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(71) Applicants: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) [FR/FR]; 101 rue de Tolbiac, 75013 Paris (FR). CENTRE HOSPITALIER UNIVERSITAIRE DE QUEBEC [CA/CA]; 11 Côte du Palais, Quebec, G1R 2J6 (CA). CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) [FR/FR]; 3, rue Michel Ange, 75016 Paris (FR). UNIVERSITÉ D'AIX-MARSEILLE [FR/FR]; 58 boulevard Charles Livon, 13007 Marseille 7 (FR). INSTITUT JEAN PAOLI & IRENE CALMETTES [FR/FR]; Centre régional de Lutte contre le Cancer, 232 boulevard de Sainte Marguerite, 13009 Marseille (FR).

(72) Inventors: DUSETTI, Nelson; Inserm U. 1068 CRMC, 163 Avenue de Luminy Case 915, 13288 Marseille Cedex 09 (FR). IOVANNA, Juan Lucio; Inserm U1068 163 Avenue de Luminy, Campus de Luminy, Bat TPR2, 13288 Marseille (FR). CALVO, Ezequiel; Plateforme d'Expression Génique, Centre de recherche du CHU de Québec, 2705 Boulevard Laurier, Québec G1V 4G2, 13288 (CA). GAYET, Odile; CRMC, U1068 163 avenue de Luminy

Case 915, 13288 Marseille Cedex 09 (FR). LONCLE, Céline; Inserm U1068, équipe stresscell, 163 avenue de Luminy, case 915, Bâtiment TPR2 - entrée A, 13288 Marseille Cedex 09 (FR).

(74) Agent: JUPIN, Claude; Cabinet Nony, 3 rue de Penthievre, 75008 Paris (FR).

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(54) Title: METHODS, KITS AND COMPOSITIONS FOR PHENOTYPING PANCREATIC DUCTAL ADENOCARCINOMA BEHAVIOUR BY TRANSCRIPTOMICS

(57) Abstract: An *in vitro* or *ex vivo* method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating PDAC in said individual, comprising the steps of: a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group of PDAC marker genes consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; a2) measuring, in a biological sample from said individual, the expression level of one or more gene selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D; b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).



METHODS, KITS AND COMPOSITIONS FOR PHENOTYPING
PANCREATIC DUCTAL ADENOCARCINOMA BEHAVIOUR BY
TRANSCRIPTOMICS

5 **FIELD OF THE INVENTION**

The invention relates to the field of transcriptomics, for effective treatment and follow-up of individuals having Pancreatic Ductal Adenocarcinoma (PDAC). It also relates to kits, compositions and solid supports, suitable for use in methods for determining the prognosis of an individual having PDAC, or the efficiency of a compound for treating
10 PDAC in said individual.

BACKGROUND OF THE INVENTION

Pancreatic Ductal Adenocarcinoma (PDAC) is one of the most lethal human malignancies and a major health problem. PDAC causes about 10,000 deaths per year in
15 France and 230,000 in the worldwide (Jemal et al.; Cancer statistics, 2003. CA: a cancer journal for clinicians 2003, 53:5-26). The ratio of incidence/death is almost 1 indicating that virtually all patients presenting a PDAC will be killed by their disease. This is due to their short survival median that is about 6 months, the shortest of all tumors, because the treatments are relatively inefficient. Despite considerable research efforts in the past
20 decades, conventional treatment approaches, including surgery, radiation, chemotherapy, or combinations of these, had very limited impact. The prognosis is dismal with only 20% of patients alive one year after diagnosis (Jemal et al, 2003). Given this scenario, the search for new treatments that will counter PDAC progression and thereby increase patient life expectancy and quality of life has been given high priority.

25 Recently phase III clinical trials in unselected PDAC populations have been reported with Bevacizumab (Van Cutsem et al.; Journal of clinican oncology: official journal of the American Society of Cinical Oncology; 2009; 27:2231-7), Erlotinib (Moore et al.; Journal of clinican oncology: official journal of the American Society of Cinical Oncology; 2007; 25:1960-6) and Axitinib (Kindler et al.; The Lancet Oncology; 2011;
30 12:256-62), that are molecularly targeted agents, combined with gemcitabine. All these

trials do not show robust survival benefits, probably because they were assayed on unselected PDAC populations that were highly heterogeneous.

This may be explained by the fact that each PDAC has a combination of several modifications in intracellular pathways that will results in a variable susceptibility to drugs, metastasis development and therefore survival.

Thus, a major impediment to the effective treatment of patients with PDAC (Pancreatic Ductal Adenocarcinoma) is the molecular heterogeneity of the disease, which is reflected in an equally diverse pattern of clinical responses to therapy.

The proposed treatments do not take into account this heterogeneity.

Yet, the drugs received by patients suffering from PDAC are chosen according to their general performance status and the stage of their disease. No study of the tumor can predict its responsiveness to the treatment, nor give a prognosis to the disease progression. For example, the objective response rate was 31.6% for multidrug FOLFIRINOX-treated patients, and only 9.4% for patients treated with gemcitabine, thus showing that about 70% to 90% of patients were not responders respectively (Conroy et al.; The New England Journal of Medicine; 2011; 364:1817-25).

Another explanation for the low-efficiency, or high-resistance, to systemic therapies is that PDAC tumors are hypovascularised and very rich in stroma, representing from 15 to 90% of the tumor mass, which may form a barrier for drug delivery to the transformed cells.

Particularly, future therapeutic agents are expected to be “patients-targeted” in order to specifically affect PDAC cells by targeting their weaknesses, while leaving normal tissues preferably undamaged.

Notably, the availability of improved prognosis or monitoring methods would allow a better selection of patients for appropriate therapeutic treatments, including before and after surgery. Such methods would also allow a better selection of patients which may benefit from surgery, in particular by determining the level of differentiation of the Pancreatic Adenocarcinoma.

Gene profiling of whole PDAC tumors has been largely reported in the prior Art (see Abdollahi et al, 2007; Abiatari et al, 2009; Buchholz et al, 2005a; Buchholz et al, 2005b; Cavard et al, 2009; Crnogorac-Jurcevic et al, 2002; Gress et al, 1997; Ishikawa et al, 2005; Marcotte et al, 2012; Verma et al, 2012; Wang et al, 2013). However, the low

reproducibility of those studies had discouraged the authors to go on exploring this direction.

The reasons for the failure of those approaches may be due to inappropriate tools, tools of insufficient quality, poor quality of the samples, or they may also be inherent to the pathology itself since PDAC tumors can contain from 15 to 90% of stroma tissue associated with variable areas of inflammation and necrosis.

Another approach has been recently reported, laser-capture of transformed epithelial cells is used, followed by their pangenomic expression analysis (**Collisson *et al*; Nature Medicine; 2011; 17:500-3**).

This study showed a significant correlation between the expression profile and the patient outcome, including responsiveness to some treatments. However, according to this prior art technique, analysis was performed only on surgically resected tumors, which correspond to a minority of patients with a relative better prognosis because they were detected earlier. Another deficiency of this prior art technique is that tissue samples were obtained from formalin-fixed paraffin-embedded (FFPE) tissue specimens collected from 1993 to 2006, wherein the RNA contained therein was likely to be altered and thus of highly variable quality.

Thus, and to the inventors knowledge, there are still no available prognostic biomarkers, or combinations of biomarkers for patients with PDAC; nor biomarkers of predictive response, or efficiency, to possible treatments.

Thus, there remains a need for *in vitro* or *ex vivo* methods for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating said individual.

In particular, there remains a need for *in vitro* or *ex vivo* methods for determining the short-term and long-term survival of said individual; or alternatively for determining the level of differentiation of Pancreatic Adenocarcinoma in said individual.

In particular, there also remains a need for *in vitro* or *ex vivo* methods for determining the efficiency of therapeutic treatments of PDAC, which includes therapeutic treatments with active principles such as gemcitabine, oxaliplatin, 5-fluorouracil (5FU), docetaxel, Irinotecan, and/or derivatives thereof, for treating said individual.

There also remains a need for *in vitro* or *ex vivo* methods for screening compounds which are efficient for treating PDAD in an individual, or alternatively for improving the prognosis, the condition or clinical outcome, of an individual having PDAC.

There also remains a need for compositions and/or kits and/or solid supports,
5 which are suitable for use for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating said individual.

SUMMARY OF THE INVENTION

The present invention relates to an *in vitro* or *ex vivo* method for determining
10 the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating PDAC in said individual, comprising the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3;
15 YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a second group consisting of: DUSP5;
20 FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D;

b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

25 The invention further relates to kits and compositions and solid supports, suitable for use in methods for determining the prognosis of an individual having PDAC, or the efficiency of a compound for treating PDAC in said individual.

Thus, the invention also relates to a composition comprising:

- at least one probe allowing the quantitative measurement of the expression levels of one
30 or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7;

KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

The invention also relates to a kit comprising:

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

The invention also relates to a solid support comprising:

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1: RNA expression analysis of PDAC. **(A)** Principal Component Analysis obtained from the Affymetrix data. Each patient is represented in double since data was obtained from two independent experiments. Grey plots are representing long-term survival patients whereas black plots are representing patients with short-term survival. **(B)** Histogram representing the survival time of patients included in this study. **(C)** The Heatmap showing the RNA expression profile of patients with long-term and short-term survival.

Figure 2: Primary cell cultures of PDAC samples. Histogram representing the duplication folds in 24 hours of each cell line.

Figure 3: Chemogram. PDAC-derived cells were treated with increasing concentrations of Gemcitabine, Docetaxel, 5-Fluouracil (5FU), Oxaliplatin and the active metabolite of Irinotecan known as SN-38 and the survival cells were measured after 72 h of treatment. A sensitivity profile was obtained for each drug. The point indicated with a red discontinue line was used to establish the score used in Figure 4.

Figure 4: RNA expression and drug sensitivity. Heatmaps and Dendograms showing the RNA expression profiles of PDAC-derived cells with resistance or sensitivity to the treatments with **(A)** Gemcitabine, **(B)** Oxaliplatin, **(C)** 5-Fluouracil (5FU), **(D)** Docetaxel, and **(E)** SN-38.

DETAILED DESCRIPTION OF THE INVENTION

The invention has for purpose to meet the aforementioned needs.

The inventors have explored the possibility that the variable sensitivity of patients with PDAC to therapeutic treatment that is known in the art is mainly due to the intrinsic molecular characteristics of the cancer cells.

In order to test this hypothesis, the inventors have conceived an assay allowing the availability of human PDAC tumor tissue which is devoid of surrounding stromal cells. More precisely, the inventors have used xenografted PDAC tissue in order to characterize the whole expression profile of the tumor tissue, so that tumors would maintain their

morphological characteristics but lose the stroma cells, the inflammatory cells and cells undergoing necrosis.

Thus, the inventors have developed an efficient strategy in which PDAC samples from patients were obtained by Endoscopic Ultrasound-Guided Fine-Needle Aspiration (EUS-FNA) biopsies or surgery, their cells maintained as a primary culture and tumors as breathing tumors by xenografting in immunosuppressed mice. For these patients a clinical follow up was obtained. On the breathing tumors the RNA expression profile was analysed by using DNA microarray chips.

Using Principal Component Analysis (PCA), the inventors have then determined, for a plurality of tumor samples or primary cell cultures thereof, the RNA expression profile of a collection of PDAC-marker genes.

Principal Component Analysis (PCA) is a statistical method that transforms data to a new coordinate system such that the greatest variance by any projection of the data comes to lie on the first coordinate (called the first principal component), the second greatest variance on the second coordinate, and so on. PCA can be used for dimensionality reduction in a data set by retaining those characteristics of the data set that contribute most to its variance, by keeping lower- order principal components and ignoring higher-order ones.

Thus, Principal components analysis (PCA) is a statistical technique for determining the key variables in a multidimensional data set that explain the differences in the observations, and which can then be used to simplify the analysis and visualization of multidimensional data sets. PCA is known in the Art and is further detailed in Raychaudhuri et al. («Principal Components analysis to summarize microarray experiments: application to sporulation time series; Pac Symp Biocomput. 2000: 455-466).

25

In particular, the inventors have shown that the transcriptome analysis of tumor tissue samples obtained from patients is indicative of the long- or short-time survival of those patients, which also corresponds to the level of differentiation of the PDAC tumor (moderately- or poorly-differentiated respectively).

Without wishing to be bound by any particular theory, the inventors believe that the predictability of this expression analysis is explained by the fact that it was

30

performed with human tumor tissue samples comprising almost exclusively cancerous cells, in contrast to the prior art studies.

Another originality of to the present inventors assay resides in the use of an *in vitro* test with cells from tumors as primary culture for defining the precise sensitivity to the anticancer drugs. This approach has proven to be useful herein, in order to determine the sensitivity of a patient's tumor tissue to a panel of candidate therapeutic molecules because the assay described herein allows performing a large dose-response analysis (from 0.001 to 1000 μ M) towards a plurality of drugs.

Using cultured patient's tumor cells allowed the present inventors to analyze the relative sensitivity of these tumor cells to several anticancer drugs *in vitro* by developing a chemiogram assay, with a plurality of known anticancer drugs, for the purpose of obtaining an individual profile of drug sensitivity. As shown in the examples herein, the response to each drug tested was patient-dependent.

Surprisingly, using this assay, the inventors have shown that the transcriptome analysis of patient's tumor tissue or of patient's tumor cells allows predicting the sensitivity of patients having PDAC to known drugs, including anticancer drugs, as well as to candidate drug compounds. The inventors have also shown that the assay described herein allows predicting the clinical outcome of those patients.

Surprisingly, the inventors have also found that the specific transcriptome analysis performed according to the invention allows predicting the sensitivity of cells to the five anticancer drugs that are the most frequently used for treating patients with PDAC.

It is disclosed herein a collection of sets of genes, the expression level of which, or alternatively the expression levels of specific combinations thereof, is indicative of the clinical outcome, or condition, of patients affected with PDAC, which clinical outcome encompasses a prognosis of progression of PDAC in PDAC-affected patients.

It is also disclosed herein a collection of sets of genes, the expression level of which, or alternatively the expression levels of specific combinations thereof, is indicative of the sensitivity of the PDAC tumor originating from a PDAC-affected individual to a treatment with one or more selected compounds, which encompasses treatment with one or more known drug compounds, including one or more known anti-cancer drugs.

A gene comprised in a set of genes as disclosed herein may also be termed a “PDAC marker gene” for the purpose of the present specification.

As it is shown in the present specification, the assay that has been conceived by the inventors has allowed determining a large number of PDAC-marker genes that are all
5 usable (i) for the purpose of predicting the clinical outcome of patients affected with PDAC and (ii) for predicting the sensitivity of a particular PDAC-affected patient to one or more drugs.

As it is also disclosed herein, subsets of PDAC-marker genes may be determined from the whole collection of gene sets described in the present specification.
10 Although any combination of the PDAC-marker genes disclosed herein may be used for the purpose of performing the methods according to the invention, it is readily understood that, for practical reasons, the use of only sub-sets of the disclosed PDAC-marker genes allows performing the methods according to the invention more rapidly, and also less costly, than when an entire gene set is assayed.

15 Based on the variation of the expression of the sets of PDAC-marker genes described herein, the inventors have notably categorized the said PDAC-marker genes into two distinct groups, according to the sense of variation of their expression level compared to a reference value, namely (i) PDAC-marker genes whose relative expression level is increased in PDAC-affected patients and (ii) PDAC-marker genes whose relative
20 expression level is decreased in PDAC-affected patients.

Then, according to the present invention, the finding of a decreased expression level of one or more PDAC-marker genes comprised in the said first group or subset of PDAC-marker genes in a sample originating from a PDAC-affected individual is indicative of a good clinical outcome of the said PDAC-affected individual.

25 Alternatively, the finding of a decreased expression level of one or more PDAC-marker genes comprised in the said first group or subset of PDAC-marker genes in a sample originating from a PDAC-affected individual treated with one given compound may be indicative of a therapeutic activity of the said given compound for the said PDAC-affected individual.

30 Then, according to the present invention, the finding of an increased expression level of one or more PDAC-marker genes comprised in the said second group or subset of

PDAC-marker genes in a sample originating from a PDAC-affected individual is indicative of a good clinical outcome of the said PDAC-affected individual.

Alternatively, the finding of an increased expression level of one or more PDAC-marker genes comprised in the said second group or subset of PDAC-marker genes
5 in a sample originating from a PDAC-affected individual treated with one given compound is indicative of a therapeutic activity of the said given compound for the said PDAC-affected individual.

In certain embodiments, the combination of (i) the finding of a decreased expression of one or more PDAC-marker genes comprised in the said first group or subset
10 of PDAC-marker genes and (ii) the finding of an increased expression of one or more PDAC-marker genes comprised in the said second group of PDAC-marker genes, in a sample originating from a PDAC-affected individual is indicative of a good clinical outcome of the said PDAC-affected individual.

Alternatively, the combination of (i) the finding of a decreased expression of
15 one or more PDAC-marker genes comprised in the said first group or subset of PDAC-marker genes and (ii) the finding of an increased expression of one or more PDAC-marker genes comprised in the said second group or subset of PDAC-marker genes, in a sample originating from a PDAC-affected individual treated with one given compound is indicative of a therapeutic activity of the said given compound for the said PDAC-affected
20 individual.

The inventors have determined that an increased predicting value, either relating to the individual clinical outcome or relating to the individual's tumor sensitivity to drugs, may be obtained by measuring the expression level of at least one PDAC-marker gene belonging to each of the first and second group described above, or subsets.

25 In particular the inventors have determined that the prognosis of clinical outcome of an individual having PDAC or the efficiency of one compound for treating PDAC in the said individual is good when:

- (i) the expression level value of one or more PDAC-marker genes selected from the first group of PDAC-marker genes described herein is below a first reference value, and
30 (ii) the expression level value of one or more PDAC-marker genes selected from the second group of PDAC-marker genes described herein is above a second reference value; or alternatively when

- the expression level ratio [expression level value of one or more PDAC-marker genes selected from the said first group / expression level value of one or more PDAC-marker genes selected from the said second group] is below a reference expression level ratio.

5 As used herein, the term “PDAC-marker gene” means a gene for which the expression level is a parameter contributing to indicate (i) the prognosis, condition or clinical outcome, of an individual affected with PDAC or (ii) the sensitivity of the tumor tissue of a PDAC-affected individual to a compound used, or alternatively assayed, for the purpose of a PDAC therapeutic treatment.

10 As used herein, the expression level of a PDAC-marker gene according to the invention encompasses (i) the RNA level which is found in a sample as a consequence of the corresponding gene transcription and (ii) the protein level which is found in a sample as the consequence of the translation of the corresponding RNA.

15 Thus, the inventors have also shown herein that a particular variation of the first group relatively to the second group represents a novel “signature” in PDAC tumors.

It is disclosed herein a collection of sets of genes which have been identified as PDAC-marker genes, in **tables 3 to 8**.

20 For each group, the PDAC-marker genes which have a negative fold-change represent a down-regulated gene. Accordingly, the PDAC-marker genes which have a positive fold-change represent an up-regulated gene.

25 In view of the above, each one of the collections of genes which are recited in tables 3 to 8 is considered, which includes **table 3, 4, 5, 6, 7, 8**, and preferred subsets of genes, which includes **tables 9, 10, 11, 12, 13 and 14**.

30 According to a most general embodiment, one up-regulated PDAC marker gene in one group may also be considered as an up-regulated in another group. Thus, one down-regulated PDAC marker gene in one group may also be considered as down-regulated in another group.

However it does not necessarily flow from the above that one compound identified as efficient for treating PDAC in one individual would necessarily improve the prognosis, or clinical outcome of the said individual. Although such correlation is likely to occur for a vast majority of compounds, it is also known in the Art that the improvement of
5 clinical outcome in an individual having PDAC is also dependent on other factors.

It also does not necessarily flow from the above, that a compound that has been identified as efficient for treating PDAC in one individual is necessarily efficient, or efficient to the same extent, for treating another individual.

It also does not necessarily flow from the above that one PDAC-marker gene
10 which has been identified as being particularly indicative of the efficiency of one compound for treating PDAC in an individual, is also indicative to the same extent of the efficiency of another compound for treating PDAC in the same individual.

In view of the above, the PDAC-marker genes that have been identified herein
15 have been grouped based on their preferred use in **tables 3 to 8**, which includes **tables 9 to 14**.

Thus, each collection of PDAC-marker genes is grouped based on its preferred use as a PDAC-marker gene, which may include:

- 20 (i) determining the prognosis of an individual having PDAC;
(ii) determining the efficiency of a compound for treating PDAC in said individual; wherein said compound is preferably chosen from Irinotecan; oxaliplatin; gemcitabine; docetaxel or 5-fluorouracil.

25 According to this most general embodiment, the invention thus relates to an *in vitro* or *ex vivo* method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating PDAC in said individual, comprising the steps of:

- 30 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-markers chosen from **tables 3 to 8**, which includes **tables 9 to 14**;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group of up-regulated PDAC-markers chosen from **tables 3 to 8**, which includes **tables 9 to 14**;

5 b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

Steps a1) and a2) may be performed at the same time period or at distinct time periods.

10 In the embodiments wherein steps a1) and a2) are performed at distinct time periods, these steps may be performed in a chronological sequence comprising performing step a1) before step a2). Alternatively, these steps may be performed in a chronological sequence comprising performing step a2) before step a1).

In the sense of the invention, the expression "*comprising the steps of*" may encompass "*consisting of the steps of*".

15

The expression level of a PDAC-marker gene is preferably a relative value that is obtained after comparison of the absolute expression level value with a reference expression value.

20 In the sense of the invention, a "*reference value*" or "*reference expression value*" refers to any value measured in one or more comparable control cells, tissue samples and/or individuals, including groups of individuals, which may or may not be disease free, and which in particular may be PDAC disease free. The said reference value may be from the same individual or from another individual who is normal or does not
25 present with the same disease from which the disease or test sample is obtained.

Thus, a "*reference value*" can be an absolute or relative value, a range of values, an average value, a median value, a mean value, a ratio, or a value as compared to a particular control or baseline value. A reference value can be based on an individual sample value, such as, a value obtained from a sample from an individual with PDAC, but
30 at an earlier point in time or prior to treatment, or a value obtained from a sample from a patient diagnosed with PDAC other than the individual being tested, or a "normal" individual, that is an individual not diagnosed with PDAC. The reference value can be

based on a large number of samples, such as from patients diagnosed with PDAC, or normal individuals, or based on a pool of samples including or excluding the sample to be tested

When the method is for determining the prognosis of an individual having
5 Pancreatic Adenocarcinoma (PDAC), the reference value can be determined from one or more control cells, tissue samples and/or individuals, that is/are not diagnosed with PDAC

When the method is for determining the efficiency of a compound for treating an individual having Pancreatic Adenocarcinoma (PDAC), the reference value can be determined from one or more control cells, tissue samples and/or individuals that is/are not
10 diagnosed with PDAC, or alternatively measured from the same individual prior to administration of the said compound.

The man skilled in the Art can readily determine, based on his/her general knowledge, a suitable reference value, including absolute and relative reference values, for each sample and/or group of samples.

15

In particular, a variation of the expression level of one given PDAC-marker gene, or collection of PDAC-marker genes from a reference value, including an absolute or a relative value, can be determined using multivariate statistical analysis.

More particularly, multivariate statistical analysis is selected from the group
20 consisting of principal component analysis, discriminant analysis, principal component analysis with discriminant analysis, partial least squares, partial least squares with discriminant analysis, canonical correlation, kernel principal component analysis, non-linear principal component analysis, factor analysis, multidimensional scaling, and cluster analysis.

25 According to an exemplary embodiment, the multivariate statistical analysis is Principal Component Analysis (PCA).

Principal Component Analysis can be performed using the Partek Genomics Suite®.

As in cluster analysis, a PCA is based on a similarity (or distance) matrix
30 between objects. In gene expression, it is common to use a correlation matrix.

In that case, the first principal component is the direction along which there is the greatest variation in the data. If one has J genes, the first principal component is

described by a vector of “loadings” of length J, consisting of weights to be applied to each gene’s expression; a loading close to 0 implies that a gene does not vary much across arrays. Large negative and large positive loadings imply that a gene shows considerable variation across arrays in the dataset. The second principal component is created so that it is orthogonal to the first principal component. It can be interpreted as the weighted average across the genes that explains the largest amount of variation in the data after controlling for the variation explained by the first principal component. The principles of determination of a reference value and multiivariate statistical analysis of Gene Expression are known in the Art, and further detailed in Parmigiani *et al.* (The Analysis of Gene Expression Data: Methods and Software; Springer).

In particular the prognosis of said individual as determined in step b) is good if said individual has a higher life expectancy than said reference, which includes determining whether said individual has a short-term or long-term life expectancy compared to a reference value.

The efficiency of said compound as determined in step b) is good if the condition of said individual is expected to improve after administration of said compound, or alternatively if the life expectancy of said individual is expected to improve after administration of said compound.

As intended herein, the expression “prognosis” or “prognosis of progression of PDAC” encompasses the prognosis, in a patient wherein the occurrence of PDAC has already been diagnosed, of various events, including:

- (i) the chances of occurrence of metastasis;
- (ii) the chances of occurrence of loco-regional recurrence of cancer, including PDAC; and
- (iii) the chances of occurrence of “short-term” or “long-term” survival following testing with the *in vitro* or *ex vivo* prognosis method according to the invention.

According to one particular embodiment, the invention relates to an *in vitro* or *ex vivo* method as defined above, for determining the short-term and long-term survival of said individual; or alternatively for determining the level of differentiation of Pancreatic Adenocarcinoma in said individual.

In the sense of the invention, “*short-term*” and “*long-term*” survival relate to the life expectancy of one given individual having Pancreatic Adenocarcinoma (PDAC). In particular, a “*short-term survival*” may refer to a life expectancy of one given individual having PDAC which does not exceed 8 months. A “*long-term survival*” may refer to a life expectancy of one given individual having PDAC which exceeds 8 months.

Thus, determining the prognosis of an individual having PDAC also encompasses determining whether said individual has a good prognosis, or clinical outcome, compared to a reference individual having PDAC, of which life expectancy is determinable.

In view of the above, a method for determining the prognosis of an individual having PDAC encompasses methods for determining whether said individual has a short-term or a long-term survival rate.

Advantageously, when the method is used for determining the efficiency of a compound for treating Pancreatic Adenocarcinoma (PDAC) in said individual, it can be used for screening purposes.

Accordingly, the invention also relates to *in vitro* or *ex vivo* methods for screening compounds, including novel compounds, which are efficient for treating PDAC in an individual, or alternatively for improving the prognosis, the condition or clinical outcome, of an individual having PDAC.

In the sense of the invention, “*determining the efficiency of a compound for treating PDAC in said individual*” encompasses determining if the compound is suitable for killing cells, in particular primary cells or xenografts, derived from said PDAC.

Quantification of this efficiency may be further tested *in vitro* by performing a chemiogram on primary cultured derived from the PDAC, as shown in Example 2.

The efficiency of a compound for treating PDAC in said individual may also be indicative of the efficiency of a compound for improving the condition of said individual.

Thus, the efficiency of a compound for treating PDAC in said individual may also be indicative of the efficiency of a compound for improving the prognosis of said individual.

It is also disclosed herein a subset of genes which have been identified as particularly efficient PDAC-marker genes, and which are listed in **tables 9 to 14**.

In particular, it is disclosed herein a first group, or subset, of 28 PDAC-marker gene consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1. The first group of PDAC-marker genes includes the PDAC-marker genes which are preferably down-regulated when the prognosis of one individual having PDAC is good, or alternatively when a given compound is deemed as efficient for treating PDAC in the said individual.

It is also disclosed herein a second group, or subset, of 19 PDAC-marker genes consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D. The second group of PDAC-marker genes includes the PDAC-marker genes which are preferably up-regulated when the prognosis of one individual having PDAC is good, or alternatively when a given compound is deemed as efficient for treating PDAC in the said individual.

According to a particular embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating PDAC in said individual, comprising the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1;

SNORD14E; PRKX; PKIA; RHOTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D;

b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

5

According to some embodiments, the method further includes a step of providing a biological sample from said individual having PDAC.

According to said embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating PDAC in said individual, comprising the steps of:

a0) providing a biological sample from said individual having PDAC;

a1) measuring, in said biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group consisting of:

15 CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1;

a2) measuring, in said biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a second group consisting of:

20 DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D;

b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

As intended herein, a "tumor sample" or "tumor tissue sample" encompasses (i) a global primary tumor (as a whole), (ii) a tissue sample from the center of the tumor, (iii) a tissue sample from the tissue directly surrounding the tumor which tissue may be more specifically named the "invasive margin" of the tumor, (iv) lymphoid islets in close proximity with the tumor, (v) the lymph nodes located at the closest proximity of the tumor, (vi) a tumor tissue sample collected prior surgery (for follow-up of patients after

30

treatment for example), (vii) a tumor tissue sample collected after surgery, (viii) a tumor tissue sample derived from the head of the pancreas, (viii) a tumor tissue sample derived from the tail of the pancreas, and (ix) a distant metastasis.

According to a preferred embodiment, the biological sample from said
5 individual is a tumour sample derived from a Pancreatic Adenocarcinoma (PDAC), including a tumor sample derived from the head or the tail of the pancreas.

A tumor tissue sample, irrespective of whether it is derived from the tail or the head of the pancreas, the center of the tumor, from the invasive margin of the tumor, or from the closest lymph nodes, encompasses pieces or slices of tissue, or even cell samples,
10 that have been removed from the tumor, including following a surgical tumor resection or following the collection of a tissue sample for biopsy, for further quantification of one or several biological markers, notably through histology or immunohistochemistry methods, through flow cytometry methods and through methods of gene or protein expression analysis, including genomic and proteomic analysis.

15 The tumour sample derived from PDAC can be a sample collected by endoscopic aspiration, including Endoscopic Ultrasound-Guided Fine-Needle Aspiration, or by surgery.

More particularly, the tumour sample is a biological sample selected from the group consisting of a xenograft or a primary culture, including a primary culture of
20 epithelial cells.

In the sense of the invention, “*measuring the expression of at least one gene*” encompasses measuring the expression of at least one nucleic acid encoded by said at least one gene, which includes RNA molecules encoded by said at least one gene. In a non-
25 limitative manner, the product of one gene may comprise RNA molecules including mRNA, tRNA, rRNA, small-interfering RNAs (siRNA), non-coding RNAs and microRNAs, which can be modified or not.

The expression of at least one gene may also encompass, in a more indirect manner, measuring the expression of at least one protein encoded by said at least one gene.

30 Methods for measuring the expression of at least one gene in a biological sample are known in the Art.

In a non-limitative manner, the expression of a protein may be achieved using Western blot, Slot blot, Dot blot, ELISA (Enzyme Linked Immuno-Sorbent Assay), immunofluorescence, electronic or confocal microscopy FRET (fluorescence resonance energy transfer), TR-FRET (time resolved FRET/FRET), FLIM (fluorescence lifetime
5 imaging microscopy), FSPIM (fluorescence spectral imaging microscopy), FRAP (fluorescence recovery after photobleaching, flux cytometry, enzymatic tests.

Preferably, measuring the expression of at least one gene includes measuring the expression of at least one nucleic acid encoded by said at least one gene.

In a non-limitative manner, the expression of a nucleic acid may be achieved
10 using polymerase-chain reaction (PCR), reverse transcriptase polymerase-chain reaction (RT-PCR), Northern Blot, Ribonuclease protection assays, microarrays, in situ hybridation.

In the sense of the invention, a “*probe*” refers to a nucleic acid that is complementary to another nucleic acid, for which the concentration must be assessed in one given sample. Such probe may be in a labelled or unlabelled form, and encompasses
15 both DNA oligonucleotides and RNA oligonucleotides, and mixtures thereof.

Such probes are generally used in combination with other probes, in a manner suitable for amplification using a variety of polymerase chain reaction methods.

According to one exemplary embodiment, the expression of at least one gene in steps a1 and a2) can be achieved by using at least one labelled or unlabelled probe,
20 preferably selected from the group consisting of DNA oligonucleotides and RNA oligonucleotides.

Thus, according to said exemplary embodiment, the expression of at least one gene in steps a1 and a2) can be achieved by using at least one labelled or unlabelled probe that is complementary to the product of at least one gene selected from the first group; and
25 at least one labelled or unlabelled probe that is complementary to the product of at least one gene selected from the second group.

As used herein, amplification probes, or « *primers* », are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene and/or a gene
30 product (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are of at least 7 nucleotides in length, which includes from about 7 to 50 nucleotides in length, which includes 7, 8, 9, 10, 11, 12, 13,

14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50 nucleotides in length, in particular 10 to 30 nucleotides in length.

Amplification probes generally flank a region from about 50 to 200 nucleotides
5 in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

In one preferred embodiment, the expression level of a PDAC marker gene is
10 assessed by preparing mRNA/cDNA (i.e. a transcribed polynucleotide) from cells in a patient tumor tissue sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a marker nucleic acid, or a fragment thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction methods.

15 In a related embodiment, a mixture of nucleic acids obtained from the sample is contacted with a substrate having fixed thereto a probe complementary to or homologous with at least a portion (e.g. at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a biological marker nucleic acid. If polynucleotides complementary to or homologous with are differentially detectable on the substrate (e.g. detectable using
20 different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (e.g. a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of assessing marker expression is used which involves hybridization of one nucleic acid with another (i.e. a probe), it is preferred that the hybridization be
25 performed under stringent hybridization conditions.

In one format, the nucleic acid to be detected, including mRNAs, is immobilized on a solid surface and contacted with a probe, for example by running the isolated nucleic acid on an agarose gel and transferring the nucleic acid from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on
30 a solid surface and the nucleic acid is contacted with the probe(s), for example, in an Affymetrix gene chip array.

Thus, according to one exemplary embodiment, a method of choice for measuring the expression of a nucleic acid is by using microarrays, such as microarrays of the Affymetrix type.

5 In the sense of the invention, “*measuring the expression of at least one gene*” includes measuring the expression of at least two, three, four, five, six, seven, eight, nine, ten, or even more than ten genes, which includes 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or even more than 100 genes, which also includes measuring the expression of all the genes belonging to the first group and all the genes belonging to the second group.

10

Preferred combinations of PDAC marker genes have been further individualized for determining the efficiency of a selection of compounds, and for determining the prognosis of an individual having PDAC, which advantageously can encompass the heterogeneity of PDAC tumors for each individual.

15

According to a **general** embodiment:

- the first group may consist of at least one gene selected from: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; 20 KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- the second group may consist of at least one gene selected from: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

25

Of note, each one of those combinations is considered individually.

References for each preferred combination are further detailed in **tables 9 to 14**, as defined in example 2, and in the sequence listing. Each PDAC-marker gene is grouped based on its preferred use as a biomarker.

30

According to said general embodiment, when the aforementioned methods include a step of measuring the expression of at least one gene by using at least one probe, the said labelled or unlabelled probe is complementary to:

- at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 1-8; SEQ ID NOs 14-16; SEQ ID NOs 20-26; SEQ ID NOs 31-32; SEQ ID NOs 34-35; SEQ ID NOs 38-43 or
 - at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 9-13;
- 5 SEQ ID NOs 17-19; SEQ ID NOs 27-30; SEQ ID NO 33; SEQ ID NOs 36-37; SEQ ID NOs 44-47.

Methods for determining the prognosis of an individual having PDAC

According to some embodiments, the invention relates to an *in vitro* or *ex vivo* method as defined above, for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC).

In particular, the invention relates to an *in vitro* or *ex vivo* method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), comprising the steps of:

15 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-markers chosen from **table 3**, which includes **table 9**;

 a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group of up-regulated PDAC-markers chosen from **table 3**, which includes **table 9**;

20 b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

More particularly, the invention relates to a method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), comprising the steps of:

 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1;

30 a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM;

b) determining the prognosis of said individual from the measurement performed in steps a1) and a2).

According to said embodiment, the invention also relates to a method for
5 determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC),
comprising the steps of:

a0) providing a biological sample from said individual having PDAC;

a1) measuring, in said biological sample from said individual, the expression
level of one or more PDAC-marker genes selected from a first group consisting of:
10 CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1;

a2) measuring, in said biological sample from said individual, the expression
level of one or more PDAC-marker genes selected from a second group consisting of:
DUSP5; FJX1; ITGA10; MT1A; VIM;

b) determining the prognosis of said individual from the measurement
15 performed in steps a1) and a2).

The first group may consist of at least one PDAC-marker gene selected from:
CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1.

The second group may consist of at least one PDAC-marker gene selected
20 from: DUSP5; FJX1; ITGA10; MT1A; VIM.

Methods for determining the efficiency of a compound on PDAC

According to some embodiments, the invention relates in particular to an *in vitro* or *ex vivo* method as defined above, for determining the efficiency of a compound for
25 treating Pancreatic Adenocarcinoma (PDAC) in an individual.

In particular, the invention relates to an *in vitro* or *ex vivo* method for
determining the efficiency of a compound for treating PDAC in an individual, comprising
at least the steps of:

a1) measuring, in a biological sample from said individual, the expression level
30 of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-
markers chosen from **table 4 to 8**;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group of up-regulated PDAC-markers chosen from **table 4 to 8**;

5 b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

According to one particular embodiment, the invention relates to an *in vitro* or *ex vivo* method as defined above, for determining the efficiency of a compound for treating PDAC in an individual, wherein the compound is selected from the group consisting of:
10 gemcitabine; oxaliplatin; 5-fluorouracil (5FU); docetaxel; Irinotecan or SN-38; and/or derivatives thereof and/or combinations thereof.

According to one embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of Irinotecan for treating PDAC in an individual,
15 comprising at least the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-markers chosen from **table 4**, which includes **table 10**;

a2) measuring, in a biological sample from said individual, the expression level
20 of one or more PDAC marker genes selected from a second group of up-regulated PDAC-marker genes chosen from **table 4**, which includes **table 10**;

b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

25 According to one embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of oxaliplatin for treating PDAC in an individual, comprising at least the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-
30 markers chosen from **table 5**, which includes **table 11**;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group of up-regulated PDAC-marker genes chosen from **table 5**, which includes **table 11**;

5 b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

According to one embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of gemcitabine for treating PDAC in an individual, comprising at least the steps of:

10 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-markers chosen from **table 6**, which includes **table 12**;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group of up-regulated PDAC-
15 markers chosen from **table 6**, which includes **table 12**;

b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

According to one embodiment, the invention relates to an *in vitro* or *ex vivo*
20 method for determining the efficiency of docetaxel for treating PDAC in an individual, comprising at least the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-markers chosen from **table 7**, which includes **table 13**;

25 a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group of up-regulated PDAC-markers chosen from **table 7**, which includes **table 13**;

b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

According to one embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of 5-fluorouracil (5FU) for treating PDAC in an individual, comprising at least the steps of:

a1) measuring, in a biological sample from said individual, the expression level
5 of one or more PDAC-marker genes selected from a first group of down-regulated PDAC-markers chosen from **table 8**, which includes **table 14**;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group of up-regulated PDAC-markers chosen from **table 8**, which includes **table 14**;

10 b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

Gemcitabine (IUPAC name: 4-amino-1-(2-deoxy-2,2-difluoro- β -D-erythro-pentofuranosyl)pyrimidin-2(1H)-on) is a nucleoside analogue which has shown effect for
15 the treatment of neoplastic conditions in both *in vitro* and *in vivo* studies. Gemcitabine is activated inside the cell by deoxycytidine kinase to its active form, the triphosphate of Gemcitabine (dFdCTP). Parallel to this Gemcitabine is deactivated by deoxycytidine deaminase to the corresponding uracil derivative (inactive). Gemcitabine is generally sold under its generic name « gemcitabine hydrochloride » and/or its tradename GEMZAR®
20 (Lilly).

Oxaliplatin (IUPAC name : [(1R,2R)-cyclohexane-1,2-diamine](ethanedioato-O,O')platinum(II)) is a cytostatic, platinum-based, antineoplastic agent which is useful in the therapeutic treatment of various types of susceptible cancers and tumors. Oxaliplatin is generally sold under its generic name « oxaliplatin » and/or its tradenames
25 OXALIPLATIN® or ELOXATIN® (Sanofi Aventis).

5-Fluorouracil (5FU) (IUPAC name : 5-Fluoro-1H,3H-pyrimidine-2,4-dione) is a pyrimidine analog used as an antitumour agent or as an intermediate for various antitumour agents, and is generally sold under its generic name « fluorouracil », and/or its tradenames ADRUCIL®, CARAC®, EFUDEX®, and EFUDIX®.

30 Docetaxel (IUPAC name: 1,7 β ,10 β -trihydroxy-9-oxo-5 β ,20-epoxytax-11-ene-2 α ,4,13 α -triyl 4-acetate 2-benzoate 13-{(2R,3S)-3-[(tert-butoxycarbonyl)amino]-2-hydroxy-3-phenylpropanoate}) is an anti-mitotic member of the taxane drug class, which

also includes the chemotherapeutic medication paclitaxel. Docetaxel is generally sold under its generic name « docetaxel » and/or its tradenames DOCECAD® or TAXOTERE® (Sanofi Aventis).

5 Irinotecan (IUPAC name : (S)-4,11-diethyl-3,4,12,14-tetrahydro-4-hydroxy-3,14-dioxo1H-pyrano[3',4':6,7]-indolizino[1,2-b]quinolin-9-yl-[1,4'bipiperidine]-1'-carboxylate) is an antineoplastic enzyme inhibitor generally sold under its generic name « irinotecan hydrochloride » and/or its tradename CAMPTOSAR® (Pfizer). According to an exemplary embodiment, an active metabolite of Irinotecan that is particularly considered by the invention is SN-38, or 7-Ethyl-10-hydroxy-camptothecin. SN-38 is
10 generally formed via hydrolysis of irinotecan by carboxylesterases and metabolized via glucuronidation by UGT1A1.

In the sense of the invention, a “*compound*” is understood as any compound which may have a potential therapeutic effect for treating Pancreatic Adenocarcinoma in said individual, or alternatively for improving or maintaining the prognosis of said
15 individual.

In the sense of the invention, a “*derivative*” of said compound may comprise any active metabolite that is susceptible to be obtained *in vivo* from said compound after its administration, which thus includes any active metabolite of said compound, and/or salt thereof.

20 Of note, the aforementioned compounds and derivatives thereof may be considered either alone or in combination, without departing from the scope of the invention. In particular, any pharmaceutical composition comprising said compounds, either alone or in combination is considered by the invention.

When the aforementioned compounds are considered in combination, they may
25 be administered either individually or sequentially.

In particular, 5-Fluorouracil (5-FU), Irinotecan and oxaliplatin are three compounds used in combination in the FOLFIRINOX chemotherapy regimen for treatment of advanced pancreatic cancer (Conroy et al.; "The role of the FOLFIRINOX regimen for advanced pancreatic cancer". Current Oncology Reports; 2013 15 (2): 182–189).

30 Thus, the following combinations of compounds are particularly considered:

- 5-fluorouracil (5FU); Irinotecan; oxaliplatin;
- 5-fluorouracil (5FU); oxaliplatin;

-5-fluorouracil (5FU); Irinotecan;

and derivatives thereof; each one of those combinations being administered alone or in complement to other compounds, including adjuvants, and more particularly vitamin B derivatives such as folinic acid (leucovorin); and their salts.

5

Other combinations of compounds are also considered, including:

- gemcitabine; docetaxel; 5-fluorouracil (5FU); Irinotecan; oxaliplatin;
- gemcitabine; docetaxel; 5-fluorouracil (5FU); Irinotecan;
- gemcitabine; docetaxel; 5-fluorouracil (5FU); oxaliplatin;
- 10 - gemcitabine; docetaxel; 5-fluorouracil (5FU);
- gemcitabine; docetaxel; Irinotecan; oxaliplatin;
- gemcitabine; docetaxel; Irinotecan;
- gemcitabine; docetaxel; oxaliplatin;
- gemcitabine; docetaxel;
- 15 - docetaxel; 5-fluorouracil (5FU); Irinotecan; oxaliplatin;
- docetaxel; 5-fluorouracil (5FU); Irinotecan;
- docetaxel; 5-fluorouracil (5FU); oxaliplatin;
- docetaxel; 5-fluorouracil (5FU);
- docetaxel; Irinotecan; oxaliplatin;
- 20 - docetaxel; Irinotecan;

and derivatives thereof; each one of those combinations being administered alone or in complement to other compounds, including adjuvants, and more particularly vitamin B derivatives such as folinic acid (leucovorin); and their salts.

- 25 Bevacizumab (Van Cutsem et al.; Journal of clinical oncology: official journal of the American Society of Clinical Oncology; 2009; 27:2231-7), Erlotinib (Moore et al.; Journal of clinical oncology: official journal of the American Society of Clinical Oncology; 2007; 25:1960-6) and Axitinib are also examples of compounds for treating PDAC.

- 30 In a non-limitative manner, examples of compounds which are also considered by the invention are disclosed in US 6384019 B1, WO 2006090029 A1, US 20040138142 A1, US 3971784 A, EP 0222155 A1.

According to one particular embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of Irinotecan and derivatives thereof, including SN-38, for treating PDAC in an individual comprising the steps of:

5 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group consisting of: HSD17B3; YAE1D1; and MIPOL1;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group consisting of: CCNE1; THBS3; and TRAF5;

10 b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

According to one particular embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of oxaliplatin and derivatives thereof, for treating PDAC in an individual, comprising the steps of:

15 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group consisting of: ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7;

20 a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group consisting of: LTA4H; SAMHD1; SNORD14E; PRKX;

b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

25 According to one particular embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of gemcitabine and derivatives thereof, for treating PDAC in an individual, comprising the steps of:

30 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group consisting of: KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group consisting of: PKIA; RHOBTB1; AK128855; CMBL;

5 b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

According to one particular embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of docetaxel and derivatives thereof, for treating PDAC in an individual, comprising the steps of:

10 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group consisting of: DDX26B and WDR78;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group consisting of: SMAD4;

15 b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

According to one particular embodiment, the invention relates to an *in vitro* or *ex vivo* method for determining the efficiency of 5-fluorouracil (5FU) and derivatives thereof, for treating PDAC in an individual, comprising the steps of:

20 a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group consisting of: AGMO and EDN1;

a2) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a second group consisting of: ARRB2 and HIST2H3D;

b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

According to some embodiments, the methods described herein further include
30 a step a0) of providing a biological sample from said individual having PDAC.

Compositions, kits and solid supports

The invention further relates to compositions and/or kits and solid supports which are suitable for use in any method according to the invention.

5 In particular, the invention relates to compositions and/or kits and/or solid supports comprising probes and/or combinations of probes, including pairs of probes, which can be used for measuring the expression of at least one gene according to the invention.

Thus, the compositions and kits and solid supports may comprise at least one probe allowing the quantitative measurement of the expression levels of at least one
10 nucleic acid selected from a first group of down-regulated PDAC-marker genes; and at least one probe allowing the quantitative measurement of the expression levels of at least one nucleic acid selected from a second group of up-regulated PDAC-marker genes.

Most preferably, the compositions, kits and solid supports consist of such probes and/or combinations of probes.

15 Indeed, for practical reasons, the use of only sub-sets of the disclosed PDAC-marker genes allows performing the methods according to the invention more rapidly, and also less costly, than when an entire gene set is assayed.

According to one general embodiment, the compositions and kits and solid supports comprise, or consist of:

- 20 - at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC marker genes selected from said first group of down-regulated PDAC-marker genes chosen from **tables 3 to 8**, which includes **tables 9 to 14**; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC marker genes selected from said second group of up-regulated PDAC-
25 marker genes chosen from **tables 3 to 8**, which includes **tables 9 to 14**.

Thus, the compositions and kits and solid supports may comprise at least one labelled or unlabelled probe that is complementary to the product of at least one gene selected from a first group of down-regulated PDAC-marker genes; and at least one labelled or unlabelled probe that is complementary to the product of at least one
30 selected from a second group of up-regulated PDAC-marker genes.

In particular, the compositions and kits and solid supports comprise, or even consist of:

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC marker genes selected from said first group of down-regulated PDAC-marker genes chosen from **tables 9 to 14**; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC marker genes selected from said second group of up-regulated PDAC-marker genes chosen from **tables 9 to 14**.

In a non-limitative manner, kits may be in the form of combinations of probes, preferably pairs of probes, and combinations of compositions comprising said probes or pairs of probes, including kits for producing microarrays.

The invention further relates to solid supports comprising said probes and combinations of probes, including solid supports which are suitable for use as microarrays.

Probes of the invention can be complementary to, or homologous with, at least a portion of nucleic acid, including 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues, which encompasses at least 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and 50 nucleotide residues, which may be consecutive or not, and preferably which are complementary consecutive nucleotide residues.

Probes of the invention can be of various length, which includes probes having a length of at least (meaning equal or superior to) 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and 50 nucleotide residues.

In certain embodiments, a kit or a solid support or a composition according to the invention comprises one or a combination or a set of pairs of probes, each kind of pair of probes hybridising specifically with one nucleic acid encoded by a gene of the invention.

In one embodiment, said kit or composition or solid support comprises a combination or a set of pair of probes comprising at least two kind of pair of probes, each kind of pair of probes hybridising with at least one nucleic acid encoded by a gene selected from the first group and at least one nucleic acid encoded by a gene product selected from the second group.

Thus, a kit or composition of solid support may comprise 2 to 50 kinds of pair or probes, each kind of pair of probes hybridizing specifically with one nucleic acid encoded by a gene of the invention, which includes 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 5 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 kinds of pairs of probes, each kind of pair of probes hybridizing specifically against one nucleic acid encoded by a gene of the invention.

When the sequences of probes or combinations of probes are chosen in order to hybridise specifically with one nucleic acid encoded by a gene of the invention, it is 10 understood that such hybridisation should be as specific as possible to the said gene. Thus, such probes or combinations of probes should preferably hybridise with a characteric part of the said nucleic acid, which generally excludes the poly-adenylation motif.

According to a **first** particular selection of PDAC-marker genes:

- the first group may consist of one or more PDAC-marker genes selected from: 15 CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; and
- the second group may consist of one or more PDAC-marker genes selected from: DUSP5; FJX1; ITGA10; MT1A; and VIM.

According to said **first** particular selection of PDAC-marker genes, when the aforementioned methods include a step of measuring the expression of at least one PDAC- 20 marker genes by using at least one probe, the said labelled or unlabelled probe being complementary to:

- at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 1-8; or
- at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 9-13.

25 According to a **second** particular selection of PDAC-marker genes:

- the first group may consist of one or more PDAC-marker genes selected from: HSD17B3; YAE1D1; MIPOL1; and
- the second group may consist of one or more PDAC-marker genes selected from: CCNE1; THBS3; and TRAF5.

30 According to said **second** particular selection of PDAC-marker genes, when the aforementioned methods include a step of measuring the expression of at least one

PDAC-marker genes by using at least one probe, the said labelled or unlabelled probe being complementary to:

- at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 14-16; or
- at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 17-19.

5

According to a **third** particular selection of PDAC-marker genes:

- the first group may consist of one or more PDAC-marker genes selected from: ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; and
- the second group may consist of one or more PDAC-marker genes selected from:

10 LTA4H; SAMHD1; SNORD14E; PRKX.

According to said **third** particular selection of PDAC-marker genes, when the aforementioned methods include a step of measuring the expression of at least one PDAC-marker gene by using at least one probe, the said labelled or unlabelled probe being complementary to:

- 15
- at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 20-26; or
 - at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 27-30.

According to a **fourth** particular selection of PDAC-marker genes:

- 20
- the first group may consist of one or more gene selected from: DDX26B and WDR78; and
 - the second group may consist of one or more gene selected from: SMAD4.

According to said **fourth** particular selection of PDAC-marker genes, when the aforementioned methods include a step of measuring the expression of at least one gene by using at least one probe, the said labelled or unlabelled probe being complementary to:

- 25
- at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 31-32; or
 - at least one nucleic acid selected from a second group consisting of SEQ ID NO 33.

According to a **fifth** particular selection of PDAC-marker genes:

- 30
- the first group may consist of one or more gene selected from: AGMO and EDN1; and
 - the second group may consist of one or more gene selected from: ARRB2 and HIST2H3D.

According to said **fifth** particular selection of PDAC-marker genes, when the aforementioned methods include a step of measuring the expression of at least one gene by using at least one probe, the said labelled or unlabelled probe being complementary to:

- at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 34-35; or
- 5 - at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 36-37.

According to a **sixth** particular selection of PDAC-marker genes:

- the first group may consist of one or more PDAC-marker genes selected from: KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; and
- 10 - the second group may consist of one or more PDAC-marker genes selected from: PKIA; RHOBTB1; AK128855; CMBL.

According to said **sixth** particular selection of PDAC-marker genes, when the aforementioned methods include a step of measuring the expression of at least one gene by using at least one probe, the said labelled or unlabelled probe being complementary to:

- 15 - at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 38-43; or
- at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 44-47.

The above mentioned selections may be further categorized in two parts whether they belong to (i) preferred PDAC marker genes for determining the prognosis of
20 an individual having PDAC; and (ii) preferred PDAC marker genes for determining the efficiency of a compound for treating PDAC in said individual.

According to a **seventh** particular selection of PDAC-marker genes:

- the first group may consist of one or more PDAC-marker genes selected from:
25 HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- the second group may consist of one or more PDAC-marker genes selected from:
CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1;
30 AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

According to said **seventh** particular selection of PDAC-marker genes, when the aforementioned methods include a step of measuring the expression of at least one gene by using at least one probe, the said labelled or unlabelled probe being complementary to:

- at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 14-16;
- 5 SEQ ID NOs 20-26; SEQ ID NOs 31-32; SEQ ID NOs 34-35; SEQ ID NOS 38-43 or
- at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 17-19; SEQ ID NOs 27-30; SEQ ID NO 33; SEQ ID NOs 36-37; SEQ ID NOs 44-47.

The invention further relates to a composition comprising:

- 10 - at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO;
- 15 and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

20

The invention further relates to a kit comprising:

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1;
- 25 MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1;
- 30 ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

The invention further relates to a solid support comprising:

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; 5 MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1; 10 ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

The invention further relates to a composition, a kit, or a solid support as defined above, comprising:

- 15 - at least one probe allowing the quantitative measurement of the expression levels of at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 1-8; SEQ ID NOs 14-16; SEQ ID NOs 20-26; SEQ ID NOs 31-32; SEQ ID NOs 34-35; SEQ ID NOs 48-53 and
- at least one probe allowing the quantitative measurement of the expression levels of at 20 least one nucleic acid selected from a second group consisting of: SEQ ID NOs 9-13; SEQ ID NOs 17-19; SEQ ID NOs 27-30; SEQ ID NO 33; SEQ ID NOs 36-37 and SEQ ID NO 44-47.

As already mentioned, the term “*comprising*” encompasses “*consisting of*”.

25

The invention further relates to a composition, a kit, or a solid support as defined above, for use for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating said individual.

30

EXAMPLES**MATERIAL & METHODS**

PDAC samples: Patients included in this project correspond to the Institut Paoli Calmettes clinical trial number 2011-A01439-32 (PaCaOmics project). Consents of informed patients were collected. The tumor tissue used for xenograft development was deemed excess to that required for the patient's diagnosis and standard of care and treatment. All samples were anonymized and obtained in accordance with institutional review boards. Post-surgical anatomopathology reports were provided for specimens from each patient.

Histopathologic evaluation was performed on 5- μ m H&E-stained sections of patient tumors and xenograft and examined under a light microscope. These sections were compared to the original human tumor when available.

Studies on cancer cells, analyzed on whole tumors, introduce a high background in systemic analysis. Therefore, we have optimized the conditions of primary culture for PDAC cells obtained by Endoscopic Ultrasound-Guided Fine-Needle Aspiration (EUS-FNA), a technique systematically employed for diagnosis in our hospitals, and by surgery. Each sample obtained from EUS-FNA was mixed with 100 μ l of Matrigel (BD Biosciences) and injected in the upper right flank in a nude mouse. Each sample derived from surgery resection was fragmented, mixed with 100 μ l of Matrigel and implanted with a trocar (10 Gauge) in the subcutaneous right upper flank of an anesthetized and disinfected mouse. When tumors reached 1 cm³, mice were sacrificed and tumors removed.

The samples which are reported herein are derived from individuals with the following characteristics:

Table 1: Samples characteristics

Models	Age/Sex	Pathology	Stage	PFS	S	A/D
D-IPC	53/F	Resectable invasive pancreatic cancer located on the body. Final histological	pT3N1M0	6	24	A

Models	Age/Sex	Pathology	Stage	PFS	S	A/D
		datas found moderately differentiated ductal adenocarcinoma (4cm) with perinervous/vascular emboli and lymph node invasion. Progression with carcinomatosis and metastasis				
01.001	69/M	Head pancreatic ductal adenocarcinoma with pulmonary metastasis at diagnosis	pT3N1M1	5	7	D
HN-01	43/M	Tail pancreatic adenocarcinoma with liver metastasis at diagnosis	pT3N1M1	3	8	D
HN-03	70/M	Resectable invasive head pancreatic cancer. Locally lung adenocarcinoma 2 years earlier treated by surgery. Final pancreatic histology datas found moderately differentiated ductal adenocarcinoma with lymph node invasion. No metastasis. No progression until censored date	pT3N1M0	-	18	A
J-IPC	60/M	Resectable invasive head pancreatic cancer. Final histology datas found moderately differentiated ductal adenocarcinoma, tumor size 2.5 cm, with incomplete carcinologic surgery (R1 based on vascular invasion). Progression with liver metastasis	pT3N1M0	8	22	A
AD-IPC	82/F	Resectable invasive pancreatic cancer located on the tail. Melanoma disease treated by surgery one year earlier. Final pancreatic histological datas found moderately differentiated adenocarcinoma (3.5 cm) with	pT3N1M0	-	12	A

Models	Age/Sex	Pathology	Stage	PFS	S	A/D
		perinervous/vascular emboli and lymph node invasion. Incomplete carcinologic surgery (R1 based on pancreatic margins). No metastasis. No progression until censored date				
AH-IPC	76/M	Resectable invasive pancreatic cancer located on the head. Final histological datas found moderately to poorly differentiated ductal adenocarcinoma (3 cm) with perinervous/vascular emboli and lymph node invasion. Regional recurrence but no metastasis	pT3N1M0	6	12	A
AO-IPC	64/F	Resectable invasive pancreatic cancer located on the head. Final histological datas found moderately differentiated ductal adenocarcinoma, tumor size 3.5 cm, with perinervous emboli and lymph node invasion. Explosive progression with liver, lung, carcinomatosis metastasis during adjuvant treatment	pT3N1M0	2	3	D
01.030	67/F	Head pancreatic ductal adenocarcinoma with liver, pulmonary and lymph node metastasis at diagnosis. No response to chemotherapy treatment with pulmonary emboli and visceral progression	pT3N1M1	1	3	D
HN-14	70/M	Head pancreatic adenocarcinoma with lung metastasis at diagnosis. Progression lung metastasis during	pT3N1M1	8	10	A

Models	Age/Sex	Pathology	Stage	PFS	S	A/D
		chemotherapy				
C-NOR	64/M	Resectable isthmic pancreatic adenocarcinoma. Final histological datas found good differentiated ductal adenocarcinoma, tumor size 2.5 cm. Liver and bone metastatic progression	pT3N1M0	7	12	D
E-NOR	74/M	Resectable invasive pancreatic cancer located on the tail. Epidermoid lung cancer treated by surgery + chemotherapy one year earlier. Final pancreatic histological datas found good and poorly differentiated ductal adenocarcinoma, tumor size 3 cm, with lymph node invasion. No metastasis. No progression until censored date.	pT3N1M0	-	17	A
H-NOR	70/M	Resectable invasive head pancreatic cancer. Locally lung adenocarcinoma 2 years earlier treated by surgery. Final pancreatic histological datas found moderately differentiated ductal adenocarcinoma with lymph node invasion. No metastasis. No progression until censored date	pT3N1M0	-	18	A
B-TIM	77/M	Resectable invasive pancreatic cancer located on the tail. Final pancreatic histological datas found moderately differentiated ductal adenocarcinoma, tumor size 4 cm, with perinervous emboli and lymph node invasion. Liver metastatic progression	pT3N1M0	6	12	D
L-IPC	60/M	Resectable invasive pancreatic cancer	pT3N1M0	2	5	D

Models	Age/Sex	Pathology	Stage	PFS	S	A/D
		located on the head. Final pancreatic histological datas found poorly differentiated carcinoma, with an anaplastic form, tumor size 3.5 cm, with perinervous emboli and lymph node invasion. Rapid lung and liver metastatic progression during chemotherapy.				
Foie-8b	56/F	Pancreatic adenocarcinoma with liver metastasis at diagnosis. No response to chemotherapy course	pT3N1M1	3	3	D
A-NOR	89/M	Resectable invasive pancreatic cancer located on the tail. Final histological datas found poorly differentiated adenocarcinoma, tumor size 1.8 cm, with perinervous emboli and lymph node invasion. No metastasis. No progression until censored date.	pT2N1M0	-	20	A

PFS = Progression Free Survival (in months)

S= Survival (in months)

A/D= Alive/Dead (respectively)

- 5 **Xenografted tumor processing and cell culture:** Tumors obtained from the mice were split into several small pieces and used for cell culture, histological analyses, re-implantation into mouse and frozen. The fragment designated to cell culture was processed in a biosafety chamber: after a fine mincing, it was treated with collagenase type V and trypsin/EDTA and suspended in DMEM supplemented with 1% w/w
- 10 Penicillin/Streptomycin and 10% Fetal Bovine Serum. After centrifugation, cells were re-suspended in a media adapted from Schreiber et al. (Schreiber et al, 2004). Cells were then cultured in SFDM media at 37°C with 5% CO₂. Amplified cells were stored in N₂. Cells were weaned from antibiotics for at least 48 h before performing tests.

Gene expression microarrays: For RNA preparation samples xenografted tumor were removed from the mouse at passage 2 and immediately drawn in cold guanidinium thiocyanate (4 M) solution, followed by protein denaturation and RNAs extraction according to Chirgwin's protocol (Chirgwin JM, Przybyla AE, MacDonald RJ, Rutter WJ.

- 5 Isolation of biologically active ribonucleic acid from sources enriched in ribonuclease. *Biochemistry*. 1979 Nov 27;18(24):5294-9). Total RNA (1.0 µg) was isolated and reverse transcribed for hybridization to the human oligonucleotide array Human Gene 2.0 (Genechip, Affymetrix) as described previously (Hamidi et al.: Nuclear protein 1 promotes pancreatic cancer development and protects cells from stress by inhibiting apoptosis. The
10 *Journal of clinical investigation* 2012, 122:2092-103).

- Arrays were processed using the Affymetrix GeneChip Fluidic Station 450 (protocol EukGE-WS2v5_450) and scanned using a GeneChip Scanner 3000 G7 (Affymetrix). The GeneChip Operating Software (Affymetrix GCOS v1.4) was used to obtain chip images with quality control performed using the AffyQCReport software. Background subtraction
15 and normalization of probe set intensities were performed using the method of Robust Multiarray Analysis (RMA) (Irizarry et al, 2003). PCA analysis was performed using Genomics Suite software (from Partek, St Louis, MO). Gene set enrichment analysis (GSEA) was performed on the Broad Institute Platform and statistical significance (false discovery rate, FDR) was set at 0.25. Microarray analysis was performed by the CRCHUL
20 (CHUQ) Gene Expression Platform, Quebec, Canada.

- Chemigrams:** Cells were screened for chemiosensitivity to the 5 clinically used drugs in patients with a PDAC: gemcitabine, 5-fluorouracil, oxaliplatin, docetaxel, and irinotecan active metabolite SN38. These cells were treated for 72 h at increasing concentrations from 0 to 1000 µM. Five thousand cells per well in 96-wells plates were plated in SFBM
25 medium. Twenty four hours later the medium was supplemented with increasing concentrations of drugs and incubating by an additional 72 h period. Each drug was done in triplicate and experiments were repeated two or three times. Cell viability was estimated after addition of the PrestoBlue reagent (Life Technologies) by 3 h following the PrestoBlue cell viability reagent protocol provided by the supplier. Cell viability was
30 measured at day 0 and day 3 to calculate the replication rate of the cells.

EXAMPLE 1. Correlation between transcriptome and clinical outcome.

A total of 11 primary tumors obtained from surgery and 6 biopsies from EUS-FNA were implanted subcutaneously into mice and preserved as xenografts by re-implantation. The histopathological and clinical characteristics of the patients are displayed in supplementary Table 1. Histologically, all specimens were pancreatic ductal adenocarcinomas, which were moderately to poorly differentiated. Growth rates to reach a tumor volume of 1 cm³ ranged from 2 to 6 months. Histopathologically comparisons between patient's primary tumors and xenograft were performed. H&E-stained tissue sections showed that xenografts retained the original morphology of the human primary tumor. The relative state of differentiation was also retained upon passaging until at least 6 times (data not shown). As is typical of PDAC, a high degree of stroma density was observed in the primary tumors but was progressively lost in xenografts.

Total RNA was obtained from 17 xenografts and the transcriptome performed by Affymetrix microchips. The first approach to grouping patients by their expression profile was done using a Principal Component Analysis (PCA) analysis. We found that the transcriptome from two patients-derived xenografts, L-IPC and 01.001, highly detached from the main group of patients. We analyzed their clinical data and found that both corresponded to a two particularly short-term survival patients with poorly-differentiated PDAC (Figure 1). We then explored the presence of other short-term survival patients with poorly-differentiated PDAC within our collection and found that 3 additional patients-derived xenografts, named 01.030, AO-IPC and Foie_8b, corresponded to patients with short-survival times of less than 8 months (Figure 1) and that their tumors were also poorly-differentiated (data not shown). More interestingly, we found that their transcriptome resulted relatively close to the L-IPC and 01.001 ones, indicating a relatively similar expression profile in short-term survival patients with poorly-differentiated tumors (data not shown).

We next performed a heatmap analysis to identify all genes differentially expressed between short-term and long-term survival patients. Five hundred and five genes appeared as overexpressed and 439 genes underexpressed in short-term compared to the long-term survivors as showed in Figure 2C and on **table 3 and 9**. Importantly, a Gene Ontology analysis, with a Fold Change of > 1.5 and a False Discovery Rate of > 0.001, on

differential expression showed a significantly gene enrichment in biological process associated with cancer such as cell cycle, mitosis, response to cellular stresses, DNA metabolism, chromosome organization and cellular metabolism. Interestingly, the majority of these genes were overexpressed in short-term survivals with poorly-differentiated
5 PDAC suggesting that these pathways were preferentially activated.

EXAMPLE 2. Correlation between transcriptome and drug resistance in PDAC.

I- Seventeen primary cultures of PDAC cells were obtained from xenografts
10 derived from PDAC patients. Cells were characterized to assess their epithelial origin by immunofluorescence with CK19 antibody, Kras mutation were identified by PCR followed by DNA sequencing and their transformed status was confirmed by subcutaneous injection of 10^7 cells in nude mice. All these primary cell cultures are strongly stained with the anti-CK19 antibody, carry the Kras mutation at position 12 or 61 and produced big tumors in
15 mice within the 8 weeks after injection (data not shown). Fibroblast contamination was estimated by immunofluorescence using the anti-S100A4 antibody. No more than 5% of fibroblast contamination was observed. Cell lines were microscopically analyzed presenting a high degree of heterogeneity between them.

20 To study their sensitivity to chemotherapeutical drugs the cells were submitted to increasing concentrations (from 0.001 to 1000 μ M) of a set of anticancer drugs and their sensitivity measured to obtaining a dose-response curve characterizing each patient.

Using this approach we were able to estimate their relative chemosensitivity. As shown in Figure 3, each patient-derived cell line shows its own chemogram. Whereas
25 L-IPC, H-N14, H-N01, 01.030 and D-IPC are the 5 most sensitive patient derived cells lines to gemcitabine; the J-IPC, 01.030, L-IPC, H-N14 and B-Tim are the most sensitives to SN-38 (the active irinotecan metabolite); L-IPC, E-NOR, H-NOR, Foie_8b and H-NO3 are sensitives to 5FU; Foie_8b, L-IPC, A-NOR, 01.030 and H-NOR are sensitives to oxal-iplatin and L-IPC, HN-14, A-NOR, AH-IPC and J-IPC to docetaxel. Concerning the most
30 chemoresistant cells, we found that the 5 more resistant were Foie_8b, H-NO3, H-NOR, 01.001 and C-NOR to gemcitabine; D-IPC, 01.001, A-DIPC, E-NOR and C-NOR to SN-38; A-DIPC, AO-IPC, C-NOR, AH-IPC and H-N14 for 5FU; AO-IPC, H-N14, AH-IPC,

C-NOR and J-IPC to oxaliplatin and H-NOR, 01-001, 01-030, AO-IPC, D-IPC to docetaxel (Table 1). Altogether, these results suggest that each PDAC-derived primary culture line has a particular profile of response. In other words, sensitivity or resistance to one drug does not necessarily predict sensitivity or resistance to another one in an identical manner.

An interesting point to be noted is that after 72 hours of incubation some drugs were unable to kill all the cells even with very high concentration such as 1000 μ M for gemcitabine, oxaliplatin, docetaxel or 5FU or 100 μ M for SN-38 (Figure 3). For example, 20 to 50% of cells were resistant to 1000 μ M of gemcitabine; 5 to 30% remained alive when treated with 100 μ M of SN-38; 10 to 70% when treated with 1000 μ M 5FU; 0 to 25% for 1000 μ M oxaliplatin. A particular behavior was found when cells were treated with docetaxel, whereas small doses of some drugs as low as 0.001 μ M were able to kill from 90 to 20%, depending of the primary culture, increasing the doses to 3.9 μ M resulted in almost no changes in its effect. However, almost all cells were killed by 62.5 μ M.

These results suggest that there is more than one cellular population within the tumor, each with a different sensitivity, including complete insensitivity, to drugs which is agreement with the intratumoral heterogeneity of PDAC.

Concerning the most resistant cells to the drugs, we found that the 5 more resistant were Foie_8b, H-NO3, H-NOR, 01.001 and C-NOR for gemcitabine; D-IPC, 01.001, A-DIPC, E-NOR and C-NOR for SN38; A-DIPC, AO-IPC, C-NOR, AH-IPC and H-N14 for 5FU; AO-IPC, H-N14, AH-IPC, C-NOR and J-IPC for oxaliplatin and D-IPC, AH-IPC, 01.001, C-NOR and AD-IPC for docetaxel. Altogether, these results suggest that each PDAC-derived cell have a particular profile of response. In other words, sensitivity or resistance for one drug does not necessarily predict sensitivity or resistance for another one in an identical manner

The most sensitive and most resistant cell lines were determined based on the scores obtained for each line and further detailed hereafter in **table 2**:

Table 2: Resistance score by cell line

Score	Gemcitabine	Docetaxel	5-FU	Oxaliplatin	SN-38
1	L-IPC	L-IPC	L-IPC	Foie-8b	J-IPC
2	HN-14	HN-14	E-NOR	L-IPC	01.030
3	HN-01	A-NOR	H-NOR	A-NOR	L-IPC
4	01.030	AH-IPC	Foie-8b	01.030	HN-14
5	D-IPC	J-IPC	HN-03	H-NOR	B-TIM
6	E-NOR	E-NOR	A-NOR	HN-03	H-NOR
7	AO-IPC	HN-01	B-TIM	E-NOR	HN-01
8	J-IPC	AD-IPC	D-IPC	HN-01	HN-03
9	B-TIM	HN-03	J-IPC	01.001	A-NOR
10	A-NOR	B-Tim	HN-01	B-TIM	Foie-8b
11	AH-IPC	Foie-8B	01.001	D-IPC	AH-IPC
12	AD-IPC	C-NOR	01.030	AD-IPC	AO-IPC
13	C-NOR	D-IPC	HN-14	J-IPC	C-NOR
14	01.001	AO-IPC	AH-IPC	C-NOR	E-NOR
15	H-NOR	01-030	C-NOR	AH-IPC	AD-IPC
16	HN-03	01-001	AO-IPC	HN-14	01.001
17	Foie-8b	H-NOR	AD-IPC	AO-IPC	D-IPC

II- To study whether or not there is a **correlation between drug resistance and sensitivity with the transcriptome** we selected the 4 most sensitive and the 4 most resistant cell lines and analyzed a possible relationship with the transcriptome by performing a heatmap analysis.

As described in Figure 4, sets of genes were identified as specifically overexpressed or underexpressed in resistant and in sensitive cells. These modulations in the expression profiles allowed us to identify 671 genes associated with gemcitabine, 1107 with oxaliplatin, 308 with 5FU, 149 with docetaxel and only 46 with SN-38 respectively (see figure 4). Ninety eight genes were common between oxaliplatin and 5FU, which is in agreement with their close mechanism of action. On the contrary, there are a small number of common genes associated with sensitivity and resistance to the other drugs.

Lastly, another important point to be noted is the fact that genes which are the most associated to the sensitivity or to the resistance to the drugs are not common with

genes which are the most associated to short-term or long-term survival, as shown in Figure 4, indicating that both survival and drug sensitivity may relate, at least in part, to different mechanisms.

5 Herebelow (see tables 3 to 8) are listed collections of sets of genes, of which the variation of the expression level is based on the reference value established by PCA analysis, along with its corresponding individual p-values and fold-changes.

Those sets of genes are grouped based on their preferred use as combinations of PDAC marker genes for:

- 10 - determining the prognosis of an individual having PDAC (table 3);
- determining, on a PDAC tumor sample from said individual, the efficiency of SN-38/Irinotecan (table 4); oxaliplatin (table 5); gemcitabine (table 6); docetaxel (table 7) and 5-fluorouracil (table 8).

15 The fold-change column indicates the variation of the expression of the corresponding gene product, compared to a reference value. The reference value is calculated as shown in the Material & Methods section, using Gene set enrichment analysis (GSEA) performed on the Broad Institute Platform and statistical significance (false discovery rate, FDR) was set at 0.25.

20 The gene symbol is indicated (if available), along with a reference number for its corresponding product in the corresponding database (REFSEQ, ENSEMBL, GENBANK, and/or LNCipedia).

Table 3: Short VS Long-term survival

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
AF007194 // GenBank // Homo sapiens mucin (MUC3) mRNA, partial cds. // chr7 // 83 // 77	MUC3A	1,54E-12	-18,8374
AJ001402 // GenBank // Homo sapiens mRNA for MUC5AC protein (tracheal), partial. // chr	MUC5AC	1,90E-08	-10,2058
AJ420564 // GenBank // Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 153400	LOC100422737	5,72E-06	-3,74451
AK022139 // GenBank // Homo sapiens cDNA FLJ12077 fis, clone HEMBB1002453. // chr6 // 9		5,23E-08	-2,05368
AK023317 // GenBank // Homo sapiens cDNA FLJ13255 fis, clone OVARC1000800, moderately s	HSPA9	3,89E-07	2,10736
AK056431 // GenBank // Homo sapiens cDNA	FLG-AS1	2,19E-06	2,1437

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
FLJ31869 fis, clone NT2RP7002151. // chr1 // 1			
AK092802 // GenBank // Homo sapiens cDNA FLJ35483 fis, clone SMINT2008277. // chr11 //		3,62E-09	-3,34868
AK094559 // GenBank // Homo sapiens cDNA FLJ37240 fis, clone BRAMY2003926. // chr8 // 1		4,80E-06	2,58938
AK095353 // GenBank // Homo sapiens cDNA FLJ38034 fis, clone CTONG2013393. // chrX // 9		8,77E-06	1,5907
AK095849 // GenBank // Homo sapiens cDNA FLJ38530 fis, clone HCHON2001039. // chr11 //	SNHG1	6,87E-06	1,85694
AK097323 // GenBank // Homo sapiens cDNA FLJ40004 fis, clone STOMA2004194. // chr14 //		3,79E-06	1,72889
AK097428 // GenBank // Homo sapiens cDNA FLJ40109 fis, clone TESTI2007685. // chr7 // 1	LOC286009	2,58E-09	1,87085
AK123096 // GenBank // Homo sapiens cDNA FLJ41101 fis, clone BLADE2004670. // chr11 //		4,31E-07	-10,5573
AK123177 // GenBank // Homo sapiens cDNA FLJ41182 fis, clone BRACE2043349. // chr1 // 1	C1orf132	3,30E-07	-1,62266
AK125494 // GenBank // Homo sapiens cDNA FLJ43505 fis, clone PEBLM2007140. // chr1 // 1	FAM177B	2,27E-07	-7,5829
AK125871 // GenBank // Homo sapiens cDNA FLJ43883 fis, clone TESTI4009123. // chr2 // 1		1,66E-09	-1,85794
AK128707 // GenBank // Homo sapiens cDNA FLJ46874 fis, clone UTERU3014274. // chr12 //	LOC100129940	1,19E-07	1,65035
AK303587 // GenBank // Homo sapiens cDNA FLJ52041 complete cds. // chr14 // 100 // 100	TRDJ2	5,92E-06	-2,09804
AK307179 // GenBank HTC // Homo sapiens cDNA, FLJ97127. // chr12 // 80 // 36 // 4 // 5	C12orf36	5,80E-06	-3,55218
BC035345 // GenBank // Homo sapiens, clone IM- AGE:5180681, mRNA. // chr14 // 100 // 100		3,87E-06	-1,72487
BC040915 // GenBank // Homo sapiens cDNA clone IMAGE:5745842, partial cds. // chrX // 1		1,88E-05	-2,25504
BC044941 // GenBank HTC // Homo sapiens similar to Apoptosis-related protein 2 (APR-2),	FAM215B	8,26E-07	-1,93435
BC045769 // GenBank // Homo sapiens hypothetical protein LOC339192, mRNA (cDNA clone IM	LOC339192	1,11E-06	2,31983
BC047238 // GenBank // Homo sapiens chromosome 1 open reading frame 51, mRNA (cDNA clon	C1orf51	2,01E-08	2,32978
BC047404 // GenBank // Homo sapiens cDNA clone IMAGE:5300528. // chr10 // 100 // 100 //	LOC100507212	5,12E-09	1,85708
BC052236 // GenBank // Homo sapiens chromosome 19 open reading frame 21, mRNA (cDNA clo	C19orf21	8,34E-07	-2,61612
DQ080207 // GenBank // Homo sapiens MIG7 (MIG7) mRNA, complete cds. // chr1 // 92 // 93	MIG7	1,58E-06	3,47111
DQ080207 // GenBank // Homo sapiens MIG7 (MIG7) mRNA, complete cds. // chr1 // 95 // 83	MIG7	1,82E-05	2,72111

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000014914 // ENSEMBL // cdna:known chromosome:GRCh37:12:13043716:13070871:1 gene:	GPRC5A	3,40E-06	-1,69405
ENST000000166345 // ENSEMBL // cdna:known chromosome:GRCh37:5:892758:918235:1 gene:ENSG0	TRIP13	5,95E-06	2,03887
ENST000000167586 // ENSEMBL // cdna:known chromosome:GRCh37:17:39738531:39743173:-1 gene	KRT14	2,86E-05	4,24169
ENST000000215531 // ENSEMBL // cdna:known chromosome:GRCh37:19:3474405:3480540:-1 gene:E	C19orf77	1,93E-06	-5,26903
ENST000000216445 // ENSEMBL // cdna:known chromosome:GRCh37:14:57936019:57960570:-1 gene	C14orf105	1,37E-10	-11,4255
ENST000000228438 // ENSEMBL // cdna:known chromosome:GRCh37:12:10005583:10022735:-1 gene	CLEC2B	3,48E-06	3,20926
ENST000000228705 // ENSEMBL // cdna:known chromosome:GRCh37:12:63038367:63328817:-1 gene	PPM1H	6,26E-06	-2,42928
ENST000000230990 // ENSEMBL // cdna:known chromosome:GRCh37:5:139712428:139726216:-1 gen	HBEGF	4,05E-06	2,63736
ENST000000231368 // ENSEMBL // cdna:known chromosome:GRCh37:5:96271168:96373219:1 gene:E	LNPEP	5,83E-08	1,62846
ENST000000231498 // ENSEMBL // cdna:known chromosome:GRCh37:5:37288239:37371283:-1 gene:	NUP155	5,35E-08	1,81071
ENST000000231524 // ENSEMBL // cdna:known chromosome:GRCh37:5:64885507:64920473:-1 gene:	TRIM23	3,50E-08	1,56997
ENST000000237380 // ENSEMBL // cdna:known chromosome:GRCh37:4:17616254:17627254:1 gene:E	MED28	1,53E-05	1,53548
ENST000000238379 // ENSEMBL // cdna:known chromosome:GRCh37:9:116135699:116138455:-1 gen	HDHD3	2,87E-08	-2,54813
ENST000000243706 // ENSEMBL // cdna:known chromosome:GRCh37:4:2230076:2243860:-1 gene:EN	HAUS3	6,82E-07	1,59818
ENST000000245185 // ENSEMBL // cdna:known chromosome:GRCh37:16:56642111:56643409:1 gene:	MT2A	1,36E-07	3,33636
ENST000000252011 // ENSEMBL // cdna:known chromosome:GRCh37:20:37590978:37668366:1 gene:	DHX35	1,86E-06	1,51979

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000257555 // ENSEMBL // cdna:known chromosome:GRCh37:12:121416346:121442296:1 gen	HNF1A	3,55E-07	-1,58254
ENST00000258436 // ENSEMBL // cdna:known chromosome:GRCh37:2:103332299:103353313:-1 gen	MFSD9	1,97E-06	-1,65392
ENST00000259056 // ENSEMBL // cdna:known chromosome:GRCh37:2:158114110:158170723:1 gene	GALNT5	1,56E-05	-4,024
ENST00000259915 // ENSEMBL // cdna:known chromosome:GRCh37:6:31130253:31138451:-1 gene:	POU5F1	1,67E-06	-2,40385
ENST00000260118 // ENSEMBL // cdna:known chromosome:GRCh37:8:63927644:63951730:-1 gene:	GGH	1,49E-10	2,00035
ENST00000261024 // ENSEMBL // cdna:known chromosome:GRCh37:2:190425305:190445613:-1 gen	SLC40A1	5,36E-16	-9,56377
ENST00000261267 // ENSEMBL // cdna:known chromosome:GRCh37:12:69742121:69748014:1 gene:	LYZ	2,89E-07	-10,4793
ENST00000261435 // ENSEMBL // cdna:known chromosome:GRCh37:4:40058446:40159872:1 gene:E	N4BP2	1,77E-05	1,54748
ENST00000262067 // ENSEMBL // cdna:known chromosome:GRCh37:7:16793160:16824161:1 gene:E	TSPAN13	8,80E-07	-2,74653
ENST00000262219 // ENSEMBL // cdna:known chromosome:GRCh37:8:124693034:124749642:-1 gen	ANXA13	5,77E-11	-13,6486
ENST00000264596 // ENSEMBL // cdna:known chromosome:GRCh37:4:178230990:178284097:1 gene	NEIL3	1,46E-07	1,92523
ENST00000264954 // ENSEMBL // cdna:known chromosome:GRCh37:4:7060633:7069924:-1 gene:EN	GRPEL1	1,56E-06	1,71636
ENST00000265140 // ENSEMBL // cdna:known chromosome:GRCh37:5:93954052:94033326:1 gene:E	ANKRD32	2,36E-10	1,98326
ENST00000265465 // ENSEMBL // cdna:known chromosome:GRCh37:11:65029233:65066156:1 gene:	POLA2	1,20E-06	1,55067
ENST00000265769 // ENSEMBL // cdna:known chromosome:GRCh37:8:24151553:24216531:1 gene:E	ADAM28	2,76E-06	-6,26412
ENST00000268099 // ENSEMBL // cdna:known chromosome:GRCh37:15:75136071:75165706:-1 gene	SCAMP2	2,89E-09	-1,72027

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000268485 // ENSEMBL // cdna:known chromosome:GRCh37:16:71660089:71670368:1 gene:	MARVELD3	1,37E-06	-3,28586
ENST00000272233 // ENSEMBL // cdna:known chromosome:GRCh37:2:20646835:20649200:1 gene:E	RHOB	1,02E-05	-1,7032
ENST00000274242 // ENSEMBL // cdna:known chromosome:GRCh37:5:40825364:40835437:-1 gene:	RPL37	1,87E-05	1,5104
ENST00000278071 // ENSEMBL // cdna:known chromosome:GRCh37:10:106071901:106093663:-1 ge	ITPRIP	1,38E-07	3,7993
ENST00000278612 // ENSEMBL // cdna:known chromosome:GRCh37:11:108027942:108093369:-1 ge	NPAT	9,07E-07	1,56184
ENST00000278618 // ENSEMBL // cdna:known chromosome:GRCh37:11:105948216:105969437:1 gen	AASDH-PPT	9,87E-08	1,60547
ENST00000278836 // ENSEMBL // cdna:known chromosome:GRCh37:11:61520121:61555990:1 gene:	C11orf9	2,15E-06	-2,09287
ENST00000281092 // ENSEMBL // cdna:known chromosome:GRCh37:5:108083523:108532542:1 gene	FER	2,06E-10	2,46467
ENST00000282185 // ENSEMBL // cdna:known chromosome:GRCh37:5:81267844:81551958:1 gene:E	ATG10	6,37E-08	1,5706
ENST00000283122 // ENSEMBL // cdna:known chromosome:GRCh37:5:89688078:89705603:-1 gene:	CETN3	3,93E-06	1,75708
ENST00000283249 // ENSEMBL // cdna:known chromosome:GRCh37:2:160956177:161056812:-1 gen	ITGB6	7,89E-06	-5,32274
ENST00000289248 // ENSEMBL // cdna:known chromosome:GRCh37:1:39351968:39392509:-1 gene:	RHBDL2	1,33E-05	-2,38393
ENST00000290130 // ENSEMBL // cdna:known chromosome:GRCh37:21:33640530:33651380:-1 gene	MIS18A	1,04E-05	1,66541
ENST00000290705 // ENSEMBL // cdna:known chromosome:GRCh37:16:56672578:56673999:1 gene:	MT1A	5,64E-08	9,37706
ENST00000291527 // ENSEMBL // cdna:known chromosome:GRCh37:21:43782391:43786703:-1 gene	TFF1	2,60E-08	-8,93598
ENST00000295101 // ENSEMBL // cdna:known chromosome:GRCh37:2:155554811:155714863:1 gene	KCNJ3	7,14E-06	-4,34784

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000295966 // ENSEMBL // cdna:known chromosome:GRCh37:3:58727733:59035810:-1 gene:	C3orf67	3,42E-08	2,70802
ENST00000296498 // ENSEMBL // cdna:known chromosome:GRCh37:4:119201193:119274158:-1 gen	PRSS12	1,65E-05	-2,92394
ENST00000296702 // ENSEMBL // cdna:known chromosome:GRCh37:5:145826875:145891524:1 gene	TCERG1	8,97E-07	1,52288
ENST00000297261 // ENSEMBL // cdna:known chromosome:GRCh37:7:155592680:155604967:-1 gen	SHH	2,10E-05	-1,58643
ENST00000297540 // ENSEMBL // cdna:known chromosome:GRCh37:5:125935960:125962944:1 gene	PHAX	4,08E-07	1,52673
ENST00000299155 // ENSEMBL // cdna:known chromosome:GRCh37:14:103388993:103397529:1 gen	AMN	1,95E-08	-1,82158
ENST00000300091 // ENSEMBL // cdna:known chromosome:GRCh37:18:51884955:51908402:1 gene:	C18orf54	1,14E-06	3,89087
ENST00000301187 // ENSEMBL // cdna:known chromosome:GRCh37:19:54663846:54676865:-1 gene	TMC4	1,79E-08	-2,37711
ENST00000302609 // ENSEMBL // cdna:known chromosome:GRCh37:10:38238500:38265561:-1 gene	ZNF25	6,91E-07	2,22809
ENST00000302764 // ENSEMBL // cdna:known chromosome:GRCh37:5:162880494:162887146:-1 gen	NUDCD2	7,82E-06	1,67039
ENST00000303225 // ENSEMBL // cdna:known chromosome:GRCh37:19:5842900:5851485:-1 gene:E	FUT3	1,81E-05	-3,45597
ENST00000304043 // ENSEMBL // cdna:known chromosome:GRCh37:5:130494720:130501178:-1 gen	HINT1	3,00E-05	1,5621
ENST00000304788 // ENSEMBL // cdna:known chromosome:GRCh37:20:25593571:25604811:-1 gene	NANP	1,31E-05	1,54366
ENST00000304858 // ENSEMBL // cdna:known chromosome:GRCh37:5:132387654:132442141:1 gene	HSPA4	2,91E-09	1,79418
ENST00000304874 // ENSEMBL // cdna:known chromosome:GRCh37:7:65540785:65558545:1 gene:E	ASL	7,33E-06	-1,59167
ENST00000305354 // ENSEMBL // cdna:known chromosome:GRCh37:3:149191761:149221068:1 gene	TM4SF4	4,16E-09	-20,4295

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000306151 // ENSEMBL // cdna:known chromosome:GRCh37:7:100663353:100702020:1 gene	MUC17	1,77E-09	-16,1252
ENST00000306862 // ENSEMBL // cdna:known chromosome:GRCh37:5:43486803:43515247:-1 gene:	C5orf34	1,26E-05	1,83942
ENST00000308650 // ENSEMBL // cdna:known chromosome:GRCh37:19:9404951:9415795:-1 gene:E	ZNF699	1,13E-05	1,99429
ENST00000309328 // ENSEMBL // cdna:known chromosome:GRCh37:11:65337901:65339241:1 gene:	SSSCA1	2,95E-07	1,56325
ENST00000311083 // ENSEMBL // cdna:known chromosome:GRCh37:12:77252495:77272840:-1 gene	CSRP2	8,58E-07	1,52868
ENST00000311191 // ENSEMBL // cdna:known chromosome:GRCh37:13:47127303:47325710:1 gene:	LRCH1	2,11E-05	-1,82976
ENST00000312087 // ENSEMBL // cdna:known chromosome:GRCh37:4:1894572:1983930:1 gene:ENS	WHSC1	1,10E-08	1,8641
ENST00000316356 // ENSEMBL // cdna:known chromosome:GRCh37:11:85405318:85522172:-1 gene	SYTL2	6,68E-06	-3,86509
ENST00000316660 // ENSEMBL // cdna:known chromosome:GRCh37:18:57567180:57571538:1 gene:	PMAIP1	5,78E-08	3,2424
ENST00000316788 // ENSEMBL // cdna:known chromosome:GRCh37:5:115177178:115249778:1 gene	AP3S1	1,93E-07	1,71622
ENST00000317702 // ENSEMBL // cdna:known chromosome:GRCh37:18:12308070:12326568:1 gene:	TUBB6	4,51E-06	3,39017
ENST00000321276 // ENSEMBL // cdna:known chromosome:GRCh37:2:223289236:223425667:1 gene	SGPP2	5,74E-07	-5,1189
ENST00000321521 // ENSEMBL // cdna:known chromosome:GRCh37:5:102455904:102538910:1 gene	PPIP5K2	2,11E-07	1,69936
ENST00000325617 // ENSEMBL // cdna:known chromosome:GRCh37:4:141309609:141349122:-1 gen	CLGN	1,33E-05	3,13393
ENST00000327355 // ENSEMBL // cdna:known chromosome:GRCh37:15:93160673:93199188:-1 gene	FAM174B	4,92E-12	-1,91327
ENST00000328376 // ENSEMBL // cdna:known chromosome:GRCh37:3:37440653:37476988:1 gene:E	C3orf35	9,10E-06	-1,5887

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000330688 // ENSEMBL // cdna:known chromosome:GRCh37:3:25469802:25639423:1 gene:E	RARB	7,31E-07	-3,51426
ENST00000331495 // ENSEMBL // cdna:known chromosome:GRCh37:17:43299292:43324681:1 gene:	FMNL1	1,90E-05	2,53729
ENST00000331659 // ENSEMBL // cdna:known chromosome:GRCh37:3:171509580:171527714:-1 gen		2,03E-05	-1,67767
ENST00000331803 // ENSEMBL // cdna:known chromosome:GRCh37:7:48128241:48148330:1 gene:E	UPP1	3,57E-06	1,95518
ENST00000332707 // ENSEMBL // cdna:known chromosome:GRCh37:12:64798130:64844907:1 gene:	XPOT	2,34E-06	1,89895
ENST00000333926 // ENSEMBL // cdna:known chromosome:GRCh37:10:60028818:60049346:1 gene:	CISD1	5,91E-06	1,67318
ENST00000334082 // ENSEMBL // cdna:known chromosome:GRCh37:5:78668459:78810040:-1 gene:	HOMER1	3,48E-10	2,46028
ENST00000334121 // ENSEMBL // cdna:known chromosome:GRCh37:5:65440046:65479443:1 gene:E	SREK1	5,30E-07	1,53684
ENST00000336219 // ENSEMBL // cdna:known chromosome:GRCh37:14:105475910:105487485:-1 ge	CDCA4	1,85E-05	1,53599
ENST00000342694 // ENSEMBL // cdna:known chromosome:GRCh37:9:35792151:35809729:1 gene:E	NPR2	7,31E-06	-1,51607
ENST00000342947 // ENSEMBL // cdna:known chromosome:GRCh37:7:24737972:24797732:-1 gene:	DFNA5	1,07E-05	1,95882
ENST00000345146 // ENSEMBL // cdna:known chromosome:GRCh37:2:209100951:209119857:-1 gen	IDH1	1,80E-06	-1,72611
ENST00000354377 // ENSEMBL // cdna:known chromosome:GRCh37:15:90895477:90906079:1 gene:	ZNF774	1,19E-08	-2,27881
ENST00000354728 // ENSEMBL // cdna:known chromosome:GRCh37:2:234580499:234681946:1 gene	UGT1A9	2,64E-09	-5,52995
ENST00000354868 // ENSEMBL // cdna:known chromosome:GRCh37:5:68665639:68710628:1 gene:E	RAD17	1,01E-06	1,80925
ENST00000354921 // ENSEMBL // cdna:known chromosome:GRCh37:1:177897923:177991679:-1 gen	SEC16B	1,43E-05	-3,52253

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000355417 // ENSEMBL // cdna:known chromosome:GRCh37:5:150560613:150603706:-1 gen	CCDC69	1,58E-07	2,88037
ENST00000355999 // ENSEMBL // cdna:known chromosome:GRCh37:2:168810530:169104651:-1 gen	STK39	5,27E-06	-1,76378
ENST00000356458 // ENSEMBL // cdna:novel chromosome:GRCh37:2:54951679:55199154:1 gene:E	EML6	2,18E-08	2,77028
ENST00000357164 // ENSEMBL // cdna:known chromosome:GRCh37:5:150632453:150650001:1 gene	GM2A	1,04E-05	1,78642
ENST00000357759 // ENSEMBL // cdna:known chromosome:GRCh37:3:108021332:108097132:1 gene	HHLA2	3,72E-06	-7,4667
ENST00000357909 // ENSEMBL // cdna:known chromosome:GRCh37:19:4675238:4723875:-1 gene:E	DPP9	9,06E-06	1,74894
ENST00000359651 // ENSEMBL // cdna:known chromosome:GRCh37:1:201977073:201985137:1 gene	ELF3	1,34E-05	-3,43293
ENST00000363271 // ENSEMBL // ncRNA:misc_RNA chromosome:GRCh37:9:34194810:34194905:-1 g		2,35E-05	-1,6832
ENST00000363666 // ENSEMBL // ncRNA:snoRNA chromosome:GRCh37:1:110815106:110815229:1 ge		9,23E-06	-1,7702
ENST00000363960 // ENSEMBL // ncRNA:misc_RNA chromosome:GRCh37:12:14706636:14706904:-1		2,59E-05	-1,64191
ENST00000364353 // ENSEMBL // ncRNA:snRNA chromosome:GRCh37:5:36155221:36155324:1 gene:		6,74E-06	1,60767
ENST00000365211 // ENSEMBL // ncRNA:snRNA chromosome:GRCh37:15:86194753:86194859:-1 gen		1,72E-05	-1,85422
ENST00000366630 // ENSEMBL // cdna:known chromosome:GRCh37:1:232533711:232697304:-1 gen	SIPA1L2	3,00E-05	-3,12866
ENST00000366773 // ENSEMBL // cdna:known chromosome:GRCh37:6:170151721:170181680:1 gene	C6orf70	1,51E-05	1,7337
ENST00000367342 // ENSEMBL // cdna:known chromosome:GRCh37:1:200860469:200884863:1 gene	C1orf106	1,21E-05	-2,64782
ENST00000367816 // ENSEMBL // cdna:known chromosome:GRCh37:1:169074935:169101960:1 gene	ATP1B1	3,75E-09	-2,36237
ENST00000368407 // ENSEMBL // cdna:known chromosome:GRCh37:1:155099936:155107333:1 gene	EFNA1	5,98E-06	-2,28495
ENST00000368702 // ENSEMBL // cdna:known	S100A14	7,84E-06	-4,0198

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:1:153586731:153589462:-1 gen			
ENST00000369308 // ENSEMBL // cdna:known chromosome:GRCh37:1:145477085:145501669:1 gene	LIX1L	8,14E-06	2,33971
ENST00000369583 // ENSEMBL // cdna:known chromosome:GRCh37:10:112257596:112271302:1 gen	DUSP5	3,95E-09	3,05393
ENST00000370626 // ENSEMBL // cdna:known chromosome:GRCh37:10:99437181:99447080:-1 gene	AVPI1	1,07E-06	1,8057
ENST00000370828 // ENSEMBL // cdna:known chromosome:GRCh37:X:132434131:132549518:-1 gen	GPC4	4,11E-08	-4,44227
ENST00000371361 // ENSEMBL // cdna:known chromosome:GRCh37:10:96092983:96122696:-1 gene	NOC3L	2,26E-05	2,0923
ENST00000372013 // ENSEMBL // cdna:known chromosome:GRCh37:10:88727949:88730672:1 gene:	C10orf116	1,59E-06	3,23654
ENST00000372462 // ENSEMBL // cdna:known chromosome:GRCh37:1:43824684:43828874:1 gene:E	CDC20	8,61E-06	1,66976
ENST00000372950 // ENSEMBL // cdna:known chromosome:GRCh37:10:75002582:75008620:-1 gene	DNAJC9	2,16E-06	1,80882
ENST00000372979 // ENSEMBL // cdna:known chromosome:GRCh37:10:74893414:74927817:-1 gene	ECD	4,79E-08	1,5934
ENST00000373030 // ENSEMBL // cdna:known chromosome:GRCh37:20:42219571:42275936:1 gene:	IFT52	8,66E-07	1,74059
ENST00000373382 // ENSEMBL // cdna:known chromosome:GRCh37:10:70883268:70932617:1 gene:	VPS26A	8,95E-06	1,54495
ENST00000373585 // ENSEMBL // cdna:known chromosome:GRCh37:10:70661034:70706603:1 gene:	DDX50	5,42E-06	1,55282
ENST00000373894 // ENSEMBL // cdna:known chromosome:GRCh37:1:28261504:28285668:1 gene:E	SMPDL3 B	8,23E-06	-2,43858
ENST00000374298 // ENSEMBL // cdna:known chromosome:GRCh37:1:26160497:26185903:-1 gene:	C1orf135	2,08E-05	1,62927
ENST00000374317 // ENSEMBL // cdna:known chromosome:GRCh37:10:46994087:47000573:1 gene:	GPRIN2	7,27E-08	-1,73423

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000376032 // ENSEMBL // cdna:known chromosome:GRCh37:13:103418460:103426161:-1 gene	TEX30	5,66E-08	2,08748
ENST00000376447 // ENSEMBL // cdna:known chromosome:GRCh37:9:85594500:85678043:-1 gene:	RASEF	1,20E-06	-6,37777
ENST00000377103 // ENSEMBL // cdna:known chromosome:GRCh37:20:23026270:23030378:-1 gene	THBD	2,19E-07	2,88419
ENST00000377603 // ENSEMBL // cdna:known chromosome:GRCh37:20:18447771:18465287:1 gene:	POLR3F	7,30E-08	1,78276
ENST00000377666 // ENSEMBL // cdna:known chromosome:GRCh37:13:74269536:74708394:-1 gene	KLF12	2,63E-13	5,3038
ENST00000378746 // ENSEMBL // cdna:known chromosome:GRCh37:5:132028368:132073330:-1 gen	KIF3A	6,62E-06	2,05153
ENST00000379380 // ENSEMBL // cdna:known chromosome:GRCh37:5:130506503:130541119:1 gene	LYRM7	6,69E-09	2,33632
ENST00000379433 // ENSEMBL // cdna:known chromosome:GRCh37:6:11198541:11232891:-1 gene:	NEDD9	1,56E-06	-2,14598
ENST00000379433 // ENSEMBL // cdna:known chromosome:GRCh37:6:11198541:11232891:-1 gene:	NEDD9	1,56E-06	-2,14598
ENST00000380009 // ENSEMBL // cdna:known chromosome:GRCh37:5:94890778:94940768:1 gene:E	ARSK	5,08E-08	2,30834
ENST00000381271 // ENSEMBL // cdna:known chromosome:GRCh37:12:27932953:27955973:1 gene:	KLHDC5	5,15E-06	2,06966
ENST00000381571 // ENSEMBL // cdna:known chromosome:GRCh37:4:47452885:47465736:-1 gene:	COMMD8	1,24E-05	1,55809
ENST00000382745 // ENSEMBL // cdna:known chromosome:GRCh37:16:1494936:1525581:-1 gene:E	CLCN7	6,20E-06	1,71357
ENST00000384277 // ENSEMBL // ncna:snRNA chromosome:GRCh37:14:52190821:52190927:1 gene		1,83E-07	3,95819
ENST00000392701 // ENSEMBL // cdna:known chromosome:GRCh37:2:166604101:166651192:-1 gen	GALNT3	1,67E-07	-5,74173
ENST00000393249 // ENSEMBL // cdna:known chromosome:GRCh37:12:76745577:76953315:-1 gene	OSBPL8	9,30E-06	1,71791
ENST00000393330 // ENSEMBL // cdna:known chromosome:GRCh37:12:71518865:71835678:-1 gene	TSPAN8	5,48E-08	-16,0254

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000393964 // ENSEMBL // cdna:known chromosome:GRCh37:5:159848917:159855746:1 gene	PTTG1	5,84E-07	1,91722
ENST00000396328 // ENSEMBL // cdna:known chromosome:GRCh37:15:53805938:54055075:-1 gene	WDR72	2,33E-05	-7,09968
ENST00000396700 // ENSEMBL // cdna:known chromosome:GRCh37:14:25278862:25519270:-1 gene	STXBP6	6,26E-07	-2,21547
ENST00000396946 // ENSEMBL // cdna:known chromosome:GRCh37:7:2945775:3083579:-1 gene:EN	CARD11	1,91E-05	-2,30095
ENST00000399231 // ENSEMBL // cdna:known chromosome:GRCh37:15:52599480:52821247:-1 gene	MYO5A	1,19E-05	3,24207
ENST00000400613 // ENSEMBL // cdna:known chromosome:GRCh37:9:112961841:112970469:-1 gen	C9orf152	5,29E-07	-2,84623
ENST00000402384 // ENSEMBL // cdna:known chromosome:GRCh37:7:8152814:8301911:-1 gene:EN	ICA1	6,30E-06	-2,74468
ENST00000403027 // ENSEMBL // cdna:known chromosome:GRCh37:5:154238077:154256352:1 gene	CNOT8	8,26E-10	1,51209
ENST00000403681 // ENSEMBL // cdna:known chromosome:GRCh37:12:66217911:66360075:1 gene:	HMGA2	1,74E-06	3,00375
ENST00000403796 // ENSEMBL // cdna:known chromosome:GRCh37:11:124932963:124959131:1 gen	SLC37A2	1,10E-06	3,63178
ENST00000406381 // ENSEMBL // cdna:known chromosome:GRCh37:17:37844393:37884915:1 gene:	ERBB2	2,21E-05	-1,69685
ENST00000406396 // ENSEMBL // cdna:known chromosome:GRCh37:18:60994971:61034743:-1 gene	KDSR	4,60E-07	2,04634
ENST00000406854 // ENSEMBL // cdna:known chromosome:GRCh37:14:60558637:60601532:1 gene:	C14orf135	1,49E-07	1,95465
ENST00000407647 // ENSEMBL // cdna:known chromosome:GRCh37:22:29702572:29708774:1 gene:	GAS2L1	3,47E-07	1,64026
ENST00000409054 // ENSEMBL // ensembl_havana_lincrna:lincRNA chromosome:GRCh37:2:877548	LOC541471	1,39E-05	2,0655

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000409150 // ENSEMBL // cdna:known chromosome:GRCh37:2:191369068:191399448:-1 gen	TMEM194B	6,18E-07	2,4164
ENST00000409977 // ENSEMBL // cdna:known chromosome:GRCh37:11:93551398:93583697:-1 gene	VSTM5	2,08E-10	-2,66012
ENST00000410414 // ENSEMBL // ncna:rRNA chromosome:GRCh37:7:111593708:111593820:-1 gen	RN5S237	1,14E-05	4,91148
ENST00000411255 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:11:47636450:47636546:-1		1,51E-05	2,11559
ENST00000412497 // ENSEMBL // cdna:known chromosome:GRCh37:20:1342266:1343229:1 gene:EN		2,11E-05	1,77068
ENST00000413231 // ENSEMBL // havana:lincRNA chromosome:GRCh37:1:113550876:113589677:1		1,84E-06	1,78865
ENST00000414053 // ENSEMBL // cdna:known chromosome:GRCh37:X:2822945:2824122:1 gene:ENS	ARSD-AS1	1,14E-05	-1,54362
ENST00000414948 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:1:8935847:8938066	ENO1-IT1	4,02E-06	1,74427
ENST00000416614 // ENSEMBL // cdna:known chromosome:GRCh37:4:2939660:2965112:-1 gene:EN	NOP14	1,67E-05	1,66598
ENST00000418814 // ENSEMBL // cdna:known chromosome:GRCh37:6:71123011:71270877:1 gene:E	FAM135A	1,61E-05	-2,05478
ENST00000418835 // ENSEMBL // cdna:putative chromosome:GRCh37:2:10987703:10995081:1 gen		4,25E-09	-1,53891
ENST00000419190 // ENSEMBL // cdna:known chromosome:GRCh37:1:201969222:201979481:-1 gen	LOC100289488	4,56E-07	-3,08419
ENST00000419304 // ENSEMBL // cdna:known chromosome:GRCh37:7:16831435:16844704:-1 gene:	AGR2	8,27E-06	-7,30195
ENST00000420080 // ENSEMBL // cdna:known chromosome:GRCh37:7:100606878:100611410:-1 gen		1,71E-07	-1,74066
ENST00000425645 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:4:77558776:775655		2,54E-08	-12,7879
ENST00000426901 // ENSEMBL // cdna:known chromosome:GRCh37:1:54751078:54753044:1 gene:E	LOC100653134	7,95E-06	-1,68866
ENST00000429644 // ENSEMBL // cdna:known	GBE1	1,08E-08	2,668

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:3:81538850:81811312:-1 gene:ENST00000429869 // ENSEMBL // cdna:known chromosome:GRCh37:11:107663341:107799019:-1 ge	SLC35F2	8,15E-09	1,82692
ENST00000430363 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:10:76185995:76186		1,50E-05	2,08073
ENST00000430430 // ENSEMBL // cdna:known chromosome:GRCh37:8:81397902:81438500:1 gene:E	ZBTB10	5,52E-06	2,01541
ENST00000431813 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:9:90168369:901693	DAPK1-IT1	1,10E-08	-5,72031
ENST00000431906 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:10:52348409:52349		6,29E-07	1,71371
ENST00000432268 // ENSEMBL // ensembl_havana_lincrna:lincRNA chromosome:GRCh37:2:112249		2,18E-05	1,90834
ENST00000434178 // ENSEMBL // cdna:known chromosome:GRCh37:3:127407909:127542028:-1 gen	MGLL	3,28E-08	-1,92076
ENST00000436258 // ENSEMBL // cdna:known chromosome:GRCh37:7:35129456:35147346:-1 gene:	DPY19L2 P1	1,91E-05	2,76141
ENST00000436636 // ENSEMBL // cdna:known chromosome:GRCh37:3:170779128:171178197:-1 gen	TNIK	3,91E-09	-4,68215
ENST00000437088 // ENSEMBL // havana:lincRNA chromosome:GRCh37:7:12693804:12694610:1 ge		8,49E-08	-5,90157
ENST00000438576 // ENSEMBL // cdna:known chromosome:GRCh37:11:65684279:65686588:-1 gene	C11orf68	5,19E-06	1,51593
ENST00000438925 // ENSEMBL // cdna:known chromosome:GRCh37:10:99218081:99258477:-1 gene	MMS19	6,75E-06	1,69939
ENST00000442605 // ENSEMBL // cdna:putative chromosome:GRCh37:21:43980484:43982044:-1 g		1,75E-05	-1,50651
ENST00000447019 // ENSEMBL // havana:lincRNA chromosome:GRCh37:2:158582220:158592517:-1		2,72E-05	-1,79248
ENST00000448015 // ENSEMBL // cdna:known chromosome:GRCh37:1:28265386:28286704:-1 gene:		2,70E-05	-1,52077
ENST00000448869 // ENSEMBL // cdna:putative chromosome:GRCh37:1:156616299:156631216:-1		1,68E-07	-1,75367
ENST00000451126 // ENSEMBL // cdna:putative chromosome:GRCh37:X:41379289:41381589:1 gen	CASK-AS1	2,08E-08	-1,62649

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000452009 // ENSEMBL // cdna:putative chromosome:GRCh37:7:116182772:116192023:-1		2,28E-06	1,96946
ENST00000453549 // ENSEMBL // cdna:putative chromosome:GRCh37:21:33650174:33653299:1 ge	MIS18A-AS1	3,38E-06	1,59237
ENST00000454337 // ENSEMBL // cdna:known chromosome:GRCh37:16:1682260:1736716:1 gene:EN		7,11E-06	1,68454
ENST00000456018 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:6:150945813:15094		6,66E-06	-1,72485
ENST00000456355 // ENSEMBL // cdna:putative chromosome:GRCh37:10:17275324:17276832:-1 g		1,59E-05	2,68701
ENST00000457383 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:9:4070906:4071884		5,06E-07	-4,25769
ENST00000458367 // ENSEMBL // cdna:putative chromosome:GRCh37:6:128821672:128822321:1 g		1,37E-08	-2,4029
ENST00000458869 // ENSEMBL // ncRNA:snoRNA chromosome:GRCh37:2:219193303:219193403:1 ge		3,33E-06	-3,58431
ENST00000463534 // ENSEMBL // cdna:known chromosome:GRCh37:2:233877602:233880594:1 gene		1,86E-08	-2,56521
ENST00000470972 // ENSEMBL // cdna:known chromosome:GRCh37:9:108006903:108159627:1 gene	SLC44A1	3,04E-06	-2,08967
ENST00000477313 // ENSEMBL // cdna:known chromosome:GRCh37:20:44527402:44540686:-1 gene	PLTP	1,43E-06	2,64916
ENST00000477853 // ENSEMBL // cdna:known chromosome:GRCh37:1:19542158:19578046:-1 gene:	EMC1	7,16E-06	1,56938
ENST00000477922 // ENSEMBL // cdna:putative chromosome:GRCh37:7:141811549:141921088:1 g		7,50E-10	-31,1994
ENST00000481149 // ENSEMBL // cdna:known chromosome:GRCh37:9:99276785:99284885:-1 gene:	CDC14B	4,06E-06	-2,15255
ENST00000483209 // ENSEMBL // cdna:known chromosome:GRCh37:3:118930579:118959486:-1 gen	B4GALT4	2,11E-05	-1,98019
ENST00000489418 // ENSEMBL // cdna:known chromosome:GRCh37:4:1694527:1714282:-1 gene:EN	SLBP	2,19E-06	1,64398
ENST00000493385 // ENSEMBL // cdna:known chromosome:GRCh37:10:101462315:101503080:1 gen	CUTC	6,28E-07	1,83694
ENST00000498004 // ENSEMBL // cdna:known chromosome:GRCh37:X:15706953:15782788:1	CA5B	2,39E-09	1,97521

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
gene:E			
ENST00000504156 // ENSEMBL // cdna:known chromosome:GRCh37:5:140052758:140071609:-1 gen	HARS	3,04E-08	1,50764
ENST00000504273 // ENSEMBL // cdna:known chromosome:GRCh37:4:186125391:186285125:1 gene	SNX25	1,43E-05	1,59626
ENST00000504352 // ENSEMBL // cdna:known chromosome:GRCh37:5:134240863:134343649:1 gene	PCBD2	4,38E-07	1,54666
ENST00000504592 // ENSEMBL // cdna:known chromosome:GRCh37:4:102341118:102995969:1 gene	BANK1	1,87E-05	-2,00135
ENST00000506538 // ENSEMBL // cdna:known chromosome:GRCh37:5:110427414:110466200:1 gene	WDR36	1,23E-06	1,71762
ENST00000508177 // ENSEMBL // cdna:known chromosome:GRCh37:5:141380243:141392359:-1 gen	GNPDA1	1,57E-06	1,72993
ENST00000510158 // ENSEMBL // cdna:known chromosome:GRCh37:5:79703843:79774959:1 gene:E	ZFYVE16	1,08E-10	1,6899
ENST00000510636 // ENSEMBL // cdna:known chromosome:GRCh37:5:175969512:176022975:1 gene	CDHR2	2,24E-05	-4,32505
ENST00000511059 // ENSEMBL // cdna:known chromosome:GRCh37:4:106848217:106850735:-1 gen		7,19E-06	-2,48461
ENST00000514459 // ENSEMBL // cdna:putative chromosome:GRCh37:5:135549736:135557847:1 g	TRPC7-AS1	1,88E-05	-1,79131
ENST00000515949 // ENSEMBL // ncna:snRNA chromosome:GRCh37:4:16010299:16010410:-1 gene		1,05E-15	-19,1331
ENST00000516126 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:2:191417990:191418206:-1		7,73E-07	1,92034
ENST00000516141 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:10:52345310:52345463:-1		5,47E-07	1,68345
ENST00000516178 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:3:53564349:53564428:-1 gen		6,41E-07	-2,14685
ENST00000516361 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:3:121964613:121964684:1 ge		1,93E-05	-17,1425
ENST00000516446 // ENSEMBL // ncna:snRNA chromosome:GRCh37:11:125519641:125519782:1 ge		1,43E-06	1,90863
ENST00000516465 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:17:70814975:70815111:-1 ge		2,88E-06	-2,49087
ENST00000517031 // ENSEMBL // ncna:snoRNA		3,66E-07	-1,90594

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:1:151500307:151500414:-1 g			
ENST00000521118 // ENSEMBL // cdna:known chromosome:GRCh37:5:133635116:133702761:-1 gen	CDKL3	2,35E-05	1,60465
ENST00000521389 // ENSEMBL // cdna:known chromosome:GRCh37:5:179382067:179499118:-1 gen	RNF130	4,27E-07	2,12345
ENST00000523037 // ENSEMBL // cdna:known chromosome:GRCh37:5:154320630:154348971:1 gene	MRPL22	1,20E-05	1,54547
ENST00000524142 // ENSEMBL // cdna:known chromosome:GRCh37:5:151122383:151152093:-1 gen	ATOX1	1,37E-09	1,51504
ENST00000525239 // ENSEMBL // cdna:known chromosome:GRCh37:11:62600384:62609281:-1 gene	WDR74	3,65E-06	1,57954
ENST00000525450 // ENSEMBL // cdna:putative chromosome:GRCh37:11:76834749:76835776:-1 g		4,62E-06	-1,53239
ENST00000526533 // ENSEMBL // cdna:putative chromosome:GRCh37:11:3529210:3593217:-1 gen		2,58E-05	-3,80805
ENST00000530960 // ENSEMBL // havana:lincRNA chromosome:GRCh37:11:29181503:29288281:1 g		2,40E-05	2,52178
ENST00000533301 // ENSEMBL // cdna:known chromosome:GRCh37:8:38258054:38259201:-1 gene:		2,57E-05	1,78198
ENST00000534892 // ENSEMBL // cdna:known chromosome:GRCh37:5:137621269:137674022:-1 gen	CDC25C	5,55E-08	1,75471
ENST00000537269 // ENSEMBL // cdna:known chromosome:GRCh37:12:7072409:7073610:1 gene:EN		1,41E-05	-1,85022
ENST00000544279 // ENSEMBL // cdna:putative chromosome:GRCh37:12:66328557:66342259:-1 g		2,50E-05	2,11707
ENST00000544347 // ENSEMBL // cdna:known chromosome:GRCh37:11:114271404:114314654:1 gen		5,67E-07	2,35935
ENST00000546072 // ENSEMBL // cdna:putative chromosome:GRCh37:12:27091430:27113779:1 ge	FGFR1OP 2	1,59E-05	1,95642
ENST00000553410 // ENSEMBL // havana:lincRNA chromosome:GRCh37:15:92076121:92078325:1 g		1,74E-05	-1,91346
ENST00000555265 // ENSEMBL // cdna:known chromosome:GRCh37:14:80962821:81408129:-1 gene	CEP128	1,44E-06	2,04629
ENST00000555313 // ENSEMBL // havana:lincRNA chromosome:GRCh37:14:75081510:75083350:-1		1,10E-06	3,0174
ENST00000556024 // ENSEMBL // cdna:known		2,75E-05	-3,80521

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:14:38025363:38036300:-1 gene			
ENST00000556640 // ENSEMBL // cdna:known chromosome:GRCh37:14:64889653:64915275:-1 gene		2,11E-05	1,59764
ENST00000558143 // ENSEMBL // cdna:known chromosome:GRCh37:17:36105206:36108563:1 gene:		1,32E-09	-4,30807
ENST00000558757 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:15:86244340:86246		4,04E-06	-1,91924
ENST00000558905 // ENSEMBL // cdna:known chromosome:GRCh37:15:63362224:63364110:-1 gene		3,25E-09	-2,63764
ENST00000559899 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:15:40105424:40107		2,75E-07	1,80125
ENST00000561241 // ENSEMBL // cdna:known chromosome:GRCh37:15:63338233:63341586:-1 gene	LOC100128979	1,10E-07	-1,83151
EU250749 // GenBank // Homo sapiens clone HA_003010 mRNA sequence. // chr1 // 100 // 17	C1orf98	2,48E-05	2,51128
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		5,07E-10	-10,2514
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		8,89E-10	-17,1922
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		9,13E-10	-8,80386
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		9,89E-10	-23,0739
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		1,07E-09	-21,2941
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		1,07E-09	-19,1253
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		1,35E-09	-16,4556
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromosome:GRCh37:7:141672558:141941111:1		1,86E-09	-16,311

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromo-some:GRCh37:7:141672558:141941111:1		1,98E-09	-11,2116
GENSCAN00000014965 // ENSEMBL // cdna:genscan chromo-some:GRCh37:7:141672558:141941111:1		3,19E-09	-8,64275
NM_000024 // RefSeq // Homo sapiens adrenoceptor beta 2, surface (ADRB2), mRNA. // chr5	ADRB2	1,97E-10	3,37262
NM_000046 // RefSeq // Homo sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA.	ARSB	2,09E-06	1,59341
NM_000053 // RefSeq // Homo sapiens ATPase, Cu++ transporting, beta polypeptide (ATP7B)	ATP7B	2,91E-08	-4,8711
NM_000082 // RefSeq // Homo sapiens excision repair cross-complementing rodent repair d	ERCC8	2,02E-06	1,73062
NM_000112 // RefSeq // Homo sapiens solute carrier family 26 (sulfate transporter), mem	SLC26A2	5,44E-07	1,73286
NM_000150 // RefSeq // Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferas	FUT6	1,34E-05	-1,85068
NM_000166 // RefSeq // Homo sapiens gap junction protein, beta 1, 32kDa (GJB1), transcr	GJB1	8,51E-10	-3,23481
NM_000179 // RefSeq // Homo sapiens mutS homolog 6 (E. coli) (MSH6), mRNA. // chr2 // 1	MSH6	2,73E-06	1,55527
NM_000260 // RefSeq // Homo sapiens myosin VIIA (MYO7A), transcript variant 1, mRNA. //	MYO7A	1,35E-06	-1,63887
NM_000311 // RefSeq // Homo sapiens prion protein (PRNP), transcript variant 1, mRNA. /	PRNP	5,37E-07	2,41853
NM_000329 // RefSeq // Homo sapiens retinal pigment epithelium-specific protein 65kDa (	RPE65	1,50E-08	2,62922
NM_000343 // RefSeq // Homo sapiens solute carrier family 5 (sodium/glucose cotransport	SLC5A1	8,88E-10	-4,59938
NM_000366 // RefSeq // Homo sapiens tropomyosin 1 (alpha) (TPM1), transcript variant 5,	TPM1	1,09E-10	-2,75385
NM_000367 // RefSeq // Homo sapiens thiopurine S-methyltransferase (TPMT), mRNA. // chr	TPMT	4,01E-06	-2,27401
NM_000433 // RefSeq // Homo sapiens neutrophil cytosolic factor 2 (NCF2), transcript va	NCF2	9,32E-07	3,01189
NM_000458 // RefSeq // Homo sapiens HNF1 homeobox B (HNF1B), transcript variant 1, mRNA	HNF1B	6,12E-11	-7,59197
NM_000492 // RefSeq // Homo sapiens cystic fibrosis transmembrane conductance regulator	CFTR	8,40E-12	-19,4273
NM_000507 // RefSeq // Homo sapiens fructose-1,6-bisphosphatase 1 (FBP1), transcript va	FBP1	1,94E-07	-4,34747
NM_000681 // RefSeq // Homo sapiens adrenoceptor alpha 2A (ADRA2A), mRNA. // chr10 // 1	ADRA2A	2,09E-10	-6,8359
NM_000690 // RefSeq // Homo sapiens aldehyde	ALDH2	2,35E-05	-3,53973

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
dehydrogenase 2 family (mitochondrial) (AL			
NM_000720 // RefSeq // Homo sapiens calcium channel, voltage-dependent, L type, alpha 1	CACNA1D	7,09E-18	-5,47623
NM_000767 // RefSeq // Homo sapiens cytochrome P450, family 2, subfamily B, polypeptide	CYP2B6	9,15E-06	-4,09662
NM_000772 // RefSeq // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide	CYP2C18	4,19E-07	-11,3016
NM_000789 // RefSeq // Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptida	ACE	1,10E-06	-1,64035
NM_000899 // RefSeq // Homo sapiens KIT ligand (KITLG), transcript variant b, mRNA. //	KITLG	4,02E-06	-3,34446
NM_000901 // RefSeq // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR	NR3C2	5,08E-06	-2,5153
NM_000919 // RefSeq // Homo sapiens peptidylglycine alpha-amidating monooxygenase (PAM)	PAM	4,26E-11	1,95029
NM_001001791 // RefSeq // Homo sapiens chromosome 10 open reading frame 55 (C10orf55),	C10orf55	1,50E-05	2,25223
NM_001002796 // RefSeq // Homo sapiens multiple C2 domains, transmembrane 1 (MCTP1), tr	MCTP1	1,82E-08	5,08908
NM_001006657 // RefSeq // Homo sapiens WD repeat domain 35 (WDR35), transcript variant	WDR35	9,35E-06	2,09791
NM_001008723 // RefSeq // Homo sapiens coiled-coil domain containing 147 (CCDC147), mRN	CCDC147	7,79E-08	1,73869
NM_001008749 // RefSeq // Homo sapiens RAB19, member RAS oncogene family (RAB19), mRNA.	RAB19	4,86E-07	-2,11397
NM_001008938 // RefSeq // Homo sapiens cytoskeleton associated protein 5 (CKAP5), trans	CKAP5	1,66E-08	1,55595
NM_001009999 // RefSeq // Homo sapiens lysine (K)-specific demethylase 1A (KDM1A), tran	KDM1A	6,12E-06	2,1216
NM_001010887 // RefSeq // Homo sapiens alkaline ceramidase 2 (ACER2), mRNA. // chr9 //	ACER2	1,09E-05	-2,73782
NM_001010922 // RefSeq // Homo sapiens BCL2-like 15 (BCL2L15), mRNA. // chr1 // 100 //	BCL2L15	6,58E-10	-6,27269
NM_001011663 // RefSeq // Homo sapiens polycomb group ring finger 6 (PCGF6), transcript	PCGF6	1,06E-07	2,25652
NM_001012515 // RefSeq // Homo sapiens ferrochelatase (FECH), nuclear gene encoding mit	FECH	1,48E-05	1,57238
NM_001012662 // RefSeq // Homo sapiens solute carrier family 3 (activators of dibasic a	SLC3A2	5,87E-06	1,55809
NM_001012761 // RefSeq // Homo sapiens RGM domain family, member B (RGMB), mRNA. // chr	RGMB	3,00E-06	2,11088
NM_001018077 // RefSeq // Homo sapiens nuclear receptor subfamily 3, group C, member 1	NR3C1	2,89E-08	1,84521
NM_001024611 // RefSeq // Homo sapiens leucine rich repeat containing 66 (LRRC66), mRNA	LRRC66	1,66E-06	-5,9514

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001024948 // RefSeq // Homo sapiens formin binding protein 1-like (FNBP1L), transcri	FNBP1L	4,73E-06	-3,19797
NM_001029996 // RefSeq // Homo sapiens primary ciliary dyskinesia protein 1 (PCDP1), mR	PCDP1	1,21E-05	-3,09884
NM_001033 // RefSeq // Homo sapiens ribonucleotide reductase M1 (RRM1), mRNA. // chr11	RRM1	6,48E-07	1,68276
NM_001034194 // RefSeq // Homo sapiens exosome component 9 (EXOSC9), transcript variant	EXOSC9	4,34E-06	1,72092
NM_001034850 // RefSeq // Homo sapiens family with sequence similarity 134, member B (F	FAM134B	2,59E-05	-2,70656
NM_001039395 // RefSeq // Homo sapiens spermatogenesis associated 6-like (SPATA6L), mRN	SPATA6L	1,39E-05	-2,31593
NM_001040022 // RefSeq // Homo sapiens signal-regulatory protein alpha (SIRPA), transcr	SIRPA	4,48E-06	-2,56297
NM_001042413 // RefSeq // Homo sapiens GLIS family zinc finger 3 (GLIS3), transcript va	GLIS3	1,28E-06	-2,46753
NM_001042471 // RefSeq // Homo sapiens gasdermin B (GSDMB), transcript variant 1, mRNA.	GSDMB	1,51E-06	-3,22959
NM_001042481 // RefSeq // Homo sapiens FERM domain containing 6 (FRMD6), transcript var	FRMD6	2,07E-07	3,59922
NM_001047 // RefSeq // Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-o	SRD5A1	3,13E-07	1,802
NM_001056 // RefSeq // Homo sapiens sulfotransferase family, cytosolic, 1C, member 2 (S	SULT1C2	7,47E-07	-8,03899
NM_001077181 // RefSeq // Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerev	CDC14B	1,03E-07	-1,92902
NM_001080416 // RefSeq // Homo sapiens v-myb myeloblastosis viral oncogene homolog (avi	MYBL1	6,72E-06	4,84232
NM_001080429 // RefSeq // Homo sapiens calmodulin regulated spectrin-associated protein	CAM-SAP3	3,64E-06	-2,00599
NM_001080527 // RefSeq // Homo sapiens myosin VIIIB (MYO7B), mRNA. // chr2 // 100 // 76	MYO7B	4,01E-06	-2,9353
NM_001083 // RefSeq // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transc	PDE5A	2,09E-07	-3,28726
NM_001085377 // RefSeq // Homo sapiens mutated in colorectal cancers (MCC), transcript	MCC	3,38E-07	2,52646
NM_001085411 // RefSeq // Homo sapiens NAD kinase domain containing 1 (NADKD1), transcr	NADKD1	1,36E-05	1,74438
NM_001098484 // RefSeq // Homo sapiens solute carrier family 4, sodium bicarbonate cotr	SLC4A4	3,18E-13	-20,7327
NM_001098511 // RefSeq // Homo sapiens kinesin heavy chain member 2A (KIF2A), transcrip	KIF2A	6,33E-06	1,7595
NM_001099287 // RefSeq // Homo sapiens NIPA-like domain containing 4 (NIPAL4), transcri	NIPAL4	2,97E-05	1,58641
NM_001100399 // RefSeq // Homo sapiens PDS5,	PDS5A	2,19E-08	1,54595

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
regulator of cohesion maintenance, homolog			
NM_001100812 // RefSeq // Homo sapiens chemokine (C-X-C motif) ligand 16 (CXCL16), tran	CXCL16	1,72E-05	-3,95261
NM_001104546 // RefSeq // Homo sapiens ribonuclease P/MRP 30kDa subunit (RPP30), transc	RPP30	4,65E-09	2,18302
NM_001105248 // RefSeq // Homo sapiens transmembrane channel-like 5 (TMC5), transcript	TMC5	1,26E-07	-7,77774
NM_001112 // RefSeq // Homo sapiens adenosine deaminase, RNA-specific, B1 (ADARB1), tra	ADARB1	2,98E-08	2,41172
NM_001112706 // RefSeq // Homo sapiens scinderin (SCIN), transcript variant 1, mRNA. //	SCIN	4,31E-07	-4,31068
NM_001114106 // RefSeq // Homo sapiens solute carrier family 44, member 3 (SLC44A3), tr	SLC44A3	1,79E-05	-4,21928
NM_001114132 // RefSeq // Homo sapiens neurobeachin-like 1 (NBEAL1), mRNA. // chr2 // 1	NBEAL1	4,52E-06	-1,65626
NM_001123 // RefSeq // Homo sapiens adenosine kinase (ADK), transcript variant 1, mRNA.	ADK	1,10E-07	2,39255
NM_001126129 // RefSeq // Homo sapiens GINS complex subunit 3 (Psf3 homolog) (GINS3), t	GINS3	2,44E-05	1,61209
NM_001127357 // RefSeq // Homo sapiens putative homeodomain transcription factor 2 (PHT	PHTF2	4,54E-06	1,81065
NM_001130524 // RefSeq // Homo sapiens adaptor-related protein complex 1, mu 1 subunit	AP1M1	2,07E-06	1,79694
NM_001130823 // RefSeq // Homo sapiens DNA (cytosine-5-)-methyltransferase 1 (DNMT1), t	DNMT1	8,25E-06	1,69113
NM_001130960 // RefSeq // Homo sapiens phospholipase C, eta 1 (PLCH1), transcript varia	PLCH1	2,80E-05	-3,10193
NM_001130963 // RefSeq // Homo sapiens transmembrane protein 194A (TMEM194A), transcrip	TMEM194A	9,14E-06	2,00629
NM_001131007 // RefSeq // Homo sapiens KIAA0922 (KIAA0922), transcript variant 1, mRNA.	KIAA0922	6,64E-09	2,93127
NM_001134437 // RefSeq // Homo sapiens pleckstrin homology-like domain, family B, membe	PHLDB2	1,99E-05	2,03956
NM_001134779 // RefSeq // Homo sapiens importin 11 (IPO11), transcript variant 1, mRNA.	IPO11	1,31E-07	1,91863
NM_001135050 // RefSeq // Homo sapiens immunoglobulin superfamily, member 9 (IGSF9), tr	IGSF9	1,74E-09	-2,27848
NM_001135648 // RefSeq // Homo sapiens protein tyrosine phosphatase, receptor type, K (	PTPRK	4,19E-08	-2,11352
NM_001136191 // RefSeq // Homo sapiens KN motif and ankyrin repeat domains 2 (KANK2), t	KANK2	8,39E-06	1,54045
NM_001136216 // RefSeq // Homo sapiens transmembrane protein 51 (TMEM51), transcript va	TMEM51	1,88E-06	-2,37228
NM_001142286 // RefSeq // Homo sapiens structural maintenance of chromosomes 6 (SMC6),	SMC6	1,17E-05	1,59291

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001142550 // RefSeq // Homo sapiens WD repeat domain 47 (WDR47), transcript variant	WDR47	1,71E-07	1,66269
NM_001143820 // RefSeq // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog	ETS1	9,39E-06	1,99545
NM_001143962 // RefSeq // Homo sapiens calpain 8 (CAPN8), mRNA. // chr1 // 100 // 52 //	CAPN8	8,27E-06	-5,968
NM_001143979 // RefSeq // Homo sapiens nude nuclear distribution E homolog 1 (A. nidula	NDE1	5,62E-06	1,59099
NM_001144832 // RefSeq // Homo sapiens tetratricopeptide repeat domain 39A (TTC39A), tr	TTC39A	3,78E-11	-2,58826
NM_001144889 // RefSeq // Homo sapiens solute carrier family 23 (nucleobase transporter	SLC23A3	1,05E-06	-1,6463
NM_001144994 // RefSeq // Homo sapiens chromosome 2 open reading frame 72 (C2orf72), mR	C2orf72	4,11E-07	-2,59372
NM_001145 // RefSeq // Homo sapiens angiogenin, ribonuclease, RNase A family, 5 (ANG),	ANG	4,28E-07	-2,88934
NM_001145065 // RefSeq // Homo sapiens family with sequence similarity 190, member A (F	FAM190A	1,78E-06	-2,82469
NM_001145313 // RefSeq // Homo sapiens fibronectin type III and SPRY domain containing	FSD1L	6,52E-06	2,39936
NM_001145775 // RefSeq // Homo sapiens FK506 binding protein 5 (FKBP5), transcript vari	FKBP5	4,88E-08	1,82034
NM_001146188 // RefSeq // Homo sapiens TOX high mobility group box family member 3 (TOX	TOX3	1,42E-07	-5,22885
NM_001153 // RefSeq // Homo sapiens annexin A4 (ANXA4), mRNA. // chr2 // 100 // 68 // 1	ANXA4	2,31E-10	-2,5913
NM_001159352 // RefSeq // Homo sapiens regenerating islet-derived family, member 4 (REG	REG4	2,61E-08	-27,5098
NM_001164386 // RefSeq // Homo sapiens Rap guanine nucleotide exchange factor (GEF) 6 (	RAPGEF6	5,16E-08	1,72561
NM_001164507 // RefSeq // Homo sapiens nebulin (NEB), transcript variant 1, mRNA. // ch	NEB	2,85E-07	-4,39602
NM_001164664 // RefSeq // Homo sapiens microtubule associated serine/threonine kinase f	MAST4	1,15E-05	1,81579
NM_001164694 // RefSeq // Homo sapiens iodotyrosine deiodinase (IYD), transcript varian	IYD	2,92E-11	-3,82576
NM_001166271 // RefSeq // Homo sapiens spermatogenesis associated 13 (SPATA13), transcr	SPATA13	1,67E-05	-1,6413
NM_001170464 // RefSeq // Homo sapiens cyclin-dependent kinase 17 (CDK17), transcript v	CDK17	1,83E-05	2,31788
NM_001171203 // RefSeq // Homo sapiens ubiquitin associated protein 1 (UBAP1), transcri	UBAP1	1,01E-07	-1,76989
NM_001171631 // RefSeq // Homo sapiens nitric oxide synthase trafficker (NOSTRIN), tran	NOSTRIN	2,82E-08	-4,42321
NM_001172 // RefSeq // Homo sapiens arginase, type	ARG2	5,23E-07	2,01206

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
II (ARG2), nuclear gene encoding mit			
NM_001172895 // RefSeq // Homo sapiens caveolin 1, caveolae protein, 22kDa (CAV1), tran	CAV1	8,57E-08	3,53007
NM_001182 // RefSeq // Homo sapiens aldehyde dehydrogenase 7 family, member A1 (ALDH7A1	ALDH7A1	2,92E-07	1,91575
NM_001184690 // RefSeq // Homo sapiens nephronectin (NPNT), transcript variant 1, mRNA.	NPNT	2,78E-05	-4,26002
NM_001184783 // RefSeq // Homo sapiens voltage-dependent anion channel 2 (VDAC2), nucle	VDAC2	1,86E-07	1,58317
NM_001184975 // RefSeq // Homo sapiens protein kinase C and casein kinase substrate in	PACSIN3	8,66E-09	2,33726
NM_001190482 // RefSeq // Homo sapiens proprotein convertase subtilisin/kexin type 5 (P	PCSK5	8,80E-10	-5,22046
NM_001190708 // RefSeq // Homo sapiens MT-RNR2-like 10 (MTRNR2L10), mRNA. // chrX // 10	MTRNR2L10	2,65E-05	-1,60716
NM_001195381 // RefSeq // Homo sapiens G protein-coupled receptor 35 (GPR35), transcrip	GPR35	1,75E-05	-2,77572
NM_001198608 // RefSeq // Homo sapiens microtubule-associated protein 7 (MAP7), transcr	MAP7	1,92E-06	-3,19656
NM_001199397 // RefSeq // Homo sapiens NIMA (never in mitosis gene a)-related kinase 1	NEK1	4,29E-09	1,7036
NM_001199799 // RefSeq // Homo sapiens immunoglobulin-like domain containing receptor 1	ILDR1	9,62E-06	-2,39787
NM_001201480 // RefSeq // Homo sapiens oxysterol binding protein-like 6 (OSBPL6), trans	OSBPL6	6,57E-07	4,23777
NM_001201483 // RefSeq // Homo sapiens enolase 1, (alpha) (ENO1), transcript variant 2,	ENO1	1,31E-06	1,70797
NM_001242348 // RefSeq // Homo sapiens uncharacterized LOC100287177 (LOC100287177), mRN	LOC100287177	5,55E-08	1,61643
NM_001242729 // RefSeq // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 38	ARHGEF38	2,66E-07	-5,69206
NM_001242903 // RefSeq // Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), transc	AKAP1	2,08E-05	-1,63284
NM_001256617 // RefSeq // Homo sapiens tubulin, gamma complex associated protein 2 (TUB	TUBGCP2	2,06E-08	1,69833
NM_001258355 // RefSeq // Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), tran	HNF4A	5,19E-07	-3,42073
NM_001258438 // RefSeq // Homo sapiens threonyl-tRNA synthetase (TARS), transcript vari	TARS	1,54E-05	1,59711
NM_001316 // RefSeq // Homo sapiens CSE1 chromosome segregation 1-like (yeast) (CSE1L),	CSE1L	4,15E-06	1,88153
NM_001398 // RefSeq // Homo sapiens enoyl CoA hydratase 1, peroxisomal (ECH1), mRNA. //	ECH1	5,35E-06	-1,80321
NM_001425 // RefSeq // Homo sapiens epithelial membrane protein 3 (EMP3), mRNA. // chr1	EMP3	5,54E-07	5,39192

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001482 // RefSeq // Homo sapiens glycine amidinotransferase (L-arginine:glycine amid	GATM	1,93E-06	-3,08419
NM_001486 // RefSeq // Homo sapiens glucokinase (hexokinase 4) regulator (GCKR), mRNA.	GCKR	5,61E-06	-3,36354
NM_001498 // RefSeq // Homo sapiens glutamate-cysteine ligase, catalytic subunit (GCLC)	GCLC	1,89E-08	1,66864
NM_001628 // RefSeq // Homo sapiens aldo-keto reductase family 1, member B1 (aldose red	AKR1B1	2,14E-06	2,47241
NM_001644 // RefSeq // Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic pol	APO-BEC1	1,59E-08	-7,48678
NM_001740 // RefSeq // Homo sapiens calbindin 2 (CALB2), transcript variant CALB2, mRNA	CALB2	1,27E-08	9,78639
NM_001745 // RefSeq // Homo sapiens calcium modulating ligand (CAMLG), mRNA. // chr5 //	CAMLG	1,07E-06	2,21494
NM_001799 // RefSeq // Homo sapiens cyclin-dependent kinase 7 (CDK7), mRNA. // chr5 //	CDK7	1,36E-08	1,8092
NM_001910 // RefSeq // Homo sapiens cathepsin E (CTSE), transcript variant 1, mRNA. //	CTSE	3,07E-09	-18,1044
NM_001931 // RefSeq // Homo sapiens dihydrolipoamide S-acetyltransferase (DLAT), nuclea	DLAT	9,46E-08	1,779
NM_001947 // RefSeq // Homo sapiens dual specificity phosphatase 7 (DUSP7), mRNA. // ch	DUSP7	1,84E-06	1,70218
NM_001983 // RefSeq // Homo sapiens excision repair cross-complementing rodent repair d	ERCC1	5,00E-06	1,84238
NM_002079 // RefSeq // Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspar	GOT1	1,52E-06	1,76056
NM_002153 // RefSeq // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2),	HSD17B2	1,32E-13	-14,8399
NM_002317 // RefSeq // Homo sapiens lysyl oxidase (LOX), transcript variant 1, mRNA. //	LOX	1,70E-05	2,66729
NM_002372 // RefSeq // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mR	MAN2A1	2,71E-05	1,68938
NM_002423 // RefSeq // Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MM	MMP7	1,62E-05	-8,00839
NM_002431 // RefSeq // Homo sapiens menage a trois homolog 1, cyclin H assembly factor	MNAT1	5,02E-07	1,53426
NM_002447 // RefSeq // Homo sapiens macrophage stimulating 1 receptor (c-met-related ty	MST1R	1,19E-05	-2,05841
NM_002483 // RefSeq // Homo sapiens carcinoembryonic antigen-related cell adhesion mole	CEACAM6	3,06E-06	-22,3709
NM_002495 // RefSeq // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18k	NDUFS4	2,04E-06	1,65785
NM_002622 // RefSeq // Homo sapiens prefoldin subunit 1 (PFDN1), mRNA. // chr5 // 100 /	PFDN1	1,87E-08	1,72168
NM_002644 // RefSeq // Homo sapiens polymeric	PIGR	1,79E-06	-18,0893

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
immunoglobulin receptor (PIGR), mRNA. //			
NM_002670 // RefSeq // Homo sapiens plastin 1 (PLS1), transcript variant 2, mRNA. // ch	PLS1	1,69E-06	-2,96555
NM_002743 // RefSeq // Homo sapiens protein kinase C substrate 80K-H (PRKCSH), transcri	PRKCSH	2,93E-08	1,5656
NM_002775 // RefSeq // Homo sapiens HtrA serine peptidase 1 (HTRA1), mRNA. // chr10 //	HTRA1	2,85E-06	4,27353
NM_002851 // RefSeq // Homo sapiens protein tyrosine phosphatase, receptor-type, Z poly	PTPRZ1	4,83E-07	9,17265
NM_002890 // RefSeq // Homo sapiens RAS p21 protein activator (GTPase activating protei	RASA1	2,83E-07	1,9742
NM_002895 // RefSeq // Homo sapiens retinoblastoma-like 1 (p107) (RBL1), transcript var	RBL1	7,24E-07	1,86968
NM_002913 // RefSeq // Homo sapiens replication factor C (activator 1) 1, 145kDa (RFC1)	RFC1	3,11E-06	1,85897
NM_002939 // RefSeq // Homo sapiens ribonuclease/angiogenin inhibitor 1 (RNH1), transcr	RNH1	1,42E-09	1,62874
NM_003025 // RefSeq // Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), transcript variant	SH3GL1	3,39E-07	1,50451
NM_003048 // RefSeq // Homo sapiens solute carrier family 9, subfamily A (NHE2, cation	SLC9A2	1,58E-10	-4,82266
NM_003059 // RefSeq // Homo sapiens solute carrier family 22 (organic cation/ergothione	SLC22A4	6,92E-06	2,13731
NM_003082 // RefSeq // Homo sapiens small nuclear RNA activating complex, polypeptide 1	SNAPC1	2,60E-05	2,04491
NM_003100 // RefSeq // Homo sapiens sorting nexin 2 (SNX2), mRNA. // chr5 // 100 // 70	SNX2	4,87E-06	1,70353
NM_003146 // RefSeq // Homo sapiens structure specific recognition protein 1 (SSRP1), m	SSRP1	1,77E-06	1,50754
NM_003155 // RefSeq // Homo sapiens stanniocalcin 1 (STC1), mRNA. // chr8 // 100 // 86	STC1	5,57E-06	7,56609
NM_003171 // RefSeq // Homo sapiens suppressor of var1, 3-like 1 (S. cerevisiae) (SUPV3	SUPV3L1	5,39E-07	1,92745
NM_003249 // RefSeq // Homo sapiens thimet oligopeptidase 1 (THOP1), mRNA. // chr19 //	THOP1	5,00E-06	1,61004
NM_003314 // RefSeq // Homo sapiens tetratricopeptide repeat domain 1 (TTC1), mRNA. //	TTC1	4,66E-07	1,54851
NM_003380 // RefSeq // Homo sapiens vimentin (VIM), mRNA. // chr10 // 100 // 55 // 18 /	VIM	7,03E-06	3,82123
NM_003389 // RefSeq // Homo sapiens coronin, actin binding protein, 2A (CORO2A), transc	CORO2A	1,20E-06	-2,77405
NM_003468 // RefSeq // Homo sapiens frizzled family receptor 5 (FZD5), mRNA. // chr2 //	FZD5	1,34E-05	-1,91449
NM_003473 // RefSeq // Homo sapiens signal transducing adaptor molecule (SH3 domain and	STAM	7,44E-06	1,87745

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_003558 // RefSeq // Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I,	PIP5K1B	3,49E-09	-5,27062
NM_003561 // RefSeq // Homo sapiens phospholipase A2, group X (PLA2G10), mRNA. // chr16	PLA2G10	1,72E-08	-6,64273
NM_003621 // RefSeq // Homo sapiens PTPRF interacting protein, binding protein 2 (lipri	PPFIBP2	2,55E-06	-2,44237
NM_003637 // RefSeq // Homo sapiens integrin, alpha 10 (ITGA10), mRNA. // chr1 // 100 /	ITGA10	7,88E-09	4,32095
NM_003657 // RefSeq // Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), mRNA	BCAS1	9,67E-07	-5,32311
NM_003688 // RefSeq // Homo sapiens calcium/calmodulin-dependent serine protein kinase	CASK	1,79E-06	-1,70133
NM_003730 // RefSeq // Homo sapiens ribonuclease T2 (RNASET2), mRNA. // chr6 // 100 //	RNASET2	2,76E-06	-2,68746
NM_003740 // RefSeq // Homo sapiens potassium channel, subfamily K, member 5 (KCNK5), m	KCNK5	8,27E-10	-3,26274
NM_003786 // RefSeq // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), memb	ABCC3	3,65E-07	-3,12547
NM_003803 // RefSeq // Homo sapiens myomesin 1, 185kDa (MYOM1), transcript variant 1, m	MYOM1	2,32E-05	-3,392
NM_003839 // RefSeq // Homo sapiens tumor necrosis factor receptor superfamily, member	TNFRSF11A	3,34E-11	-4,92878
NM_003883 // RefSeq // Homo sapiens histone deacetylase 3 (HDAC3), mRNA. // chr5 // 100	HDAC3	7,46E-10	1,70453
NM_003889 // RefSeq // Homo sapiens nuclear receptor subfamily 1, group I, member 2 (NR	NR1I2	3,82E-07	-4,09907
NM_003927 // RefSeq // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcr	MBD2	2,55E-05	1,59749
NM_004055 // RefSeq // Homo sapiens calpain 5 (CAPN5), mRNA. // chr11 // 100 // 74 // 2	CAPN5	1,52E-06	-3,40528
NM_004079 // RefSeq // Homo sapiens cathepsin S (CTSS), transcript variant 1, mRNA. //	CTSS	2,44E-06	-2,56738
NM_004126 // RefSeq // Homo sapiens guanine nucleotide binding protein (G protein), gam	GNG11	1,12E-05	5,04648
NM_004133 // RefSeq // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /	HNF4G	1,38E-07	-3,44075
NM_004134 // RefSeq // Homo sapiens heat shock 70kDa protein 9 (mortalin) (HSPA9), nucl	HSPA9	4,78E-08	1,73539
NM_004170 // RefSeq // Homo sapiens solute carrier family 1 (neuronal/epithelial high a	SLC1A1	6,50E-09	-7,74362
NM_004235 // RefSeq // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. // chr9 /	KLF4	7,12E-06	-1,74298
NM_004240 // RefSeq // Homo sapiens thyroid hormone receptor interactor 10 (TRIP10), mR	TRIP10	1,49E-05	1,51893
NM_004249 // RefSeq // Homo sapiens RAB28,	RAB28	1,60E-06	1,54275

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
member RAS oncogene family (RAB28), transcri			
NM_004281 // RefSeq // Homo sapiens BCL2-associated athanogene 3 (BAG3), mRNA. // chr10	BAG3	5,51E-06	1,74201
NM_004282 // RefSeq // Homo sapiens BCL2-associated athanogene 2 (BAG2), mRNA. // chr6	BAG2	7,40E-07	2,96914
NM_004293 // RefSeq // Homo sapiens guanine deaminase (GDA), transcript variant 2, mRNA	GDA	2,00E-07	-4,98333
NM_004307 // RefSeq // Homo sapiens amyloid beta (A4) precursor protein-binding, family	APBB2	2,83E-06	1,97486
NM_004329 // RefSeq // Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI	BMPR1A	6,24E-06	1,69451
NM_004390 // RefSeq // Homo sapiens cathepsin H (CTSH), mRNA. // chr15 // 100 // 38 //	CTSH	3,10E-09	-2,87544
NM_004417 // RefSeq // Homo sapiens dual specificity phosphatase 1 (DUSP1), mRNA. // ch	DUSP1	1,68E-07	2,1245
NM_004420 // RefSeq // Homo sapiens dual specificity phosphatase 8 (DUSP8), mRNA. // ch	DUSP8	1,51E-05	-1,70935
NM_004472 // RefSeq // Homo sapiens forkhead box D1 (FOXD1), mRNA. // chr5 // 100 // 67	FOXD1	9,61E-07	2,86306
NM_004477 // RefSeq // Homo sapiens FSHD region gene 1 (FRG1), mRNA. // chr4 // 100 //	FRG1	3,07E-06	1,62969
NM_004497 // RefSeq // Homo sapiens forkhead box A3 (FOXA3), mRNA. // chr19 // 100 // 1	FOXA3	2,81E-05	-1,7194
NM_004607 // RefSeq // Homo sapiens tubulin folding cofactor A (TBCA), mRNA. // chr5 //	TBCA	7,79E-07	1,62625
NM_004636 // RefSeq // Homo sapiens sema domain, immunoglobulin domain (Ig), short basi	SEMA3B	6,84E-06	-2,39322
NM_004641 // RefSeq // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithor	MLLT10	4,11E-07	1,81768
NM_004661 // RefSeq // Homo sapiens cell division cycle 23 homolog (S. cerevisiae) (CDC	CDC23	4,16E-09	1,6899
NM_004672 // RefSeq // Homo sapiens mitogen-activated protein kinase kinase kinase 6 (M	MAP3K6	1,19E-05	1,6318
NM_004724 // RefSeq // Homo sapiens ZW10, kinetochore associated, homolog (Drosophila)	ZW10	6,66E-06	1,60086
NM_004726 // RefSeq // Homo sapiens RALBP1 associated Eps domain containing 2 (REPS2),	REPS2	6,02E-11	-3,83928
NM_004817 // RefSeq // Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2),	TJP2	1,28E-05	-1,93552
NM_004852 // RefSeq // Homo sapiens one cut homeobox 2 (ONECUT2), mRNA. // chr18 // 100	ONECUT2	1,48E-12	-3,51155
NM_004866 // RefSeq // Homo sapiens secretory carrier membrane protein 1 (SCAMP1), mRNA	SCAMP1	1,16E-07	1,53148
NM_004938 // RefSeq // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. //	DAPK1	8,78E-08	-4,66228

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_004978 // RefSeq // Homo sapiens potassium voltage-gated channel, Shaw-related subfa	KCNC4	9,13E-06	-1,68861
NM_004995 // RefSeq // Homo sapiens matrix metalloproteinase 14 (membrane-inserted) (MMP	MMP14	1,91E-05	1,68308
NM_004999 // RefSeq // Homo sapiens myosin VI (MYO6), mRNA. // chr6 // 100 // 97 // 31	MYO6	5,62E-09	-2,15877
NM_005060 // RefSeq // Homo sapiens RAR-related orphan receptor C (RORC), transcript va	RORC	6,72E-07	-2,2321
NM_005257 // RefSeq // Homo sapiens GATA binding protein 6 (GATA6), mRNA. // chr18 // 1	GATA6	2,25E-07	-4,74869
NM_005261 // RefSeq // Homo sapiens GTP binding protein overexpressed in skeletal muscle	GEM	1,58E-05	2,01863
NM_005271 // RefSeq // Homo sapiens glutamate dehydrogenase 1 (GLUD1), nuclear gene enc	GLUD1	9,93E-07	1,57385
NM_005276 // RefSeq // Homo sapiens glycerol-3-phosphate dehydrogenase 1 (soluble) (GPD	GPD1	4,69E-06	-1,81233
NM_005349 // RefSeq // Homo sapiens recombination signal binding protein for immunoglob	RBPJ	1,46E-05	1,56501
NM_005429 // RefSeq // Homo sapiens vascular endothelial growth factor C (VEGFC), mRNA.	VEGFC	3,21E-06	2,75523
NM_005445 // RefSeq // Homo sapiens structural maintenance of chromosomes 3 (SMC3), mRN	SMC3	1,36E-05	1,73547
NM_005472 // RefSeq // Homo sapiens potassium voltage-gated channel, Isk-related family	KCNE3	1,64E-06	-5,41251
NM_005486 // RefSeq // Homo sapiens target of myb1 (chicken)-like 1 (TOM1L1), mRNA. //	TOM1L1	1,76E-05	-1,86045
NM_005550 // RefSeq // Homo sapiens kinesin family member C3 (KIFC3), transcript varian	KIFC3	4,08E-07	1,80767
NM_005573 // RefSeq // Homo sapiens lamin B1 (LMNB1), transcript variant 1, mRNA. // ch	LMNB1	3,09E-07	1,602
NM_005578 // RefSeq // Homo sapiens LIM domain containing preferred translocation partn	LPP	4,17E-07	-1,65196
NM_005724 // RefSeq // Homo sapiens tetraspanin 3 (TSPAN3), transcript variant 1, mRNA.	TSPAN3	3,10E-11	-2,17613
NM_005727 // RefSeq // Homo sapiens tetraspanin 1 (TSPAN1), mRNA. // chr1 // 100 // 71	TSPAN1	8,67E-07	-3,00503
NM_005732 // RefSeq // Homo sapiens RAD50 homolog (S. cerevisiae) (RAD50), mRNA. // chr	RAD50	3,84E-06	1,58783
NM_005733 // RefSeq // Homo sapiens kinesin family member 20A (KIF20A), mRNA. // chr5 /	KIF20A	1,53E-07	1,72119
NM_005746 // RefSeq // Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT), mRN	NAMPT	2,29E-05	2,00349
NM_005764 // RefSeq // Homo sapiens PDZK1 interacting protein 1 (PDZK1IP1), mRNA. // ch	PDZK1IP1	8,36E-07	-3,77744
NM_005767 // RefSeq // Homo sapiens lysophospha-	LPAR6	3,24E-06	-1,82469

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
tidic acid receptor 6 (LPAR6), transcrip			
NM_005780 // RefSeq // Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. // chr13	LHFP	5,61E-06	1,54322
NM_005865 // RefSeq // Homo sapiens protease, serine, 16 (thymus) (PRSS16), mRNA. // ch	PRSS16	1,36E-06	-1,60344
NM_005869 // RefSeq // Homo sapiens CWC27 spliceosome-associated protein homolog (S. ce	CWC27	1,04E-05	1,75413
NM_005967 // RefSeq // Homo sapiens NGFI-A binding protein 2 (EGR1 binding protein 2) (	NAB2	1,71E-05	1,71749
NM_005969 // RefSeq // Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), mRNA	NAP1L4	1,15E-06	1,53719
NM_005982 // RefSeq // Homo sapiens SIX homeobox 1 (SIX1), mRNA. // chr14 // 100 // 45	SIX1	3,40E-07	1,77984
NM_006017 // RefSeq // Homo sapiens prominin 1 (PROM1), transcript variant 1, mRNA. //	PROM1	7,29E-16	-14,3953
NM_006083 // RefSeq // Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA. /	IK	6,35E-06	1,53955
NM_006149 // RefSeq // Homo sapiens lectin, galactoside-binding, soluble, 4 (LGALS4), m	LGALS4	1,69E-09	-12,2815
NM_006282 // RefSeq // Homo sapiens serine/threonine kinase 4 (STK4), mRNA. // chr20 //	STK4	7,94E-06	1,6133
NM_006397 // RefSeq // Homo sapiens ribonuclease H2, subunit A (RNASEH2A), mRNA. // chr	RNASEH2A	2,78E-07	1,8307
NM_006442 // RefSeq // Homo sapiens DR1-associated protein 1 (negative cofactor 2 alpha	DRAP1	1,98E-09	1,73334
NM_006615 // RefSeq // Homo sapiens calpain 9 (CAPN9), transcript variant 1, mRNA. // c	CAPN9	2,07E-05	-4,01722
NM_006633 // RefSeq // Homo sapiens IQ motif containing GTPase activating protein 2 (IQ	IQGAP2	7,41E-10	-11,3352
NM_006738 // RefSeq // Homo sapiens A kinase (PRKA) anchor protein 13 (AKAP13), transcr	AKAP13	1,57E-05	-1,65705
NM_006769 // RefSeq // Homo sapiens LIM domain only 4 (LMO4), mRNA. // chr1 // 100 // 6	LMO4	2,19E-05	-2,69509
NM_006809 // RefSeq // Homo sapiens translocase of outer mitochondrial membrane 34 (TOM	TOMM34	3,00E-05	1,8995
NM_006871 // RefSeq // Homo sapiens receptor-interacting serine-threonine kinase 3 (RIP	RIPK3	1,88E-05	-2,47697
NM_006887 // RefSeq // Homo sapiens zinc finger protein 36, C3H type-like 2 (ZFP36L2),	ZFP36L2	7,74E-07	-1,97496
NM_006895 // RefSeq // Homo sapiens histamine N-methyltransferase (HNMT), transcript va	HNMT	3,00E-07	-3,01755
NM_006930 // RefSeq // Homo sapiens S-phase kinase-associated protein 1 (SKP1), transcr	SKP1	3,46E-07	1,79509
NM_006933 // RefSeq // Homo sapiens solute carrier family 5 (sodium/myo-inositol cotran	SLC5A3	1,11E-09	2,57353

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_006951 // RefSeq // Homo sapiens TAF5 RNA polymerase II, TATA box binding protein (T	TAF5	3,01E-06	1,7264
NM_006999 // RefSeq // Homo sapiens PAP associated domain containing 7 (PAPD7), transcr	PAPD7	8,53E-09	1,79709
NM_007011 // RefSeq // Homo sapiens abhydrolase domain containing 2 (ABHD2), transcript	ABHD2	1,22E-07	-2,19797
NM_007103 // RefSeq // Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 1, 51k	NDUFV1	6,58E-08	1,51326
NM_007129 // RefSeq // Homo sapiens Zic family member 2 (ZIC2), mRNA. // chr13 // 100 /	ZIC2	2,40E-06	2,36547
NM_007173 // RefSeq // Homo sapiens protease, serine, 23 (PRSS23), mRNA. // chr11 // 10	PRSS23	1,35E-06	2,20939
NM_007186 // RefSeq // Homo sapiens centrosomal protein 250kDa (CEP250), mRNA. // chr20	CEP250	5,88E-09	1,96026
NM_007195 // RefSeq // Homo sapiens polymerase (DNA directed) iota (POLI), mRNA. // chr	POL1	1,48E-05	2,05477
NM_007213 // RefSeq // Homo sapiens PRA1 domain family, member 2 (PRAF2), mRNA. // chrX	PRAF2	6,40E-06	1,8937
NM_007220 // RefSeq // Homo sapiens carbonic anhydrase VB, mitochondrial (CA5B), nuclea	CA5B	2,03E-06	1,76794
NM_007223 // RefSeq // Homo sapiens G protein-coupled receptor 176 (GPR176), mRNA. // c	GPR176	2,58E-07	2,32054
NM_012112 // RefSeq // Homo sapiens TPX2, microtubule-associated, homolog (Xenopus laev	TPX2	1,37E-05	1,62922
NM_012120 // RefSeq // Homo sapiens CD2-associated protein (CD2AP), mRNA. // chr6 // 10	CD2AP	1,18E-07	-1,53535
NM_012177 // RefSeq // Homo sapiens F-box protein 5 (FBXO5), transcript variant 1, mRNA	FBXO5	1,48E-05	1,89663
NM_012200 // RefSeq // Homo sapiens beta-1,3-glucuronyltransferase 3 (glucuronosyltrans	B3GAT3	1,19E-09	1,55988
NM_012238 // RefSeq // Homo sapiens sirtuin 1 (SIRT1), transcript variant 1, mRNA. // c	SIRT1	8,30E-07	2,02532
NM_012289 // RefSeq // Homo sapiens kelch-like ECH-associated protein 1 (KEAP1), transc	KEAP1	1,96E-06	1,52174
NM_012291 // RefSeq // Homo sapiens extra spindle pole bodies homolog 1 (S. cerevisiae)	ESPL1	1,69E-06	1,56875
NM_012340 // RefSeq // Homo sapiens nuclear factor of activated T-cells, cytoplasmic, c	NFATC2	2,94E-06	-1,82662
NM_012454 // RefSeq // Homo sapiens T-cell lymphoma invasion and metastasis 2 (TIAM2),	TIAM2	1,09E-07	-2,32022
NM_013230 // RefSeq // Homo sapiens CD24 molecule (CD24), mRNA. // chrY // 68 // 100 //	CD24	8,43E-09	-10,0061
NM_013337 // RefSeq // Homo sapiens translocase of inner mitochondrial membrane 22 homo	TIMM22	1,72E-05	1,71899
NM_013389 // RefSeq // Homo sapiens NPC1 (Nie-	NPC1L1	3,07E-18	-10,3772

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
mann-Pick disease, type C1, gene)-like 1 (			
NM_013390 // RefSeq // Homo sapiens transmembrane protein 2 (TMEM2), transcript variant	TMEM2	1,33E-10	-4,63651
NM_013402 // RefSeq // Homo sapiens fatty acid desaturase 1 (FADS1), mRNA. // chr11 //	FADS1	1,26E-05	1,66257
NM_013437 // RefSeq // Homo sapiens low density lipoprotein receptor-related protein 12	LRP12	6,94E-08	3,00003
NM_013451 // RefSeq // Homo sapiens myoferlin (MYOF), transcript variant 1, mRNA. // ch	MYOF	3,39E-06	1,73353
NM_014035 // RefSeq // Homo sapiens sorting nexin 24 (SNX24), mRNA. // chr5 // 100 // 3	SNX24	5,84E-06	1,79881
NM_014226 // RefSeq // Homo sapiens MOK protein kinase (MOK), mRNA. // chr14 // 100 //	MOK	1,31E-06	2,08795
NM_014241 // RefSeq // Homo sapiens protein tyrosine phosphatase-like (proline instead	PTPLA	1,18E-08	4,17505
NM_014312 // RefSeq // Homo sapiens V-set and immunoglobulin domain containing 2 (VSIG2	VSIG2	2,28E-08	-4,2413
NM_014326 // RefSeq // Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. //	DAPK2	3,02E-06	-2,27857
NM_014344 // RefSeq // Homo sapiens four jointed box 1 (Drosophila) (FJX1), mRNA. // ch	FJX1	1,35E-07	4,3145
NM_014373 // RefSeq // Homo sapiens G protein-coupled receptor 160 (GPR160), mRNA. // c	GPR160	2,35E-06	-2,82018
NM_014391 // RefSeq // Homo sapiens ankyrin repeat domain 1 (cardiac muscle) (ANKRD1),	ANKRD1	2,66E-06	3,95638
NM_014394 // RefSeq // Homo sapiens growth hormone inducible transmembrane protein (GHI	GHITM	1,77E-07	1,54607
NM_014470 // RefSeq // Homo sapiens Rho family GTPase 1 (RND1), mRNA. // chr12 // 100 /	RND1	1,70E-05	-1,70826
NM_014473 // RefSeq // Homo sapiens DIM1 dimethyladenosine transferase 1 homolog (S. ce	DIMT1	6,66E-06	1,8146
NM_014553 // RefSeq // Homo sapiens transcription factor CP2-like 1 (TFCP2L1), mRNA. //	TFCP2L1	1,03E-08	-3,83608
NM_014639 // RefSeq // Homo sapiens tetratricopeptide repeat domain 37 (TTC37), mRNA. /	TTC37	3,72E-06	1,6999
NM_014669 // RefSeq // Homo sapiens nucleoporin 93kDa (NUP93), transcript variant 1, mR	NUP93	2,55E-05	1,64157
NM_014698 // RefSeq // Homo sapiens transmembrane protein 63A (TMEM63A), mRNA. // chr1	TMEM63A	1,76E-06	-2,15003
NM_014755 // RefSeq // Homo sapiens SERTA domain containing 2 (SERTAD2), mRNA. // chr2	SERTAD2	6,74E-08	2,02911
NM_014801 // RefSeq // Homo sapiens pecanex-like 2 (Drosophila) (PCNXL2), mRNA. // chr1	PCNXL2	3,16E-07	-2,62205
NM_014808 // RefSeq // Homo sapiens FERM, RhoGEF and pleckstrin domain protein 2 (FARP2	FARP2	3,70E-07	-1,55286

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_014819 // RefSeq // Homo sapiens praja ring finger 2, E3 ubiquitin protein ligase (P	PJA2	3,45E-11	1,80215
NM_014824 // RefSeq // Homo sapiens FCH and double SH3 domains 2 (FCHSD2), mRNA. // chr	FCHSD2	2,55E-08	2,06135
NM_014829 // RefSeq // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 (DDX46),	DDX46	1,57E-10	1,62102
NM_014840 // RefSeq // Homo sapiens NUA1 family, SNF1-like kinase, 1 (NUAK1), mRNA. //	NUAK1	5,87E-07	2,11629
NM_014861 // RefSeq // Homo sapiens ATPase, Ca++ transporting, type 2C, member 2 (ATP2C	ATP2C2	3,96E-07	-3,56944
NM_014874 // RefSeq // Homo sapiens mitofusin 2 (MFN2), nuclear gene encoding mitochond	MFN2	2,44E-05	1,6586
NM_014935 // RefSeq // Homo sapiens pleckstrin homology domain containing, family A mem	PLEKHA6	1,13E-05	-2,79537
NM_014982 // RefSeq // Homo sapiens pecanex homolog (Drosophila) (PCNX), mRNA. // chr14	PCNX	5,56E-06	1,58249
NM_015018 // RefSeq // Homo sapiens dopey family member 1 (DOPEY1), transcript variant	DOPEY1	1,37E-05	-1,63396
NM_015027 // RefSeq // Homo sapiens pyridoxal-dependent decarboxylase domain containing	PDXDC1	2,38E-07	-1,50753
NM_015041 // RefSeq // Homo sapiens clusterin associated protein 1 (CLUAP1), transcript	CLUAP1	1,80E-08	1,85354
NM_015179 // RefSeq // Homo sapiens ribosomal RNA processing 12 homolog (S. cerevisiae)	RRP12	1,66E-05	1,65573
NM_015187 // RefSeq // Homo sapiens sel-1 suppressor of lin-12-like 3 (C. elegans) (SEL	SEL1L3	2,19E-05	-3,25169
NM_015198 // RefSeq // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. // chr7 /	COBL	8,52E-07	-2,38065
NM_015261 // RefSeq // Homo sapiens non-SMC condensin II complex, subunit D3 (NCAPD3),	NCAPD3	1,68E-05	1,60627
NM_015265 // RefSeq // Homo sapiens SATB homeobox 2 (SATB2), transcript variant 2, mRNA	SATB2	7,52E-07	1,87255
NM_015279 // RefSeq // Homo sapiens TBC1 domain family, member 30 (TBC1D30), mRNA. // c	TBC1D30	1,11E-08	-2,71759
NM_015342 // RefSeq // Homo sapiens peptidylprolyl isomerase domain and WD repeat conta	PPWD1	7,10E-06	1,55324
NM_015465 // RefSeq // Homo sapiens gem (nuclear organelle) associated protein 5 (GEMIN	GEMIN5	2,65E-05	1,82836
NM_015523 // RefSeq // Homo sapiens REX2, RNA exonuclease 2 homolog (S. cerevisiae) (RE	REXO2	5,69E-06	1,83576
NM_015675 // RefSeq // Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD4	GADD45B	6,24E-08	2,82559
NM_015714 // RefSeq // Homo sapiens G0/G1 switch 2 (G0S2), mRNA. // chr1 // 100 // 100 /	G0S2	1,84E-05	2,47245
NM_015831 // RefSeq // Homo sapiens acetylcho-	ACHE	4,74E-07	-2,30919

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
linesterase (ACHE), transcript variant E4-			
NM_015873 // RefSeq // Homo sapiens villin-like (VILL), mRNA. // chr3 // 100 // 65 // 1	VILL	1,15E-07	-3,1407
NM_015942 // RefSeq // Homo sapiens MTERF domain containing 1 (MTERFD1), nuclear gene e	MTERFD1	2,80E-07	1,51271
NM_015960 // RefSeq // Homo sapiens cutC copper transporter homolog (E. coli) (CUTC), m	CUTC	3,69E-07	1,75155
NM_016010 // RefSeq // Homo sapiens zinc finger, C2HC-type containing 1A (ZC2HC1A), mRN	ZC2HC1A	6,63E-07	1,84085
NM_016032 // RefSeq // Homo sapiens zinc finger, DHHC-type containing 9 (ZDHHC9), trans	ZDHHC9	1,92E-05	-1,53184
NM_016218 // RefSeq // Homo sapiens polymerase (DNA directed) kappa (POLK), mRNA. // ch	POLK	6,87E-06	1,5116
NM_016240 // RefSeq // Homo sapiens scavenger receptor class A, member 3 (SCARA3), tran	SCARA3	1,29E-06	2,75506
NM_016277 // RefSeq // Homo sapiens RAB23, member RAS oncogene family (RAB23), transcri	RAB23	2,87E-05	2,19716
NM_016283 // RefSeq // Homo sapiens TAF9 RNA polymerase II, TATA box binding protein (T	TAF9	2,42E-07	1,69866
NM_016308 // RefSeq // Homo sapiens cytidine monophosphate (UMP-CMP) kinase 1, cytosoli	CMPK1	1,74E-05	-1,53193
NM_016356 // RefSeq // Homo sapiens doublecortin domain containing 2 (DCDC2), transcrip	DCDC2	1,67E-07	-4,51992
NM_016361 // RefSeq // Homo sapiens acid phosphatase 6, lysophosphatidic (ACP6), mRNA.	ACP6	1,94E-06	-1,85025
NM_016441 // RefSeq // Homo sapiens cysteine rich transmembrane BMP regulator 1 (chordi	CRIM1	1,47E-05	1,58447
NM_016657 // RefSeq // Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protei	KDEL3	1,44E-05	-2,03177
NM_017420 // RefSeq // Homo sapiens SIX homeobox 4 (SIX4), mRNA. // chr14 // 100 // 67	SIX4	3,46E-07	2,29441
NM_017640 // RefSeq // Homo sapiens leucine rich repeat containing 16A (LRRC16A), trans	LRRC16A	2,35E-07	-3,77497
NM_017688 // RefSeq // Homo sapiens B-box and SPRY domain containing (BSPRY), mRNA. //	BSPRY	6,76E-06	-1,95831
NM_017708 // RefSeq // Homo sapiens family with sequence similarity 83, member E (FAM83	FAM83E	3,92E-09	-2,24897
NM_017712 // RefSeq // Homo sapiens pyroglutamyl-peptidase I (PGPEP1), mRNA. // chr19 /	PGPEP1	8,11E-06	-2,26798
NM_017752 // RefSeq // Homo sapiens TBC1 domain family, member 8B (with GRAM domain) (T	TBC1D8B	4,81E-07	-2,5223
NM_017755 // RefSeq // Homo sapiens NOP2/Sun RNA methyltransferase family, member 2 (NS	NSUN2	2,61E-05	1,50241
NM_017816 // RefSeq // Homo sapiens Lyl antibody reactive homolog (mouse) (LYAR), trans	LYAR	1,15E-08	2,74029

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_017824 // RefSeq // Homo sapiens membrane-associated ring finger (C3HC4) 5 (MARCH5),	MARCH5	1,07E-06	1,58164
NM_017848 // RefSeq // Homo sapiens family with sequence similarity 120C (FAM120C), tra	FAM120C	1,59E-05	1,64572
NM_017893 // RefSeq // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembr	SEMA4G	1,24E-06	-3,82476
NM_017987 // RefSeq // Homo sapiens RUN and FYVE domain containing 2 (RUFY2), transcrip	RUFY2	9,92E-07	1,59015
NM_018120 // RefSeq // Homo sapiens armadillo repeat containing 1 (ARMC1), mRNA. // chr	ARMC1	2,89E-06	1,50314
NM_018121 // RefSeq // Homo sapiens family with sequence similarity 178, member A (FAM1	FAM178A	5,42E-10	1,63729
NM_018131 // RefSeq // Homo sapiens centrosomal protein 55kDa (CEP55), transcript varia	CEP55	2,15E-06	2,29507
NM_018178 // RefSeq // Homo sapiens golgi phosphoprotein 3-like (GOLPH3L), mRNA. // chr	GOLPH3L	5,58E-08	-1,71613
NM_018226 // RefSeq // Homo sapiens arginyl aminopeptidase (aminopeptidase B)-like 1 (R	RNPEPL1	4,58E-10	-1,58752
NM_018240 // RefSeq // Homo sapiens kin of IRRE like (Drosophila) (KIRREL), mRNA. // ch	KIRREL	1,79E-06	2,74686
NM_018268 // RefSeq // Homo sapiens WD repeat domain 41 (WDR41), mRNA. // chr5 // 100 /	WDR41	2,86E-06	1,54487
NM_018270 // RefSeq // Homo sapiens chromosome 20 open reading frame 20 (C20orf20), mRN	C20orf20	2,04E-06	1,76087
NM_018288 // RefSeq // Homo sapiens PHD finger protein 10 (PHF10), transcript variant 1	PHF10	5,27E-06	1,72185
NM_018290 // RefSeq // Homo sapiens phosphoglucomutase 2 (PGM2), mRNA. // chr4 // 100 /	PGM2	2,48E-05	1,59095
NM_018302 // RefSeq // Homo sapiens chromosome 4 open reading frame 19 (C4orf19), trans	C4orf19	3,79E-06	-3,1795
NM_018303 // RefSeq // Homo sapiens exocyst complex component 2 (EXOC2), mRNA. // chr6	EXOC2	2,80E-05	1,56773
NM_018319 // RefSeq // Homo sapiens tyrosyl-DNA phosphodiesterase 1 (TDP1), transcript	TDP1	4,16E-08	1,61671
NM_018343 // RefSeq // Homo sapiens RIO kinase 2 (yeast) (RIOK2), transcript variant 1,	RIOK2	4,34E-09	1,94851
NM_018397 // RefSeq // Homo sapiens choline dehydrogenase (CHDH), nuclear gene encoding	CHDH	9,72E-06	-2,38333
NM_018409 // RefSeq // Homo sapiens LRP2 binding protein (LRP2BP), mRNA. // chr4 // 100	LRP2BP	7,40E-06	1,55085
NM_018429 // RefSeq // Homo sapiens B double prime 1, subunit of RNA polymerase III tra	BDP1	4,88E-10	1,634
NM_018456 // RefSeq // Homo sapiens ELL associated factor 2 (EAF2), mRNA. // chr3 // 10	EAF2	1,94E-06	-2,25283
NM_018651 // RefSeq // Homo sapiens zinc finger	ZNF167	2,44E-05	-1,73535

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
protein 167 (ZNF167), transcript varian			
NM_018842 // RefSeq // Homo sapiens BAI1-associated protein 2-like 1 (BAIAP2L1), mRNA.	BAIAP2L1	1,50E-05	-2,70286
NM_018964 // RefSeq // Homo sapiens solute carrier family 37 (glycerol-3-phosphate tran	SLC37A1	2,09E-05	-2,19597
NM_018976 // RefSeq // Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA.	SLC38A2	6,35E-11	2,11953
NM_018984 // RefSeq // Homo sapiens slingshot homolog 1 (Drosophila) (SSH1), transcript	SSH1	1,04E-06	1,70245
NM_018989 // RefSeq // Homo sapiens RNA binding motif protein 27 (RBM27), mRNA. // chr5	RBM27	6,36E-09	1,53409
NM_018999 // RefSeq // Homo sapiens family with sequence similarity 190, member B (FAM1	FAM190B	2,54E-08	2,05467
NM_019030 // RefSeq // Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 29 (DHX29),	DHX29	3,32E-07	1,8447
NM_019072 // RefSeq // Homo sapiens small glutamine-rich tetratricopeptide repeat (TPR)	SGTB	1,96E-05	2,70842
NM_019859 // RefSeq // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 7, adenyly	HTR7	1,15E-05	2,20274
NM_020117 // RefSeq // Homo sapiens leucyl-tRNA synthetase (LARS), mRNA. // chr5 // 100	LARS	3,63E-06	1,91859
NM_020208 // RefSeq // Homo sapiens solute carrier family 6 (proline IMINO transporter)	SLC6A20	3,78E-14	-6,2697
NM_020340 // RefSeq // Homo sapiens KIAA1244 (KIAA1244), mRNA. // chr6 // 100 // 100 //	KIAA1244	1,34E-06	-2,24402
NM_020343 // RefSeq // Homo sapiens Ral GTPase activating protein, alpha subunit 2 (cat	RALGA-PA2	2,29E-05	-2,4487
NM_020453 // RefSeq // Homo sapiens ATPase, class V, type 10D (ATP10D), mRNA. // chr4 /	ATP10D	1,73E-07	2,49698
NM_020529 // RefSeq // Homo sapiens nuclear factor of kappa light polypeptide gene enha	NFKBIA	8,81E-06	1,76041
NM_020722 // RefSeq // Homo sapiens KIAA1211 (KIAA1211), mRNA. // chr4 // 100 // 74 //	KIAA1211	1,83E-09	-2,59744
NM_020726 // RefSeq // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), nucl	NLN	2,99E-05	1,79955
NM_020770 // RefSeq // Homo sapiens cingulin (CGN), mRNA. // chr1 // 100 // 79 // 15 //	CGN	1,08E-05	-2,87225
NM_020773 // RefSeq // Homo sapiens TBC1 domain family, member 14 (TBC1D14), transcript	TBC1D14	7,69E-07	1,61063
NM_020801 // RefSeq // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. // chr	ARRDC3	4,71E-07	2,20374
NM_020859 // RefSeq // Homo sapiens shroom family member 3 (SHROOM3), mRNA. // chr4 //	SHROOM3	2,94E-08	-3,96414
NM_020873 // RefSeq // Homo sapiens leucine rich repeat neuronal 1 (LRRN1), mRNA. // ch	LRRN1	1,17E-05	-3,09541

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_020886 // RefSeq // Homo sapiens ubiquitin specific peptidase 28 (USP28), mRNA. // c	USP28	9,84E-06	1,71757
NM_021200 // RefSeq // Homo sapiens pleckstrin homology domain containing, family B (ev	PLEKHB1	9,82E-06	-1,71345
NM_021214 // RefSeq // Homo sapiens family with sequence similarity 108, member C1 (FAM	FAM108C1	1,02E-05	-2,18379
NM_021947 // RefSeq // Homo sapiens serine racemase (SRR), mRNA. // chr17 // 100 // 100	SRR	9,89E-08	2,02806
NM_021999 // RefSeq // Homo sapiens integral membrane protein 2B (ITM2B), mRNA. // chr1	ITM2B	1,44E-05	-1,5076
NM_022145 // RefSeq // Homo sapiens centromere protein K (CENPK), transcript variant 1,	CENPK	1,55E-05	1,89702
NM_022346 // RefSeq // Homo sapiens non-SMC condensin I complex, subunit G (NCAPG), mRN	NCAPG	1,62E-08	2,18889
NM_022449 // RefSeq // Homo sapiens RAB17, member RAS oncogene family (RAB17), transcri	RAB17	8,42E-06	-1,80027
NM_022481 // RefSeq // Homo sapiens ArfGAP with RhoGAP domain, ankyrin repeat and PH do	ARAP3	2,20E-06	1,77549
NM_022825 // RefSeq // Homo sapiens porcupine homolog (Drosophila) (PORCN), transcript	PORCN	3,48E-06	1,81584
NM_022909 // RefSeq // Homo sapiens centromere protein H (CENPH), mRNA. // chr5 // 100	CENPH	5,74E-08	2,64595
NM_022970 // RefSeq // Homo sapiens fibroblast growth factor receptor 2 (FGFR2), transc	FGFR2	1,07E-06	-3,05461
NM_024092 // RefSeq // Homo sapiens transmembrane protein 109 (TMEM109), mRNA. // chr11	TMEM109	1,08E-07	1,95659
NM_024101 // RefSeq // Homo sapiens melanophilin (MLPH), transcript variant 1, mRNA. //	MLPH	1,50E-05	-2,76966
NM_024306 // RefSeq // Homo sapiens fatty acid 2-hydroxylase (FA2H), mRNA. // chr16 //	FA2H	1,04E-05	-3,1323
NM_024320 // RefSeq // Homo sapiens proline rich 15-like (PRR15L), mRNA. // chr17 // 10	PRR15L	1,17E-07	-5,5807
NM_024420 // RefSeq // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dep	PLA2G4A	2,07E-08	-3,367
NM_024539 // RefSeq // Homo sapiens ring finger protein 128, E3 ubiquitin protein ligas	RNF128	1,50E-07	-4,2009
NM_024576 // RefSeq // Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA	OGFRL1	6,24E-06	2,03059
NM_024577 // RefSeq // Homo sapiens SH3 domain and tetratricopeptide repeats 2 (SH3TC2)	SH3TC2	6,82E-06	1,9706
NM_024608 // RefSeq // Homo sapiens nei endonuclease VIII-like 1 (E. coli) (NEIL1), tra	NEIL1	1,56E-07	-2,12245
NM_024628 // RefSeq // Homo sapiens solute carrier family 12 (potassium/chloride transp	SLC12A8	1,19E-06	-1,75792
NM_024642 // RefSeq // Homo sapiens UDP-N-	GALNT12	3,20E-06	-3,80907

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
acetyl-alpha-D-galactosamine:polypeptide N-ac			
NM_024712 // RefSeq // Homo sapiens engulfment and cell motility 3 (ELMO3), mRNA. // ch	ELMO3	2,17E-05	-1,62831
NM_024727 // RefSeq // Homo sapiens leucine rich repeat containing 31 (LRRC31), mRNA. /	LRRC31	2,12E-05	-3,81382
NM_024754 // RefSeq // Homo sapiens pentatricopeptide repeat domain 2 (PTCD2), mRNA. //	PTCD2	1,69E-06	1,81064
NM_024756 // RefSeq // Homo sapiens multimerin 2 (MMRN2), mRNA. // chr10 // 100 // 57 /	MMRN2	5,36E-06	1,59057
NM_024790 // RefSeq // Homo sapiens centrosome and spindle pole associated protein 1 (C	CSPP1	2,77E-05	1,6024
NM_024795 // RefSeq // Homo sapiens transmembrane 4 L six family member 20 (TM4SF20), m	TM4SF20	4,78E-08	-13,9678
NM_024834 // RefSeq // Homo sapiens minichromosome maintenance complex binding protein	MCMBP	3,57E-06	1,77466
NM_024921 // RefSeq // Homo sapiens premature ovarian failure, 1B (POF1B), mRNA. // chr	POF1B	6,45E-06	-5,26964
NM_024936 // RefSeq // Homo sapiens zinc finger, CCHC domain containing 4 (ZCCHC4), mRN	ZCCHC4	1,01E-05	1,548
NM_024954 // RefSeq // Homo sapiens ubiquitin domain containing 1 (UBTD1), mRNA. // chr	UBTD1	1,25E-08	1,67307
NM_025004 // RefSeq // Homo sapiens coiled-coil domain containing 15 (CCDC15), mRNA. //	CCDC15	1,17E-06	2,41792
NM_025106 // RefSeq // Homo sapiens splA/ryanodine receptor domain and SOCS box contain	SPSB1	3,18E-06	1,7784
NM_025132 // RefSeq // Homo sapiens WD repeat domain 19 (WDR19), mRNA. // chr4 // 100 /	WDR19	7,52E-06	2,35118
NM_025164 // RefSeq // Homo sapiens SIK family kinase 3 (SIK3), mRNA. // chr11 // 100 /	SIK3	2,05E-05	1,5795
NM_025245 // RefSeq // Homo sapiens pre-B-cell leukemia homeobox 4 (PBX4), transcript v	PBX4	4,16E-06	1,59466
NM_030622 // RefSeq // Homo sapiens cytochrome P450, family 2, subfamily S, polypeptide	CYP2S1	1,17E-05	-4,58802
NM_030628 // RefSeq // Homo sapiens integrator complex subunit 5 (INTS5), mRNA. // chr1	INTS5	3,61E-08	1,52049
NM_030630 // RefSeq // Homo sapiens chromosome 17 open reading frame 28 (C17orf28), mRN	C17orf28	4,89E-12	-5,3555
NM_030751 // RefSeq // Homo sapiens zinc finger E-box binding homeobox 1 (ZEB1), transc	ZEB1	1,20E-05	3,43139
NM_030767 // RefSeq // Homo sapiens AT-hook transcription factor (AKNA), mRNA. // chr9	AKNA	2,96E-06	-1,50389
NM_030783 // RefSeq // Homo sapiens phosphatidylserine synthase 2 (PTDSS2), mRNA. // ch	PTDSS2	6,59E-09	1,67521
NM_030919 // RefSeq // Homo sapiens family with	FAM83D	1,30E-05	1,69234

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
sequence similarity 83, member D (FAM83			
NM_030926 // RefSeq // Homo sapiens integral membrane protein 2C (ITM2C), transcript va	ITM2C	2,54E-08	-2,17254
NM_030964 // RefSeq // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), transcript	SPRY4	1,92E-05	1,83423
NM_031212 // RefSeq // Homo sapiens solute carrier family 25 (mitochondrial iron transp	SLC25A28	1,78E-05	1,67648
NM_031217 // RefSeq // Homo sapiens kinesin family member 18A (KIF18A), mRNA. // chr11	KIF18A	2,64E-08	2,08959
NM_031302 // RefSeq // Homo sapiens glycosyltransferase 8 domain containing 2 (GLT8D2),	GLT8D2	4,68E-06	3,41962
NM_031415 // RefSeq // Homo sapiens gasdermin C (GSDMC), mRNA. // chr8 // 100 // 86 //	GSDMC	2,15E-05	6,33453
NM_031419 // RefSeq // Homo sapiens nuclear factor of kappa light polypeptide gene enha	NFKBIZ	1,10E-05	-2,14027
NM_031439 // RefSeq // Homo sapiens SRY (sex determining region Y)-box 7 (SOX7), mRNA.	SOX7	3,13E-08	2,17199
NM_031457 // RefSeq // Homo sapiens membrane-spanning 4-domains, subfamily A, member 8B	MS4A8B	5,01E-06	-3,62687
NM_031463 // RefSeq // Homo sapiens hydroxysteroid dehydrogenase like 1 (HSDL1), transc	HSDL1	2,24E-07	1,93101
NM_031469 // RefSeq // Homo sapiens SH3 domain binding glutamic acid-rich protein like	SH3BGR L2	2,54E-06	-3,87722
NM_031966 // RefSeq // Homo sapiens cyclin B1 (CCNB1), mRNA. // chr5 // 100 // 85 // 17	CCNB1	1,13E-08	2,1201
NM_032042 // RefSeq // Homo sapiens family with sequence similarity 172, member A (FAM1	FAM172A	2,47E-08	1,53397
NM_032175 // RefSeq // Homo sapiens UTP15, U3 small nucleolar ribonucleoprotein, homolo	UTP15	1,09E-06	1,72995
NM_032208 // RefSeq // Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript varia	ANTXR1	4,13E-07	3,60105
NM_032898 // RefSeq // Homo sapiens centrosomal protein 19kDa (CEP19), mRNA. // chr3 //	CEP19	7,28E-07	1,54008
NM_033049 // RefSeq // Homo sapiens mucin 13, cell surface associated (MUC13), mRNA. //	MUC13	3,33E-08	-18,5751
NM_033102 // RefSeq // Homo sapiens solute carrier family 45, member 3 (SLC45A3), mRNA.	SLC45A3	7,72E-07	-2,37482
NM_033103 // RefSeq // Homo sapiens rhophilin, Rho GTPase binding protein 2 (RHPN2), mR	RHPN2	1,02E-10	-3,25777
NM_033266 // RefSeq // Homo sapiens endoplasmic reticulum to nucleus signaling 2 (ERN2)	ERN2	5,59E-06	-4,31539
NM_033386 // RefSeq // Homo sapiens MICAL-like 1 (MICALL1), mRNA. // chr22 // 100 // 85	MICALL1	7,37E-07	1,64994
NM_033421 // RefSeq // Homo sapiens sorting nexin family member 21 (SNX21), transcript	SNX21	2,74E-05	1,58739

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_033498 // RefSeq // Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochond	HK1	1,16E-05	1,87167
NM_052950 // RefSeq // Homo sapiens WD repeat and FYVE domain containing 2 (WDFY2), mRN	WDFY2	3,51E-08	2,25194
NM_052966 // RefSeq // Homo sapiens family with sequence similarity 129, member A (FAM1	FAM129A	2,64E-05	2,4835
NM_058165 // RefSeq // Homo sapiens monoacyl-glycerol O-acyltransferase 1 (MOGAT1), mRNA	MOGAT1	1,18E-07	-4,14775
NM_058237 // RefSeq // Homo sapiens protein phosphatase 4, regulatory subunit 4 (PPP4R4	PPP4R4	6,13E-06	2,69477
NM_080489 // RefSeq // Homo sapiens syndecan binding protein (syntenin) 2 (SDCBP2), tra	SDCBP2	4,40E-07	-2,35397
NM_080656 // RefSeq // Homo sapiens CDKN2A interacting protein N-terminal like (CDKN2AI	CDKN2AI PNL	1,92E-07	1,79298
NM_133372 // RefSeq // Homo sapiens folliculin interacting protein 1 (FNIP1), transcrip	FNIP1	3,56E-08	1,7533
NM_133447 // RefSeq // Homo sapiens ankyrin repeat and GTPase domain Arf GTPase activat	AGAP11	2,43E-08	2,62118
NM_133637 // RefSeq // Homo sapiens DEAQ box RNA-dependent ATPase 1 (DQX1), mRNA. // ch	DQX1	2,98E-05	-3,15917
NM_138333 // RefSeq // Homo sapiens family with sequence similarity 122A (FAM122A), mRN	FAM122A	7,29E-07	-1,51479
NM_138370 // RefSeq // Homo sapiens protein kinase domain containing, cytoplasmic homol	PKDCC	1,61E-09	-3,33428
NM_138383 // RefSeq // Homo sapiens metastasis suppressor 1-like (MTSS1L), mRNA. // chr	MTSS1L	3,48E-06	2,34633
NM_138409 // RefSeq // Homo sapiens melanocortin 2 receptor accessory protein 2 (MRAP2)	MRAP2	2,31E-05	-3,30067
NM_138424 // RefSeq // Homo sapiens kinesin family member 12 (KIF12), mRNA. // chr9 //	KIF12	1,53E-06	-1,95439
NM_138694 // RefSeq // Homo sapiens polycystic kidney and hepatic disease 1 (autosomal	PKHD1	1,42E-05	-3,1775
NM_138962 // RefSeq // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript v	MSI2	9,15E-06	-2,292
NM_139053 // RefSeq // Homo sapiens EPS8-like 3 (EPS8L3), transcript variant 1, mRNA. /	EPS8L3	2,06E-07	-5,96732
NM_139241 // RefSeq // Homo sapiens FYVE, RhoGEF and PH domain containing 4 (FGD4), mRN	FGD4	1,50E-05	-3,20747
NM_144626 // RefSeq // Homo sapiens transmembrane protein 125 (TMEM125), mRNA. // chr1	TMEM125	1,91E-09	-1,77259
NM_144632 // RefSeq // Homo sapiens transmembrane protein 182 (TMEM182), mRNA. // chr2	TMEM182	3,69E-06	-1,57896
NM_144633 // RefSeq // Homo sapiens potassium voltage-gated channel, subfamily H (eag-r	KCNH8	1,14E-05	-4,08341
NM_144691 // RefSeq // Homo sapiens calpain 12	CAPN12	9,60E-08	-1,76735

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
(CAPN12), mRNA. // chr19 // 100 // 100 /			
NM_144717 // RefSeq // Homo sapiens interleukin 20 receptor beta (IL20RB), mRNA. // chr	IL20RB	9,68E-06	3,15609
NM_145051 // RefSeq // Homo sapiens ring finger protein 183 (RNF183), mRNA. // chr9 //	RNF183	5,47E-08	-2,08144
NM_145168 // RefSeq // Homo sapiens short chain dehydrogenase/reductase family 42E, mem	SDR42E1	1,13E-05	-1,60021
NM_145246 // RefSeq // Homo sapiens fragile site, folic acid type, rare, fra(10)(q23.3)	FRA10AC1	1,46E-05	1,63614
NM_145291 // RefSeq // Homo sapiens zinc finger and BTB domain containing 49 (ZBTB49),	ZBTB49	3,59E-09	1,72442
NM_145798 // RefSeq // Homo sapiens oxysterol binding protein-like 7 (OSBPL7), mRNA. //	OSBPL7	7,80E-08	-2,63201
NM_145865 // RefSeq // Homo sapiens ankyrin repeat and sterile alpha motif domain conta	ANKS4B	4,67E-06	-3,31564
NM_152309 // RefSeq // Homo sapiens phosphoinositide-3-kinase adaptor protein 1 (PIK3AP	PIK3AP1	1,13E-08	-3,16626
NM_152406 // RefSeq // Homo sapiens actin filament associated protein 1-like 1 (AFAP1L1	AFAP1L1	4,90E-06	2,48081
NM_152407 // RefSeq // Homo sapiens GrpE-like 2, mitochondrial (E. coli) (GRPEL2), nucl	GRPEL2	3,64E-07	1,73853
NM_152546 // RefSeq // Homo sapiens serum response factor binding protein 1 (SRFBP1), m	SRFBP1	8,49E-07	1,57634
NM_152599 // RefSeq // Homo sapiens major facilitator superfamily domain containing 6-l	MFSD6L	1,10E-06	-1,51532
NM_152624 // RefSeq // Homo sapiens DCP2 decapping enzyme homolog (S. cerevisiae) (DCP2	DCP2	1,18E-09	1,59207
NM_152701 // RefSeq // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1	ABCA13	1,54E-05	-2,9658
NM_152716 // RefSeq // Homo sapiens protein associated with topoisomerase II homolog 1	PATL1	3,39E-09	1,54271
NM_153223 // RefSeq // Homo sapiens centrosomal protein 120kDa (CEP120), transcript var	CEP120	3,35E-09	1,85572
NM_153229 // RefSeq // Homo sapiens transmembrane protein 92 (TMEM92), transcript varia	TMEM92	8,93E-06	-2,16814
NM_153246 // RefSeq // Homo sapiens chromosome 6 open reading frame 223 (C6orf223), tra	C6orf223	6,92E-07	-1,94305
NM_153354 // RefSeq // Homo sapiens transmembrane protein 161B (TMEM161B), mRNA. // chr	TMEM161B	1,38E-07	1,57601
NM_153676 // RefSeq // Homo sapiens Usher syndrome 1C (autosomal recessive, severe) (US	USH1C	3,88E-06	-4,27153
NM_153704 // RefSeq // Homo sapiens transmembrane protein 67 (TMEM67), transcript varia	TMEM67	2,64E-05	1,82612
NM_153705 // RefSeq // Homo sapiens KDEL (Lys-Asp-Glu-Leu) containing 2 (KDELC2), mRNA.	KDELC2	2,23E-05	1,92081

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_153811 // RefSeq // Homo sapiens solute carrier family 38, member 6 (SLC38A6), trans	SLC38A6	1,64E-09	1,93536
NM_170739 // RefSeq // Homo sapiens mitochondrial ribosomal protein L11 (MRPL11), nucle	MRPL11	2,54E-05	1,53304
NM_172069 // RefSeq // Homo sapiens pleckstrin homology domain containing, family H (wi	PLEKHH2	2,90E-06	-3,63821
NM_172089 // RefSeq // Homo sapiens TNFSF12-TNFSF13 readthrough (TNFSF12-TNFSF13), mRNA	TNFSF12-TNFSF13	9,22E-07	-1,94812
NM_173500 // RefSeq // Homo sapiens tau tubulin kinase 2 (TTBK2), mRNA. // chr15 // 100	TTBK2	4,81E-08	1,66259
NM_173596 // RefSeq // Homo sapiens solute carrier family 39 (metal ion transporter), m	SLC39A5	1,61E-06	-2,73305
NM_173630 // RefSeq // Homo sapiens rotatin (RTTN), mRNA. // chr18 // 100 // 100 // 45	RTTN	1,21E-06	1,77726
NM_173829 // RefSeq // Homo sapiens SREK1-interacting protein 1 (SREK1IP1), mRNA. // ch	SREK1IP1	1,22E-06	1,53161
NM_173853 // RefSeq // Homo sapiens keratinocyte associated protein 3 (KRTCAP3), transc	KRTCAP3	8,65E-07	-2,07297
NM_174954 // RefSeq // Homo sapiens ATPase, Ca++ transporting, ubiquitous (ATP2A3), tra	ATP2A3	5,79E-09	-3,10241
NM_175617 // RefSeq // Homo sapiens metallothionein 1E (MT1E), mRNA. // chr16 // 100 //	MT1E	8,72E-14	2,60459
NM_175748 // RefSeq // Homo sapiens ubiquitin protein ligase E3 component n-recogin 7	UBR7	3,13E-07	1,53645
NM_175887 // RefSeq // Homo sapiens proline rich 15 (PRR15), mRNA. // chr7 // 100 // 77	PRR15	2,56E-06	-2,69486
NM_176813 // RefSeq // Homo sapiens anterior gradient 3 homolog (Xenopus laevis) (AGR3)	AGR3	1,41E-11	-11,9405
NM_176870 // RefSeq // Homo sapiens metallothionein 1M (MT1M), mRNA. // chr16 // 100 //	MT1M	1,12E-08	4,8387
NM_177937 // RefSeq // Homo sapiens golgi membrane protein 1 (GOLM1), transcript varian	GOLM1	2,44E-08	-2,46822
NM_177964 // RefSeq // Homo sapiens LY6/PLAUR domain containing 6B (LYPD6B), mRNA. // c	LYPD6B	9,53E-09	-4,00458
NM_178313 // RefSeq // Homo sapiens spectrin, beta, non-erythrocytic 1 (SPTBN1), transc	SPTBN1	3,39E-08	-1,82948
NM_178314 // RefSeq // Homo sapiens Rab interacting lysosomal protein-like 1 (RILPL1),	RILPL1	1,27E-05	1,86601
NM_178832 // RefSeq // Homo sapiens MORN repeat containing 4 (MORN4), transcript varian	MORN4	4,07E-06	2,34797
NM_178868 // RefSeq // Homo sapiens CKLF-like MARVEL transmembrane domain containing 8	CMTM8	2,53E-07	-2,21936
NM_181471 // RefSeq // Homo sapiens replication factor C (activator 1) 2, 40kDa (RFC2),	RFC2	5,39E-07	1,6244
NM_181659 // RefSeq // Homo sapiens nuclear recep-	NCOA3	6,18E-06	1,60504

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
tor coactivator 3 (NCOA3), transcript			
NM_181802 // RefSeq // Homo sapiens ubiquitin-conjugating enzyme E2C (UBE2C), transcrip	UBE2C	2,23E-06	1,79928
NM_182513 // RefSeq // Homo sapiens SPC24, NDC80 kinetochore complex component, homolog	SPC24	1,61E-05	1,66149
NM_182848 // RefSeq // Homo sapiens claudin 10 (CLDN10), transcript variant a, mRNA. //	CLDN10	4,74E-10	-12,9355
NM_182948 // RefSeq // Homo sapiens protein kinase, cAMP-dependent, catalytic, beta (PR	PRKACB	1,98E-05	-3,27267
NM_183001 // RefSeq // Homo sapiens SHC (Src homology 2 domain containing) transforming	SHC1	1,23E-07	1,50809
NM_194283 // RefSeq // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 21 (DNAJC	DNAJC21	3,30E-06	1,53247
NM_197977 // RefSeq // Homo sapiens zinc finger protein 189 (ZNF189), transcript varian	ZNF189	1,59E-05	-2,00268
NM_198270 // RefSeq // Homo sapiens Nance-Horan syndrome (congenital cataracts and dent	NHS	1,82E-06	-2,55426
NM_198681 // RefSeq // Homo sapiens pleckstrin homology domain containing, family G (wi	PLEKHG5	3,12E-07	2,01973
NM_201649 // RefSeq // Homo sapiens solute carrier family 6 (neurotransmitter transport	SLC6A9	4,39E-11	1,80695
NM_203394 // RefSeq // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. // chr12 /	E2F7	9,51E-06	2,81599
NM_207317 // RefSeq // Homo sapiens zinc finger protein 474 (ZNF474), mRNA. // chr5 //	ZNF474	3,99E-06	2,28257
NM_212503 // RefSeq // Homo sapiens cyclin-dependent kinase 18 (CDK18), transcript vari	CDK18	2,40E-05	-1,51027
NM_213566 // RefSeq // Homo sapiens DNA fragmentation factor, 45kDa, alpha polypeptide	DFFA	1,62E-05	1,62044
NR_000022 // RefSeq // Homo sapiens small nuclear RNA, C/D box 14A (SNORD14A), small	SNORD14A	8,55E-06	1,5123
NR_001278 // RefSeq // Homo sapiens cytochrome P450, family 2, subfamily B, polypeptide	CYP2B7P1	2,91E-05	-3,48269
NR_001447 // RefSeq // Homo sapiens metallothionein 1L (gene/pseudogene) (MT1L), non-co	MT1L	5,37E-09	5,33311
NR_002950 // RefSeq // Homo sapiens small nuclear RNA, H/ACA box 2A (SNORA2A), small	SNO-RA2A	2,73E-05	1,52306
NR_003059 // RefSeq // Homo sapiens small nuclear RNA, C/D box 71 (SNORD71), small nu	SNORD71	3,18E-07	-1,64467
NR_003610 // RefSeq // Homo sapiens pyridoxal-dependent decarboxylase domain containing	PDXDC2P	3,67E-06	-2,30662
NR_003715 // RefSeq // Homo sapiens maltase-glucoamylase (alpha-glucosidase) pseudogene	LOC93432	9,97E-10	-12,1234
NR_003717 // RefSeq // Homo sapiens maltase-glucoamylase (alpha-glucosidase) pseudogene	LOC100124692	7,05E-10	-18,7092

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NR_024084 // RefSeq // Homo sapiens SAP30-like (SAP30L), transcript variant 4, non-codi	SAP30L	1,65E-07	1,51349
NR_024345 // RefSeq // Homo sapiens HNF1A antisense RNA 1 (non-protein coding) (HNF1A-A	HNF1A-AS1	2,75E-11	-7,00022
NR_024413 // RefSeq // Homo sapiens uncharacterized LOC401105 (FLJ42393), non-coding RN	FLJ42393	3,56E-06	-1,5441
NR_024546 // RefSeq // Homo sapiens thioredoxin-like 1 (TXNL1), transcript variant 2, n	TXNL1	6,86E-06	1,66398
NR_026586 // RefSeq // Homo sapiens EF-hand calcium binding domain 2 (EFCAB2), transcri	EFCAB2	2,79E-05	1,67842
NR_027136 // RefSeq // Homo sapiens chromosome 1 open reading frame 126 (C1orf126), non	C1orf126	1,30E-09	-2,99279
NR_027654 // RefSeq // Homo sapiens SMAD family member 6 (SMAD6), transcript variant 3,	SMAD6	1,74E-05	-3,16759
NR_027921 // RefSeq // Homo sapiens CCL14-CCL15 readthrough (CCL14-CCL15), transcript v	CCL14-CCL15	6,01E-06	-2,87146
NR_029497 // RefSeq // Homo sapiens microRNA 24-2 (MIR24-2), microRNA. // chr19 // 100	MIR24-2	1,53E-06	1,74847
NR_029578 // RefSeq // Homo sapiens microRNA 192 (MIR192), microRNA. // chr11 // 100 //	MIR192	2,12E-07	-4,01248
NR_029635 // RefSeq // Homo sapiens microRNA 221 (MIR221), microRNA. // chrX // 100 //	MIR221	1,23E-05	2,10295
NR_029636 // RefSeq // Homo sapiens microRNA 222 (MIR222), microRNA. // chrX // 100 //	MIR222	2,21E-06	2,30276
NR_030295 // RefSeq // Homo sapiens microRNA 569 (MIR569), microRNA. // chr3 // 100 //	MIR569	1,62E-12	-3,36092
NR_033807 // RefSeq // Homo sapiens cytochrome P450, family 3, subfamily A, polypeptide	CYP3A5	2,65E-05	-4,76011
NR_033876 // RefSeq // Homo sapiens long intergenic non-protein coding RNA 511 (LINC005	LINC00511	1,17E-05	-1,63527
NR_033932 // RefSeq // Homo sapiens uncharacterized protein FLJ35946 (FLJ35946), non-co	FLJ35946	4,86E-06	2,02692
NR_034091 // RefSeq // Homo sapiens uncharacterized LOC100129046 (LOC100129046), non-co	LOC100129046	2,17E-07	-2,40725
NR_036057 // RefSeq // Homo sapiens microRNA 3115 (MIR3115), microRNA. // chr1 // 100 /	MIR3115	2,37E-05	2,44155
NR_036491 // RefSeq // Homo sapiens F-box protein 43 (FBXO43), transcript variant 1, no	FBXO43	1,78E-05	1,59251
NR_036497 // RefSeq // Homo sapiens LPP antisense RNA 2 (non-protein coding) (LPP-AS2),	LPP-AS2	5,58E-07	-1,93976
NR_036575 // RefSeq // Homo sapiens uncharacterized LOC729966 (LOC729966), non-coding R	LOC729966	2,96E-07	-3,87461
NR_036581 // RefSeq // Homo sapiens uncharacterized LOC100289255 (LOC100289255), non-co	LOC100289255	8,16E-06	-3,99448
NR_037167 // RefSeq // Homo sapiens quinone oxi-	LOC7301	3,69E-06	-2,38905

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
doreductase-like protein 2 pseudogene (L	02		
NR_037631 // RefSeq // Homo sapiens uncharacterized LOC100288911 (LOC100288911), non-co	LOC100288911	1,41E-06	1,50797
NR_038258 // RefSeq // Homo sapiens transmembrane phosphoinositide 3-phosphatase and te	TPTE2P5	2,03E-06	-2,12082
NR_038269 // RefSeq // Homo sapiens uncharacterized LOC100506844 (LOC100506844), non-co	LOC100506844	1,58E-08	1,62653
NR_038291 // RefSeq // Homo sapiens uncharacterized LOC100507127 (LOC100507127), non-co	LOC100507127	5,53E-07	5,02658
NR_038834 // RefSeq // Homo sapiens uncharacterized LOC100505989 (LOC100505989), non-co	LOC100505989	7,31E-09	-6,74071
NR_038842 // RefSeq // Homo sapiens uncharacterized LOC728431 (LOC728431), non-coding R	LOC728431	6,13E-06	-1,73164
NR_038849 // RefSeq // Homo sapiens uncharacterized LOC100505633 (LOC100505633), non-co	LOC100505633	1,64E-11	-9,51391
NR_038886 // RefSeq // Homo sapiens uncharacterized LOC100506385 (LOC100506385), transc	LOC100506385	1,37E-05	-1,82358
NR_039667 // RefSeq // Homo sapiens microRNA 378h (MIR378H), microRNA. // chr5 // 100 /	MIR378H	4,25E-07	1,77042
NR_039990 // RefSeq // Homo sapiens uncharacterized LOC100507299 (LOC100507299), non-co	LOC100507299	6,69E-07	-1,79412
NR_045994 // RefSeq // Homo sapiens eukaryotic translation termination factor 1 (ETF1),	ETF1	4,02E-08	1,60646
NR_046207 // RefSeq // Homo sapiens solute carrier family 12 (sodium/potassium/chloride	SLC12A2	4,70E-07	-2,55573
NR_046320 // RefSeq // Homo sapiens glutathione peroxidase 2 (gastrointestinal) (GPX2),	GPX2	1,44E-06	-4,9979
NR_046533 // RefSeq // Homo sapiens CLDN10 antisense RNA 1 (non-protein coding) (CLDN10	CLDN10-AS1	4,53E-06	-7,21832
NR_046840 // RefSeq // Homo sapiens ARHGEF38 intronic transcript 1 (non-protein coding)	ARHGEF38-IT1	6,87E-06	-3,10262
NR_047477 // RefSeq // Homo sapiens FRMD6 antisense RNA 2 (non-protein coding) (FRMD6-A	FRMD6-AS2	4,03E-07	1,53959
TCONS_00001602-XLOC_000932 // Rinn lincRNA // linc-DPYD-1 chr1:-:98389796-98394621 // c		1,21E-07	1,63968
TCONS_00003042-XLOC_001738 // Rinn lincRNA // linc-XIRP2-4 chr2:+:166651360-166666520 /		2,66E-05	-1,84419
TCONS_00003266-XLOC_002070 // Rinn lincRNA // linc-HAAO-6 chr2:-:43324883-43329829 // c		6,88E-06	-1,517
TCONS_00003518-XLOC_002531 // Rinn lincRNA // linc-COL6A3-2 chr2:-:238337562-238343465		3,53E-06	3,07246
TCONS_00003519-XLOC_002536 // Rinn lincRNA // linc-PER2-1 chr2:-:239207350-239209261 //		5,35E-07	-1,83619
TCONS_00004225-XLOC_002067 // Rinn lincRNA // linc-HAAO-4 chr2:-:43199537-43228604 // c		6,90E-10	-2,07419

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
TCONS_00005686-XLOC_002962 // Rinn lincRNA // linc-LPP-5 chr3:+:187166632-187167238 //		4,04E-06	-2,72907
TCONS_00005695-XLOC_002973 // Rinn lincRNA // linc-HES1-3 chr3:+:193558616-193561016 //		5,33E-07	-1,99679
TCONS_00006739-XLOC_003378 // Rinn lincRNA // linc-ATP13A4-2 chr3:-:193551437-193555388		1,82E-05	-2,80749
TCONS_00007517-XLOC_003515 // Rinn lincRNA // linc-WDR19 chr4:+:39135532-39137228 // ch		7,44E-06	2,66332
TCONS_00009612-XLOC_004747 // Rinn lincRNA // linc-MYO10-3 chr5:-:18704541-18746282 //		1,12E-05	2,15835
TCONS_00010966-XLOC_004901 // Rinn lincRNA // linc-DMGDH-1 chr5:-:78654496-78663947 //		2,57E-08	1,56471
TCONS_00011960-XLOC_005473 // Rinn lincRNA // linc-MAP7-BP chr6:+:136871938-136872729 /		1,10E-09	-2,30569
TCONS_00012690-XLOC_005677 // Rinn lincRNA // linc-POU5F1-1 chr6:-:31139385-31144598 //		2,61E-05	-2,74463
TCONS_00012969-XLOC_006009 // Rinn lincRNA // linc-IL6-1 chr7:+:22629323-22631241 // ch		9,60E-07	1,74149
TCONS_00013399-XLOC_006028 // Rinn lincRNA // linc-TAX1BP1 chr7:+:27427803-27449622 //		2,91E-12	-10,8879
TCONS_00013576-XLOC_006231 // Rinn lincRNA // linc-ARF5-8 chr7:+:124638323-124641124 //		1,98E-05	-1,77792
TCONS_00014003-XLOC_006644 // Rinn lincRNA // linc-ZNF467-2 chr7:-:149903392-149917567		1,28E-06	-2,11402
TCONS_00015651-XLOC_007291 // Rinn lincRNA // linc-CNTLN-4 chr9:+:16121130-16122432 //		7,93E-06	2,1406
TCONS_00015691-XLOC_007398 // Rinn lincRNA // linc-TMC1-2 chr9:+:74872251-74872699 // c		1,49E-06	-2,02453
TCONS_00016324-XLOC_007698 // Rinn lincRNA // linc-FAM75A6-4 chr9:-:46122188-46123597 /		1,64E-05	-2,25016
TCONS_00017313-XLOC_008149 // Rinn lincRNA // linc-CXorf36-1 chrX:-:45629145-45629608 /		7,53E-08	2,3005
TCONS_00018036-XLOC_008937 // Rinn lincRNA // linc-ITPRIP-1 chr10:-:106111348-106113333		2,06E-07	1,63964
TCONS_00018334-XLOC_008611 // Rinn lincRNA // linc-SMC3 chr10:+:112306237-112307703 //		3,23E-08	3,31117
TCONS_00018558-XLOC_008875 // Rinn lincRNA // linc-DYDC1-3 chr10:-:83633134-83634234 //		2,38E-05	-2,63052
TCONS_00019615-XLOC_009415 // Rinn lincRNA // linc-APIP-1 chr11:-:35086672-35095505 //		1,65E-05	1,81003
TCONS_00020456-XLOC_009788 // Rinn lincRNA // linc-HMGA2 chr12:+:65996599-66010730 // c		1,19E-05	2,18813
TCONS_00021594-XLOC_010491 // Rinn lincRNA // linc-COL4A2-7 chr13:+:109934320-109940081		2,69E-07	1,95057
TCONS_00021940-XLOC_010534 // Rinn lincRNA		1,90E-05	-1,70705

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
// linc-C1QTNF9B chr13:-:24911521-24913410 /			
TCONS_00022264-XLOC_010579 // Rinn lincRNA // linc-MRPS31 chr13:-:41448189-41455780 //		1,34E-06	-2,09995
TCONS_00022761-XLOC_011044 // Rinn lincRNA // linc-C14orf39 chr14:-:61108285-61109382 /		7,84E-08	1,50651
TCONS_00023506-XLOC_011350 // Rinn lincRNA // linc-FURIN chr15:+:91382984-91384570 // c		4,32E-08	-1,58202
TCONS_00023790-XLOC_011585 // Rinn lincRNA // linc-VPS33B-2 chr15:-:93137349-93139933 /		1,53E-05	-1,79128
TCONS_00024596-XLOC_011889 // Rinn lincRNA // linc-SMG1 chr16:-:19365543-19405174 // ch		8,95E-07	-2,41212
TCONS_00025308-XLOC_012111 // Rinn lincRNA // linc-SHISA6-2 chr17:+:10750779-10751687 /		3,78E-06	-1,58083
TCONS_00025543-XLOC_012370 // Rinn lincRNA // linc-TEKT1-3 chr17:-:6778552-6784435 // c		5,23E-10	2,79825
TCONS_00026289-XLOC_012631 // Rinn lincRNA // linc-TUBB6 chr18:+:12288321-12291290 // c		1,35E-07	1,57765
TCONS_12_00004461-XLOC_12_002271 // Broad TUCP // linc-FSHB-2 chr11:+:29059301-29085806		1,08E-05	2,95848
TCONS_12_00005499-XLOC_12_002886 // Broad TUCP // linc-CLEC2D-1 chr12:+:9795445-9814706	LOC374443	1,56E-05	2,534
TCONS_12_00014416-XLOC_12_007884 // Broad TUCP // linc-CMPK2-10 chr2:-:8708041-8720165		1,80E-09	-2,00811
TCONS_12_00015910-XLOC_12_008203 // Broad TUCP // linc-BUB1-2 chr2:-:111996295-11225259	LOC100128130	1,66E-09	2,62287
TCONS_12_00016754-XLOC_12_008600 // Broad TUCP // linc-DEFB115-3 chr20:+:26035249-26067	FAM182A	1,89E-07	1,51072
TCONS_12_00020301-XLOC_12_010491 // Broad TUCP // linc-ATP13A4-3 chr3:-:193560348-19356		2,25E-13	-4,39979
TCONS_12_00020391-XLOC_12_010558 // Broad TUCP // linc-S100P-2 chr4:+:6676003-6678711 /	LOC93622	9,71E-07	2,01416
TCONS_12_00022010-XLOC_12_011291 // Broad TUCP // linc-RNF150-2 chr4:-:142242282-142247		3,21E-06	-4,64232
TCONS_12_00022497-XLOC_12_011737 // Broad TUCP // linc-SNCAIP chr5:+:121492826-12151544	ZNF474	2,13E-05	1,50141
TCONS_12_00023557-XLOC_12_011793 // Broad TUCP // linc-SPRY4-BP chr5:+:141704857-141843		4,70E-07	1,62441
TCONS_12_00023567-XLOC_12_011805 // Broad TUCP // linc-SH3TC2-BP chr5:+:148442879-14845		4,38E-08	2,57157
U02020 // GenBank // Human pre-B cell enhancing factor (PBEF) mRNA, complete cds. // ch	NAMPT	1,25E-07	2,37943
XR_109952 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100507307 (LOC100507307)	LOC100507307	5,86E-06	1,62059
XR_110188 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100507624 (LOC100507624)	LOC100507624	3,36E-06	2,57222

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
XR_133524 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100653206 (LOC100653206)	LOC100653206	6,22E-06	-1,59858

Table 4: Efficiency of SN-38 (Irinotecan active metabolite)

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000253110 // ENSEMBL // cdna:known chromosome:GRCh37:19:10196806:10203927:1 gene:	C19orf66	4,91E-05	-1,41413
ENST00000256545 // ENSEMBL // cdna:known chromosome:GRCh37:15:34376218:34394149:-1 gene	EMC7	2,49E-05	-1,34823
ENST00000262367 // ENSEMBL // cdna:known chromosome:GRCh37:16:3775055:3930727:-1 gene:E	CREBBP	1,82E-06	1,36423
ENST00000341861 // ENSEMBL // cdna:known chromosome:GRCh37:15:65734801:65809611:-1 gene	DPP8	4,47E-06	-1,45274
ENST00000359775 // ENSEMBL // cdna:known chromosome:GRCh37:6:157802165:158099178:1 gene	ZDHHC14	5,49E-05	1,49934
ENST00000367001 // ENSEMBL // cdna:known chromosome:GRCh37:1:211744910:211752084:-1 gen	SLC30A1	1,28E-05	1,80378
ENST00000373043 // ENSEMBL // cdna:known chromosome:GRCh37:1:38272651:38275124:1 gene:E	C1orf122	5,71E-05	-1,22797
ENST00000395491 // ENSEMBL // cdna:putative chromosome:GRCh37:17:21188049:21218525:1 ge	MAP2K3	1,09E-05	-1,47207
ENST00000410851 // ENSEMBL // ncRNA:misc_RNA chromosome:GRCh37:3:130530612:130530939:-1		3,75E-06	1,43148
ENST00000414676 // ENSEMBL // cdna:known chromosome:GRCh37:20:300957:305878:-1 gene:ENS	LOC100507459	1,13E-05	1,74729
ENST00000497194 // ENSEMBL // cdna:putative chromosome:GRCh37:11:71709659:71714799:1 ge	IL18BP	1,64E-05	1,26609
ENST00000558443 // ENSEMBL // cdna:putative chromosome:GRCh37:15:64762452:64763563:1 ge		1,79E-05	-2,2321
NM_000197 // RefSeq // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 3 (HSD17B3),	HSD17B3	1,28E-07	-2,74982
NM_000288 // RefSeq // Homo sapiens peroxisomal biogenesis factor 7 (PEX7), mRNA. // ch	PEX7	2,33E-05	-1,41622
NM_001100876 // RefSeq // Homo sapiens phytanoyl-	PHYHD1	3,13E-07	1,47854

CoA dioxygenase domain containing 1 (P			
NM_001126 // RefSeq // Homo sapiens adenylosuccinate synthase (ADSS), mRNA. // chr1 //	ADSS	1,51E-05	1,29195
NM_001130009 // RefSeq // Homo sapiens Gen endonuclease homolog 1 (Drosophila) (GEN1),	GEN1	1,13E-06	1,42069
NM_001195296 // RefSeq // Homo sapiens mirror-image polydactyly 1 (MIPOL1), transcript	MIPOL1	1,52E-06	-1,61943
NM_001238 // RefSeq // Homo sapiens cyclin E1 (CCNE1), mRNA. // chr19 // 100 // 100 //	CCNE1	6,75E-08	1,70632
NM_004339 // RefSeq // Homo sapiens pituitary tumor-transforming 1 interacting protein	PTTG1IP	1,11E-05	1,26909
NM_004619 // RefSeq // Homo sapiens TNF receptor-associated factor 5 (TRAF5), transcrip	TRAF5	2,68E-05	3,13128
NM_004719 // RefSeq // Homo sapiens SR-related CTD-associated factor 11 (SCAF11), mRNA.	SCAF11	4,64E-05	1,20729
NM_006026 // RefSeq // Homo sapiens H1 histone family, member X (H1FX), mRNA. // chr3 /	H1FX	1,40E-05	1,43588
NM_012241 // RefSeq // Homo sapiens sirtuin 5 (SIRT5), transcript variant 1, mRNA. // c	SIRT5	4,97E-05	1,44938
NM_014246 // RefSeq // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (fla	CELSR1	5,57E-05	2,8642
NM_018259 // RefSeq // Homo sapiens tetratricopeptide repeat domain 17 (TTC17), mRNA. /	TTC17	5,96E-05	1,3538
NM_018413 // RefSeq // Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (C	CHST11	2,41E-05	2,8737
NM_018602 // RefSeq // Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 4 (DNAJA4	DNAJA4	1,84E-05	-1,87107
NM_020192 // RefSeq // Homo sapiens Yae1 domain containing 1 (YAE1D1), mRNA. // chr7 //	YAE1D1	9,70E-07	-1,61835
NM_021982 // RefSeq // Homo sapiens SEC24 family, member A (S. cerevisiae) (SEC24A), tr	SEC24A	2,78E-05	-1,38482
NM_138768 // RefSeq // Homo sapiens myeloma overexpressed (in a subset of t(11;14) posi	MYEOV	1,18E-05	1,4116
NM_152744 // RefSeq // Homo sapiens sidekick cell adhesion molecule 1 (SDK1), transcrip	SDK1	1,82E-05	-1,34953
NM_181719 // RefSeq // Homo sapiens transmembrane and coiled-coil domains 4 (TMCO4), mR	TMCO4	5,77E-05	1,27538
NR_002196 // RefSeq // Homo sapiens H19, imprinted maternally expressed transcript (non	H19	1,34E-06	4,35208
NR_003008 // RefSeq // Homo sapiens small Cajal body-specific RNA 5 (SCARNA5), guide RN	SCARNA5	4,59E-05	3,57866
NR_026862 // RefSeq // Homo sapiens protein phosphatase 1, regulatory subunit 3E (PPP1R	PPP1R3E	6,77E-06	1,3635
NR_036474 // RefSeq // Homo sapiens G patch domain containing 8 (GPATCH8), transcript v	GPATCH8	4,93E-06	-1,2289
NR_040252 // RefSeq // Homo sapiens ankyrin repeat and sterile alpha motif domain conta	ANKS3	1,21E-05	1,20509

NR_045553 // RefSeq // Homo sapiens thrombospondin 3 (THBS3), transcript variant 4, non	THBS3	8,00E-06	1,93413
TCONS_00000324-XLOC_000441 // Rinn lincRNA // linc-FCGR2A chr1+:161337811-161341754 //		3,97E-05	-1,46789
TCONS_00003558-XLOC_001334 // Rinn lincRNA // linc-ASAP2-4 chr2+:9144181-9148968 // ch		3,29E-05	1,26364
TCONS_00015020-XLOC_007094 // Rinn lincRNA // linc-CA8-2 chr8:-:61377162-61378147 // ch		4,72E-05	-1,9219
TCONS_00020978-XLOC_010244 // Rinn lincRNA // linc-DHX37-4 chr12:-:127214600-127232784	LOC387895	3,96E-05	1,88561
TCONS_00024123-XLOC_011480 // Rinn lincRNA // linc-BCL2L10 chr15:-:52407273-52409155 //		3,83E-06	-1,40259
TCONS_00029585-XLOC_014219 // Rinn lincRNA // linc-RASD2 chr22+:35846033-35851349 // c		2,45E-05	1,64874
TCONS_12_00028315-XLOC_12_014585 // Broad TUCP // linc-TMEM55A-1 chr8:-:92080145-920823	LOC100506365	5,12E-05	-1,40029

Table 5: Efficiency of oxaliplatin

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
AF086261 // GenBank // Homo sapiens full length insert cDNA clone ZD42A11. // chr15 //	LOC100507311	0,00092669	-1,63804
AF086310 // GenBank // Homo sapiens full length insert cDNA clone ZD51F08. // chr4 // 1		0,00012871	-3,47383
AF147354 // GenBank // Homo sapiens full length insert cDNA clone YB43H03. // chr20 //	LINC00493	0,0008703	1,38961
AF520800 // GenBank // Homo sapiens clone 958LR MRDS1 protein (MRDS1) mRNA, complete cd	OFCC1	0,0009487	-1,93359
AK056431 // GenBank // Homo sapiens cDNA FLJ31869 fis, clone NT2RP7002151. // chr1 // 1	FLG-AS1	0,00142515	1,89868
AK057443 // GenBank // Homo sapiens cDNA FLJ32881 fis, clone TESTI2004153. // chr22 //		7,00E-05	1,57188
AK093576 // GenBank // Homo sapiens cDNA FLJ36257 fis, clone THYMU2002376. // chr2 // 1		0,00157934	1,25081
AK096045 // GenBank // Homo sapiens cDNA FLJ38726 fis, clone KIDNE2010271, moderately s	SHANK2	1,82E-06	2,55588
AK097401 // GenBank // Homo sapiens cDNA FLJ40082 fis, clone TESTI2002282, highly simil		6,25E-05	-1,51377
AK123224 // GenBank // Homo sapiens cDNA FLJ41230 fis, clone BRAMY2030703. // chr16 //	LOC100506928	0,00065449	-1,72222
AK123971 // GenBank // Homo sapiens cDNA FLJ41977 fis, clone SKNMC2007961. // chr12 //		6,08E-05	2,11232
AK124207 // GenBank // Homo sapiens cDNA FLJ42213 fis, clone THYMU2037081. // chr19 //	LOC100132272	0,00044379	-1,28444

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
AK124321 // GenBank // Homo sapiens cDNA FLJ42330 fis, clone TSTOM1000135. // chr7 // 9	LOC389602	0,00063529	-2,59503
AK124544 // GenBank // Homo sapiens cDNA FLJ42553 fis, clone BRACE3005225. // chr7 // 1	LOC644841	0,00027133	-1,26561
AK125790 // GenBank // Homo sapiens cDNA FLJ43802 fis, clone TESTI4000462. // chr7 // 1	LOC401357	0,00062933	-1,23391
AK127497 // GenBank // Homo sapiens cDNA FLJ45590 fis, clone BRTHA3014691. // chr12 //		0,00028051	1,75552
AK127825 // GenBank // Homo sapiens cDNA FLJ45928 fis, clone PLACE6019674. // chr14 //		0,00115628	-1,32115
AK295794 // GenBank // Homo sapiens cDNA FLJ53557 complete cds. // chrX // 100 // 96 //	LOC100133957	0,00041384	1,23553
AK299170 // GenBank // Homo sapiens cDNA FLJ58610 complete cds. // chr12 // 90 // 65 //	C12orf43	0,00101109	1,33346
AY077697 // GenBank // Homo sapiens clone qa81f10 C21ORF9 (C21orf9) mRNA, complete cds.	GRIK1-AS1	0,00135624	-1,44849
BC007540 // GenBank // Homo sapiens chromosome 11 open reading frame 84, mRNA (cDNA clo	C11orf84	0,00040398	1,83304
BC038379 // GenBank // Homo sapiens, clone IMAGE:5194896, mRNA. // chr15 // 100 // 100		0,0015726	-1,35245
BC039376 // GenBank // Homo sapiens cDNA clone IMAGE:5271474. // chr6 // 100 // 58 // 1		0,00106878	-1,23951
BC039382 // GenBank // Homo sapiens cDNA clone IMAGE:5271897. // chr2 // 100 // 62 // 1		0,00062192	-1,20648
BC040901 // GenBank // Homo sapiens, clone IMAGE:5743779, mRNA. // chr5 // 100 // 100 /		0,00016115	1,33801
BC041487 // GenBank // Homo sapiens, clone IMAGE:5493056, mRNA. // chr2 // 100 // 100 /		6,87E-06	1,86446
BC047404 // GenBank // Homo sapiens cDNA clone IMAGE:5300528. // chr10 // 100 // 100 //	LOC100507212	0,0006522	1,78698
BX648677 // GenBank // Homo sapiens mRNA; cDNA DKFZp686D0374 (from clone DKFZp686D0374)	FLJ33630	0,00034036	1,38398
CR457332 // GenBank // Homo sapiens full open reading frame cDNA clone RZPDo834A0110D f	C11orf67	0,00025408	1,38856
ENST00000007516 // ENSEMBL // cdna:known chromosome:GRCh37:16:23592323:23607677:-1 gene	NDU-FAB1	0,00032987	1,37938
ENST00000202017 // ENSEMBL // cdna:known chromosome:GRCh37:20:30532758:30539895:-1 gene	PDRG1	0,00076135	1,4287
ENST00000216127 // ENSEMBL // cdna:known chromosome:GRCh37:22:35936915:35950048:1 gene:	RASD2	9,96E-05	-1,25882
ENST00000217109 // ENSEMBL // cdna:known	CSTF1	0,000619	1,33752

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:20:54967450:54979518:1 gene:		17	
ENST00000217244 // ENSEMBL // cdna:known chromosome:GRCh37:20:461741:524465:-1 gene:ENS	CSNK2A1 P	3,75E-06	1,65862
ENST00000219139 // ENSEMBL // cdna:known chromosome:GRCh37:16:67143891:67182442:1 gene:	C16orf70	6,55E-05	1,27398
ENST00000220062 // ENSEMBL // cdna:known chromosome:GRCh37:15:65345679:65360450:-1 gene	RASL12	0,000294 72	-1,24282
ENST00000222644 // ENSEMBL // cdna:known chromosome:GRCh37:7:24612965:24729159:1 gene:E	MPP6	0,000449 94	2,54923
ENST00000223129 // ENSEMBL // cdna:known chromosome:GRCh37:7:7676149:7758238:-1 gene:EN	RPA3	6,75E-05	1,36251
ENST00000225964 // ENSEMBL // cdna:known chromosome:GRCh37:17:48260650:48278993:-1 gene	COL1A1	0,000206 93	-1,36223
ENST00000229390 // ENSEMBL // cdna:known chromosome:GRCh37:12:120899471:120907596:-1 ge	GATC	0,000457 6	1,54452
ENST00000239007 // ENSEMBL // cdna:known chromosome:GRCh37:10:111985751:112046264:1 gen	MXI1	0,000141 31	1,76321
ENST00000242576 // ENSEMBL // cdna:known chromosome:GRCh37:12:109535379:109548797:1 gen	UNG	0,001485 12	1,64417
ENST00000254262 // ENSEMBL // cdna:known chromosome:GRCh37:19:33463148:33467946:1 gene:	C19orf40	0,000456 24	1,33988
ENST00000254605 // ENSEMBL // cdna:known chromosome:GRCh37:11:6616305:6624850:-1 gene:E	RRP8	0,001515 31	1,31301
ENST00000254691 // ENSEMBL // cdna:known chromosome:GRCh37:5:40841286:40855456:1 gene:E	CARD6	0,001363 34	-1,3984
ENST00000256682 // ENSEMBL // cdna:known chromosome:GRCh37:12:49329506:49351334:-1 gene	ARF3	0,000757 85	1,22761
ENST00000257245 // ENSEMBL // cdna:known chromosome:GRCh37:11:57295936:57298238:-1 gene	TIMM10	9,35E-05	1,5048
ENST00000259808 // ENSEMBL // cdna:known chromosome:GRCh37:6:3068741:3115419:1 gene:ENS	RIPK1	0,000535 43	-1,81904

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000260453 // ENSEMBL // cdna:known chromosome:GRCh37:15:56720929:56757335:-1 gene	MNS1	0,00091012	1,9289
ENST00000260970 // ENSEMBL // cdna:known chromosome:GRCh37:2:170440850:170497916:1 gene	PPIG	0,00024151	-1,22291
ENST00000261263 // ENSEMBL // cdna:known chromosome:GRCh37:12:72148654:72184699:1 gene:	RAB21	8,18E-06	1,47141
ENST00000261735 // ENSEMBL // cdna:known chromosome:GRCh37:12:112451120:112461255:1 gen	ERP29	0,0004558	1,55097
ENST00000262878 // ENSEMBL // cdna:known chromosome:GRCh37:20:35518632:35580246:-1 gene	SAMHD1	7,20E-06	3,98971
ENST00000263341 // ENSEMBL // cdna:known chromosome:GRCh37:2:113587328:113594480:-1 gen	IL1B	0,00078698	-1,57183
ENST00000264228 // ENSEMBL // cdna:known chromosome:GRCh37:4:56212276:56239263:1 gene:E	SRD5A3	1,46E-08	-3,81237
ENST00000264260 // ENSEMBL // cdna:known chromosome:GRCh37:2:103035149:103069025:1 gene	IL18RAP	0,00117957	-1,24329
ENST00000265140 // ENSEMBL // cdna:known chromosome:GRCh37:5:93954052:94033326:1 gene:E	ANKRD32	0,00074107	1,7776
ENST00000266735 // ENSEMBL // cdna:known chromosome:GRCh37:12:96252706:96260831:1 gene:	SNRPF	0,00024249	1,91437
ENST00000267199 // ENSEMBL // cdna:known chromosome:GRCh37:12:122715292:122751068:-1 ge	VPS33A	0,00037094	1,58685
ENST00000268138 // ENSEMBL // cdna:known chromosome:GRCh37:15:90118713:90171250:1 gene:	C15orf42	0,00122047	1,72611
ENST00000268379 // ENSEMBL // cdna:known chromosome:GRCh37:16:21963981:21994981:1 gene:	UQCRC2	7,96E-08	1,3405
ENST00000269033 // ENSEMBL // cdna:known chromosome:GRCh37:17:27952956:28257170:-1 gene	SSH2	0,00045979	-1,42412
ENST00000272321 // ENSEMBL // cdna:known chromosome:GRCh37:2:63348518:63815933:-1 gene:	WDPCP	0,00056261	1,58517
ENST00000274063 // ENSEMBL // cdna:known chromosome:GRCh37:4:154701744:154710272:-1	SFRP2	0,00074275	-2,03144

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
gen			
ENST00000274255 // ENSEMBL // cdna:known chromosome:GRCh37:5:36152169:36184421:1 gene:E	SKP2	0,00021914	1,60315
ENST00000274629 // ENSEMBL // cdna:known chromosome:GRCh37:5:169805168:169816681:-1 gene	KCNMB1	0,00028475	-1,25267
ENST00000280557 // ENSEMBL // cdna:known chromosome:GRCh37:12:123237321:123255611:1 gene	DENR	7,96E-05	1,65214
ENST00000282032 // ENSEMBL // cdna:known chromosome:GRCh37:11:30344598:30359774:1 gene:	ARL14EP	0,00066841	1,39067
ENST00000282570 // ENSEMBL // cdna:known chromosome:GRCh37:2:70056774:70108528:1 gene:E	GMCL1	0,00015899	1,56067
ENST00000283122 // ENSEMBL // cdna:known chromosome:GRCh37:5:89688078:89705603:-1 gene:	CETN3	0,00123302	1,77012
ENST00000283943 // ENSEMBL // cdna:known chromosome:GRCh37:2:230631930:230786725:-1 gene	TRIP12	5,86E-05	-1,32651
ENST00000285735 // ENSEMBL // cdna:known chromosome:GRCh37:1:113243755:113249749:-1 gene	RHOC	0,00018049	-1,35758
ENST00000288235 // ENSEMBL // cdna:known chromosome:GRCh37:15:59427113:59665099:-1 gene	MYO1E	3,15E-06	-1,60901
ENST00000295121 // ENSEMBL // cdna:known chromosome:GRCh37:2:68356935:68384692:-1 gene:	WDR92	4,73E-06	1,55956
ENST00000295268 // ENSEMBL // cdna:known chromosome:GRCh37:4:98480027:99064391:-1 gene:	C4orf37	0,00027006	-1,36673
ENST00000295640 // ENSEMBL // cdna:known chromosome:GRCh37:1:201951752:201975275:1 gene	RNPEP	1,98E-10	-1,49315
ENST00000295685 // ENSEMBL // cdna:known chromosome:GRCh37:2:219081933:219119079:1 gene	ARPC2	1,83E-06	-1,28366
ENST00000295930 // ENSEMBL // cdna:known chromosome:GRCh37:3:157827841:158262624:1 gene	RSRC1	3,33E-06	1,50201
ENST00000296498 // ENSEMBL // cdna:known chromosome:GRCh37:4:119201193:119274158:-1 gene	PRSS12	0,00122289	-3,42438
ENST00000296805 // ENSEMBL // cdna:known chromosome:GRCh37:5:74017029:74063196:-1 gene:	GFM2	0,00090184	1,88142

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000296824 // ENSEMBL // cdna:known chromosome:GRCh37:5:204872:218330:-1 gene:ENSG	CCDC127	0,0013935	1,29272
ENST00000302188 // ENSEMBL // cdna:known chromosome:GRCh37:2:28004231:28113965:-1 gene:	RBKS	0,00161435	1,60836
ENST00000302764 // ENSEMBL // cdna:known chromosome:GRCh37:5:162880494:162887146:-1 gene	NUDCD2	0,00108933	1,62788
ENST00000302824 // ENSEMBL // cdna:known chromosome:GRCh37:15:81601394:81616466:-1 gene	STARD5	0,00023123	-1,57932
ENST00000306910 // ENSEMBL // cdna:known chromosome:GRCh37:19:58920063:58929690:1 gene:	ZNF584	9,57E-05	2,06623
ENST00000307366 // ENSEMBL // cdna:known chromosome:GRCh37:11:62557443:62559493:-1 gene	TMEM223	0,00039167	1,27965
ENST00000308091 // ENSEMBL // cdna:known chromosome:GRCh37:2:204306196:204400058:-1 gene	RAPH1	5,86E-07	-2,01855
ENST00000308342 // ENSEMBL // cdna:known chromosome:GRCh37:11:65601112:65621172:1 gene:	SNX32	7,31E-05	-1,23638
ENST00000308418 // ENSEMBL // cdna:known chromosome:GRCh37:11:65485144:65488418:-1 gene	RNASEH2C	4,73E-06	1,47745
ENST00000308448 // ENSEMBL // cdna:known chromosome:GRCh37:10:89511269:89577917:-1 gene	ATAD1	0,00097375	1,39443
ENST00000308724 // ENSEMBL // cdna:known chromosome:GRCh37:14:24028774:24037279:-1 gene	AP1G2	0,00051108	-1,63218
ENST00000309050 // ENSEMBL // cdna:known chromosome:GRCh37:12:110478983:110505500:-1 ge	C12orf76	1,40E-05	1,35762
ENST00000313601 // ENSEMBL // cdna:known chromosome:GRCh37:3:50273384:50296787:1 gene:E	GNAI2	0,00075699	1,26032
ENST00000314400 // ENSEMBL // cdna:known chromosome:GRCh37:3:112721287:112738686:-1 gene	C3orf17	0,00089895	1,20723
ENST00000315691 // ENSEMBL // cdna:known chromosome:GRCh37:3:143690640:143711201:1 gene	C3orf58	0,00023042	1,55782
ENST00000316788 // ENSEMBL // cdna:known chromosome:GRCh37:5:115177178:115249778:1	AP3S1	9,89E-05	1,61739

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
gene			
ENST00000317058 // ENSEMBL // cdna:known chromosome:GRCh37:16:28565247:28603111:1 gene:	CCDC101	0,00128876	1,31303
ENST00000317702 // ENSEMBL // cdna:known chromosome:GRCh37:18:12308070:12326568:1 gene:	TUBB6	0,00105767	2,62451
ENST00000318066 // ENSEMBL // cdna:known chromosome:GRCh37:12:93800981:93836038:-1 gene	UBE2N	0,00026708	1,90259
ENST00000318967 // ENSEMBL // cdna:known chromosome:GRCh37:1:153700543:153746555:1 gene	INTS3	0,00022297	-1,35866
ENST00000322342 // ENSEMBL // cdna:known chromosome:GRCh37:18:72907063:72921303:-1 gene	ZADH2	0,00067071	1,49416
ENST00000326153 // ENSEMBL // cdna:known chromosome:GRCh37:X:220025:230886:-1 gene:ENSG	GTPBP6	4,26E-05	1,45659
ENST00000327772 // ENSEMBL // cdna:known chromosome:GRCh37:12:95365109:95397546:-1 gene	NDU-FA12	0,00036155	1,34605
ENST00000328379 // ENSEMBL // cdna:known chromosome:GRCh37:2:25012855:25016251:-1 gene:	PTRHD1	0,00020925	1,215
ENST00000329146 // ENSEMBL // cdna:known chromosome:GRCh37:14:105940487:105946499:1 gen	CRIP2	0,00155516	1,62754
ENST00000330479 // ENSEMBL // cdna:known chromosome:GRCh37:12:123868320:123893898:1 gen	SETD8	0,00049325	1,43373
ENST00000334082 // ENSEMBL // cdna:known chromosome:GRCh37:5:78668459:78810040:-1 gene:	HOMER1	4,70E-05	2,35761
ENST00000334736 // ENSEMBL // cdna:known chromosome:GRCh37:11:76156069:76262586:1 gene:	C11orf30	3,84E-05	1,43131
ENST00000334982 // ENSEMBL // cdna:known chromosome:GRCh37:20:19997760:20014273:1 gene:	NAA20	0,00014244	1,61091
ENST00000336702 // ENSEMBL // cdna:known chromosome:GRCh37:11:118978093:118989252:1 gen	C2CD2L	2,42E-05	1,57185
ENST00000337179 // ENSEMBL // cdna:known chromosome:GRCh37:12:93771659:93797024:1 gene:	NUDT4	0,0013692	1,70135
ENST00000338121 // ENSEMBL // cdna:known	GZF1	0,000666	1,45228

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:20:23342819:23353700:1 gene:		03	
ENST00000338508 // ENSEMBL // cdna:known chromosome:GRCh37:11:70315540:70858372:-1 gene	SHANK2	0,000213 87	1,74823
ENST00000338569 // ENSEMBL // cdna:novel chro- mosome:GRCh37:11:6789218:6790286:-1 gene:E	OR2AG2	2,89E-05	1,84466
ENST00000340080 // ENSEMBL // cdna:known chromosome:GRCh37:7:7606503:7647127:1 gene:ENS	MIOS	0,000117 07	1,46544
ENST00000340934 // ENSEMBL // cdna:known chromosome:GRCh37:1:222885895:222908538:1 gene	BROX	4,11E-05	-1,65638
ENST00000342788 // ENSEMBL // cdna:known chromosome:GRCh37:2:212240446:213403565:-1 gen	ERBB4	0,000571 26	-1,32193
ENST00000342927 // ENSEMBL // cdna:known chromosome:GRCh37:1:248616077:248617130:1 gene	OR2T2	0,000386 83	-1,22499
ENST00000343605 // ENSEMBL // cdna:known chromosome:GRCh37:22:31031639:31043880:1 gene:	SLC35E4	0,000538 58	1,46572
ENST00000344063 // ENSEMBL // cdna:known chromosome:GRCh37:19:55896713:55903453:1 gene:	RPL28	0,000114 7	1,39614
ENST00000350777 // ENSEMBL // cdna:known chromosome:GRCh37:11:118992297:119006752:1 gen	HINFP	0,000468 93	1,2477
ENST00000354488 // ENSEMBL // cdna:known chromosome:GRCh37:20:3170996:3185331:-1 gene:E	DDRKG1	2,87E-07	1,25455
ENST00000354921 // ENSEMBL // cdna:known chromosome:GRCh37:1:177897923:177991679:-1 gen	SEC16B	1,24E-05	-4,95166
ENST00000354921 // ENSEMBL // cdna:known chromosome:GRCh37:1:177897923:177991679:-1 gen	SEC16B	2,37E-05	-5,52141
ENST00000354921 // ENSEMBL // cdna:known chromosome:GRCh37:1:177897923:177991679:-1 gen	SEC16B	3,70E-05	-4,25942
ENST00000354921 // ENSEMBL // cdna:known chromosome:GRCh37:1:177897923:177991679:-1 gen	SEC16B	0,000213 02	-3,18455
ENST00000355938 // ENSEMBL // cdna:known chromosome:GRCh37:17:46970127:46973233:1 gene:	ATP5G1	0,000500 78	1,42057

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000356891 // ENSEMBL // cdna:known chromosome:GRCh37:12:88429223:88443937:1 gene:	C12orf29	0,00012497	2,17905
ENST00000357388 // ENSEMBL // cdna:known chromosome:GRCh37:3:160117092:160152750:1 gene	SMC4	0,0007008	1,54032
ENST00000357618 // ENSEMBL // cdna:known chromosome:GRCh37:6:26087547:26098571:1 gene:E	HFE	0,00020568	-1,46294
ENST00000358230 // ENSEMBL // cdna:known chromosome:GRCh37:12:66529626:66563852:-1 gene	TMBIM4	0,0003641	-1,4589
ENST00000359193 // ENSEMBL // cdna:known chromosome:GRCh37:6:27100832:27103070:1 gene:E	HIST1H2AH	0,00137009	2,67438
ENST00000360244 // ENSEMBL // cdna:known chromosome:GRCh37:1:150237806:150241703:-1 gen	APH1A	9,22E-05	-1,29702
ENST00000360820 // ENSEMBL // cdna:known chromosome:GRCh37:12:100661162:100735502:1 gen	SCYL2	3,80E-05	1,43871
ENST00000361205 // ENSEMBL // cdna:known chromosome:GRCh37:18:13218786:13652753:1 gene:	C18orf1	9,77E-05	-1,58899
ENST00000361714 // ENSEMBL // cdna:known chromosome:GRCh37:6:112375462:112392171:1 gene	WISP3	0,0006417	-3,93656
ENST00000362007 // ENSEMBL // cdna:known chromosome:GRCh37:1:156262479:156265463:-1 gen	C1orf85	8,93E-05	-1,46907
ENST00000363200 // ENSEMBL // ncna:snRNA chromosome:GRCh37:15:59504847:59504987:-1 gen		3,17E-05	-1,74369
ENST00000363371 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:2:86387079:86387189:-1 g		0,00079416	1,66803
ENST00000363507 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:2:154303327:154303397:-1 g		0,00146901	-1,41723
ENST00000364281 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:20:33704939:33705010:-1 ge		8,94E-05	1,67302
ENST00000364339 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:22:28628744:28628811:-1 ge		3,48E-06	2,55884
ENST00000364506 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:14:51710808:51710942:1 gen		1,30E-05	1,67586
ENST00000364746 // ENSEMBL // ncna:snRNA chromosome:GRCh37:11:3069589:3069751:-1 gene:		0,00099141	1,45526
ENST00000365211 // ENSEMBL // ncna:snRNA chromo-		3,45E-06	-1,77207

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
some:GRCh37:15:86194753:86194859:-1 gen			
ENST00000365538 // ENSEMBL // ncma:snRNA chromo-some:GRCh37:1:147806736:147806886:-1 ge		0,000927 17	-1,70832
ENST00000366472 // ENSEMBL // cdna:known chromosome:GRCh37:1:249104650:249120832:-1 gen	SH3BP5L	0,000329 95	-1,26433
ENST00000366510 // ENSEMBL // cdna:known chromosome:GRCh37:1:246887349:246931439:1 gene	SCCPDH	0,001246 41	-2,06558
ENST00000366628 // ENSEMBL // cdna:known chromosome:GRCh37:1:233086370:233114548:1 gene	NTPCR	0,000142 75	-1,53288
ENST00000366731 // ENSEMBL // cdna:known chromosome:GRCh37:1:228294389:228297000:-1 gen	MRPL55	0,001216 79	-1,21889
ENST00000366769 // ENSEMBL // cdna:known chromosome:GRCh37:1:227177566:227506175:-1 gen	CDC42BP A	1,45E-06	-2,14792
ENST00000366862 // ENSEMBL // cdna:known chromosome:GRCh37:1:224301789:224349749:1 gene	FBXO28	0,000181 01	-1,79493
ENST00000366960 // ENSEMBL // cdna:known chromosome:GRCh37:1:213224597:213448116:1 gene	RPS6KC1	0,000944 89	-1,3482
ENST00000367265 // ENSEMBL // cdna:known chromosome:GRCh37:1:202696526:202778598:-1 gen	KDM5B	0,000538 19	-1,76782
ENST00000367602 // ENSEMBL // cdna:known chromosome:GRCh37:1:180123969:180173165:1 gene	QSOX1	1,20E-05	-2,33289
ENST00000367669 // ENSEMBL // cdna:known chromosome:GRCh37:1:175913967:176176629:-1 gen	RFWD2	1,07E-05	-1,55878
ENST00000367723 // ENSEMBL // cdna:known chromosome:GRCh37:1:172501489:172580971:1 gene	C1orf9	4,37E-05	-1,84555
ENST00000367763 // ENSEMBL // cdna:known chromosome:GRCh37:1:170501270:170522587:1 gene	GORAB	0,000819 94	-1,63236
ENST00000367772 // ENSEMBL // cdna:known chromosome:GRCh37:1:169821804:169863076:-1 gen	SCYL3	4,71E-06	-1,75313
ENST00000368454 // ENSEMBL // cdna:known chromosome:GRCh37:6:122764499:122907269:-1 gen	SERINC1	3,23E-05	-1,25266

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000368547 // ENSEMBL // cdna:known chromosome:GRCh37:10:135175984:135187193:-1 ge	ECHS1	0,00015632	1,42215
ENST00000368918 // ENSEMBL // cdna:known chromosome:GRCh37:1:151043080:151098018:1 gene	GABPB2	7,92E-05	-1,58075
ENST00000369684 // ENSEMBL // cdna:known chromosome:GRCh37:1:113051400:113065288:1 gene	WNT2B	0,00035294	-1,47545
ENST00000370580 // ENSEMBL // cdna:known chromosome:GRCh37:1:85731931:85742773:-1 gene:	BCL10	0,00019153	-1,5469
ENST00000370859 // ENSEMBL // cdna:known chromosome:GRCh37:1:75667816:76076801:-1 gene:	SLC44A5	0,00026431	-8,55671
ENST00000372013 // ENSEMBL // cdna:known chromosome:GRCh37:10:88727949:88730672:1 gene:	C10orf116	0,00056961	3,32952
ENST00000373030 // ENSEMBL // cdna:known chromosome:GRCh37:20:42219571:42275936:1 gene:	IFT52	3,52E-05	1,59356
ENST00000373281 // ENSEMBL // cdna:known chromosome:GRCh37:9:130493804:130497573:-1 gen	TOR2A	0,00021486	1,27663
ENST00000373921 // ENSEMBL // cdna:known chromosome:GRCh37:1:28199079:28213184:1 gene:E	C1orf38	7,96E-05	-1,61447
ENST00000374796 // ENSEMBL // cdna:known chromosome:GRCh37:20:33302578:33409442:-1 gene	NCOA6	0,00138719	1,28788
ENST00000374980 // ENSEMBL // cdna:known chromosome:GRCh37:20:32676104:32700138:-1 gene	EIF2S2	0,00129448	1,30923
ENST00000376317 // ENSEMBL // cdna:known chromosome:GRCh37:X:49031151:49042845:-1 gene:	PRICKLE3	0,00045488	1,33185
ENST00000377275 // ENSEMBL // cdna:known chromosome:GRCh37:10:18948334:18970568:1 gene:	ARL5B	0,00015454	1,49238
ENST00000377768 // ENSEMBL // cdna:known chromosome:GRCh37:20:17922241:17949623:-1 gene	SNX5	0,00108104	1,45515
ENST00000377921 // ENSEMBL // cdna:known chromosome:GRCh37:10:16632610:16859382:-1 gene	RSU1	0,00058313	1,59813
ENST00000378090 // ENSEMBL // cdna:known chromosome:GRCh37:12:104343985:104351042:-1 ge	C12orf73	0,00083164	1,63671

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000378106 // ENSEMBL // cdna:known chromosome:GRCh37:20:13765596:13799067:1 gene:	NDU-FAF5	0,00145084	1,66888
ENST00000378372 // ENSEMBL // cdna:known chromosome:GRCh37:10:14880163:14913740:1 gene:	HSPA14	0,00027114	1,92698
ENST00000378669 // ENSEMBL // cdna:known chromosome:GRCh37:2:42576478:42596150:-1 gene:	COX7A2L	0,00103693	1,25986
ENST00000378699 // ENSEMBL // cdna:putative chromosome:GRCh37:5:132093835:132113908:-1	08-sept	0,00011557	1,43419
ENST00000378746 // ENSEMBL // cdna:known chromosome:GRCh37:5:132028368:132073330:-1 gen	KIF3A	0,00038205	1,79786
ENST00000379433 // ENSEMBL // cdna:known chromosome:GRCh37:6:11198541:11232891:-1 gene:	NEDD9	7,14E-05	-2,5124
ENST00000379433 // ENSEMBL // cdna:known chromosome:GRCh37:6:11198541:11232891:-1 gene:	NEDD9	7,14E-05	-2,5124
ENST00000379661 // ENSEMBL // cdna:known chromosome:GRCh37:16:57769642:57791162:1 gene:	KATNB1	0,0014013	1,47482
ENST00000380274 // ENSEMBL // cdna:known chromosome:GRCh37:6:3849620:3851551:1 gene:ENS	FAM50B	3,48E-05	-1,5746
ENST00000380834 // ENSEMBL // cdna:known chromosome:GRCh37:2:25016014:25045245:1 gene:E	CENPO	0,00017621	1,48142
ENST00000381401 // ENSEMBL // cdna:known chromosome:GRCh37:X:1505045:1511617:-1 gene:EN	SLC25A6	0,00144553	1,29435
ENST00000381962 // ENSEMBL // cdna:known chromosome:GRCh37:20:627259:634014:-1 gene:ENS	SRXN1	0,00029025	1,68569
ENST00000382352 // ENSEMBL // cdna:known chromosome:GRCh37:20:277737:280965:1 gene:ENSG	ZCCHC3	9,88E-05	1,33252
ENST00000382456 // ENSEMBL // cdna:known chromosome:GRCh37:3:183892477:183901879:1 gene	AP2M1	0,00010295	1,41754
ENST00000384785 // ENSEMBL // ncRNA:snoRNA chromosome:GRCh37:15:45829448:45829575:1 gen		0,00021325	-1,66552
ENST00000390291 // ENSEMBL // cdna:known chromosome:GRCh37:22:22681658:22682172:1 gene:	IGLV1-50	0,00051052	1,79869
ENST00000391835 // ENSEMBL // cdna:putative chromosome:GRCh37:19:50372303:50381285:-1 g	AKT1S1	0,00132378	1,39675

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000392133 // ENSEMBL // cdna:known chromosome:GRCh37:2:216972187:217071026:1 gene	XRCC5	0,000233 36	-1,27542
ENST00000393249 // ENSEMBL // cdna:known chromosome:GRCh37:12:76745577:76953315:-1 gene	OSBPL8	0,000723 76	1,85943
ENST00000394167 // ENSEMBL // cdna:known chromosome:GRCh37:6:42714696:42836128:1 gene:E	KIAA0240	0,000176 21	-1,43343
ENST00000394697 // ENSEMBL // cdna:known chromosome:GRCh37:16:50300427:50352046:1 gene:	ADCY7	0,001176 32	1,81853
ENST00000394795 // ENSEMBL // cdna:known chromosome:GRCh37:5:138678131:138705406:1 gene	PAIP2	0,000981 65	1,26046
ENST00000394986 // ENSEMBL // cdna:known chromosome:GRCh37:4:90647204:90758290:-1 gene:	SNCA	1,34E-05	-1,49814
ENST00000395471 // ENSEMBL // cdna:known chromosome:GRCh37:7:56078761:56119297:-1 gene:	PSPH	0,000854 2	1,87258
ENST00000395601 // ENSEMBL // cdna:known chromosome:GRCh37:8:121547985:121825513:-1 gen	SNTB1	3,44E-08	-4,19721
ENST00000395787 // ENSEMBL // cdna:known chromosome:GRCh37:11:34903842:34938046:-1 gene	APIP	2,96E-05	1,7195
ENST00000395841 // ENSEMBL // cdna:known chromosome:GRCh37:20:55926066:55954267:1 gene:	RAE1	0,000792 8	1,41155
ENST00000395879 // ENSEMBL // cdna:known chromosome:GRCh37:7:43678856:43689895:-1 gene:	COA1	0,000717 26	1,27678
ENST00000396880 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:5:81287814:812883	ATG10-IT1	0,000286 27	2,04241
ENST00000397203 // ENSEMBL // cdna:known chromosome:GRCh37:12:1100404:1605090:1 gene:EN	ERC1	0,000622 64	2,04145
ENST00000398004 // ENSEMBL // cdna:known chromosome:GRCh37:12:69139886:69162470:1 gene:	SLC35E3	0,000324 91	1,65104
ENST00000404924 // ENSEMBL // cdna:known chromosome:GRCh37:2:24150182:24223073:1 gene:E	UBXN2A	0,000331 99	1,42582
ENST00000407418 // ENSEMBL // cdna:known chromosome:GRCh37:22:39257455:39268319:-1 gene	CBX6	0,000202 85	2,35432

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000408647 // ENSEMBL // ncna:snRNA chromosome:GRCh37:11:10420739:10420864:-1 gen		4,31E-07	-1,45401
ENST00000410528 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:20:34231065:34231384:1 g		0,000999 85	1,20817
ENST00000410545 // ENSEMBL // ncna:snRNA chromosome:GRCh37:11:64915055:64915249:1 gene		0,000844 56	1,41325
ENST00000410613 // ENSEMBL // ncna:miRNA chromosome:GRCh37:17:70710522:70710610:-1 gen		0,000692 14	-1,72657
ENST00000411194 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:12:94402515:94402823:-1		0,001430 5	-1,58174
ENST00000411349 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:8:99933461:99933778:-1 g		0,000577 73	1,6413
ENST00000414676 // ENSEMBL // cdna:known chromosome:GRCh37:20:300957:305878:-1 gene:ENS	LOC100507459	5,99E-05	1,64586
ENST00000416191 // ENSEMBL // cdna:known chromosome:GRCh37:10:101190948:101195542:1 gen		0,000494 29	1,42159
ENST00000416575 // ENSEMBL // cdna:known chromosome:GRCh37:2:20189978:20203971:1 gene:E		4,39E-05	1,56048
ENST00000417257 // ENSEMBL // cdna:known chromosome:GRCh37:15:44162962:44487429:-1 gene	FRMD5	0,001494 52	-1,82467
ENST00000418930 // ENSEMBL // cdna:known chromosome:GRCh37:8:86089460:86126753:1 gene:E	E2F5	0,000262 99	1,94281
ENST00000422143 // ENSEMBL // cdna:known chromosome:GRCh37:7:142448053:142448741:1 gene	TRBV29-1	8,19E-06	-4,60396
ENST00000422931 // ENSEMBL // cdna:known chromosome:GRCh37:13:76203370:76206271:-1 gene	LMO7-AS1	0,000521 44	-1,29513
ENST00000423045 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:21:47170542:47172		0,000434 38	-1,54534
ENST00000423793 // ENSEMBL // cdna:known chromosome:GRCh37:9:138799658:138805359:1 gene		0,000124 01	1,83448
ENST00000424014 // ENSEMBL // cdna:known chromosome:GRCh37:12:124104953:124118313:-1 ge	EIF2B1	0,001582	1,33112
ENST00000424075 // ENSEMBL // cdna:known chromosome:GRCh37:12:133464428:133465169:1 gen		0,000996 3	1,306
ENST00000425008 // ENSEMBL // cdna:putative chromosome:GRCh37:3:183525552:183526729:-1	YEATS2-AS1	0,000142	1,66192
ENST00000425585 // ENSEMBL // cdna:novel chromosome:GRCh37:11:70798846:70798972:-1 gene	SHANK2	3,37E-05	1,39819
ENST00000426595 // ENSEMBL // cdna:putative	MRPS17	0,000889	-1,33918

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:7:55954970:56022932:1 gen		02	
ENST00000428777 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:2:207985608:20798	KLF7-IT1	1,25E-05	-1,98817
ENST00000429352 // ENSEMBL // cdna:known chromosome:GRCh37:1:152178334:152179533:1 gene		0,00030766	1,74297
ENST00000431906 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:10:52348409:52349		0,0009047	1,82342
ENST00000433121 // ENSEMBL // havana:lincRNA chromosome:GRCh37:20:61004604:61006568:1 g		0,00029913	-1,20087
ENST00000433526 // ENSEMBL // cdna:putative chromosome:GRCh37:10:18820778:18822265:-1 g		0,00074216	1,3397
ENST00000433837 // ENSEMBL // cdna:putative chromosome:GRCh37:1:227179841:227180907:1 g		1,15E-05	-1,73003
ENST00000434147 // ENSEMBL // cdna:known chromosome:GRCh37:10:75573276:75574495:1 gene:		0,00072963	1,35512
ENST00000436557 // ENSEMBL // cdna:known chromosome:GRCh37:2:186648418:186664877:-1 gen		3,07E-06	-2,0687
ENST00000436877 // ENSEMBL // cdna:known chromosome:GRCh37:10:45395062:45415668:-1 gene		4,92E-05	-1,2743
ENST00000436893 // ENSEMBL // cdna:known chromosome:GRCh37:X:38660821:38663136:-1 gene:	MID1IP1-AS1	0,00041182	1,38978
ENST00000438113 // ENSEMBL // havana:lincRNA chromosome:GRCh37:22:27299303:27316574:1 g		0,00127048	-1,25923
ENST00000438206 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:9:127885377:12788		0,00032457	1,56336
ENST00000438551 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:1:22843967:228462	ZBTB40-IT1	0,00025302	1,21198
ENST00000443515 // ENSEMBL // cdna:known chromosome:GRCh37:1:204346978:204404974:1 gene		0,00044204	-1,4105
ENST00000443649 // ENSEMBL // cdna:known chromosome:GRCh37:12:122692216:122712081:-1 ge	DIABLO	7,28E-05	1,47994
ENST00000446193 // ENSEMBL // cdna:known chromosome:GRCh37:10:14033815:14049525:1 gene:		0,00143044	-1,39613
ENST00000446992 // ENSEMBL // cdna:known chromosome:GRCh37:2:115591407:115593165:-1 gen		0,00089655	-1,24657
ENST00000449821 // ENSEMBL // cdna:known chromosome:GRCh37:20:36611424:36642305:-1 gene	TTI1	8,37E-05	1,48828
ENST00000450852 // ENSEMBL // cdna:known chromosome:GRCh37:5:52393882:52405602:-1 gene:	MOCS2	8,92E-06	1,65389
ENST00000450930 // ENSEMBL // cdna:putative chromo-		0,000224	-1,20112

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
some:GRCh37:6:16762143:16762849:1 gen		93	
ENST00000451507 // ENSEMBL // cdna:putative chromo-some:GRCh37:20:3868886:3869515:-1 gen		2,43E-05	1,5211
ENST00000452366 // ENSEMBL // havana:lincRNA chromo-some:GRCh37:1:172876040:172876824:1		0,001217 51	-1,35327
ENST00000452637 // ENSEMBL // cdna:known chromosome:GRCh37:1:149284645:149287106:1 gene	FAM91A2	0,001153 56	-1,5681
ENST00000454029 // ENSEMBL // cdna:known chromo-some:GRCh37:7:23719814:23720405:-1 gene:		0,000104 13	1,20098
ENST00000454400 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:10:72577323:72577		0,000179	1,54955
ENST00000455336 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:9:77624744:776309		0,000599 79	1,72663
ENST00000455566 // ENSEMBL // cdna:known chromosome:GRCh37:10:133747955:133773331:1 gen	PPP2R2D	0,001596 33	1,5885
ENST00000455707 // ENSEMBL // cdna:known chromo-some:GRCh37:2:120932461:120974120:-1 gen		0,001527 33	-3,07134
ENST00000455791 // ENSEMBL // cdna:known chromo-some:GRCh37:20:25604695:25657688:1 gene:		3,19E-08	2,33683
ENST00000457016 // ENSEMBL // cdna:known chromosome:GRCh37:5:112043218:112181936:1 gene	APC	0,000370 64	1,47383
ENST00000457116 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:6:82434439:824460		0,001188 75	-1,54484
ENST00000457162 // ENSEMBL // cdna:putative chromo-some:GRCh37:21:30430394:30431977:-1 g		0,000833 82	1,43391
ENST00000457290 // ENSEMBL // cdna:known chromosome:GRCh37:2:105992323:105995298:1 gene	LOC100506494	0,000513 55	-1,36522
ENST00000457319 // ENSEMBL // cdna:known chromo-some:GRCh37:6:116565350:116565891:-1 gen		0,000169 33	1,26391
ENST00000458178 // ENSEMBL // cdna:known chromosome:GRCh37:22:22292665:22297799:1 gene:	LOC100286925	0,000691 73	-1,39737
ENST00000458261 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:9:128047877:12804		0,000761 3	1,65978
ENST00000458509 // ENSEMBL // cdna:known chromosome:GRCh37:5:131973740:131991846:-1 gen	LOC100506030	0,000666 66	1,24575
ENST00000458754 // ENSEMBL // ncRNA:snoRNA chromo-some:GRCh37:10:12187662:12187765:1 gen		1,14E-05	2,95278
ENST00000459385 // ENSEMBL // ncRNA:snoRNA chromo-some:GRCh37:2:208938785:208938886:-1 g		0,000646 97	-1,37551

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000459496 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:1:171451046:171451148:1 ge		0,00043463	1,31547
ENST00000460977 // ENSEMBL // cdna:putative chromosome:GRCh37:3:142184157:142191179:-1		0,0010472	1,75625
ENST00000461096 // ENSEMBL // cdna:known chromosome:GRCh37:1:109605121:109618593:-1 gen	TAF13	0,00098579	-1,61297
ENST00000463534 // ENSEMBL // cdna:known chromosome:GRCh37:2:233877602:233880594:1 gene		0,00111825	-1,98252
ENST00000467082 // ENSEMBL // havana:lincRNA chromosome:GRCh37:8:76079939:76088891:-1 g		1,07E-06	-5,19749
ENST00000477153 // ENSEMBL // havana:lincRNA chromosome:GRCh37:3:147878698:147944382:1		0,00111062	-1,20165
ENST00000477313 // ENSEMBL // cdna:known chromosome:GRCh37:20:44527402:44540686:-1 gene	PLTP	0,00045289	2,73334
ENST00000477703 // ENSEMBL // cdna:known chromosome:GRCh37:3:52570621:52575907:1 gene:E	C3orf78	0,00037553	1,35684
ENST00000477892 // ENSEMBL // cdna:known chromosome:GRCh37:3:122103029:122131181:1 gene	FAM162A	0,00034168	1,43865
ENST00000481585 // ENSEMBL // cdna:known chromosome:GRCh37:3:149498063:149686172:-1 gen	ANKUB1	0,0012284	1,25428
ENST00000491614 // ENSEMBL // cdna:known chromosome:GRCh37:10:12207324:12238123:-1 gene	NUDT5	0,00119632	1,77745
ENST00000494238 // ENSEMBL // cdna:putative chromosome:GRCh37:3:132379206:132396626:1 g	UBA5	5,16E-05	1,45905
ENST00000496455 // ENSEMBL // cdna:known chromosome:GRCh37:3:155588325:155658457:1 gene	GMPS	6,11E-05	1,60653
ENST00000497366 // ENSEMBL // cdna:putative chromosome:GRCh37:7:150076943:150080973:-1		0,00018614	-1,22759
ENST00000498508 // ENSEMBL // cdna:known chromosome:GRCh37:1:214161274:214209775:1 gene	PROX1	0,00016956	-1,72824
ENST00000498967 // ENSEMBL // havana:lincRNA chromosome:GRCh37:12:124066767:124069662:-		0,00026687	1,34749
ENST00000499653 // ENSEMBL // cdna:known chromosome:GRCh37:8:103255837:103265561:1 gene		2,04E-06	1,52328
ENST00000504204 // ENSEMBL // havana:lincRNA chromosome:GRCh37:5:144602173:144608545:-1		9,24E-05	-1,48305
ENST00000504469 // ENSEMBL // cdna:known chromosome:		0,001218	1,43301

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
some:GRCh37:5:43484061:43488542:-1 gene:E		66	
ENST00000504592 // ENSEMBL // cdna:known chromosome:GRCh37:4:102341118:102995969:1 gene	BANK1	0,00048312	-2,50627
ENST00000508632 // ENSEMBL // cdna:known chromosome:GRCh37:4:48887036:48908845:-1 gene:	OCIAD2	1,21E-07	-1,51418
ENST00000509136 // ENSEMBL // cdna:known chromosome:GRCh37:4:30777879:30795592:-1 gene:		2,18E-05	-2,09047
ENST00000509578 // ENSEMBL // cdna:known chromosome:GRCh37:5:85913773:85916578:1 gene:E	COX7C	0,00110932	1,34119
ENST00000511331 // ENSEMBL // cdna:known chromosome:GRCh37:5:180673523:180699168:1 gene	LOC100507619	0,00070558	1,42899
ENST00000516072 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:15:80434400:80434469:1 gen		0,00070487	-1,56093
ENST00000516141 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:10:52345310:52345463:-1		0,00060721	1,83558
ENST00000516154 // ENSEMBL // ncna:miRNA chromosome:GRCh37:8:18667010:18667136:-1 gene		0,00139772	2,10268
ENST00000516383 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:12:122976660:122976788:-1		0,00039633	1,77877
ENST00000516847 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:1:145044651:145044900:1		0,00040291	-2,25769
ENST00000516947 // ENSEMBL // ncna:snRNA chromosome:GRCh37:2:37094541:37094638:-1 gene		0,0009123	1,69045
ENST00000516991 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:14:63945990:63946131:1 gen		0,00056437	1,22773
ENST00000517008 // ENSEMBL // ncna:miRNA chromosome:GRCh37:1:154226921:154226997:1 gen		8,05E-06	-1,49301
ENST00000517065 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:11:47841755:47841844:-1		0,00100986	1,58332
ENST00000517074 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:12:62511668:62511739:-1 ge		0,00070136	-1,95715
ENST00000517126 // ENSEMBL // ncna:snRNA chromosome:GRCh37:8:79310750:79310857:-1 gene		0,00045448	-1,69285
ENST00000517211 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:3:174349613:174349892:1		1,21E-05	-1,40338
ENST00000518105 // ENSEMBL // cdna:known chromosome:GRCh37:4:98307111:98554974:-1 gene:		0,00028423	-1,50542
ENST00000518498 // ENSEMBL // cdna:known chromosome:GRCh37:21:43731777:43735761:-1 gene	TFF3	0,00086647	-2,51423
ENST00000520149 // ENSEMBL // havana:lincRNA chromosome:GRCh37:8:134898739:134914575:1		0,00034818	-1,24194

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000520778 // ENSEMBL // cdna:putative chromosome:GRCh37:8:75938663:75941695:-1 ge		5,52E-05	-2,66621
ENST00000523577 // ENSEMBL // cdna:known chromosome:GRCh37:8:94712781:94741478:1 gene:E	FAM92A1	0,000928 82	1,68262
ENST00000523790 // ENSEMBL // cdna:known chromosome:GRCh37:7:27208713:27211384:1 gene:E	MIR196B	0,000985 07	-1,47379
ENST00000525500 // ENSEMBL // cdna:known chromosome:GRCh37:11:62357121:62357959:-1 gene		4,20E-05	1,53044
ENST00000526310 // ENSEMBL // cdna:putative chromosome:GRCh37:11:102100582:102101653:-1		0,000803 5	1,39884
ENST00000526453 // ENSEMBL // cdna:putative chromosome:GRCh37:11:118866905:118868714:-1		0,000360 17	1,56516
ENST00000527997 // ENSEMBL // havana:lincRNA chromosome:GRCh37:11:12108438:12110988:1 g		0,000901 04	-1,71049
ENST00000529689 // ENSEMBL // cdna:known chromosome:GRCh37:11:82970139:82997450:-1 gene	CCDC90B	0,001215 75	1,30395
ENST00000531268 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:11:44093012:44093		0,001429 68	1,58826
ENST00000531323 // ENSEMBL // cdna:known chromosome:GRCh37:11:62437745:62441049:1 gene:	C11orf83	0,000278 35	1,2612
ENST00000531742 // ENSEMBL // cdna:known chromosome:GRCh37:11:118267810:118272024:-1 ge		0,000375 74	1,20253
ENST00000533028 // ENSEMBL // cdna:known chromosome:GRCh37:1:100435992:100492535:1 gene	SLC35A3	0,000592 03	-1,47538
ENST00000533166 // ENSEMBL // cdna:known chromosome:GRCh37:11:65770052:65771602:1 gene:	BANF1	5,23E-06	1,28516
ENST00000535318 // ENSEMBL // cdna:known chromosome:GRCh37:16:57126519:57181878:1 gene:	CPNE2	0,000311 29	2,87766
ENST00000536183 // ENSEMBL // cdna:known chromosome:GRCh37:7:95034175:95064510:-1 gene:	PON2	0,000150 7	-2,00045
ENST00000538010 // ENSEMBL // cdna:known chromosome:GRCh37:12:122457328:122499948:1 gen	BCL7A	5,52E-05	1,63861
ENST00000540410 // ENSEMBL // cdna:known chromosome:GRCh37:11:47241769:47243302:-1 gene		0,000741 25	1,32153
ENST00000542440 // ENSEMBL // cdna:putative chromosome:GRCh37:12:122242086:122270490:1	SETD1B	9,06E-06	1,44079
ENST00000542678 // ENSEMBL // cdna:known	ABCB9	0,000765	1,21722

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:12:123413547:123466196:-1 ge		31	
ENST00000543341 // ENSEMBL // cdna:known chromosome:GRCh37:12:124118376:124146479:1 gen	GTF2H3	4,12E-05	1,9056
ENST00000543473 // ENSEMBL // cdna:known chromosome:GRCh37:12:118814185:118855836:1 gen	SUDS3	0,0001534	1,50495
ENST00000544627 // ENSEMBL // cdna:putative chromosome:GRCh37:12:14537998:14651697:1 ge	ATF7IP	0,00044287	1,34258
ENST00000546455 // ENSEMBL // cdna:known chromosome:GRCh37:12:47473386:47630443:1 gene:	PCED1B	0,00067564	-2,15546
ENST00000547748 // ENSEMBL // cdna:known chromosome:GRCh37:12:47631517:47672804:-1 gene		1,85E-07	-3,02862
ENST00000549373 // ENSEMBL // havana:non_coding chromosome:GRCh37:12:116612307:11661910		5,67E-06	1,65719
ENST00000550908 // ENSEMBL // havana:lincRNA chromosome:GRCh37:12:53553370:53554784:1 g		1,39E-05	-1,20398
ENST00000552864 // ENSEMBL // cdna:known chromosome:GRCh37:12:81186299:81331704:-1 gene	LIN7A	0,00145697	-1,20575
ENST00000553780 // ENSEMBL // cdna:known chromosome:GRCh37:14:95027779:95059133:1 gene:	SERPIN A5	0,00069404	-1,33316
ENST00000556949 // ENSEMBL // cdna:putative chromosome:GRCh37:14:32476108:32487891:1 ge		4,79E-05	-2,39868
ENST00000558749 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:15:59640847:59652		5,04E-06	-1,66675
ENST00000559041 // ENSEMBL // havana:sense_overlapping chromosome:GRCh37:15:90061754:90		0,00030979	1,63133
ENST00000563192 // ENSEMBL // havana:lincRNA chromosome:GRCh37:16:2204798:2205359:-1 ge	LOC100507303	0,00120023	1,57117
ENST00000564376 // ENSEMBL // cdna:known chromosome:GRCh37:16:57282459:57286664:-1 gene	LOC100653273	0,00041618	1,41418
ENST00000566741 // ENSEMBL // cdna:putative chromosome:GRCh37:6:147830362:148058683:1 g	SAMD5	0,00063294	-3,22175
NC_001807 // GenBank // gi 17981852 ref NC_001807.4 :10406-10470; gene=TRNR; product=tR		0,00104053	2,02382
NC_001807 // GenBank // gi 17981852 ref NC_001807.4 :12139-12207; gene=TRNH; product=tR		0,00064851	1,54923
NC_001807 // GenBank // gi 17981852 ref NC_001807.4 :12267-12337; gene=TRNL2; product=t		0,00148681	1,85219
NC_001807 // GenBank // gi 17981852 ref NC_001807.4 :9992-		1,35E-05	2,57351

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
10059; gene=TRNG; product=tRN			
NM_000070 // RefSeq // Homo sapiens calpain 3, (p94) (CAPN3), transcript variant 1, mRN	CAPN3	5,23E-05	-2,50154
NM_000092 // RefSeq // Homo sapiens collagen, type IV, alpha 4 (COL4A4), mRNA. // chr2	COL4A4	0,00120659	-1,47865
NM_000107 // RefSeq // Homo sapiens damage-specific DNA binding protein 2, 48kDa (DDB2)	DDB2	0,00050351	1,79357
NM_000109 // RefSeq // Homo sapiens dystrophin (DMD), transcript variant Dp427c, mRNA.	DMD	0,00028804	-1,43397
NM_000153 // RefSeq // Homo sapiens galactosylceramidase (GALC), transcript variant 1,	GALC	1,64E-06	-2,44218
NM_000179 // RefSeq // Homo sapiens mutS homolog 6 (E. coli) (MSH6), mRNA. // chr2 // 1	MSH6	0,00092599	1,45217
NM_000182 // RefSeq // Homo sapiens hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiola	HADHA	3,24E-06	1,44575
NM_000201 // RefSeq // Homo sapiens intercellular adhesion molecule 1 (ICAM1), mRNA. //	ICAM1	0,00118348	-1,98895
NM_000204 // RefSeq // Homo sapiens complement factor I (CFI), mRNA. // chr4 // 100 //	CFI	7,31E-06	-5,68645
NM_000234 // RefSeq // Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA. // chr19	LIG1	4,21E-07	1,29522
NM_000274 // RefSeq // Homo sapiens ornithine aminotransferase (OAT), nuclear gene enco	OAT	6,95E-05	2,15728
NM_000367 // RefSeq // Homo sapiens thiopurine S-methyltransferase (TPMT), mRNA. // chr	TPMT	9,66E-06	-1,96134
NM_000396 // RefSeq // Homo sapiens cathepsin K (CTSK), mRNA. // chr1 // 100 // 91 // 2	CTSK	0,00014606	-1,68832
NM_000431 // RefSeq // Homo sapiens mevalonate kinase (MVK), transcript variant 1, mRNA	MVK	0,00048061	1,3952
NM_000535 // RefSeq // Homo sapiens PMS2 postmeiotic segregation increased 2 (S. cerevi	PMS2	0,00036354	1,39858
NM_000546 // RefSeq // Homo sapiens tumor protein p53 (TP53), transcript variant 1, mRN	TP53	0,00069436	1,67829
NM_000574 // RefSeq // Homo sapiens CD55 molecule, decay accelerating factor for comple	CD55	0,00024293	-1,84036
NM_000584 // RefSeq // Homo sapiens interleukin 8 (IL8), mRNA. // chr4 // 100 // 62 //	IL8	2,46E-05	-5,87816
NM_000715 // RefSeq // Homo sapiens complement component 4 binding protein, alpha (C4BP	C4BPA	0,00077329	-1,49347
NM_000867 // RefSeq // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2B, G prot	HTR2B	0,00100932	-1,33096
NM_000895 // RefSeq // Homo sapiens leukotriene A4 hydrolase (LTA4H), transcript varian	LTA4H	2,94E-06	2,35941
NM_000906 // RefSeq // Homo sapiens natriuretic peptide receptor A/guanylate cyclase A	NPR1	0,0008733	-1,37524

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_000963 // RefSeq // Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandi	PTGS2	0,00044848	-5,13436
NM_001001323 // RefSeq // Homo sapiens ATPase, Ca ⁺⁺ transporting, plasma membrane 1 (AT	ATP2B1	0,0002789	1,94477
NM_001001419 // RefSeq // Homo sapiens SMAD family member 5 (SMAD5), transcript variant	SMAD5	5,19E-05	1,51318
NM_001001973 // RefSeq // Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1	ATP5C1	0,00014739	1,51094
NM_001002265 // RefSeq // Homo sapiens membrane-associated ring finger (C3HC4) 8, E3 ub	MARCH8	4,39E-05	1,48212
NM_001002762 // RefSeq // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 12 (DN	DNAJB12	0,00127392	1,37654
NM_001002857 // RefSeq // Homo sapiens annexin A2 (ANXA2), transcript variant 2, mRNA.	ANXA2	6,44E-05	-1,61672
NM_001005203 // RefSeq // Homo sapiens olfactory receptor, family 8, subfamily S, membe	OR8S1	0,00077375	-1,23703
NM_001005493 // RefSeq // Homo sapiens olfactory receptor, family 6, subfamily C, membe	OR6C6	0,00079147	1,23247
NM_001005741 // RefSeq // Homo sapiens glucosidase, beta, acid (GBA), transcript varian	GBA	0,00127574	-1,29666
NM_001008708 // RefSeq // Homo sapiens ChaC, cation transport regulator homolog 2 (E. c	CHAC2	0,00162046	1,85546
NM_001009880 // RefSeq // Homo sapiens KIAA0930 (KIAA0930), transcript variant 2, mRNA.	KIAA0930	4,46E-06	1,50115
NM_001010888 // RefSeq // Homo sapiens zinc finger CCCH-type containing 12B (ZC3H12B),	ZC3H12B	0,00051311	-1,70592
NM_001010922 // RefSeq // Homo sapiens BCL2-like 15 (BCL2L15), mRNA. // chr1 // 100 //	BCL2L15	7,99E-05	-4,67039
NM_001011724 // RefSeq // Homo sapiens heterogeneous nuclear ribonucleoprotein A1-like	HNRNPA1L2	0,00015565	1,60651
NM_001012515 // RefSeq // Homo sapiens ferrochelatase (FECH), nuclear gene encoding mit	FECH	1,17E-05	1,60873
NM_001014437 // RefSeq // Homo sapiens cysteinyl-tRNA synthetase (CARS), transcript var	CARS	0,00086522	1,23829
NM_001014443 // RefSeq // Homo sapiens ubiquitin specific peptidase 21 (USP21), transcr	USP21	0,00018706	-1,2041
NM_001014450 // RefSeq // Homo sapiens small proline-rich protein 2F (SPRR2F), mRNA. //	SPRR2F	0,00031069	-1,41659
NM_001017402 // RefSeq // Homo sapiens laminin, beta 3 (LAMB3), transcript variant 2, m	LAMB3	0,00032431	-1,87364
NM_001023561 // RefSeq // Homo sapiens zinc finger protein 749 (ZNF749), mRNA. // chr19	ZNF749	2,64E-05	1,38312
NM_001030060 // RefSeq // Homo sapiens sterile alpha motif domain containing 5 (SAMD5),	SAMD5	0,00038478	-2,19646
NM_001032281 // RefSeq // Homo sapiens tissue fac-	TFPI	0,000393	-3,46002

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
tor pathway inhibitor (lipoprotein-ass		23	
NM_001037165 // RefSeq // Homo sapiens forkhead box K1 (FOXK1), mRNA. // chr7 // 100 //	FOXK1	6,30E-05	1,42961
NM_001037984 // RefSeq // Homo sapiens solute carrier family 38, member 10 (SLC38A10),	SLC38A10	0,00135348	-1,28079
NM_001039091 // RefSeq // Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2	PRPS2	0,00098688	1,72913
NM_001039361 // RefSeq // Homo sapiens PRAME family member 10 (PRAMEF10), mRNA. // chr1	PRAMEF10	1,34E-06	-1,4122
NM_001048226 // RefSeq // Homo sapiens dysbindin (dystrobrevin binding protein 1) domai	DBNDD2	0,00011949	1,49289
NM_001076786 // RefSeq // Homo sapiens glutamine and serine rich 1 (QSER1), mRNA. // ch	QSER1	0,00048227	1,44388
NM_001079559 // RefSeq // Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 2	HNRNPUL2	0,00141417	1,2318
NM_001080401 // RefSeq // Homo sapiens protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1N (pu	PPM1N	1,69E-05	1,41467
NM_001080533 // RefSeq // Homo sapiens unc-119 homolog B (C. elegans) (UNC119B), mRNA.	UNC119B	7,23E-05	1,8408
NM_001083 // RefSeq // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transc	PDE5A	0,00045544	-3,04833
NM_001083602 // RefSeq // Homo sapiens patched 1 (PTCH1), transcript variant 1a, mRNA.	PTCH1	0,00068102	1,53049
NM_001098511 // RefSeq // Homo sapiens kinesin heavy chain member 2A (KIF2A), transcrip	KIF2A	0,00124134	1,53114
NM_001098616 // RefSeq // Homo sapiens chromosome 1 open reading frame 43 (C1orf43), tr	C1orf43	0,00011383	-1,32891
NM_001098638 // RefSeq // Homo sapiens ring finger protein 169 (RNF169), mRNA. // chr11	RNF169	0,00067824	1,51561
NM_001099678 // RefSeq // Homo sapiens leucine rich repeat containing 58 (LRRC58), mRNA	LRRC58	0,00054893	1,54347
NM_001100422 // RefSeq // Homo sapiens spermatogenesis associated, serine-rich 2-like (	SPATS2L	0,00063845	-1,43625
NM_001102366 // RefSeq // Homo sapiens chromosome 14 open reading frame 159 (C14orf159)	C14orf159	0,00024922	1,33575
NM_001104546 // RefSeq // Homo sapiens ribonuclease P/MRP 30kDa subunit (RPP30), transc	RPP30	0,00132594	1,68722
NM_001104647 // RefSeq // Homo sapiens solute carrier family 25 (pyrimidine nucleotide	SLC25A36	0,0005822	1,51822
NM_001105570 // RefSeq // Homo sapiens nudix (nucleoside diphosphate linked moiety X)-t	NUDT19	4,76E-05	1,53021
NM_001110822 // RefSeq // Homo sapiens tudor domain containing 12 (TDRD12), mRNA. // ch	TDRD12	0,00135346	-1,20318
NM_001112808 // RefSeq // Homo sapiens FPGT-TNNI3K readthrough (FPGT-TNNI3K), transcrip	FPGT-TNNI3K	0,00015929	-1,47344

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001113493 // RefSeq // Homo sapiens septin 9 (SEPT9), transcript variant 2, mRNA. //	09-sept	0,000991 23	-1,30732
NM_001116 // RefSeq // Homo sapiens adenylate cyclase 9 (ADCY9), mRNA. // chr16 // 100	ADCY9	0,001597 25	1,59723
NM_001123375 // RefSeq // Homo sapiens histone cluster 2, H3d (HIST2H3D), mRNA. // chr1	HIST2H3D	0,000192 82	2,28785
NM_001127221 // RefSeq // Homo sapiens calcium channel, voltage-dependent, P/Q type, $\alpha 1$	CACNA1A	0,001538 6	-1,21835
NM_001128205 // RefSeq // Homo sapiens sulfatase 1 (SULF1), transcript variant 1, mRNA.	SULF1	0,000423 26	-1,26557
NM_001128310 // RefSeq // Homo sapiens SPARC-like 1 (hevin) (SPARCL1), transcript varia	SPARCL1	0,000952 33	-1,71251
NM_001129993 // RefSeq // Homo sapiens KIAA1841 (KIAA1841), transcript variant 1, mRNA.	KIAA1841	0,000113 87	1,40579
NM_001130440 // RefSeq // Homo sapiens signal recognition particle 9kDa (SRP9), transcr	SRP9	0,000876 63	-1,26458
NM_001130518 // RefSeq // Homo sapiens chondroitin sulfate N-acetylgalactosaminyltransf	CSGALNACT1	0,000410 98	-1,80869
NM_001130699 // RefSeq // Homo sapiens interaction protein for cytohesin exchange facto	IPCEF1	0,001399 9	-1,58711
NM_001130966 // RefSeq // Homo sapiens thromboxane A synthase 1 (platelet) (TBXAS1), tr	TBXAS1	0,001259 83	-1,49448
NM_001131007 // RefSeq // Homo sapiens KIAA0922 (KIAA0922), transcript variant 1, mRNA.	KIAA0922	0,000732 49	2,57886
NM_001134745 // RefSeq // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LR	LRRTM4	0,000617 12	-1,24574
NM_001134779 // RefSeq // Homo sapiens importin 11 (IPO11), transcript variant 1, mRNA.	IPO11	0,000247 04	1,74127
NM_001135638 // RefSeq // Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type	PIP5K1A	6,03E-06	-1,36912
NM_001135773 // RefSeq // Homo sapiens spermatogenesis associated 2 (SPATA2), transcrip	SPATA2	7,11E-05	1,52604
NM_001135924 // RefSeq // Homo sapiens von Willebrand factor D and EGF domains (VWDE),	VWDE	1,03E-05	-4,16521
NM_001136223 // RefSeq // Homo sapiens REST corepressor 3 (RCOR3), transcript variant 1	RCOR3	0,001141 56	-1,27312
NM_001136538 // RefSeq // Homo sapiens acyl-CoA dehydrogenase family, member 10 (ACAD10	ACAD10	3,02E-05	1,64528
NM_001137550 // RefSeq // Homo sapiens leucine rich repeat (in FLII) interacting protei	LRRFIP1	7,49E-05	-1,42505
NM_001143906 // RefSeq // Homo sapiens TRAF-type zinc finger domain containing 1 (TRAFD	TRAFD1	4,23E-05	1,40898
NM_001145260 // RefSeq // Homo sapiens nuclear receptor coactivator 4 (NCOA4), transcri	NCOA4	0,000789 12	1,3858
NM_001145345 // RefSeq // Homo sapiens zinc finger	ZNF566	0,000811	1,42612

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
protein 566 (ZNF566), transcript var		27	
NM_001145418 // RefSeq // Homo sapiens tetratricopeptide repeat domain 28 (TTC28), mRNA	TTC28	6,59E-05	1,84335
NM_001145547 // RefSeq // Homo sapiens RNA binding motif protein 17 (RBM17), transcript	RBM17	6,65E-05	1,94998
NM_001159767 // RefSeq // Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), tr	BZW2	0,00068853	1,67003
NM_001161766 // RefSeq // Homo sapiens adenosylhomocysteinase (AHCY), transcript varian	AHCY	1,73E-05	1,60835
NM_001162893 // RefSeq // Homo sapiens KIAA0040 (KIAA0040), transcript variant 1, mRNA.	KIAA0040	2,60E-06	-2,58796
NM_001162893 // RefSeq // Homo sapiens KIAA0040 (KIAA0040), transcript variant 1, mRNA.	KIAA0040	0,00105225	-1,37926
NM_001164811 // RefSeq // Homo sapiens PET117 homolog (S. cerevisiae) (PET117), mRNA. /	PET117	0,00023943	1,40319
NM_001167674 // RefSeq // Homo sapiens cell adhesion molecule 2 (CADM2), transcript var	CADM2	0,00061349	-2,17204
NM_001167856 // RefSeq // Homo sapiens strawberry notch homolog 1 (Drosophila) (SBNO1),	SBNO1	2,78E-05	1,70916
NM_001172303 // RefSeq // Homo sapiens microtubule associated serine/threonine kinase-1	MASTL	0,00094602	2,11393
NM_001173454 // RefSeq // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 1 (PDHA	PDHA1	0,00073466	1,57999
NM_001177 // RefSeq // Homo sapiens ADP-ribosylation factor-like 1 (ARL1), mRNA. // chr	ARL1	0,00064166	1,45845
NM_001177802 // RefSeq // Homo sapiens RAN guanine nucleotide release factor (RANGRF),	RANGRF	0,00079908	1,44664
NM_001185093 // RefSeq // Homo sapiens nitrilase 1 (NIT1), transcript variant 3, mRNA.	NIT1	0,00039593	-1,57835
NM_001185118 // RefSeq // Homo sapiens myoneurin (MYNN), transcript variant 2, mRNA. //	MYNN	0,00146892	1,3656
NM_001193434 // RefSeq // Homo sapiens pleckstrin homology domain containing, family S	PLEKHS1	0,00059998	-6,65282
NM_001194995 // RefSeq // Homo sapiens chromosome 12 open reading frame 65 (C12orf65),	C12orf65	9,03E-05	1,64746
NM_001197097 // RefSeq // Homo sapiens protease, serine, 3 (PRSS3), transcript variant	PRSS3	6,72E-06	-2,87571
NM_001197104 // RefSeq // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trit	MLL	0,00135135	1,24154
NM_001198842 // RefSeq // Homo sapiens chaperonin containing TCP1, subunit 2 (beta) (CC	CCT2	0,00069794	1,78291
NM_001199260 // RefSeq // Homo sapiens torsin A interacting protein 2 (TOR1AIP2), trans	TOR1AIP2	7,95E-05	-1,59076
NM_001199815 // RefSeq // Homo sapiens gamma-glutamylcyclotransferase (GGCT), transcrip	GGCT	3,16E-05	1,6749

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001201 // RefSeq // Homo sapiens bone morpho-genetic protein 3 (BMP3), mRNA. // chr4	BMP3	0,001111 35	-1,21306
NM_001204 // RefSeq // Homo sapiens bone morpho-genetic protein receptor, type II (serin	BMPR2	0,001014 88	-1,46829
NM_001204397 // RefSeq // Homo sapiens paired-like homeodomain 2 (PITX2), transcript va	PITX2	8,09E-05	-1,29379
NM_001204406 // RefSeq // Homo sapiens arachido-nate 5-lipoxygenase-activating protein (	ALOX5A P	0,001296 68	-1,31725
NM_001206651 // RefSeq // Homo sapiens SH3-domain GRB2-like endophilin B1 (SH3GLB1), tr	SH3GLB1	0,000845 48	-1,51161
NM_001242307 // RefSeq // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), nuclear	PITRM1	0,000496 75	1,92544
NM_001243121 // RefSeq // Homo sapiens phospho-diesterase 4A, cAMP-specific (PDE4A), tra	PDE4A	0,001273 57	-1,81771
NM_001252100 // RefSeq // Homo sapiens kinesin family member 21B (KIF21B), transcript v	KIF21B	0,000320 94	-1,67712
NM_001252406 // RefSeq // Homo sapiens zinc finger and BTB domain containing 7B (ZBTB7B	ZBTB7B	0,000700 87	-1,29393
NM_001256165 // RefSeq // Homo sapiens trans-membrane and coiled-coil domains 1 (TMCO1),	TMCO1	0,000159 86	-1,70566
NM_001256410 // RefSeq // Homo sapiens RAB18, member RAS oncogene family (RAB18), trans	RAB18	1,29E-05	1,58657
NM_001258438 // RefSeq // Homo sapiens threonyl-tRNA synthetase (TARS), transcript vari	TARS	0,001337 87	1,61221
NM_001267578 // RefSeq // Homo sapiens torsin A interacting protein 1 (TOR1AIP1), trans	TOR1AIP 1	0,000532 39	-1,5063
NM_001267806 // RefSeq // Homo sapiens pro-teasomal ATPase-associated factor 1 (PAAF1),	PAAF1	0,000215 72	1,57539
NM_001281 // RefSeq // Homo sapiens tubulin fold-ing cofactor B (TBCB), mRNA. // chr19 /	TBCB	0,001368 45	1,3556
NM_001297 // RefSeq // Homo sapiens cyclic nucleo-tide gated channel beta 1 (CNGB1), tra	CNGB1	0,001248 75	-1,23801
NM_001412 // RefSeq // Homo sapiens eukaryotic translation initiation factor 1A, X-link	EIF1AX	0,001470 83	1,59057
NM_001483 // RefSeq // Homo sapiens glioblastoma amplified sequence (GBAS), nuclear gen	GBAS	0,000724 32	1,69679
NM_001494 // RefSeq // Homo sapiens GDP dissocia-tion inhibitor 2 (GDI2), transcript var	GDI2	0,000200 18	1,59581
NM_001531 // RefSeq // Homo sapiens major histo-compatibility complex, class I-related (	MR1	1,77E-06	-2,32707
NM_001536 // RefSeq // Homo sapiens protein argi-nine methyltransferase 1 (PRMT1), trans	PRMT1	0,000501 63	1,2935
NM_001540 // RefSeq // Homo sapiens heat shock 27kDa protein 1 (HSPB1), mRNA. // chr7 /	HSPB1	0,000527 72	1,3797
NM_001628 // RefSeq // Homo sapiens aldo-keto re-	AKR1B1	0,001282	1,99198

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ductase family 1, member B1 (aldose red		46	
NM_001631 // RefSeq // Homo sapiens alkaline phosphatase, intestinal (ALPI), mRNA. // c	ALPI	0,0015973	-1,27247
NM_001632 // RefSeq // Homo sapiens alkaline phosphatase, placental (ALPP), mRNA. // ch	ALPP	0,00012277	-1,39519
NM_001647 // RefSeq // Homo sapiens apolipoprotein D (APOD), mRNA. // chr3 // 100 // 73	APOD	0,00132312	-2,42082
NM_001665 // RefSeq // Homo sapiens ras homolog family member G (RHOG), mRNA. // chr11	RHOG	0,00065311	1,30759
NM_001668 // RefSeq // Homo sapiens aryl hydrocarbon receptor nuclear translocator (ARN	ARNT	1,53E-06	-1,32541
NM_001693 // RefSeq // Homo sapiens ATPase, H ⁺ transporting, lysosomal 56/58kDa, V1 sub	ATP6V1B2	0,00101333	1,6069
NM_001745 // RefSeq // Homo sapiens calcium modulating ligand (CAMLG), mRNA. // chr5 //	CAMLG	0,00072404	2,22836
NM_001799 // RefSeq // Homo sapiens cyclin-dependent kinase 7 (CDK7), mRNA. // chr5 //	CDK7	0,00139085	1,58626
NM_001876 // RefSeq // Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A),	CPT1A	0,00057874	1,57343
NM_001964 // RefSeq // Homo sapiens early growth response 1 (EGR1), mRNA. // chr5 // 10	EGR1	0,00056386	-1,67519
NM_001976 // RefSeq // Homo sapiens enolase 3 (beta, muscle) (ENO3), transcript variant	ENO3	0,0005075	1,4093
NM_002079 // RefSeq // Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspar	GOT1	0,00044201	1,76797
NM_002080 // RefSeq // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial	GOT2	0,00025391	1,6705
NM_002202 // RefSeq // Homo sapiens ISL LIM homeobox 1 (ISL1), mRNA. // chr5 // 100 //	ISL1	0,00130185	-1,77133
NM_002245 // RefSeq // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), m	KCNK1	4,17E-06	-2,4294
NM_002296 // RefSeq // Homo sapiens lamin B receptor (LBR), transcript variant 1, mRNA.	LBR	2,70E-05	-1,28615
NM_002381 // RefSeq // Homo sapiens matrilin 3 (MATN3), mRNA. // chr2 // 100 // 87 // 1	MATN3	9,71E-05	1,86256
NM_002389 // RefSeq // Homo sapiens CD46 molecule, complement regulatory protein (CD46)	CD46	0,00070188	-1,40216
NM_002392 // RefSeq // Homo sapiens Mdm2, p53 E3 ubiquitin protein ligase homolog (mous	MDM2	0,00027261	1,66699
NM_002393 // RefSeq // Homo sapiens Mdm4 p53 binding protein homolog (mouse) (MDM4), tr	MDM4	1,19E-05	-1,37419
NM_002480 // RefSeq // Homo sapiens protein phosphatase 1, regulatory subunit 12A (PPP1	PPP1R12A	8,81E-05	1,41056
NM_002489 // RefSeq // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	NDUFA4	0,00107631	1,40944

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_002570 // RefSeq // Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK	PCSK6	2,38E-06	-1,54374
NM_002651 // RefSeq // Homo sapiens phosphatidylinositol 4-kinase, catalytic, beta (PI4	PI4KB	3,95E-05	-1,47366
NM_002696 // RefSeq // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide G (P	POLR2G	3,38E-05	1,32237
NM_002769 // RefSeq // Homo sapiens protease, serine, 1 (trypsin 1) (PRSS1), mRNA. // c	PRSS1	0,00051069	-1,88649
NM_002824 // RefSeq // Homo sapiens parathyrosin (PTMS), mRNA. // chr12 // 100 // 65 //	PTMS	0,00040146	2,03167
NM_002834 // RefSeq // Homo sapiens protein tyrosine phosphatase, non-receptor type 11	PTPN11	0,00090274	1,59947
NM_002857 // RefSeq // Homo sapiens peroxisomal biogenesis factor 19 (PEX19), transcrip	PEX19	0,00013968	-1,28994
NM_002886 // RefSeq // Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA.	RAP2B	5,50E-05	1,41129
NM_002956 // RefSeq // Homo sapiens CAP-GLY domain containing linker protein 1 (CLIP1),	CLIP1	0,00024805	1,71171
NM_002973 // RefSeq // Homo sapiens ataxin 2 (ATXN2), mRNA. // chr12 // 100 // 68 // 28	ATXN2	0,00072364	1,49264
NM_003001 // RefSeq // Homo sapiens succinate dehydrogenase complex, subunit C, integra	SDHC	0,00034269	-1,23218
NM_003092 // RefSeq // Homo sapiens small nuclear ribonucleoprotein polypeptide B (SNRP	SNRPB2	0,00055796	1,31392
NM_003096 // RefSeq // Homo sapiens small nuclear ribonucleoprotein polypeptide G (SNRP	SNRPG	0,00100417	1,3593
NM_003098 // RefSeq // Homo sapiens syntrophin, alpha 1 (SNTA1), mRNA. // chr20 // 100	SNTA1	0,00010054	1,44719
NM_003107 // RefSeq // Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA.	SOX4	0,00012087	-2,05885
NM_003332 // RefSeq // Homo sapiens TYRO protein tyrosine kinase binding protein (TYROB	TYROBP	0,000332	-1,24025
NM_003344 // RefSeq // Homo sapiens ubiquitin-conjugating enzyme E2H (UBE2H), transcrip	UBE2H	5,56E-05	-1,47325
NM_003392 // RefSeq // Homo sapiens wingless-type MMTV integration site family, member	WNT5A	0,00150039	-1,24142
NM_003450 // RefSeq // Homo sapiens zinc finger protein 174 (ZNF174), transcript varian	ZNF174	0,0004611	1,4252
NM_003463 // RefSeq // Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PT	PTP4A1	0,00064902	-1,22373
NM_003477 // RefSeq // Homo sapiens pyruvate dehydrogenase complex, component X (PDHX),	PDHX	0,00044234	1,35677
NM_003532 // RefSeq // Homo sapiens histone cluster 1, H3e (HIST1H3E), mRNA. // chr6 //	HIST1H3E	7,33E-06	-4,39238
NM_003566 // RefSeq // Homo sapiens early endo-	EEA1	0,000527	1,72506

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
some antigen 1 (EEA1), mRNA. // chr12 //		93	
NM_003661 // RefSeq // Homo sapiens apolipoprotein L, 1 (APOL1), transcript variant 1,	APOL1	0,00160498	-2,62681
NM_003666 // RefSeq // Homo sapiens basic leucine zipper nuclear factor 1 (BLZF1), mRNA	BLZF1	2,90E-06	-1,7224
NM_003707 // RefSeq // Homo sapiens RuvB-like 1 (E. coli) (RUVBL1), mRNA. // chr3 // 10	RUVBL1	0,00078266	1,48803
NM_003762 // RefSeq // Homo sapiens vesicle-associated membrane protein 4 (VAMP4), tran	VAMP4	0,00040257	-1,68248
NM_003785 // RefSeq // Homo sapiens P antigen family, member 1 (prostate associated) (P	PAGE1	0,00072855	1,21394
NM_003805 // RefSeq // Homo sapiens CASP2 and RIPK1 domain containing adaptor with deat	CRADD	4,07E-05	1,48819
NM_003818 // RefSeq // Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidyl	CDS2	0,00026594	1,45671
NM_003849 // RefSeq // Homo sapiens succinate-CoA ligase, alpha subunit (SUCLG1), nucle	SUCLG1	0,0012371	1,56949
NM_003901 // RefSeq // Homo sapiens sphingosine-1-phosphate lyase 1 (SGPL1), mRNA. // c	SGPL1	1,75E-05	1,37937
NM_003972 // RefSeq // Homo sapiens BTAF1 RNA polymerase II, B-TFIID transcription fact	BTAF1	0,00022503	1,54822
NM_003993 // RefSeq // Homo sapiens CDC-like kinase 2 (CLK2), mRNA. // chr1 // 100 // 3	CLK2	5,33E-05	-1,23759
NM_004134 // RefSeq // Homo sapiens heat shock 70kDa protein 9 (mortalin) (HSPA9), nucl	HSPA9	0,00070049	1,54933
NM_004288 // RefSeq // Homo sapiens cytohesin 1 interacting protein (CYTIP), mRNA. // c	CYTIP	0,00108851	-1,85581
NM_004292 // RefSeq // Homo sapiens Ras and Rab interactor 1 (RIN1), mRNA. // chr11 //	RIN1	0,00111312	1,33952
NM_004311 // RefSeq // Homo sapiens ADP-ribosylation factor-like 3 (ARL3), mRNA. // chr	ARL3	0,00019557	1,62357
NM_004384 // RefSeq // Homo sapiens casein kinase 1, gamma 3 (CSNK1G3), transcript vari	CSNK1G3	7,05E-05	1,44168
NM_004539 // RefSeq // Homo sapiens asparaginyl-tRNA synthetase (NARS), mRNA. // chr18	NARS	2,70E-05	1,81563
NM_004562 // RefSeq // Homo sapiens parkinson protein 2, E3 ubiquitin protein ligase (p	PARK2	0,00159509	-1,52523
NM_004591 // RefSeq // Homo sapiens chemokine (C-C motif) ligand 20 (CCL20), transcript	CCL20	3,89E-05	-4,73731
NM_004626 // RefSeq // Homo sapiens wntless-type MMTV integration site family, member	WNT11	0,00078462	-1,40856
NM_004655 // RefSeq // Homo sapiens axin 2 (AXIN2), mRNA. // chr17 // 100 // 100 // 24	AXIN2	0,00122224	-1,46793
NM_004661 // RefSeq // Homo sapiens cell division cycle 23 homolog (S. cerevisiae) (CDC	CDC23	0,00118021	1,48785

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_004698 // RefSeq // Homo sapiens PRP3 pre-mRNA processing factor 3 homolog (S. cerev	PRPF3	0,000316 45	-1,34337
NM_004738 // RefSeq // Homo sapiens VAMP (vesicle-associated membrane protein)-associat	VAPB	0,000648 18	1,30044
NM_004744 // RefSeq // Homo sapiens lecithin retinol acyltransferase (phosphatidylcholi	LRAT	8,21E-05	-1,50068
NM_004795 // RefSeq // Homo sapiens klotho (KL), mRNA. // chr13 // 100 // 78 // 18 // 1	KL	0,000361 32	-1,43606
NM_004866 // RefSeq // Homo sapiens secretory carrier membrane protein 1 (SCAMP1), mRNA	SCAMP1	0,001213 16	1,45803
NM_005044 // RefSeq // Homo sapiens protein kinase, X-linked (PRKX), mRNA. // chrX // 1	PRKX	1,36E-05	2,58025
NM_005067 // RefSeq // Homo sapiens siah E3 ubiquitin protein ligase 2 (SIAH2), mRNA. /	SIAH2	0,001512 07	1,34349
NM_005202 // RefSeq // Homo sapiens collagen, type VIII, alpha 2 (COL8A2), mRNA. // chr	COL8A2	0,001486 8	-1,23495
NM_005325 // RefSeq // Homo sapiens histone cluster 1, H1a (HIST1H1A), mRNA. // chr6 //	HIST1H1A	1,46E-05	-3,583
NM_005333 // RefSeq // Homo sapiens holocytochrome c synthase (HCCS), transcript varian	HCCS	0,000642 82	1,63165
NM_005470 // RefSeq // Homo sapiens abl-interactor 1 (ABI1), transcript variant 1, mRNA	ABI1	0,000574 03	1,30702
NM_005562 // RefSeq // Homo sapiens laminin, gamma 2 (LAMC2), transcript variant 1, mRN	LAMC2	0,000521 06	-2,78732
NM_005608 // RefSeq // Homo sapiens protein tyrosine phosphatase, receptor type, C-asso	PTPRCAP	0,000652 17	-1,27802
NM_005629 // RefSeq // Homo sapiens solute carrier family 6 (neurotransmitter transport	SLC6A8	0,000459 17	-1,79906
NM_005717 // RefSeq // Homo sapiens actin related protein 2/3 complex, subunit 5, 16kDa	ARPC5	0,000431 41	-1,327
NM_005729 // RefSeq // Homo sapiens peptidylprolyl isomerase F (PPIF), nuclear gene enc	PPIF	9,02E-05	2,11747
NM_005733 // RefSeq // Homo sapiens kinesin family member 20A (KIF20A), mRNA. // chr5 /	KIF20A	0,001286 28	1,47779
NM_005762 // RefSeq // Homo sapiens tripartite motif containing 28 (TRIM28), mRNA. // c	TRIM28	0,001519 38	1,44075
NM_005814 // RefSeq // Homo sapiens glycoprotein A33 (transmembrane) (GPA33), mRNA. //	GPA33	0,000168 81	-3,88549
NM_005869 // RefSeq // Homo sapiens CWC27 spliceosome-associated protein homolog (S. ce	CWC27	0,000171 6	1,64652
NM_005928 // RefSeq // Homo sapiens milk fat globule-EGF factor 8 protein (MFGE8), tran	MFGE8	0,001018 9	-2,14504
NM_005973 // RefSeq // Homo sapiens papillary renal cell carcinoma (translocation-assoc	PRCC	0,001007 03	-1,2169
NM_006023 // RefSeq // Homo sapiens cell division	CDC123	0,001066	1,67128

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
cycle 123 homolog (S. cerevisiae) (CD		73	
NM_006047 // RefSeq // Homo sapiens RNA binding motif protein 12 (RBM12), transcript va	RBM12	7,20E-06	1,35344
NM_006071 // RefSeq // Homo sapiens polycystic kidney disease (polycystin) and REJ homo	PKDREJ	4,11E-05	-1,52425
NM_006092 // RefSeq // Homo sapiens nucleotide-binding oligomerization domain containin	NOD1	0,0002099	1,42976
NM_006118 // RefSeq // Homo sapiens HCLS1 associated protein X-1 (HAX1), transcript var	HAX1	0,00038059	-1,23547
NM_006166 // RefSeq // Homo sapiens nuclear transcription factor Y, beta (NFYB), mRNA.	NFYB	4,11E-05	1,83094
NM_006180 // RefSeq // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTR	NTRK2	0,00066319	-1,39428
NM_006196 // RefSeq // Homo sapiens poly(rC) binding protein 1 (PCBP1), mRNA. // chr2 /	PCBP1	0,00099509	1,3228
NM_006233 // RefSeq // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide I, 1	POLR2I	0,00015891	1,40564
NM_006363 // RefSeq // Homo sapiens Sec23 homolog B (S. cerevisiae) (SEC23B), transcrip	SEC23B	0,00024909	1,2751
NM_006469 // RefSeq // Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), mR	IVNS1ABP	0,00143714	-1,73159
NM_006494 // RefSeq // Homo sapiens Ets2 repressor factor (ERF), mRNA. // chr19 // 100	ERF	0,000193	1,37107
NM_006584 // RefSeq // Homo sapiens chaperonin containing TCP1, subunit 6B (zeta 2) (CC	CCT6B	0,00153637	1,43154
NM_006602 // RefSeq // Homo sapiens transcription factor-like 5 (basic helix-loop-helix	TCFL5	0,00121912	2,22333
NM_006654 // RefSeq // Homo sapiens fibroblast growth factor receptor substrate 2 (FRS2	FRS2	6,22E-05	1,53387
NM_006714 // RefSeq // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPD	SMPDL3A	0,00023575	-2,66292
NM_006715 // RefSeq // Homo sapiens mannosidase, alpha, class 2C, member 1 (MAN2C1), tr	MAN2C1	0,00053952	-1,31738
NM_006738 // RefSeq // Homo sapiens A kinase (PRKA) anchor protein 13 (AKAP13), transcr	AKAP13	0,00032542	-1,53359
NM_006768 // RefSeq // Homo sapiens BRCA1 associated protein (BRAP), mRNA. // chr12 //	BRAP	0,00027643	1,61836
NM_006782 // RefSeq // Homo sapiens zinc finger protein-like 1 (ZFPL1), mRNA. // chr11	ZFPL1	0,00121596	1,29865
NM_006814 // RefSeq // Homo sapiens proteasome (prosome, macropain) inhibitor subunit 1	PSMF1	2,54E-06	1,42048
NM_006819 // RefSeq // Homo sapiens stress-induced-phosphoprotein 1 (STIP1), mRNA. // c	STIP1	0,00048871	1,43574
NM_006839 // RefSeq // Homo sapiens inner membrane protein, mitochondrial (IMMT), nucle	IMMT	0,00044915	1,48509

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_006861 // RefSeq // Homo sapiens RAB35, member RAS oncogene family (RAB35), transcri	RAB35	0,000156 47	1,52171
NM_006888 // RefSeq // Homo sapiens calmodulin 1 (phosphorylase kinase, delta) (CALM1),	CALM1	0,001121 92	1,5505
NM_006909 // RefSeq // Homo sapiens Ras protein-specific guanine nucleotide-releasing f	RASGRF2	0,000638 18	-1,7884
NM_006923 // RefSeq // Homo sapiens stromal cell-derived factor 2 (SDF2), transcript va	SDF2	0,001432 35	-1,29388
NM_006939 // RefSeq // Homo sapiens son of seven-less homolog 2 (Drosophila) (SOS2), mRNA	SOS2	0,000239 75	-1,29436
NM_006943 // RefSeq // Homo sapiens SRY (sex determining region Y)-box 12 (SOX12), mRNA	SOX12	0,001255 26	1,38149
NM_007007 // RefSeq // Homo sapiens cleavage and polyadenylation specific factor 6, 68k	CPSF6	0,000784 73	1,59417
NM_007043 // RefSeq // Homo sapiens KRR1, small subunit (SSU) processome component, hom	KRR1	0,000855 82	1,59834
NM_007048 // RefSeq // Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), tran	BTN3A1	0,001535 88	-1,4829
NM_007195 // RefSeq // Homo sapiens polymerase (DNA directed) iota (POLI), mRNA. // chr	POLI	4,31E-05	2,18364
NM_007219 // RefSeq // Homo sapiens ring finger protein 24 (RNF24), transcript variant	RNF24	0,000724 51	2,98562
NM_007259 // RefSeq // Homo sapiens vacuolar protein sorting 45 homolog (S. cerevisiae)	VPS45	0,000424 76	-1,49916
NM_007261 // RefSeq // Homo sapiens CD300a molecule (CD300A), transcript variant 1, mRN	CD300A	0,000612 42	-1,27958
NM_007346 // RefSeq // Homo sapiens opioid growth factor receptor (OGFR), mRNA. // chr2	OGFR	0,000560 49	1,53927
NM_007348 // RefSeq // Homo sapiens activating transcription factor 6 (ATF6), mRNA. //	ATF6	1,68E-06	-1,47806
NM_007357 // RefSeq // Homo sapiens component of oligomeric golgi complex 2 (COG2), tra	COG2	0,001064 81	-1,32704
NM_007361 // RefSeq // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. // chr14 //	NID2	0,000392	-1,32729
NM_009586 // RefSeq // Homo sapiens single-minded homolog 2 (Drosophila) (SIM2), transc	SIM2	0,001149 87	1,57869
NM_012120 // RefSeq // Homo sapiens CD2-associated protein (CD2AP), mRNA. // chr6 // 10	CD2AP	9,78E-05	-1,66455
NM_012124 // RefSeq // Homo sapiens cysteine and histidine-rich domain (CHORD) containi	CHORDC 1	0,000984 77	1,91504
NM_012139 // RefSeq // Homo sapiens secretion regulating guanine nucleotide exchange fa	SERGEF	0,000525 9	1,29655
NM_012193 // RefSeq // Homo sapiens frizzled family receptor 4 (FZD4), mRNA. // chr11 /	FZD4	0,001337 99	1,47718
NM_012215 // RefSeq // Homo sapiens meningioma	MGEA5	0,000231	1,27569

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
expressed antigen 5 (hyaluronidase) (MGE		51	
NM_012231 // RefSeq // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), tr	PRDM2	0,001157 57	-1,27503
NM_012247 // RefSeq // Homo sapiens selenophosphate synthetase 1 (SEPHS1), transcript v	SEPHS1	0,001262 11	1,63736
NM_012311 // RefSeq // Homo sapiens KIN, antigenic determinant of recA protein homolog	KIN	0,001138 59	1,40937
NM_012330 // RefSeq // Homo sapiens K(lysine) acetyltransferase 6B (KAT6B), transcript	KAT6B	0,000114 93	1,29998
NM_012426 // RefSeq // Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA	SF3B3	0,000880 38	1,32098
NM_012467 // RefSeq // Homo sapiens tryptase gamma 1 (TPSG1), mRNA. // chr16 // 100 //	TPSG1	1,30E-05	-1,27549
NM_013402 // RefSeq // Homo sapiens fatty acid desaturase 1 (FADS1), mRNA. // chr11 //	FADS1	0,000251 64	1,5219
NM_014042 // RefSeq // Homo sapiens anaphase promoting complex subunit 15 (ANAPC15), mR	ANAPC15	0,000772 02	1,3619
NM_014051 // RefSeq // Homo sapiens transmembrane protein 14A (TMEM14A), mRNA. // chr6	TMEM14A	0,000308 92	-1,35545
NM_014055 // RefSeq // Homo sapiens intraflagellar transport 81 homolog (Chlamydomonas)	IFT81	0,000150 24	2,00152
NM_014155 // RefSeq // Homo sapiens zinc finger and BTB domain containing 44 (ZBTB44),	ZBTB44	0,001190 97	1,41955
NM_014286 // RefSeq // Homo sapiens neuronal calcium sensor 1 (NCS1), transcript varian	NCS1	0,000318 43	2,4069
NM_014325 // RefSeq // Homo sapiens coronin, actin binding protein, 1C (CORO1C), transc	CORO1C	0,001125 72	1,7456
NM_014394 // RefSeq // Homo sapiens growth hormone inducible transmembrane protein (GHI	GHITM	2,30E-05	1,59817
NM_014458 // RefSeq // Homo sapiens kelch-like 20 (Drosophila) (KLHL20), mRNA. // chr1	KLHL20	0,001115 95	-1,46899
NM_014464 // RefSeq // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA.	TINAG	0,001563 09	-1,8053
NM_014484 // RefSeq // Homo sapiens molybdenum cofactor synthesis 3 (MOCS3), mRNA. // c	MOCS3	0,000200 61	1,4925
NM_014502 // RefSeq // Homo sapiens PRP19/PSO4 pre-mRNA processing factor 19 homolog (S	PRPF19	9,75E-05	1,56017
NM_014570 // RefSeq // Homo sapiens ADP-ribosylation factor GTPase activating protein 3	ARFGAP3	0,000349 59	-1,65063
NM_014624 // RefSeq // Homo sapiens S100 calcium binding protein A6 (S100A6), mRNA. //	S100A6	4,63E-07	-1,53785
NM_014639 // RefSeq // Homo sapiens tetratricopeptide repeat domain 37 (TTC37), mRNA. /	TTC37	0,000227 33	1,69732
NM_014688 // RefSeq // Homo sapiens USP6 N-terminal like (USP6NL), transcript variant 1	USP6NL	0,000148 73	1,4676

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_014698 // RefSeq // Homo sapiens transmembrane protein 63A (TMEM63A), mRNA. // chr1	TMEM63A	0,00027864	-2,09532
NM_014706 // RefSeq // Homo sapiens squamous cell carcinoma antigen recognized by T cel	SART3	0,00059671	1,5482
NM_014729 // RefSeq // Homo sapiens thymocyte selection-associated high mobility group	TOX	6,76E-06	-4,36237
NM_014735 // RefSeq // Homo sapiens PHD finger protein 16 (PHF16), transcript variant 1	PHF16	0,00036236	1,76908
NM_014763 // RefSeq // Homo sapiens mitochondrial ribosomal protein L19 (MRPL19), nucle	MRPL19	0,00118984	1,31797
NM_014810 // RefSeq // Homo sapiens centrosomal protein 350kDa (CEP350), mRNA. // chr1	CEP350	6,25E-05	-1,47514
NM_014827 // RefSeq // Homo sapiens zinc finger CCCH-type containing 11A (ZC3H11A), mRN	ZC3H11A	3,99E-05	-1,32586
NM_014847 // RefSeq // Homo sapiens ubiquitin associated protein 2-like (UBAP2L), trans	UBAP2L	0,00051243	-1,25372
NM_014864 // RefSeq // Homo sapiens family with sequence similarity 20, member B (FAM20	FAM20B	0,00118319	-1,63175
NM_014977 // RefSeq // Homo sapiens apoptotic chromatin condensation inducer 1 (ACIN1),	ACIN1	0,00043289	-1,29995
NM_015100 // RefSeq // Homo sapiens pogo transposable element with ZNF domain (POGZ), t	POGZ	0,00050702	-1,28401
NM_015120 // RefSeq // Homo sapiens Alstrom syndrome 1 (ALMS1), mRNA. // chr2 // 100 //	ALMS1	0,00037383	1,78252
NM_015172 // RefSeq // Homo sapiens proline-rich coiled-coil 2C (PRRC2C), mRNA. // chr1	PRRC2C	2,91E-06	-1,56704
NM_015261 // RefSeq // Homo sapiens non-SMC condensin II complex, subunit D3 (NCAPD3),	NCAPD3	0,00037066	1,5389
NM_015331 // RefSeq // Homo sapiens nicastrin (NCSTN), mRNA. // chr1 // 100 // 68 // 17	NCSTN	0,00012771	-1,60014
NM_015335 // RefSeq // Homo sapiens mediator complex subunit 13-like (MED13L), mRNA. //	MED13L	1,78E-05	1,6504
NM_015360 // RefSeq // Homo sapiens superkiller viralicidic activity 2-like 2 (S. cerev	SKIV2L2	0,00053077	1,51697
NM_015388 // RefSeq // Homo sapiens Yip1 domain family, member 3 (YIPF3), mRNA. // chr6	YIPF3	6,78E-06	-1,3296
NM_015428 // RefSeq // Homo sapiens zinc finger protein 473 (ZNF473), transcript varian	ZNF473	0,00089076	1,44132
NM_015441 // RefSeq // Homo sapiens olfactomedin-like 2B (OLFML2B), mRNA. // chr1 // 10	OLFML2B	0,00152426	-1,24995
NM_015469 // RefSeq // Homo sapiens nipsnap homolog 3A (C. elegans) (NIPSNAP3A), mRNA.	NIPSNAP3A	0,00036804	1,33118
NM_015471 // RefSeq // Homo sapiens NSL1, MIND kinetochore complex component, homolog (	NSL1	0,00057604	-1,28648
NM_015523 // RefSeq // Homo sapiens REX2, RNA	REXO2	0,001535	1,64473

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
exonuclease 2 homolog (S. cerevisiae) (RE		02	
NM_015607 // RefSeq // Homo sapiens chromatin target of PRMT1 (CHTOP), transcript varia	CHTOP	7,05E-05	-1,34448
NM_015655 // RefSeq // Homo sapiens zinc finger protein 337 (ZNF337), mRNA. // chr20 //	ZNF337	5,26E-09	1,43625
NM_015666 // RefSeq // Homo sapiens GTP binding protein 5 (putative) (GTPBP5), mRNA. //	GTPBP5	0,00071086	1,21123
NM_015909 // RefSeq // Homo sapiens neuroblastoma amplified sequence (NBAS), transcript	NBAS	0,00092477	1,25504
NM_015949 // RefSeq // Homo sapiens golgi to ER traffic protein 4 homolog (S. cerevisia	GET4	0,0001004	1,39888
NM_016045 // RefSeq // Homo sapiens slowmo homolog 2 (Drosophila) (SLMO2), transcript v	SLMO2	0,0006579	1,32832
NM_016055 // RefSeq // Homo sapiens mitochondrial ribosomal protein L48 (MRPL48), nucle	MRPL48	0,00077237	1,39848
NM_016065 // RefSeq // Homo sapiens mitochondrial ribosomal protein S16 (MRPS16), nucle	MRPS16	0,00064195	1,56009
NM_016071 // RefSeq // Homo sapiens mitochondrial ribosomal protein S33 (MRPS33), nucle	MRPS33	0,00098973	1,51408
NM_016121 // RefSeq // Homo sapiens potassium channel tetramerisation domain containing	KCTD3	7,55E-05	-2,11292
NM_016138 // RefSeq // Homo sapiens coenzyme Q7 homolog, ubiquinone (yeast) (COQ7), nuc	COQ7	0,00030095	1,39177
NM_016143 // RefSeq // Homo sapiens NSFL1 (p97) cofactor (p47) (NSFL1C), transcript var	NSFL1C	0,00026839	1,25182
NM_016196 // RefSeq // Homo sapiens RNA binding motif protein 19 (RBM19), transcript va	RBM19	0,00053219	1,8271
NM_016202 // RefSeq // Homo sapiens zinc finger protein 580 (ZNF580), transcript varian	ZNF580	0,00060488	1,33616
NM_016237 // RefSeq // Homo sapiens anaphase promoting complex subunit 5 (ANAPC5), tran	ANAPC5	0,00086832	1,59121
NM_016240 // RefSeq // Homo sapiens scavenger receptor class A, member 3 (SCARA3), tran	SCARA3	0,00023999	3,27654
NM_016243 // RefSeq // Homo sapiens cytochrome b5 reductase 1 (CYB5R1), mRNA. // chr1 /	CYB5R1	0,00031316	-1,46734
NM_016265 // RefSeq // Homo sapiens zinc finger protein 12 (ZNF12), transcript variant	ZNF12	0,00136559	1,28019
NM_016374 // RefSeq // Homo sapiens AT rich interactive domain 4B (RBP1-like) (ARID4B),	ARID4B	5,92E-06	-1,50202
NM_016399 // RefSeq // Homo sapiens TP53 regulated inhibitor of apoptosis 1 (TRIAP1), m	TRIAP1	0,00026869	1,55788
NM_016470 // RefSeq // Homo sapiens chromosome 20 open reading frame 111 (C20orf111), m	C20orf111	3,08E-06	1,50047
NM_016544 // RefSeq // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 27 (DNAJC	DNAJC27	5,85E-07	1,54363

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_016584 // RefSeq // Homo sapiens interleukin 23, alpha subunit p19 (IL23A), mRNA. //	IL23A	2,65E-06	-1,83192
NM_016605 // RefSeq // Homo sapiens family with sequence similarity 53, member C (FAM53	FAM53C	0,00010366	1,47316
NM_016652 // RefSeq // Homo sapiens crooked neck pre-mRNA splicing factor-like 1 (Droso	CRNKL1	0,00013341	1,52294
NM_016732 // RefSeq // Homo sapiens RNA binding protein, autoantigenic (hnRNP-associate	RALY	0,00079455	1,25761
NM_017440 // RefSeq // Homo sapiens Mdm1 nuclear protein homolog (mouse) (MDM1), transc	MDM1	0,00024198	1,56152
NM_017495 // RefSeq // Homo sapiens RNA binding motif protein 38 (RBM38), transcript va	RBM38	0,00028982	1,4799
NM_017547 // RefSeq // Homo sapiens FAD-dependent oxidoreductase domain containing 1 (F	FOXRED1	0,00083092	1,39435
NM_017583 // RefSeq // Homo sapiens tripartite motif containing 44 (TRIM44), mRNA. // c	TRIM44	0,00069422	1,59217
NM_017584 // RefSeq // Homo sapiens myo-inositol oxygenase (MIOX), mRNA. // chr22 // 10	MIOX	0,0001701	-1,5449
NM_017664 // RefSeq // Homo sapiens ankyrin repeat domain 10 (ANKRD10), mRNA. // chr13	ANKRD10	0,00147031	-1,45306
NM_017676 // RefSeq // Homo sapiens gypsy retrotransposon integrase 1 (GIN1), mRNA. //	GIN1	0,00116773	1,4977
NM_017782 // RefSeq // Homo sapiens family with sequence similarity 208, member B (FAM2	FAM208B	3,13E-06	1,83464
NM_017838 // RefSeq // Homo sapiens NHP2 ribonucleoprotein homolog (yeast) (NHP2), tran	NHP2	0,00038003	1,56437
NM_017847 // RefSeq // Homo sapiens chromosome 1 open reading frame 27 (C1orf27), trans	C1orf27	3,42E-06	-1,63888
NM_017895 // RefSeq // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 (DDX27),	DDX27	5,42E-05	1,46956
NM_017987 // RefSeq // Homo sapiens RUN and FYVE domain containing 2 (RUFY2), transcrip	RUFY2	0,00051102	1,55483
NM_018040 // RefSeq // Homo sapiens G patch domain containing 2 (GPATCH2), mRNA. // chr	GPATCH2	4,03E-05	-1,52906
NM_018109 // RefSeq // Homo sapiens mitochondrial poly(A) polymerase (MTPAP), nuclear g	MTPAP	0,00022197	1,90657
NM_018178 // RefSeq // Homo sapiens golgi phosphoprotein 3-like (GOLPH3L), mRNA. // chr	GOLPH3L	0,00103389	-1,70765
NM_018182 // RefSeq // Homo sapiens family with sequence similarity 222, member B (FAM2	FAM222B	0,00148065	-1,37895
NM_018244 // RefSeq // Homo sapiens ubiquinol-cytochrome c reductase complex chaperone	UQCC	0,00047053	1,40054
NM_018268 // RefSeq // Homo sapiens WD repeat domain 41 (WDR41), mRNA. // chr5 // 100 /	WDR41	6,51E-06	1,52299
NM_018328 // RefSeq // Homo sapiens methyl-CpG	MBD5	0,000276	-1,93365

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
binding domain protein 5 (MBD5), mRNA. /		77	
NM_018475 // RefSeq // Homo sapiens transmembrane protein 165 (TMEM165), mRNA. // chr4	TMEM165	0,00126284	-1,7905
NM_018489 // RefSeq // Homo sapiens ash1 (absent, small, or homeotic)-like (Drosophila)	ASH1L	5,93E-05	-1,40378
NM_018649 // RefSeq // Homo sapiens H2A histone family, member Y2 (H2AFY2), mRNA. // ch	H2AFY2	0,00034615	2,44595
NM_018694 // RefSeq // Homo sapiens ADP-ribosylation-like factor 6 interacting protein	ARL6IP4	3,33E-06	1,50431
NM_018704 // RefSeq // Homo sapiens CTTNBP2 N-terminal like (CTTNBP2NL), mRNA. // chr1	CTTNBP2NL	0,00056343	-1,48332
NM_018848 // RefSeq // Homo sapiens McKusick-Kaufman syndrome (MKKS), transcript varian	MKKS	0,00091775	1,69538
NM_018945 // RefSeq // Homo sapiens phosphodiesterase 7B (PDE7B), mRNA. // chr6 // 100	PDE7B	0,00042538	-1,24337
NM_018984 // RefSeq // Homo sapiens slingshot homolog 1 (Drosophila) (SSH1), transcript	SSH1	8,33E-06	1,94783
NM_019044 // RefSeq // Homo sapiens coiled-coil domain containing 93 (CCDC93), mRNA. //	CCDC93	0,00061187	-1,30461
NM_019046 // RefSeq // Homo sapiens ankyrin repeat domain 16 (ANKRD16), transcript vari	ANKRD16	5,94E-05	1,95099
NM_019082 // RefSeq // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box helicase 56 (DDX56), tra	DDX56	0,00043445	1,34578
NM_019090 // RefSeq // Homo sapiens KIAA1383 (KIAA1383), mRNA. // chr1 // 100 // 100 //	KIAA1383	0,00150442	-1,54064
NM_019096 // RefSeq // Homo sapiens GTP binding protein 2 (GTPBP2), mRNA. // chr6 // 10	GTPBP2	6,77E-06	-1,28367
NM_019609 // RefSeq // Homo sapiens carboxypeptidase X (M14 family), member 1 (CPXM1),	CPXM1	1,11E-05	-1,44051
NM_019886 // RefSeq // Homo sapiens carbohydrate (N-acetylglucosamine 6-O) sulfotransfe	CHST7	1,22E-05	1,6393
NM_020127 // RefSeq // Homo sapiens tuftelin 1 (TUFT1), transcript variant 1, mRNA. //	TUFT1	0,00015961	-1,54195
NM_020151 // RefSeq // Homo sapiens StAR-related lipid transfer (START) domain containi	STARD7	0,00016801	1,26853
NM_020167 // RefSeq // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. // chr5 // 1	NMUR2	0,00084048	-2,77709
NM_020192 // RefSeq // Homo sapiens Yae1 domain containing 1 (YAE1D1), mRNA. // chr7 //	YAE1D1	0,00056556	1,25222
NM_020312 // RefSeq // Homo sapiens coenzyme Q9 homolog (S. cerevisiae) (COQ9), nuclear	COQ9	4,51E-07	1,36879
NM_020336 // RefSeq // Homo sapiens Ral GTPase activating protein, beta subunit (non-ca	RAL-GAPB	0,00023981	1,24099
NM_020470 // RefSeq // Homo sapiens Yip1 interacting factor homolog A (S. cerevisiae) (	YIF1A	0,00127004	1,23556

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_020652 // RefSeq // Homo sapiens zinc finger protein 286A (ZNF286A), transcript vari	ZNF286A	2,70E-05	2,56101
NM_020689 // RefSeq // Homo sapiens solute carrier family 24 (sodium/potassium/calcium	SLC24A3	0,001184 84	-1,48299
NM_020805 // RefSeq // Homo sapiens kelch-like 14 (Drosophila) (KLHL14), mRNA. // chr18	KLHL14	0,000260 09	-1,23455
NM_020848 // RefSeq // Homo sapiens KIAA1462 (KIAA1462), mRNA. // chr10 // 100 // 88 //	KIAA1462	7,49E-05	-1,52479
NM_020883 // RefSeq // Homo sapiens zinc finger, SWIM-type containing 5 (ZSWIM5), mRNA.	ZSWIM5	0,000179 68	-2,3067
NM_020899 // RefSeq // Homo sapiens zinc finger and BTB domain containing 4 (ZBTB4), tr	ZBTB4	2,76E-05	1,31497
NM_021046 // RefSeq // Homo sapiens keratin associated protein 5-8 (KRTAP5-8), mRNA. //	KRTAP5-8	0,000143 57	-1,59939
NM_021133 // RefSeq // Homo sapiens ribonuclease L (2',5'-oligoadenylate synthetase-	RNASEL	0,001385 36	-2,48178
NM_021163 // RefSeq // Homo sapiens RB-associated KRAB zinc finger (RBAK), transcript v	RBAK	0,001451 43	1,29484
NM_021215 // RefSeq // Homo sapiens regulation of nuclear pre-mRNA domain containing 1B	RPRD1B	0,001212 23	1,33094
NM_021222 // RefSeq // Homo sapiens prune homolog (Drosophila) (PRUNE), mRNA. // chr1 /	PRUNE	6,18E-05	-1,59692
NM_021233 // RefSeq // Homo sapiens deoxyribonuclease II beta (DNASE2B), transcript var	DNASE2B	0,000615 13	-1,22419
NM_021630 // RefSeq // Homo sapiens PDZ and LIM domain 2 (mystique) (PDLIM2), transcrip	PDLIM2	0,001190 11	1,45662
NM_021639 // RefSeq // Homo sapiens GC-rich promoter binding protein 1-like 1 (GPBP1L1)	GPBP1L1	3,88E-05	-1,24636
NM_021648 // RefSeq // Homo sapiens TSPY-like 4 (TSPYL4), mRNA. // chr6 // 100 // 100 /	TSPYL4	0,000726 16	1,29882
NM_021873 // RefSeq // Homo sapiens cell division cycle 25 homolog B (S. pombe) (CDC25B	CDC25B	0,001457 09	2,11315
NM_021943 // RefSeq // Homo sapiens zinc finger, AN1-type domain 3 (ZFAND3), mRNA. // c	ZFAND3	1,64E-07	-1,41275
NM_021988 // RefSeq // Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1),	UBE2V1	0,001371 68	1,2635
NM_022073 // RefSeq // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. // c	EGLN3	4,12E-07	-1,91309
NM_022132 // RefSeq // Homo sapiens methylcrotonoyl-CoA carboxylase 2 (beta) (MCCC2), n	MCCC2	0,001146 78	1,49278
NM_022350 // RefSeq // Homo sapiens endoplasmic reticulum aminopeptidase 2 (ERAP2), tra	ERAP2	0,000644 42	2,88687
NM_022469 // RefSeq // Homo sapiens gremlin 2 (GREM2), mRNA. // chr1 // 100 // 100 // 2	GREM2	0,000608 11	-1,23154
NM_022489 // RefSeq // Homo sapiens inverted for-	INF2	0,000105	-1,31497

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
min, FH2 and WH2 domain containing (INF		17	
NM_022492 // RefSeq // Homo sapiens tetratricopeptide repeat domain 31 (TTC31), transcr	TTC31	0,001533 98	1,24286
NM_022496 // RefSeq // Homo sapiens ARP6 actin-related protein 6 homolog (yeast) (ACTR6	ACTR6	0,001382 3	1,62155
NM_022769 // RefSeq // Homo sapiens CREB regulated transcription coactivator 3 (CRTC3),	CRTC3	9,19E-05	1,52917
NM_023016 // RefSeq // Homo sapiens sosondowah ankyrin repeat domain family member C (S	SOWAHC	0,001157 68	1,42712
NM_024075 // RefSeq // Homo sapiens tRNA splicing endonuclease 34 homolog (S. cerevisia	TSEN34	0,000134 71	1,40567
NM_024312 // RefSeq // Homo sapiens N-acetylglucosamine-1-phosphate transferase, alpha	GNPTAB	0,000706 93	1,41694
NM_024325 // RefSeq // Homo sapiens zinc finger protein 343 (ZNF343), mRNA. // chr20 //	ZNF343	7,97E-05	1,58815
NM_024529 // RefSeq // Homo sapiens cell division cycle 73, Paf1/RNA polymerase II comp	CDC73	0,000560 39	-1,58931
NM_024662 // RefSeq // Homo sapiens N-acetyltransferase 10 (GCN5-related) (NAT10), tran	NAT10	0,000467 29	1,46162
NM_024676 // RefSeq // Homo sapiens SH3 domain containing 21 (SH3D21), transcript varia	SH3D21	0,000384 52	-2,13835
NM_024685 // RefSeq // Homo sapiens Bardet-Biedl syndrome 10 (BBS10), mRNA. // chr12 //	BBS10	2,25E-05	1,60638
NM_024715 // RefSeq // Homo sapiens thioredoxin domain containing 15 (TXNDC15), mRNA. /	TXNDC15	0,000191 56	1,34752
NM_024747 // RefSeq // Homo sapiens Hermansky-Pudlak syndrome 6 (HPS6), mRNA. // chr10	HPS6	0,000420 57	1,3725
NM_024754 // RefSeq // Homo sapiens pentatricopeptide repeat domain 2 (PTCD2), mRNA. //	PTCD2	5,06E-05	1,97563
NM_024766 // RefSeq // Homo sapiens calmodulin-lysine N-methyltransferase (CAMKMT), mRN	CAM-KMT	0,000988 11	1,46028
NM_024784 // RefSeq // Homo sapiens zinc finger and BTB domain containing 3 (ZBTB3), mR	ZBTB3	0,000999 56	1,32429
NM_024825 // RefSeq // Homo sapiens podocan-like 1 (PODNL1), transcript variant 1, mRNA	PODNL1	0,000129 47	1,2926
NM_024855 // RefSeq // Homo sapiens ARP5 actin-related protein 5 homolog (yeast) (ACTR5	ACTR5	0,000249 23	1,61346
NM_024864 // RefSeq // Homo sapiens mitochondrial rRNA methyltransferase 1 homolog (S.	MRM1	0,001300 76	1,48867
NM_024866 // RefSeq // Homo sapiens adrenomedullin 2 (ADM2), transcript variant 1, mRNA	ADM2	1,43E-06	-1,38512
NM_025079 // RefSeq // Homo sapiens zinc finger CCCH-type containing 12A (ZC3H12A), mRN	ZC3H12A	0,000329 76	-1,9546
NM_025114 // RefSeq // Homo sapiens centrosomal protein 290kDa (CEP290), mRNA. // chr12	CEP290	0,000423 71	2,25352

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_025146 // RefSeq // Homo sapiens N(alpha)-acetyltransferase 50, NatE catalytic subun	NAA50	0,0001979	1,37115
NM_025180 // RefSeq // Homo sapiens centrosomal protein 63kDa (CEP63), transcript varia	CEP63	0,00092898	1,22257
NM_025191 // RefSeq // Homo sapiens ER degradation enhancer, mannosidase alpha-like 3 (	EDEM3	7,24E-06	-2,38595
NM_025212 // RefSeq // Homo sapiens CXXC finger protein 4 (CXXC4), mRNA. // chr4 // 100	CXXC4	0,00048344	-1,44564
NM_025232 // RefSeq // Homo sapiens receptor accessory protein 4 (REEP4), mRNA. // chr8	REEP4	1,16E-05	1,57104
NM_025246 // RefSeq // Homo sapiens solute carrier family 35, member G2 (SLC35G2), tran	SLC35G2	0,00143901	1,83948
NM_030624 // RefSeq // Homo sapiens kelch-like 15 (Drosophila) (KLHL15), mRNA. // chrX	KLHL15	0,00145873	1,63855
NM_030637 // RefSeq // Homo sapiens DDHD domain containing 1 (DDHD1), transcript varian	DDHD1	0,00015031	1,73324
NM_030819 // RefSeq // Homo sapiens glucose-fructose oxidoreductase domain containing 2	GFOD2	0,00077554	1,30658
NM_030919 // RefSeq // Homo sapiens family with sequence similarity 83, member D (FAM83	FAM83D	4,33E-05	1,87557
NM_030973 // RefSeq // Homo sapiens mediator complex subunit 25 (MED25), mRNA. // chr19	MED25	8,69E-05	1,37006
NM_031232 // RefSeq // Homo sapiens N-terminal EF-hand calcium binding protein 3 (NECAB	NECAB3	4,36E-05	1,28785
NM_031900 // RefSeq // Homo sapiens alanine--glyoxylate aminotransferase 2 (AGXT2), nuc	AGXT2	0,00045954	-1,20218
NM_031954 // RefSeq // Homo sapiens potassium channel tetramerisation domain containing	KCTD10	6,93E-05	1,5303
NM_032013 // RefSeq // Homo sapiens NDRG family member 3 (NDRG3), transcript variant 1,	NDRG3	0,00037453	1,74198
NM_032118 // RefSeq // Homo sapiens WD repeat domain 54 (WDR54), mRNA. // chr2 // 100 /	WDR54	0,00081234	1,98573
NM_032139 // RefSeq // Homo sapiens ankyrin repeat domain 27 (VPS9 domain) (ANKRD27), m	ANKRD27	9,22E-05	1,52115
NM_032228 // RefSeq // Homo sapiens fatty acyl CoA reductase 1 (FAR1), mRNA. // chr11 /	FAR1	0,00022511	1,43801
NM_032322 // RefSeq // Homo sapiens ring finger protein 135 (RNF135), transcript varian	RNF135	0,00019196	-1,29605
NM_032354 // RefSeq // Homo sapiens transmembrane protein 107 (TMEM107), transcript var	TMEM107	0,00024605	1,34677
NM_032389 // RefSeq // Homo sapiens ADP-ribosylation factor GTPase activating protein 2	ARFGAP2	0,00148935	1,22121
NM_032429 // RefSeq // Homo sapiens leucine zipper, putative tumor suppressor 2 (LZTS2)	LZTS2	0,00060698	1,54315
NM_032457 // RefSeq // Homo sapiens protocadherin	PCDH7	2,47E-05	-6,06759

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
7 (PCDH7), transcript variant c, mRNA			
NM_032599 // RefSeq // Homo sapiens family with sequence similarity 71, member F1 (FAM7	FAM71F1	0,00049127	-1,23937
NM_032663 // RefSeq // Homo sapiens ubiquitin specific peptidase 30 (USP30), mRNA. // c	USP30	0,00011015	1,30046
NM_032807 // RefSeq // Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript va	FBXO18	0,00037898	1,80784
NM_032816 // RefSeq // Homo sapiens centrosomal protein 89kDa (CEP89), mRNA. // chr19 /	CEP89	0,00021635	1,51514
NM_032826 // RefSeq // Homo sapiens solute carrier family 35, member B4 (SLC35B4), mRNA	SLC35B4	0,00060907	2,05363
NM_032834 // RefSeq // Homo sapiens asparagine-linked glycosylation 10, alpha-1,2-gluco	ALG10	0,00045294	1,60864
NM_032890 // RefSeq // Homo sapiens dispatched homolog 1 (Drosophila) (DISP1), mRNA. //	DISP1	0,00021879	-2,41308
NM_033081 // RefSeq // Homo sapiens death inducer-oblierator 1 (DIDO1), transcript var	DIDO1	0,00078773	1,22185
NM_033109 // RefSeq // Homo sapiens polyribonucleotide nucleotidyltransferase 1 (PNPT1)	PNPT1	1,36E-05	1,55054
NM_033121 // RefSeq // Homo sapiens ankyrin repeat domain 13A (ANKRD13A), mRNA. // chr1	ANKRD13A	0,00094682	1,86212
NM_033198 // RefSeq // Homo sapiens phosphatidylinositol glycan anchor biosynthesis, cl	PIGS	0,00042031	-1,35094
NM_033281 // RefSeq // Homo sapiens mitochondrial ribosomal protein S36 (MRPS36), nucle	MRPS36	2,07E-05	1,47483
NM_033624 // RefSeq // Homo sapiens F-box protein 21 (FBXO21), transcript variant 1, mR	FBXO21	0,00160899	1,37753
NM_052847 // RefSeq // Homo sapiens guanine nucleotide binding protein (G protein), gam	GNG7	0,00103317	-1,29628
NM_052875 // RefSeq // Homo sapiens vacuolar protein sorting 26 homolog B (S. pombe) (V	VPS26B	8,25E-05	1,4459
NM_052893 // RefSeq // Homo sapiens BTB (POZ) domain containing 9 (BTBD9), transcript v	BTBD9	0,00032742	-1,4213
NM_052972 // RefSeq // Homo sapiens leucine-rich alpha-2-glycoprotein 1 (LRG1), mRNA. /	LRG1	0,00087777	-2,62197
NM_053052 // RefSeq // Homo sapiens synaptosomal-associated protein, 47kDa (SNAP47), mR	SNAP47	0,00143037	-1,20285
NM_057169 // RefSeq // Homo sapiens G protein-coupled receptor kinase interacting ArfGA	GIT2	0,00029292	1,46617
NM_080599 // RefSeq // Homo sapiens UPF2 regulator of nonsense transcripts homolog (yea	UPF2	0,00014393	1,67195
NM_080600 // RefSeq // Homo sapiens myelin associated glycoprotein (MAG), transcript va	MAG	0,000229	-1,32911
NM_080656 // RefSeq // Homo sapiens CDKN2A interacting protein N-terminal like (CDKN2AI	CDKN2AI PNL	0,00030379	1,65033

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_080667 // RefSeq // Homo sapiens coiled-coil domain containing 104 (CCDC104), mRNA.	CCDC104	1,18E-05	1,52447
NM_080821 // RefSeq // Homo sapiens family with sequence similarity 210, member B (FAM2	FAM210B	0,000516 39	1,76357
NM_130466 // RefSeq // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript va	UBE3B	1,55E-08	1,57749
NM_130906 // RefSeq // Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 3 (PPIL	PPIL3	0,001534 34	-1,60762
NM_133259 // RefSeq // Homo sapiens leucine-rich pentatricopeptide repeat containing (L	LRPPRC	2,40E-05	1,67421
NM_133263 // RefSeq // Homo sapiens peroxisome proliferator-activated receptor gamma, c	PPARGC1B	0,000155 95	1,90548
NM_133447 // RefSeq // Homo sapiens ankyrin repeat and GTPase domain Arf GTPase activat	AGAP11	0,001295 92	2,53933
NM_133496 // RefSeq // Homo sapiens solute carrier family 30 (zinc transporter), member	SLC30A7	0,000928 32	-1,20954
NM_138499 // RefSeq // Homo sapiens PWWP domain containing 2B (PWWP2B), transcript vari	PWWP2B	0,000345 72	1,44521
NM_138773 // RefSeq // Homo sapiens solute carrier family 25, member 46 (SLC25A46), mRN	SLC25A46	0,000262 65	1,46163
NM_139015 // RefSeq // Homo sapiens signal peptide peptidase like 3 (SPPL3), mRNA. // c	SPPL3	0,000438 83	1,48281
NM_139055 // RefSeq // Homo sapiens ADAM metalloproteinase with thrombospondin type 1 mo	ADAMTS15	0,000594 74	-1,3551
NM_139312 // RefSeq // Homo sapiens YME1-like 1 (S. cerevisiae) (YME1L1), nuclear gene	YME1L1	0,000429 02	1,40919
NM_144563 // RefSeq // Homo sapiens ribose 5-phosphate isomerase A (RPIA), mRNA. // chr	RPIA	0,000738 53	1,7074
NM_144650 // RefSeq // Homo sapiens alcohol dehydrogenase, iron containing, 1 (ADHFE1),	ADHFE1	2,16E-07	-1,6318
NM_144660 // RefSeq // Homo sapiens sterile alpha motif domain containing 8 (SAMD8), tr	SAMD8	0,000376 43	1,48792
NM_144736 // RefSeq // Homo sapiens chromosome 2 open reading frame 56 (C2orf56), nucle	C2orf56	0,000145	1,4022
NM_144775 // RefSeq // Homo sapiens Smith-Magenis syndrome chromosome region, candidate	SMCR8	0,000293 17	1,36704
NM_144982 // RefSeq // Homo sapiens zinc finger, C3H1-type containing (ZFC3H1), mRNA. /	ZFC3H1	3,12E-05	1,5588
NM_145176 // RefSeq // Homo sapiens solute carrier family 2 (facilitated glucose transp	SLC2A12	0,000103 68	-1,58611
NM_152345 // RefSeq // Homo sapiens ankyrin repeat domain 13B (ANKRD13B), mRNA. // chr1	ANKRD13B	0,000553 29	1,9531
NM_152380 // RefSeq // Homo sapiens T-box 15 (TBX15), mRNA. // chr1 // 100 // 88 // 22	TBX15	0,000745 52	-2,82976
NM_152442 // RefSeq // Homo sapiens RAD9 homo-	RAD9B	8,40E-05	1,36039

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
log B (S. pombe) (RAD9B), mRNA. // chr12 /			
NM_152503 // RefSeq // Homo sapiens chromosome 20 open reading frame 132 (C20orf132), t	C20orf132	0,001132 68	1,42846
NM_152519 // RefSeq // Homo sapiens KAT8 regulatory NSL complex subunit 1-like (KANSL1L	KANSL1 L	0,000134 4	-2,44698
NM_152545 // RefSeq // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /	RASGEF1 B	0,000283 89	-2,80615
NM_152605 // RefSeq // Homo sapiens zinc finger protein 781 (ZNF781), mRNA. // chr19 //	ZNF781	0,001298 79	-1,20798
NM_152686 // RefSeq // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 18 (DNAJC	DNAJC18	0,000776 18	1,86226
NM_152787 // RefSeq // Homo sapiens TGF-beta activated kinase 1/MAP3K7 binding protein	TAB3	0,000353 12	1,47134
NM_152905 // RefSeq // Homo sapiens neural precursor cell expressed, developmentally do	NEDD1	0,000118 2	1,88129
NM_153450 // RefSeq // Homo sapiens mediator complex subunit 19 (MED19), mRNA. // chr11	MED19	0,000654 23	1,33905
NM_153451 // RefSeq // Homo sapiens oral cancer overexpressed 1 (ORAOV1), mRNA. // chr1	ORAOV1	2,10E-05	1,42326
NM_153477 // RefSeq // Homo sapiens ubiquitously-expressed, prefoldin-like chaperone (U	UXT	0,000659 56	1,46217
NM_153640 // RefSeq // Homo sapiens pantothenate kinase 2 (PANK2), transcript variant 2	PANK2	0,001237 53	1,5008
NM_153810 // RefSeq // Homo sapiens CDK2-associated, cullin domain 1 (CACUL1), mRNA. //	CACUL1	8,20E-05	1,42134
NM_170739 // RefSeq // Homo sapiens mitochondrial ribosomal protein L11 (MRPL11), nucle	MRPL11	0,000122 85	1,60909
NM_170746 // RefSeq // Homo sapiens chromosome 11 open reading frame 31 (C11orf31), mRN	C11orf31	0,000763 58	1,2109
NM_173179 // RefSeq // Homo sapiens solute carrier family 35, member C2 (SLC35C2), tran	SLC35C2	0,000631 11	1,29149
NM_173555 // RefSeq // Homo sapiens trypsin domain containing 1 (TYSND1), transcript va	TYSND1	0,001221 76	1,57321
NM_173651 // RefSeq // Homo sapiens fibrous sheath interacting protein 2 (FSIP2), mRNA.	FSIP2	7,83E-05	-2,04693
NM_173810 // RefSeq // Homo sapiens tetratricopeptide repeat domain 9C (TTC9C), mRNA. /	TTC9C	1,33E-05	1,30773
NM_173852 // RefSeq // Homo sapiens keratinocyte associated protein 2 (KRTCAP2), mRNA.	KRTCAP 2	0,000680 06	-1,2311
NM_175929 // RefSeq // Homo sapiens fibroblast growth factor 14 (FGF14), transcript var	FGF14	0,001544	-1,24276
NM_176787 // RefSeq // Homo sapiens phosphatidylinositol glycan anchor biosynthesis, cl	PIGN	6,54E-06	1,97638
NM_176818 // RefSeq // Homo sapiens glutamyl-tRNA(Gln) amidotransferase, subunit C homo	GATC	1,38E-06	1,8109

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_177455 // RefSeq // Homo sapiens basic helix-loop-helix family, member a15 (BHLHA15)	BHLHA15	0,00115641	-1,27898
NM_177553 // RefSeq // Homo sapiens growth arrest-specific 2 (GAS2), transcript variant	GAS2	0,00025742	-1,32308
NM_178580 // RefSeq // Homo sapiens histocompatibility (minor) 13 (HM13), transcript va	HM13	0,00019896	1,31016
NM_181515 // RefSeq // Homo sapiens mitochondrial ribosomal protein L21 (MRPL21), nucle	MRPL21	0,00046098	1,31757
NM_181578 // RefSeq // Homo sapiens replication factor C (activator 1) 5, 36.5kDa (RFC5	RFC5	0,00050888	1,92089
NM_181699 // RefSeq // Homo sapiens protein phosphatase 2, regulatory subunit A, beta (	PPP2R1B	0,00140413	1,31989
NM_181783 // RefSeq // Homo sapiens transmembrane and tetratricopeptide repeat containi	TMTC3	3,61E-08	1,95925
NM_181838 // RefSeq // Homo sapiens ubiquitin-conjugating enzyme E2D 2 (UBE2D2), transc	UBE2D2	0,00119777	1,34504
NM_181846 // RefSeq // Homo sapiens zinc finger and SCAN domain containing 22 (ZSCAN22)	ZSCAN22	0,00061831	1,2937
NM_182612 // RefSeq // Homo sapiens Parkinson disease 7 domain containing 1 (PDDC1), mR	PDDC1	0,0012706	1,33877
NM_183013 // RefSeq // Homo sapiens cAMP responsive element modulator (CREM), transcrip	CREM	0,00032436	1,51244
NM_183240 // RefSeq // Homo sapiens transmembrane protein 37 (TMEM37), mRNA. // chr2 //	TMEM37	9,30E-05	-1,65575
NM_194271 // RefSeq // Homo sapiens ring finger protein 34, E3 ubiquitin protein ligase	RNF34	0,00043436	1,49997
NM_194314 // RefSeq // Homo sapiens zinc finger and BTB domain containing 41 (ZBTB41),	ZBTB41	0,00010528	-1,72205
NM_198046 // RefSeq // Homo sapiens zinc finger, DHHC-type containing 16 (ZDHHC16), tra	ZDHHC16	0,00030026	1,61426
NM_198281 // RefSeq // Homo sapiens GPRIN family member 3 (GPRIN3), mRNA. // chr4 // 10	GPRIN3	0,00149765	-1,67612
NM_198529 // RefSeq // Homo sapiens EF-hand calcium binding domain 5 (EFCAB5), transcri	EFCAB5	6,48E-06	-1,56597
NM_198551 // RefSeq // Homo sapiens melanoma inhibitory activity family, member 3 (MIA3	MIA3	0,00037754	-1,60087
NM_199421 // RefSeq // Homo sapiens suppressor of cytokine signaling 4 (SOCS4), transcr	SOCS4	0,00072564	1,35866
NM_199460 // RefSeq // Homo sapiens calcium channel, voltage-dependent, L type, alpha 1	CACNA1C	0,00021915	-1,49252
NM_201555 // RefSeq // Homo sapiens four and a half LIM domains 2 (FHL2), transcript va	FHL2	0,00017763	-2,3147
NM_203406 // RefSeq // Homo sapiens metallo-beta-lactamase domain containing 2 (MBLAC2)	MBLAC2	0,00021729	1,95145
NM_207012 // RefSeq // Homo sapiens adaptor-	AP3M1	0,000207	1,40305

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
related protein complex 3, mu 1 subunit (AP		75	
NM_212503 // RefSeq // Homo sapiens cyclin-dependent kinase 18 (CDK18), transcript vari	CDK18	0,00031244	-1,52993
NM_214462 // RefSeq // Homo sapiens dapper, antagonist of beta-catenin, homolog 2 (Xeno	DACT2	0,00111571	-1,29867
NR_001539 // RefSeq // Homo sapiens testis-specific transcript, Y-linked 22 (non-protei	TTY22	0,00021464	-1,30581
NR_001562 // RefSeq // Homo sapiens annexin A2 pseudogene 1 (ANXA2P1), non-coding RNA.	ANXA2P1	8,18E-05	-1,26755
NR_002710 // RefSeq // Homo sapiens arachidonate 12-lipoxygenase pseudogene 2 (ALOX12P2	ALOX12P2	2,09E-06	-5,70699
NR_002751 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 41 (SNORD41), small nu	SNORD41	0,00129016	1,66004
NR_002779 // RefSeq // Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type	NUDT9P1	0,0002891	1,89134
NR_002809 // RefSeq // Homo sapiens uncharacterized LOC338799 (LOC338799), non-coding R	LOC338799	0,00112762	1,45715
NR_002913 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 63 (SNORD63), small nu	SNORD63	0,0009154	2,16873
NR_002940 // RefSeq // Homo sapiens leucine rich repeat containing 37, member A4, pseud	LRRC37A4P	7,36E-06	1,94338
NR_002998 // RefSeq // Homo sapiens small Cajal body-specific RNA 3 (SCARNA3), guide RN	SCARNA3	0,00035419	-1,50753
NR_003056 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 67 (SNORD67), small nu	SNORD67	7,48E-06	1,41457
NR_003079 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 111 (SNORD111), small	SNORD111	4,95E-06	1,54511
NR_003125 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 14E (SNORD14E), small	SNORD14E	1,14E-05	2,40066
NR_003684 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 119 (SNORD119), small	SNORD119	0,00014332	2,24693
NR_004384 // RefSeq // Homo sapiens small ILF3/NF90-associated RNA F (SNAR-F), small nu	SNAR-F	6,11E-05	-1,37739
NR_004395 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 1A (SNORD1A), small nu	SNORD1A	2,02E-05	1,75932
NR_015378 // RefSeq // Homo sapiens uncharacterized LOC401588 (LOC401588), non-coding R	LOC401588	0,0005025	1,75307
NR_015427 // RefSeq // Homo sapiens long intergenic non-protein coding RNA 94 (LINC0009	LINC00094	0,00035394	1,44212
NR_024457 // RefSeq // Homo sapiens uncharacterized LOC100190940 (LOC100190940), non-co	LOC100190940	0,00115874	-1,24906
NR_024458 // RefSeq // Homo sapiens TPT1 antisense RNA 1 (non-protein coding) (TPT1-AS1	TPT1-AS1	0,00158902	-1,5234
NR_024505 // RefSeq // Homo sapiens long intergenic non-protein coding RNA 598 (LINC005	LINC00598	0,00120991	-1,33847

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NR_024577 // RefSeq // Homo sapiens Sec61 alpha 2 subunit (S. cerevisiae) (SEC61A2), tr	SEC61A2	0,001203 51	1,78705
NR_024585 // RefSeq // Homo sapiens uncharacterized LOC100128292 (LOC100128292), non-co	LOC100128292	0,001549 93	1,23815
NR_026052 // RefSeq // Homo sapiens CENPB DNA-binding domains containing 1 pseudogene (	MGC2752	0,000146 15	1,3821
NR_026664 // RefSeq // Homo sapiens uncharacterized LOC85009 (MGC16025), non-coding RNA	MGC16025	0,000129 67	-1,2694
NR_026835 // RefSeq // Homo sapiens tigger transposable element derived 2 pseudogene (F	FLJ37201	2,92E-05	1,57934
NR_026846 // RefSeq // Homo sapiens anaphase promoting complex subunit 1 pseudogene (LO	LOC285074	0,001012 84	1,32505
NR_026954 // RefSeq // Homo sapiens uncharacterized LOC90246 (LOC90246), non-coding RNA	LOC90246	0,000318 42	-1,70983
NR_027157 // RefSeq // Homo sapiens TMPO antisense RNA 1 (non-protein coding) (TMPO-AS1	TMPO-AS1	0,001468 2	1,38027
NR_027258 // RefSeq // Homo sapiens prolyl-tRNA synthetase associated domain containing	PRORS1P	0,000543 93	1,23688
NR_027280 // RefSeq // Homo sapiens SUMO1 activating enzyme subunit 1 (SAE1), transcrip	SAE1	0,001089 66	1,32461
NR_027451 // RefSeq // Homo sapiens uncharacterized LOC647979 (LOC647979), non-coding R	LOC647979	0,000558 57	1,36491
NR_027709 // RefSeq // Homo sapiens IDI2 antisense RNA 1 (non-protein coding) (IDI2-AS1	IDI2-AS1	2,51E-05	1,67902
NR_028138 // RefSeq // Homo sapiens uncharacterized LOC338758 (LOC338758), non-coding R	LOC338758	0,000645 82	1,39864
NR_028383 // RefSeq // Homo sapiens translocase of inner mitochondrial membrane 8 homol	TIMM8B	0,000107 59	1,40999
NR_028402 // RefSeq // Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant	CSRP2BP	0,000203 76	1,67052
NR_028407 // RefSeq // Homo sapiens armadillo repeat containing, X-linked 4 (ARMCX4), t	ARMCX4	0,001068 78	-1,78257
NR_028474 // RefSeq // Homo sapiens LSM3 homolog, U6 small nuclear RNA associated (S. c	LOC100303749	0,000345 36	1,22385
NR_029493 // RefSeq // Homo sapiens microRNA 21 (MIR21), microRNA. // chr17 // 100 // 1	MIR21	2,02E-05	-2,22993
NR_029663 // RefSeq // Homo sapiens microRNA 15b (MIR15B), microRNA. // chr3 // 100 //	MIR15B	1,19E-06	1,88837
NR_030350 // RefSeq // Homo sapiens microRNA 619 (MIR619), microRNA. // chr12 // 100 //	MIR619	0,001247 46	1,41009
NR_030597 // RefSeq // Homo sapiens microRNA 876 (MIR876), microRNA. // chr9 // 100 //	MIR876	0,000680 03	1,21556
NR_030722 // RefSeq // Homo sapiens family with sequence similarity 104, member B (FAM1	FAM104B	0,000469 96	1,57985
NR_033189 // RefSeq // Homo sapiens phosphodiester-	LOC1001	0,000343	-1,37703

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
rase 4D interacting protein pseudogene	30000	79	
NR_033362 // RefSeq // Homo sapiens autophagy related 12 (ATG12), transcript variant 2,	ATG12	1,27E-06	1,40396
NR_033373 // RefSeq // Homo sapiens uncharacterized FLJ39534 (FLJ39534), non-coding RNA	FLJ39534	0,000233 29	1,29691
NR_033697 // RefSeq // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	NDUFA2	0,000925 75	1,47748
NR_033759 // RefSeq // Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial Fo com	ATP5L	6,40E-07	1,57276
NR_033805 // RefSeq // Homo sapiens uncharacterized LOC220906 (LOC220906), non-coding R	LOC220906	0,000192 52	1,40749
NR_033876 // RefSeq // Homo sapiens long intergenic non-protein coding RNA 511 (LINC00511)	LINC00511	2,89E-05	-1,56208
NR_036155 // RefSeq // Homo sapiens microRNA 3188 (MIR3188), microRNA. // chr19 // 100	MIR3188	0,001269 15	1,38135
NR_036179 // RefSeq // Homo sapiens microRNA 4297 (MIR4297), microRNA. // chr10 // 100	MIR4297	0,001532 13	-1,33616
NR_036227 // RefSeq // Homo sapiens microRNA 2355 (MIR2355), microRNA. // chr2 // 100 /	MIR2355	5,76E-05	-1,78443
NR_036435 // RefSeq // Homo sapiens arginine/serine-rich coiled-coil 2 (RSRC2), transcr	RSRC2	0,001254 6	1,4655
NR_036539 // RefSeq // Homo sapiens uncharacterized LOC644656 (LOC644656), non-coding R	LOC644656	0,000626 74	1,42322
NR_036676 // RefSeq // Homo sapiens interferon, alpha 22, pseudogene (IFNA22P), non-cod	IFNA22P	0,000343 34	1,26319
NR_036679 // RefSeq // Homo sapiens alpha-2-glycoprotein 1, zinc-binding pseudogene 1 (	AZGP1P1	0,000647 98	-1,24752
NR_037167 // RefSeq // Homo sapiens quinone oxidoreductase-like protein 2 pseudogene (L	LOC730102	0,000204 06	-2,56698
NR_037606 // RefSeq // Homo sapiens mitochondrial ribosomal protein S14 (MRPS14), trans	MRPS14	1,14E-05	-1,2987
NR_037638 // RefSeq // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside	SLC28A3	0,001619 14	-2,87347
NR_037804 // RefSeq // Homo sapiens NPHP3-ACAD11 readthrough (NPHP3-ACAD11), non-coding	NPHP3-ACAD11	2,29E-05	1,2902
NR_037851 // RefSeq // Homo sapiens uncharacterized LOC100505918 (LOC100505918), non-co	LOC100505918	7,36E-05	-1,62737
NR_037869 // RefSeq // Homo sapiens uncharacterized LOC653160 (LOC653160), non-coding R	LOC653160	4,97E-05	-1,3028
NR_038262 // RefSeq // Homo sapiens MIR210 host gene (non-protein coding) (MIR210HG), n	MIR210HG	0,001104 07	-1,57369
NR_038360 // RefSeq // Homo sapiens SPTY2D1 antisense RNA 1 (non-protein coding) (SPTY2	SPTY2D1-AS1	1,48E-05	1,42639
NR_038379 // RefSeq // Homo sapiens leucine car-	LOC5542	0,000127	1,5339

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
boxyl methyltransferase 1 pseudogene (LO	06	12	
NR_038396 // RefSeq // Homo sapiens uncharacterized LOC100506469 (LOC100506469), non-co	LOC100506469	0,00058663	1,31795
NR_038844 // RefSeq // Homo sapiens uncharacterized LOC644838 (LOC644838), non-coding R	LOC644838	0,00043769	-1,29986
NR_038857 // RefSeq // Homo sapiens uncharacterized LOC441009 (LOC441009), non-coding R	LOC441009	0,0015708	-1,33274
NR_038923 // RefSeq // Homo sapiens uncharacterized LOC254100 (LOC254100), non-coding R	LOC254100	4,54E-05	1,40365
NR_038937 // RefSeq // Homo sapiens uncharacterized LOC100505761 (LOC100505761), transc	LOC100505761	0,00079709	1,36927
NR_039625 // RefSeq // Homo sapiens microRNA 4427 (MIR4427), microRNA. // chr1 // 100 /	MIR4427	8,74E-05	-2,91825
NR_040047 // RefSeq // Homo sapiens uncharacterized LOC100507495 (LOC100507495), transc	LOC100507495	9,58E-05	1,43768
NR_046020 // RefSeq // Homo sapiens transmembrane protease, serine 3 (TMPRSS3), transcr	TMPRSS3	0,00132837	-4,43879
NR_046229 // RefSeq // Homo sapiens uncharacterized LOC100508120 (LOC100508120), non-co	LOC100508120	4,08E-06	-2,80569
NR_046262 // RefSeq // Homo sapiens uncharacterized LOC646719 (LOC646719), non-coding R	LOC646719	0,00063277	1,70791
NR_046437 // RefSeq // Homo sapiens solute carrier family 30, member 10 (SLC30A10), tra	SLC30A10	7,00E-07	-2,08218
NR_046512 // RefSeq // Homo sapiens SAMSN1 antisense RNA 1 (non-protein coding) (SAMSN1	SAMSN1-AS1	0,00057445	-1,21031
NR_046578 // RefSeq // Homo sapiens CACNA1C antisense RNA 4 (non-protein coding) (CACNA	CACNA1C-AS4	0,00060464	1,22108
NR_046935 // RefSeq // Homo sapiens RNA, U6 small nuclear 64 (RNU6-64), small nuclear R	RNU6-64	0,00147312	-1,27085
NR_051962 // RefSeq // Homo sapiens inversin (INVS), transcript variant 3, non-coding R	INVS	0,00066744	1,42107
NR_072995 // RefSeq // Homo sapiens GLI pathogenesis-related 1 like 2 (GLIPR1L2), trans	GLIPR1L2	0,00094341	1,20363
TCONS_00000362-XLOC_000509 // Rinn lincRNA // linc-CFH-3 chr1+:193648023-193696313 //		1,47E-05	-1,56805
TCONS_00000576-XLOC_000922 // Rinn lincRNA // linc-F3-4 chr1:-:95086706-95089740 // chr		9,98E-05	-3,37385
TCONS_00000618-XLOC_000982 // Rinn lincRNA // linc-TBX15 chr1:-:119542966-119544015 //		0,00142693	-1,34283
TCONS_00000674-XLOC_001085 // Rinn lincRNA // linc-DPT-1 chr1:-:168732602-168743728 //		0,00012228	-1,25348
TCONS_00001247-XLOC_000529 // Rinn lincRNA // linc-PRELP chr1+:203343737-203369257 //		0,00150559	-1,22519
TCONS_00001318-XLOC_000600 // Rinn lincRNA // linc-RHOU chr1+:228688982-228697976 // c		4,75E-06	-1,65525

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
TCONS_00001333-XLOC_000628 // Rinn lincRNA // linc-GPR137B-3 chr1+:236120926-236138865		0,00100781	-1,70849
TCONS_00001555-XLOC_000897 // Rinn lincRNA // linc-ODF2L chr1:-:86966981-86969353 // ch		0,00044431	-1,38592
TCONS_00001577-XLOC_000913 // Rinn lincRNA // linc-GBP5-6 chr1:-:90752759-90763021 // c		0,00083119	-1,24236
TCONS_00001762-XLOC_001134 // Rinn lincRNA // linc-FAM5C-4 chr1:-:192904812-192916494 /		2,80E-06	-1,7964
TCONS_00001789-XLOC_001178 // Rinn lincRNA // linc-YOD1-5 chr1:-:207574927-207589566 //		0,00160281	-1,28979
TCONS_00001821-XLOC_001205 // Rinn lincRNA // linc-GPATCH2-3 chr1:-:219150088-219164653		0,00095408	-1,34678
TCONS_00001854-XLOC_001242 // Rinn lincRNA // linc-HIST3H2A-2 chr1:-:229027197-22903356		7,20E-05	-1,53468
TCONS_00001882-XLOC_001265 // Rinn lincRNA // linc-IRF2BP2-1 chr1:-:235087870-235100203		0,00010731	-1,7331
TCONS_00002744-XLOC_001974 // Rinn lincRNA // linc-CMPK2-2 chr2:-:8347272-8468549 // ch	LINC00299	0,00152082	-1,26509
TCONS_00003265-XLOC_002069 // Rinn lincRNA // linc-HAAO-2 chr2:-:43268331-43270921 // c		0,00012011	-1,32581
TCONS_00003286-XLOC_002099 // Rinn lincRNA // linc-SMEK2 chr2:-:55852072-55858573 // ch		0,00048635	1,36088
TCONS_00003900-XLOC_001703 // Rinn lincRNA // linc-TNFAIP6-6 chr2+:150683557-150704743		0,00015587	-1,70016
TCONS_00003986-XLOC_001809 // Rinn lincRNA // linc-CASP10-1 chr2+:202038290-202042899		0,00062558	-1,77498
TCONS_00004059-XLOC_001907 // Rinn lincRNA // linc-MLPH-5 chr2+:238059251-238061515 //		0,00084222	-1,35492
TCONS_00004196-XLOC_002042 // Rinn lincRNA // linc-SRD5A2-2 chr2:-:31935274-31990384 //		0,00034328	-1,30111
TCONS_00004354-XLOC_002229 // Rinn lincRNA // linc-RFX8 chr2:-:102168064-102184370 // c		6,44E-05	-1,37061
TCONS_00006134-XLOC_002735 // Rinn lincRNA // linc-COL8A1-4 chr3+:98621202-98623886 //		0,00104861	-1,32621
TCONS_00006171-XLOC_002779 // Rinn lincRNA // linc-NDUFB4-5 chr3+:119814170-119819230		0,00128337	1,32221
TCONS_00007239-XLOC_003221 // Rinn lincRNA // linc-KIAA2018 chr3:-:113432277-113433137		0,00108982	1,79005
TCONS_00007654-XLOC_003729 // Rinn lincRNA // linc-DCLK2-5 chr4+:149614183-149615475 /		0,00083444	-1,8603
TCONS_00007710-XLOC_003862 // Rinn lincRNA // linc-LRPAP1-2 chr4:-:3760474-3765117 // c		0,00073022	-1,20479
TCONS_00007810-XLOC_004040 // Rinn lincRNA // linc-INTS12-3 chr4:-:106924473-106943635		0,00159581	-1,57193
TCONS_00007969-XLOC_003438 // Rinn lincRNA // linc-		0,000287	-1,24193

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
MAN2B2-2 chr4:+:6315485-6319667 // c		92	
TCONS_00007986-XLOC_003455 // Rinn lincRNA // linc-CPEB2-11 chr4:+:11315419-11344598 //		0,00099613	-1,96696
TCONS_00008078-XLOC_003544 // Rinn lincRNA // linc-TMEM165 chr4:+:56251872-56253958 //		1,44E-06	-2,93117
TCONS_00008368-XLOC_003823 // Rinn lincRNA // linc-ZFP42-9 chr4:+:187980347-187980856 /		0,00011406	-1,29189
TCONS_00008546-XLOC_004041 // Rinn lincRNA // linc-PAPSS1 chr4:-:108908047-108910629 //		0,00014044	-1,37898
TCONS_00008717-XLOC_004231 // Rinn lincRNA // linc-TRIML2-6 chr4:-:190598434-190600102		0,00100767	1,22442
TCONS_00009213-XLOC_004382 // Rinn lincRNA // linc-FST chr5:+:52405686-52410950 // chr5	LOC257396	0,00055016	1,51762
TCONS_00009341-XLOC_004275 // Rinn lincRNA // linc-ADCY2-6 chr5:+:6868671-6886900 // ch		0,00027874	-1,24952
TCONS_00009498-XLOC_004529 // Rinn lincRNA // linc-FTMT-2 chr5:+:120658244-120661532 //		0,00110706	1,43624
TCONS_00009609-XLOC_004740 // Rinn lincRNA // linc-ANKH-1 chr5:-:15192247-15266650 // c		0,00116578	-1,22349
TCONS_00009708-XLOC_004894 // Rinn lincRNA // linc-ZBED3 chr5:-:76393281-76393984 // ch		0,00057297	1,44645
TCONS_00009981-XLOC_004407 // Rinn lincRNA // linc-PPWD1 chr5:+:64361892-64366318 // ch		0,00130685	-1,23843
TCONS_00010096-XLOC_004556 // Rinn lincRNA // linc-TCF7-1 chr5:+:133304442-133306019 //		0,00069696	1,30042
TCONS_00010119-XLOC_004585 // Rinn lincRNA // linc-ARHGAP26-5 chr5:+:141615465-14161601		0,00054444	-1,22277
TCONS_00010366-XLOC_004863 // Rinn lincRNA // linc-CD180-12 chr5:-:68430028-68455323 //		0,00066946	1,43349
TCONS_00010530-XLOC_005050 // Rinn lincRNA // linc-CSNK1A1 chr5:-:149016982-149020628 /		0,00010314	-1,453
TCONS_00010663-XLOC_004339 // Rinn lincRNA // linc-NIPBL chr5:+:36871456-36876605 // ch		0,00039131	1,45209
TCONS_00010939-XLOC_004848 // Rinn lincRNA // linc-SGTB-3 chr5:-:65220459-65221176 // c		7,45E-05	1,35403
TCONS_00012990-XLOC_006040 // Rinn lincRNA // linc-NPSR1 chr7:+:34249137-34295955 // ch		1,64E-05	-3,76707
TCONS_00013102-XLOC_006310 // Rinn lincRNA // linc-NOM1-1 chr7:+:156737414-156738339 //		0,00026931	-1,3724
TCONS_00013176-XLOC_006463 // Rinn lincRNA // linc-ZNF479-10 chr7:-:62505204-62514809 /		0,00017292	1,23332
TCONS_00013576-XLOC_006231 // Rinn lincRNA // linc-ARF5-8 chr7:+:124638323-124641124 //		0,00010867	-2,10369
TCONS_00013655-XLOC_006312 // Rinn lincRNA // linc-UBE3C-3 chr7:+:156775940-156777103 /		0,0015459	1,50533

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
TCONS_00013748-XLOC_006388 // Rinn lincRNA // linc-HNRNPA2B1-3 chr7:-:26584207-26590534		0,000662 25	-1,32379
TCONS_00014518-XLOC_007098 // Rinn lincRNA // linc-ASP1-1 chr8:-:62671659-62678528 // c		0,001267 38	-1,30911
TCONS_00014546-XLOC_006923 // Rinn lincRNA // linc-EFR3A-6 chr8+:128938354-128943402 /	PVT1	0,000343 1	1,90337
TCONS_00014977-XLOC_007055 // Rinn lincRNA // linc-DUSP26-1 chr8:-:37455061-37456790 //	LOC157860	0,000136	-1,41976
TCONS_00014998-XLOC_007078 // Rinn lincRNA // linc-RNF170-1 chr8:-:47722339-47730705 //		3,15E-05	-1,2676
TCONS_00015354-XLOC_006922 // Rinn lincRNA // linc-EFR3A-7 chr8+:128867393-128944934 /	PVT1	0,001089 66	2,06859
TCONS_00015582-XLOC_007500 // Rinn lincRNA // linc-ZNF462-3 chr9+:108870331-109173662		0,000436 39	-1,30328
TCONS_00016076-XLOC_007467 // Rinn lincRNA // linc-HIATL1-3 chr9+:97075821-97076871 //		0,001450 82	1,20451
TCONS_00016123-XLOC_007508 // Rinn lincRNA // linc-ACTL7A-8 chr9+:110329106-110338504		0,000424 02	-1,40776
TCONS_00016944-XLOC_008094 // Rinn lincRNA // linc-SPRY3-1 chrX+:154697946-154716706 /		0,001419 83	-1,36726
TCONS_00017190-XLOC_008005 // Rinn lincRNA // linc-FAM155B chrX+:68250821-68256955 //		0,000264 01	-1,71756
TCONS_00017353-XLOC_008198 // Rinn lincRNA // linc-GLA-1 chrX:-:100759567-100764657 //		0,000305 35	-1,38426
TCONS_00017652-XLOC_008328 // Rinn lincRNA // linc-KDM5D-2 chrY:-:22681833-22686319 //		0,001509 14	-1,2496
TCONS_00017675-XLOC_008480 // Rinn lincRNA // linc-ANXA8L2-1 chr10+:47658233-47701446	ANTXRL	0,000164 37	-1,20606
TCONS_00017835-XLOC_008501 // Rinn lincRNA // linc-LRRTM3-2 chr10+:67345445-67441220 /		0,000826 62	-1,59698
TCONS_00017851-XLOC_008542 // Rinn lincRNA // linc-OPN4-1 chr10+:88281701-88282443 //		8,79E-05	1,97892
TCONS_00018003-XLOC_008867 // Rinn lincRNA // linc-SFTPA2-1 chr10:-:81390510-81391942 /		0,000931 16	-1,3366
TCONS_00018097-XLOC_008366 // Rinn lincRNA // linc-PFKFB3 chr10+:6182720-6183545 // ch		8,70E-05	-1,35384
TCONS_00018537-XLOC_008855 // Rinn lincRNA // linc-AGAP5-1 chr10:-:75540422-75541627 //		0,001190 04	1,72402
TCONS_00018588-XLOC_008922 // Rinn lincRNA // linc-PDZD7 chr10:-:102819375-102820683 //		3,19E-05	2,60033
TCONS_00019181-XLOC_009016 // Rinn lincRNA // linc-B4GALNT4-2 chr11+:331733-333645 //		0,001529 64	-1,28327
TCONS_00019266-XLOC_009094 // Rinn lincRNA // linc-FSHB-4 chr11+:28535560-28548491 //		0,000440 34	-1,71633
TCONS_00019401-XLOC_009224 // Rinn lincRNA	LOC1002	0,001195	1,49126

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
// linc-USP35 chr11+:77850805-77852799 // c	89388	18	
TCONS_00019443-XLOC_009252 // Rinn lincRNA // linc-AMOTL1-3 chr11+:94371178-94373474 /		1,49E-05	-1,25024
TCONS_00019646-XLOC_009452 // Rinn lincRNA // linc-FTH1-1 chr11:-:61883943-61891289 //		0,001453 18	1,24973
TCONS_00019712-XLOC_009507 // Rinn lincRNA // linc-PRKRIR chr11:-:76154344-76155704 //		5,61E-07	1,94492
TCONS_00019769-XLOC_009563 // Rinn lincRNA // linc-CADM1-4 chr11:-:115754859-115757277		0,000234 46	-1,37598
TCONS_00020353-XLOC_009683 // Rinn lincRNA // linc-PDE3A-3 chr12+:19804642-19806912 //		0,001247 13	-2,40963
TCONS_00020848-XLOC_010133 // Rinn lincRNA // linc-OSBPL8 chr12:-:77086299-77088341 //		0,000600 26	-1,23625
TCONS_00020906-XLOC_010185 // Rinn lincRNA // linc-APPL2-3 chr12:-:106180060-106404785		0,000495 76	-1,54517
TCONS_00020988-XLOC_010253 // Rinn lincRNA // linc-DHX37-14 chr12:-:128151535-128155451		5,83E-05	-1,37219
TCONS_00021063-XLOC_009661 // Rinn lincRNA // linc-PRH2-3 chr12+:10705978-10710816 //		0,000958 53	-1,22126
TCONS_00021113-XLOC_009728 // Rinn lincRNA // linc-SLC48A1-3 chr12+:47808466-47814022		0,000148 64	-1,50083
TCONS_00021481-XLOC_010315 // Rinn lincRNA // linc-ATP12A-3 chr13+:24905587-24911256 /	LINC0056 6	0,000782 01	-1,23402
TCONS_00021772-XLOC_010368 // Rinn lincRNA // linc-SERP2-4 chr13+:44596391-44614387 //	LINC0028 4	0,000673 49	-1,23137
TCONS_00021794-XLOC_010397 // Rinn lincRNA // linc-PRR20A-5 chr13+:53631290-53650848 /		0,001428 64	-1,65999
TCONS_00022476-XLOC_010804 // Rinn lincRNA // linc-SSTR1-5 chr14+:38033433-38048129 //		5,26E-05	-1,43864
TCONS_00022880-XLOC_011134 // Rinn lincRNA // linc-RTL1-2 chr14:-:101819693-101822512 /		0,000453 83	-3,03365
TCONS_00022976-XLOC_010811 // Rinn lincRNA // linc-LRFN5-3 chr14+:39903870-39962715 //		0,001393 57	-1,46134
TCONS_00023300-XLOC_011169 // Rinn lincRNA // linc-C15orf2-13 chr15+:23873168-23874538		1,38E-05	-1,36677
TCONS_00024334-XLOC_011650 // Rinn lincRNA // linc-BFAR chr16+:14416112-14420490 // ch		0,001412 64	1,75618
TCONS_00024378-XLOC_011704 // Rinn lincRNA // linc-PHKB-2 chr16+:47007716-47012770 //		5,98E-06	1,48532
TCONS_00024390-XLOC_011715 // Rinn lincRNA // linc-TMEM188 chr16+:49488184-49494684 //		5,59E-05	-1,26342
TCONS_00025258-XLOC_012064 // Rinn lincRNA // linc-C17orf97-3 chr17+:47994-49628 // ch		0,000290 32	-1,27904
TCONS_00025293-XLOC_012095 // Rinn lincRNA // linc-ALOX12-1 chr17+:6840593-6857728 //	ALOX12P 2	3,35E-09	-6,94788

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
TCONS_00025544-XLOC_012371 // Rinn lincRNA // linc-TEKT1-2 chr17:-:6856978-6859935 // c		0,00010179	-1,51281
TCONS_00025602-XLOC_012430 // Rinn lincRNA // linc-SEZ6-1 chr17:-:27337874-27339680 //		0,00075899	1,3394
TCONS_00025687-XLOC_012503 // Rinn lincRNA // linc-COPZ2 chr17:-:46124280-46125406 // c		5,94E-05	1,46319
TCONS_00025761-XLOC_012571 // Rinn lincRNA // linc-SDK2-1 chr17:-:71940478-71945993 //		0,00072093	-1,27592
TCONS_00026215-XLOC_012692 // Rinn lincRNA // linc-NEDD4L-1 chr18:+:55471011-55474049 /		0,0005428	1,40698
TCONS_00026294-XLOC_012638 // Rinn lincRNA // linc-CABLES1 chr18:+:20685924-20686303 //		0,0001148	-1,37746
TCONS_00026681-XLOC_012784 // Rinn lincRNA // linc-POTEC-3 chr18:-:15301184-15303066 //		0,0003215	-2,4629
TCONS_00027011-XLOC_013056 // Rinn lincRNA // linc-ZNF382-1 chr19:+:37025702-37026137 /		0,00124697	1,25574
TCONS_00027301-XLOC_013301 // Rinn lincRNA // linc-ANKRD27 chr19:-:33177953-33182862 //		0,00024326	2,28984
TCONS_00027541-XLOC_013072 // Rinn lincRNA // linc-LGALS13 chr19:+:40018979-40019553 //		0,00060244	1,23361
TCONS_00027828-XLOC_013429 // Rinn lincRNA // linc-ZNF837 chr19:-:58917723-58919829 //		0,00016144	1,64973
TCONS_00027888-XLOC_013737 // Rinn lincRNA // linc-KIAA1755-3 chr20:-:37034659-37045444		3,26E-05	1,91261
TCONS_00028857-XLOC_013973 // Rinn lincRNA // linc-C21orf70-5 chr21:+:46222491-46224632		4,20E-05	1,46727
TCONS_00029024-XLOC_013947 // Rinn lincRNA // linc-UMODL1-5 chr21:+:42953358-42954625 /		0,00060526	-1,37463
TCONS_00029355-XLOC_014420 // Rinn lincRNA // linc-ARSA-2 chr22:-:51174258-51176567 //	LOC100506917	0,00025032	-1,23968
TCONS_00029709-XLOC_014393 // Rinn lincRNA // linc-LDOC1L-1 chr22:-:45057491-45063704 /		0,00082912	-1,20718
TCONS_I2_00002247-XLOC_I2_000514 // Broad TUCP // linc-RASAL2-2 chr1:+:177320721-177335		0,00129273	-1,28228
TCONS_I2_00004657-XLOC_I2_002407 // Broad TUCP // linc-PRKRIR-BP chr11:+:76092015-76121	LOC100506127	4,01E-06	1,55781
TCONS_I2_00005499-XLOC_I2_002886 // Broad TUCP // linc-CLEC2D-1 chr12:+:9795445-9814706	LOC374443	0,00117902	1,63563
TCONS_I2_00007360-XLOC_I2_003627 // Broad TUCP // linc-FGF9-2 chr13:+:21872277-21878694	LINC00539	0,00078261	1,69306
TCONS_I2_00014462-XLOC_I2_007928 // Broad TUCP // linc-PUM2-3 chr2:-:20786002-20793177		0,00157761	-1,22302
TCONS_I2_00014537-XLOC_I2_007986 // Broad TUCP // linc-HAAO-4 chr2:-:43258947-43266681		0,00017949	-6,27918
TCONS_I2_00015367-XLOC_I2_007359 // Broad TUCP // linc-		0,001016	-1,68373

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ETAA1-3 chr2+:67267677-67269098		7	
TCONS_l2_00016216-XLOC_l2_008596 // Broad TUCP // linc-DEFB115-7 chr20+:25731895-25733		0,00018336	1,62011
TCONS_l2_00021564-XLOC_l2_010631 // Broad TUCP // linc-DTHD1-3 chr4+:33852212-33893771		0,00092651	-1,2169
TCONS_l2_00023729-XLOC_l2_012023 // Broad TUCP // linc-FGF10-3 chr5-:44777167-44808828	LOC100506674	0,00125653	-1,53522
TCONS_l2_00025079-XLOC_l2_012374 // Broad TUCP // linc-LY86-2 chr6+:5892672-5986353 //		0,00130622	-1,45816
TCONS_l2_00027197-XLOC_l2_013564 // Broad TUCP // linc-TES-2 chr7+:114719011-114766368		5,93E-05	-1,26181
TCONS_l2_00028605-XLOC_l2_014694 // Broad TUCP // linc-SLC1A1-1 chr9+:3663779-3694788		0,0005533	-1,78587
TCONS_l2_00029674-XLOC_l2_014694 // Broad TUCP // linc-SLC1A1-1 chr9+:3526722-3671624		0,00048301	-2,41707
TCONS_l2_00029675-XLOC_l2_014694 // Broad TUCP // linc-SLC1A1-1 chr9+:3647334-3648338		0,00010498	-1,58698
TCONS_l2_00029789-XLOC_l2_014891 // Broad TUCP // linc-C9orf79-2 chr9+:90479080-904812		0,00034007	-1,26413
TCONS_l2_00030536-XLOC_l2_015760 // Broad TUCP // linc-NAP1L2-3 chrX-:73492775-7350467	FTX	0,00140457	-1,2648
TCONS_l2_00030882-XLOC_l2_015855 // Broad TUCP // linc-CLIC2-1 chrX-:154564166-1545812		9,68E-05	-1,47293
X58060 // GenBank // H.sapiens U13 snRNA pseudo-gene U13.32A. // chr7 // 100 // 100 // 1	SNORD13P2	0,00077484	1,40796
XM_001713850 // RefSeq // PREDICTED: Homo sapiens anaphase-promoting complex subunit 1-	LOC730268	0,00030747	1,46366
XR_108724 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100505531 (LOC100505531)	LOC100505531	0,00014046	1,51312
XR_109972 // RefSeq // PREDICTED: Homo sapiens SOS1 intronic transcript 1 (non-protein	SOS1-IT1	1,00E-06	1,79962
XR_110412 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100507196 (LOC100507196)		0,0001363	1,41455
XR_111249 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100509976 (LOC100509976)	LOC100509976	1,49E-05	2,76581
XR_111611 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100506670 (LOC100506670)	LOC100506670	0,00020987	1,45269
XR_132525 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100288712 (LOC100288712)	LOC100288712	0,00078818	1,22288
XR_133207 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100505703 (LOC100505703)	LOC100505703	0,00126179	-1,36872

Table 6: Efficiency of gemcitabine

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
AK054868 // GenBank // Homo sapiens cDNA FLJ30306 fis, clone BRACE2003319. // chr19 //	ERVK3-1	0,000696 237	-1,52016
AK091161 // GenBank // Homo sapiens cDNA FLJ33842 fis, clone CTONG2005049. // chr14 //		0,000262 963	1,21991
AK091355 // GenBank // Homo sapiens cDNA FLJ34036 fis, clone FCBBF2005069. // chr22 //	LOC2849 26	8,52E-05	1,77735
AK091883 // GenBank // Homo sapiens cDNA FLJ34564 fis, clone KIDNE2002845. // chr3 // 1		0,000221 048	5,56898
AK096237 // GenBank // Homo sapiens cDNA FLJ38918 fis, clone NT2NE2010633. // chr8 // 1		0,000315 424	2,04575
AK096500 // GenBank // Homo sapiens cDNA FLJ39181 fis, clone OCBBF2004235. // chr14 //		1,03E-05	-2,20704
AK124321 // GenBank // Homo sapiens cDNA FLJ42330 fis, clone TSTOM1000135. // chr7 // 9	LOC3896 02	0,000349 943	3,83049
AK125386 // GenBank // Homo sapiens cDNA FLJ43396 fis, clone OCBBF2009095. // chr4 // 1		1,34E-05	1,84765
AK128202 // GenBank // Homo sapiens cDNA FLJ46334 fis, clone TESTI4045955. // chr3 // 1		0,000816 377	-1,23261
AK128855 // GenBank // Homo sapiens cDNA FLJ46652 fis, clone TRACH3005102. // chr5 // 1		8,85E-07	3,27341
AK289402 // GenBank // Homo sapiens cDNA FLJ77641 complete cds. // chr6 // 94 // 75 //	C6orf72	6,52E-05	-2,03391
AK297111 // GenBank // Homo sapiens cDNA FLJ57124 complete cds, highly similar to Actin	ARPC1A	0,000242 88	1,46571
AY358789 // GenBank // Homo sapiens clone DNA129794 TSSP3028 (UNQ3028) mRNA	LOC1001 31826	6,92E-05	1,63451
BX641037 // GenBank // Homo sapiens mRNA; cDNA DKFZp686H10114 (from clone DKFZp686H1011	BAZ2B	0,000588 76	-1,33689
ENST00000215071 // ENSEMBL // cdna:known chromosome:GRCh37:19:38865176:38874464:1 gene:	PSMD8	7,23E-07	-1,32389
ENST00000220822 // ENSEMBL // cdna:known chromosome:GRCh37:8:75262617:75279111:1 gene:E	GDAP1	2,89E-06	-2,49444
ENST00000221315 // ENSEMBL // cdna:known chromosome:GRCh37:19:52536361:52552106:-1 gene	ZNF432	0,000325 158	-1,49169
ENST00000223210 // ENSEMBL // cdna:known chromosome:GRCh37:7:149535456:149564568:1 gene	ZNF862	0,000494 549	1,23597
ENST00000233557 // ENSEMBL // cdna:known chromosome:GRCh37:2:27650657:27665126:1 gene:E	NRBP1	4,22E-06	-1,51348
ENST00000239231 // ENSEMBL // cdna:known	PANK3	0,000116	1,57179

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:5:167975500:168006605:-1 gen		545	
ENST00000240719 // ENSEMBL // cdna:known chromosome:GRCh37:19:58038693:58052124:1 gene:	ZNF549	8,96E-06	-1,82687
ENST00000258733 // ENSEMBL // cdna:known chromosome:GRCh37:7:23286182:23314727:1 gene:E	GPNMB	4,05E-06	-2,29169
ENST00000260810 // ENSEMBL // cdna:known chromosome:GRCh37:3:133319417:133380737:-1 gen	TOPBP1	0,000159 579	1,52012
ENST00000261811 // ENSEMBL // cdna:known chromosome:GRCh37:5:139554227:139623372:1 gene	CYSTM1	7,75E-05	1,98413
ENST00000262109 // ENSEMBL // cdna:known chromosome:GRCh37:8:614200:681239:-1 gene:ENSG	ERICH1	5,36E-05	1,75401
ENST00000262990 // ENSEMBL // cdna:known chromosome:GRCh37:4:142142041:142155851:1 gene	ZNF330	0,000393 899	1,83509
ENST00000263593 // ENSEMBL // cdna:known chromosome:GRCh37:11:124503009:124543777:-1 ge	SIAE	0,000818 232	1,83348
ENST00000263674 // ENSEMBL // cdna:known chromosome:GRCh37:11:73019334:73080136:1 gene:	ARHGEF 17	0,000422 284	-1,56321
ENST00000264230 // ENSEMBL // cdna:known chromosome:GRCh37:4:57829536:57844989:-1 gene:	NOA1	1,89E-05	2,06548
ENST00000264255 // ENSEMBL // cdna:known chromosome:GRCh37:2:99935445:99952925:-1 gene:	TXNDC9	8,37E-06	-1,40503
ENST00000264690 // ENSEMBL // cdna:known chromosome:GRCh37:4:187148556:187179625:1 gene	KLKB1	4,43E-05	-1,7182
ENST00000264808 // ENSEMBL // cdna:known chromosome:GRCh37:4:121613070:121844004:-1 gen	PRDM5	0,000171 838	3,43061
ENST00000264893 // ENSEMBL // cdna:known chromosome:GRCh37:4:77870856:77959767:1 gene:E	11-sept	3,45E-07	1,55783
ENST00000265565 // ENSEMBL // cdna:known chromosome:GRCh37:3:47455203:47517603:-1 gene:	SCAP	0,000632 991	-1,24856
ENST00000273853 // ENSEMBL // cdna:known chromosome:GRCh37:4:68337521:68411324:-1 gene:	CENPC1	0,000896 59	1,59838
ENST00000276282 // ENSEMBL // cdna:known chromosome:GRCh37:8:8640864:8751155:-1	MFHAS1	8,20E-05	1,71336

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
gene:EN			
ENST00000278426 // ENSEMBL // cdna:known chromosome:GRCh37:11:57252007:57283259:-1 gene	SLC43A1	0,000878 286	2,55747
ENST00000278550 // ENSEMBL // cdna:known chromosome:GRCh37:11:78363876:79151695:-1 gene	ODZ4	0,000347 848	2,18428
ENST00000279488 // ENSEMBL // cdna:known chromosome:GRCh37:12:89741050:89747048:-1 gene	DUSP6	1,08E-05	-2,14826
ENST00000282292 // ENSEMBL // cdna:known chromosome:GRCh37:19:58011309:58019508:1 gene:	ZNF773	7,98E-05	-1,65026
ENST00000284818 // ENSEMBL // cdna:known chromosome:GRCh37:8:74903587:74941322:1 gene:E	LY96	0,000749 825	-5,28224
ENST00000286692 // ENSEMBL // cdna:known chromosome:GRCh37:1:111659955:111682662:-1 gen	DRAM2	0,000338 303	1,23307
ENST00000292330 // ENSEMBL // cdna:known chromosome:GRCh37:7:100032905:100034188:-1 gen	PPP1R35	0,000234 909	1,53457
ENST00000295704 // ENSEMBL // cdna:known chromosome:GRCh37:2:219528587:219537134:-1 gen	RNF25	0,000314 862	-1,29553
ENST00000296277 // ENSEMBL // cdna:known chromosome:GRCh37:3:186838736:186857311:-1 gen	RPL39L	0,000279 281	3,53523
ENST00000299954 // ENSEMBL // cdna:known chromosome:GRCh37:17:65373924:65689645:1 gene:	PITPNC1	4,19E-05	-3,24324
ENST00000301464 // ENSEMBL // cdna:known chromosome:GRCh37:12:53491229:53496124:1 gene:	IGFBP6	0,000731 019	-1,9813
ENST00000303204 // ENSEMBL // cdna:known chromosome:GRCh37:5:176730775:176733960:1 gene	PRELID1	0,000780 397	1,45856
ENST00000306121 // ENSEMBL // cdna:known chromosome:GRCh37:1:99127279:99226056:1 gene:E	SNX7	2,30E-06	2,04272
ENST00000310473 // ENSEMBL // cdna:known chromosome:GRCh37:11:73685712:73694352:-1 gene	UCP2	8,26E-05	-1,75262
ENST00000312134 // ENSEMBL // cdna:known chromosome:GRCh37:11:65779312:65780976:1	CST6	4,58E-05	-2,69328

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
gene:			
ENST00000313401 // ENSEMBL // cdna:known chromosome:GRCh37:17:30813637:30818274:1 gene:	CDK5R1	0,000202586	-1,49651
ENST00000315870 // ENSEMBL // cdna:known chromosome:GRCh37:7:120590803:120617270:1 gene	ING3	0,0004981	1,69923
ENST00000316403 // ENSEMBL // cdna:known chromosome:GRCh37:8:27454434:27472548:-1 gene:	CLU	4,91E-05	2,08183
ENST00000317749 // ENSEMBL // cdna:known chromosome:GRCh37:22:23950639:23974508:-1 gene	C22orf43	0,0002042	-1,24446
ENST00000317932 // ENSEMBL // cdna:known chromosome:GRCh37:18:24034874:24209206:-1 gene	KCTD1	7,66E-05	3,37668
ENST00000322088 // ENSEMBL // cdna:known chromosome:GRCh37:19:52693292:52730687:1 gene:	PPP2R1A	0,000273871	-1,39357
ENST00000323060 // ENSEMBL // cdna:known chromosome:GRCh37:19:46030685:46088100:-1 gene	OPA3	2,36E-05	-1,36129
ENST00000325134 // ENSEMBL // cdna:known chromosome:GRCh37:19:58053208:58071207:-1 gene	ZNF550	6,10E-09	-1,69453
ENST00000328205 // ENSEMBL // cdna:known chromosome:GRCh37:1:226418858:226497434:-1 gen	LIN9	9,40E-05	1,39651
ENST00000328697 // ENSEMBL // cdna:known chromosome:GRCh37:11:27360076:27385415:-1 gene	CCDC34	0,000180662	2,2432
ENST00000334744 // ENSEMBL // cdna:known chromosome:GRCh37:5:145138582:145214867:-1 gen	PRELID2	0,000146481	1,54003
ENST00000336034 // ENSEMBL // cdna:known chromosome:GRCh37:19:42702752:42721813:-1 gene	DEDD2	3,64E-06	-1,67946
ENST00000339526 // ENSEMBL // cdna:known chromosome:GRCh37:1:182352029:182360927:-1 gen	GLUL	0,000779167	-5,69582
ENST00000341084 // ENSEMBL // cdna:known chromosome:GRCh37:8:101269570:101322555:-1 gen	RNF19A	0,000772526	-1,65425
ENST00000341199 // ENSEMBL // cdna:known chromosome:GRCh37:5:175665365:175772988:1 gene	C5orf25	0,000601107	1,82196

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000341695 // ENSEMBL // cdna:known chromosome:GRCh37:4:106290234:106395238:-1 gen	PPA2	4,51E-05	1,62066
ENST00000343735 // ENSEMBL // cdna:known chromosome:GRCh37:3:137717577:137752494:1 gene	CLDN18	0,000649 245	19,6112
ENST00000344850 // ENSEMBL // cdna:known chromosome:GRCh37:2:144703583:145052885:-1 gen	GTDC1	0,000352 571	-1,55546
ENST00000348956 // ENSEMBL // cdna:known chromosome:GRCh37:14:103985996:103989448:-1 ge	CKB	6,80E-05	-1,42423
ENST00000353107 // ENSEMBL // cdna:known chromosome:GRCh37:8:101162812:101166230:1 gene	POLR2K	7,75E-05	-1,82141
ENST00000355196 // ENSEMBL // cdna:known chromosome:GRCh37:4:83740164:83821691:-1 gene:	SEC31A	0,000156 189	1,61823
ENST00000355327 // ENSEMBL // cdna:known chromosome:GRCh37:15:71389291:72075722:1 gene:	THSD4	0,000871 04	-2,17992
ENST00000356056 // ENSEMBL // cdna:known chromosome:GRCh37:15:72114632:72410422:-1 gene	MYO9A	0,000549 188	-1,5253
ENST00000356584 // ENSEMBL // cdna:known chromosome:GRCh37:19:57984413:57988900:-1 gene	ZNF772	0,000307 021	-1,98976
ENST00000357884 // ENSEMBL // cdna:known chromosome:GRCh37:19:40826973:40854421:-1 gene	C19orf47	1,27E-05	-1,39691
ENST00000357927 // ENSEMBL // cdna:known chromosome:GRCh37:9:33548830:33573007:1 gene:E	ANKRD18B	6,37E-05	-2,18228
ENST00000357949 // ENSEMBL // cdna:known chromosome:GRCh37:19:40927499:40931932:-1 gene	SERTAD1	1,33E-06	-1,71314
ENST00000358055 // ENSEMBL // cdna:known chromosome:GRCh37:2:220492049:220506693:1 gene	SLC4A3	0,000555 798	-1,60227
ENST00000361951 // ENSEMBL // cdna:known chromosome:GRCh37:1:173793641:173827684:1 gene	DARS2	2,86E-06	1,77141
ENST00000364675 // ENSEMBL // ncna:snRNA chromosome:GRCh37:3:20038295:20038417:1 gene:		8,08E-06	-2,22379
ENST00000365473 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:6:149915761:149915895:1 ge		0,000138 9	-2,01644

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000367073 // ENSEMBL // cdna:known chromosome:GRCh37:6:159290954:159331385:1 gene	C6orf99	3,36E-05	-1,27229
ENST00000367434 // ENSEMBL // cdna:known chromosome:GRCh37:1:193148175:193155784:-1 gen	B3GALT2	0,000138 974	1,46892
ENST00000370548 // ENSEMBL // cdna:known chromosome:GRCh37:1:87458692:87634887:1 gene:E	LOC3395 24	0,000301 854	1,3582
ENST00000372054 // ENSEMBL // cdna:known chromosome:GRCh37:X:109589700:109590201:-1 gen	GNG5P2	0,000362 306	1,39732
ENST00000372987 // ENSEMBL // cdna:putative chromosome:GRCh37:6:41902694:41909257:-1 ge	CCND3	0,000124 999	-1,47882
ENST00000373004 // ENSEMBL // cdna:known chromosome:GRCh37:X:99899215:99926296:1 gene:E	SRPX2	9,60E-06	-3,06264
ENST00000374227 // ENSEMBL // cdna:known chromosome:GRCh37:9:115800660:115818996:-1 gen	ZFP37	0,000444 011	-1,54377
ENST00000374279 // ENSEMBL // cdna:known chromosome:GRCh37:9:114659046:114697649:1 gene	UGCG	0,000100 999	1,53097
ENST00000381227 // ENSEMBL // cdna:known chromosome:GRCh37:4:57843908:57897324:1 gene:E	POLR2B	0,000895 037	1,4927
ENST00000381867 // ENSEMBL // cdna:known chromosome:GRCh37:20:1246999:1289972:1 gene:EN	SNPH	0,000596 78	-1,44308
ENST00000382480 // ENSEMBL // cdna:known chromosome:GRCh37:4:8594435:8621488:1 gene:ENS	CPZ	0,000321 835	-1,30817
ENST00000383657 // ENSEMBL // cdna:known chromosome:GRCh37:3:123210401:123304032:-1 gen	PTPLB	0,000117 874	1,48231
ENST00000384211 // ENSEMBL // ncna:snRNA chromo- some:GRCh37:7:156664772:156664912:1 gen		0,000689 4	1,28896
ENST00000384391 // ENSEMBL // ncna:snoRNA chromo- some:GRCh37:15:69750281:69750488:-1 ge		0,000756 596	-1,57419
ENST00000384551 // ENSEMBL // ncna:misc_RNA chromo- some:GRCh37:19:40844966:40845071:-1		0,000688 653	-1,63531
ENST00000389386 // ENSEMBL // cdna:known chromosome:GRCh37:16:89773542:89787394:-1 gene	C16orf7	1,64E-05	-1,52188
ENST00000390658 // ENSEMBL // cdna:known	EID2	0,000101	-1,36795

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:19:40028890:40030870:-1 gene		693	
ENST00000391017 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:3:101347154:101347250:-1		0,000858488	-1,9397
ENST00000391195 // ENSEMBL // ncna:rRNA chromosome:GRCh37:19:12138728:12138836:-1 gene	RN5S465	0,000113338	-3,28665
ENST00000391684 // ENSEMBL // cdna:known chromosome:GRCh37:8:71485681:71486671:1 gene:E		0,000597096	-1,66854
ENST00000391835 // ENSEMBL // cdna:putative chromosome:GRCh37:19:50372303:50381285:-1 g	AKT1S1	0,000540615	-1,37139
ENST00000394735 // ENSEMBL // cdna:known chromosome:GRCh37:4:106603784:106629238:-1 gen	INTS12	0,000318897	1,59886
ENST00000395091 // ENSEMBL // cdna:known chromosome:GRCh37:16:30565085:30569819:-1 gene	ZNF764	1,33E-06	1,40782
ENST00000395491 // ENSEMBL // cdna:putative chromosome:GRCh37:17:21188049:21218525:1 ge	MAP2K3	9,28E-07	-1,5359
ENST00000396161 // ENSEMBL // cdna:known chromosome:GRCh37:19:58125628:58134721:1 gene:	ZNF134	5,95E-10	-2,49719
ENST00000396822 // ENSEMBL // cdna:known chromosome:GRCh37:8:49830327:49834299:-1 gene:	SNAI2	0,000720222	-3,19124
ENST00000396842 // ENSEMBL // cdna:known chromosome:GRCh37:3:15468862:15484120:1 gene:E	EAF1	0,000100148	-1,2134
ENST00000398499 // ENSEMBL // cdna:known chromosome:GRCh37:21:43408746:43430475:-1 gene	ZNF295	0,000120332	-1,40126
ENST00000401867 // ENSEMBL // cdna:known chromosome:GRCh37:5:131527531:131563508:-1 gen	P4HA2	0,000212031	-1,61629
ENST00000404190 // ENSEMBL // cdna:known chromosome:GRCh37:10:90484301:90512543:1 gene:	LIPK	0,000616088	-2,33798
ENST00000408925 // ENSEMBL // cdna:novel chromosome:GRCh37:6:42858005:42858554:-1 gene:	C6orf226	0,000298282	-1,34005
ENST00000409890 // ENSEMBL // cdna:known chromosome:GRCh37:2:85581843:85618873:1 gene:E	ELMOD3	0,000127393	-1,36737
ENST00000410023 // ENSEMBL // cdna:known chromosome:GRCh37:2:102759246:102796334:1 gene	IL1R1	0,000753922	-2,33905
ENST00000410113 // ENSEMBL // cdna:known	FAM176A	0,000614	-2,46861

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:2:75719612:75788064:-1 gene:		694	
ENST00000410125 // ENSEMBL // ncna:snRNA chromosome:GRCh37:3:121374322:121374451:-1 ge		0,000495 236	-1,80601
ENST00000410832 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:6:141807278:141807549:-1		0,000173 371	-5,84677
ENST00000414686 // ENSEMBL // cdna:putative chromosome:GRCh37:1:101461029:101461816:1 g		0,000612 986	1,32817
ENST00000418393 // ENSEMBL // cdna:known chromosome:GRCh37:17:39077682:39132178:1 gene:		0,000299 834	-3,4005
ENST00000418639 // ENSEMBL // cdna:known chromosome:GRCh37:4:114372188:114683083:-1 gen	CAMK2D	0,000105 367	1,59597
ENST00000420917 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:X:62890076:628913	ARHGEF9-IT1	0,000127 286	1,58709
ENST00000421055 // ENSEMBL // cdna:known chromosome:GRCh37:1:203096387:203097082:-1 gen		0,000149 3	-1,25654
ENST00000426015 // ENSEMBL // havana:lincRNA chromosome:GRCh37:9:36332947:36334969:-1 g		0,000203 212	-1,40533
ENST00000429768 // ENSEMBL // cdna:known chromosome:GRCh37:1:186420213:186420881:1 gene		0,000552 06	-1,44623
ENST00000430825 // ENSEMBL // cdna:known chromosome:GRCh37:7:156461646:156469257:-1 gen		0,000102 682	1,48161
ENST00000436429 // ENSEMBL // cdna:known chromosome:GRCh37:21:16343791:16365175:1 gene:		0,000795 857	-1,49708
ENST00000439326 // ENSEMBL // cdna:known chromosome:GRCh37:19:12175514:12192380:1 gene:	ZNF844	0,000662 012	-2,95647
ENST00000441212 // ENSEMBL // cdna:known chromosome:GRCh37:2:173292502:173293331:-1 gen		0,000469 07	-1,31166
ENST00000444739 // ENSEMBL // cdna:known chromosome:GRCh37:11:104813593:104840163:-1 ge	CASP4	0,000572 724	-1,47994
ENST00000445927 // ENSEMBL // cdna:known chromosome:GRCh37:2:47314130:47382517:-1 gene:	C2orf61	7,49E-05	-1,53314
ENST00000447975 // ENSEMBL // cdna:putative chromosome:GRCh37:3:194868600:194873519:1 g	XXYLT1-AS2	9,04E-05	-2,49146
ENST00000449181 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:6:52262356:522629		0,000472 539	2,65913
ENST00000451832 // ENSEMBL // ha-vana:sense_intronic chromosome:GRCh37:7:110364215:11036	IMMP2L-IT1	1,30E-06	1,51431
ENST00000458860 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:4:103780550:103780653:-1 g		0,000342 08	1,89982
ENST00000458921 // ENSEMBL // ncna:snoRNA chromosome:		0,000855	1,33675

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
some:GRCh37:16:58652579:58652668:1 gen		926	
ENST00000459130 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:7:110749324:110749413:-1 g		0,000155 979	2,05344
ENST00000469539 // ENSEMBL // cdna:known chromosome:GRCh37:7:155435895:155437100:-1 gen	LOC100506302	0,000321 81	1,36226
ENST00000473000 // ENSEMBL // cdna:known chromosome:GRCh37:6:3259195:3268284:1 gene:ENS	PSMG4	0,000411 217	1,53932
ENST00000477973 // ENSEMBL // cdna:known chromosome:GRCh37:3:72423744:72496069:-1 gene:	RYBP	2,40E-06	-1,23294
ENST00000480669 // ENSEMBL // cdna:known chromosome:GRCh37:3:169165655:169194840:1 gene	LOC100505473	0,000601 39	1,92979
ENST00000502781 // ENSEMBL // cdna:known chromosome:GRCh37:4:147096881:147111198:1 gene	LSM6	0,000347 388	1,43004
ENST00000504123 // ENSEMBL // cdna:known chromosome:GRCh37:4:78634541:78740522:-1 gene:	CNOT6L	0,000577 056	1,54781
ENST00000504754 // ENSEMBL // cdna:known chromosome:GRCh37:4:108828356:108829383:1 gene	SGMS2	0,000118 24	1,31737
ENST00000506265 // ENSEMBL // cdna:known chromosome:GRCh37:5:113998658:114004103:-1 gen		0,000734 852	1,32966
ENST00000516685 // ENSEMBL // ncna:snRNA chromosome:GRCh37:11:77844466:77844568:-1 gen		0,000346 598	1,75775
ENST00000517183 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:11:117134515:117134668:1 g		0,000519 145	1,20846
ENST00000517608 // ENSEMBL // cdna:known chromosome:GRCh37:8:74698455:74791145:-1 gene:	UBE2W	1,30E-05	-1,49257
ENST00000518448 // ENSEMBL // cdna:known chromosome:GRCh37:8:124191287:124222002:1 gene	FAM83A	9,39E-06	-3,32026
ENST00000519389 // ENSEMBL // cdna:known chromosome:GRCh37:X:65382391:65488709:1 gene:E	HEPH	0,000208 635	7,18637
ENST00000521586 // ENSEMBL // havana:lincRNA chromosome:GRCh37:8:128351519:128404876:1		0,000791 7	1,60312
ENST00000522560 // ENSEMBL // havana:lincRNA chromosome:GRCh37:8:74281005:74281530:-1 g		0,000499 322	-1,40786
ENST00000522769 // ENSEMBL // havana:lincRNA chromosome:GRCh37:5:157600609:157603430:-1		4,51E-07	1,20768
ENST00000523411 // ENSEMBL // cdna:putative chromosome:GRCh37:8:36924959:36926936:-1 ge		0,000193 564	-1,52387
ENST00000527441 // ENSEMBL // cdna:known	PPP2R5B	4,84E-06	-1,43679

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:11:64692198:64701947:1 gene:			
ENST00000527726 // ENSEMBL // cdna:putative chromosome:GRCh37:11:11591631:11595329:1 ge		4,89E-06	1,84128
ENST00000530705 // ENSEMBL // cdna:known chromosome:GRCh37:13:45911313:45915505:-1 gene	TPT1	0,000566 051	1,36389
ENST00000532272 // ENSEMBL // havana:lincRNA chromosome:GRCh37:11:133896882:133898013:1		0,000113 735	1,219
ENST00000532740 // ENSEMBL // cdna:putative chromosome:GRCh37:11:14720385:14722472:1 ge	PDE3B	0,000112 868	2,12587
ENST00000533992 // ENSEMBL // havana:lincRNA chromosome:GRCh37:8:123426571:123440790:-1		0,000411 202	-2,20409
ENST00000535380 // ENSEMBL // cdna:known chromosome:GRCh37:11:18720326:18724657:1 gene:	TMEM86 A	0,000557 232	-2,4282
ENST00000535512 // ENSEMBL // cdna:known chromosome:GRCh37:17:7293053:7307416:-1 gene:E	PLSCR3	0,000153 989	-1,35601
ENST00000536931 // ENSEMBL // cdna:known chromosome:GRCh37:12:18867729:18890812:1 gene:		0,000751 849	3,36421
ENST00000542678 // ENSEMBL // cdna:known chromosome:GRCh37:12:123413547:123466196:-1 ge	ABCB9	0,000606 38	-1,32417
ENST00000543026 // ENSEMBL // cdna:known chromosome:GRCh37:12:31240579:31246654:1 gene:	DDX11	0,000500 058	1,21651
ENST00000546566 // ENSEMBL // cdna:known chromosome:GRCh37:12:53433383:53440834:-1 gene	LOC2833 35	7,44E-05	1,69798
ENST00000546591 // ENSEMBL // cdna:known chromosome:GRCh37:12:56510370:56511727:1 gene:	RPL41	0,000847 422	1,36638
ENST00000547688 // ENSEMBL // cdna:putative chromosome:GRCh37:12:51381722:51422349:-1 g	SLC11A2	0,000153 493	1,70546
ENST00000552360 // ENSEMBL // cdna:known chromosome:GRCh37:19:47777710:47778964:1 gene:	PRR24	7,79E-05	-1,66618
ENST00000554595 // ENSEMBL // havana:non_coding chromosome:GRCh37:14:37566267:37567768:		0,000193 093	-1,50142
ENST00000555325 // ENSEMBL // cdna:known chromosome:GRCh37:15:93349000:93351797:-1 gene		0,000416 756	1,79801
ENST00000558238 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:15:52237616:52238		0,000483 972	-2,02093
ENST00000560268 // ENSEMBL // cdna:known chromosome:GRCh37:15:34150918:34157026:-1 gene		0,000401 682	1,71696

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ENST00000561394 // ENSEMBL // havana:lincRNA chromosome:GRCh37:15:36262559:36544458:-1		0,00028679	1,26726
ENST00000576221 // ENSEMBL // cdna:known chromosome:GRCh37:17:53848538:53920191:1 gene:	PCTP	0,000403024	1,37123
NM_000521 // RefSeq // Homo sapiens hexosaminidase B (beta polypeptide) (HEXB), mRNA. /	HEXB	5,02E-05	1,50615
NM_000523 // RefSeq // Homo sapiens homeobox D13 (HOXD13), mRNA. // chr2 // 100 // 100	HOXD13	9,97E-06	1,37541
NM_000641 // RefSeq // Homo sapiens interleukin 11 (IL11), transcript variant 1, mRNA.	IL11	3,91E-05	-1,8859
NM_000671 // RefSeq // Homo sapiens alcohol dehydrogenase 5 (class III), chi polypeptid	ADH5	0,000602119	1,43083
NM_000786 // RefSeq // Homo sapiens cytochrome P450, family 51, subfamily A, polypeptid	CYP51A1	0,000818085	1,59522
NM_000824 // RefSeq // Homo sapiens glycine receptor, beta (GLRB), transcript variant 1	GLRB	0,000267102	3,28788
NM_000922 // RefSeq // Homo sapiens phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA.	PDE3B	0,000141479	2,5712
NM_000930 // RefSeq // Homo sapiens plasminogen activator, tissue (PLAT), transcript va	PLAT	0,00015803	-5,59179
NM_000969 // RefSeq // Homo sapiens ribosomal protein L5 (RPL5), mRNA. // chr1 // 100 /	RPL5	0,00036192	1,33607
NM_001002034 // RefSeq // Homo sapiens family with sequence similarity 109, member B (F	FAM109B	4,68E-05	1,49774
NM_001002236 // RefSeq // Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 ant	SERPIN A1	0,000298105	-2,31174
NM_001002923 // RefSeq // Homo sapiens IGF-like family member 4 (IGFL4), mRNA. // chr19	IGFL4	0,000511422	-2,67778
NM_001004318 // RefSeq // Homo sapiens iron/zinc purple acid phosphatase-like protein (	PAPL	0,000468278	-2,67004
NM_001004320 // RefSeq // Homo sapiens alkylglycerol monooxygenase (AGMO), mRNA. // chr	AGMO	6,29E-05	8,06425
NM_001005360 // RefSeq // Homo sapiens dynamin 2 (DNM2), transcript variant 1, mRNA. //	DNM2	0,000490022	1,32152
NM_001006 // RefSeq // Homo sapiens ribosomal protein S3A (RPS3A), transcript variant 1	RPS3A	8,60E-05	1,65182
NM_001007559 // RefSeq // Homo sapiens synovial sarcoma translocation, chromosome 18 (S	SS18	0,000761038	1,91375
NM_001008390 // RefSeq // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), t	CGGBP1	0,000396308	-1,37792
NM_001009562 // RefSeq // Homo sapiens solute carrier organic anion transporter family,	SLCO1B7	0,00050148	-8,902
NM_001011880 // RefSeq // Homo sapiens C-type lectin domain family 18, member B (CLEC18	CLEC18B	0,000128672	-1,42747

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001017928 // RefSeq // Homo sapiens coiled-coil domain containing 58 (CCDC58), mRNA.	CCDC58	0,000353 427	1,49667
NM_001025389 // RefSeq // Homo sapiens adenosine monophosphate deaminase 3 (AMPD3), tra	AMPD3	0,000298 983	-1,60416
NM_001031835 // RefSeq // Homo sapiens phosphor-ylase kinase, beta (PHKB), transcript va	PHKB	0,000864 315	1,40848
NM_001037442 // RefSeq // Homo sapiens RUN and FYVE domain containing 3 (RUFY3), transc	RUFY3	0,000252 175	1,37668
NM_001038707 // RefSeq // Homo sapiens CDC42 small effector 1 (CDC42SE1), transcript va	CDC42SE1	2,61E-06	-1,29465
NM_001039671 // RefSeq // Homo sapiens Yip1 interacting factor homolog B (S. cerevisiae	YIF1B	0,000355 643	-1,41043
NM_001040402 // RefSeq // Homo sapiens DCN1, defective in cullin neddylation 1, domain	DCUN1D4	8,02E-05	1,80786
NM_001040716 // RefSeq // Homo sapiens pyruvate carboxylase (PC), nuclear gene encoding	PC	0,000353 343	-1,29792
NM_001042423 // RefSeq // Homo sapiens solute carrier family 16, member 3 (monocarboxyl	SLC16A3	0,000262 502	-2,35895
NM_001042521 // RefSeq // Homo sapiens chromosome 2 open reading frame 88 (C2orf88), tr	C2orf88	9,10E-06	1,99661
NM_001042552 // RefSeq // Homo sapiens TatD DNase domain containing 3 (TATDN3), transcr	TATDN3	0,000703 324	1,52517
NM_001048210 // RefSeq // Homo sapiens chloride channel CLIC-like 1 (CLCC1), transcript	CLCC1	0,000874 74	1,45649
NM_001049 // RefSeq // Homo sapiens somatostatin receptor 1 (SSTR1), mRNA. // chr14 //	SSTR1	0,000411 241	1,89356
NM_001101330 // RefSeq // Homo sapiens hCG1645220 (LOC728819), mRNA. // chr2 // 94 // 1	LOC728819	0,000143 303	-1,58684
NM_001103 // RefSeq // Homo sapiens actinin, alpha 2 (ACTN2), mRNA. // chr1 // 100 // 7	ACTN2	0,000196 637	-1,3708
NM_001113411 // RefSeq // Homo sapiens FGGY carbohydrate kinase domain containing (FGGY	FGGY	0,000226 823	1,37144
NM_001124758 // RefSeq // Homo sapiens spinster homolog 2 (Drosophila) (SPNS2), mRNA. /	SPNS2	0,000579 421	-4,62005
NM_001128429 // RefSeq // Homo sapiens SWI/SNF-related, matrix-associated actin-depende	SMARCA D1	0,000738 123	1,58261
NM_001128431 // RefSeq // Homo sapiens solute carrier family 39 (zinc transporter), mem	SLC39A14	0,000459 731	3,12873
NM_001130144 // RefSeq // Homo sapiens latent transforming growth factor beta binding p	LTBP3	0,000898 569	-1,5144
NM_001130475 // RefSeq // Homo sapiens THAP domain containing 5 (THAP5), transcript var	THAP5	6,53E-05	1,23023
NM_001130929 // RefSeq // Homo sapiens chromosome 7 open reading frame 73 (C7orf73), nu	C7orf73	0,000630 645	1,64204
NM_001134382 // RefSeq // Homo sapiens IQ motif	IQSEC1	3,41E-05	-1,43344

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
and Sec7 domain 1 (IQSEC1), transcript			
NM_001134479 // RefSeq // Homo sapiens leucine rich repeat containing 8 family, member	LRRC8D	0,000117045	1,56754
NM_001134848 // RefSeq // Homo sapiens coiled-coil domain containing 152 (CCDC152), mRNA	CCDC152	0,000248709	-2,3558
NM_001142292 // RefSeq // Homo sapiens lectin, mannose-binding 2-like (LMAN2L), transcr	LMAN2L	0,00054543	-1,51167
NM_001142343 // RefSeq // Homo sapiens chemo-kinase-like receptor 1 (CMKLR1), transcript v	CMKLR1	0,000432359	1,2915
NM_001142416 // RefSeq // Homo sapiens aminoacyl tRNA synthetase complex-interacting mu	AIMP1	0,000844505	1,45334
NM_001142502 // RefSeq // Homo sapiens protein phosphatase 1, regulatory subunit 13 lik	PPP1R13L	0,000218174	-1,84965
NM_001143676 // RefSeq // Homo sapiens serum/glucocorticoid regulated kinase 1 (SGK1),	SGK1	0,000802596	-2,85707
NM_001145078 // RefSeq // Homo sapiens zinc finger protein 805 (ZNF805), transcript var	ZNF805	0,000487418	-1,46138
NM_001145354 // RefSeq // Homo sapiens muskellin 1, intracellular mediator containing ke	MKLN1	3,12E-05	1,29035
NM_001145548 // RefSeq // Homo sapiens zinc finger, DHHC-type containing 7 (ZDHHC7), tr	ZDHHC7	0,000677847	1,52576
NM_001160170 // RefSeq // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransfe	NAT1	0,000344721	1,66591
NM_001164277 // RefSeq // Homo sapiens solute carrier family 37 (glucose-6-phosphate tr	SLC37A4	2,68E-05	1,42023
NM_001165 // RefSeq // Homo sapiens baculoviral IAP repeat containing 3 (BIRC3), transc	BIRC3	1,79E-05	2,25422
NM_001172477 // RefSeq // Homo sapiens ribonucleotide reductase M2 B (TP53 inducible) (	RRM2B	0,000301415	-1,95744
NM_001177716 // RefSeq // Homo sapiens Kruppel-like factor 11 (KLF11), transcript varia	KLF11	4,44E-05	1,83245
NM_001178106 // RefSeq // Homo sapiens zinc finger protein 185 (LIM domain) (ZNF185), t	ZNF185	9,63E-06	-2,93461
NM_001184705 // RefSeq // Homo sapiens hydroxyacyl-CoA dehydrogenase (HADH), nuclear ge	HADH	0,000417731	1,77472
NM_001190849 // RefSeq // Homo sapiens CCR4-NOT transcription complex, subunit 4 (CNOT4	CNOT4	2,04E-05	1,28959
NM_001195132 // RefSeq // Homo sapiens cyclin-dependent kinase inhibitor 2A (CDKN2A), t	CDKN2A	0,000699063	-5,7807
NM_001195291 // RefSeq // Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin),	SERPINB6	6,86E-06	1,66561
NM_001195597 // RefSeq // Homo sapiens uncharacterized LOC100507203 (LOC100507203), mRNA	LOC100507203	0,000483994	1,2554
NM_001198 // RefSeq // Homo sapiens PR domain containing 1, with ZNF domain (PRDM1), tr	PRDM1	1,59E-05	-2,31008

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001199324 // RefSeq // Homo sapiens zinc finger protein 615 (ZNF615), transcript var	ZNF615	0,000366 397	-2,26976
NM_001229 // RefSeq // Homo sapiens caspase 9, apoptosis-related cysteine peptidase (CA	CASP9	8,21E-05	-1,59112
NM_001242394 // RefSeq // Homo sapiens synapto-tagmin-like 3 (SYTL3), transcript variant	SYTL3	0,000508 259	-1,58732
NM_001242498 // RefSeq // Homo sapiens MIF4G domain containing (MIF4GD), transcript var	MIF4GD	0,000622 388	-1,4261
NM_001243571 // RefSeq // Homo sapiens myotubularin related protein 2 (MTMR2), transcri	MTMR2	0,000405 397	1,88056
NM_001243794 // RefSeq // Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 12	CHST12	0,000569 308	-1,41903
NM_001251962 // RefSeq // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 26	ARHGEF 26	0,000480 656	-2,00735
NM_001254738 // RefSeq // Homo sapiens Rho family GTPase 3 (RND3), transcript variant 1	RND3	2,24E-05	-2,51389
NM_001256312 // RefSeq // Homo sapiens serine/threonine kinase 3 (STK3), transcript var	STK3	0,000299 53	-1,89043
NM_001256530 // RefSeq // Homo sapiens translocator protein (18kDa) (TSPO), transcript	TSPO	0,000449 578	1,44089
NM_001265597 // RefSeq // Homo sapiens zinc finger protein 211 (ZNF211), transcript var	ZNF211	0,000514 918	-2,30733
NM_001267708 // RefSeq // Homo sapiens zinc finger protein 706 (ZNF706), transcript var	ZNF706	0,000123 325	-1,7641
NM_001343 // RefSeq // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprote	DAB2	0,000519 307	-3,92156
NM_001393 // RefSeq // Homo sapiens extracellular matrix protein 2, female organ and ad	ECM2	9,76E-05	2,24396
NM_001407 // RefSeq // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 3 (fla	CELSR3	0,000829 472	-1,551
NM_001532 // RefSeq // Homo sapiens solute carrier family 29 (nucleoside transporters),	SLC29A2	8,19E-05	1,68744
NM_001661 // RefSeq // Homo sapiens ADP-ribosylation factor-like 4D (ARL4D), mRNA. // c	ARL4D	6,76E-08	-5,20681
NM_001706 // RefSeq // Homo sapiens B-cell CLL/lymphoma 6 (BCL6), transcript variant 1,	BCL6	2,06E-05	-2,05698
NM_001749 // RefSeq // Homo sapiens calpain, small subunit 1 (CAPNS1), transcript varia	CAPNS1	0,000190 856	-1,31634
NM_001785 // RefSeq // Homo sapiens cytidine deaminase (CDA), mRNA. // chr1 // 100 // 1	CDA	0,000245 901	-4,255
NM_001861 // RefSeq // Homo sapiens cytochrome c oxidase subunit IV isoform 1 (COX4I1),	COX4I1	0,000260 048	1,29733
NM_001967 // RefSeq // Homo sapiens eukaryotic translation initiation factor 4A2 (EIF4A	EIF4A2	0,000429 724	1,54564
NM_001983 // RefSeq // Homo sapiens excision re-	ERCC1	0,000166	-1,76995

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
pair cross-complementing rodent repair d		515	
NM_001986 // RefSeq // Homo sapiens ets variant 4 (ETV4), transcript variant 1, mRNA. /	ETV4	0,000877 273	-1,68646
NM_001993 // RefSeq // Homo sapiens coagulation factor III (thromboplastin, tissue fact	F3	0,000482 213	-5,80008
NM_002064 // RefSeq // Homo sapiens glutaredoxin (thioltransferase) (GLRX), transcript	GLRX	0,000797 405	-1,97137
NM_002092 // RefSeq // Homo sapiens G-rich RNA sequence binding factor 1 (GRSF1), trans	GRSF1	0,000629 916	1,60764
NM_002162 // RefSeq // Homo sapiens intercellular adhesion molecule 3 (ICAM3), mRNA. //	ICAM3	1,83E-06	1,43223
NM_002531 // RefSeq // Homo sapiens neurotensin receptor 1 (high affinity) (NTSR1), mRN	NTSR1	0,000150 506	-6,19041
NM_002546 // RefSeq // Homo sapiens tumor necrosis factor receptor superfamily, member	TNFRSF1 1B	0,000749 525	-5,31434
NM_002582 // RefSeq // Homo sapiens poly(A)-specific ribonuclease (PARN), transcript va	PARN	9,64E-05	1,33441
NM_002601 // RefSeq // Homo sapiens phosphodiesterase 6D, cGMP-specific, rod, delta (PD	PDE6D	0,000164 304	-1,52387
NM_002924 // RefSeq // Homo sapiens regulator of G-protein signaling 7 (RGS7), mRNA. //	RGS7	0,000546 182	-3,50229
NM_002982 // RefSeq // Homo sapiens chemokine (C-C motif) ligand 2 (CCL2), mRNA. // chr	CCL2	0,000391 267	8,61057
NM_003087 // RefSeq // Homo sapiens synuclein, gamma (breast cancer-specific protein 1)	SNCG	0,000814 077	-1,37279
NM_003169 // RefSeq // Homo sapiens suppressor of Ty 5 homolog (S. cerevisiae) (SUPT5H)	SUPT5H	0,000514 663	-1,47521
NM_003214 // RefSeq // Homo sapiens TEA domain family member 3 (TEAD3), mRNA. // chr6 /	TEAD3	0,000229 856	-1,26253
NM_003236 // RefSeq // Homo sapiens transforming growth factor, alpha (TGFA), transcrip	TGFA	0,000241 211	-1,9813
NM_003292 // RefSeq // Homo sapiens translocated promoter region, nuclear basket protei	TPR	0,000436 055	1,26378
NM_003379 // RefSeq // Homo sapiens ezrin (EZR), transcript variant 1, mRNA. // chr6 //	EZR	0,000168 322	-1,3654
NM_003401 // RefSeq // Homo sapiens X-ray repair complementing defective repair in Chin	XRCC4	0,000141 991	3,20011
NM_003406 // RefSeq // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	YWHAZ	0,000143 04	-1,46884
NM_003470 // RefSeq // Homo sapiens ubiquitin specific peptidase 7 (herpes virus-associ	USP7	1,47E-05	1,37228
NM_003518 // RefSeq // Homo sapiens histone cluster 1, H2bg (HIST1H2BG), mRNA. // chr6	HIST1H2 BG	0,000136 898	-4,51926
NM_003658 // RefSeq // Homo sapiens BARX homeobox 2 (BARX2), mRNA. // chr11 // 100 // 5	BARX2	3,59E-07	-4,15642

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_003687 // RefSeq // Homo sapiens PDZ and LIM domain 4 (PDLIM4), transcript variant 1	PDLIM4	4,88E-05	-2,14248
NM_003715 // RefSeq // Homo sapiens USO1 vesicle docking protein homolog (yeast) (USO1)	USO1	0,000788 674	1,43571
NM_003794 // RefSeq // Homo sapiens sorting nexin 4 (SNX4), mRNA. // chr3 // 100 // 100	SNX4	2,99E-05	1,48131
NM_003826 // RefSeq // Homo sapiens N-ethylmaleimide-sensitive factor attachment protei	NAPG	7,84E-05	-1,48986
NM_003941 // RefSeq // Homo sapiens Wiskott-Aldrich syndrome-like (WASL), mRNA. // chr7	WASL	0,000205 855	1,36174
NM_003969 // RefSeq // Homo sapiens ubiquitin-conjugating enzyme E2M (UBE2M), mRNA. //	UBE2M	0,000655 961	-1,30263
NM_003998 // RefSeq // Homo sapiens nuclear factor of kappa light polypeptide gene enha	NFKB1	0,000226 853	1,90719
NM_004069 // RefSeq // Homo sapiens adaptor-related protein complex 2, sigma 1 subunit	AP2S1	0,000729 629	-1,33855
NM_004209 // RefSeq // Homo sapiens synaptogyrin 3 (SYNGR3), mRNA. // chr16 // 100 // 1	SYNGR3	0,000298 206	-1,23225
NM_004252 // RefSeq // Homo sapiens solute carrier family 9, subfamily A (NHE3, cation	SLC9A3R 1	0,000219 286	-1,7649
NM_004279 // RefSeq // Homo sapiens peptidase (mitochondrial processing) beta (PMPCB),	PMPCB	5,78E-05	1,60227
NM_004285 // RefSeq // Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydro	H6PD	0,000618 377	-1,75418
NM_004347 // RefSeq // Homo sapiens caspase 5, apoptosis-related cysteine peptidase (CA	CASP5	0,000763 706	1,48837
NM_004396 // RefSeq // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box helicase 5 (DDX5), mRNA.	DDX5	8,74E-06	-1,33353
NM_004408 // RefSeq // Homo sapiens dynamin 1 (DNM1), transcript variant 1, mRNA. // ch	DNM1	0,000207 772	-3,26653
NM_004425 // RefSeq // Homo sapiens extracellular matrix protein 1 (ECM1), transcript v	ECM1	1,23E-08	-2,695
NM_004456 // RefSeq // Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2), tr	EZH2	0,000263 091	2,03696
NM_004489 // RefSeq // Homo sapiens G protein pathway suppressor 2 (GPS2), mRNA. // chr	GPS2	8,41E-05	-1,35008
NM_004569 // RefSeq // Homo sapiens phosphatidylinositol glycan anchor biosynthesis, cl	PIGH	0,000567 481	-1,32564
NM_004579 // RefSeq // Homo sapiens mitogen-activated protein kinase kinase kinase kina	MAP4K2	0,000270 645	-1,53383
NM_004651 // RefSeq // Homo sapiens ubiquitin specific peptidase 11 (USP11), mRNA. // c	USP11	0,000114 691	-1,63242
NM_004663 // RefSeq // Homo sapiens RAB11A, member RAS oncogene family (RAB11A), transc	RAB11A	6,67E-05	-1,26527
NM_004719 // RefSeq // Homo sapiens SR-related	SCAF11	0,000462	1,23776

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
CTD-associated factor 11 (SCAF11), mRNA.		182	
NM_004798 // RefSeq // Homo sapiens kinesin family member 3B (KIF3B), mRNA. // chr20 //	KIF3B	0,000456076	1,24459
NM_004889 // RefSeq // Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial Fo com	ATP5J2	0,000753912	1,32863
NM_004890 // RefSeq // Homo sapiens sperm associated antigen 7 (SPAG7), mRNA. // chr17	SPAG7	6,48E-05	-1,53009
NM_004891 // RefSeq // Homo sapiens mitochondrial ribosomal protein L33 (MRPL33), nucle	MRPL33	0,000412155	-1,39785
NM_004923 // RefSeq // Homo sapiens metallothionein-like 5, testis-specific (tesmin) (M	MTL5	0,000540822	1,9187
NM_004941 // RefSeq // Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 8 (DHX8), mR	DHX8	4,29E-08	-1,43201
NM_004973 // RefSeq // Homo sapiens jumonji, AT rich interactive domain 2 (JARID2), tra	JARID2	0,000563521	-1,77431
NM_004979 // RefSeq // Homo sapiens potassium voltage-gated channel, Shal-related subfa	KCND1	0,000444632	-1,5521
NM_004991 // RefSeq // Homo sapiens MDS1 and EVI1 complex locus (MECOM), transcript var	MECOM	3,25E-05	2,8483
NM_005207 // RefSeq // Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian)-1	CRKL	2,39E-05	1,28839
NM_005234 // RefSeq // Homo sapiens nuclear receptor subfamily 2, group F, member 6 (NR	NR2F6	0,000826876	1,51014
NM_005321 // RefSeq // Homo sapiens histone cluster 1, H1e (HIST1H1E), mRNA. // chr6 //	HIST1H1E	0,000713866	1,41021
NM_005324 // RefSeq // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. // chr	H3F3B	9,61E-05	-1,3704
NM_005342 // RefSeq // Homo sapiens high mobility group box 3 (HMGB3), mRNA. // chrX //	HMGB3	0,000671081	1,20975
NM_005455 // RefSeq // Homo sapiens zinc finger, RAN-binding domain containing 2 (ZRANB	ZRANB2	2,77E-05	1,26006
NM_005474 // RefSeq // Homo sapiens histone deacetylase 5 (HDAC5), transcript variant 1	HDAC5	7,49E-06	-1,72069
NM_005515 // RefSeq // Homo sapiens motor neuron and pancreas homeobox 1 (MXN1), transc	MNX1	0,000704808	1,50401
NM_005612 // RefSeq // Homo sapiens RE1-silencing transcription factor (REST), transcri	REST	0,000239743	1,34567
NM_005716 // RefSeq // Homo sapiens GIPC PDZ domain containing family, member 1 (GIPC1)	GIPC1	0,000203046	-1,23473
NM_006005 // RefSeq // Homo sapiens Wolfram syndrome 1 (wolframin) (WFS1), transcript v	WFS1	1,69E-05	-2,85621
NM_006044 // RefSeq // Homo sapiens histone deacetylase 6 (HDAC6), mRNA. // chrX // 100	HDAC6	0,000117075	-1,64883
NM_006099 // RefSeq // Homo sapiens protein inhibitor of activated STAT, 3 (PIAS3), mRN	PIAS3	0,000768421	-1,50387

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_006136 // RefSeq // Homo sapiens capping protein (actin filament) muscle Z-line, alp	CAPZA2	3,22E-06	1,57006
NM_006184 // RefSeq // Homo sapiens nucleobindin 1 (NUCB1), mRNA. // chr19 // 100 // 65	NUCB1	0,000410 265	-1,26674
NM_006233 // RefSeq // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide I, 1	POLR2I	0,000840 742	-1,40612
NM_006278 // RefSeq // Homo sapiens ST3 beta-galactoside alpha-2,3-sialyltransferase 4	ST3GAL4	0,000235 949	-1,81199
NM_006323 // RefSeq // Homo sapiens SEC24 family, member B (S. cerevisiae) (SEC24B), tr	SEC24B	0,000334 897	1,54512
NM_006340 // RefSeq // Homo sapiens BAI1-associated protein 2 (BAIAP2), transcript vari	BAIAP2	0,000370 249	-2,0633
NM_006349 // RefSeq // Homo sapiens zinc finger, HIT-type containing 1 (ZNHIT1), mRNA.	ZNHIT1	0,000265 674	1,28554
NM_006503 // RefSeq // Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase	PSMC4	4,26E-05	-1,40083
NM_006519 // RefSeq // Homo sapiens dynein, light chain, Tctex-type 1 (DYNLT1), mRNA. /	DYNLT1	7,04E-05	-1,62122
NM_006520 // RefSeq // Homo sapiens dynein, light chain, Tctex-type 3 (DYNLT3), mRNA. /	DYNLT3	3,50E-06	-1,92108
NM_006576 // RefSeq // Homo sapiens advillin (AVIL), mRNA. // chr12 // 100 // 46 // 17	AVIL	0,000323 698	-1,91468
NM_006662 // RefSeq // Homo sapiens Snf2-related CREBBP activator protein (SRCAP), mRNA	SRCAP	8,70E-06	1,24864
NM_006670 // RefSeq // Homo sapiens trophoblast glycoprotein (TPBG), transcript variant	TPBG	0,000295 368	-1,9724
NM_006694 // RefSeq // Homo sapiens jumping translocation breakpoint (JTB), mRNA. // ch	JTB	0,000326 852	1,44031
NM_006765 // RefSeq // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript va	TUSC3	0,000369 097	8,61268
NM_006823 // RefSeq // Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibito	PKIA	6,46E-10	7,40614
NM_006959 // RefSeq // Homo sapiens zinc finger protein 17 (ZNF17), mRNA. // chr19 // 1	ZNF17	0,000487 315	-1,568
NM_007121 // RefSeq // Homo sapiens nuclear receptor subfamily 1, group H, member 2 (NR	NR1H2	8,40E-06	-1,49957
NM_007202 // RefSeq // Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), nuclear	AKAP10	7,62E-05	-1,33875
NM_007207 // RefSeq // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcrip	DUSP10	0,000207 631	-4,83062
NM_007255 // RefSeq // Homo sapiens xylosylprotein beta 1,4-galactosyltransferase, poly	B4GALT7	0,000722 147	1,37816
NM_007257 // RefSeq // Homo sapiens paraneoplastic Ma antigen 2 (PNMA2), mRNA. // chr8	PNMA2	0,000101 706	1,92845
NM_012267 // RefSeq // Homo sapiens HSPA (heat	HSPBP1	2,64E-05	-1,27672

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
shock 70kDa) binding protein, cytoplasmic			
NM_012367 // RefSeq // Homo sapiens olfactory receptor, family 2, subfamily B, member 6	OR2B6	0,000305 265	-3,04291
NM_012478 // RefSeq // Homo sapiens WW domain binding protein 2 (WBP2), mRNA. // chr17	WBP2	1,15E-06	-1,64786
NM_013256 // RefSeq // Homo sapiens zinc finger protein 180 (ZNF180), mRNA. // chr19 //	ZNF180	0,000513 508	-1,42914
NM_013302 // RefSeq // Homo sapiens eukaryotic elongation factor-2 kinase (EEF2K), mRNA	EEF2K	2,87E-05	1,79718
NM_013360 // RefSeq // Homo sapiens zinc finger protein 222 (ZNF222), transcript variant	ZNF222	0,000427 923	-1,54723
NM_013396 // RefSeq // Homo sapiens ubiquitin specific peptidase 25 (USP25), mRNA. // c	USP25	0,000601 869	-1,52444
NM_014053 // RefSeq // Homo sapiens feline leukemia virus subgroup C cellular receptor	FLVCR1	0,000757 75	1,76921
NM_014059 // RefSeq // Homo sapiens regulator of cell cycle (RGCC), mRNA. // chr13 // 1	RGCC	0,000664 532	-2,02054
NM_014153 // RefSeq // Homo sapiens zinc finger CCH-type containing 7A (ZC3H7A), mRNA.	ZC3H7A	0,000145 153	1,37325
NM_014203 // RefSeq // Homo sapiens adaptor-related protein complex 2, alpha 1 subunit	AP2A1	0,000109 055	-1,35066
NM_014232 // RefSeq // Homo sapiens vesicle-associated membrane protein 2 (synaptobrevin)	VAMP2	0,000156 22	-1,34177
NM_014236 // RefSeq // Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA.	GNPAT	0,000764 504	1,30866
NM_014305 // RefSeq // Homo sapiens TDP-glucose 4,6-dehydratase (TGDS), mRNA. // chr13	TGDS	0,000626 997	1,42438
NM_014372 // RefSeq // Homo sapiens ring finger protein 11 (RNF11), mRNA. // chr1 // 10	RNF11	0,000106 794	-1,24245
NM_014400 // RefSeq // Homo sapiens LY6/PLAUR domain containing 3 (LYPD3), mRNA. // chr	LYPD3	0,000869 584	-5,98257
NM_014505 // RefSeq // Homo sapiens potassium large conductance calcium-activated channel	KCNMB4	6,35E-11	-3,3897
NM_014547 // RefSeq // Homo sapiens tropomodulin 3 (ubiquitous) (TMOD3), mRNA. // chr15	TMOD3	0,000185 07	-1,51616
NM_014548 // RefSeq // Homo sapiens tropomodulin 2 (neuronal) (TMOD2), transcript variant	TMOD2	0,000549 144	-2,48044
NM_014601 // RefSeq // Homo sapiens EH-domain containing 2 (EHD2), mRNA. // chr19 // 10	EHD2	0,000105 966	-1,5327
NM_014713 // RefSeq // Homo sapiens lysosomal protein transmembrane 4 alpha (LAPTM4A),	LAPTM4A	0,000694 398	-1,23092
NM_014911 // RefSeq // Homo sapiens AP2 associated kinase 1 (AAK1), mRNA. // chr2 // 10	AAK1	0,000574 658	-1,72334
NM_014931 // RefSeq // Homo sapiens protein phosphatase 6, regulatory subunit 1 (PPP6R1)	PPP6R1	0,000223 448	-1,55494

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_014964 // RefSeq // Homo sapiens epsin 2 (EPN2), transcript variant 2, mRNA. // chr1	EPN2	4,10E-05	-1,72126
NM_015040 // RefSeq // Homo sapiens phosphoinositide kinase, FYVE finger containing (PI	PIKFYVE	0,000832 262	-1,23084
NM_015044 // RefSeq // Homo sapiens golgi-associated, gamma adaptin ear containing, ARF	GGA2	0,000406 7	1,44491
NM_015049 // RefSeq // Homo sapiens trafficking protein, kinesin binding 2 (TRAK2), mRN	TRAK2	2,88E-05	-1,43795
NM_015069 // RefSeq // Homo sapiens zinc finger protein 423 (ZNF423), mRNA. // chr16 //	ZNF423	0,000552 678	1,20408
NM_015143 // RefSeq // Homo sapiens methionyl aminopeptidase 1 (METAP1), mRNA. // chr4	METAP1	1,54E-05	1,55048
NM_015207 // RefSeq // Homo sapiens OTU domain containing 3 (OTUD3), mRNA. // chr1 // 1	OTUD3	7,69E-05	-1,33735
NM_015252 // RefSeq // Homo sapiens EH domain binding protein 1 (EHBP1), transcript var	EHBP1	6,58E-05	-1,71059
NM_015310 // RefSeq // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), tra	PSD3	0,000193 01	2,6915
NM_015416 // RefSeq // Homo sapiens LETM1 domain containing 1 (LETMD1), nuclear gene en	LETMD1	1,29E-05	1,69204
NM_015603 // RefSeq // Homo sapiens coiled-coil domain containing 9 (CCDC9), mRNA. // c	CCDC9	4,28E-05	-1,43959
NM_015627 // RefSeq // Homo sapiens low density lipoprotein receptor adaptor protein 1	LDLRAP1	0,000157 637	-1,741
NM_015629 // RefSeq // Homo sapiens PRP31 pre-mRNA processing factor 31 homolog (S. cer	PRPF31	2,06E-05	-1,34607
NM_015836 // RefSeq // Homo sapiens tryptophanyl tRNA synthetase 2, mitochondrial (WARS	WARS2	0,000434 877	1,44684
NM_015902 // RefSeq // Homo sapiens ubiquitin protein ligase E3 component n-recogin 5	UBR5	0,000746 269	-1,59776
NM_015914 // RefSeq // Homo sapiens thioredoxin domain containing 11 (TXNDC11), mRNA. /	TXNDC1 1	0,000568 452	1,39512
NM_015953 // RefSeq // Homo sapiens nitric oxide synthase interacting protein (NOSIP),	NOSIP	0,000110 277	-1,29593
NM_016057 // RefSeq // Homo sapiens coatomer protein complex, subunit zeta 1 (COPZ1), m	COPZ1	0,000163 738	1,24018
NM_016200 // RefSeq // Homo sapiens N(alpha)-acetyltransferase 38, NatC auxiliary subun	NAA38	0,000483 72	1,40998
NM_016406 // RefSeq // Homo sapiens ubiquitin-fold modifier conjugating enzyme 1 (UFC1)	UFC1	0,000584 754	1,30922
NM_016429 // RefSeq // Homo sapiens coatomer protein complex, subunit zeta 2 (COPZ2), m	COPZ2	0,000269 299	-1,60225
NM_016641 // RefSeq // Homo sapiens glycerophosphodiester phosphodiesterase 1 (GDE1), m	GDE1	1,54E-05	1,42932
NM_016648 // RefSeq // Homo sapiens La ribonu-	LARP7	0,000723	1,49349

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
cleoprotein domain family, member 7 (LARP7		325	
NM_017432 // RefSeq // Homo sapiens prostate tumor overexpressed 1 (PTOV1), mRNA. // ch	PTOV1	0,000297 575	-1,20982
NM_017514 // RefSeq // Homo sapiens plexin A3 (PLXNA3), mRNA. // chrX // 100 // 86 // 2	PLXNA3	0,000351 785	-1,34289
NM_017567 // RefSeq // Homo sapiens N-acetylglucosamine kinase (NAGK), mRNA. // chr2 //	NAGK	0,000803 027	-1,49187
NM_017595 // RefSeq // Homo sapiens NFkB inhibitor interacting Ras-like 2 (NKIRAS2), tr	NKIRAS2	0,000702 664	-1,3554
NM_017654 // RefSeq // Homo sapiens sterile alpha motif domain containing 9 (SAMD9), tr	SAMD9	0,000382 814	-2,7255
NM_017728 // RefSeq // Homo sapiens transmembrane protein 104 (TMEM104), mRNA. // chr17	TMEM104	0,000102 602	-1,40477
NM_017879 // RefSeq // Homo sapiens zinc finger protein 416 (ZNF416), mRNA. // chr19 //	ZNF416	1,07E-05	-1,61003
NM_017983 // RefSeq // Homo sapiens WD repeat domain, phosphoinositide interacting 1 (W	WIP1	0,000177 262	-2,02652
NM_018003 // RefSeq // Homo sapiens uveal autoantigen with coiled-coil domains and anky	UACA	0,000346 391	-1,72232
NM_018028 // RefSeq // Homo sapiens sterile alpha motif domain containing 4B (SAMD4B),	SAMD4B	0,000527 89	-1,42244
NM_018060 // RefSeq // Homo sapiens isoleucyl-tRNA synthetase 2, mitochondrial (IARS2),	IARS2	0,000793 147	1,39318
NM_018113 // RefSeq // Homo sapiens limb region 1 homolog (mouse)-like (LMBR1L), mRNA.	LMBR1L	8,15E-07	-1,57303
NM_018115 // RefSeq // Homo sapiens SDA1 domain containing 1 (SDAD1), mRNA. // chr4 //	SDAD1	3,72E-05	1,62122
NM_018184 // RefSeq // Homo sapiens ADP-ribosylation factor-like 8B (ARL8B), mRNA. // c	ARL8B	6,87E-05	-1,34728
NM_018246 // RefSeq // Homo sapiens coiled-coil domain containing 25 (CCDC25), mRNA. //	CCDC25	0,000438 81	1,87372
NM_018259 // RefSeq // Homo sapiens tetratricopeptide repeat domain 17 (TTC17), mRNA. /	TTC17	0,000286 301	1,37035
NM_018352 // RefSeq // Homo sapiens translation machinery associated 16 homolog (S. cer	TMA16	3,90E-05	1,45216
NM_018374 // RefSeq // Homo sapiens transmembrane protein 106B (TMEM106B), transcript v	TMEM106B	2,75E-08	-1,46927
NM_018420 // RefSeq // Homo sapiens solute carrier family 22, member 15 (SLC22A15), mRN	SLC22A15	0,000349 26	-3,64877
NM_018490 // RefSeq // Homo sapiens leucine-rich repeat containing G protein-coupled re	LGR4	3,11E-05	2,4669
NM_018561 // RefSeq // Homo sapiens ubiquitin specific peptidase 49 (USP49), mRNA. // c	USP49	0,000113 383	-1,5503
NM_018602 // RefSeq // Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 4 (DNAJA4	DNAJA4	0,000396 672	-1,62023

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_018660 // RefSeq // Homo sapiens zinc finger protein 395 (ZNF395), mRNA. // chr8 //	ZNF395	0,000239 944	1,47923
NM_019028 // RefSeq // Homo sapiens zinc finger, DHHC-type containing 13 (ZDHHC13), tra	ZDHHC13	0,000493 147	-1,55561
NM_019088 // RefSeq // Homo sapiens Paf1, RNA polymerase II associated factor, homolog	PAF1	7,03E-07	-1,6404
NM_019104 // RefSeq // Homo sapiens lin-37 homolog (C. elegans) (LIN37), mRNA. // chr19	LIN37	0,000120 927	-1,52126
NM_019108 // RefSeq // Homo sapiens smg-9 homolog, nonsense mediated mRNA decay factor	SMG9	9,41E-05	-1,48116
NM_019556 // RefSeq // Homo sapiens motile sperm domain containing 1 (MOSPD1), mRNA. //	MOSPD1	0,000120 877	-2,02203
NM_020133 // RefSeq // Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 4 (lys	AGPAT4	0,000802 249	-1,6154
NM_020185 // RefSeq // Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. //	DUSP22	0,000724 319	1,60139
NM_020218 // RefSeq // Homo sapiens ataxin 7-like 3 (ATXN7L3), transcript variant 1, mR	ATXN7L3	2,11E-05	-1,32871
NM_020414 // RefSeq // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 (DDX24),	DDX24	0,000154 496	-1,37919
NM_020429 // RefSeq // Homo sapiens SMAD specific E3 ubiquitin protein ligase 1 (SMURF1	SMURF1	2,37E-05	1,56555
NM_020437 // RefSeq // Homo sapiens aspartate beta-hydroxylase domain containing 2 (ASP	ASPHD2	0,000482 138	2,51121
NM_020448 // RefSeq // Homo sapiens NIPA-like domain containing 3 (NIPAL3), mRNA. // ch	NIPAL3	2,86E-05	-1,65519
NM_020632 // RefSeq // Homo sapiens ATPase, H ⁺ -transporting, lysosomal V0 subunit a4 (A	ATP6V0A4	1,77E-05	-1,75119
NM_020664 // RefSeq // Homo sapiens 2,4-dienoyl CoA reductase 2, peroxisomal (DEC2R2), m	DEC2R2	6,51E-05	1,30586
NM_020765 // RefSeq // Homo sapiens ubiquitin protein ligase E3 component n-recogin 4	UBR4	0,000102 398	-1,40087
NM_020803 // RefSeq // Homo sapiens kelch-like 8 (Drosophila) (KLHL8), mRNA. // chr4 //	KLHL8	0,000232 071	1,82758
NM_020880 // RefSeq // Homo sapiens zinc finger protein 530 (ZNF530), mRNA. // chr19 //	ZNF530	0,000395 105	-1,35847
NM_021065 // RefSeq // Homo sapiens histone cluster 1, H2ad (HIST1H2AD), mRNA. // chr6	HIST1H2AD	0,000208 018	-2,15029
NM_021089 // RefSeq // Homo sapiens zinc finger protein 8 (ZNF8), mRNA. // chr19 // 100	ZNF8	2,03E-07	-1,57901
NM_021135 // RefSeq // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (	RPS6KA2	0,000760 68	-1,81987
NM_021167 // RefSeq // Homo sapiens GATA zinc finger domain containing 1 (GATAD1), tran	GATAD1	9,00E-05	1,22999
NM_021228 // RefSeq // Homo sapiens SR-related	SCAF1	0,000888	-1,40377

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
CTD-associated factor 1 (SCAF1), mRNA. /		645	
NM_021807 // RefSeq // Homo sapiens exocyst complex component 4 (EXOC4), transcript var	EXOC4	2,98E-05	1,52739
NM_021962 // RefSeq // Homo sapiens active BCR-related (ABR), transcript variant 1, mRN	ABR	0,000231115	1,53359
NM_021969 // RefSeq // Homo sapiens nuclear receptor subfamily 0, group B, member 2 (NR	NR0B2	0,000339648	2,05228
NM_021994 // RefSeq // Homo sapiens zinc finger protein 277 (ZNF277), mRNA. // chr7 //	ZNF277	3,51E-05	1,45306
NM_022071 // RefSeq // Homo sapiens SH2 domain containing 4A (SH2D4A), transcript varia	SH2D4A	2,08E-05	2,66162
NM_022081 // RefSeq // Homo sapiens Hermansky-Pudlak syndrome 4 (HPS4), transcript vari	HPS4	2,66E-06	1,40447
NM_022445 // RefSeq // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), transcript vari	TPK1	6,16E-06	2,57981
NM_022727 // RefSeq // Homo sapiens tRNA methyltransferase 2 homolog A (S. cerevisiae)	TRMT2A	4,16E-05	1,21513
NM_022746 // RefSeq // Homo sapiens mitochondrial amidoxime reducing component 1 (MARC1	MARC1	8,69E-07	2,2723
NM_022757 // RefSeq // Homo sapiens coiled-coil domain containing 14 (CCDC14), mRNA. //	CCDC14	0,000363066	1,34168
NM_022835 // RefSeq // Homo sapiens pleckstrin homology domain containing, family G (wi	PLEKHG2	0,000417527	-1,7062
NM_024090 // RefSeq // Homo sapiens ELOVL fatty acid elongase 6 (ELOVL6), transcript va	ELOVL6	0,00045942	1,86685
NM_024298 // RefSeq // Homo sapiens membrane bound O-acyltransferase domain containing	MBOAT7	0,000146738	-1,75347
NM_024321 // RefSeq // Homo sapiens RNA binding motif protein 42 (RBM42), mRNA. // chr1	RBM42	0,000394402	-1,33722
NM_024334 // RefSeq // Homo sapiens transmembrane protein 43 (TMEM43), mRNA. // chr3 //	TMEM43	0,000251036	-1,54047
NM_024546 // RefSeq // Homo sapiens ring finger protein 219 (RNF219), mRNA. // chr13 //	RNF219	0,000295069	1,55798
NM_024599 // RefSeq // Homo sapiens rhomboid 5 homolog 2 (Drosophila) (RHBDF2), transcr	RHBDF2	7,54E-05	-1,89983
NM_024620 // RefSeq // Homo sapiens zinc finger protein 329 (ZNF329), mRNA. // chr19 //	ZNF329	9,96E-05	-1,56211
NM_024682 // RefSeq // Homo sapiens TBC1 domain family, member 17 (TBC1D17), transcript	TBC1D17	3,50E-07	-1,61794
NM_024707 // RefSeq // Homo sapiens gem (nuclear organelle) associated protein 7 (GEMIN	GEMIN7	0,000106435	-1,60472
NM_024847 // RefSeq // Homo sapiens transmembrane channel-like 7 (TMC7), transcript var	TMC7	4,30E-05	1,53843
NM_024893 // RefSeq // Homo sapiens synapse differentiation inducing 1 (SYNDIG1), mRNA.	SYNDIG1	0,000865658	1,93541

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_025015 // RefSeq // Homo sapiens heat shock 70kDa protein 12A (HSPA12A), mRNA. // ch	HSPA12A	0,000652709	-2,08983
NM_025040 // RefSeq // Homo sapiens zinc finger protein 614 (ZNF614), mRNA. // chr19 //	ZNF614	6,23E-05	-2,08337
NM_030927 // RefSeq // Homo sapiens tetraspanin 14 (TSPAN14), transcript variant 1, mRN	TSPAN14	3,46E-06	-1,69729
NM_030972 // RefSeq // Homo sapiens zinc finger protein 611 (ZNF611), transcript varian	ZNF611	2,49E-05	-1,54955
NM_031271 // RefSeq // Homo sapiens testis expressed 15 (TEX15), mRNA. // chr8 // 100 /	TEX15	0,000189962	2,09968
NM_031415 // RefSeq // Homo sapiens gasdermin C (GSDMC), mRNA. // chr8 // 100 // 86 //	GSDMC	3,43E-05	-8,10653
NM_031417 // RefSeq // Homo sapiens MAP/microtubule affinity-regulating kinase 4 (MARK4	MARK4	5,37E-05	-1,50481
NM_031444 // RefSeq // Homo sapiens chromosome 22 open reading frame 13 (C22orf13), mRN	C22orf13	0,000463429	1,26404
NM_031485 // RefSeq // Homo sapiens glutamate-rich WD repeat containing 1 (GRWD1), mRNA	GRWD1	0,000329926	-1,36462
NM_031905 // RefSeq // Homo sapiens armadillo repeat containing 10 (ARMC10), transcript	ARMC10	1,79E-06	1,56017
NM_031908 // RefSeq // Homo sapiens C1q and tumor necrosis factor related protein 2 (C1	C1QTNF2	5,01E-05	-1,37685
NM_032211 // RefSeq // Homo sapiens lysyl oxidase-like 4 (LOXL4), mRNA. // chr10 // 100	LOXL4	5,16E-06	-2,21943
NM_032217 // RefSeq // Homo sapiens ankyrin repeat domain 17 (ANKRD17), transcript vari	ANKRD17	2,20E-05	1,46788
NM_032283 // RefSeq // Homo sapiens zinc finger, DHHC-type containing 18 (ZDHHC18), mRN	ZDHHC18	0,000729905	-1,57247
NM_032409 // RefSeq // Homo sapiens PTEN induced putative kinase 1 (PINK1), nuclear gen	PINK1	9,10E-05	-2,04163
NM_032410 // RefSeq // Homo sapiens hook homolog 3 (Drosophila) (HOOK3), mRNA. // chr8	HOOK3	7,92E-05	-1,42225
NM_032442 // RefSeq // Homo sapiens neuralized homolog 4 (Drosophila) (NEURL4), transcr	NEURL4	9,19E-05	-1,29159
NM_032515 // RefSeq // Homo sapiens BCL2-related ovarian killer (BOK), mRNA. // chr2 //	BOK	0,000623475	-1,65855
NM_032530 // RefSeq // Homo sapiens zinc finger protein 594 (ZNF594), mRNA. // chr17 //	ZNF594	0,000102382	-1,57187
NM_032549 // RefSeq // Homo sapiens IMP2 inner mitochondrial membrane peptidase-like (S	IMMP2L	8,61E-06	1,81822
NM_032792 // RefSeq // Homo sapiens zinc finger and BTB domain containing 45 (ZBTB45),	ZBTB45	0,000160789	-1,49652
NM_032813 // RefSeq // Homo sapiens transmembrane and tetratricopeptide repeat containi	TMTC4	0,000822269	1,66863

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_032836 // RefSeq // Homo sapiens FLT3-interacting zinc finger 1 (FIZ1), mRNA. // chr	FIZ1	0,000515 313	-1,34828
NM_032861 // RefSeq // Homo sapiens serine active site containing 1 (SERAC1), mRNA. //	SERAC1	6,05E-05	-1,52789
NM_032999 // RefSeq // Homo sapiens general transcription factor Ili (GTF2I), transcrip	GTF2I	0,000214 966	1,27657
NM_033017 // RefSeq // Homo sapiens tripartite motif containing 4 (TRIM4), transcript v	TRIM4	8,60E-05	1,3946
NM_033141 // RefSeq // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (M	MAP3K9	0,000380 881	-2,72236
NM_033625 // RefSeq // Homo sapiens ribosomal protein L34 (RPL34), transcript variant 2	RPL34	2,20E-05	1,67708
NM_052883 // RefSeq // Homo sapiens thioredoxin reductase 3 (TXNRD3), transcript varian	TXNRD3	8,39E-05	1,63902
NM_053282 // RefSeq // Homo sapiens SH2 domain containing 1B (SH2D1B), mRNA. // chr1 //	SH2D1B	0,000887 864	-1,67602
NM_054013 // RefSeq // Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acety	MGAT4B	2,62E-05	1,47036
NM_133178 // RefSeq // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTP	PTPRU	7,58E-05	-2,43936
NM_133502 // RefSeq // Homo sapiens zinc finger protein 274 (ZNF274), transcript varian	ZNF274	0,000215 353	-1,41605
NM_138374 // RefSeq // Homo sapiens zinc finger protein 845 (ZNF845), mRNA. // chr19 //	ZNF845	0,000396 171	-1,22981
NM_138392 // RefSeq // Homo sapiens SH3KBP1 binding protein 1 (SHKBP1), mRNA. // chr19	SHKBP1	0,000130 387	-1,70089
NM_138439 // RefSeq // Homo sapiens FLYWCH family member 2 (FLYWCH2), transcript varian	FLY-WCH2	0,000103 143	-1,3144
NM_138639 // RefSeq // Homo sapiens BCL2-like 12 (proline rich) (BCL2L12), transcript v	BCL2L12	0,000236 635	-1,29172
NM_138806 // RefSeq // Homo sapiens CD200 receptor 1 (CD200R1), transcript variant 1, m	CD200R1	4,66E-05	-1,3429
NM_138809 // RefSeq // Homo sapiens carboxy-methylenebutenolidase homolog (Pseudomonas)	CMBL	1,77E-06	2,74107
NM_139163 // RefSeq // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromoso	ALS2CR1 2	0,000403 151	-1,87959
NM_139165 // RefSeq // Homo sapiens retinoic acid early transcript 1E (RAET1E), transcr	RAET1E	0,000382 797	-1,68602
NM_139239 // RefSeq // Homo sapiens nuclear factor of kappa light polypeptide gene enha	NFKBID	0,000401 81	-1,25134
NM_144643 // RefSeq // Homo sapiens sodium channel and clathrin linker 1 (SCLT1), mRNA.	SCLT1	4,36E-05	1,47543
NM_144680 // RefSeq // Homo sapiens zinc finger protein 18 (ZNF18), mRNA. // chr17 // 1	ZNF18	0,000451 991	-1,4086
NM_145249 // RefSeq // Homo sapiens interferon,	IFI27L1	0,000435	-1,37161

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
alpha-inducible protein 27-like 1 (IFI2		565	
NM_145260 // RefSeq // Homo sapiens odd-skipped related 1 (Drosophila) (OSR1), mRNA. //	OSR1	0,000118411	-1,37549
NM_145792 // RefSeq // Homo sapiens microsomal glutathione S-transferase 1 (MGST1), tra	MGST1	6,76E-05	1,50692
NM_152244 // RefSeq // Homo sapiens sorting nexin 11 (SNX11), transcript variant 1, mRN	SNX11	0,000714939	-1,28327
NM_152262 // RefSeq // Homo sapiens zinc finger protein 439 (ZNF439), mRNA. // chr19 //	ZNF439	0,000790075	-1,59248
NM_152292 // RefSeq // Homo sapiens tRNA methyl-transferase 10 homolog A (S. cerevisiae)	TRMT10A	0,000649916	1,37031
NM_152336 // RefSeq // Homo sapiens ATP/GTP binding protein-like 1 (AGBL1), mRNA. // ch	AGBL1	0,000460694	1,29346
NM_152458 // RefSeq // Homo sapiens zinc finger protein 785 (ZNF785), mRNA. // chr16 //	ZNF785	0,000139475	1,23971
NM_152540 // RefSeq // Homo sapiens sec1 family domain containing 2 (SCFD2), mRNA. // c	SCFD2	2,13E-06	1,55505
NM_152730 // RefSeq // Homo sapiens chromosome 6 open reading frame 170 (C6orf170), mRN	C6orf170	3,90E-05	-1,84595
NM_153213 // RefSeq // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 19 (AR	ARHGEF19	0,000854193	-1,51734
NM_153230 // RefSeq // Homo sapiens F-box protein 39 (FBXO39), mRNA. // chr17 // 100 //	FBXO39	8,19E-05	-1,29957
NM_153267 // RefSeq // Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. // chr9 //	MAMDC2	0,000475674	-2,24897
NM_153373 // RefSeq // Homo sapiens alanine-glyoxylate aminotransferase 2-like 2 (AGXT2	AGXT2L2	4,42E-07	1,48762
NM_153690 // RefSeq // Homo sapiens family with sequence similarity 43, member A (FAM43	FAM43A	4,77E-08	-2,59262
NM_170732 // RefSeq // Homo sapiens brain-derived neurotrophic factor (BDNF), transcrip	BDNF	0,000681043	-1,79376
NM_172195 // RefSeq // Homo sapiens eukaryotic translation initiation factor 2B, subuni	EIF2B4	0,000878249	-1,46683
NM_173505 // RefSeq // Homo sapiens ankyrin repeat domain 29 (ANKRD29), mRNA. // chr18	ANKRD29	0,000654302	3,60246
NM_174898 // RefSeq // Homo sapiens lysozyme G-like 1 (LYG1), mRNA. // chr2 // 100 // 1	LYG1	4,19E-05	-1,36589
NM_175875 // RefSeq // Homo sapiens SIX homeobox 5 (SIX5), mRNA. // chr19 // 100 // 90	SIX5	2,33E-06	-1,20606
NM_178562 // RefSeq // Homo sapiens tetraspanin 33 (TSPAN33), mRNA. // chr7 // 100 // 8	TSPAN33	0,000272558	1,6253
NM_178566 // RefSeq // Homo sapiens zinc finger, DHHC-type containing 21 (ZDHHC21), mRN	ZDHHC21	0,000331668	-1,43307
NM_178820 // RefSeq // Homo sapiens F-box protein 27 (FBXO27), mRNA. // chr19 // 100 //	FBXO27	0,000747319	-2,52259

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_182691 // RefSeq // Homo sapiens SRSF protein kinase 2 (SRPK2), transcript variant 2	SRPK2	3,74E-05	1,52103
NM_182703 // RefSeq // Homo sapiens ankyrin repeat and death domain containing 1A (ANKD1A)	ANKD1A	0,000361769	-1,2451
NM_182776 // RefSeq // Homo sapiens minichromosome maintenance complex component 7 (MCM7)	MCM7	0,000545722	1,62408
NM_194071 // RefSeq // Homo sapiens cAMP responsive element binding protein 3-like 2 (CREB3L2)	CREB3L2	9,16E-05	-1,8041
NM_198467 // RefSeq // Homo sapiens round spermatid basic protein 1-like (RSBN1L), mRNA	RSBN1L	1,11E-09	1,60102
NM_198489 // RefSeq // Homo sapiens coiled-coil domain containing 84 (CCDC84), mRNA. //	CCDC84	0,000713857	-1,42244
NM_198562 // RefSeq // Homo sapiens chromosome 3 open reading frame 62 (C3orf62), mRNA.	C3orf62	0,000103136	-1,70768
NM_198686 // RefSeq // Homo sapiens RAB15, member RAS oncogene family (RAB15), mRNA. //	RAB15	0,000218391	-2,55595
NM_198850 // RefSeq // Homo sapiens pleckstrin homology-like domain, family B, member 3 (PHLDB3)	PHLDB3	0,00058687	-1,88141
NM_199320 // RefSeq // Homo sapiens PHD finger protein 17 (PHF17), transcript variant L	PHF17	6,05E-05	1,89743
NM_205853 // RefSeq // Homo sapiens musculoskeletal, embryonic nuclear protein 1 (MUSTN1)	MUSTN1	6,73E-05	-1,36668
NM_207113 // RefSeq // Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter) (SLC37A3)	SLC37A3	6,52E-05	1,53532
NM_207351 // RefSeq // Homo sapiens proline-rich transmembrane protein 3 (PRRT3), mRNA.	PRRT3	0,000258606	-1,27858
NM_212550 // RefSeq // Homo sapiens biogenesis of lysosomal organelles complex-1, subunit 3 (BLOC1S3)	BLOC1S3	6,16E-05	-1,3341
NM_212559 // RefSeq // Homo sapiens XK, Kell blood group complex subunit-related, X-linked (XKRX)	XKRX	0,000376005	-2,04521
NM_213598 // RefSeq // Homo sapiens zinc finger protein 543 (ZNF543), mRNA. // chr19 //	ZNF543	3,79E-05	-1,55628
NR_002785 // RefSeq // Homo sapiens GNAS antisense RNA 1 (non-protein coding) (GNAS-AS1)	GNAS-AS1	4,85E-06	4,20833
NR_002806 // RefSeq // Homo sapiens FAM13A antisense RNA 1 (non-protein coding) (FAM13A-AS1)	FAM13A-AS1	1,39E-07	1,43629
NR_002911 // RefSeq // Homo sapiens small nucleolar RNA, H/ACA box 71A (SNORA71A), small	SNORA71A	9,30E-05	1,75134
NR_002941 // RefSeq // Homo sapiens phosphatidylethanolamine-binding protein 3 pseudogene (LOC285359), non-coding	LOC285359	0,000350562	-1,44857
NR_003014 // RefSeq // Homo sapiens small nucleolar RNA, H/ACA box 47 (SNORA47), small	SNORA47	0,000797356	2,14719
NR_003529 // RefSeq // Homo sapiens CDKN2B antisense RNA 1 (non-protein coding) (CDKN2B-AS1)	CDKN2B-AS1	0,000591483	-3,02225
NR_015379 // RefSeq // Homo sapiens urothelial carcinoma (UCA1)	UCA1	0,000543	-2,31695

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
cer associated 1 (non-protein coding)		923	
NR_024063 // RefSeq // Homo sapiens zinc finger and SCAN domain containing 12 pseudogen	ZSCAN12P1	0,00023091	-2,35094
NR_024170 // RefSeq // Homo sapiens late endosomal/lysosomal adaptor, MAPK and MTOR act	LAM-TOR3	0,000153994	1,80448
NR_024176 // RefSeq // Homo sapiens MAP kinase interacting serine/threonine kinase 1 (M	MKNK1	6,66E-06	-1,59683
NR_024178 // RefSeq // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	LOC284100	0,000267456	1,79347
NR_024199 // RefSeq // Homo sapiens Cbl proto-oncogene, E3 ubiquitin protein ligase-lik	CBLL1	8,31E-05	1,31022
NR_024322 // RefSeq // Homo sapiens male-specific lethal 3 homolog (Drosophila) pseudog	MSL3P1	0,000268237	-1,67614
NR_024554 // RefSeq // Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), tran	RHOBTB1	7,69E-08	2,75759
NR_024618 // RefSeq // Homo sapiens uncharacterized LOC100129550 (LOC100129550), non-co	LOC100129550	0,000410664	-1,51029
NR_026052 // RefSeq // Homo sapiens CENPB DNA-binding domains containing 1 pseudogene (	MGC2752	0,000313693	-1,33581
NR_026583 // RefSeq // Homo sapiens Rac GTPase activating protein 1 pseudogene (RACGAP1	RACGAP1P	0,000882981	1,24476
NR_026650 // RefSeq // Homo sapiens biphenyl hydrolase-like (serine hydrolase) (BPHL),	BPHL	0,000157942	1,99326
NR_026778 // RefSeq // Homo sapiens HNRNPU antisense RNA 1 (non-protein coding) (HNRNPU	HNRNPU-AS1	5,39E-06	1,75828
NR_026865 // RefSeq // Homo sapiens chromosome 7 open reading frame 13 (C7orf13), non-c	C7orf13	3,85E-05	1,73876
NR_026892 // RefSeq // Homo sapiens AFAP1 antisense RNA 1 (non-protein coding) (AFAP1-A	AFAP1-AS1	0,000535337	3,15772
NR_026921 // RefSeq // Homo sapiens chromosome 5 open reading frame 25 pseudogene (LOC2	LOC202181	0,000132	5,93496
NR_027003 // RefSeq // Homo sapiens uncharacterized LOC93429 (DKFZp434J0226), non-codin	DKFZp434J0226	0,000714032	-1,93606
NR_027107 // RefSeq // Homo sapiens uncharacterized LOC90768 (MGC45800), non-coding RNA	MGC45800	0,000466578	1,34131
NR_027280 // RefSeq // Homo sapiens SUMO1 activating enzyme subunit 1 (SAE1), transcrip	SAE1	0,000790559	-1,38962
NR_027774 // RefSeq // Homo sapiens pleckstrin homology domain containing, family M (wi	PLEKHM1	0,000102552	-1,56662
NR_028090 // RefSeq // Homo sapiens uncharacterized LOC202781 (LOC202781), non-coding R	LOC202781	3,81E-07	1,71214
NR_028103 // RefSeq // Homo sapiens DDB1 and CUL4 associated factor 8 (DCAF8), transcri	DCAF8	0,000487055	1,28223
NR_028459 // RefSeq // Homo sapiens ataxin 3 (ATXN3), transcript variant m, non-coding	ATXN3	0,000582436	-1,37831

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NR_029636 // RefSeq // Homo sapiens microRNA 222 (MIR222), microRNA. // chrX // 100 //	MIR222	0,000719 859	-2,35412
NR_029886 // RefSeq // Homo sapiens microRNA 330 (MIR330), microRNA. // chr19 // 100 //	MIR330	0,000391 606	-1,21744
NR_030255 // RefSeq // Homo sapiens microRNA 455 (MIR455), microRNA. // chr9 // 100 //	MIR455	0,000773 182	1,44537
NR_030365 // RefSeq // Homo sapiens microRNA 635 (MIR635), microRNA. // chr17 // 100 //	MIR635	0,000549 592	-2,20312
NR_030598 // RefSeq // Homo sapiens microRNA 708 (MIR708), microRNA. // chr11 // 100 //	MIR708	0,000152 35	3,66493
NR_031611 // RefSeq // Homo sapiens microRNA 1206 (MIR1206), microRNA. // chr8 // 100 //	MIR1206	5,51E-06	-7,06005
NR_033248 // RefSeq // Homo sapiens glycine cleavage system protein H (aminomethyl carr	GCSHP3	3,60E-06	-1,61256
NR_033322 // RefSeq // Homo sapiens NOP2/Sun domain family, member 5 pseudogene 1 (NSUN	NSUN5P1	0,000397 788	1,34196
NR_033396 // RefSeq // Homo sapiens solute carrier family 22, member 20 (SLC22A20), tra	SLC22A20	0,000420 652	-1,82501
NR_033646 // RefSeq // Homo sapiens lipase maturation factor 1 (LMF1), transcript varia	LMF1	0,000844 324	1,64505
NR_033829 // RefSeq // Homo sapiens MIR4500 host gene (non-protein coding) (MIR4500HG),	MIR4500HG	1,18E-05	-2,597
NR_033897 // RefSeq // Homo sapiens EPHA1 antisense RNA 1 (non-protein coding) (EPHA1-A	EPHA1-AS1	0,000447 922	-1,44666
NR_033914 // RefSeq // Homo sapiens long intergenic non-protein coding RNA 254 (LINC002	LINC00254	0,000486 907	1,24413
NR_033957 // RefSeq // Homo sapiens uncharacterized LOC643650 (LOC643650), non-coding R	LOC643650	0,000482 995	-2,40882
NR_034146 // RefSeq // Homo sapiens sirtuin 2 (SIRT2), transcript variant 4, non-coding	SIRT2	0,000270 408	-1,22398
NR_036639 // RefSeq // Homo sapiens Yip1 domain family, member 1 (YIPF1), transcript va	YIPF1	0,000103 1	-1,53376
NR_037606 // RefSeq // Homo sapiens mitochondrial ribosomal protein S14 (MRPS14), trans	MRPS14	0,000377 113	1,2155
NR_037638 // RefSeq // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside	SLC28A3	0,000398 623	-3,61015
NR_037897 // RefSeq // Homo sapiens uncharacterized LOC386627 (FLJ38109), non-coding RN	FLJ38109	8,47E-06	1,33859
NR_038064 // RefSeq // Homo sapiens perilipin 2 (PLIN2), transcript variant 2, non-codi	PLIN2	4,56E-05	-1,81769
NR_038125 // RefSeq // Homo sapiens capping protein (actin filament) muscle Z-line, bet	CAPZB	0,000359 775	-1,30811
NR_038221 // RefSeq // Homo sapiens uncharacterized LOC201617 (LOC201617), non-coding R	LOC201617	0,000749 039	1,26238
NR_038340 // RefSeq // Homo sapiens uncharacter-	LOC1005	0,000387	-16,657

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ized LOC100505817 (LOC100505817), non-co	05817	011	
NR_038835 // RefSeq // Homo sapiens uncharacterized LOC645249 (LOC645249), non-coding R	LOC645249	0,000103643	1,34015
NR_039722 // RefSeq // Homo sapiens microRNA 4500 (MIR4500), microRNA. // chr13 // 100	MIR4500	5,51E-09	-27,9959
NR_039969 // RefSeq // Homo sapiens microRNA 5047 (MIR5047), microRNA. // chr17 // 100	MIR5047	0,000597691	-1,54287
NR_040001 // RefSeq // Homo sapiens uncharacterized LOC375295 (LOC375295), non-coding R	LOC375295	0,000516498	3,81932
NR_040006 // RefSeq // Homo sapiens cleft lip and palate associated transmembrane prote	CLPTM1	1,36E-06	-1,61167
NR_046008 // RefSeq // Homo sapiens zinc finger, matrin-type 1 (ZMAT1), transcript vari	ZMAT1	0,000253172	3,70656
NR_046088 // RefSeq // Homo sapiens uncharacterized LOC729987 (LOC729987), non-coding R	LOC729987	0,000314965	3,06482
NR_046224 // RefSeq // Homo sapiens uncharacterized LOC100652730 (LOC100652730), transc	LOC100652730	0,000245568	1,43106
NR_046240 // RefSeq // Homo sapiens uncharacterized LOC100506100 (LOC100506100), non-co	LOC100506100	1,24E-07	-1,83546
NR_046793 // RefSeq // Homo sapiens RPS6KA2 intronic transcript 1 (non-protein coding)	RPS6KA2-IT1	0,00044991	-1,69521
NR_046824 // RefSeq // Homo sapiens EPN2 intronic transcript 1 (non-protein coding) (EP	EPN2-IT1	0,000425865	-1,47957
TCONS_00000159-XLOC_000068 // Rinn lincRNA // linc-PAD11-1 chr1+:17516277-17524112 //	LOC400743	3,53E-06	-1,40789
TCONS_00000159-XLOC_000068 // Rinn lincRNA // linc-PAD11-1 chr1+:17516277-17524112 //	LOC400743	7,34E-06	-1,42537
TCONS_00001037-XLOC_000302 // Rinn lincRNA // linc-SLC44A3-2 chr1+:95007607-95008571 //		1,96E-06	-4,13922
TCONS_00001448-XLOC_000771 // Rinn lincRNA // linc-FABP3-2 chr1:-:31933167-31944351 //		0,000588915	-1,67127
TCONS_00001550-XLOC_000893 // Rinn lincRNA // linc-TTL7-6 chr1:-:84920351-84924713 //		0,000371881	-1,21769
TCONS_00001926-XLOC_000031 // Rinn lincRNA // linc-AJAP1-5 chr1+:4037027-4058260 // ch		0,000307348	1,21471
TCONS_00003039-XLOC_001728 // Rinn lincRNA // linc-PSMD14 chr2+:162101265-162103965 //		0,000390421	-2,76654
TCONS_00003057-XLOC_001765 // Rinn lincRNA // linc-HNRNPA3-4 chr2+:177502437-177520686		0,000561159	1,75699
TCONS_00004099-XLOC_001948 // Rinn lincRNA // linc-MYT1L-2 chr2:-:2886699-2898250 // ch		0,000635893	1,2547
TCONS_00004125-XLOC_001971 // Rinn lincRNA // linc-CMPK2-5 chr2:-:8007543-8009432 // ch		0,000616141	1,40959
TCONS_00005559-XLOC_002736 // Rinn lincRNA // linc-COL8A1-3 chr3+:98699901-98701940 //		0,000423396	-16,4077

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
TCONS_00005633-XLOC_002891 // Rinn lincRNA // linc-PTX3-5 chr3:+:156799629-156806336 //		0,000536452	-1,28956
TCONS_00007505-XLOC_003499 // Rinn lincRNA // linc-DTHD1-7 chr4:+:32352659-32354842 //		0,000755516	1,28673
TCONS_00007610-XLOC_003680 // Rinn lincRNA // linc-FAT4-3 chr4:+:124426433-124448680 //		0,000808553	1,61816
TCONS_00008202-XLOC_003656 // Rinn lincRNA // linc-NDST3-5 chr4:+:116102448-116191383 /		2,43E-06	1,36186
TCONS_00008471-XLOC_003934 // Rinn lincRNA // linc-APBB2-3 chr4:-:41222114-41223379 //		4,17E-05	1,24977
TCONS_00009717-XLOC_004914 // Rinn lincRNA // linc-CCNH-1 chr5:-:87008951-87029086 // c		3,91E-05	-1,37898
TCONS_00009795-XLOC_005037 // Rinn lincRNA // linc-NR3C1 chr5:-:142869419-142910915 //		0,000640911	1,22263
TCONS_00010319-XLOC_004802 // Rinn lincRNA // linc-SEPP1-2 chr5:-:42918465-42920126 //		0,000542759	-1,81594
TCONS_00010320-XLOC_004803 // Rinn lincRNA // linc-SEPP1-3 chr5:-:42985139-42992726 //	FLJ32255	0,000345075	-2,77265
TCONS_00010376-XLOC_004879 // Rinn lincRNA // linc-ZNF366-6 chr5:-:72408840-72413568 //		0,000515921	1,81771
TCONS_00012358-XLOC_005917 // Rinn lincRNA // linc-PDE10A-1 chr6:-:166253091-166253578		0,000646916	1,21054
TCONS_00014650-XLOC_006740 // Rinn lincRNA // linc-RHOBTB2-1 chr8:+:22808335-22814153 /		0,000637075	1,33522
TCONS_00014681-XLOC_006779 // Rinn lincRNA // linc-C8orf4-2 chr8:+:39891375-39891902 //		0,00061212	1,3039
TCONS_00014909-XLOC_006976 // Rinn lincRNA // linc-ERICH1-4 chr8:-:1741067-1744122 // c		0,000275069	1,27392
TCONS_00015946-XLOC_007323 // Rinn lincRNA // linc-PRSS3-4 chr9:+:33583982-33585615 //		0,000863093	-1,82072
TCONS_00016159-XLOC_007570 // Rinn lincRNA // linc-STXBP1-2 chr9:+:130342615-130343098		4,15E-05	-2,51168
TCONS_00016465-XLOC_007830 // Rinn lincRNA // linc-C9orf80 chr9:-:115505050-115512795 /		0,00015219	1,35857
TCONS_00016665-XLOC_007505 // Rinn lincRNA // linc-ACTL7A-11 chr9:+:110100226-110101430		0,000788805	-1,36119
TCONS_00018677-XLOC_008381 // Rinn lincRNA // linc-GATA3-1 chr10:+:8093126-8094726 // c		0,000297137	-1,30622
TCONS_00020348-XLOC_009679 // Rinn lincRNA // linc-PLEKHA5-2 chr12:+:18906532-18926324		4,82E-05	2,30686
TCONS_00020678-XLOC_009983 // Rinn lincRNA // linc-PARP11-1 chr12:-:4017194-4029987 //		0,000109318	1,31993
TCONS_00020723-XLOC_010023 // Rinn lincRNA // linc-GUCY2C chr12:-:14898793-14903603 //		8,63E-05	-3,44753
TCONS_00021677-XLOC_010682 // Rinn lincRNA // linc-		0,000227	-1,79851

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
SLITRK6-7 chr13:-:88079468-88080528		162	
TCONS_00022382-XLOC_011104 // Rinn lincRNA // linc-TRIP11 chr14:-:92511119-92516990 //		0,000582 973	-2,24763
TCONS_00022775-XLOC_011059 // Rinn lincRNA // linc-C14orf181 chr14:-:69283615-69284659		0,000479 353	-1,24444
TCONS_00023282-XLOC_011521 // Rinn lincRNA // linc-TLE3-1 chr15:-:70863297-70878945 //		5,62E-05	-1,56672
TCONS_00023504-XLOC_011348 // Rinn lincRNA // linc-CRTC3 chr15+:91061799-91068340 // c		0,000439 486	-1,60682
TCONS_00023631-XLOC_011430 // Rinn lincRNA // linc-MEIS2-4 chr15:-:38363067-38365188 //		7,46E-05	1,48546
TCONS_00023687-XLOC_011486 // Rinn lincRNA // linc-ALDH1A2-1 chr15:-:58572414-58576475		0,000596 414	-4,40333
TCONS_00025120-XLOC_012197 // Rinn lincRNA // linc-TMEM99-4 chr17+:38673277-38683253 /		0,000355 171	-1,51121
TCONS_00026909-XLOC_012981 // Rinn lincRNA // linc-OR10H4 chr19+:15945758-15946461 //		0,000515 535	-9,62033
TCONS_00028551-XLOC_013534 // Rinn lincRNA // linc-WFDC2-2 chr20+:44058263-44077210 //	LOC1001 30157	9,64E-05	-1,22992
TCONS_00029009-XLOC_013932 // Rinn lincRNA // linc-CHAF1B chr21+:37756424-37757219 //	MORC3	0,000401 113	-1,46957
TCONS_00029062-XLOC_013983 // Rinn lincRNA // linc-COL18A1-2 chr21+:46767516-46773433		5,55E-05	1,35484
TCONS_00029585-XLOC_014219 // Rinn lincRNA // linc-RASD2 chr22+:35846033-35851349 // c		2,07E-05	1,67681
TCONS_I2_00004768-XLOC_I2_002469 // Broad TUCP // linc-NCAM1-3 chr11+:112161097-112164	LOC2831 40	0,000821 801	1,43834
TCONS_I2_00007341-XLOC_I2_004113 // Broad TUCP // linc-GRTP1 chr13:-:114053726-11406528	DKFZp45 1A211	5,80E-06	-1,25913
TCONS_I2_00009421-XLOC_I2_004598 // Broad TUCP // linc-ARHGAP11B-6 chr15+:29967193-299	LOC1001 30111	4,13E-08	2,06385
TCONS_I2_00016247-XLOC_I2_008622 // Broad TUCP // linc-SLC32A1 chr20+:37230530-3727925	ARHGAP 40	3,66E-05	-2,80957
TCONS_I2_00017147-XLOC_I2_009139 // Broad TUCP // linc-SAMSN1-3 chr21:-:16189150-162300		0,000375 346	-1,77573
TCONS_I2_00020756-XLOC_I2_010831 // Broad TUCP // linc-PHF17-2 chr4+:129387804-1294405		0,000748 312	2,80774
TCONS_I2_00021702-XLOC_I2_010831 // Broad TUCP // linc-PHF17-2 chr4+:129349224-1294405		0,000335 994	2,45244
TCONS_I2_00025074-XLOC_I2_012365 // Broad TUCP // linc-PECI-BP chr6+:4136305-4157619 /	LOC1005 07506	0,000455 314	1,36554
TCONS_I2_00025502-XLOC_I2_013149 // Broad TUCP // linc-HIVEP2-2 chr6:-:143360561-143363		0,000171 428	-1,9421
TCONS_I2_00030323-XLOC_I2_015593 // Broad TUCP // linc-PRPS1 chrX+:106773651-106848480	FRMPD3	0,000409 836	-1,88413

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
XR_111249 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100509976 (LOC100509976)	LOC100509976	0,000680072	-2,00309
XR_111788 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100505529 (LOC100505529)	LOC100505529	5,83E-05	-1,25515
XR_111837 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100507503 (LOC100507503)	LOC100507503	0,000259017	1,40679
XR_133191 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100653303 (LOC100653303)	LOC100653303	0,000546361	1,20938

Table 7: Efficiency of docetaxel

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_002727 // RefSeq // Homo sapiens serglycin (SRGN), transcript variant 1, mRNA. // ch	SRGN	0,00010316	-8,6479
NM_002531 // RefSeq // Homo sapiens neurotensin receptor 1 (high affinity) (NTSR1), mRN	NTSR1	0,000157721	-5,10623
NM_019029 // RefSeq // Homo sapiens carboxypeptidase, vitellogenic-like (CPVL), transcr	CPVL	4,07E-05	-3,87573
NM_015278 // RefSeq // Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. // c	SASH1	5,49E-05	-3,06266
ENST00000467369 // ENSEMBL // cdna:known chromosome:GRCh37:6:31430962:31445283:1 gene:E	HCP5	2,30E-05	-3,0544
NM_052916 // RefSeq // Homo sapiens ring finger protein 157 (RNF157), mRNA. // chr17 //	RNF157	5,21E-05	-2,80706
NM_001142386 // RefSeq // Homo sapiens pyruvate dehydrogenase kinase, isozyme 3 (PDK3),	PDK3	9,45E-05	-2,78885
NM_006623 // RefSeq // Homo sapiens phosphoglycerate dehydrogenase (PHGDH), mRNA. // ch	PHGDH	1,24E-06	-2,68742
NM_001002236 // RefSeq // Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 ant	SERPIN A1	0,000176717	-2,6201
OTTHUMT00000370461 // Havana transcript // cdna:all chromosome:VEGA52:5:90522292:905228	OTTHUMG0000162808	0,000123488	-2,61951
NM_001199324 // RefSeq // Homo sapiens zinc finger protein 615 (ZNF615), transcript var	ZNF615	3,33E-05	-2,60408
NR_029636 // RefSeq // Homo sapiens microRNA 222 (MIR222), microRNA. // chrX // 100 //	MIR222	0,000164313	-2,53655
ENST00000369562 // ENSEMBL // cdna:known chromosome:GRCh37:6:88117701:88174183:1 gene:E	C6orf165	3,55E-05	-2,44894
ENST00000263056 // ENSEMBL // cdna:known chromosome:GRCh37:10:30722866:30750761:1	MAP3K8	0,000203356	-2,36483

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
gene:			
NM_001010892 // RefSeq // Homo sapiens radial spoke head 4 homolog A (Chlamydomonas) (R	RSPH4A	0,000147188	-2,33328
ENST00000279488 // ENSEMBL // cdna:known chromosome:GRCh37:12:89741009:89747048:-1 gene	DUSP6	3,88E-06	-2,25701
NM_001127899 // RefSeq // Homo sapiens chloride channel, voltage-sensitive 5 (CLCN5), t	CLCN5	4,48E-05	-2,21887
NM_025145 // RefSeq // Homo sapiens WD repeat domain 96 (WDR96), mRNA. // chr10 // 100	WDR96	3,56E-05	-2,20641
NM_024763 // RefSeq // Homo sapiens WD repeat domain 78 (WDR78), transcript variant 1,	WDR78	4,79E-07	-2,20452
NM_000784 // RefSeq // Homo sapiens cytochrome P450, family 27, subfamily A, polypeptid	CYP27A1	0,000133547	-2,2037
NR_027263 // RefSeq // Homo sapiens ARHGAP5 antisense RNA 1 (head to head) (ARHGAP5-AS1	ARHGAP5-AS1	1,40E-05	-2,20004
n366450 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		3,88E-05	-2,18667
n376497 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		1,03E-05	-2,16336
NM_007220 // RefSeq // Homo sapiens carbonic anhydrase VB, mitochondrial (CA5B), nuclea	CA5B	1,38E-06	-2,12654
NM_030964 // RefSeq // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), transcript	SPRY4	6,98E-05	-2,11768
ENST00000356031 // ENSEMBL // cdna:known chromosome:GRCh37:5:35617946:35814713:1 gene:E	SPEF2	1,16E-05	-2,07984
NM_182540 // RefSeq // Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B (D	DDX26B	1,05E-07	-2,07652
NM_001080850 // RefSeq // Homo sapiens coiled-coil domain containing 30 (CCDC30), mRNA.	CCDC30	2,37E-05	-2,06986
NM_005842 // RefSeq // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. // ch	SPRY2	7,50E-05	-2,05999
NM_194318 // RefSeq // Homo sapiens beta 1,3-galactosyltransferase-like (B3GALT), mRNA	B3GALT L	9,16E-06	-2,01518
ENST00000492422 // ENSEMBL // cdna:known chromosome:GRCh37:1:42929593:42939231:1 gene:E	CCDC30	0,000123017	-1,9016
NM_021979 // RefSeq // Homo sapiens heat shock 70kDa protein 2 (HSPA2), mRNA. // chr14	HSPA2	2,21E-05	-1,88733
NM_020962 // RefSeq // Homo sapiens immunoglobulin superfamily, DCC subclass, member 4	IGDCC4	3,25E-05	-1,82229
NR_038380 // RefSeq // Homo sapiens SLC7A11 antisense RNA 1 (SLC7A11-AS1), non-coding R	SLC7A11-AS1	4,65E-05	-1,80631
NM_000124 // RefSeq // Homo sapiens excision re-	ERCC6	6,13E-05	-1,80348

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
pair cross-complementing rodent repair d			
NM_017950 // RefSeq // Homo sapiens coiled-coil domain containing 40 (CCDC40), transcri	CCDC40	1,74E-05	-1,7932
n375630 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		0,000123 988	-1,77963
NM_001099287 // RefSeq // Homo sapiens NIPA-like domain containing 4 (NIPAL4), transcri	NIPAL4	0,000141 498	-1,76541
NR_003021 // RefSeq // Homo sapiens small nucleolar RNA, H/ACA box 79 (SNORA79), small	SNORA79	4,28E-06	-1,75966
NM_174890 // RefSeq // Homo sapiens zinc finger, AN1-type domain 4 (ZFAND4), transcript	ZFAND4	3,99E-05	-1,75147
ENST00000381501 // ENSEMBL // cdna:known chromosome:GRCh37:4:48137800:48271881:-1 gene:	TEC	0,000145 164	-1,65816
NM_003410 // RefSeq // Homo sapiens zinc finger protein, X-linked (ZFX), transcript var	ZFX	8,76E-06	-1,65553
AK074471 // GenBank // Homo sapiens cDNA FLJ23891 fis, clone LNG14431. // chr10 // 90 /	LOC143188	0,000102 202	-1,65356
NM_001146321 // RefSeq // Homo sapiens GRAM domain containing 3 (GRAMD3), transcript va	GRAMD3	0,000125 579	-1,64708
NM_006079 // RefSeq // Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-r	CITED2	0,000103 799	-1,64134
NM_004651 // RefSeq // Homo sapiens ubiquitin specific peptidase 11 (USP11), mRNA. // c	USP11	0,000101 809	-1,60502
NR_030354 // RefSeq // Homo sapiens microRNA 624 (MIR624), microRNA. // chr14 // 100 //	MIR624	0,000184 996	-1,58923
ENST00000322213 // ENSEMBL // cdna:known chromosome:GRCh37:X:53401070:53449677:-1 gene:	SMC1A	0,000105 872	-1,58004
NR_038386 // RefSeq // Homo sapiens uncharacterized LOC728537 (LOC728537), non-coding R	LOC728537	0,000174 809	-1,57328
NR_046408 // RefSeq // Homo sapiens fructosamine 3 kinase related protein (FN3KRP), tra	FN3KRP	0,000128 848	-1,56413
NM_153218 // RefSeq // Homo sapiens laccase (multicopper oxidoreductase) domain contain	LACC1	0,000111 361	-1,56264
NR_038971 // RefSeq // Homo sapiens long intergenic non-protein coding RNA 641 (LINC006	LINC00641	7,64E-05	-1,55954
n372506 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		3,18E-05	-1,53004
NR_040096 // RefSeq // Homo sapiens uncharacterized LOC643339 (LOC643339), non-coding R	LOC643339	3,16E-05	-1,51852
NM_145047 // RefSeq // Homo sapiens organic solute carrier partner 1 (OSCP1), transcrip	OSCP1	0,000115 259	-1,50284
n364117 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		0,000175 972	-1,49439
n366425 // NONCODE // accn=NULL class=lncRNA		8,97E-05	-1,48485

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
name=Human lincRNA ref=BodyMapLinc transcr			
NR_024176 // RefSeq // Homo sapiens MAP kinase interacting serine/threonine kinase 1 (M	MKNK1	2,77E-05	-1,47961
NM_005765 // RefSeq // Homo sapiens ATPase, H+ transporting, lysosomal accessory protei	ATP6AP2	0,000181 311	-1,45823
ENST00000391265 // ENSEMBL // ncna:snoRNA chromo-some:GRCh37:5:40790179:40790306:-1 gen		0,000112 73	-1,45519
NM_001654 // RefSeq // Homo sapiens v-raf murine sarcoma 3611 viral oncogene homolog (A	ARAF	6,50E-06	-1,45052
NM_003334 // RefSeq // Homo sapiens ubiquitin-like modifier activating enzyme 1 (UBA1),	UBA1	0,000127 309	-1,44636
NM_015698 // RefSeq // Homo sapiens G patch do-main and KOW motifs (GPKOW), mRNA. // chr	GPKOW	0,000181 843	-1,44071
ENST00000439131 // ENSEMBL // cdna:known chromosome:GRCh37:14:78227173:78236085:1 gene:	C14orf178	9,31E-05	-1,43968
ENST00000601961 // ENSEMBL // cdna:known chromo-some:GRCh37:HG1433_PATCH:53175722:531760		4,68E-05	-1,43809
OTTHUMT00000050408 // Havana transcript // cdna:all chromosome:VEGA52:10:114648494:1146	OT-THUMG0000019067	0,000211 094	-1,42955
n366327 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		0,000132 112	-1,42665
NM_206907 // RefSeq // Homo sapiens protein ki-nase, AMP-activated, alpha 1 catalytic su	PRKAA1	0,000116 055	-1,42008
AF086476 // GenBank // Homo sapiens full length insert cDNA clone ZD88F12. // chr17 //	LOC400590	8,00E-05	-1,40857
NM_001024593 // RefSeq // Homo sapiens MSS51 mitochondrial translational activator (MSS	MSS51	2,13E-05	-1,40763
NM_006297 // RefSeq // Homo sapiens X-ray repair complementing defective repair in Chin	XRCC1	0,000122 008	-1,39256
NM_016049 // RefSeq // Homo sapiens ER membrane protein complex subunit 9 (EMC9), mRNA.	EMC9	6,79E-06	-1,3891
NM_031407 // RefSeq // Homo sapiens HECT, UBA and WWE domain containing 1, E3 ubiquitin	HUWE1	8,51E-06	-1,38609
NM_001008390 // RefSeq // Homo sapiens CGG tri-plet repeat binding protein 1 (CGGBP1), t	CGGBP1	0,000145 189	-1,37358
NM_207368 // RefSeq // Homo sapiens family with sequence similarity 195, member B (FAM1	FAM195B	0,000195 999	-1,37338
NM_020137 // RefSeq // Homo sapiens GRIP1 asso-ciated protein 1 (GRIPAP1), transcript va	GRIPAP1	0,000149 647	-1,3641
ENST00000288616 // ENSEMBL // cdna:known chromosome:GRCh37:12:121087888:121104835:1 gen	CABP1	1,47E-05	-1,35928

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_001167947 // RefSeq // Homo sapiens translocase of inner mitochondrial membrane 17 h	TIMM17B	5,39E-05	-1,35282
NM_153367 // RefSeq // Homo sapiens zinc finger, CCHC domain containing 24 (ZCCHC24), m	ZCCHC24	9,31E-05	-1,35175
NM_014828 // RefSeq // Homo sapiens TOX high mobility group box family member 4 (TOX4),	TOX4	0,000141446	-1,3414
NR_037717 // RefSeq // Homo sapiens RNASEK-C17orf49 readthrough (non-protein coding) (R	RNASEK-C17orf49	7,83E-05	-1,33293
NM_001085487 // RefSeq // Homo sapiens Myb-like, SWIRM and MPN domains 1 (MYSM1), mRNA.	MYSM1	4,82E-05	-1,3198
ENST00000348513 // ENSEMBL // cdna:known chromosome:GRCh37:17:38781214:38804760:-1 gene	SMARCE1	1,87E-05	-1,31328
NM_173527 // RefSeq // Homo sapiens RAS (RAD and GEM)-like GTP binding 2 (REM2), mRNA.	REM2	1,32E-05	-1,29457
ENST00000453573 // ENSEMBL // cdna:known chromosome:GRCh37:1:51731525:51732716:1 gene:E		0,000166479	-1,26492
NM_001199822 // RefSeq // Homo sapiens magnesium-dependent phosphatase 1 (MDP1), transc	MDP1	0,000168386	-1,22068
ENST00000265260 // ENSEMBL // cdna:known chromosome:GRCh37:3:101292939:101313281:1 gene	PCNP	0,000122455	1,21859
AK127434 // GenBank // Homo sapiens cDNA FLJ45526 fis, clone BRTHA2027227. // chr16 //	LOC100129215	4,77E-05	1,22826
NM_005832 // RefSeq // Homo sapiens potassium large conductance calcium-activated chann	KCNMB2	0,00015353	1,22955
ENST00000451415 // ENSEMBL // cdna:known chromosome:GRCh37:6:114551305:114560363:1 gene	LOC441167	2,90E-05	1,23387
NM_013356 // RefSeq // Homo sapiens solute carrier family 16, member 8 (monocarboxylic	SLC16A8	4,44E-06	1,23566
NM_001105579 // RefSeq // Homo sapiens synapse differentiation inducing 1-like (SYNDIG1	SYNDIG1L	8,80E-05	1,24069
NM_017806 // RefSeq // Homo sapiens Lck interacting transmembrane adaptor 1 (LIME1), mR	LIME1	5,21E-05	1,24701
ENST00000416090 // ENSEMBL // cdna:known chromosome:GRCh37:13:110380629:110382354:1 gen	LINC00676	8,59E-05	1,24871
OTTHUMT00000050714 // Havana transcript // cdna:all chromosome:VEGA52:10:123374939:1233	OTTHUMG0000019174	0,000172169	1,24874
n376918 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		2,71E-05	1,2536
ENST00000293883 // ENSEMBL // cdna:known	WDR24	6,29E-05	1,25377

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:16:734622:740400:-1 gene:ENS			
ENST00000461943 // ENSEMBL // cdna:known chromosome:GRCh37:3:150479724:150480325:1 gene	SIAH2-AS1	5,51E-05	1,25689
ENST00000449451 // ENSEMBL // cdna:known chromo- some:GRCh37:2:47713153:47715691:-1 gene:		6,40E-05	1,25957
ENST00000480018 // ENSEMBL // cdna:known chromo- some:GRCh37:7:129648694:129666391:1 gene		1,63E-05	1,27141
NM_182917 // RefSeq // Homo sapiens eukaryotic translation initiation factor 4 gamma, 1	EIF4G1	2,68E-05	1,28023
ENST00000560026 // ENSEMBL // cdna:known chromo- some:GRCh37:15:22747313:22782336:-1 gene		0,000210 584	1,30463
NM_002950 // RefSeq // Homo sapiens ribophorin I (RPN1), mRNA. // chr3 // 100 // 67 //	RPN1	1,47E-05	1,30517
ENST00000391089 // ENSEMBL // ncna:snoRNA chromo- some:GRCh37:2:227833705:227833838:-1 g		0,000188 667	1,3125
n370415 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		4,42E-05	1,32222
NM_173591 // RefSeq // Homo sapiens otogelin-like (OTOGL), mRNA. // chr12 // 100 // 96	OTOGL	5,54E-05	1,33091
AB073349 // GenBank // Homo sapiens primary neuroblastoma cDNA, clone:Nbla00110, full i		7,89E-05	1,33494
NM_002928 // RefSeq // Homo sapiens regulator of G-protein signaling 16 (RGS16), mRNA.	RGS16	0,000182 747	1,34078
OTTHUMT00000343105 // Havana transcript // cdna:all chromosome:VEGA52:1:166117019:16613	OT-THUMG0000156136	5,46E-05	1,36304
BC070375 // GenBank // Homo sapiens cDNA clone IM- AGE:4730954, with apparent retained in		1,81E-05	1,36566
NM_004798 // RefSeq // Homo sapiens kinesin family member 3B (KIF3B), mRNA. // chr20 //	KIF3B	0,000158 215	1,38449
NM_138769 // RefSeq // Homo sapiens ras homolog family member T2 (RHOT2), nuclear gene	RHOT2	0,000145 864	1,40282
ENST00000394077 // ENSEMBL // cdna:known chromosome:GRCh37:3:101399936:101405626:-1 gen	RPL24	1,89E-05	1,40358
OTTHUMT00000410900 // Havana transcript // cdna:all chromosome:VEGA52:2:119591401:11959	OT-THUMG0000170896	1,27E-05	1,41217
NM_014612 // RefSeq // Homo sapiens family with sequence similarity 120A (FAM120A), mRN	FAM120A	8,23E-05	1,42127
NR_027460 // RefSeq // Homo sapiens RNA polyme-	RRN3P3	9,53E-05	1,44031

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
rase I transcription factor homolog (S. c			
NM_006026 // RefSeq // Homo sapiens H1 histone family, member X (H1FX), mRNA. // chr3 /	H1FX	0,000170 726	1,44106
NR_033437 // RefSeq // Homo sapiens uridine mono-phosphate synthetase (UMPS), transcript	UMPS	0,000161 562	1,44749
NM_001199198 // RefSeq // Homo sapiens TBC1 domain family, member 23 (TBC1D23), transcr	TBC1D23	2,20E-05	1,45157
NM_014770 // RefSeq // Homo sapiens ArfGAP with GTPase domain, ankyrin repeat and PH do	AGAP2	1,15E-06	1,46867
NM_080653 // RefSeq // Homo sapiens ATPase, H+ transporting, lysosomal 31kDa, V1 subuni	ATP6V1E2	3,65E-05	1,49544
NM_001085451 // RefSeq // Homo sapiens leukemia NUP98 fusion partner 1 (LNP1), mRNA. //	LNP1	1,65E-05	1,50202
NM_019095 // RefSeq // Homo sapiens cardiolipin synthase 1 (CRLS1), transcript variant	CRLS1	1,10E-05	1,5252
NM_017945 // RefSeq // Homo sapiens solute carrier family 35, member A5 (SLC35A5), mRNA	SLC35A5	0,000162 375	1,53733
NR_027766 // RefSeq // Homo sapiens nudix (nucleo-side diphosphate linked moiety X)-type	NUDT16P1	5,89E-05	1,55496
NM_001083308 // RefSeq // Homo sapiens pyrin domain containing 2 (PYDC2), mRNA. // chr3	PYDC2	1,33E-05	1,55882
NM_001042533 // RefSeq // Homo sapiens MYC induced nuclear antigen (MINA), transcript v	MINA	1,50E-05	1,56356
OTTHUMT00000143657 // Havana transcript // cdna:all chromosome:VEGA52:9:39395734:393974	OT-THUMG0000067120	3,08E-05	1,57852
ENST00000423367 // ENSEMBL // cdna:known chromosome:GRCh37:18:25534483:25543651:1 gene:		1,14E-05	1,57934
ENST00000457928 // ENSEMBL // cdna:known chromosome:GRCh37:3:176741108:176915256:-1 gen	TBL1XR1	7,71E-07	1,59191
NR_102705 // RefSeq // Homo sapiens MMP24 antisense RNA 1 (MMP24-AS1), transcript varia	MMP24-AS1	0,000103 453	1,59246
NM_004451 // RefSeq // Homo sapiens estrogen-related receptor alpha (ESRRA), mRNA. // c	ESRRA	0,000117 381	1,60729
NM_173683 // RefSeq // Homo sapiens XK, Kell blood group complex subunit-related family	XKR6	0,000181 986	1,80799
NR_038387 // RefSeq // Homo sapiens uncharacterized LOC730091 (LOC730091), non-coding R	LINC00886	3,32E-05	1,83953
NM_001390 // RefSeq // Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, m	DTNA	3,87E-07	1,84096
NM_001802 // RefSeq // Homo sapiens cerebellar degeneration-related protein 2, 62kDa (C	CDR2	0,000141 363	1,85348
OTTHUMT00000343510 // Havana transcript //	IL1RAP	8,36E-05	1,87877

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
cdna:all chromosome:VEGA52:3:190234008:19023			
OTTHUMT00000343232 // Havana transcript // cdna:all chromosome:VEGA52:3:191275113:19130	OT-THUMG0000156168	5,65E-06	1,9162
NM_032501 // RefSeq // Homo sapiens acyl-CoA synthetase short-chain family member 1 (AC	ACSS1	0,000146721	1,96382
n365833 // NONCODE // accn=NULL class=lncRNA name=Human lincRNA ref=BodyMapLinc transcr		6,82E-05	1,96778
NM_183373 // RefSeq // Homo sapiens PX domain containing 1 (PXDC1), mRNA. // chr6 // 10	PXDC1	0,000110145	2,0936
NM_001080392 // RefSeq // Homo sapiens KIAA1147 (KIAA1147), mRNA. // chr7 // 100 // 81	KIAA1147	2,52E-05	2,20155
NM_014427 // RefSeq // Homo sapiens copine VII (CPNE7), transcript variant 2, mRNA. //	CPNE7	4,10E-05	2,31564
AK125860 // GenBank // Homo sapiens cDNA FLJ43872 fis, clone TESTI4008417. // chr8 // 1		0,000158592	2,36231
NR_003284 // RefSeq // Homo sapiens proliferation-associated 2G4 pseudogene 4 (PA2G4P4)	PA2G4P4	8,99E-05	2,59897
BC137525 // GenBank // Homo sapiens chromosome 8 open reading frame 16, mRNA (cDNA clon		0,00010038	2,88566
BC132953 // GenBank // Homo sapiens chromosome 8 open reading frame 15, mRNA (cDNA clon		0,000191222	3,20541
ENST00000369663 // ENSEMBL // cdna:known chromosome:GRCh37:6:85444157:85474237:-1 gene:	TBX18	9,66E-05	3,37111
NM_005359 // RefSeq // Homo sapiens SMAD family member 4 (SMAD4), mRNA. // chr18 // 100	SMAD4	2,36E-06	4,58279

Table 8: Efficiency of 5-fluorouracil (5FU)

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
AK093576 // GenBank // Homo sapiens cDNA FLJ36257 fis, clone THYMU2002376. // chr2 // 1		2,03E-05	1,34515
AK096045 // GenBank // Homo sapiens cDNA FLJ38726 fis, clone KIDNE2010271, moderately s	SHANK2	0,00027191	1,92893
AK098314 // GenBank // Homo sapiens cDNA FLJ40995 fis, clone UTERU2015830. // chr15 //		5,93E-05	1,50957
AK128544 // GenBank // Homo sapiens cDNA FLJ46703 fis, clone TRACH3014580. // chr19 //		6,28E-05	1,30817

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
AK131222 // GenBank // Homo sapiens cDNA FLJ16120 fis, clone BLADE2000579. // chr19 //	HSH2D	0,000411 92	-2,10555
AY623011 // GenBank // Homo sapiens DIPLA1-antisense expressed (DIPLAS) mRNA, complete	PAPPA-AS1	8,11E-07	-1,50982
BC002469 // GenBank // Homo sapiens chromosome 1 open reading frame 56, mRNA (cDNA clon	C1orf56	8,69E-05	1,25652
BC034253 // GenBank // Homo sapiens chromosome 4 open reading frame 29, mRNA (cDNA clon	C4orf29	3,40E-05	-1,40195
BC041487 // GenBank // Homo sapiens, clone IMAGE:5493056, mRNA. // chr2 // 100 // 100 /		0,000271 37	1,60265
BC043386 // GenBank // Homo sapiens chromosome 19 open reading frame 68, mRNA (cDNA clo	C19orf68	7,80E-06	1,38556
ENST00000014935 // ENSEMBL // cdna:known chromosome:GRCh37:X:153630099:153638375:-1 gen	DNASE1L1	0,000304 52	-1,21873
ENST000000216807 // ENSEMBL // cdna:known chromosome:GRCh37:14:36295524:36341140:1 gene:	BRMS1L	0,000158 41	1,5124
ENST000000235090 // ENSEMBL // cdna:known chromosome:GRCh37:1:111982512:111991998:-1 gen	WDR77	0,000315	1,33902
ENST000000258457 // ENSEMBL // cdna:known chromosome:GRCh37:2:105953816:105965668:1 gene	C2orf49	3,27E-05	1,202
ENST000000264228 // ENSEMBL // cdna:known chromosome:GRCh37:4:56212276:56239263:1 gene:E	SRD5A3	0,000170 94	-2,92546
ENST000000264434 // ENSEMBL // cdna:known chromosome:GRCh37:2:70377012:70418203:-1 gene:	C2orf42	0,000362 55	1,30412
ENST000000264716 // ENSEMBL // cdna:known chromosome:GRCh37:2:28615725:28640179:1 gene:E	FOSL2	9,65E-05	1,55547
ENST000000270586 // ENSEMBL // cdna:known chromosome:GRCh37:17:4699439:4701790:1 gene:EN	PSMB6	3,59E-06	1,35052
ENST000000282292 // ENSEMBL // cdna:known chromosome:GRCh37:19:58011309:58019508:1 gene:	ZNF773	8,07E-06	1,88021
ENST000000286692 // ENSEMBL // cdna:known chromosome:GRCh37:1:111659955:111682662:-1 gen	DRAM2	0,000391	-1,21978
ENST000000290374 // ENSEMBL // cdna:known chromosome:GRCh37:15:35043233:35047166:-1 gene	GJD2	0,000203 65	-1,2476
ENST000000295121 // ENSEMBL // cdna:known	WDR92	7,50E-05	1,57754

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:2:68356935:68384692:-1 gene:			
ENST00000295268 // ENSEMBL // cdna:known chromosome:GRCh37:4:98480027:99064391:-1 gene:	C4orf37	1,76E-05	-1,36187
ENST00000295640 // ENSEMBL // cdna:known chromosome:GRCh37:1:201951752:201975275:1 gene	RNPEP	1,60E-05	-1,30039
ENST00000306910 // ENSEMBL // cdna:known chromosome:GRCh37:19:58920063:58929690:1 gene:	ZNF584	7,58E-05	2,14006
ENST00000306984 // ENSEMBL // cdna:known chromosome:GRCh37:7:40172342:40174258:-1 gene:	MPLKIP	1,31E-06	1,45083
ENST00000313143 // ENSEMBL // cdna:known chromosome:GRCh37:3:183873176:183891398:1 gene	DVL3	0,00031266	1,25901
ENST00000318967 // ENSEMBL // cdna:known chromosome:GRCh37:1:153700543:153746555:1 gene	INTS3	0,00020296	-1,39546
ENST00000325134 // ENSEMBL // cdna:known chromosome:GRCh37:19:58053208:58071207:-1 gene	ZNF550	0,00034554	1,82104
ENST00000327428 // ENSEMBL // cdna:known chromosome:GRCh37:2:74362525:74375121:-1 gene:	BOLA3	0,00027086	1,62836
ENST00000337768 // ENSEMBL // cdna:known chromosome:GRCh37:2:27873679:27886676:-1 gene:	SUPT7L	2,02E-05	1,35931
ENST00000338508 // ENSEMBL // cdna:known chromosome:GRCh37:11:70315540:70858372:-1 gene	SHANK2	0,00017107	1,68848
ENST00000340080 // ENSEMBL // cdna:known chromosome:GRCh37:7:7606503:7647127:1 gene:ENS	MIOS	2,02E-06	1,54664
ENST00000341928 // ENSEMBL // cdna:known chromosome:GRCh37:18:5392383:5544241:-1 gene:E	EPB41L3	0,00042139	-1,41844
ENST00000344063 // ENSEMBL // cdna:known chromosome:GRCh37:19:55896713:55903453:1 gene:	RPL28	1,66E-06	1,49974
ENST00000360820 // ENSEMBL // cdna:known chromosome:GRCh37:12:100661162:100735502:1 gen	SCYL2	0,00012417	1,36683
ENST00000361716 // ENSEMBL // cdna:known chromosome:GRCh37:12:6571403:6580153:-1 gene:E	VAMP1	7,13E-07	1,72688
ENST00000363200 // ENSEMBL // ncna:snRNA chromosome:GRCh37:15:59504847:59504987:-1 gen		0,00040235	-1,46828
ENST00000363221 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:6:76364686:76365015:-1 g		2,84E-05	1,66874
ENST00000366510 // ENSEMBL // cdna:known	SCCPDH	9,41E-05	-2,38749

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:1:246887349:246931439:1 gene			
ENST00000368564 // ENSEMBL // cdna:known chromosome:GRCh37:6:117002350:117056807:1 gene	KPNA5	6,99E-05	1,7103
ENST00000368918 // ENSEMBL // cdna:known chromosome:GRCh37:1:151043080:151098018:1 gene	GABPB2	1,04E-05	-1,66795
ENST00000369084 // ENSEMBL // cdna:known chromosome:GRCh37:1:150266340:150281414:1 gene	MRPS21	0,00038893	-1,20225
ENST00000370206 // ENSEMBL // cdna:known chromosome:GRCh37:1:95362507:95392834:-1 gene:	CNN3	0,00011078	3,74929
ENST00000370580 // ENSEMBL // cdna:known chromosome:GRCh37:1:85731931:85742773:-1 gene:	BCL10	2,07E-05	-1,46157
ENST00000371964 // ENSEMBL // cdna:known chromosome:GRCh37:9:136223428:136228045:1 gene	SURF2	4,37E-05	1,60293
ENST00000373996 // ENSEMBL // cdna:known chromosome:GRCh37:9:119187504:120177216:-1 gen	ASTN2	0,00014433	-1,22639
ENST00000377526 // ENSEMBL // cdna:known chromosome:GRCh37:2:74753775:74757066:-1 gene:	AUP1	6,13E-05	1,30544
ENST00000378387 // ENSEMBL // cdna:known chromosome:GRCh37:9:35659341:35665284:-1 gene:	C9orf100	2,74E-05	-1,39206
ENST00000378746 // ENSEMBL // cdna:known chromosome:GRCh37:5:132028368:132073330:-1 gen	KIF3A	0,00036532	1,5834
ENST00000381341 // ENSEMBL // cdna:known chromosome:GRCh37:2:15731302:15771225:1 gene:E	DDX1	0,00015847	1,46473
ENST00000390291 // ENSEMBL // cdna:known chromosome:GRCh37:22:22681658:22682172:1 gene:	IGLV1-50	2,34E-05	1,59231
ENST00000390658 // ENSEMBL // cdna:known chromosome:GRCh37:19:40028890:40030870:-1 gene	EID2	0,00041541	1,45924
ENST00000390998 // ENSEMBL // ncna:snoRNA chromosome:GRCh37:4:159621843:159622060:1 ge		0,00032647	-1,37147
ENST00000391835 // ENSEMBL // cdna:putative chromosome:GRCh37:19:50372303:50381285:-1 g	AKT1S1	2,02E-06	1,59522
ENST00000391857 // ENSEMBL // cdna:known chromosome:GRCh37:19:49990811:49995565:1 gene:	SNORD32 A	0,00031523	1,27385
ENST00000391945 // ENSEMBL // cdna:known	ERCC2	5,66E-05	1,70038

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
chromosome:GRCh37:19:45854246:45873876:-1 gene			
ENST00000395787 // ENSEMBL // cdna:known chromosome:GRCh37:11:34903842:34938046:-1 gene	APIP	0,00040488	1,40164
ENST00000396049 // ENSEMBL // cdna:known chromosome:GRCh37:2:74382165:74405995:-1 gene:	MOB1A	0,00037436	1,43653
ENST00000404924 // ENSEMBL // cdna:known chromosome:GRCh37:2:24150182:24223073:1 gene:E	UBXN2A	0,00024523	1,42216
ENST00000407418 // ENSEMBL // cdna:known chromosome:GRCh37:22:39257455:39268319:-1 gene	CBX6	0,00015417	2,32883
ENST00000408152 // ENSEMBL // ncna:miRNA chromosome:GRCh37:4:89415047:89415167:-1 gene		0,00031385	1,26787
ENST00000410682 // ENSEMBL // ncna:misc_RNA chromosome:GRCh37:19:47239569:47239676:1 g		7,44E-06	1,7438
ENST00000413451 // ENSEMBL // cdna:known chromosome:GRCh37:1:21069480:21070455:1 gene:E		5,76E-07	1,66593
ENST00000417210 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:10:65086093:65086		0,00010457	-2,20279
ENST00000419113 // ENSEMBL // cdna:known chromosome:GRCh37:19:54606129:54612011:1 gene:	NDUFA3	5,39E-05	1,51833
ENST00000428443 // ENSEMBL // cdna:known chromosome:GRCh37:2:179966483:180129517:-1 gen	SESTD1	1,03E-05	-2,86002
ENST00000428463 // ENSEMBL // cdna:known chromosome:GRCh37:X:47842756:47930508:-1 gene:	ZNF630	2,47E-05	-1,4488
ENST00000428463 // ENSEMBL // cdna:known chromosome:GRCh37:X:47842756:47930508:-1 gene:	ZNF630	0,00042517	-2,72234
ENST00000433452 // ENSEMBL // cdna:known chromosome:GRCh37:10:135160650:135166187:1 gen	PRAP1	0,00016688	-1,3514
ENST00000435136 // ENSEMBL // cdna:known chromosome:GRCh37:4:2814031:2836015:1 gene:ENS	SH3BP2	0,00026774	-1,45604
ENST00000435478 // ENSEMBL // cdna:known chromosome:GRCh37:3:49936735:49941190:1 gene:E		6,89E-05	-1,2073
ENST00000436877 // ENSEMBL // cdna:known chromosome:GRCh37:10:45395062:45415668:-1 gene		0,00018185	-1,20746
ENST00000438551 // ENSEMBL // ha-vana:sense_intronic chromo-	ZBTB40-IT1	0,00019472	1,2402

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
some:GRCh37:1:22843967:228462			
ENST00000446992 // ENSEMBL // cdna:known chromosome:GRCh37:2:115591407:115593165:-1 gen		0,00011975	-1,28973
ENST00000450709 // ENSEMBL // cdna:known chromosome:GRCh37:2:286419:287496:1 gene:ENSG0		0,00029899	1,20228
ENST00000453103 // ENSEMBL // cdna:known chromosome:GRCh37:2:74174769:74208568:-1 gene:	DGUOK-AS1	2,51E-05	2,21859
ENST00000459226 // ENSEMBL // ncRNA:snoRNA chromosome:GRCh37:6:34660557:34660660:1 gene		0,00013454	1,59243
ENST00000459496 // ENSEMBL // ncRNA:snoRNA chromosome:GRCh37:1:171451046:171451148:1 ge		0,00039211	1,30193
ENST00000460977 // ENSEMBL // cdna:putative chromosome:GRCh37:3:142184157:142191179:-1		0,00013835	1,55597
ENST00000497885 // ENSEMBL // cdna:known chromosome:GRCh37:17:4607525:4608824:1 gene:EN		0,00022258	1,43127
ENST00000507521 // ENSEMBL // cdna:known chromosome:GRCh37:5:139750476:139780952:-1 gen		0,00014841	1,32745
ENST00000508632 // ENSEMBL // cdna:known chromosome:GRCh37:4:48887036:48908845:-1 gene:	OCIAD2	2,44E-07	-1,60924
ENST00000516170 // ENSEMBL // ncRNA:snoRNA chromosome:GRCh37:4:160428047:160428180:-1 g		0,00021845	-1,26237
ENST00000516439 // ENSEMBL // ncRNA:miRNA chromosome:GRCh37:7:68527371:68527457:1 gene:		0,00040339	-1,7645
ENST00000516474 // ENSEMBL // ncRNA:misc_RNA chromosome:GRCh37:17:26388993:26389094:1 g		0,0003624	1,22844
ENST00000520840 // ENSEMBL // cdna:known chromosome:GRCh37:8:22928890:22932001:-1 gene:		0,00027289	-1,5516
ENST00000532917 // ENSEMBL // cdna:known chromosome:GRCh37:11:118215071:118225876:1 gen	CD3G	0,00028294	-1,22972
ENST00000538010 // ENSEMBL // cdna:known chromosome:GRCh37:12:122457328:122499948:1 gen	BCL7A	0,00040092	1,58483
ENST00000549860 // ENSEMBL // cdna:known chromosome:GRCh37:12:56694496:56708592:1 gene:		0,00030324	1,50229
ENST00000553046 // ENSEMBL // havana:lincRNA chromosome:GRCh37:14:36343063:36344509:1 g		6,99E-05	1,59145
ENST00000553270 // ENSEMBL // havana:non_coding chromosome:GRCh37:14:102095321:10209886		0,00026937	-1,41407
ENST00000555212 // ENSEMBL // havana:sense_intronic chromosome:GRCh37:14:100730118:1007		0,00019511	1,34974
ENST00000557322 // ENSEMBL // cdna:known chromosome:GRCh37:14:58731380:58736399:1 gene:		3,08E-05	1,437
GENSCAN00000034805 // ENSEMBL // cdna:genscan chromosome:GRCh37:18:14335864:14357900:1		6,35E-05	-1,93557

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_000165 // RefSeq // Homo sapiens gap junction protein, alpha 1, 43kDa (GJA1), mRNA.	GJA1	0,000229 46	5,04133
NM_000208 // RefSeq // Homo sapiens insulin receptor (INSR), transcript variant 1, mRNA	INSR	0,000179 75	-2,69344
NM_000234 // RefSeq // Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA. // chr19	LIG1	5,52E-05	1,34088
NM_000584 // RefSeq // Homo sapiens interleukin 8 (IL8), mRNA. // chr4 // 100 // 62 //	IL8	0,000314 35	-5,01122
NM_000607 // RefSeq // Homo sapiens orosomucoid 1 (ORM1), mRNA. // chr9 // 100 // 45 //	ORM1	2,05E-05	-1,36683
NM_000660 // RefSeq // Homo sapiens transforming growth factor, beta 1 (TGFB1), mRNA. /	TGFB1	0,000412 72	2,48992
NM_000880 // RefSeq // Homo sapiens interleukin 7 (IL7), transcript variant 1, mRNA. //	IL7	0,000299 12	-2,88692
NM_001001563 // RefSeq // Homo sapiens translocase of inner mitochondrial membrane 50 h	TIMM50	8,83E-06	1,39074
NM_001002836 // RefSeq // Homo sapiens zinc finger protein 787 (ZNF787), mRNA. // chr19	ZNF787	9,18E-05	1,60299
NM_001004320 // RefSeq // Homo sapiens alkylglycerol monooxygenase (AGMO), mRNA. // chr	AGMO	8,17E-06	-5,67111
NM_001009 // RefSeq // Homo sapiens ribosomal protein S5 (RPS5), mRNA. // chr19 // 100	RPS5	2,74E-05	1,37861
NM_001010853 // RefSeq // Homo sapiens peptidase M20 domain containing 2 (PM20D2), mRNA	PM20D2	0,000136 69	2,29387
NM_001011724 // RefSeq // Homo sapiens heterogeneous nuclear ribonucleoprotein A1-like	HNRN-PA1L2	0,000324 46	1,53175
NM_001020 // RefSeq // Homo sapiens ribosomal protein S16 (RPS16), mRNA. // chr19 // 10	RPS16	1,45E-05	1,46978
NM_001031853 // RefSeq // Homo sapiens inscuteable homolog (Drosophila) (INSC), transcr	INSC	5,50E-05	-1,33459
NM_001032281 // RefSeq // Homo sapiens tissue factor pathway inhibitor (lipoprotein-ass	TFPI	0,000371 57	-3,41298
NM_001040056 // RefSeq // Homo sapiens mitogen-activated protein kinase 3 (MAPK3), tran	MAPK3	0,000349 32	-1,3027
NM_001080533 // RefSeq // Homo sapiens unc-119 homolog B (C. elegans) (UNC119B), mRNA.	UNC119B	0,000300 16	1,6389
NM_001083953 // RefSeq // Homo sapiens thyroid adenoma associated (THADA), transcript v	THADA	9,59E-06	1,33863
NM_001099337 // RefSeq // Homo sapiens coenzyme Q10 homolog A (S. cerevisiae) (COQ10A),	COQ10A	6,00E-07	1,54954
NM_001105244 // RefSeq // Homo sapiens protein tyrosine phosphatase, receptor type, M (	PTPRM	2,60E-07	-4,09702
NM_001114093 // RefSeq // Homo sapiens LSM14A, SCD6 homolog A (S. cerevisiae) (LSM14A),	LSM14A	0,000358 17	1,41516
NM_001123375 // RefSeq // Homo sapiens histone	HIST2H3	1,05E-06	2,96225

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
cluster 2, H3d (HIST2H3D), mRNA. // chr1	D		
NM_001129993 // RefSeq // Homo sapiens KIAA1841 (KIAA1841), transcript variant 1, mRNA.	KIAA1841	0,00010954	1,57702
NM_001136156 // RefSeq // Homo sapiens zinc finger protein 507 (ZNF507), transcript var	ZNF507	0,00028985	1,49007
NM_001159767 // RefSeq // Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), tr	BZW2	0,00026221	1,60965
NM_001162893 // RefSeq // Homo sapiens KIAA0040 (KIAA0040), transcript variant 1, mRNA.	KIAA0040	2,26E-05	-1,50042
NM_001162893 // RefSeq // Homo sapiens KIAA0040 (KIAA0040), transcript variant 1, mRNA.	KIAA0040	0,00012464	-2,16198
NM_001195605 // RefSeq // Homo sapiens zinc finger protein 865 (ZNF865), mRNA. // chr19	ZNF865	3,04E-05	1,55085
NM_001197097 // RefSeq // Homo sapiens protease, serine, 3 (PRSS3), transcript variant	PRSS3	0,00020336	-2,13193
NM_001198801 // RefSeq // Homo sapiens eukaryotic translation initiation factor 4 gamma	EIF4G3	1,88E-05	1,32335
NM_001289 // RefSeq // Homo sapiens chloride intracellular channel 2 (CLIC2), mRNA. //	CLIC2	2,55E-05	-1,70538
NM_001483 // RefSeq // Homo sapiens glioblastoma amplified sequence (GBAS), nuclear gen	GBAS	2,98E-05	1,90245
NM_001536 // RefSeq // Homo sapiens protein arginine methyltransferase 1 (PRMT1), trans	PRMT1	1,48E-07	1,4486
NM_001631 // RefSeq // Homo sapiens alkaline phosphatase, intestinal (ALPI), mRNA. // c	ALPI	4,48E-05	-1,22218
NM_001955 // RefSeq // Homo sapiens endothelin 1 (EDN1), transcript variant 1, mRNA. //	EDN1	5,30E-05	-4,42114
NM_002381 // RefSeq // Homo sapiens matrilin 3 (MATN3), mRNA. // chr2 // 100 // 87 // 1	MATN3	8,58E-05	2,51599
NM_002486 // RefSeq // Homo sapiens nuclear cap binding protein subunit 1, 80kDa (NCBP1	NCBP1	2,87E-06	1,20111
NM_002557 // RefSeq // Homo sapiens oviductal glycoprotein 1, 120kDa (OVGP1), mRNA. //	OVGP1	4,36E-05	-1,35733
NM_002609 // RefSeq // Homo sapiens platelet-derived growth factor receptor, beta polyp	PDGFRB	0,00017565	-1,5889
NM_002612 // RefSeq // Homo sapiens pyruvate dehydrogenase kinase, isozyme 4 (PDK4), nu	PDK4	0,00026309	-2,80794
NM_002824 // RefSeq // Homo sapiens parathymosin (PTMS), mRNA. // chr12 // 100 // 65 //	PTMS	0,00012629	1,86795
NM_003041 // RefSeq // Homo sapiens solute carrier family 5 (sodium/glucose cotransport	SLC5A2	0,00027548	-1,23505
NM_003263 // RefSeq // Homo sapiens toll-like receptor 1 (TLR1), mRNA. // chr4 // 100 /	TLR1	0,0001973	-2,10905
NM_003344 // RefSeq // Homo sapiens ubiquitin-conjugating enzyme E2H (UBE2H), transcrip	UBE2H	0,0003788	-1,39585

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_003432 // RefSeq // Homo sapiens zinc finger protein 131 (ZNF131), mRNA. // chr5 //	ZNF131	0,00032051	1,38427
NM_003672 // RefSeq // Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisi	CDC14A	3,46E-06	1,43973
NM_003762 // RefSeq // Homo sapiens vesicle-associated membrane protein 4 (VAMP4), tran	VAMP4	6,55E-06	-1,59861
NM_003846 // RefSeq // Homo sapiens peroxisomal biogenesis factor 11 beta (PEX11B), tra	PEX11B	2,12E-05	-1,31719
NM_004069 // RefSeq // Homo sapiens adaptor-related protein complex 2, sigma 1 subunit	AP2S1	2,37E-05	1,39511
NM_004313 // RefSeq // Homo sapiens arrestin, beta 2 (ARRB2), transcript variant 1, mRN	ARRB2	3,89E-07	2,03526
NM_004562 // RefSeq // Homo sapiens parkinson protein 2, E3 ubiquitin protein ligase (p	PARK2	5,00E-06	-1,67657
NM_004591 // RefSeq // Homo sapiens chemokine (C-C motif) ligand 20 (CCL20), transcript	CCL20	7,95E-05	-4,74036
NM_004666 // RefSeq // Homo sapiens vanin 1 (VNN1), mRNA. // chr6 // 100 // 100 // 23 /	VNN1	0,00022372	-10,7979
NM_004891 // RefSeq // Homo sapiens mitochondrial ribosomal protein L33 (MRPL33), nucle	MRPL33	0,00021983	1,39891
NM_004943 // RefSeq // Homo sapiens dystrophia myotonica, WD repeat containing (DMWD),	DMWD	0,0004224	1,51374
NM_004996 // RefSeq // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), memb	ABCC1	0,00024197	1,84534
NM_005399 // RefSeq // Homo sapiens protein kinase, AMP-activated, beta 2 non-catalytic	PRKAB2	0,00015505	-1,38553
NM_005499 // RefSeq // Homo sapiens ubiquitin-like modifier activating enzyme 2 (UBA2),	UBA2	0,0002127	1,41222
NM_005608 // RefSeq // Homo sapiens protein tyrosine phosphatase, receptor type, C-asso	PTPRCAP	0,00032835	-1,2394
NM_005629 // RefSeq // Homo sapiens solute carrier family 6 (neurotransmitter transport	SLC6A8	5,01E-05	-1,7957
NM_005688 // RefSeq // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), memb	ABCC5	0,00034443	1,80486
NM_005717 // RefSeq // Homo sapiens actin related protein 2/3 complex, subunit 5, 16kDa	ARPC5	0,00024769	-1,2103
NM_005762 // RefSeq // Homo sapiens tripartite motif containing 28 (TRIM28), mRNA. // c	TRIM28	2,12E-06	1,81273
NM_005764 // RefSeq // Homo sapiens PDZK1 interacting protein 1 (PDZK1IP1), mRNA. // ch	PDZK1IP1	0,00016658	-3,66578
NM_005814 // RefSeq // Homo sapiens glycoprotein A33 (transmembrane) (GPA33), mRNA. //	GPA33	1,27E-05	-5,19703
NM_006092 // RefSeq // Homo sapiens nucleotide-binding oligomerization domain containin	NOD1	0,00022548	1,57476
NM_006196 // RefSeq // Homo sapiens poly(rC) bind-	PCBP1	0,000192	1,32624

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ing protein 1 (PCBP1), mRNA. // chr2 /		11	
NM_006233 // RefSeq // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide I, 1	POLR2I	2,30E-05	1,47761
NM_006269 // RefSeq // Homo sapiens retinitis pigmentosa 1 (autosomal dominant) (RP1),	RP1	0,00027495	-1,63607
NM_006555 // RefSeq // Homo sapiens YKT6 v-SNARE homolog (S. cerevisiae) (YKT6), mRNA.	YKT6	0,00017022	1,46334
NM_006583 // RefSeq // Homo sapiens retinal pigment epithelium-derived rhodopsin homolo	RRH	0,00038208	-1,7899
NM_006653 // RefSeq // Homo sapiens fibroblast growth factor receptor substrate 3 (FRS3	FRS3	0,00036606	1,26124
NM_006666 // RefSeq // Homo sapiens RuvB-like 2 (E. coli) (RUVBL2), mRNA. // chr19 // 1	RUVBL2	0,00024297	1,63545
NM_006949 // RefSeq // Homo sapiens syntaxin binding protein 2 (STXBP2), transcript var	STXBP2	2,41E-05	-1,47895
NM_007059 // RefSeq // Homo sapiens kaptin (actin binding protein) (KPTN), mRNA. // chr	KPTN	0,00010502	1,46326
NM_007256 // RefSeq // Homo sapiens solute carrier organic anion transporter family, me	SLCO2B1	0,00033408	-1,74676
NM_012232 // RefSeq // Homo sapiens polymerase I and transcript release factor (PTRF),	PTRF	0,00023799	2,95904
NM_012267 // RefSeq // Homo sapiens HSPA (heat shock 70kDa) binding protein, cytoplasmic	HSPBP1	0,0001105	1,24592
NM_012279 // RefSeq // Homo sapiens zinc finger protein 346 (ZNF346), mRNA. // chr5 //	ZNF346	0,00032717	1,33646
NM_012416 // RefSeq // Homo sapiens RAN binding protein 6 (RANBP6), transcript variant	RANBP6	0,00031619	1,40515
NM_012467 // RefSeq // Homo sapiens tryptase gamma 1 (TPSG1), mRNA. // chr16 // 100 //	TPSG1	1,01E-05	-1,3725
NM_013234 // RefSeq // Homo sapiens eukaryotic translation initiation factor 3, subunit	EIF3K	0,00030494	1,44265
NM_014501 // RefSeq // Homo sapiens ubiquitin-conjugating enzyme E2S (UBE2S), mRNA. //	UBE2S	0,00040904	1,63133
NM_014516 // RefSeq // Homo sapiens CCR4-NOT transcription complex, subunit 3 (CNOT3),	CNOT3	0,00010444	1,5445
NM_014624 // RefSeq // Homo sapiens S100 calcium binding protein A6 (S100A6), mRNA. //	S100A6	6,25E-06	-1,47538
NM_014681 // RefSeq // Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 34 (DHX34),	DHX34	0,00016154	1,29357
NM_014763 // RefSeq // Homo sapiens mitochondrial ribosomal protein L19 (MRPL19), nucle	MRPL19	0,00029331	1,3835
NM_014909 // RefSeq // Homo sapiens vasohibin 1 (VASH1), mRNA. // chr14 // 100 // 72 //	VASH1	4,25E-05	-1,2245
NM_014946 // RefSeq // Homo sapiens spastin (SPAST), transcript variant 1, mRNA. // chr	SPAST	7,79E-05	1,59312

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_014957 // RefSeq // Homo sapiens DENN/MADD domain containing 3 (DENND3), mRNA. // ch	DENND3	0,000224 33	-1,50109
NM_015016 // RefSeq // Homo sapiens microtubule associated serine/threonine kinase 3 (M	MAST3	0,000192 05	-1,75067
NM_015030 // RefSeq // Homo sapiens FRY-like (FRYL), mRNA. // chr4 // 100 // 83 // 55 /	FRYL	0,000174 56	-1,30584
NM_015147 // RefSeq // Homo sapiens centrosomal protein 68kDa (CEP68), mRNA. // chr2 //	CEP68	0,000250 69	1,53034
NM_015185 // RefSeq // Homo sapiens Cdc42 guanine nucleotide exchange factor (GEF) 9 (A	ARHGEF 9	0,000235 48	-1,5908
NM_015335 // RefSeq // Homo sapiens mediator complex subunit 13-like (MED13L), mRNA. //	MED13L	0,000144 34	1,57466
NM_015428 // RefSeq // Homo sapiens zinc finger protein 473 (ZNF473), transcript varian	ZNF473	1,32E-06	1,68095
NM_015475 // RefSeq // Homo sapiens family with sequence similarity 98, member A (FAM98	FAM98A	1,54E-06	1,46883
NM_015603 // RefSeq // Homo sapiens coiled-coil domain containing 9 (CCDC9), mRNA. // c	CCDC9	0,000308 04	1,41536
NM_015629 // RefSeq // Homo sapiens PRP31 pre-mRNA processing factor 31 homolog (S. cer	PRPF31	2,25E-05	1,55764
NM_015710 // RefSeq // Homo sapiens glioma tumor suppressor candidate region gene 2 (GL	GLTSCR2	5,19E-05	1,51405
NM_016107 // RefSeq // Homo sapiens zinc finger RNA binding protein (ZFR), mRNA. // chr	ZFR	0,000140 51	1,32448
NM_016121 // RefSeq // Homo sapiens potassium channel tetramerisation domain containing	KCTD3	6,19E-05	-1,89187
NM_016265 // RefSeq // Homo sapiens zinc finger protein 12 (ZNF12), transcript variant	ZNF12	3,65E-05	1,40066
NM_016307 // RefSeq // Homo sapiens paired related homeobox 2 (PRRX2), mRNA. // chr9 //	PRRX2	0,000388 58	-1,33434
NM_016377 // RefSeq // Homo sapiens A kinase (PRKA) anchor protein 7 (AKAP7), transcrip	AKAP7	0,000110 73	1,74544
NM_016516 // RefSeq // Homo sapiens vacuolar protein sorting 54 homolog (S. cerevisiae)	VPS54	0,000145 16	1,31988
NM_016544 // RefSeq // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 27 (DNAJC	DNAJC27	1,73E-05	1,47881
NM_016955 // RefSeq // Homo sapiens Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRN	SEPSECS	0,000318 18	-1,69997
NM_017440 // RefSeq // Homo sapiens Mdm1 nuclear protein homolog (mouse) (MDM1), transc	MDM1	0,000202 26	1,47567
NM_017607 // RefSeq // Homo sapiens protein phosphatase 1, regulatory subunit 12C (PPP1	PPP1R12 C	3,84E-06	1,3566
NM_017707 // RefSeq // Homo sapiens ArfGAP with SH3 domain, ankyrin repeat and PH domai	ASAP3	0,000222 71	1,5287

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_017878 // RefSeq // Homo sapiens HRAS-like suppressor 2 (HRASLS2), mRNA. // chr11 //	HRASLS2	2,35E-06	-2,78784
NM_018028 // RefSeq // Homo sapiens sterile alpha motif domain containing 4B (SAMD4B),	SAMD4B	8,25E-05	1,43155
NM_018036 // RefSeq // Homo sapiens autophagy related 2B (ATG2B), mRNA. // chr14 // 100	ATG2B	0,000308 11	1,42686
NM_018845 // RefSeq // Homo sapiens solute carrier family 50 (sugar transporter), membe	SLC50A1	0,000357 94	-1,79767
NM_018945 // RefSeq // Homo sapiens phosphodiesterase 7B (PDE7B), mRNA. // chr6 // 100	PDE7B	3,37E-05	-1,25731
NM_020143 // RefSeq // Homo sapiens partner of NOB1 homolog (S. cerevisiae) (PNO1), mRN	PNO1	0,000274 75	1,68538
NM_020151 // RefSeq // Homo sapiens StAR-related lipid transfer (START) domain containi	STARD7	0,000362 6	1,25883
NM_020158 // RefSeq // Homo sapiens exosome component 5 (EXOSC5), mRNA. // chr19 // 100	EXOSC5	0,000135 47	1,30701
NM_020652 // RefSeq // Homo sapiens zinc finger protein 286A (ZNF286A), transcript vari	ZNF286A	0,000422 53	2,19621
NM_020829 // RefSeq // Homo sapiens KIAA1432 (KIAA1432), transcript variant 1, mRNA. //	KIAA143 2	0,000154 97	1,27707
NM_020978 // RefSeq // Homo sapiens amylase, alpha 2B (pancreatic) (AMY2B), mRNA. // ch	AMY2B	1,08E-05	-2,29554
NM_021107 // RefSeq // Homo sapiens mitochondrial ribosomal protein S12 (MRPS12), nucle	MRPS12	0,000109 55	1,36171
NM_021233 // RefSeq // Homo sapiens deoxyribonuclease II beta (DNASE2B), transcript var	DNASE2 B	0,000147 69	-1,24731
NM_021648 // RefSeq // Homo sapiens TSPY-like 4 (TSPYL4), mRNA. // chr6 // 100 // 100 /	TSPYL4	0,000115 2	1,44558
NM_021818 // RefSeq // Homo sapiens salvador homolog 1 (Drosophila) (SAV1), mRNA. // ch	SAV1	0,000286 89	-1,84494
NM_024075 // RefSeq // Homo sapiens tRNA splicing endonuclease 34 homolog (S. cerevisia	TSEN34	8,85E-06	1,50582
NM_024119 // RefSeq // Homo sapiens DEXH (Asp-Glu-X-His) box polypeptide 58 (DHX58), mR	DHX58	0,000174 34	-1,61011
NM_024676 // RefSeq // Homo sapiens SH3 domain containing 21 (SH3D21), transcript varia	SH3D21	5,39E-05	-2,60288
NM_024688 // RefSeq // Homo sapiens chromosome 10 open reading frame 68 (C10orf68), mRN	C10orf68	8,01E-06	-2,12512
NM_024866 // RefSeq // Homo sapiens adrenomedullin 2 (ADM2), transcript variant 1, mRNA	ADM2	8,76E-05	-1,31143
NM_025040 // RefSeq // Homo sapiens zinc finger protein 614 (ZNF614), mRNA. // chr19 //	ZNF614	0,000261 8	1,92899
NM_025201 // RefSeq // Homo sapiens pleckstrin homology domain containing, family O mem	PLEK- HO2	0,000318 17	1,31501
NM_025246 // RefSeq // Homo sapiens solute carrier	SLC35G2	0,000120	1,62626

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
family 35, member G2 (SLC35G2), tran		51	
NM_031485 // RefSeq // Homo sapiens glutamate-rich WD repeat containing 1 (GRWD1), mRNA	GRWD1	1,81E-06	1,5296
NM_032139 // RefSeq // Homo sapiens ankyrin repeat domain 27 (VPS9 domain) (ANKRD27), m	ANKRD27	3,24E-06	1,70059
NM_032490 // RefSeq // Homo sapiens chromosome 14 open reading frame 142 (C14orf142), m	C14orf142	8,91E-05	1,3147
NM_032530 // RefSeq // Homo sapiens zinc finger protein 594 (ZNF594), mRNA. // chr17 //	ZNF594	0,00019445	1,74392
NM_032635 // RefSeq // Homo sapiens transmembrane protein 147 (TMEM147), transcript var	TMEM147	0,00040838	1,33902
NM_033224 // RefSeq // Homo sapiens purine-rich element binding protein B (PURB), mRNA.	PURB	1,08E-06	1,56758
NM_052924 // RefSeq // Homo sapiens rhophilin, Rho GTPase binding protein 1 (RHPN1), mR	RHPN1	0,00034896	-1,41282
NM_080656 // RefSeq // Homo sapiens CDKN2A interacting protein N-terminal like (CDKN2AI	CDKN2AI PNL	0,00022583	1,694
NM_080662 // RefSeq // Homo sapiens peroxisomal biogenesis factor 11 gamma (PEX11G), mR	PEX11G	0,00025273	-1,21528
NM_080667 // RefSeq // Homo sapiens coiled-coil domain containing 104 (CCDC104), mRNA.	CCDC104	9,49E-07	1,41087
NM_080676 // RefSeq // Homo sapiens MACRO domain containing 2 (MACROD2), transcript var	MA- CROD2	0,00034241	-1,92941
NM_138389 // RefSeq // Homo sapiens family with sequence similarity 114, member A1 (FAM	FAM114A 1	2,49E-06	-1,46983
NM_144607 // RefSeq // Homo sapiens cytochrome b5 domain containing 1 (CYB5D1), mRNA. /	CYB5D1	8,91E-05	1,52863
NM_144736 // RefSeq // Homo sapiens chromosome 2 open reading frame 56 (C2orf56), nucle	C2orf56	2,19E-05	1,43026
NM_144992 // RefSeq // Homo sapiens von Willebrand factor A domain containing 3B (VWA3B	VWA3B	2,00E-05	-1,36939
NM_145243 // RefSeq // Homo sapiens OMA1 zinc metallopeptidase homolog (S. cerevisiae)	OMA1	7,61E-05	-1,78106
NM_152441 // RefSeq // Homo sapiens F-box and leucine-rich repeat protein 14 (FBXL14),	FBXL14	0,00016895	1,39127
NM_153329 // RefSeq // Homo sapiens aldehyde dehydrogenase 16 family, member A1 (ALDH16	ALDH16 A1	2,70E-06	1,42633
NM_172195 // RefSeq // Homo sapiens eukaryotic translation initiation factor 2B, subuni	EIF2B4	0,00033623	1,4457
NM_177542 // RefSeq // Homo sapiens small nuclear ribonucleoprotein D2 polypeptide 16.5	SNRPD2	9,61E-05	1,51587
NM_178001 // RefSeq // Homo sapiens protein phosphatase 2A activator, regulatory subuni	PPP2R4	0,00012692	1,38247
NM_181783 // RefSeq // Homo sapiens transmembrane and tetratricopeptide repeat containi	TMTC3	0,00010148	1,63587

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_183240 // RefSeq // Homo sapiens transmembrane protein 37 (TMEM37), mRNA. // chr2 //	TMEM37	1,49E-06	-1,66592
NM_198529 // RefSeq // Homo sapiens EF-hand calcium binding domain 5 (EFCAB5), transcri	EFCAB5	0,0001342	-1,47185
NM_198963 // RefSeq // Homo sapiens DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 (DHX5	DHX57	3,65E-06	1,58895
NM_199421 // RefSeq // Homo sapiens suppressor of cytokine signaling 4 (SOCS4), transcr	SOCS4	0,00019149	1,36856
NR_002181 // RefSeq // Homo sapiens pancreatic polypeptide 2 (PPY2), non-coding RNA. //	PPY2	0,00028262	-1,44853
NR_002201 // RefSeq // Homo sapiens ferritin, heavy polypeptide 1 pseudogene 3 (FTH1P3)	FTH1P3	0,00010698	1,30473
NR_002737 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 59A (SNORD59A), small	SNORD59A	0,00013025	1,86291
NR_003056 // RefSeq // Homo sapiens small nucleolar RNA, C/D box 67 (SNORD67), small nu	SNORD67	3,45E-05	1,3861
NR_024162 // RefSeq // Homo sapiens FK506 binding protein 1A, 12kDa pseudogene 1 (FKBP1	FKBP1A1	0,00022046	1,30617
NR_024567 // RefSeq // Homo sapiens uncharacterized LOC100130557 (LOC100130557), non-co	LOC100130557	0,00026386	1,34946
NR_026052 // RefSeq // Homo sapiens CENPB DNA-binding domains containing 1 pseudogene (	MGC2752	2,96E-06	1,63126
NR_026761 // RefSeq // Homo sapiens long intergenic non-protein coding RNA 467 (LINC004	LINC00467	0,00021377	-1,70439
NR_026846 // RefSeq // Homo sapiens anaphase promoting complex subunit 1 pseudogene (LO	LOC285074	0,00025847	1,34842
NR_027280 // RefSeq // Homo sapiens SUMO1 activating enzyme subunit 1 (SAE1), transcrip	SAE1	4,34E-07	1,78488
NR_028408 // RefSeq // Homo sapiens uncharacterized LOC400027 (LOC400027), non-coding R	LOC400027	0,00038859	1,35507
NR_028450 // RefSeq // Homo sapiens branched chain amino-acid transaminase 2, mitochond	BCAT2	0,00022739	1,47055
NR_029663 // RefSeq // Homo sapiens microRNA 15b (MIR15B), microRNA. // chr3 // 100 //	MIR15B	1,89E-05	1,7084
NR_031621 // RefSeq // Homo sapiens microRNA 1289-2 (MIR1289-2), microRNA. // chr5 // 1	MIR1289-2	0,00020231	1,38227
NR_031649 // RefSeq // Homo sapiens microRNA 1247 (MIR1247), microRNA. // chr14 // 100	MIR1247	0,00032926	-1,50317
NR_033237 // RefSeq // Homo sapiens family with sequence similarity 3, member A (FAM3A)	FAM3A	0,00024153	-1,35016
NR_033998 // RefSeq // Homo sapiens hCG2028352-like (LOC729970), non-coding RNA. // chr	LOC729970	0,00040419	1,47659
NR_037504 // RefSeq // Homo sapiens microRNA 3939 (MIR3939), microRNA. // chr6 // 100 /	MIR3939	0,00024971	2,36522
NR_037869 // RefSeq // Homo sapiens uncharacter-	LOC6531	0,000335	-1,28991

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
ized LOC653160 (LOC653160), non-coding R	60	32	
NR_038262 // RefSeq // Homo sapiens MIR210 host gene (non-protein coding) (MIR210HG), n	MIR210HG	5,61E-05	-1,72839
NR_038379 // RefSeq // Homo sapiens leucine carboxyl methyltransferase 1 pseudogene (LO	LOC554206	1,37E-06	1,44265
NR_038948 // RefSeq // Homo sapiens uncharacterized LOC100506136 (LOC100506136), non-co	LOC100506136	0,00022821	1,81449
NR_045382 // RefSeq // Homo sapiens uncharacterized LOC100507066 (LOC100507066), non-co	LOC100507066	0,00040365	1,22414
NR_045789 // RefSeq // Homo sapiens NOP2/Sun domain family, member 4 (NSUN4), transcrip	NSUN4	0,0001178	-1,20429
NR_046229 // RefSeq // Homo sapiens uncharacterized LOC100508120 (LOC100508120), non-co	LOC100508120	0,00012533	-2,52892
NR_046262 // RefSeq // Homo sapiens uncharacterized LOC646719 (LOC646719), non-coding R	LOC646719	0,00020155	1,78257
TCONS_00000362-XLOC_000509 // Rinn lincRNA // linc-CFH-3 chr1:+:193648023-193696313 //		8,51E-05	-1,42106
TCONS_00001318-XLOC_000600 // Rinn lincRNA // linc-RHOU chr1:+:228688982-228697976 // c		0,00019276	-1,42061
TCONS_00002986-XLOC_001636 // Rinn lincRNA // linc-INSIG2-2 chr2:+:118593925-118595780		0,00035564	-1,40949
TCONS_00003473-XLOC_002443 // Rinn lincRNA // linc-TMEFF2-3 chr2:-:194746279-194755854		8,74E-05	1,30483
TCONS_00005118-XLOC_002032 // Rinn lincRNA // linc-RBKS-5 chr2:-:28646220-28646862 // c		0,00010592	1,38752
TCONS_00005685-XLOC_002961 // Rinn lincRNA // linc-ADIPOQ chr3:+:186525480-186535910 //		0,00037132	-1,2387
TCONS_00008078-XLOC_003544 // Rinn lincRNA // linc-TMEM165 chr4:+:56251872-56253958 //		0,00024879	-2,7085
TCONS_00011423-XLOC_005555 // Rinn lincRNA // linc-C6orf70 chr6:+:170125599-170139088 /		0,00033668	1,92401
TCONS_00013672-XLOC_006331 // Rinn lincRNA // linc-COX19 chr7:-:1019649-1020276 // chr7		4,94E-05	-1,29445
TCONS_00016692-XLOC_007556 // Rinn lincRNA // linc-RABGAP1 chr9:+:125693948-125702599 /		6,63E-05	1,47753
TCONS_00018282-XLOC_008558 // Rinn lincRNA // linc-RPP30-1 chr10:+:92618126-92621421 //		0,00042604	1,32674
TCONS_00018897-XLOC_008756 // Rinn lincRNA // linc-ABI1-1 chr10:-:27269560-27271723 //		4,08E-05	-2,45908
TCONS_00020906-XLOC_010185 // Rinn lincRNA // linc-APPL2-3 chr12:-:106180060-106404785		0,00034005	-1,4611
TCONS_00021545-XLOC_010373 // Rinn lincRNA // linc-GTF2F2-1 chr13:+:45620724-45657260 /		7,23E-05	1,22023
TCONS_00021615-XLOC_010543 // Rinn lincRNA // linc-USP12-2 chr13:-:27810418-27810948 //		2,90E-09	-3,82547

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
TCONS_00021854-XLOC_010448 // Rinn lincRNA // linc-SLITRK5-14 chr13:+:80367942-80369398		0,00035546	-1,3146
TCONS_00022239-XLOC_010544 // Rinn lincRNA // linc-USP12-5 chr13:-:27819822-27824854 //		2,20E-05	-1,78705
TCONS_00027274-XLOC_013283 // Rinn lincRNA // linc-ZNF681-5 chr19:-:28262961-28264517 //		0,00012643	1,96627
TCONS_00027541-XLOC_013072 // Rinn lincRNA // linc-LGALS13 chr19:+:40018979-40019553 //		9,73E-05	1,25089
TCONS_00028814-XLOC_013888 // Rinn lincRNA // linc-JAM2-2 chr21:+:26467334-26475983 //		2,81E-05	-1,2634
XM_001713850 // RefSeq // PREDICTED: Homo sapiens anaphase-promoting complex subunit 1-	LOC730268	8,86E-05	1,54381
XR_108351 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100505516 (LOC100505516)	LOC100505516	0,00021728	-1,41696
XR_109972 // RefSeq // PREDICTED: Homo sapiens SOS1 intronic transcript 1 (non-protein	SOS1-IT1	1,00E-05	1,74497
XR_111249 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100509976 (LOC100509976)	LOC100509976	8,35E-06	2,67012
XR_133207 // RefSeq // PREDICTED: Homo sapiens hypothetical LOC100505703 (LOC100505703)	LOC100505703	0,00018176	-1,32568
Z26248 // GenBank // H.sapiens mRNA for eosinophil granule major basic protein. // chr1	PRG2	0,00033489	-2,42157

Herebelow (see tables 9 to 14) are listed collections of sets of genes, of which the variation of the expression level is based on the reference value established by PCA analysis, along with its corresponding individual p-values and fold-changes.

5 Those sets of genes are grouped based on their most preferred use as combinations of PDAC-marker genes for:

- determining the prognosis of an individual having PDAC (table 9);
- determining, on a PDAC tumor sample from said individual, the efficiency of SN-38/Irinotecan (table 10); oxaliplatin (table 11); gemcitabine (table 12); docetaxel (table

10 13) and 5-fluorouracil (table 14).

The fold-change column indicates the variation of the expression of the corresponding gene product, compared to a reference value. The reference value is calculated as shown in the Material & Methods section, using Gene set enrichment analysis (GSEA) performed on the Broad Institute Platform and statistical significance (false discovery rate, FDR) was set at 0.25.

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The gene symbol is indicated (if available), along with its reference number in the corresponding database (REFSEQ, ENSEMBL, GENBANK, and/or LNCipedia).

Table 9: Short VS Long-term survival

Reference (REF-SEQ/ENSEMBL/GENBANK/LNCipedia)	Gene Symbol	p-value	Fold-Change
NM_013389 // RefSeq Niemann-Pick disease, type C1, gene	NPC1L1	3,07E-18	-10,3772
NM_000720 // RefSeq // calcium channel, voltage-dependent, L type, alpha 1D subunit	CACNA1D	7,09E-18	-5,47623
ENST00000261024 // ENSEMBL // solute carrier family 40 (iron-regulated transporter	SLC40A1	5,36E-16	-9,56377
NM_006017 // RefSeq // prominin 1	PROM1	7,29E-16	-14,3953
NM_020208 // RefSeq // solute carrier family 6	SLC6A20	3,78E-14	-6,2697
NM_004852 // RefSeq // one cut homeobox 2	ONECUT2	1,48E-12	-3,51155
AF007194 // GenBank // mucin 3A	MUC3A	1,54E-12	-18,8374
NM_000492 // RefSeq // cystic fibrosis transmembrane conductance regulator	CFTR	8,40E-12	-19,4273
ENST00000369583 // ENSEMBL // dual specificity phosphatase 5	DUSP5	3,95E-09	3,05393
NM_003637 // RefSeq // integrin, alpha 10	ITGA10	7,88E-09	4,32095
ENST00000290705 // ENSEMBL // metallothionein 1A	MT1A	5,64E-08	9,37706
NM_014344 // RefSeq // four jointed box 1	FJX1	1,35E-07	4,3145
NM_003380 // RefSeq // vimentin	VIM	7,03E-06	3,82123

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Table 10: Efficiency of SN-38 (Irinotecan active metabolite)

Reference	Gene Symbol	p-value	Fold-Change
NM_000197 // RefSeq // hydroxysteroid (17-beta) dehydrogenase 3	HSD17B3	1,28E-07	-2,74982
NM_020192 // RefSeq // YaeI domain containing 1	YAE1D1	9,70E-07	-1,61835
NM_001195296 // RefSeq // mirror-image polydactyly 1	MIPOL1	1,52E-06	-1,61943

NM_001238 // RefSeq // cyclin E1	CCNE1	6,75E-08	1,70632
NR_045553 // RefSeq // thrombospondin 3 (THBS3)	THBS3	8,00E-06	1,93413
NM_004619 // RefSeq // TNF receptor-associated factor 5	TRAF5	2,68E-05	3,13128

Table 11: Efficiency of oxaliplatin

Reference	Gene Symbol	p-value	Fold-Change
TCONS_00025293-XLOC_012095 // Rinn lincRNA // linc-ALOX12-1 chr17:+:6840593-6857728 // arachidonate 12-lipoxygenase pseudogene 2	ALOX12P2	3,35E-09	-6,94788
ENST00000264228 // ENSEMBL // Steroid 5-Alpha-Reductase 3	SRD5A3	1,46E-08	-3,81237
ENST00000395601 // ENSEMBL // Syntrophin, beta 1	SNTB1	3,44E-08	-4,19721
NM_002245 // RefSeq // potassium channel, subfamily K, member 1	KCNK1	4,17E-06	-2,4294
NM_003532 // RefSeq // histone cluster 1, H3e	HIST1H3E	7,33E-06	-4,39238
ENST00000354921 // ENSEMBL //	SEC16B	1,24E-05	-4,95166
NM_032457 // RefSeq // protocadherin 7	PCDH7	2,47E-05	-6,06759
NM_000895 // RefSeq // leukotriene A4 hydrolase	LTA4H	2,94E-06	2,35941
ENST00000262878 // ENSEMBL //	SAMHD1	7,20E-06	3,98971
NR_003125 // RefSeq // small nucleolar RNA, C/D box 14E	SNORD14E	1,14E-05	2,40066
NM_005044 // RefSeq // protein kinase, X-linked (PRKX)	PRKX	1,36E-05	2,58025

Table 12: Efficiency of gemcitabine

Reference	Gene Symbol	p-value	Fold-Change
NM_014505 // RefSeq // potassium large conductance calcium-activated chann	KCNMB4	6,35E-11	-3,3897
NR_039722 // RefSeq // microRNA 4500	MIR4500	5,51E-09	-27,9959
NM_001661 // RefSeq // ADP-ribosylation factor-like 4D	ARL4D	6,76E-08	-5,20681
NR_031611 // RefSeq // Homo sapiens microRNA	MIR1206	5,51E-06	-7,06005

1206 (MIR1206), microRNA. // chr8 // 100 /			
ENST00000373004 // ENSEMBL // Sushi-Repeat Containing Protein X-Linked 2	SRPX2	9,60E-06	-3,06264
NM_006005 // RefSeq // Wolfram syndrome 1	WFS1	1,69E-05	-2,85621
NM_006823 // RefSeq // protein kinase (cAMP-dependent, catalytic) inhibitor	PKIA	6,46E-10	7,40614
NR_024554 // RefSeq // Rho-related BTB domain containing 1	RHOBTB1	7,69E-08	2,75759
AK128855 // GenBank // cDNA FLJ46652 fis, clone TRACH3005102	AK128855	8,85E-07	3,27341
NM_138809 // RefSeq // carboxymethylenebutenolidase homolog	CMBL	1,77E-06	2,74107

Table 13: Efficiency of docetaxel

Reference	Gene Symbol	p-value	Fold-Change
NM_182540 // RefSeq // DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	DDX26B	1,05E-07	-2,07652
NM_024763 // RefSeq // WD repeat domain 78 (WDR78), transcript variant 1,	WDR78	4,79E-07	-2,20452
NM_005359 // RefSeq // SMAD family member 4	SMAD4	2,36E-06	4,58279

Table 14: Efficiency of 5-fluorouracil (5FU)

Reference	Gene Symbol	p-value	Fold-Change
NM_001004320 // RefSeq // alkylglycerol monooxygenase	AGMO	8,17E-06	-5,67111
NM_001955 // RefSeq // endothelin 1 (EDN1)	EDN1	5,30E-05	-4,42114
NM_004313 // RefSeq // arrestin, beta 2	ARRB2	3,89E-07	2,03526
NM_001123375 // RefSeq // histone cluster 2, H3d	HIST2H3D	1,05E-06	2,96225

SEQUENCE LISTING

For reference, one nucleic acid encoded by a PDAC-marker gene of the invention is detailed herebelow. Each sequence corresponds to the complementary DNA of the said nucleic acid encoded by said PDAC-marker gene.

5

<i>SEQID N°1-13</i>	
SEQID N°1	CACNA1D
SEQID N°2	CFTR
SEQID N°3	MUC3A
SEQID N°4	NPC1L1
SEQID N°5	ONECUT2
SEQID N°6	PROM1
SEQID N°7	SLC6A20
SEQID N°8	SLC40A1
SEQID N°9	DUSP5
SEQID N°10	FJX1
SEQID N°11	ITGA10
SEQID N°12	MT1A
SEQID N°13	VIM
<i>SEQID N°14-19</i>	
SEQID N°14	HSD17B3
SEQID N°15	YAE1D1
SEQID N°16	MIPOL1
SEQID N°17	CCNE1
SEQID N°18	THBS3
SEQID N°19	TRAF5
<i>SEQID N°20-30</i>	

SEQID N°20	ALOX12P2
SEQID N°21	SRD5A3
SEQID N°22	SNTB1
SEQID N°23	KCNK1
SEQID N°24	HIST1H3E
SEQID N°25	SEC16B
SEQID N°26	PCDH7
SEQID N°27	LTA4H
SEQID N°28	SAMHD1
SEQID N°29	SNORD14E
SEQID N°30	PRKX
<i>SEQID N°31-33</i>	
SEQID N°31	DDX26B
SEQID N°32	WDR78
SEQID N°33	SMAD4
<i>SEQID N°34-37</i>	
SEQID N°34	AGMO
SEQID N°35	EDN1
SEQID N°36	ARRB2
SEQID N°37	HIST2H3D
<i>SEQID N°38-47</i>	
SEQID N°38	KCNMB4
SEQID N°39	MIR4500
SEQID N°40	ARL4D
SEQID N°41	MIR1206
SEQID N°42	SRPX2

SEQID N°43	WFS1
SEQID N°44	PKIA
SEQID N°45	RHOBTB1
SEQID N°46	AK128855
SEQID N°47	CMBL

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> 2

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> 3

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CLAIMS

1. An *in vitro* or *ex vivo* method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency of a compound for treating PDAC in said individual, comprising the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group of PDAC marker genes consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1;

a2) measuring, in a biological sample from said individual, the expression level of one or more gene selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D;

b) determining the prognosis of said individual, or the efficiency of said compound from the measurement performed in steps a1) and a2).

2. The method according to claim 1, wherein the method is for determining the short-term and long-term survival of said individual; or alternatively for determining the level of differentiation of Pancreatic Adenocarcinoma in said individual.

3. The method according to claim 1, wherein the compound is selected from the group consisting of: gemcitabine; oxaliplatin; 5-fluorouracil (5FU); docetaxel; Irinotecan; and/or derivatives thereof and/or combinations thereof.

4. The method according to any one of the preceding claims, wherein the biological sample from said individual is a tumour sample derived from a Pancreatic Adenocarcinoma (PDAC).

5. The method according to the preceding claim, wherein the biological sample is selected from the group consisting of a xenograft or a primary culture from said individual.

6. The method according to any one of the preceding claims, wherein the measurement in steps a1) and a2) is achieved by using at least one labelled or unlabelled

probe, preferably selected from the group consisting of DNA oligonucleotides and RNA oligonucleotides.

7. The method according to the preceding claim, wherein the said labelled or unlabelled probe is complementary to:

- 5 - at least one nucleic acid selected from a first group consisting of: SEQ ID NOs 1-8; SEQ ID NOs 14-16; SEQ ID NOs 20-26; SEQ ID NOs 31-32; SEQ ID NOs 34-35; SEQ ID NOs 38-43 or
- at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 9-13; SEQ ID NOs 17-19; SEQ ID NOs 27-30; SEQ ID NO 33; SEQ ID NOs 36-37; SEQ ID
- 10 NOs 44-47.

8. A composition comprising:

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1;
- 15 MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC-marker genes selected from a second group consisting of: DUSP5; FJX1;
- 20 ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

9. A kit comprising

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC marker genes selected from a first group consisting of: CACNA1D; CFTR;
- 25 MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one
- 30 or more PDAC marker genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

10. A solid support consisting of

- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC marker genes selected from a first group consisting of: CACNA1D; CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1; HSD17B3; YAE1D1; 5 MIPOL1; ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7; KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1; DDX26B; WDR78; AGMO; and EDN1; and
- at least one probe allowing the quantitative measurement of the expression levels of one or more PDAC marker genes selected from a second group consisting of: DUSP5; FJX1; 10 ITGA10; MT1A; VIM; CCNE1; THBS3; TRAF5; LTA4H; SAMHD1; SNORD14E; PRKX; PKIA; RHOBTB1; AK128855; CMBL; SMAD4; ARRB2; and HIST2H3D.

11. A composition as claimed in claim 8, or a kit as claimed in claim 9, or a solid support as claimed in claim 10, comprising:

- at least one probe allowing the quantitative measurement of the expression levels of at 15 least one nucleic acid selected from a first group consisting of: SEQ ID NOs 1-8; SEQ ID NOs 14-16; SEQ ID NOs 20-26; SEQ ID NOs 31-32; SEQ ID NOs 34-35; SEQ ID NOs 38-43 and
- at least one probe allowing the quantitative measurement of the expression levels of at least one nucleic acid selected from a second group consisting of: SEQ ID NOs 9-13; SEQ 20 ID NOs 17-19; SEQ ID NOs 27-30; SEQ ID NO 33; SEQ ID NOs 36-37; SEQ ID NOs 44-47.

12. A composition as claimed in claims 8 or 11, or a kit as claimed in claims 9 or 11, or a solid support as claimed in claims 10 or 11, for use for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), or the efficiency 25 of a compound for treating said individual.

13. An *in vitro* or *ex vivo* method for determining the prognosis of an individual having Pancreatic Adenocarcinoma (PDAC), comprising the steps of:

- a1) measuring, in a biological sample from said individual, the expression level of one or more PDAC marker genes selected from a first group consisting of: CACNA1D; 30 CFTR; MUC3A; NPC1L1; ONECUT2; PROM1; SLC6A20; SLC40A1;

a2) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a second group consisting of: DUSP5; FJX1; ITGA10; MT1A; VIM;

5 b) determining the prognosis of said individual from the measurement performed in steps a1) and a2).

14. An *in vitro* or *ex vivo* method for determining the efficiency of Irinotecan and derivatives thereof, for treating Pancreatic Adenocarcinoma (PDAC) in said individual, comprising the steps of:

10 a1) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a first group consisting of: HSD17B3; YAE1D1; and MIPOL1;

a2) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a second group consisting of: CCNE1; THBS3; and TRAF5;

15 b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

15. An *in vitro* or *ex vivo* method for determining the efficiency of oxaliplatin and derivatives thereof, for treating Pancreatic Adenocarcinoma (PDAC) in said individual, comprising the steps of:

20 a1) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a first group consisting of: ALOX12P2; SRD5A3; SNTB1; KCNK1; HIST1H3E; SEC16B; PCDH7;

a2) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a second group consisting of: LTA4H; SAMHD1; 25 SNORD14E; PRKX;

b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

16. An *in vitro* or *ex vivo* method for determining the efficiency of gemcitabine and derivatives thereof, for treating Pancreatic Adenocarcinoma (PDAC) in said 30 individual, comprising the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a first group consisting of: KCNMB4; MIR4500; ARL4D; MIR1206; SRPX2; WFS1;

5 a2) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a second group consisting of: PKIA; RHOTB1; AK128855; CMBL;

b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

10 17. An *in vitro* or *ex vivo* method for determining the efficiency of docetaxel and derivatives thereof, for treating Pancreatic Adenocarcinoma (PDAC) in said individual, comprising the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a first group consisting of: DDX26B and WDR78;

15 a2) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a second group consisting of: SMAD4;

b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

20 18. An *in vitro* or *ex vivo* method for determining the efficiency of 5-fluorouracil (5FU) and derivatives thereof, for treating Pancreatic Adenocarcinoma (PDAC) in said individual, comprising the steps of:

a1) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a first group consisting of: AGMO and EDN1;

a2) measuring, in a biological sample from said individual, the expression level of one or more genes selected from a second group consisting of: ARRB2 and HIST2H3D;

25 b) determining the efficiency of said compound from the measurement performed in steps a1) and a2).

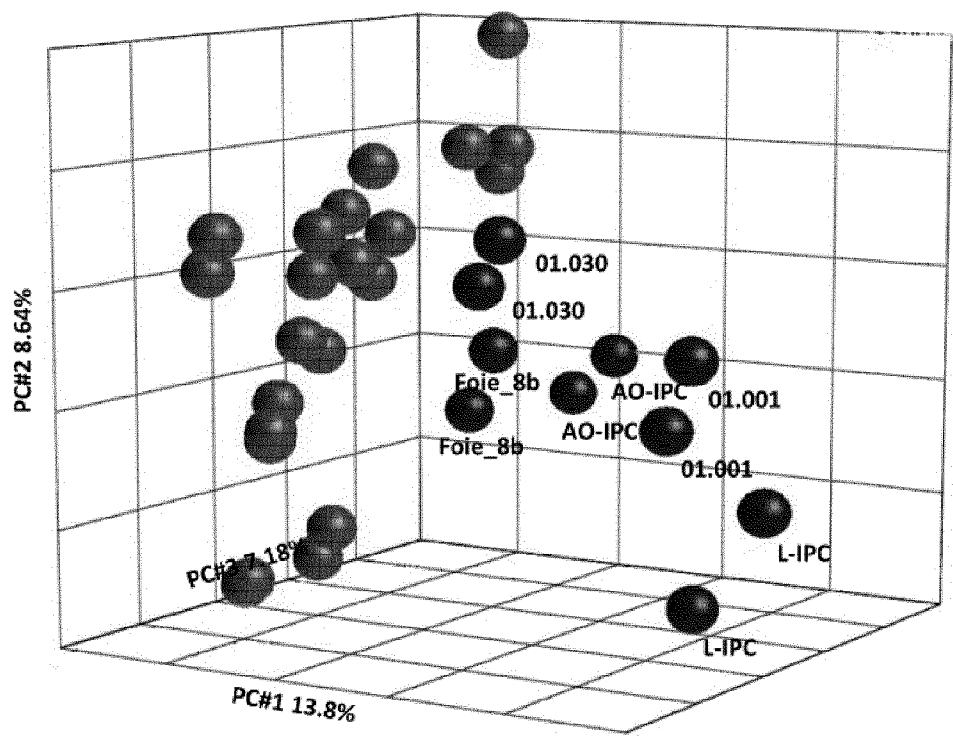


Figure 1A

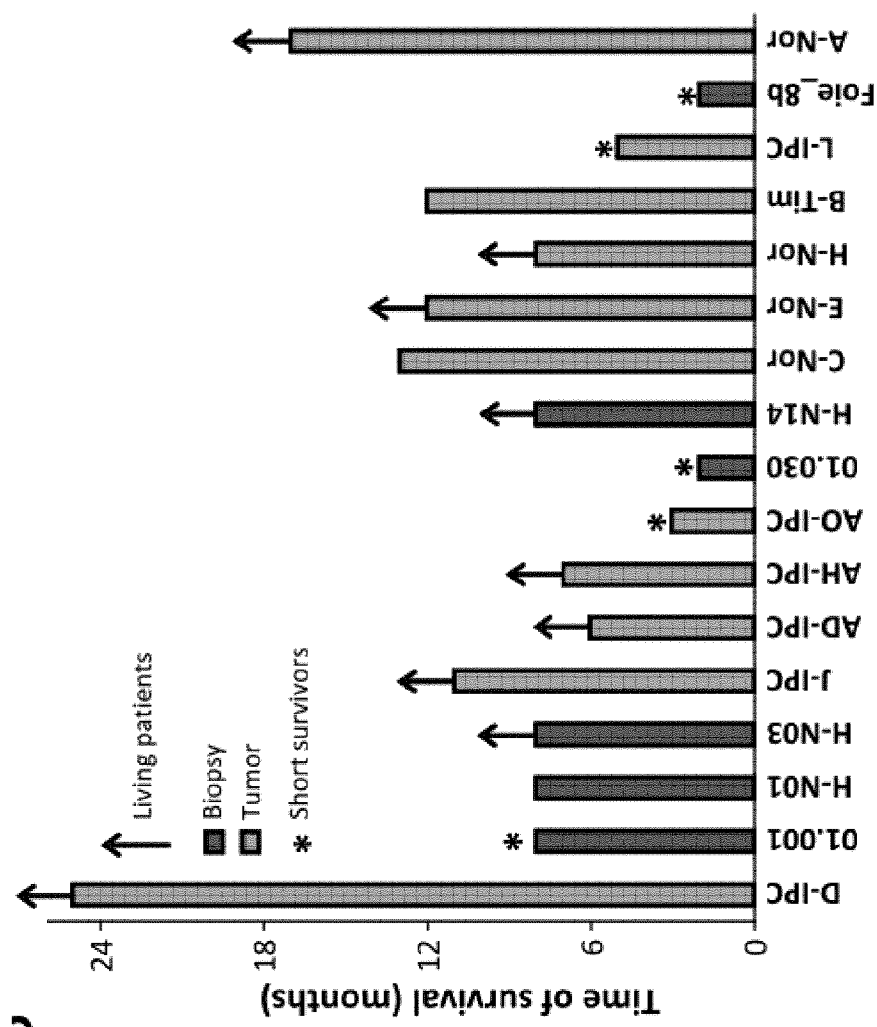


Figure 1B

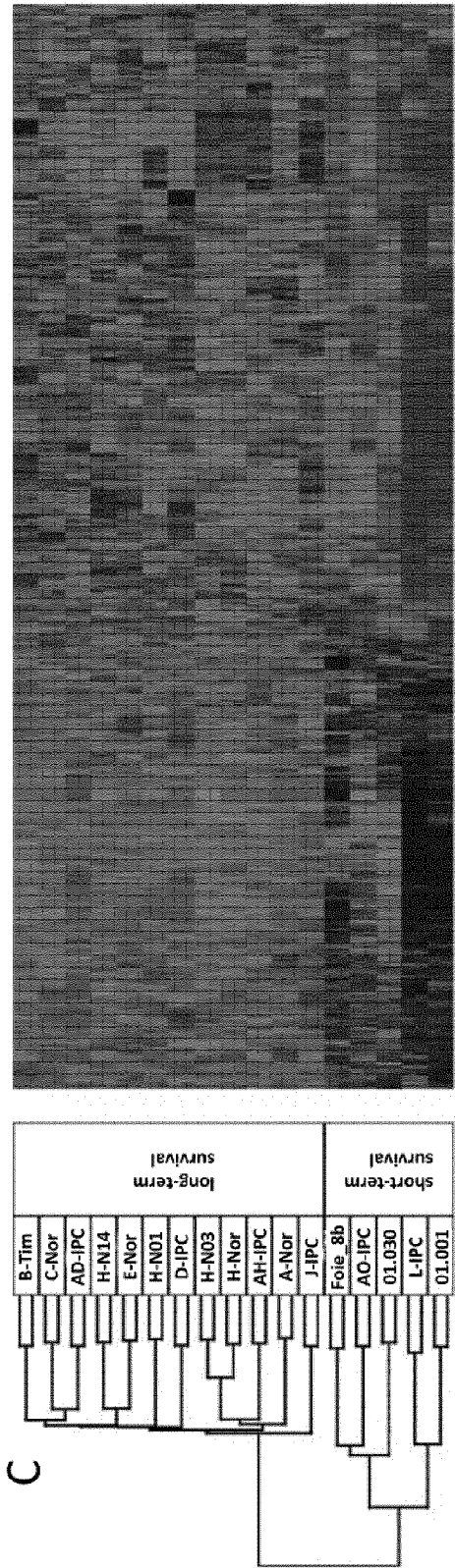


Figure 1C

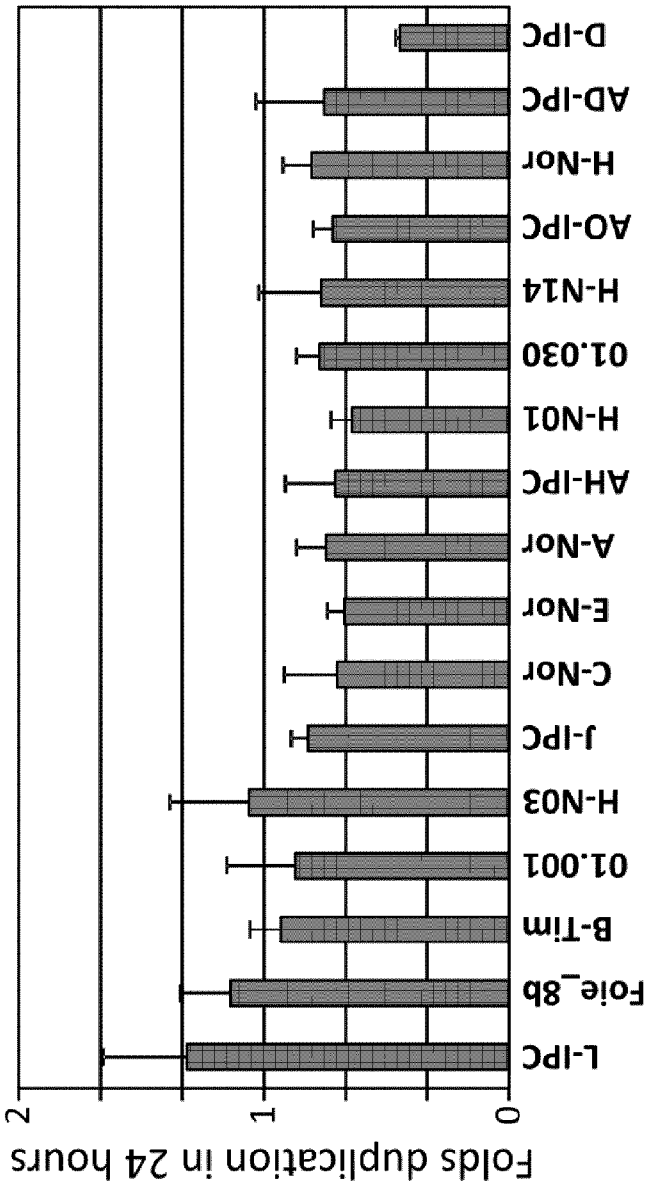
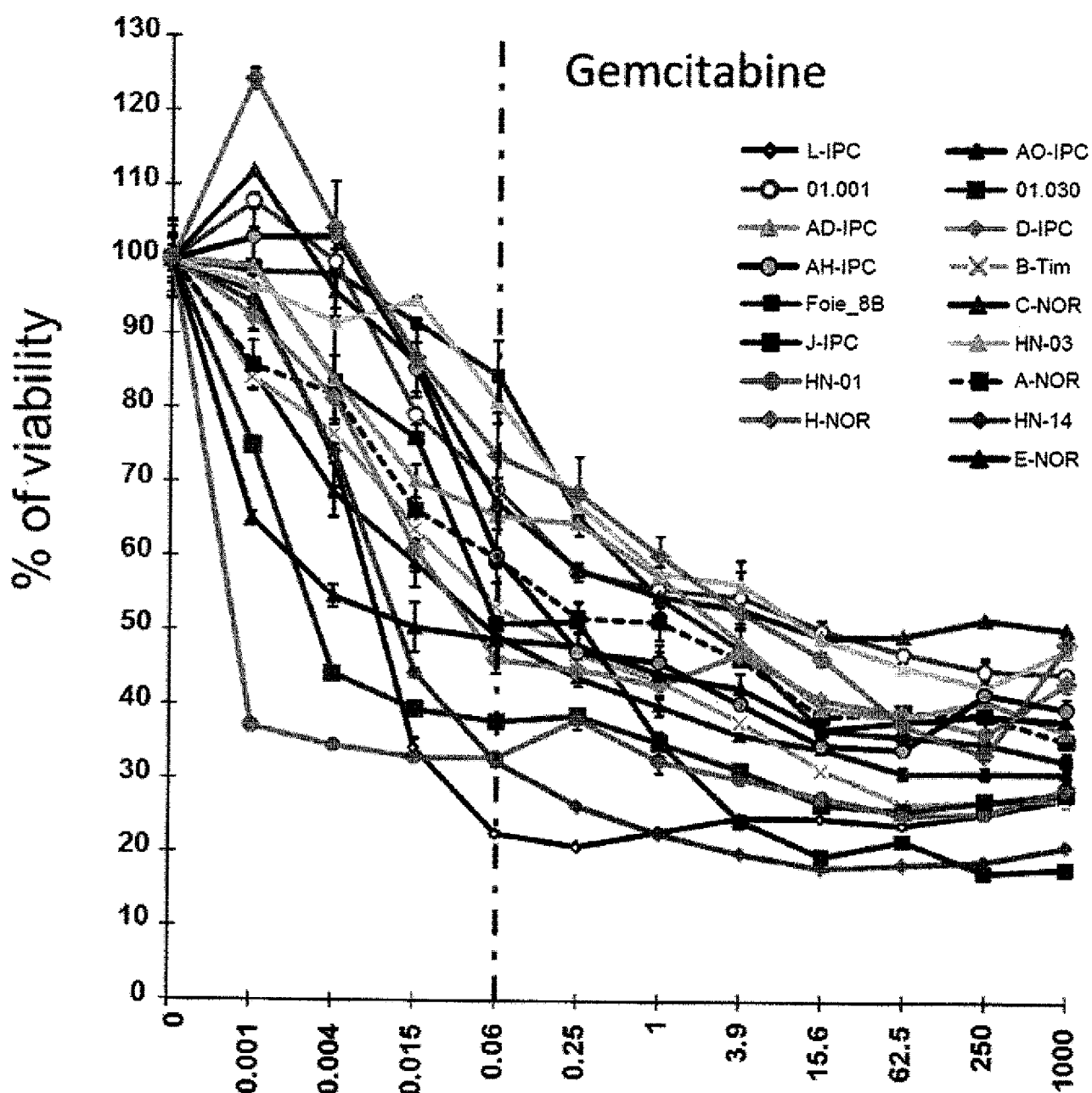
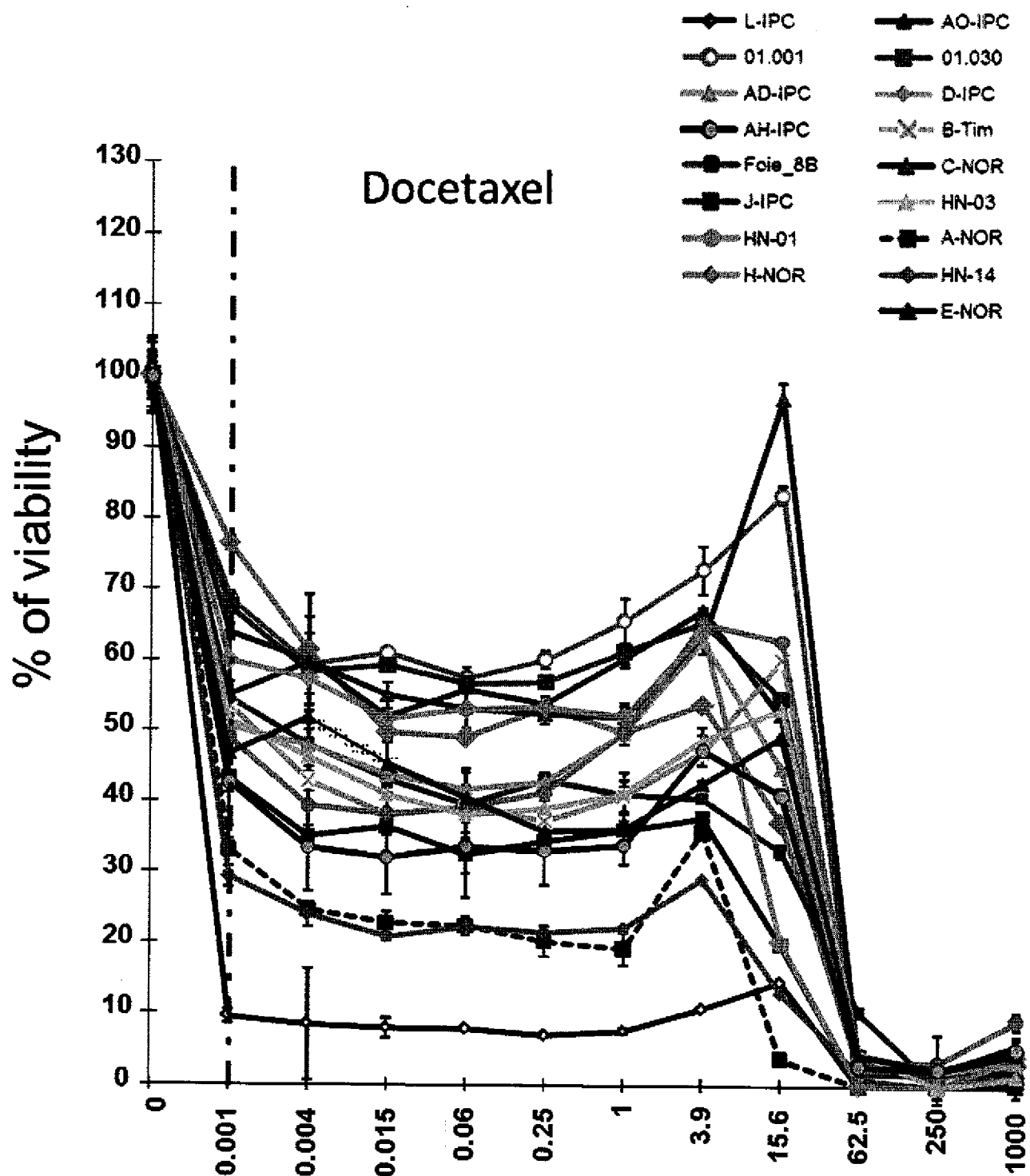
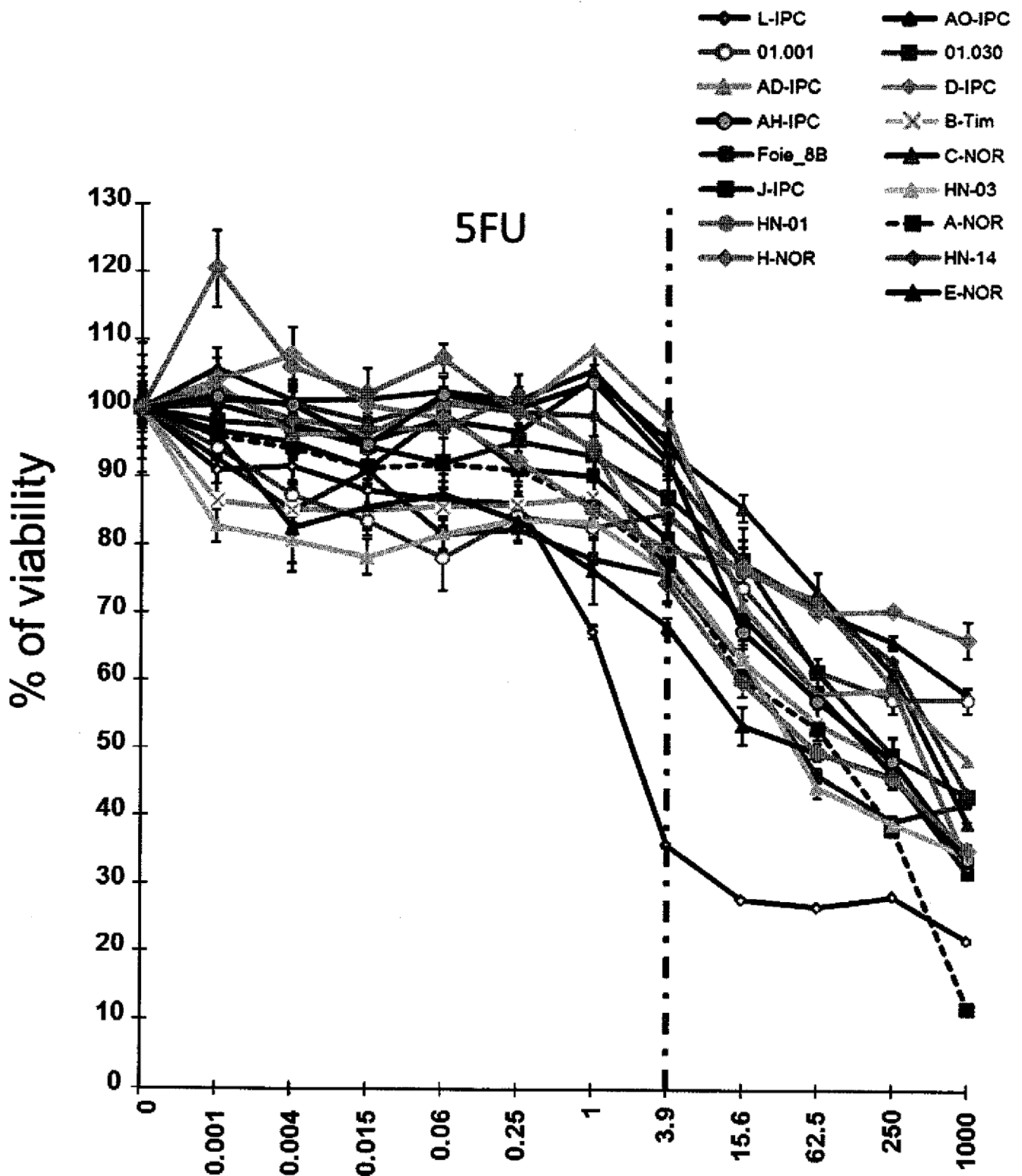
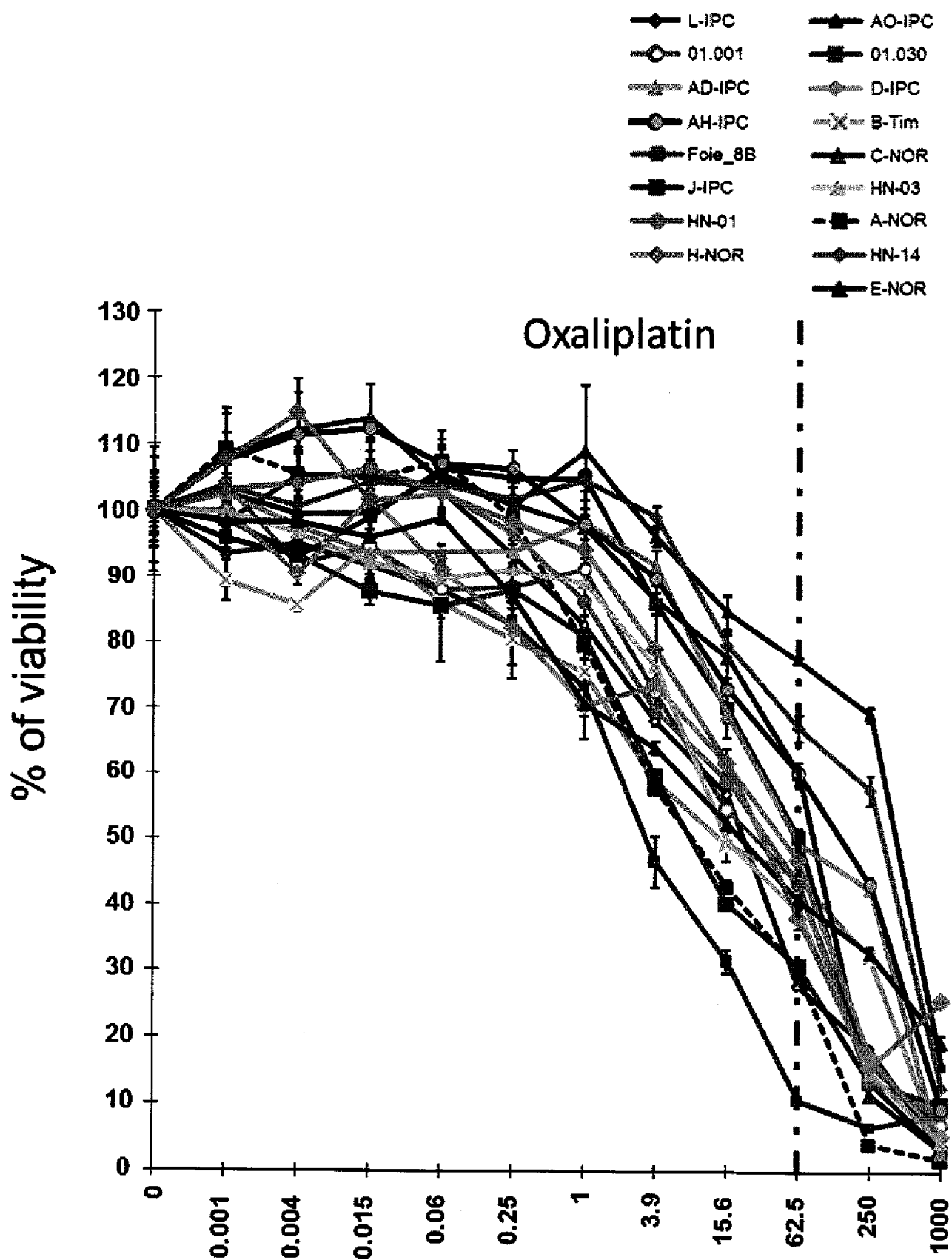


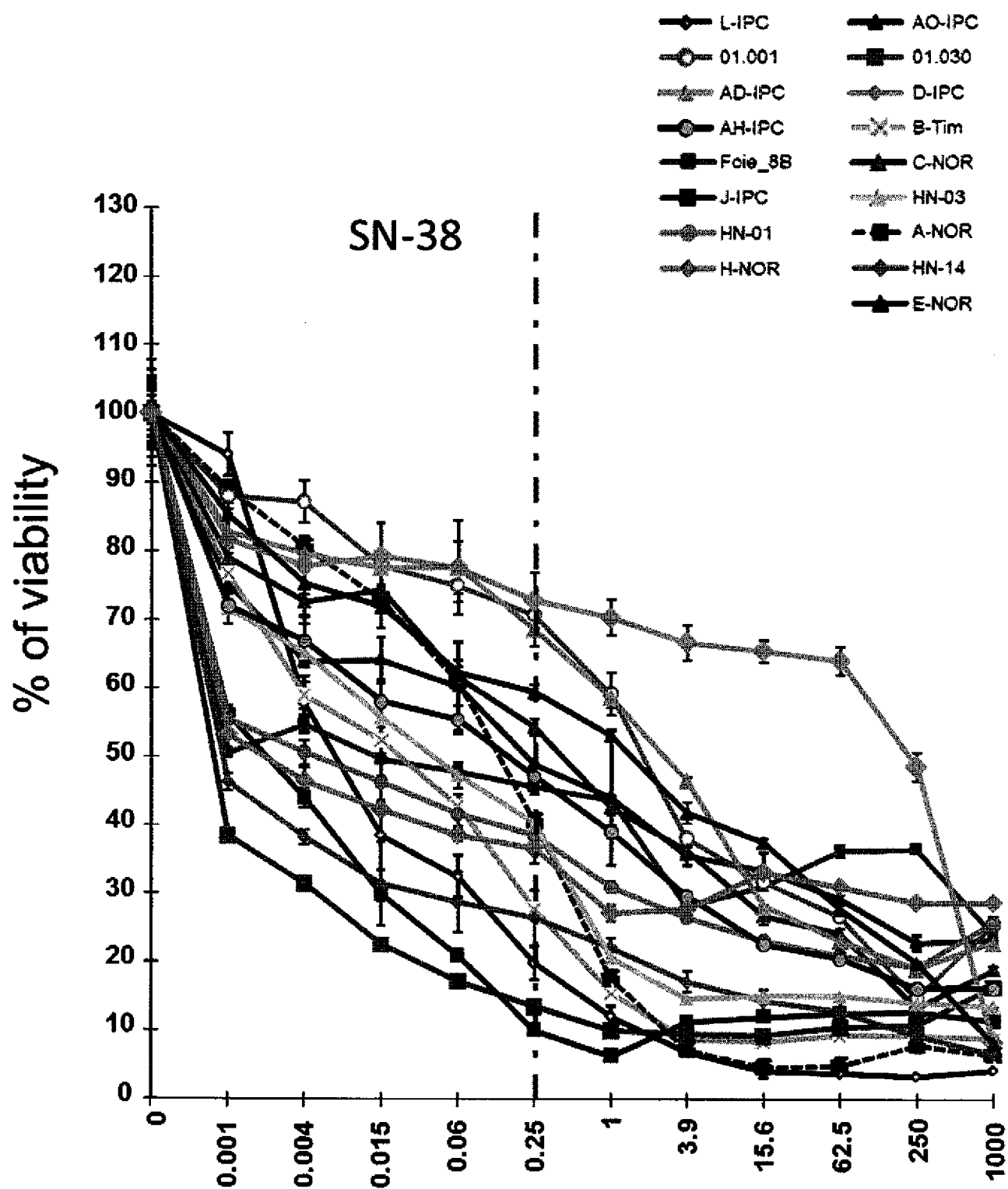
Figure 2

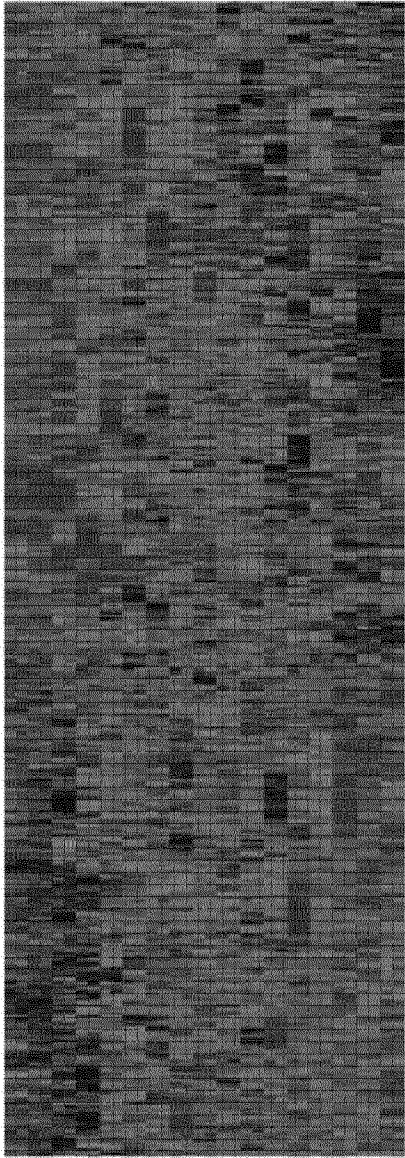
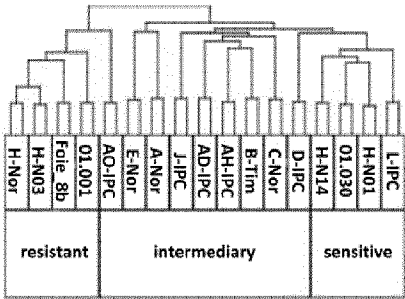
**Figure 3**

**Figure 3 (continued)**

**Figure 3 (continued)**

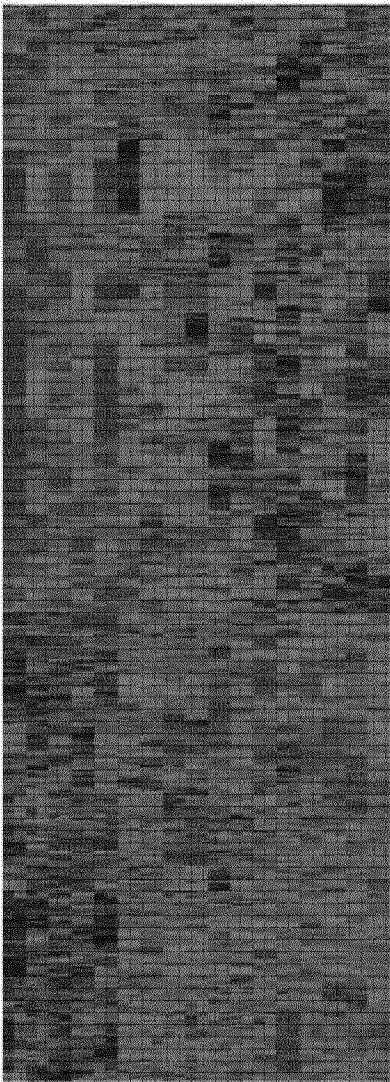
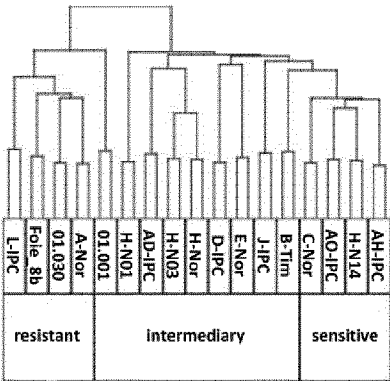
**Figure 3 (continued)**

Figure 3 (end)



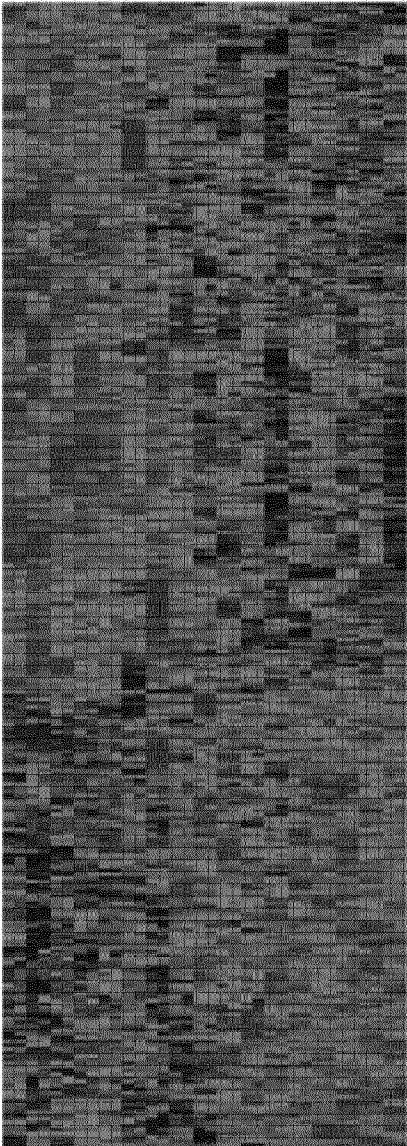
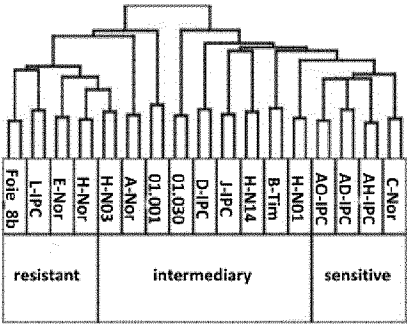
gemcitabine

Figure 4A



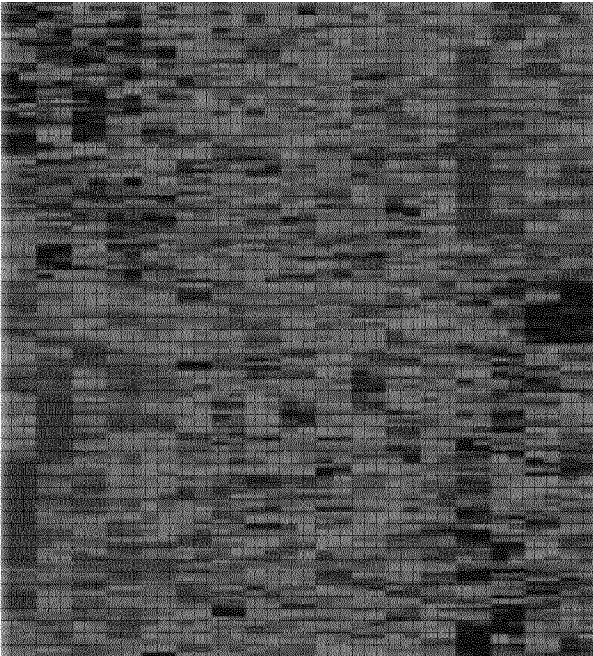
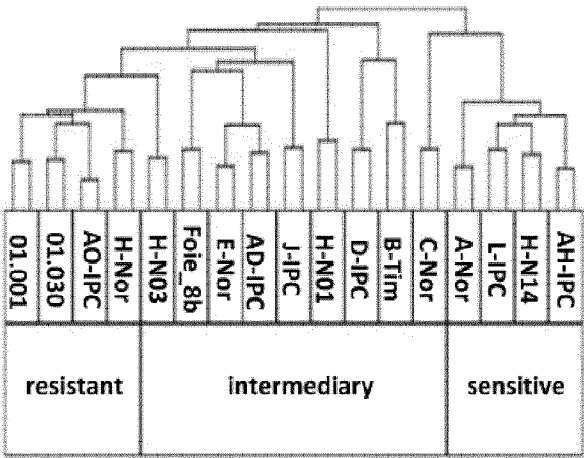
oxaliplatin

Figure 4B



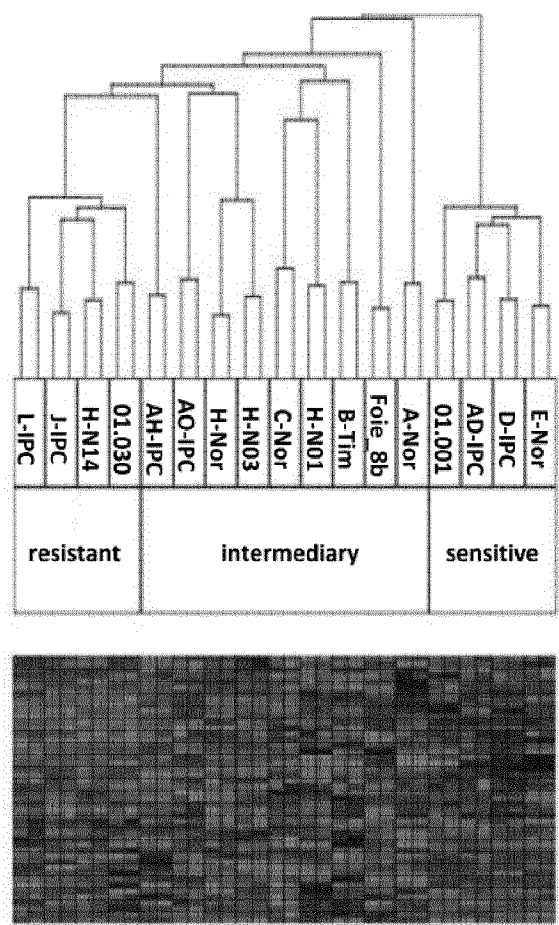
5FU

Figure 4C



docetaxel

Figure 4D



SN38

Figure 4E