RALGPS1	0.0434	1.49
1337	ADXECRS.2688_s_at	PREDICTED: Homo sapiens hypothetical LOC100127930 (LOC100127930)	LOC100127930	0.0444	1.49
1338	ADXEC.8649.C2-a_s_at	Homo sapiens erythrocyte membrane protein band 4.1-like 3	EPB41L3	0.0448	1.49
1339	ADXECEMUTR.410_at	Homo sapiens WD repeat domain 26 (WDR26) transcript variant 1	WDR26	0.0473	1.49
1340	ADXEC.30362.C1_at	Human chromosome 14 DNA sequence BAC R-300J18 of library RPCI-11 from chromosome	GPR65	0.0488	1.49
1341	ADXEC.7090.C1_at	Transcribed locus		0.0011	1.48
1342	200041_s_at	Homo sapiens HLA-B associated transcript 1 (BAT1) transcript	BAT1	0.0161	1.48
1343	ADXEC.6478.C1-a_s_at	Homo sapiens mediator complex subunit 16 (MED16) mRNA.	MED16	0.021	1.48
1344	ADXEC.2838.C1_at	splicing factor arginine/serine-rich 8 (suppressor-of-white-apricot homolog Dros	SFRS8	0.0223	1.48
1345	ADXECAD.1_at	Scavenger receptor class B member 1	SCARB1	0.0261	1.48

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1346	ADXEC.25678.C1_at	Genomic sequence from Human 6 complete sequence.	ATXN1	0.0305	1.48
1347	ADXOCEC.14969.C2_x_at	Trans-golgi network protein 2	TGOLN2	0.0335	1.48
1348	ADXEC.10617.C4_at	Homo sapiens radial spoke head 9 homolog (Chlamydomonas) (RSPH9)	RSPH9	0.0382	1.48
1349	ADXEC.7491.C1_x_at	DnaI (Hsp40) homolog subfamily C member 9	DNAJC9	0.0503	1.48
1350	ADXECRS.26272_at	Homo sapiens potassium voltage-gated channel KQT-like subfamily	KCNQ5	0.0504	1.48
1351	ADXEC.24757.C1_at	Transcribed locus		0.0505	1.48
1352	ADXECRS.10528_s_at	Homo sapiens mitochondrial ribosomal protein S7 (MRPS7) nuclear	MRPS7	0.0509	1.48
1353	ADXECADA.11791_at	hypothetical protein partial [Macaca mulatta]		0.0514	1.48
1354	ADXECAD.15819_at	Homo sapiens v-rel reticuloendotheliosis viral oncogene homolog	REL	0.0527	1.48
1355	ADXEC.16074.C1_s_at	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransf	AGPAT5	0.0531	1.48
1356	ADXECAD.26628_x_at	Homo sapiens major histocompatibility complex class I B (HLA-B)	HLA-B	0.0543	1.48
1357	ADXEC.170.C3_s_at	Homo sapiens CTAGE family member 5 (CTAGE5) transcript variant 2	CTAGE5	0.0178	1.47
1358	ADXEC.18820.C1_at	Transcribed locus		0.0203	1.47
1359	ADXECADA.21050_at	Homo sapiens solute carrier family 4 sodium bicarbonate	SLC4A7	0.0227	1.47
1360	ADXEC.7122.C1_at	AFG3 ATPase family gene 3-like 2 (yeast)	AFG3L2	0.0235	1.47
1361	ADXECADA.17436_s_at	Homo sapiens forkhead box K2 (FOXK2) mRNA.	FOXK2	0.0252	1.47
1362	ADXEC.65.C1_at	Homo sapiens palmitoyl-protein thioesterase 1 (PPT1) transcript	PPT1	0.0257	1.47
1363	ADXECNTDJ.998_at	Leucine-rich repeat kinase 1	LRRK1	0.0299	1.47
1364	ADXEC.20154.C2_at	Transcribed locus		0.0304	1.47
1365	ADXECAD.19136_x_at	ERO1-like (S. cerevisiae)	ERO1L	0.0356	1.47
1366	ADXEC.8228.C1_s_at	Homo sapiens endo-beta-N-acetylglucosaminidase (ENGASE) mRNA.	ENGASE	0.0357	1.47
1367	3819572_at			0.0421	1.47
1368	ADXOCEC.15139.C1_at	Human DNA sequence from clone RP11-710A11 on chromosome 10 Contains the 3end for	ADAMTS14	0.0424	1.47
1369	ADXECEMUTR.2098_at	Transmembrane protein 135	TMEM135	0.048	1.47

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1370	ADXOCEC.1187.C1_s_at	Homo sapiens transmembrane protein 106C (TMEM106C) transcript	TMEM106C	0.0487	1.47
1371	ADXECC.15087.C1_x_at	Homo sapiens symplekin (SYMPK) mRNA.	SYMPK	0.0544	1.47
1372	ADXECCNTDJ.676_at	Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1) transcript	FIP1L1	0.0061	1.46
1373	ADXECC.7065.C1_s_at	Homo sapiens solute carrier family 4 anion exchanger member 3	SLC4A3	0.0092	1.46
1374	ADXECC.121.C1_s_at	Homo sapiens ADP-ribosylation factor-like 5A (ARL5A) transcript	ARL5A	0.0123	1.46
1375	ADXECC.1253.C1_s_at	Homo sapiens solute carrier family 37 glycerol-3-phosphate	SLC37A1	0.0147	1.46
1376	ADXECC.119.CB1_x_at	Homo sapiens major histocompatibility complex class I B (HLA-B)	HLA-B	0.0166	1.46
1377	ADXECC.119.C14_x_at	Homo sapiens major histocompatibility complex class I B (HLA-B)	HLA-B	0.0212	1.46
1378	ADXECC.1945.C5_s_at	Homo sapiens importin 7 (IPO7) mRNA.	IPO7	0.023	1.46
1379	ADXECC.32789.C1_x_at	Homo sapiens ZKD family zinc finger C (ZXDC) transcript variant 2	ZXDC	0.0268	1.46
1380	ADXECCRS.36620_at	Homo sapiens zinc finger protein 223 (ZNF223) mRNA.	ZNF223	0.0271	1.46
1381	ADXECC.8005.C1_at	GM2 ganglioside activator	GM2A	0.0315	1.46
1382	ADXECCAD.23807_s_at	Homo sapiens inhibitor of growth family member 1 (ING1)	ING1	0.0342	1.46
1383	ADXECC.2577.C1-a_s_at	Homo sapiens ATP-binding cassette sub-family E (OABP) member 1	ABCE1	0.0432	1.46
1384	ADXECCAD.3433_at	Homo sapiens tandem acid-sensitive potassium channel TASK5 (KCNK15) gene complete	KCNK15	0.0444	1.46
1385	ADXECCAD.22835_x_at	ras-related C3 botulinum toxin substrate 2 (rho family small GTP binding protein	RAC2	0.0507	1.46
1386	ADXECC.3499.C1_at	Human DNA sequence of contig comprising 3 cosimids (HDAB HDAC HDAD).		0.0538	1.46
1387	ADXECC.13284.C2_at	Rtf1 Paf1/RNA polymerase II complex component homolog (S. cerevisiae)	RTF1	0.0133	1.45
1388	ADXECC.505.C3_x_at	Homo sapiens M-phase phosphoprotein 10 (U3 small nucleolar	MPHOSPH10	0.0251	1.45
1389	ADXECCAD.9519_at	Homo sapiens polycomb group ring finger 5 (PCGF5) mRNA.	PCGF5	0.0305	1.45
1390	ADXPCEC.3315.C3_s_at	Homo sapiens hexosaminidase A (alpha polypeptide) (HEXA) mRNA.	HEXA	0.0389	1.45
1391	ADXECC.2989.C3_s_at	Homo sapiens arginine-glutamic acid dipeptide (RE) repeats (RERE)	RERE	0.0407	1.45
1392	ADXECCAD.7737_s_at	Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1)	TM6SF1	0.0415	1.45
1393	ADXECCAD.14566_at	Homo sapiens TMC3 protein (TMC3) mRNA complete cds.	TMC3	0.0463	1.45

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1394	ADXEC.4846.C3-a_s_at	Homo sapiens TATA box binding protein (TBP)-associated factor RNA	TAF1C	0.047	1.45
1395	ADXECADA.2601_x_at	Homo sapiens full length insert cDNA YR39D03.		0.0492	1.45
1396	ADXEC.25691.C2_at	Ring finger protein 144B	RNF144B	0.05	1.45
1397	ADXEC.3724.C1-a_s_at	Homo sapiens pallidin homolog (mouse) (PLDN) mRNA.	PLDN	0.0536	1.45
1398	ADXEC.34927.C1_at	Transcribed locus		0.0539	1.45
1399	ADXEC.12953.C1_at	Homo sapiens genomic DNA chromosome 21q section 97/105.	C21orf32	0.0008	1.44
1400	ADXEC.9209.C1_x_at	Homo sapiens cardiotrophin 1 (CTF1) transcript variant 1 mRNA.	CTF1	0.0038	1.44
1401	ADXEC.6963.C1_x_at	Cut-like homeobox 1	CUX1	0.0046	1.44
1402	ADXEC.24924.C1_at	Homo sapiens mRNA for leucyl/cystinyl aminopeptidase variant protein.	LNPEP	0.0095	1.44
1403	ADXEC.1253.C2_s_at	Homo sapiens solute carrier family 37 (glycerol-3-phosphate	SLC37A1	0.0128	1.44
1404	ADXEC.11961.C1_at	Homo sapiens aquarius homolog (mouse) (AQR) mRNA.	AQR	0.018	1.44
1405	ADXEC.27232.C1_s_at	Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT)	RNGTT	0.0206	1.44
1406	ADXECADA.1528_s_at	Homo sapiens cyclin J (CCNJ) transcript variant 3 mRNA.	CCNJ	0.0207	1.44
1407	ADXECAD.17583_at	Homo sapiens zinc finger protein 154 (ZNF154) mRNA.	ZNF154	0.0225	1.44
1408	ADXECAD.4765_x_at	LIM and senescent cell antigen-like domains 1	LIMS1	0.0267	1.44
1409	ADXEC.3915.C1_at	Sad1 and UNC84 domain containing 1	SUN1	0.0297	1.44
1410	ADXEC.3168.C1_at	Transcribed locus		0.0336	1.44
1411	ADXEC.20369.C1_x_at	Homo sapiens zinc finger protein 296 (ZNF296) mRNA.	ZNF296	0.0466	1.44
1412	ADXEC.9945.C9_x_at	Transcribed locus		0.049	1.44
1413	ADXEC.6.C64_x_at	Homo sapiens NOD1 protein (NOD1) gene exons 4 through 14 and complete cds.	NOD1	0.0494	1.44
1414	ADXEC.1770.C1-a_at	Homo sapiens disabled homolog 2 mitogen-responsive phosphoprotein	DAB2	0.0118	1.43
1415	ADXECADA.17719_at	5296329		0.0129	1.43
1416	ADXECRS.25333_s_at	Homo sapiens WW domain containing adaptor with coiled-coil (WAC)	WAC	0.016	1.43
1417	ADXECAD.10768_s_at	Homo sapiens phosphatidylinositol binding clathrin assembly protein	PICALM	0.0184	1.43

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1418	ADXEC.174.C1-a_s_at	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide K	POLR2K	0.0256	1.43
1419	ADXEC.15900.C1-a_s_at	Homo sapiens family with sequence similarity 60 member A (FAM60A)	FAM60A	0.0263	1.43
1420	ADXECAD.19377_x_at	hypothetical protein [Pan troglodytes]		0.0273	1.43
1421	ADXPCEC.2037.C1_at	CDNA FLJ30575 fis clone BRAWH2006526		0.0329	1.43
1422	ADXECNTDJ.7917_at	Homo sapiens chromosome 22 open reading frame 9 (C22orf9)	C22orf9	0.0347	1.43
1423	ADXEC.3333.C1_s_at	Homo sapiens erythrocyte membrane protein band 4.1 (elliptocytosis)	EPB41	0.0383	1.43
1424	ADXEC.10085.C1_at	Homo sapiens KIAA1012 (KIAA1012) mRNA.	KIAA1012	0.0383	1.43
1425	ADXEC.3934.C1_at	Homo sapiens paired related homeobox 2 (PRRX2) mRNA.	PRRX2	0.0384	1.43
1426	ADXECAD.20409_s_at	Homo sapiens influenza virus NS1A binding protein (IVNS1ABP) mRNA.	IVNS1ABP	0.0422	1.43
1427	ADXEC.5445.C1_at	Homo sapiens embigin homolog (mouse) (EMB) mRNA.	EMB	0.0428	1.43
1428	ADXECRS.14416_s_at	Homo sapiens syntaxin 10 (STX10) mRNA.	STX10	0.0442	1.43
1429	ADXEC.2814.C3-a_s_at	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 1	AGPAT1	0.0446	1.43
1430	ADXEC.6263.C1_at	Regulator of G-protein signaling 12	RGS12	0.0508	1.43
1431	ADXECRS.41404_at	Homo sapiens interleukin 26 (IL26) mRNA.	IL26	0.0514	1.43
1432	ADXEC.2591.C1_s_at	Homo sapiens serine/threonine kinase 4 (STK4) mRNA.	STK4	0.0537	1.43
1433	ADXECAD.1876_at	Homo sapiens ADP-ribosylation factor-like 8A (ARL8A) mRNA.	ARL8A	0.0049	1.42
1434	ADXECAD.20345_s_at	Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B) mRNA.	RAD23B	0.0065	1.42
1435	ADXEC.23286.C1_x_at	G patch domain containing 2	GPATCH2	0.0166	1.42
1436	ADXEC.26923.C1_at	Transcribed locus		0.0227	1.42
1437	ADXECRS.14563_s_at	Homo sapiens ceramide kinase-like (CERKL) transcript variant 6	CERKL	0.0282	1.42
1438	ADXEC.26064.C1_s_at	Transcribed locus		0.0306	1.42
1439	ADXECADA.12699_at	Transcribed locus		0.033	1.42
1440	ADXECNTDJ.4261_s_at	Homo sapiens anaphase promoting complex subunit 4 (ANAPC4) mRNA.	ANAPC4	0.0335	1.42
1441	ADXEC.3987.C4-a_x_at	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide J	POLR2J	0.0345	1.42
1442	ADXECAD.3500_at	CDNA FLJ37191 fis clone BRALZ2003453		0.0389	1.42

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1443	ADXEC.3876.C1_s_at	Homo sapiens family with sequence similarity 100 member B	FAM100B	0.0404	1.42
1444	ADXECRS.37182_x_at	cAMP responsive element binding protein 3-like 3	CREB3L3	0.0443	1.42
1445	ADXECAD.15293_at	Transcribed locus		0.0454	1.42
1446	ADXEC.20420.C1-a_s_at	Homo sapiens ADP-ribosylation-like factor 6 interacting protein 6	ARL6IP6	0.0457	1.42
1447	ADXEC.14885.C1_s_at	BMP2 inducible kinase	BMP2K	0.0484	1.42
1448	ADXGood64_at			0.0484	1.42
1449	ADXEC.4359.C1_s_at	Homo sapiens adaptor-related protein complex 3 mu 2 subunit	AP3M2	0.0504	1.42
1450	ADXEC.23669.C1_s_at	Transcribed locus		0.0517	1.42
1451	ADXECNTDJ.4653_s_at	Homo sapiens mRNA for PREBP1 protein 5UTR	MEG3	0.0522	1.42
1452	ADXECADA.20324_s_at	Homo sapiens transient receptor potential cation channel subfamily	TRPC3	0.0531	1.42
1453	ADXECAD.14809_at	Transcribed locus		0.0537	1.42
1454	ADXEC.20671.C1_x_at	Homo sapiens N-acetyltransferase 8 (GCN5-related putative) (NAT8)	NAT8	0.0049	1.41
1455	ADXECAD.22429_x_at	Homo sapiens methyltransferase like 13 (METTL13) transcript	METTL13	0.006	1.41
1456	ADXECRS.21396_at	Homo sapiens heat shock protein 90kDa alpha (cytosolic) class B	HSP90AB2P	0.0077	1.41
1457	ADXPCEC.15942.C1_x_at	Homo sapiens ccr2b (ccr2) ccr2a (ccr2) ccr5 (ccr5) and ccr6 (ccr6) genescomplete	CCR2	0.018	1.41
1458	ADXEC.1477.C4_x_at	Homo sapiens butyrophilin subfamily 3 member A3 (BTN3A3)	BTN3A3	0.0233	1.41
1459	ADXECRS.29095_s_at	Homo sapiens MEF2 activating motif and SAP domain containing	MAMSTR	0.0242	1.41
1460	ADXEC.966.C1_at	Homo sapiens adiponectin receptor 1 (ADIPO1) transcript variant	ADIPO1	0.0378	1.41
1461	ADXECAD.6247_x_at	Homo sapiens microtubule-associated protein 1B (MAP1B) mRNA.	MAP1B	0.0392	1.41
1462	ADXECAD.16533_x_at	H.sapiens TCR V-beta 6.3 gene for TCR beta chain variable region		0.0408	1.41
1463	ADXEC.9786.C1_s_at	Transcribed locus		0.0471	1.41
1464	ADXEC.4635.C1_at	Der1-like domain family member 1	DERL1	0.0067	1.4
1465	ADXECNTDJ.2090_s_at	H.sapiens mRNA for rearranged Ig heavy chain variable domain cell-typeTB-1-P5		0.0142	1.4
1466	ADXStrongB57_at			0.0171	1.4

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1467	ADXECNTDJ.5409_s_at	Homo sapiens taxilin alpha (TXLNA) mRNA.	TXLNA	0.0183	1.4
1468	ADXECAD.5310_at	Homo sapiens p83 (DBC2) gene complete cds.	RHOBTB2	0.0188	1.4
1469	ADXEC.12173.C1_s_at	Homo sapiens coiled-coil domain containing 15 (CCDC15) mRNA.	CCDC15	0.0231	1.4
1470	ADXEC.20377.C1-a_s_at	Homo sapiens sterol O-acyltransferase 1 (SOAT1) transcript variant	SOAT1	0.0241	1.4
1471	ADXEC.4119.C4_at	Transcribed locus		0.0276	1.4
1472	ADXECAD.5485_at	Integrator complex subunit 7	INTS7	0.0376	1.4
1473	ADXECRS.19034_s_at	PREDICTED: Homo sapiens hypothetical LOC100130465 (LOC100130465)	LOC100130465	0.0413	1.4
1474	ADXEC.5198.C2_s_at	Homo sapiens heat shock 70kDa protein 4 (HSPA4) mRNA.	HSPA4	0.0442	1.4
1475	ADXECADA.20758_s_at	Homo sapiens zinc finger MYND-type containing 8 mRNA (cDNA cloneMGC:166983 IMAGE)	ZMYND8	0.0447	1.4
1476	ADXEC.1119.C2_s_at	Homo sapiens high-mobility group box 2 (HMGB2) transcript variant	HMGB2	0.0455	1.4
1477	ADXEC.32599.C1_at	Homo sapiens immunity-related GTPase family Q (IRGQ) mRNA.	IRGQ	0.0482	1.4
1478	ADXECADA.1722_s_at	Homo sapiens FYVE RhoGEF and PH domain containing 2 (FGD2) mRNA.	FGD2	0.0046	1.39
1479	ADXEC.25009.C1_x_at	Zinc finger RAN-binding domain containing 2	ZRANB2	0.0074	1.39
1480	ADXECAD.1588_x_at	Homo sapiens Pig7 (PIG7) mRNA complete cds.	LITAF	0.0132	1.39
1481	ADXECAD.7391_at	Transcribed locus		0.0171	1.39
1482	ADXEC.26052.C1_at	Homo sapiens ectodysplasin A (EDA) transcript variant 2 mRNA.	EDA	0.0213	1.39
1483	ADXECRS.6389_at	PREDICTED: Homo sapiens hypothetical LOC645177 (LOC645177) mRNA.	LOC645177	0.0245	1.39
1484	ADXEC.18691.C1_x_at	protein phosphatase Mg2? dependent 1F	PPM1F	0.0307	1.39
1485	ADXECRS.3811_s_at	PREDICTED: Homo sapiens similar to ras homolog gene family member	LOC730041	0.0312	1.39
1486	ADXEC.4151.C2-a_s_at	Homo sapiens heterogeneous nuclear ribonucleoprotein A0 (HNRNPA0)	HNRNPA0	0.0393	1.39
1487	ADXECADA.7311_at	Homo sapiens metastasis suppressor 1 (MTSS1) mRNA.	MTSS1	0.0394	1.39
1488	ADXECRS.4570_s_at	PREDICTED: Homo sapiens similar to hCG1784039 (LOC391359) mRNA.	LOC391359	0.0476	1.39
1489	ADXEC.9804.C1_s_at	Homo sapiens amyloid beta (A4) precursor protein-binding family B	APBB3	0.048	1.39
1490	ADXECRS.12050_s_at	PREDICTED: Homo sapiens similar to mCG1050952 (LOC100129711) mRNA.	LOC100129711	0.0503	1.39

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1491	ADXECNTDJ.835_at	Homo sapiens DnaJ (Hsp40) homolog subfamily A member 3 (DNAJA3)	DNAJA3	0.0503	1.39
1492	ADXEC.19665.C1-a_s_at	Homo sapiens nicotinamide nucleotide transhydrogenase (NNT)	NNT	0.0508	1.39
1493	ADXEC.34481.C1_at	CDNA FLJ11528 fis clone HEMBA1002621		0.0089	1.38
1494	ADXECAD.10771_x_at	Neurochondrin	NCDN	0.0119	1.38
1495	ADXECAD.9764_s_at	Homo sapiens dehydrogenase/reductase (SDR family) member 7 (DHR57)	DHR57	0.014	1.38
1496	ADXEC.1884.C4_x_at	Homo sapiens profilin 1 (PFN1) mRNA.	PFN1	0.0291	1.38
1497	ADXECRS.39033_at	Homo sapiens ectodysplasin A (EDA) transcript variant 4 mRNA.	EDA	0.031	1.38
1498	ADXEC.7650.C2_at	Homo sapiens transportin 1 (TNPO1) transcript variant 2 mRNA.	TNPO1	0.036	1.38
1499	ADXEC.9646.C1_at	Homo sapiens mRNA for KIAA0471 protein partial cds.	RABGAP1L	0.045	1.38
1500	ADXOCEC.9935.C1_x_at	Homo sapiens RAD9 homolog A (S. pombe) (RAD9A) gene complete cds.	RAD9A	0.0471	1.38
1501	ADXEC.20443.C1_at	Homo sapiens BAC clone RP11-571118 from 4 complete sequence.	MORF4LP4	0.0518	1.38
1502	ADXEC.23970.C1_s_at	Small nucleolar RNA host gene 10 (non-protein coding)	SNHG10	0.0094	1.37
1503	ADXECAD.7761_at	hypothetical protein [Pan troglodytes]		0.0111	1.37
1504	ADXECNTDJ.483_at	Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1)	TM6SF1	0.0137	1.37
1505	3362759_at			0.0137	1.37
1506	ADXEC.10228.C1_s_at	Homo sapiens phospholipase C delta 1 (PLCD1) transcript variant	PLCD1	0.0155	1.37
1507	ADXEC.7845.C1_at	Homo sapiens phosphoinositide kinase FYVE finger containing	PIKFYVE	0.0289	1.37
1508	ADXEC.9624.C1_s_at	similar to Sorting nexin-19 [Pan troglodytes]		0.03	1.37
1509	ADXEC.913.C1_at	Homo sapiens SAFB-like transcription modulator (SLTM) transcript	SLTM	0.0306	1.37
1510	ADXEC.32842.C1_at	Transcribed locus		0.0317	1.37
1511	ADXEC.19586.C1_at	LETM1 domain containing 1	LETM1	0.0356	1.37
1512	ADXEC.7820.C1_s_at	Transcribed locus		0.0377	1.37
1513	ADXEC.3599.C1_s_at	Homo sapiens thymidine phosphorylase (TYMP) transcript variant 1	TYMP	0.0473	1.37
1514	ADXEC.22883.C2-a_s_at	Homo sapiens GTPase activating protein (SH3 domain) binding protein	G3BP2	0.0494	1.37
1515	ADXEC.119.C44_x_at	Homo sapiens major histocompatibility complex class I A (HLA-A)	HLA-A	0.0042	1.36

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1516	ADXECAD.16634_at	Homo sapiens biorientation of chromosomes in cell division 1-like	BOD1L	0.0056	1.36
1517	ADXEC.33040.C1_x_at	Homo sapiens KIAA1161 (KIAA1161) mRNA.	KIAA1161	0.0202	1.36
1518	ADXECADA.4929_s_at	Homo sapiens male-specific lethal 1 homolog (Drosophila) (MSL1)	MSL1	0.0251	1.36
1519	ADXEC.11994.C2_s_at	Homo sapiens protein phosphatase 1 regulatory (inhibitor) subunit	PPP1R8	0.0294	1.36
1520	ADXECRS.530_s_at	PREDICTED: Homo sapiens hypothetical protein LOC100129677	LOC100129677	0.032	1.36
1521	ADXECRS.37691_x_at	Homo sapiens ovochymase 1 (OVCH1) mRNA.	OVCH1	0.0322	1.36
1522	ADXEC.5650.C1-a_s_at	Homo sapiens iduronate 2-sulfatase (IDS) transcript variant 1	IDS	0.0393	1.36
1523	ADXEC.28670.C1_s_at	Homo sapiens NOP2/Sun domain family member 3 (NSUN3) mRNA.	NSUN3	0.0405	1.36
1524	ADXECADA.4045_at	Homo sapiens TNF receptor-associated factor 5 (TRAF5) transcript	TRAF5	0.0427	1.36
1525	ADXEC.26102.C1_at	Transcribed locus		0.0449	1.36
1526	ADXEC.14515.C1_at	Homo sapiens erythrocyte membrane protein band 4.1-like 1	EPB41L1	0.0528	1.36
1527	ADXEC.10542.C1_s_at	Coiled-coil domain containing 88A	CCDC88A	0.0056	1.35
1528	ADXEC.5270.C1_s_at	Homo sapiens trans-golgi network protein 2 (TGOLN2) mRNA.	TGOLN2	0.0132	1.35
1529	ADXEC.19265.C1_s_at	Homo sapiens zinc finger DHC-type containing 2 (ZDHHC2) mRNA.	ZDHHC2	0.0162	1.35
1530	ADXECAD.14031_at	Neuroblastoma amplified sequence	NBAS	0.0166	1.35
1531	ADXECADA.11791_x_at	hypothetical protein partial [Macaca mulatta]		0.0167	1.35
1532	ADXEC.31072.C1_at	Human hereditary haemochromatosis region histone 2A-like protein genehereditary	TRIM38	0.0178	1.35
1533	ADXECAD.5572_at	Syntaxin 8	STX8	0.0182	1.35
1534	Adx-200073-up_s_at	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1	HNRNPD	0.0207	1.35
1535	ADXEC.24718.C1_s_at	Homo sapiens HRIHFB2017 mRNA partial cds.	BMP2K	0.0277	1.35
1536	ADXOCEC.15602.C1_at	Homo sapiens chromosome 19 clone CTC-450M9 complete sequence.	SIPA1L3	0.0346	1.35
1537	2775487_at			0.0358	1.35
1538	ADXECAD.13345_s_at	Transcribed locus		0.0374	1.35

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1539	ADXEC.5035.C3_x_at	Homo sapiens poly(A) binding protein cytoplasmic 1 (PABPC1) mRNA.	PABPC1	0.0417	1.35
1540	ADXLCEC.5249.C1_at	Homo sapiens mRNA for KIAA1152 protein partial cds.	C14orf118	0.0475	1.35
1541	ADXEC.7155.C3_at	Homo sapiens zinc finger protein 626 (ZNF626) transcript variant	ZNF626	0.0478	1.35
1542	ADXEC.2402.C2-a_s_at	Homo sapiens synovial apoptosis inhibitor 1 synoviolin (SYVN1)	SYVN1	0.0481	1.35
1543	ADXEC.2995.CB1_x_at	Homo sapiens ATPase Na? transporting alpha 1 polypeptide	ATP1A1	0.0532	1.35
1544	ADXEC.11944.C2-a_s_at	Homo sapiens transmembrane protein 2 (TMEM2) transcript variant 2	TMEM2	0.0544	1.35
1545	ADXECAD.9838_s_at	Ribosome binding protein 1 homolog 180kDa (dog)	RRBP1	0.0054	1.34
1546	ADXEC.13855.CB1_s_at	Homo sapiens surfactant protein C (SFTPC) transcript variant 1	SFTPC	0.0099	1.34
1547	ADXEC.6634.C2_at	Poly(A) polymerase alpha	PAPOLA	0.0113	1.34
1548	ADXEC.8227.C2_s_at	Homo sapiens ADP-ribosylation factor 6 (ARF6) mRNA.	ARF6	0.0159	1.34
1549	ADXECAD.11607_s_at	hypothetical protein [Pan troglodytes]		0.019	1.34
1550	ADXEC.31693.C1_at	Homo sapiens genomic DNA chromosome 11q clone:CTD-2542M24.	LOC100289388	0.0208	1.34
1551	ADXEC.9641.C1_s_at	Homo sapiens eukaryotic translation termination factor 1 (ETF1)	ETF1	0.0209	1.34
1552	ADXEC.1104.C1_at	Homo sapiens proteasome (prosome macropain) 26S subunit	PSMD12	0.0389	1.34
1553	ADXECRS.45667_s_at	Homo sapiens phenylalanyl-tRNA synthetase alpha subunit (FARSA)	FARSA	0.0428	1.34
1554	ADXECRS.11016_x_at	Homo sapiens golgin A8 family member F (GOLGA8F) non-coding RNA.	GOLGA8F	0.0441	1.34
1555	ADXECADA.19635_s_at	Homo sapiens WD repeat domain 83 (WDR83) transcript variant 3	WDR83	0.0484	1.34
1556	ADXEC.7837.C1_at	Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32	ANP32E	0.0079	1.33
1557	ADXECAD.9719_at	Transcribed locus		0.0164	1.33
1558	ADXEC.15770.C2_s_at	splicing factor arginine/serine-rich 8 (suppressor-of-white-apricot homolog Dros	SFRS8	0.0213	1.33
1559	ADXECRS.8603_at	Homo sapiens gigaxonin mRNA complete cds.	GAN	0.0217	1.33
1560	ADXECNTDJ.7257_s_at	Homo sapiens chromatin modifying protein 1A (CHMP1A) transcript	CHMP1A	0.0231	1.33
1561	ADXEC.5285.C1_s_at	estrogen receptor binding site associated antigen 9	EBAG9	0.0233	1.33
1562	ADXUglyB78_at			0.0246	1.33
1563	ADXECADA.15524_at	CDNA FLJ20785 fis clone COL02504		0.0297	1.33

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1564	ADXEC.16201.C1_at	Homo sapiens ubiquitin protein ligase E3 component n-recognin 2	UBR2	0.0341	1.33
1565	ADXEC.15255.C1_at	PREDICTED: Homo sapiens hypothetical protein LOC100289224	LOC100289224	0.0346	1.33
1566	ADXECRS.241_s_at	Homo sapiens isoprenoid synthase domain containing (ISPD)	ISPD	0.0359	1.33
1567	ADXEC.11385.C1_s_at	PREDICTED: Homo sapiens similar to mCG115122 (LOC100129361) mRNA.	LOC100129361	0.0459	1.33
1568	ADXEC.15096.C1_x_at	Homo sapiens H2K binding factor 2 (KBF2) mRNA complete cds.	RBPJ	0.0519	1.33
1569	ADXEC.2294.C1_x_at	Homo sapiens Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB)	ARHGDIB	0.0087	1.32
1570	ADXEC.23922.C2_x_at	Homo sapiens zinc finger protein 431 (ZNF431) mRNA.	ZNF431	0.009	1.32
1571	ADXEC.2424.C1_s_at	Homo sapiens stress-associated endoplasmic reticulum protein 1	SERP1	0.0141	1.32
1572	ADXEC.4522.C1_s_at	Homo sapiens fuzzy homolog (Drosophila) (FUZ) transcript variant	FUZ	0.016	1.32
1573	ADXEC.3894.C1_at	Homo sapiens SH3-domain GRB2-like endophilin B1 (SH3GLB1) mRNA.	SH3GLB1	0.0238	1.32
1574	ADXEC.1357.CB1_x_at	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	YWHAZ	0.0434	1.32
1575	ADXEC.673.C16_x_at	Homo sapiens ferritin light polypeptide (FTL) mRNA.	FTL	0.0451	1.32
1576	ADXECAD.1302_s_at	Homo sapiens adenylate cyclase 7 (ADCY7) mRNA.	ADCY7	0.0464	1.32
1577	ADXECADA.20635_s_at	Homo sapiens myocyte enhancer factor 2A (MEF2A) transcript variant	MEF2A	0.054	1.32
1578	ADXECNTD1.958_s_at	Homo sapiens BRF1 homolog subunit of RNA polymerase III	BRF1	0.0037	1.31
1579	ADXOCEC.11956.C1-a_s_at	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10	LRRC27	0.0117	1.31
1580	ADXEC.2060.C1_at	PREDICTED: Homo sapiens hypothetical LOC644794 (LOC644794) mRNA.	LOC644794	0.0266	1.31
1581	ADXEC.7849.C1_at	Homo sapiens kinesin family member 5B (KIF5B) mRNA.	KIF5B	0.0283	1.31
1582	ADXEC.12048.C1-a_s_at	Transcribed locus		0.0344	1.31
1583	ADXEC.6911.C2_s_at	Homo sapiens protein kinase N2 (PKN2) mRNA.	PKN2	0.035	1.31
1584	ADXECRS.5108_x_at	Human DNA sequence from clone RP4-758J18 on chromosome 1p36.31-36.33 Contains the	LOC100288271	0.036	1.31
1585	ADXECADA.1143_at	3883659 mRNA		0.0367	1.31
1586	ADXECRS.32618_at	similar to C/EBP-induced protein [Monodelphis domestica]		0.0388	1.31

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1587	ADXEC.12233.C1_at	Homo sapiens pyrroline-5-carboxylate reductase family member 2	PYCR2	0.0418	1.31
1588	ADXECAD.11993_at	Transcribed locus		0.0446	1.31
1589	ADXEC.3835.C1-a_s_at	Homo sapiens SH2 domain containing 4A (SH2D4A) transcript variant	SH2D4A	0.0473	1.31
1590	ADXECAD.23371_at	Homo sapiens CD6 molecule (CD6) mRNA.	CD6	0.0495	1.31
1591	ADXECAD.26067_at	Homo sapiens ciliary neurotrophic factor receptor (CNTFR)	CNTFR	0.0077	1.3
1592	ADXEC.3246.C3_at	Homo sapiens PHD finger protein 21A (PHF21A) transcript variant 2	PHF21A	0.0205	1.3
1593	ADXECNTDJ.7258_at	Homo sapiens chromatin modifying protein 1A (CHMP1A) transcript	CHMP1A	0.0293	1.3
1594	3362775_at			0.0314	1.3
1595	ADXECADA.17296_at	Homo sapiens ring finger protein 126 pseudogene 1 (RNF126P1)	RNF126P1	0.0422	1.3
1596	ADXECEMUTR.5836_at	CDNA FLJ43210 fis clone FEBRA2020582		0.0449	1.3
1597	ADXECNTDJ.4943_s_at	Homo sapiens centromere protein P (CENPP) mRNA.	CENPP	0.0508	1.3
1598	ADXECNTDJ.3199_s_at	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	YWHAE	0.0513	1.3
1599	ADXECAD.19045_at	Homo sapiens transmembrane 9 superfamily member 3 (TM9SF3) mRNA.	TM9SF3	0.0027	1.29
1600	ADXECEMUTR.2599_at	PREDICTED: Homo sapiens hypothetical LOC729225 (LOC729225) mRNA.	LOC729225	0.0074	1.29
1601	ADXECSR.3598_s_at	Transcribed locus		0.0083	1.29
1602	ADXECNTDJ.8317_s_at	Homo sapiens GT219 mRNA.		0.012	1.29
1603	ADXEC.3966.C1_s_at	Homo sapiens glucosidase alpha	GAA	0.0219	1.29
1604	ADXLCEC.10213.C1_at	Human DNA sequence from clone RP3-337H4 on chromosome 6 Contains the 3part of a	RPS2P29	0.0293	1.29
1605	ADXEC.3334.C1-a_s_at	Homo sapiens syntaxin 7 (STX7) mRNA.	STX7	0.0354	1.29
1606	ADXEC.28258.C1_at	Homo sapiens hypothetical protein LOC253842 mRNA (cDNA clonIMAGE:4993690) parti	LOC253842	0.0403	1.29
1607	ADXEC.32826.C1_at	Homo sapiens BR serine/threonine kinase 2 (BRSK2) mRNA.	BRSK2	0.0461	1.29
1608	ADXEC.29220.C1_s_at	Homo sapiens chromosome clone RP11-140L24 complete sequence.	RNU7-49P	0.0515	1.29
1609	ADXEC.21281.C1_at	Homo sapiens poly(A) binding protein interacting protein 2 (PAIP2)	PAIP2	0.052	1.29

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1610	ADXECAD.5688_x_at	Exocyst complex component 5	EXOC5	0.0102	1.28
1611	ADXECAD.14326_at	Homo sapiens ataxin 1-like (ATXN1L) transcript variant 2	ATXN1L	0.0174	1.28
1612	ADXEC.2995.CB1_at	Homo sapiens ATPase Na ⁺ transporting alpha 1 polypeptide	ATP1A1	0.0182	1.28
1613	ADXEC.1706.C2_s_at	Homo sapiens serrate RNA effector molecule homolog (Arabidopsis)	SRRT	0.0201	1.28
1614	ADXECRS.3441_x_at	Homo sapiens hypothetical LOC399844 (FLJ45445) non-coding RNA.	FLJ45445	0.0204	1.28
1615	ADXECNTDJ.6223_s_at	interferon-related developmental regulator 1	IFRD1	0.0208	1.28
1616	ADXECRS.5108_at	Human DNA sequence from clone RP4-758J18 on chromosome 1p36.31-36.33Contains the	LOC100288271	0.0224	1.28
1617	ADXEC.673.CB2_x_at	Homo sapiens ferritin light polypeptide (FTL) mRNA.	FTL	0.0315	1.28
1618	ADXEC.8822.C1_at	Homo sapiens round spermatid basic protein 1 (RSBN1) mRNA.	RSBN1	0.0431	1.28
1619	ADXECADA.244_at	Homo sapiens hypothetical LOC85009 (MGC16025) non-coding RNA.	MGC16025	0.0447	1.28
1620	ADXECRS.17931_at	Homo sapiens olfactory receptor family 52 subfamily W member 1	OR52W1	0.051	1.28
1621	ADXEC.11850.C1_at	Homo sapiens Ras suppressor protein 1 (RSU1) transcript variant 1	RSU1	0.0526	1.28
1622	ADXECRS.14237_s_at	Hypothetical LOC730338	LOC730338	0.053	1.28
1623	ADXEC.29050.C1_s_at	Homo sapiens fatty acyl CoA reductase 1 (FAR1) mRNA.	FAR1	0.0538	1.28
1624	ADXEC.19419.C1_s_at	Homo sapiens YTH domain containing 1 (YTHDC1) transcript variant	YTHDC1	0.011	1.27
1625	ADXEC.29244.C1_at	Homo sapiens partial TUB gene for mouse tubby homologue exons 1-9	TUB	0.0117	1.27
1626	ADXECRS.24253_x_at	Homo sapiens small nucleolar RNA H/ACA box 5B (SNORA5B) small	SNORA5B	0.0183	1.27
1627	ADXECAD.17311_at	Human DNA sequence from cDNA 16pHQG	PDIA2	0.0185	1.27
1628	ADXECEMUTR.5896_at	Hypothetical LOC100128059	LOC100128059	0.0202	1.27
1629	ADXECAD.10364_s_at	Homo sapiens myocyte enhancer factor 2A (MEF2A) transcript variant	MEF2A	0.0266	1.27
1630	ADXEC.838.C16_at	Metallothionein 2A	MT2A	0.0348	1.27
1631	ADXECRS.24303_at	Homo sapiens endonuclease polyU-specific (ENDOU) transcript	ENDOU	0.0381	1.27
1632	ADXEC.2814.C2_s_at	Homo sapiens EGF-like-domain multiple 8 (EGFL8) mRNA.	EGFL8	0.0392	1.27
1633	ADXEC.8836.C1-a_s_at	Homo sapiens nuclear cap binding protein subunit 1 80kDa (NCBP1)	NCBP1	0.0408	1.27

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1634	ADXECAD.4753_at	MRNA		0.0433	1.27
1635	ADXEC.319.C15_s_at	Homo sapiens eukaryotic translation initiation factor 2 subunit 2	EIF2S2	0.0449	1.27
1636	ADXEC.26501.C1_at	Homo sapiens tripartite motif-containing 13 (TRIM13) transcript	TRIM13	0.0468	1.27
1637	ADXECNTDJ.4173_x_at	Homo sapiens selenocysteine lyase (SCLY) mRNA.	SCLY	0.0488	1.27
1638	ADXECRS.34618_x_at	Homo sapiens chromosome 17 open reading frame 74 (C17orf74) mRNA.	C17orf74	0.0531	1.27
1639	ADXECADA.19527_at	Transcribed locus	C14orf91	0.0043	1.26
1640	ADXECNTDJ.4562_at	Homo sapiens zinc finger FYVE domain containing 1 (ZFYVE1)	ZFYVE1	0.0048	1.26
1641	ADXECRS.24957_at	Transcribed locus		0.0082	1.26
1642	ADXEC.15770.C1_s_at	splicing factor arginine/serine-rich 8 (suppressor-of-white-apricot homolog Dros	SFRS8	0.0106	1.26
1643	ADXECRS.9316_at	Homo sapiens keratin associated protein 5-3 (KRTAP5-3) mRNA.	KRTAP5-3	0.0141	1.26
1644	ADXECEMUTR.3539_at	Homo sapiens RAET1E2 mRNA complete cds.	RAET1E	0.0182	1.26
1645	ADXEC.3867.C1_x_at	3-hydroxyanthranilate 34-dioxygenase	HAAO	0.0311	1.26
1646	ADXEC.9567.C3_at	Family with sequence similarity 96 member B	FAM96B	0.0416	1.26
1647	ADXECAD.14147_at	Transcribed locus		0.0432	1.26
1648	ADXECAD.4051_x_at	Homo sapiens zinc finger protein 229 (ZNF229) mRNA.	ZNF229	0.0452	1.26
1649	ADXEC.10545.C1_s_at	Transcribed locus		0.0453	1.26
1650	ADXEC.931.C1_s_at	Homo sapiens glutathione peroxidase 1 (GPX1) transcript variant 2	GPX1	0.0468	1.26
1651	ADXEC.2886.C1_at	Homo sapiens golgi phosphoprotein 3 (coat-protein) (GOLPH3) mRNA.	GOLPH3	0.0475	1.26
1652	ADXEC.21117.C1_at	Homo sapiens ROD1 regulator of differentiation 1 (s. pombe) (ROD1)	ROD1	0.0481	1.26
1653	ADXOCEC.14434.C1_at	Transcribed locus		0.0495	1.26
1654	ADXECADA.15467_at	Homo sapiens storkhead box 2 (STOX2) mRNA.	STOX2	0.0512	1.26
1655	ADXECAD.18141_at	Homo sapiens DNA DLEC1 to ORCTL4 gene region section 1/2 (DLEC1 ORCTL3ORCTL4 gen	DLEC1	0.0539	1.26
1656	ADXECRS.13130_s_at	PREDICTED: Homo sapiens similar to hCG1770601 (LOC100128334) mRNA.	LOC100128334	0.0061	1.25
1657	ADXEC.3576.C1_x_at	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2)	LAMP2	0.0137	1.25

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1658	ADXEC.2197.C1_at	Homo sapiens family with sequence similarity 108 member A1	FAM108A1	0.0155	1.25
1659	ADXECRS.15841_s_at	Homo sapiens radial spoke head 10 homolog B2 (Chlamydomonas)	RSPH10B2	0.0215	1.25
1660	Adx-200055-up_s_at	TAF10 RNA polymerase II TATA box binding protein (TBP)-associated factor 30kDa	TAF10	0.0239	1.25
1661	ADXECRS.26052_s_at	Chromosome 14 open reading frame 81	C14orf81	0.0264	1.25
1662	ADXECAD.23938_s_at	Homo sapiens formyl peptide receptor 2 (FPR2) transcript variant	FPR2	0.0277	1.25
1663	ADXECNTDJ.9604_at			0.0291	1.25
1664	ADXEC.13397.C1_s_at	Homo sapiens myeloid leukemia factor 1 (MLF1) transcript variant	MLF1	0.0372	1.25
1665	3551874_at			0.0388	1.25
1666	ADXECADA.790_s_at	Homo sapiens zygote arrest 1 (ZAR1) mRNA.	ZAR1	0.0403	1.25
1667	ADXEC.22481.C1_s_at	Transcribed locus		0.0404	1.25
1668	ADXEC.28238.C1_at	Homo sapiens NK2 homeobox 2 (NKX2-2) mRNA.	NKX2-2	0.0428	1.25
1669	ADXEC.4918.C1_at	Homo sapiens N-acetyltransferase 15 (GCN5-related putative)	NAT15	0.0445	1.25
1670	ADXEC.2340.C1-a_s_at	Homo sapiens mediator complex subunit 29 (MED29) mRNA.	MED29	0.0469	1.25
1671	ADXECRS.13131_at	Homo sapiens baculoviral IAP repeat-containing 5 (BIRC5)	BIRC5	0.0486	1.25
1672	ADXEC.8137.C1_x_at	LUC7-like 2 (S. cerevisiae)	LUC7L2	0.0491	1.25
1673	ADXECRS.8473_at	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase	GAPDHS	0.0016	1.24
1674	ADXEC.3578.C2_at	Homo sapiens haplogroup T1a mitochondrion complete genome.		0.0171	1.24
1675	ADXEC.17731.C1_at	Homo sapiens transmembrane protein 90A (TMEM90A) mRNA.	TMEM90A	0.0201	1.24
1676	ADXEC.29873.C1_at	Transcribed locus		0.0212	1.24
1677	ADXECAD.12808_at	Protein tyrosine phosphatase non-receptor type 1	PTPN1	0.0239	1.24
1678	ADXEC.18978.C1_at	Transcribed locus		0.0284	1.24
1679	ADXEC.19816.C1_x_at	Homo sapiens carbohydrate (N-acetylgalactosamine 4-O)	CHST9	0.0296	1.24
1680	ADXECAD.5585_at	Homo sapiens kinesin light chain 3 (KLC3) mRNA.	KLC3	0.0366	1.24
1681	ADXOCEC.6950.C1_x_at	Homo sapiens v-rel reticuloendotheliosis viral oncogene homolog	REL	0.0396	1.24

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1682	3362748_at			0.0421	1.24
1683	ADXEC.141.C2_x_at	Transcribed locus		0.0455	1.24
1684	ADXEC.3578.C2_x_at	Homo sapiens haplogroup H11a1 mitochondrion complete genome.	ND6	0.0485	1.24
1685	ADXEC.2294.C1_at	Homo sapiens Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB)	ARHGDIB	0.0504	1.24
1686	ADXEC.23280.C1_at	Homo sapiens translin (TSN) mRNA.	TSN	0.0093	1.23
1687	ADXECAD.12357_at	Homo sapiens retinoic acid receptor gamma (RARG) transcript	RARG	0.0262	1.23
1688	ADXECAD.12890_s_at	Homo sapiens chromosome 17 clone RP11-24715 complete sequence.	HSF5	0.0264	1.23
1689	ADXECEMUTR.4504_x_at	Homo sapiens KCNQ1 downstream neighbor (KCNQ1DN) non-coding RNA.	KCNQ1DN	0.0278	1.23
1690	ADXECRS.20617_at	Human DNA sequence from clone RP5-1114G22 on chromosome 1q24-25 Contains the 5 en	LOC100288070	0.0285	1.23
1691	ADXECAD.10093_x_at	CDNA FLJ33454 fis clone BRAMY2000231		0.0306	1.23
1692	ADXEC.6038.C1_x_at	Homo sapiens zinc finger CCH-type containing 15 (ZC3H15) mRNA.	ZC3H15	0.0387	1.23
1693	ADXECRS.16162_s_at	Homo sapiens mRNA for hypothetical protein (ORF1) cloneTelethon(Italy_B41)_Strai	LOC100129366	0.0416	1.23
1694	ADXECADA.10529_s_at	Homo sapiens ADP-ribosylation factor 6 (ARF6) mRNA.	ARF6	0.0461	1.23
1695	ADXECAD.25526_x_at	Homo sapiens beta-adrenergic receptor kinase (ADR) gene exons 7 through 21 and co	ADRBK1	0.0471	1.23
1696	ADXEC.19839.C1_at	Homo sapiens interferon regulatory factor 2 (IRF2) gene 5 flank.		0.01	1.22
1697	ADXECRS.5544_s_at	Homo sapiens chromosome 19 BC335474 (CIT-HSPC_482H14) complete sequence.	LOC100128439	0.0129	1.22
1698	ADXEC.14371.C1_s_at	Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1)	CYFIP1	0.0156	1.22
1699	ADXECRS.24092_x_at	Homo sapiens mRNA for a disintegrin and metalloprotease with thrombospondin motif	ADAMTS7	0.0161	1.22
1700	ADXECRS.25943_at	Homo sapiens urocortin 3 (stresscopin) (UCN3) mRNA.	UCN3	0.0322	1.22
1701	ADXEC.5303.C1_at	Transcribed locus		0.038	1.22
1702	ADXECADA.3999_x_at	Homo sapiens chromosome X multiple clones map p11.23 complete sequence.		0.0387	1.22

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1703	ADXECNTDJ.7956_s_at	Homo sapiens interferon regulatory factor 5 (IRF5) gene complete cds.	IRF5	0.0419	1.22
1704	ADXEC.14042.C1_x_at	Homo sapiens SRY (sex determining region Y)-box 8 (SOX8) mRNA.	SOX8	0.0429	1.22
1705	ADXECADA.15773_x_at	Homo sapiens ferritin light polypeptide (FTL) mRNA.	FTL	0.0432	1.22
1706	ADXECRS.26593_x_at	Homo sapiens hypothetical LOC100131880 (LOC100131880)	LOC100131880	0.0435	1.22
1707	ADXECRS.13131_x_at	Homo sapiens baculoviral IAP repeat-containing 5 (BIRC5)	BIRC5	0.0444	1.22
1708	ADXECADA.13997_at	Hypothetical protein LOC100129195	LOC100129195	0.05	1.22
1709	ADXEC.4427.C11_x_at	Homo sapiens actinin alpha 4 (ACTN4) mRNA.	ACTN4	0.0519	1.22
1710	ADXECAD.18107_at	Homo sapiens BAC clone RP11-20120 from 4 complete sequence.	LOC100130872	0.0073	1.21
1711	ADXECAD.15226_s_at	DKFZP564C196 protein	DKFZP564C196	0.0109	1.21
1712	ADXEC.15164.C1_s_at	Homo sapiens coiled-coil domain containing 88A (CCDC88A)	CCDC88A	0.0135	1.21
1713	ADXECRS.5808_s_at	PREDICTED: Homo sapiens non-protein coding RNA 83 (NCRNA00083)	NCRNA00083	0.016	1.21
1714	ADXEC.28457.C1_at	Homo sapiens p21 protein (Cdc42/Rac)-activated kinase 2 (PAK2)	PAK2	0.0207	1.21
1715	ADXECNTDJ.9148_x_at	Homo sapiens HAUS augmin-like complex subunit 5 (HAUS5) mRNA.	HAUS5	0.0228	1.21
1716	ADXECRS.34985_at	Homo sapiens growth differentiation factor 7 (GDF7) mRNA.	GDF7	0.026	1.21
1717	ADXECAD.14878_s_at	Homo sapiens zinc finger protein 771 (ZNF771) transcript variant	ZNF771	0.0283	1.21
1718	ADXEC.21002.C1_at	Homo sapiens eukaryotic translation initiation factor 4 gamma 2	EIF4G2	0.036	1.21
1719	ADXECEMUTR.5129_at	Chromosome 11 open reading frame 72	C11orf72	0.0363	1.21
1720	ADXECADA.11075_at	Homo sapiens similar to hCG1994130 (LOC100293274) mRNA.	LOC100293274	0.0448	1.21
1721	ADXECRS.17207_at	Homo sapiens ADAM metalloproteinase with thrombospondin type 1	ADAMTS15	0.0515	1.21
1722	ADXECNTDJ.6711_x_at	Homo sapiens hydroxysteroid (11-beta) dehydrogenase 1-like	HSD11B1L	0.0012	1.2
1723	ADXECAD.15380_at	Homo sapiens pannexin 2 (PANX2) transcript variant 1 mRNA.	PANX2	0.0064	1.2
1724	ADXECRS.43350_at	Homo sapiens poly(A) binding protein nuclear 1-like (cytoplasmic)	PABPN1L	0.0068	1.2
1725	ADXECAD.1221_at	Homo sapiens CKLF-like MARVEL transmembrane domain containing 4	CMTM4	0.0115	1.2
1726	ADXEC.1357.CB2_s_at	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	YWHAZ	0.0119	1.2
1727	ADXECRS.38266_s_at	Homo sapiens peptidoglycan recognition protein 2 (PGLYRP2) mRNA.	PGLYRP2	0.0123	1.2

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1728	ADXECADA.9049_at	Homo sapiens hypothetical protein LOC100293168	LOC100293168	0.0126	1.2
1729	ADXECNTDJ.4124_x_at	Homo sapiens tafazzin (TAZ) transcript variant 5 non-coding RNA.	TAZ	0.017	1.2
1730	ADXEC.242.C1_x_at	Homo sapiens ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog	UBE2D3	0.0232	1.2
1731	ADXECNTDJ.10277_at	Transcribed locus moderately similar to NP_001002912.4 hypothetical protein LOC1		0.0258	1.2
1732	ADXECADA.2245_at	5272683		0.0377	1.2
1733	ADXEC.9590.C1_at			0.0451	1.2
1734	ADXECRS.1230_s_at	PREDICTED: Homo sapiens hypothetical LOC100129191 (LOC100129191)	LOC100129191	0.0484	1.2
1735	ADXEC.8415.C1_at	Insulin-like growth factor binding protein 5	IGFBP5	0.0485	1.2
1736	ADXECEMUTR.2383_at	Homo sapiens actin filament associated protein 1-like 1 mRNA (cDNA clone IMAGE:60	AFAP1L1	0.0159	1.19
1737	ADXECADA.12629_at	Transcribed locus		0.0205	1.19
1738	ADXEC.375.C5_x_at	Keratin 8	KRT8	0.021	1.19
1739	ADXECAD.4116_x_at	Hypothetical LOC340357	LOC340357	0.0242	1.19
1740	ADXEC.10563.C1_at	SWI/SNF related matrix associated actin dependent regulator of chromatin subfam1	SMARCA4	0.0277	1.19
1741	ADXECEMUTR.3328_s_at	PREDICTED: Homo sapiens hypothetical protein LOC644767 (FLJ44838)	FLJ44838	0.0283	1.19
1742	ADXECRS.7655_s_at	PREDICTED: Homo sapiens hypothetical LOC100131630 (LOC100131630)	LOC100131630	0.0293	1.19
1743	ADXStrongB53_at			0.0328	1.19
1744	ADXEC.23983.C1_at	Homo sapiens hypothetical protein FLJ13224 (FLJ13224) non-coding	FLJ13224	0.0334	1.19
1745	ADXEC.28282.C5_at	Chymotrypsin-like elastase family member 3A	CELA3A	0.0395	1.19
1746	ADXECAD.10566_at	Transcribed locus		0.0396	1.19
1747	ADXEC.9134.C1_at	Homo sapiens zinc finger CCCH-type containing 4 (ZC3H4) mRNA.	ZC3H4	0.0476	1.19
1748	ADXEC.3791.C1_at	Homo sapiens casein kinase 1 gamma 2 (CSNK1G2) mRNA.	CSNK1G2	0.0513	1.19
1749	ADXECAD.12474_at	Homo sapiens dynein axonemal heavy chain 1 (DNAH1) mRNA.	DNAH1	0.0057	1.18

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1750	ADXECRS.26595_x_at	ARP3 actin-related protein 3 homolog B pseudogene	LOC644773	0.0079	1.18
1751	ADXECAD.1597_at	Homo sapiens protein phosphatase Mg2? dependent 1F (PPM1F)	PPM1F	0.0091	1.18
1752	ADXECRS.10689_s_at	Homo sapiens keratin 84 (KRT84) mRNA.	KRT84	0.0096	1.18
1753	ADXECNTDJ.2139_at	Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region		0.0217	1.18
1754	ADXECADA.4021_at	Homo sapiens Prader-Willi region non-protein coding RNA 1 (PWRN1)	PWRN1	0.0254	1.18
1755	ADXEC.2569.C1_s_at	Transcribed locus		0.026	1.18
1756	2328475_at			0.0322	1.18
1757	ADXECRS.8910_s_at	Homo sapiens hypothetical LOC91948 (LOC91948) transcript variant	LOC91948	0.0327	1.18
1758	ADXECRS.14265_x_at	Homo sapiens chromosome 15 clone RP11-439M15 complete sequence.		0.0369	1.18
1759	ADXECADA.16192_at	pleckstrin homology domain containing family M (with RUN domain) member 1	PLEKHM1	0.042	1.18
1760	ADXECAD.14526_at	Human DNA sequence from clone RP5-1005F21 on chromosome 20 Contains thePSMA7 gen	FLJ44790	0.0443	1.18
1761	ADXECRS.657_s_at	PREDICTED: Homo sapiens hypothetical LOC652990 (LOC652990)	LOC652990	0.0458	1.18
1762	ADXECAD.10331_at	Homo sapiens BAC clone RP11-44N22 from 2 complete sequence.	NOTO	0.0489	1.18
1763	ADXECAD.18814_at	Homo sapiens growth differentiation factor 11 (GDF11) mRNA.	GDF11	0.0517	1.18
1764	ADXECAD.23363_s_at	Homo sapiens gap junction protein alpha 3 46kDa (GJA3) mRNA.	GJA3	0.0051	1.17
1765	ADXECRS.45555_at	Homo sapiens olfactory receptor family 1 subfamily K member 1	OR1K1	0.0055	1.17
1766	ADXECRS.25518_at	Homo sapiens C2 calcium-dependent domain containing 4C (C2CD4C)	C2CD4C	0.0107	1.17
1767	ADXECRS.43089_s_at	Homo sapiens family with sequence similarity 27 member E1 mRNA (cDNAclone IMAGE:	FAM27E1	0.0107	1.17
1768	ADXEC.7524.C2_s_at	Homo sapiens KIAA1984 (KIAA1984) mRNA.	KIAA1984	0.0118	1.17
1769	ADXECADA.12075_x_at	Homo sapiens partial MASP2 gene patient 23.01 exon d-g	MASP2	0.0152	1.17
1770	ADXECADA.8135_x_at	Homo sapiens chromosome 20 open reading frame 144 (C20orf144)	C20orf144	0.0169	1.17
1771	ADXECAD.26565_s_at	Homo sapiens neurogenin 1 (NEUROG1) mRNA.	NEUROG1	0.0188	1.17
1772	ADXEC.10489.C1_at	Homo sapiens ventral anterior homeobox 1 (VAX1) transcript variant	VAX1	0.0216	1.17

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1773	ADXECNTDJ.10499_at	Transcribed locus		0.0225	1.17
1774	ADXECAD.8731_x_at	Castor zinc finger 1	CASZ1	0.0227	1.17
1775	ADXECNTDJ.9589_at	Homo sapiens multimerin 2 (MMRN2) mRNA.	MMRN2	0.0254	1.17
1776	ADXECAD.16932_at	Homo sapiens zinc finger protein 324B (ZNF324B) mRNA.	ZNF324B	0.0264	1.17
1777	ADXEC.21083.C1_x_at	Homo sapiens chromosome 11 clone RP11-797J4 complete sequence.	ATP5LP8	0.0284	1.17
1778	ADXEC.9954.C1_s_at	Homo sapiens SWI/SNF related matrix associated actin dependent	SMARCD1	0.0308	1.17
1779	ADXEC.8227.C1-a_s_at	Homo sapiens ADP-ribosylation factor 6 (ARF6) mRNA.	ARF6	0.0313	1.17
1780	ADXEC.23288.C1_at	Homo sapiens coronin 6 (CORO6) mRNA.	CORO6	0.0345	1.17
1781	ADXECRS.2701_at	Homo sapiens trace amine associated receptor 5 (TAAR5) mRNA.	TAAR5	0.0347	1.17
1782	ADXECAD.457_s_at	Homo sapiens somatostatin receptor 3 (SSTR3) mRNA.	SSTR3	0.0351	1.17
1783	ADXECNTDJ.8796_s_at	H. sapiens (xs168) mRNA 381bp		0.0359	1.17
1784	ADXEC.14538.C1_s_at	CDNA FLJ36181 fis clone TESTI2026794		0.0385	1.17
1785	ADXECRS.14109_x_at	PREDICTED: Homo sapiens hypothetical LOC100132084 (LOC100132084)	LOC100132084	0.0395	1.17
1786	ADXECAD.19838_at	Homo sapiens similar to arsenic-like protein	LOC100292504	0.0475	1.17
1787	ADXECNTDJ.5995_x_at	Homo sapiens metastasis suppressor 1-like (MTSS1L) mRNA.	MTSS1L	0.0489	1.17
1788	ADXECRS.14963_s_at	hypothetical protein [Pan troglodytes]		0.0507	1.17
1789	ADXECAD.28494_s_at	Homo sapiens growth factor receptor-bound protein 7 (GRB7)	GRB7	0.0517	1.17
1790	ADXECRS.37269_x_at	Homo sapiens small nucleolar RNA C/D box 115-41 (SNORD115-41)	SNORD115-41	0.0141	1.16
1791	ADXEC.9499.C1_at	Homo sapiens opticin (OPTC) mRNA.	OPTC	0.0158	1.16
1792	ADXECNTDJ.8675_x_at	Homo sapiens catenin (cadherin-associated protein) beta 1 88kDa	CTNNB1	0.0228	1.16
1793	ADXECRS.8153_at	Homo sapiens actinin alpha 3 (ACTN3) mRNA.	ACTN3	0.0249	1.16
1794	ADXECRS.6675_at	Homo sapiens keratin 3 (KRT3) mRNA.	KRT3	0.025	1.16
1795	ADXECNTDJ.8492_s_at	Homo sapiens B lymphocyte mRNA sequence.		0.0256	1.16
1796	ADXECNTDJ.5199_s_at	Homo sapiens neuronal nitric oxide synthase (NOS1) mRNA alternative exon1b.		0.0274	1.16
1797	ADXEC.3746.C2-a_s_at	Homo sapiens kinesin family member 2C (KIF2C) mRNA.	KIF2C	0.0353	1.16

ID	Probe ID	Gene Name	Gene Symbol	p-value	Fold-Change (Cav1 Negative vs Cav1 Positive)
1798	ADXPCEC.16421.C1-a_s_at	Homo sapiens chromosome 3 clone RP11-272D20 complete sequence.	PPIAP18	0.0426	1.16
1799	ADXECAD.15076_at	Homo sapiens serum amyloid A3 pseudogene (SAA3P) non-coding RNA.	SAA3P	0.0464	1.16
1800	ADXECRS.14728_at	Human DNA sequence from clone RP1-37J18 on chromosome 1p36.2-36.3 Containstwo no		0.0501	1.16
1801	ADXECAD.1227_s_at	Homo sapiens KIAA1199 (KIAA1199) mRNA.	KIAA1199	0.0502	1.16
1802	ADXPCEC.9834.C1_at	Homo sapiens slit homolog 1 (Drosophila) (SLIT1) mRNA.	SLIT1	0.0523	1.16
1803	ADXECRS.32171_at	Homo sapiens defensin alpha 4 corticostatin (DEFA4) mRNA.	DEFA4	0.0525	1.16
1804	ADXEC.24616.C1_at	Hypothetical LOC401022	LOC401022	0.0074	1.15
1805	ADXECADA.11712_at	Homo sapiens ribosomal RNA processing 12 homolog (S. cerevisiae)	RRP12	0.016	1.15
1806	ADXECRS.3215_s_at	PREDICTED: Homo sapiens similar to S-phase kinase-associated	LOC728622	0.0173	1.15
1807	ADXECAD.7388_at	Homo sapiens Rho GTPase activating protein 23 (ARHGAP23) mRNA.	ARHGAP23	0.0184	1.15
1808	ADXEC.3261.C2_at	Homo sapiens putative sterol reductase SR-1 (TM7SF2) gene complete cds.	TM7SF2	0.0264	1.15
1809	ADXECNTDJ.8419_x_at			0.0356	1.15
1810	ADXECNTDJ.845_s_at	Homo sapiens bone morphogenetic protein 6 (BMP6) mRNA.	BMP6	0.0386	1.15
1811	ADXEC.12497.C1_at	small glutamine-rich tetratricopeptide repeat (TPR)-containing alpha	SGTA	0.0426	1.15
1812	ADXECAD.1336_s_at	FERM domain containing 8	FRMD8	0.0427	1.15
1813	ADXECADA.18200_at	Chromosome 8 open reading frame 58	C8orf58	0.044	1.15
1814	ADXECAD.4356_at	insulin activator factor [human pancreatic insulinoma mRNA Partial 2622nt].		0.0444	1.15
1815	ADXECRS.15441_s_at	PREDICTED: Homo sapiens similar to glyceraldehyde-3-phosphate	LOC391073	0.0449	1.15
1816	ADXECAD.4795_x_at	Keratin associated protein 5-2	KRTAP5-2	0.0513	1.15
1817	ADXECRS.9895_s_at	PREDICTED: Homo sapiens hypothetical LOC100132883 (LOC100132883)	LOC100132883	0.0516	1.15
1818	ADXECADA.2292_at	4829680		0.0533	1.15
1819	ADXECADA.3494_at	Vaccinia related kinase 3	VRK3	0.0538	1.15

I/We Claim:

1. A prognostic signature (also referred to herein as a biological marker or biomarker) for assessing cancer prognosis in a subject (e.g., risk of cancer recurrence, progression of a cancer in a cancer subject, overall survival of cancer by a cancer patient), said prognostic signature
5 comprising a tumor/cancer stromal signature, wherein the tumor/stromal stromal signature is derived from a genome-wide transcriptional profiling of a tumor/cancer stromal material derived from a biological sample obtained from a set of at least one or more subjects having cancer, said tumor stromal signature comprising a first set of gene transcripts that is up-regulated in the
10 the tumor stromal material.
3. The prognostic signature of claim 1, wherein said tumor stromal signature comprises at least a set of one or more gene transcripts up-regulated in Cav-1 deficient tumor/cancer stroma, the up-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental
Tables 1, 3 or combinations thereof.
- 15 4. The prognostic signature of claim 1, wherein said tumor stromal signature comprises at least a set of one or more gene transcripts down-regulated in Cav-1 deficient tumor/cancer stroma, the down-regulated gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3 or combinations thereof.
5. The prognostic signature of claim 1, wherein said tumor stromal signature comprises at
20 least a first set of one or more gene transcripts up-regulated in Cav-1 deficient tumor/cancer stroma and a second set of one or more gene transcripts down-regulated in Cav-1 deficient tumor/cancer stroma, wherein the first set of one or more gene transcripts and the second set of one or more gene transcripts are selected from the group consisting of the gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof.
- 25 6. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1-deficient cancer tumor stroma.
7. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1 positive cancer tumor stroma.
8. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived
30 from a breast cancer tumor stroma.

9. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1-deficient breast cancer tumor stroma.

10. The prognostic signature of claim of claim 9, wherein said tumor/cancer stromal material signature comprising a first set of gene transcripts that is up-regulated in the tumor/cancer stromal material.

11. The prognostic signature of claim of claim 9, wherein said tumor/cancer stromal material signature comprising a first set of gene transcripts that is down-regulated in the tumor/cancer stromal material.

12. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1-deficient breast cancer tumor stroma, and wherein the tumor/cancer stromal signature comprises the first set of up-regulated gene transcripts, wherein the first set of up-regulated gene transcripts comprises at least a set of one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3 or combinations thereof.

13. The prognostic signature of claim of claim 6, wherein said tumor/cancer stromal material signature comprises a first set of gene transcripts up-regulated in the tumor/cancer stromal material, wherein the first set of up-regulated gene transcripts comprises at least a set of one or more gene transcripts having gene names and/or gene symbols selected from the group consisting of: LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2, SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLCO2B1, PTPN1, ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GF11, AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165,

MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC, AMZ2, TYROBP, IFNGR2, RIOK2, C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT,
 5 BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.

14. The prognostic signature of claim of claim 9, wherein said tumor/cancer stromal material signature comprising a first set of gene transcripts that is down-regulated in the tumor stromal
 10 material, and wherein the tumor/cancer stromal signature comprises the first set of up-regulated gene transcripts, wherein the first set of up-regulated gene transcripts comprises at least a set of one or more genes having gene names and/or gene symbols selected from the group consisting of: LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23,
 15 CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPU5D4, C21orf7, ZNF609, SAMHD1, NFATC2,
 20 SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLCO2B1, PTPN1, ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GFI1,
 25 AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165, MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC,
 30 AMZ2, TYROBP, IFNGR2, RIOK2, C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.

15. The prognostic signature of claim 1, wherein the tumor stromal material is derived from a Cav-1-deficient breast cancer tumor stroma, and wherein the tumor stromal signature comprises the first set of down-regulated gene transcripts, wherein the first set of down-regulated gene transcripts comprises at least a set of one or more genes having gene names and/or gene symbols selected from the group consisting of: LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2, SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLCO2B1, PTPN1, ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GFI1, AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165, MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC, AMZ2, TYROBP, IFNGR2, RIOK2, C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.

16. The prognostic signature of claim of claim 9, wherein said tumor/cancer stromal material signature comprising a first set of gene transcripts that is up-regulated in the tumor stromal material, and wherein the tumor stromal signature comprises the first set of down-regulated gene transcripts, wherein the first set of down-regulated gene transcripts comprises at least a set of one or more genes having gene names and/or gene symbols selected from the group consisting of: LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D,

- LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2,
- 5 SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLCO2B1, PTPN1, ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GF11,
- 10 AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165, MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC,
- 15 AMZ2, TYROBP, IFNGR2, RIOK2, C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.
- 20 17. The prognostic signature of claim of claim 9, wherein said tumor/cancer stromal material signature comprising a first set of gene transcripts that is down-regulated in the tumor stromal material, and wherein the tumor/cancer stromal signature comprises the first set of down-regulated gene transcripts, wherein the first set of down-regulated gene transcripts comprises at least a set of one or more genes having gene names and/or gene symbols selected from the group
- 25 consisting of: LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2,
- 30 KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2, SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLCO2B1, PTPN1,

ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GF11, AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, 5 DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165, MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC, AMZ2, TYROBP, IFNGR2, RIOK2, C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, 10 BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.

18. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1 positive breast cancer tumor stroma.
- 15 19. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a breast cancer stroma, wherein the breast cancer stroma is in turn derived from a breast cancer of a subtype selected from the group consisting of ER positive (or ER(+)), ER negative (or ER(-)), and HER2 positive (or HER2(+)).
- 20 20. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1-deficient cancer tumor stroma, and wherein the cancer tumor/cancer stromal signature comprises the first set of gene transcripts up-regulated in the Cav-1-deficient tumor stroma.
- 25 21. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1-deficient cancer tumor stroma, and wherein the cancer tumor stromal signature comprises the second set of gene transcripts down-regulated in the Cav-1-deficient tumor stroma.
22. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1-positive cancer tumor stroma, and wherein the cancer tumor stromal signature comprises the first set of gene transcripts up-regulated in the Cav-1-positive tumor stroma.
- 30 23. The prognostic signature of claim 1, wherein the tumor/cancer stromal material is derived from a Cav-1-positive cancer tumor stroma, and wherein the cancer tumor stromal signature comprises the second set of gene transcripts down-regulated in the Cav-1-positive tumor stroma.

24. The prognostic signature of claim 1, wherein the cancer tumor stromal signature comprises at least one or more sets of gene transcripts from the gene transcripts in Supplemental Table 1.

25. The prognostic signature of claim 8, wherein the Cav-1-deficient tumor stromal signature comprises a set of at least one or more genes selected from the genes in Supplemental Table 1.

26. A method of assessing cancer prognosis, wherein the method comprises: (a) determining a genome-wide transcriptional profile of a first stromal material, wherein the first stromal material is derived from a biological sample obtained from a subject afflicted with cancer or suspected of having cancer; (b) comparing the genome-wide transcriptional profile (or a subgenome-transcriptional profile derived therefrom) to a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises a set of at least one or more genes selected from the genes in Supplemental Table 1, whereby an overlap of between the genome-wide transcriptional profile (or a subgenome-transcriptional profile derived therefrom) and the Cav-1-deficient tumor stromal signature indicates a poor prognosis (increased risk of recurrence, decreased overall survival, increased risk of cancer progression).

27. A method of monitoring progression of breast cancer in a subject, the method comprising:

(a) obtaining a first sample from a subject at a first time point and a second sample from said subject at a second time point;

(b) determining a genome-wide transcriptional profile of said first and second samples;

(c) comparing the genome-wide transcriptional profile (or a subgenome transcriptional profile derived therefrom) of said first sample to the genome-wide transcriptional profile (or a subgenome transcriptional profile derived therefrom) of said second sample; and

(d) thereafter, comparing any difference in transcriptional profile between the genome-wide transcriptional profile (or a subgenome transcriptional profile derived therefrom) of said first sample and the genome-wide transcriptional profile (or a subgenome transcriptional profile derived therefrom) of said second sample to a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises a set of at least one or more genes having gene names and/or gene symbols selected from Supplemental Tables 1, 3, 4, or combinations thereof, whereby an overlap of from about 25% to about 75% is indicative of a poor clinical outcome (e.g., recurrence of the cancer in said subject, or decreased overall survival of the cancer

by the subject, or is an indication that the cancer has progressed in said subject, or is an indication that the cancer has metastasized in said subject).

28. A method of stratifying a subject or a group of subjects having a cancer tumor for a clinical trial, comprising:

5 (a) providing a stromal material, wherein the stromal material is derived from a biological sample obtained from the subject or each member of the group of subjects having a cancer tumor;

(b) determining a genome-wide transcriptional profile of the stromal material;

(c) comparing the genome-wide transcriptional profile (or a set of gene transcripts derived therefrom) of said stromal material to a Cav-1-deficient tumor stromal signature, wherein the
10 Cav-1-deficient tumor stromal signature comprises a set of at least one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof; and

(d) stratifying the subject for a clinical trial based on the results of the comparison step (c).

15 29. A method of identifying a set of genes, expression of which is modulated by the status of stromal Cav-1 in a cancer tumor stroma, the method comprising:

(a) subjecting a first stromal material deficient in stromal Caveolin-1 (Cav-1) to a genome-wide transcriptional profiling to generate a first stromal transcriptional profile,

20 wherein the first stromal material is derived from a biological sample obtained from a subject having cancer or suspected of having cancer;

(b) comparing the first stromal transcriptional profile to a second stromal transcriptional profile derived from a genome-wide transcriptional profiling of a second stromal material, wherein said second stromal material is Cav-1-positive (+) (or Cav-1-(+));

25 whereby a difference in gene expression patterns between the first stromal transcriptional profile and the second stromal transcriptional profile is indicative of a set of one or more genes that is differentially expressed in the stromal Cav-1-deficient tumor relative to the stromal Cav-1 positive (+) tumor.

30. A method of stratifying a subject or a group of subjects having a cancer tumor for a clinical trial, comprising:

(a) providing a biological sample, wherein the biological sample is obtained from the subject or each member of the group of subjects having a cancer tumor;

5 (b) determining a genome-wide transcriptional profile of the biological sample;

(c) comparing the genome-wide transcriptional profile (or a set of gene transcripts derived therefrom) of said biological sample to a Cav-1-deficient tumor stromal signature, wherein the Cav-1-deficient tumor stromal signature comprises a set of at least one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof; and

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(d) stratifying the subject for a clinical trial based on the results of the comparison step (c).

31. The prognostic signature of claim 12, wherein the at least a set of one or more gene transcripts having gene names and/or gene symbols listed in Supplemental Tables 1, 3, or combinations thereof is selected from the group consisting of LOC100293390, RNF217, PGBD2, LACTB, TRIT1, RNF217, LOC654433, DFFA, DNAJC5, ZNF365, ZNF365, MDN1, ERG, CTSB, SGSM3, MYL5, HLA-Z, IKZF1, C15orf23, CD84, C21orf7, VPS26B, SUFU, MSH6, S1PR3, FCGR2B, BCL2L11, RFC5, RAB3D, LOC100128943, PSMB9, GALNT11, APOC2, ISM2, PMS2CL, RDBP, GSPT2, NOD2, USP6NL, TAF13, H2AFX, CD53, CYP3A5, HLA-Z, DCAF8, CTTNBP2NL, ISM2, KCTD20, HMMR, RYR1, METTL3, BCAT1, GSPT1, MGC27345, PGPEP1, TFEB, POLG2, RBM33, LOC80054, FABP3, GCA, FANCC, RPUSD4, C21orf7, ZNF609, SAMHD1, NFATC2, SERPINB8, CYP4F11, LOC728613, SNRK, LOC80054, SLC8A1, VMO1, IL28RA, LOC100288109, APITD1, TRIP6, TMEM165, TBXAS1, KLHL12, LY86, KLF3, WHSC1, ZBTB46, SNRK, MLL2, KCNJ13, THG1L, CYP4V2, SLC23A2, OGFRL1, SLCO2B1, PTPN1, ALOX5AP, MORC2, ABCD1P4, UCK2, TMED5, FCGR2C, FAM185A, PHF20L1, EPB41L3, LARP4B, DHRSX, PDPK1, APEX2, CTSB, MRPL9, LOC100293165, C1orf104, STX7, GFI1, AP4E1, ARHGAP5, C14orf106, SUDS3, BAT2L1, BCAS3, LMF2, INTS4, FCGR2A, ADAM10, CCZ1, RANBP9, MATR3, SENP5, PPIL2, THNSL1, DNHD1, RBMS2, SYMPK, DNASE1, FCGR2A, KIFC2, TTC17, PDPK1, BCL2L13, MFSD7, ETF1, REEP4, TMEM165, MRPL9, HAUS2, ADAP2, IL1RAP, PARVG, C14orf118, ATXN1, PDE7A, DENND4B, ZNF502, C1orf77, OPA3, TNPO3, KIF1B, RNASE1, ANXA11, FAM84A, C6orf26, CLTC, AMZ2, TYROBP, IFNGR2, RIOK2,

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C17orf63, GPBAR1, ZNF639, TBRG4, SKP2, PHKA2, SERP1, CENPC1, MICALCL, RHOG, PDE4DIP, KIAA1147, UBAP1, C20orf7, SRRT, BTN3A2, DCP2, MIR1302-3, UFM1, PDPR, DNMT1, SMC2, GALT, LOC730235, STX8, GNB1, LOC283267, WDR1, BACH1, AGFG1, PIAS1, SNX6, ROCK1, EIF2AK1, UBXN11, APAF1, THNSL1, and combinations thereof.

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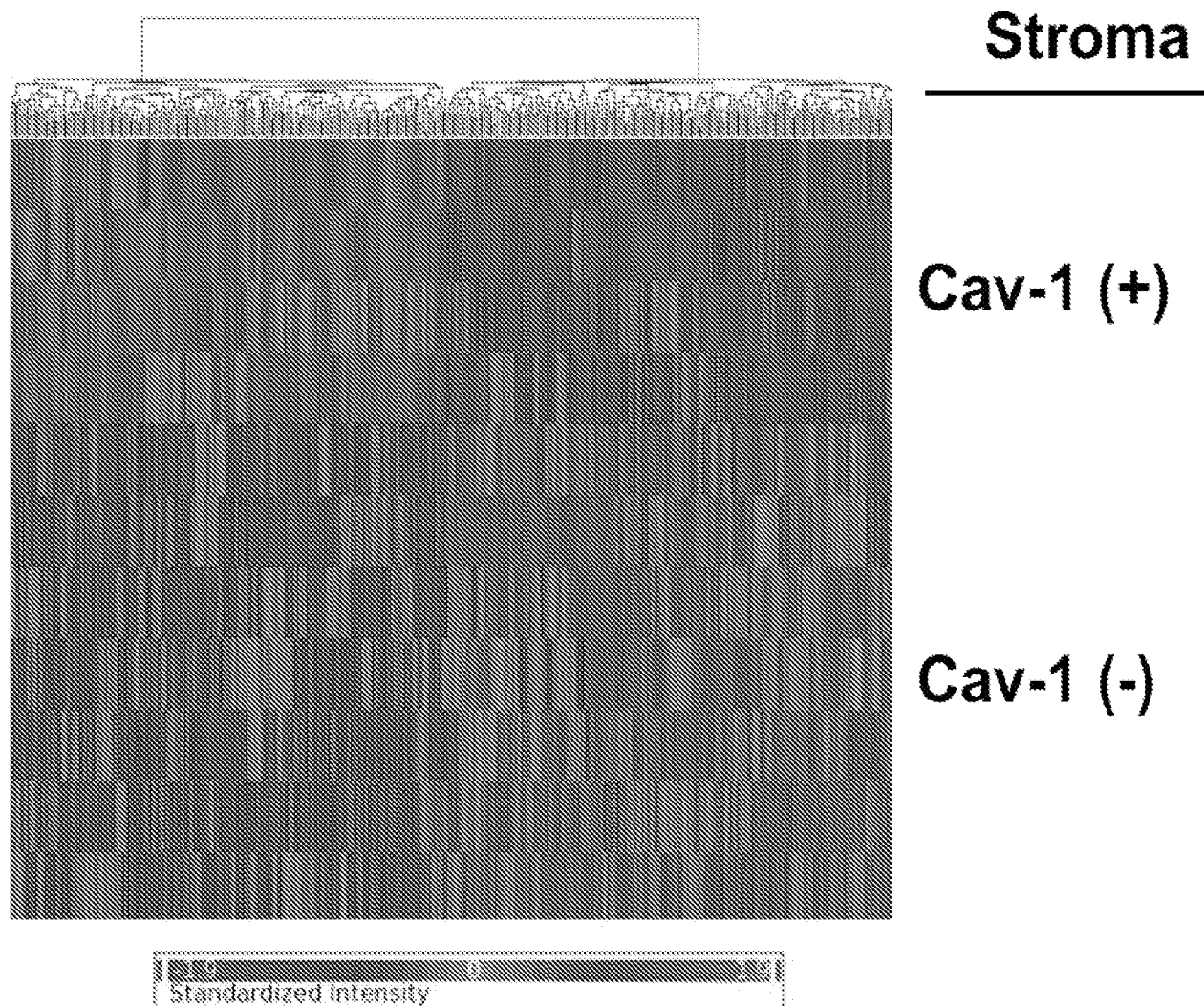
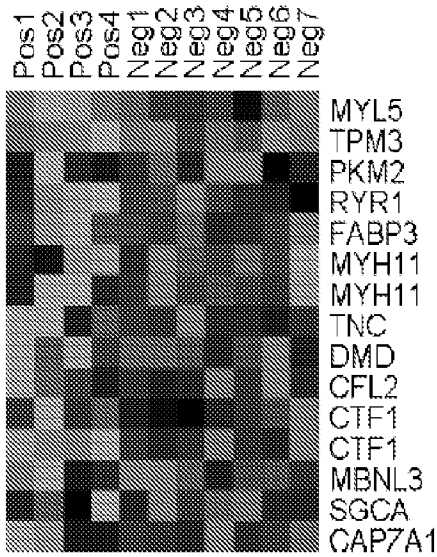
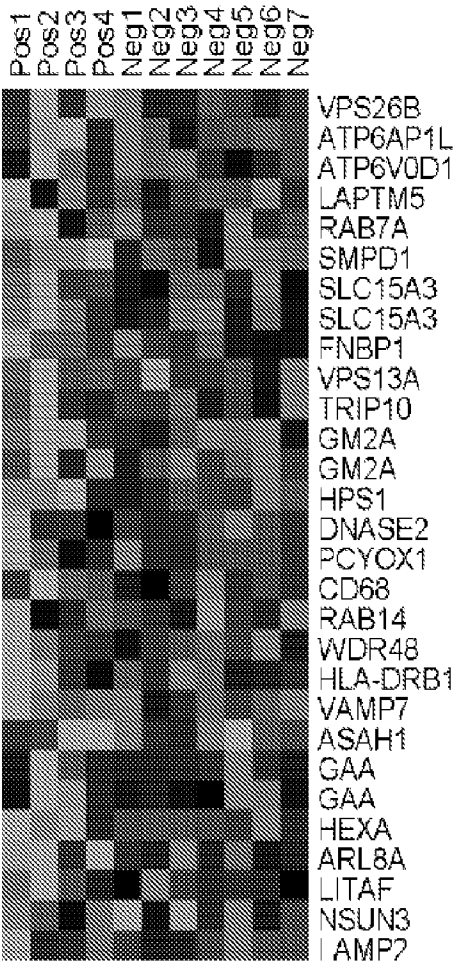


Figure 1: Heatmap illustrating stratification of human breast cancer patients into two transcriptionally distinct patient populations based on their stromal Cav-1 status.

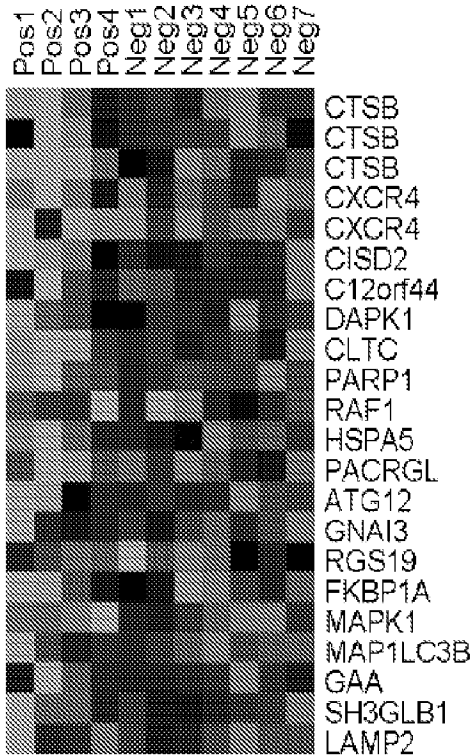
Myo-fibroblast/Muscle



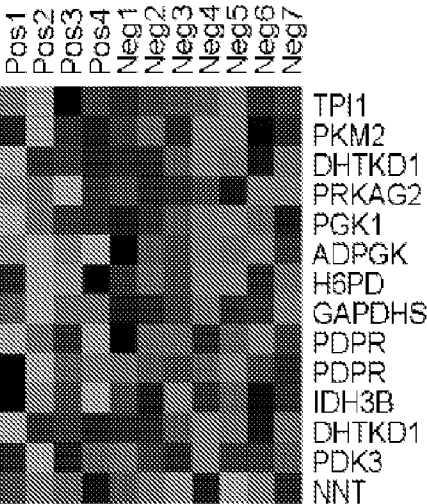
Lysosome Associated



Autophagy Associated



Glycolysis and Pyruvate Metabolism



Lysosomal Proteases

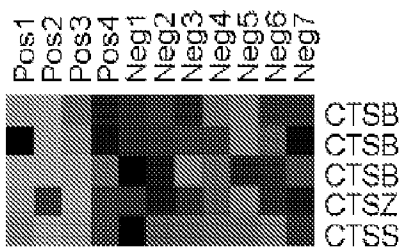
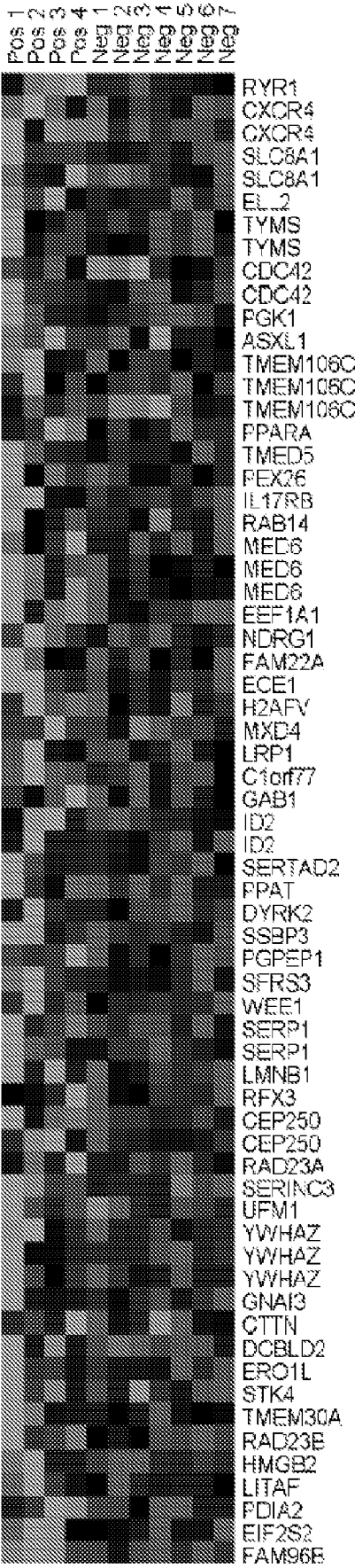


Figure 2: Heatmaps of gene transcripts associated with myofibroblast differentiation, autophagy, lysosomal degradation, and glycolysis

Response to Hypoxia

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Mitochondria Associated

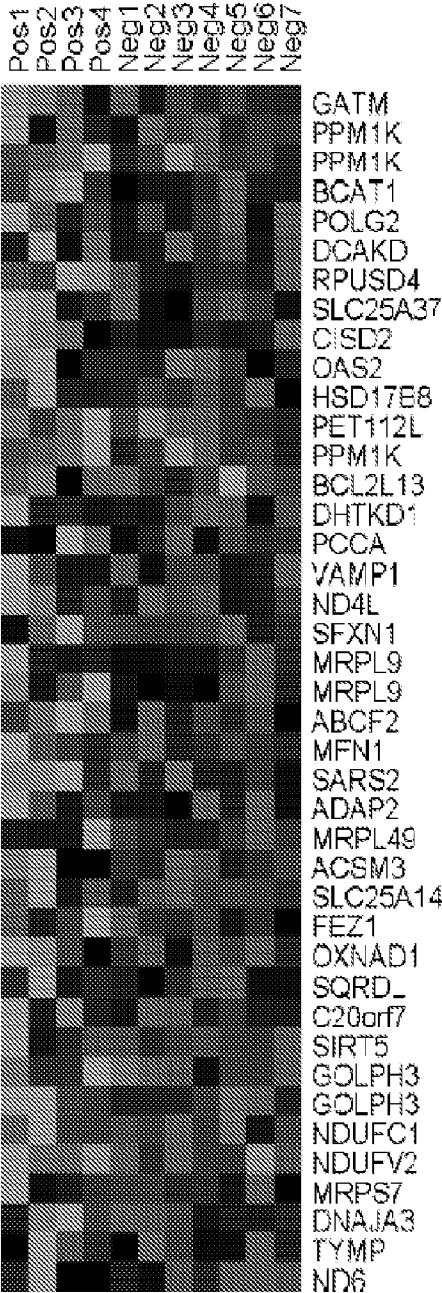
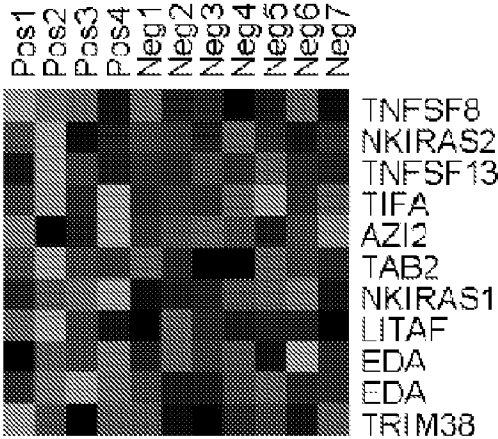
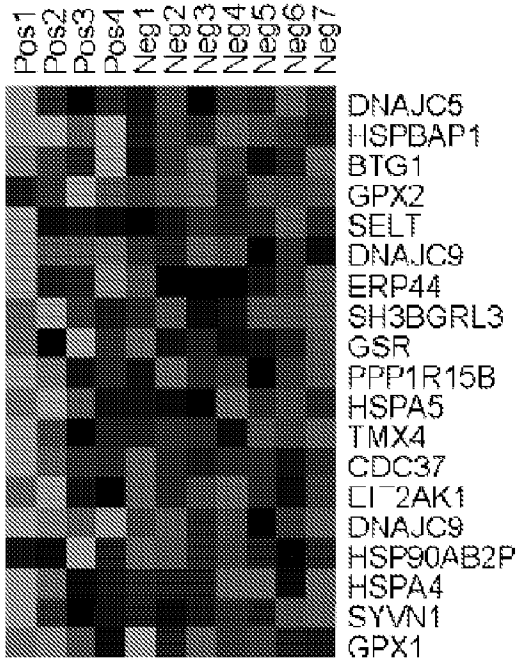


Figure 3: Heatmaps of gene transcripts associated with response to hypoxia and mitochondria

TNF/NFkB Signaling



Redox and Stress Signaling



Immune Response

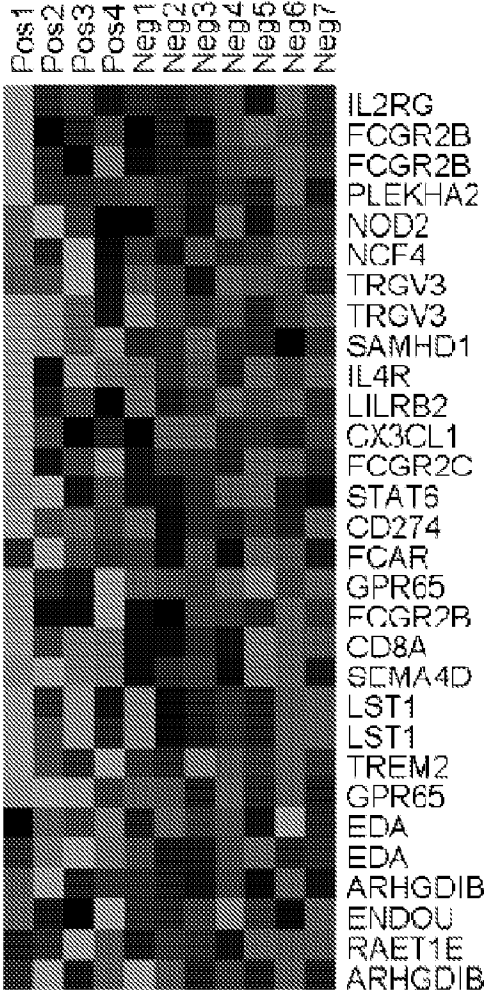


Figure 4: Heatmaps of gene transcripts associated with inflammation and redox/stress signaling

DNA Damage and Repair

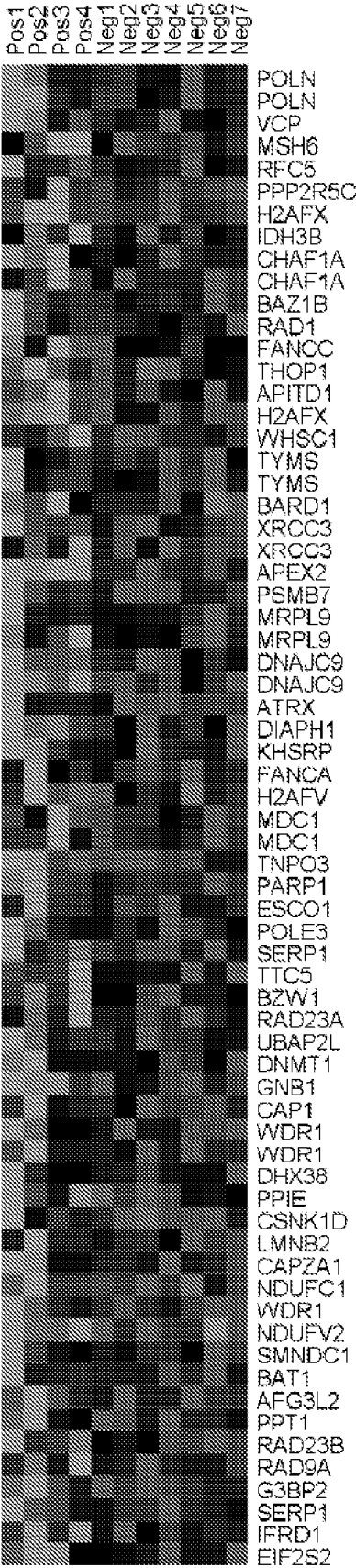
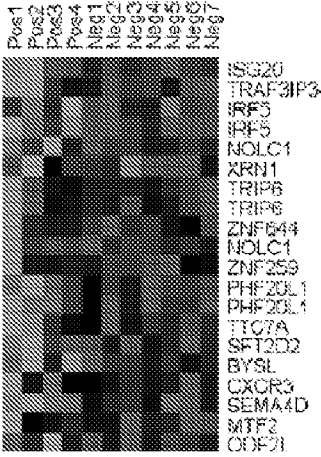
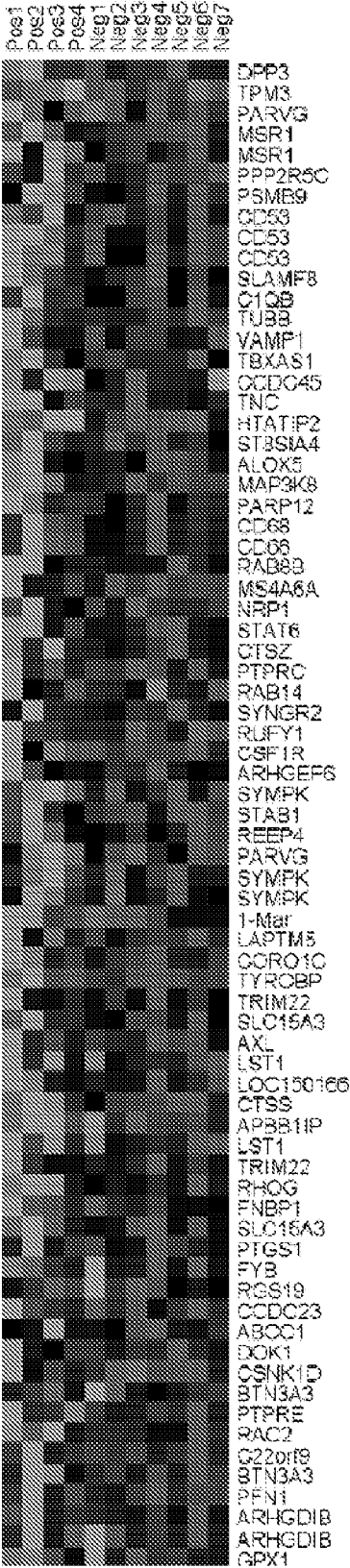


Figure 5: Heatmaps of gene transcripts associated with dna damage and repair

Aging Associated Genes

BRCA1-positive Patients



Key Regulators of Apoptosis

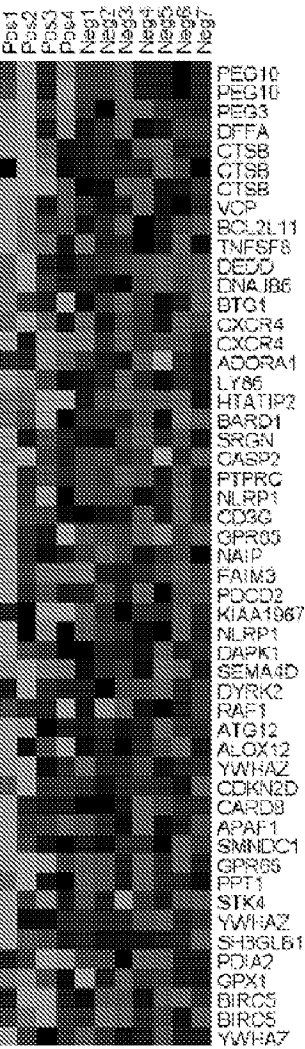


Figure 6: Heatmaps of gene transcripts associated with aging, apoptosis, and brca1-mutation positive breast cancer patients

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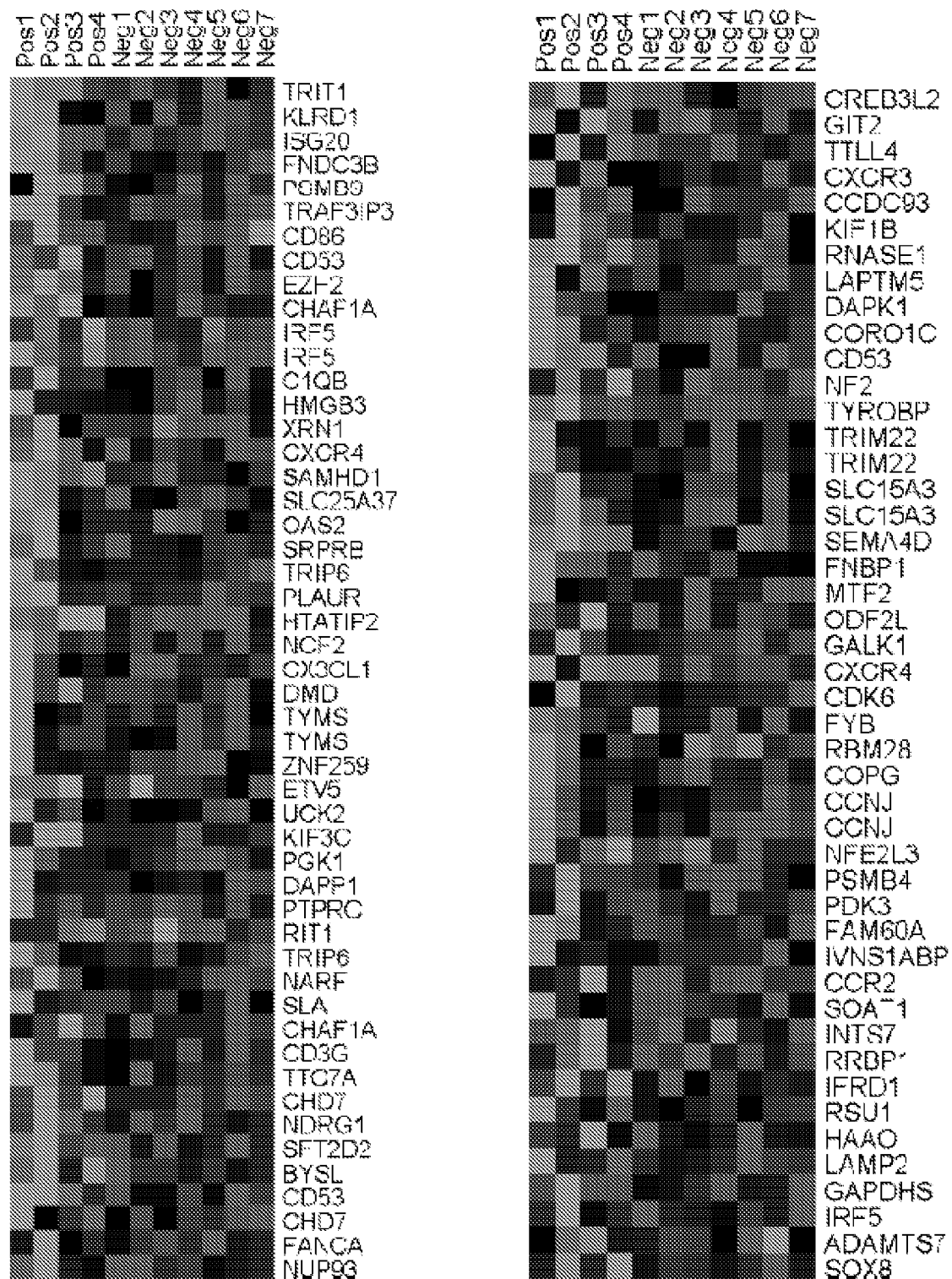


Figure 7: Overlap with Breast Tumors Derived from ER-negative Patients

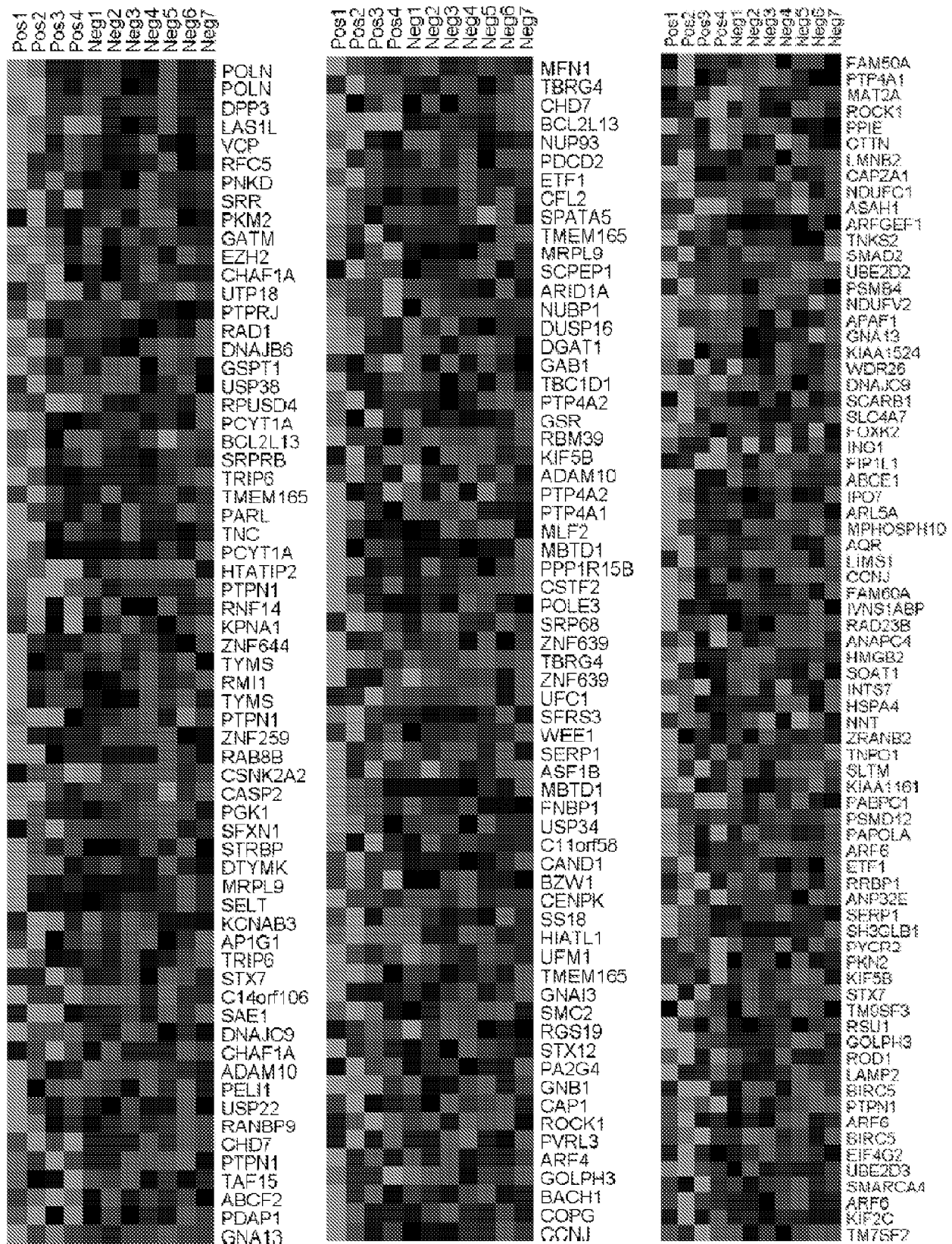


Figure 8: Neural Stem Cell Associated Genes

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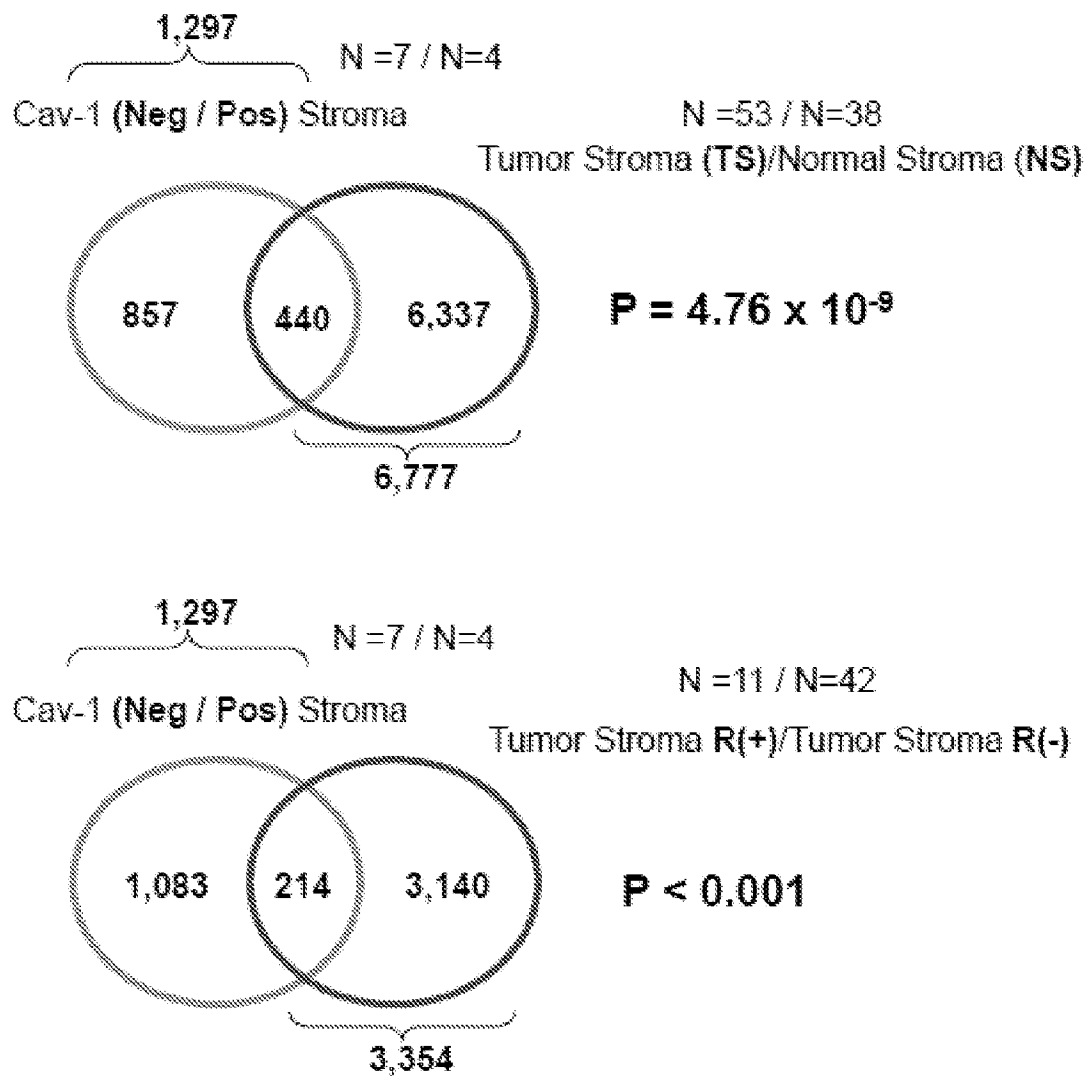
Cav-1 (-/+) vs. Tumor Stroma
Cav-1 (-/+) vs. Recurrence (R)

Figure 9: Venn diagrams for the intersection of the cav-1-deficient stromal gene signature with other breast cancer tumor stromal gene sets

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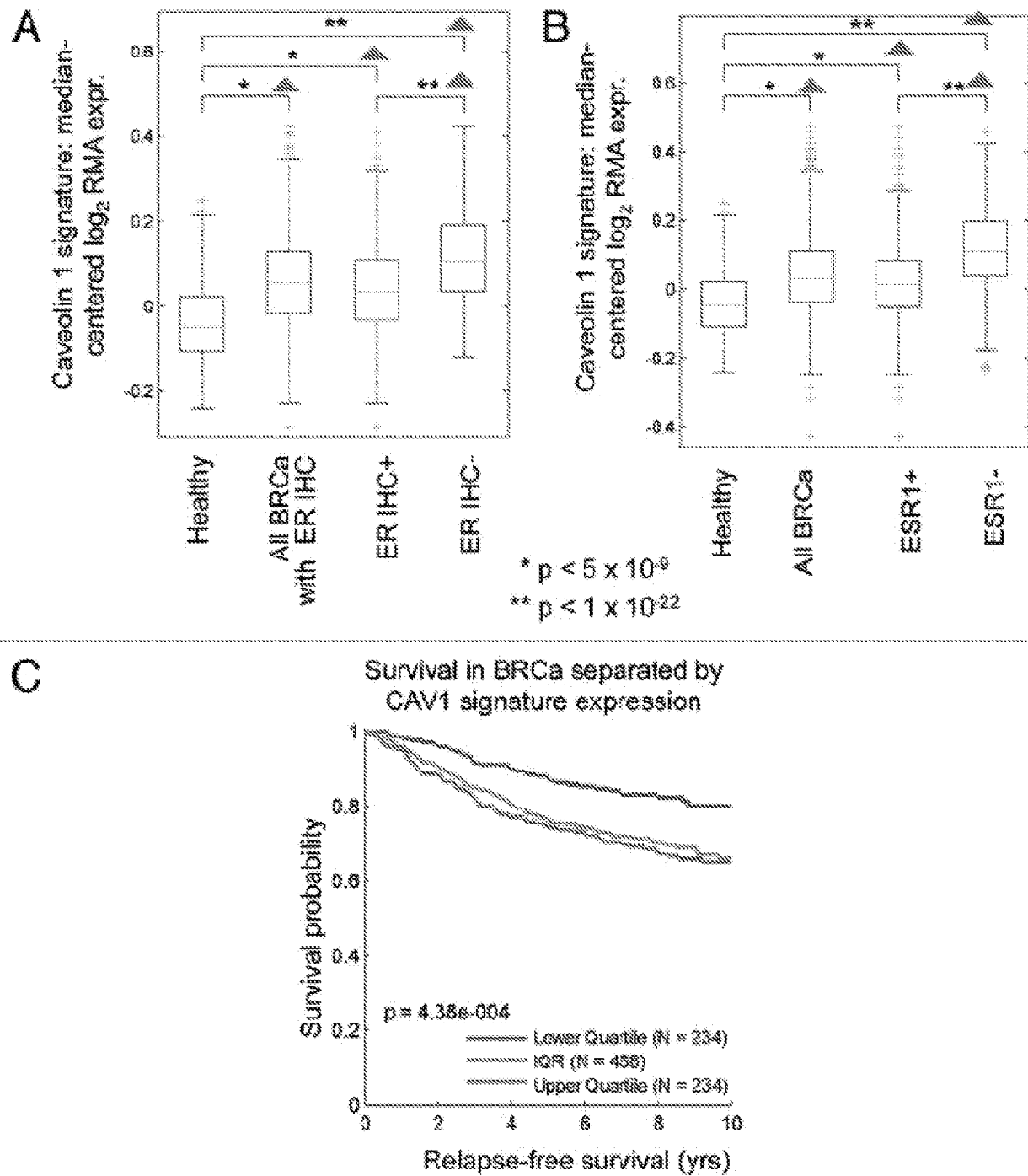


Figure 10: The Cav-1-deficient stromal gene signature is up-regulated in breast cancer and is associated with tumor recurrence

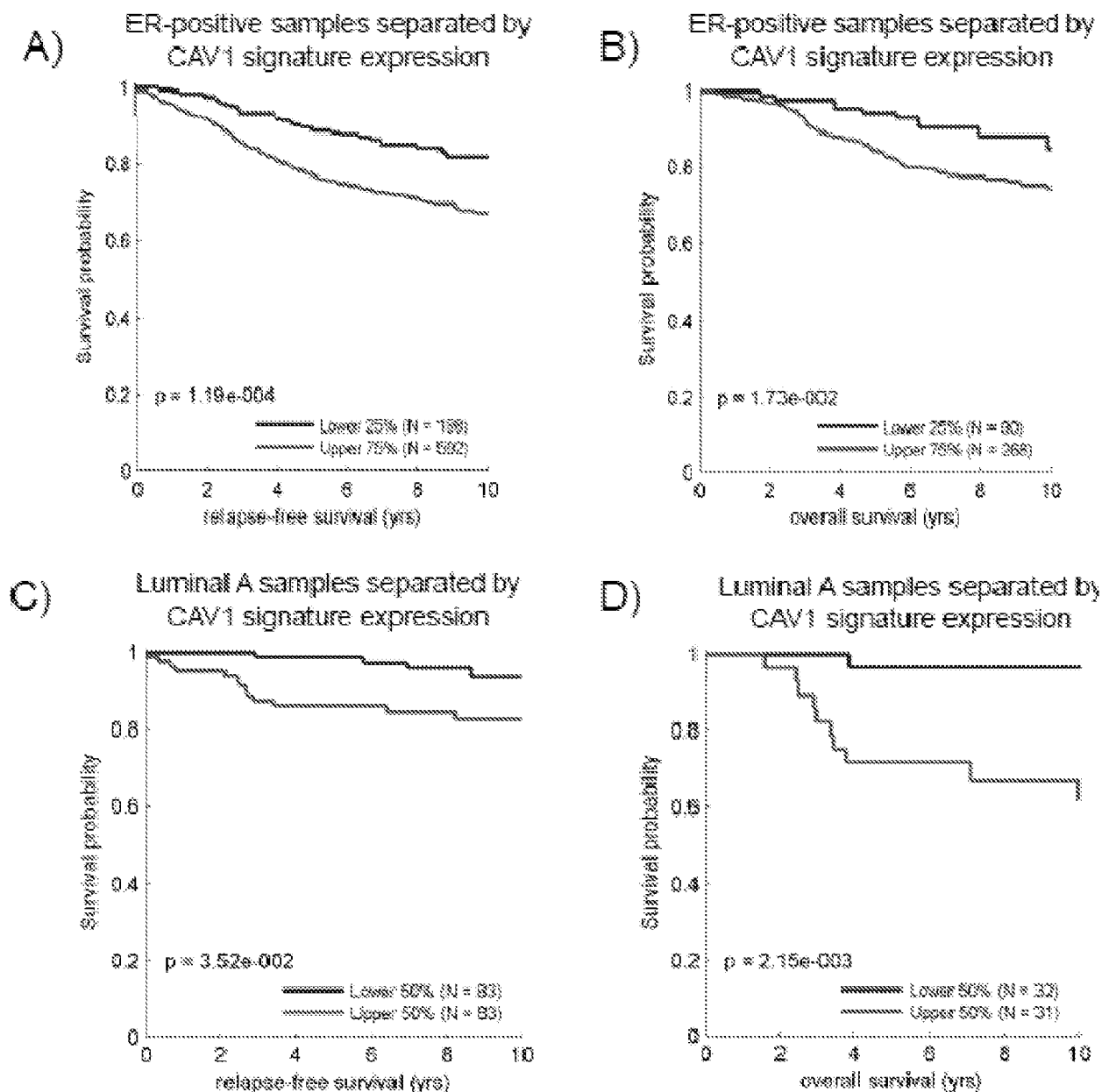


Figure 11: The Cav-1-deficient stromal gene signature is associated with tumor recurrence and poor survival in ER(+) and luminal A breast cancer patients

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A Lethal Tumor Microenvironment

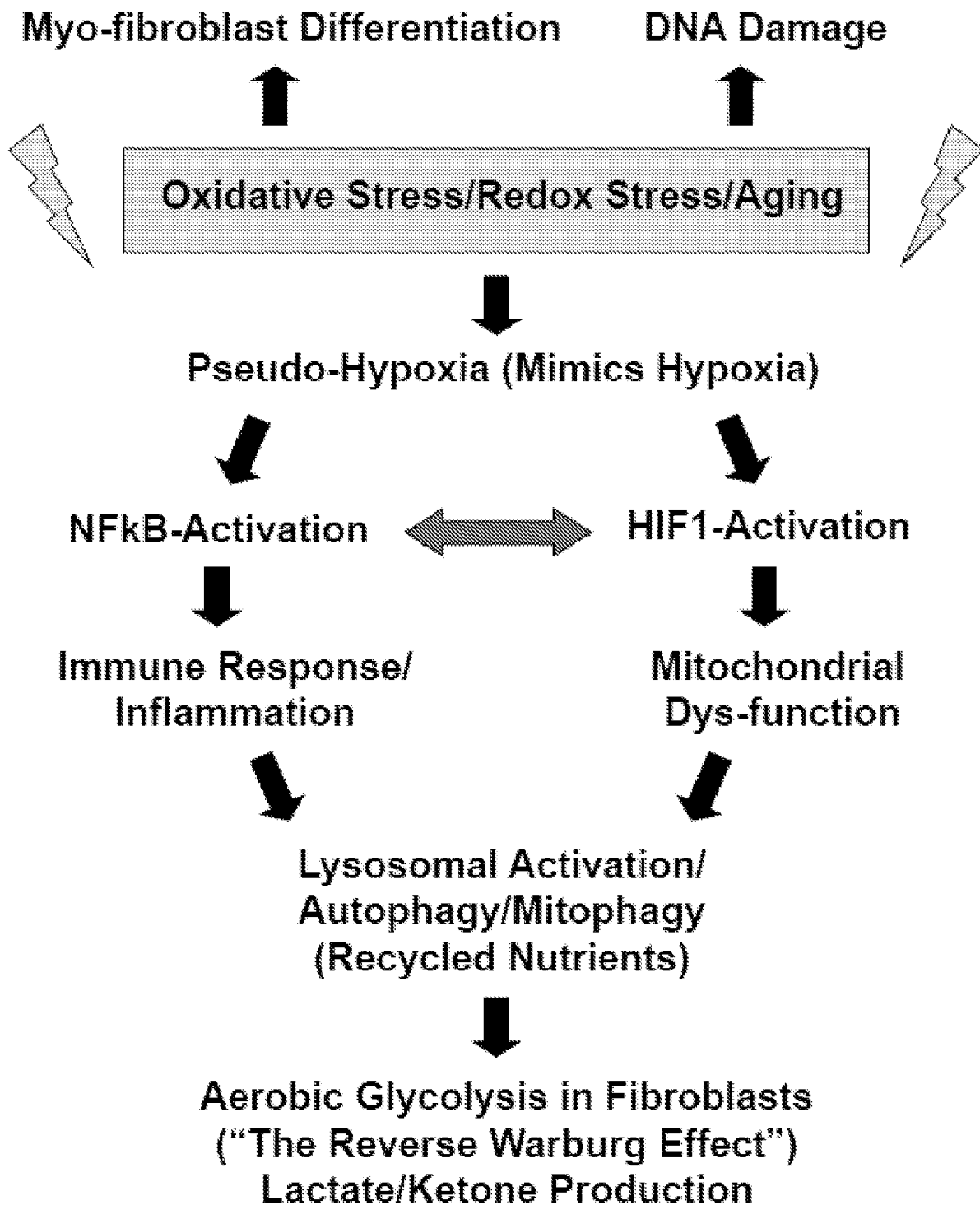


Figure 12: Hierarchy of the cellular processes associated with a Cav-1-deficient tumor microenvironment