METHOD

The present invention relates to sensitivity of tumours to therapeutic agents which can be predicted from the gene expression profile of the tumour and hence that the suitability of cancer patients for treatment with such therapeutic agents can be determined by measuring the relative expression levels of particular genes in tumour tissue.

The phosphorylation of proteins on tyrosine residues is a key element of signal transduction within cells. Enzymes capable of catalysing such reactions are termed tyrosine kinases. A number of these enzymes exist as integral components of transmembrane receptor molecules and are classified as receptor tyrosine kinases (RTKs). There are several members of this family of RTKs, class I of which includes the erbB family, e.g. epidermal growth factor receptor (EGFR), erbB2, erbB3 and erbB4. Binding of a variety of ligands to the external domain activates the EGFR tyrosine kinase domain. Activation causes EGFR itself and a number of cellular substrates to become phosphorylated on tyrosine residues. These phosphorylation reactions are a major component of growth factor induced proliferation of cells.

The erbB family of receptor tyrosine kinases are known to be frequently involved in driving the proliferation and survival of tumour cells (reviewed in Olayioye et al., EMBO J., 2000, 19, 3159). One mechanism by which this can occur is over expression of the receptor at the protein level, for example as a result of gene amplification. This has been observed in many common human cancers (reviewed in Klapper et al., Adv. Cancer Res., 2000, 77, 25) such as, non-small cell lung cancers (NSCLCs) including adenocarcinomas (Cerny et al., Brit. J. Cancer, 1986, 54, 265; Reubi et al., Int. J. Cancer, 1990, 45, 269; Rusch et al., Cancer Research, 1993, 53, 2379; Brabender et al, Clin. Cancer Res., 2001, 7, 1850) as well as other cancers of the lung (Hendler et al., Cancer Cells, 1989, 7, 347.

It is now several decades since the study of retroviral mediated cellular transformation began to revolutionize our understanding of malignant transformation. Transformation was shown to be dependent on oncogenes carried by viruses and these were shown to have mammalian cellular counterparts, proto-oncogenes. In 1984, EGFR was described as the mammalian counterpart of the retroviral oncogene, v-erbB (Downward et al). This, coupled to earlier observations describing a two component autocrine growth promoting mechanism in cancer cells consisting of EGF ligand and its receptor EGFR (Sporn & Todaro), strengthened

the hypothesis that EGFR signalling is an important contributor to tumourigenesis. Subsequent reports continued to provide evidence that EGFR is an attractive target for therapeutic intervention in Cancer (see Yarden & Sliwkowski for review). EGFR is markedly overexpressed across a large variety of epithelial Cancers (see Salomon et al) and some immunohistochemical studies have demonstrated EGFR expression is associated with poor prognosis. In addition to overexpression, it is recognised that there is potential for deregulated EGFR signalling in tumours via a number of alternative mechanisms including i) EGFR mutations ii) increased ligand expression and enhanced autocrine loop and iii) heterodimerisation and cross talk with other erbB receptor family members.

In addition, a wealth of pre-clinical information suggests that the erbB family of receptor tyrosine kinases are involved in cellular transformation. In addition to this, a number of pre-clinical studies have demonstrated that anti-proliferative effects can be induced by knocking out one or more erbB activities by small molecule inhibitors, dominant negatives or inhibitory antibodies (reviewed in Mendelsohn et al., Oncogene, 2000, 19, 6550).

Thus it has been recognised that inhibitors of these receptor tyrosine kinases should be of value as a selective inhibitor of mammalian cancer cells (Yaish et al. Science, 1988, 242, 933, Kolibaba et al, Biochimica et Biophysica Acta, 1997, 133, F217-F248; Al-Obeidi et al, 2000, Oncogene, 19, 5690-5701; Mendelsohn et al, 2000, Oncogene, 19, 6550-6565).

A number of small molecule inhibitors of erbB family of receptor tyrosine kinases are known, particularly inhibitors of EGF and erbB2 receptor tyrosine kinases. For example European Patent Application No. 0566226 and International Patent Applications WO 96/33980 and WO 97/30034 disclose that certain quinazoline derivatives which possess an anilino substituent at the 4-position possess EGFR tyrosine kinase inhibitory activity and are inhibitors of cancer tissue.

It has been disclosed by J R Woodburn et al. in Proc. Amer. Assoc. Cancer Research, 1997, 38, 633 and Pharmacol. Ther., 1999, 82, 241-250 that the compound N-(3-chloro-4-fluorophenyl)-7-methoxy-6-(3-morpholinopropoxy)quinazolin-4-amine is a potent EGFR tyrosine kinase inhibitor. This compound is also known as Iressa (registered trade mark), gefitinib (United States Adopted Name), by way of the code number ZD1839 and Chemical Abstracts Registry Number 184475-35-2. The compound is principally identified hereinafter as gefitinib.

Gefitinib was developed as an inhibitor of epidermal growth factor receptor-tyrosine kinase (EGFR-TK), which blocks signalling pathways responsible for driving proliferation, invasion, and survival of cancer cells (Wakeling, A.E., et al. Cancer Res, 2002, 62(20), p5749). Gefitinib has provided clinical validation of small molecule inhibitors of EGFR. Potent anti-tumour effects as well as rapid improvements in NSCLC-related symptoms and quality of life have been observed in clinical studies that enrolled patients with advanced NSCLC who did not respond to platinum-based chemotherapy. The Phase II 'IDEAL' trials demonstrated that single agent gefitinib resulted in objective anti-tumour activity, symptomatic improvement and limited toxicity in patients with advanced NSCLC and previously treated with cytotoxic chemotherapy (Fukuoka et al., Kris et al). Objective response rate (Complete Response + Partial Response) was 18.4% and 11.8% respectively in the IDEAL 1 and IDEAL 2 trials. The differences in response in these clinical trials has been attributed to different population groups in the two trials, predominantly Japanese in IDEAL 1 and a predominantly European-derived population in IDEAL 2. Beyond objective responses, additional patients experienced stable disease and / or symptom improvement meaning that approximately 50% of patients overall benefit from gefitinib. The tumour response data has been the basis of initial regulatory approvals of gefitinib in advanced NSCLC in several markets.

It is important to be able to understand the basis of response to anti-cancer therapeutic agents such as gefitinib since this would allow clinicians to maximise the benefit/risk ratio for each patient, potentially via the development of diagnostic tests to identify patients most likely to benefit from gefitinib treatment. An obvious candidate marker of response to gefitinib has been EGFR expression level. However, gefitinib inhibition of growth of some cancer-derived cell lines and tumour xenografts is not well correlated with the level of expression of EGFR. Furthermore, studies alongside the IDEAL trials demonstrated that EGFR protein expression as measured by IHC was not an accurate predictor of response to gefitinib (Bailey et al). Although there are now several additional hypotheses based on genetics, genomics, proteomics, biochemical and other studies, there is still no pre-treatment predictive biomarker of gefitinib response currently approved by regulatory authorities. Possibly the most significant recent breakthrough in understanding gefitinib response has come from recent data (Lynch et al, Paez et al) indicating that mutation in the EGFR kinase domain predicts gefitinib hypersensitivity in NSCLC patients. Hypersensitivity is a vague term but in this field is generally understood to mean patients experiencing objective tumour responses (i.e. marked tumour regression,

normally above 50%). As well as demonstrating the EGFR mechanism of action for gefitinib, this may provide a basis for venturing into other disease settings such as first line, adjuvant and possibly earlier cancer intervention with EGFR inhibitors in a targeted subpopulation in NSCLC patients and other types of cancers carrying the EGFR mutation.

However, it is likely that restricting prescription of gefitinib to the mutant EGFR carrying tumour subgroup will deprive many patients who could benefit from gefitinib. Firstly there are emerging reports of gefitinib hypersensitive patients with undetectable EGFR mutation in their tumour and other patients with EGFR mutation who do not respond to gefitinib. Secondly, data reported at ASCO 2004 (Shepherd et al) indicated that the EGFR small molecule tyrosine kinase inhibitor erlotinib (Roche, Genentech, OSI) prolongs survival in advanced NSCLC previously treated with chemotherapy, by ~2 months across the population with resulting 41% reduction in risk of death at one year. Most interestingly, the survival benefit appears to be is derived from patients in the stable disease response population as well as hypersensitive patients. This highlights the likely importance of identifying likely gefitinib responsive patients beyond those carrying EGFR mutation. Definitive survival benefit is also likely to be demonstrated from ongoing clinical trials with gefitinib.

The differential response of patients to chemotherapy treatments indicates that there is a need to find methods of predicting which treatment regimes best suit a particular patient.

There is an increasing body of evidence that suggests that patients' responses to numerous drugs may be related to a patients' genetic, genomic, proteomic, biochemical or profile and that determination of the genetic factors that influence, for example, response to a particular drug could be used to provide a patient with a personalised treatment regime. Such personalised treatment regimes offer the potential to maximise therapeutic benefit to the patient, whilst minimising, for example side effects that may be associated with alternative and less effective treatment regimes.

Therefore there is a need for methods that can predict a patients' response to a drug based on the results of a test that indicates whether the patient is likely to respond to treatment or to be resistant to treatment.

The present invention is based on the discovery that the sensitivity of tumours to therapeutic agents can be predicted from the gene expression profile of the tumour and hence that the suitability of tumour patients for treatment with such therapeutic agents can be determined by measuring the relative expression levels of particular genes in tumour tissue.

According to one aspect of the present invention there is provided a method of selecting a mammal having or suspected of having a tumour for treatment with an erbB receptor drug which comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 1 as defined herein whereby to predict an increased likelihood of response to the erbB receptor drug.

According to another aspect of the present invention there is provided a method of selecting a mammal having or suspected of having a tumour for treatment with an erbB receptor drug which comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 1 or DAPK2 whereby to predict an increased likelihood of response to the erbB receptor drug.

In one embodiment the method comprises testing a biological sample from the mammal for expression of any one of ACOX2, NPAS2, NES, CHST7, GSPT2, DAPK1, DAPK2 or TNNC1. More preferably the method comprises testing a biological sample from the mammal for expression of any one of NPAS2, NES, CHST7 or DAPK1. More preferably the method comprises testing a biological sample from the mammal for expression of at least two of NPAS2, NES, CHST7 or DAPK1. More preferably the method comprises testing a biological sample from the mammal for expression of at least three of NPAS2, NES, CHST7 or DAPK1. More preferably still the method comprises testing a biological sample from the mammal for expression of NPAS2, NES, CHST7 and DAPK1.

In an alternative embodiment the method comprises testing a biological sample from the mammal for expression of any one of NES, GSPT2, ETR101, TAZ, CHST7, DNAJC3, NPAS2, PIN1, TCEA2, VAMP4, DAPK1, DAPK2, MLLT3, TNNC1 or KIAA0931. More preferably the method comprises testing a biological sample from the mammal for expression of any one of DAPK1, DAPK2 or NES. More preferably the method comprises testing a biological sample from the mammal for expression of at least two of DAPK1, DAPK2 or NES. More preferably the method comprises testing a biological sample from the mammal for expression of DAPK1, DAPK2 and NES.

In a preferred embodiment the method additionally comprises testing a biological sample from the mammal for expression of any gene listed in Table 2 as defined herein. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1, SLC20A1, SPRY2 or PGM1. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

In an alternative preferred embodiment the method additionally comprises testing a biological sample from the mammal for expression of any gene listed in Table 2 as defined herein. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1, HCA127, UBL5, ZNF23, UROD, CD44, SPRY1, RAPGEF2, SLC20A1, NRP1, PGM1, SPRY2, PTGER3, SCN10A, KITLG, CDH1, HOP, BCL3 or OLFM1. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

Preferably the tumour is selected from the group consisting of leukaemia, multiple myeloma, lymphoma, bile duct, bone, bladder, brain, CNS, glioblastoma, breast, colorectal, cervical, endometrial, gastric, head, neck, hepatic, lung, muscle, neuronal, oesophageal, ovarian, pancreatic, pleural membrane, peritoneal membrane, prostate, renal, skin, testicular, thyroid, uterine and vulval. More preferably the tumour is selected from one of non-small cell lung, pancreatic, head or neck. More preferably the tumour is selected from one of non-small cell lung, head or neck.

Preferably the erbB receptor drug is selected from any one of gefitinib, erlotinib, PKI-166, EKB-569, HKI-272, lapatinib, canertinib, AEE788, XL647, BMS 5599626, cetuximab, matuzumab, panitumumab, MR1-1, IMC-11F8 or EGFRL11. Most preferably the erbB receptor drug is gefitinib.

In a further preferred embodiment of the method of the invention the mammal is a human and the method comprises testing a biological sample from the human for increased expression of DAPK1 and decreased expression of NPAS2, NES, CHST7 or EMP1 whereby to predict an increased likelihood of response to gefitinib. In an alternative preferred embodiment of the method of the invention the mammal is a human and the method comprises testing a biological sample from the human for increased expression of DAPK1 and DAPK2 and decreased expression of NES and EMP1 whereby to predict an increased likelihood of response to gefitinib.

According to another aspect of the invention there is provided an isolated set of marker genes identified as having differential expression between tumour cells that are sensitive and resistant to an erbB receptor drug said gene set comprising one or more genes selected from at least the group consisting of the genes listed in Table 1 defined herein or DAPK2, including gene specific oligonucleotides derived from said genes. Preferably the set comprises at least 2

genes, more preferably at least 3 genes, more preferably at least 4 genes. More preferably the set comprises at least one gene selected from Table 2 as defined herein.

According to another aspect of the invention there is provided an isolated set of marker genes identified as having differential expression between tumour cells that are sensitive and resistant to an erbB receptor drug said gene set comprising one or more genes selected from at least the group consisting of the genes listed in Table 1 defined herein, including gene specific oligonucleotides derived from said genes. Preferably the set comprises at least 2 genes, more preferably at least 3 genes. More preferably the set comprises at least one gene selected from Table 2 as defined herein.

The present invention permits the improved selection of a patient, having or suspected of having a tumour, for treatment with an erbB receptor drug, in order to predict an increased likelihood of response to the erbB receptor drug.

In one embodiment, the method comprises testing a biological sample from the mammal for expression of at least one or more of the following from Table 1, which are found at lower levels in sensitive cells NPAS2, NES, CHST7, ACOX2 or GSPT2 or at least one or more of the following which are found at higher levels in sensitive cells DAPK1 or TNNC1. The Affymetrix ID and Affymetrix probe sequence for these genes are displayed in Table 1. In a preferred embodiment, the method further comprises testing a biological sample from the mammal for expression of DAPK2 which is found at higher levels in sensitive cells, whereby to predict an increased likelihood of response to the erbB receptor drug.

In an alternative embodiment, the method comprises testing a biological sample from the mammal for expression of at least one or more of the following from Table 1, which are found at lower levels in sensitive cells NES, GSPT2, ETR101, TAZ, CHST7, DNAJC3, NPAS2, PIN1, TCEA2 or VAMP4 or at least one or more of the following which are found at higher levels in sensitive cells DAPK1, DAPK2, MLLT3, TNNC1 or KIAA0931. The Affymetrix ID and Affymetrix probe sequence for these genes are displayed in Table 1.

In a preferred embodiment, the method further comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 2, whereby to predict an increased likelihood of response to the erbB receptor drug. In a preferred embodiment, the method comprises testing a biological sample from the mammal for expression of any one of the following genes listed in Table 2, which are found at lower levels in sensitive cells EMP1, SLC20A1, SPRY2 or PGM1, whereby to predict an increased likelihood of response to the

erbB receptor drug. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

In an alternative preferred embodiment, the method further comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 2, whereby to predict an increased likelihood of response to the erbB receptor drug. In a preferred embodiment, the method comprises testing a biological sample from the mammal for expression of any one of the following genes listed in Table 2, which are found at lower levels in sensitive cells EMP1, HCA127, UBL5, ZNF23, UROD, CD44, SPRY1, RAPGEF2, SLC20A1, NRP1, PGM1 or SPRY2 or at least one or more of the following which are found at higher levels in sensitive cells PTGER3, SCN10A, KITLG, CDH1, HOP, BCL3 or OLFM1 whereby to predict an increased likelihood of response to the erbB receptor drug. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

In an especially preferred embodiment the method comprises testing a biological sample from the mammal for expression of NPAS2, NES, CHST7, DAPK1 and EMP1. High NPAS2, NES, CHST7 and EMP1 levels are associated with resistance to gefitinib and high DAPK1 levels are associated with sensitivity to gefitinib. Preferably, the assessment of expression comprises determination of whether DAPK1 levels are increased and NPAS2, NES, CHST7 and EMP1 levels are reduced.

In an alternative especially preferred embodiment the method comprises testing a biological sample from the mammal for expression of DAPK1, DAPK2, NES and EMP1. High EMP1 and NES levels are associated with resistance to gefitinib and high DAPK1 and DAPK2 levels are associated with sensitivity to gefitinib. Preferably, the assessment of expression comprises determination of whether DAPK1 and DAPK2 levels are increased and EMP1 and NES levels are reduced. In a most preferred embodiment the invention comprises determining the level of DAPK1 and EMP1.

According to another aspect of the invention there is provided a method for predicting clinical outcome of treatment with an erbB receptor drug for a mammal, having or suspected of having a tumour, comprising determining the level of any of the genes as described hereinabove in a biological sample taken from the tumour, or suspected tumour, wherein a poor outcome is predicted if:

a) the expression level of DAPK1 is reduced; and /or

b) the expression level of NPAS2, NES, CHST7 and EMP1 is increased.

According to another aspect of the invention there is provided a method for classifying cancer comprising, determining the level of any of the genes as described hereinabove in a biological sample taken from a tumour, or suspected tumour, wherein tumours expressing elevated levels of DAPK1 and / or reduced levels of NPAS2, NES, CHST7 or EMP1 are predicted as sensitive to treatment with erbB receptor drugs.

According to another aspect of the invention there is provided a method for predicting clinical outcome of treatment with an erbB receptor drug for a mammal, having or suspected of having a tumour, comprising determining the level of any of the genes as described hereinabove in a biological sample taken from the tumour, or suspected tumour, wherein a poor outcome is predicted if:

a) the expression level of DAPK1 or DAPK2 is reduced; and /or

b) the expression level of EMP1 or NES is increased.

According to another aspect of the invention there is provided a method for classifying cancer comprising, determining the level of any of the genes as described hereinabove in a biological sample taken from a tumour, or suspected tumour, wherein tumours expressing elevated levels of DAPK1 or DAPK2 and / or reduced levels of EMP1 or NES are predicted as sensitive to treatment with erbB receptor drugs.

According to another aspect of the invention there is provided a method for treating a disease condition in a mammal having, or suspected of having, a tumour, predicted to be resistant or non responsive to erbB receptor drug treatment based on the level of any of the genes as described hereinabove, comprising: providing a resistance-surmounting quantity of an erbB receptor drug and administering the resistance-surmounting quantity of the erbB receptor drug to the mammal.

In a preferred embodiment the mammal is a primate. In a most preferred embodiment the mammal is a human. In a preferred embodiment the patient is a primate. In a most preferred embodiment the patient is a human.

The term "erbB receptor drug" includes drugs acting upon the erbB family of receptor tyrosine kinases, which include EGFR, erbB2 (HER), erbB3 and erbB4 as described in the background to the invention above. In a preferred embodiment the erbB receptor drug is an erbB receptor tyrosine kinase inhibitor. In a preferred embodiment the erbB receptor drug is an EGFR tyrosine kinase inhibitor.

In a more preferred embodiment the EGF receptor tyrosine kinase inhibitor is selected from gefitinib, Erlotinib (OSI-774, CP-358774), PKI-166, EKB-569, HKI-272 (WAY-177820), lapatinib (GW2016, GW-572016), canertinib (CI-1033, PD183805), AEE788, XL647, BMS 5599626 or any of the compounds as disclosed in WO03/082831, WO05/012290, WO05/026157, WO05/026150, WO05/026156, WO05/028470, WO05/028469, WO2004/006846, WO03082831, WO03/082290 or PCT/GB2005/000237.

In another preferred embodiment the erbB receptor drug is an anti-EGFR antibody such as for example one of cetuximab (C225), matuzumab (EMD-72000), panitumumab (ABX-EGF/ rHuMAb-EGFr), MR1-1, IMC-11F8 or EGFRL11.

We contemplate that erbB receptor drugs may be used as monotherapy or in combination with other drugs of the same or different classes. In an especially preferred embodiment the EGF receptor tyrosine kinase inhibitor is gefitinib.

In a preferred embodiment the present invention is particularly suitable for use in predicting the response to the erbB receptor drug as described hereinbefore in those patients or patient population with a tumour which is dependent alone, or in part, on an erbB tyrosine kinase receptor. Such tumours include, for example, non-solid tumours such as leukaemia, multiple myeloma or lymphoma, and also solid tumours, for example bile duct, bone, bladder, brain/CNS, glioblastoma, breast, colorectal, cervical, endometrial, gastric, head and neck, hepatic, lung, muscle, neuronal, oesophageal, ovarian, pancreatic, pleural/peritoneal membranes, prostate, renal, skin, testicular, thyroid, uterine and vulval tumours.

In a preferred embodiment the present invention is particularly suitable for identifying a patient with head, neck, pancreatic, glioblastoma, colorectal or breast tumour for drug treatment. In an especially preferred embodiment the present invention also is particularly suitable for identifying those patients with NSCLC, more particularly advanced NSCLC including advanced adenocarcinoma that will respond to treatment with an erbB receptor drug as hereinbefore defined.

The present invention provides advantage in the treatment of tumours such as NSCLC, especially advanced NSCLC by identifying "individual cancer profiles" of NSCLC and so determining which tumours would respond to erbB receptor drug such as gefitinib.

The present invention is particularly useful in the treatment of patients with advanced NSCLC who have failed previous chemotherapy, such as platinum-based chemotherapy. The present invention is also particularly useful in the treatment of patients with locally advanced

(stage IIIB) or metastasized (stage IV) NSCLC who have received previous chemotherapy, such as platinum-based chemotherapy. The present invention is also useful in adjuvant therapy or as a first-line therapy.

In a preferred embodiment there is provided a method of selecting a human, having or suspected of having a tumour, for treatment with gefitinib which comprises testing a biological sample, from the mammal for expression of NPAS2, NES, CHST7, DAPK1 and EMP1, whereby to predict an increased likelihood of response to gefitinib.

In a preferred embodiment there is provided a method of selecting a human, having or suspected of having a tumour, for treatment with gefitinib which comprises testing a biological sample, from the mammal for expression of DAPK1, DAPK2, NES and EMP1 whereby to predict an increased likelihood of response to gefitinib.

According to another aspect of the invention there is provided a method of predicting the responsiveness of a patient or patient population with cancer, for example lung cancer, to treatment with chemotherapeutic agents, especially erbB receptor drugs, comprising comparing the differential expression of any of the genes described herein.

In one embodiment the assessment of expression is performed by gene expression profiling using oligonucleotide-based arrays or cDNA-based arrays of any type, particularly where large numbers of genes are analysed simultaneously. In an alternative embodiment, RT-PCR (reverse transcription- Polymerase Chain Reaction), real-time PCR, *in-situ* hybridisation, Northern blotting, Serial analysis of gene expression (SAGE) for example as described by Velculescu et al Science 270 (5235): 484-487, or differential display or any other method of measuring gene expression at the RNA level could be used. Details of these and other general molecular biology techniques can be found in Current Protocols in Molecular Biology Volumes1-3, edited by F M Asubel, R Brent and R E Kingston; published by John Wiley, 1998 and Sambrook, J. and Russell, D.W., Molecular Cloning: A Laboratory Manual, the third edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001.

In another embodiment the assessment of expression is performed by measurement of protein levels encoded by the aforementioned genes. For example, an immunohistochemistry-based assay or application of an alternative proteomics methodology.

In another embodiment the assessment of expression is performed by measurement of activity of the proteins encoded by the aforementioned genes, for example in a bioassay.

In a preferred embodiment the biological sample would have been obtained using a

minimally invasive technique to obtain a small sample of tumour, or suspected tumour, from which to determine gene expression profile. Such techniques include, for example tumour biopsy, such as transbronchial biopsy. The profile of gene expression of transbronchial biopsy specimens whose size is about 1 mm may be measured for example using a suitable amplification procedure.

Another aspect of the invention provides a kit for use in a method of predicting the responsiveness of a patient or patient population with a tumour, to treatment with chemotherapeutic agents, especially erbB receptor drugs, comprising a means for measuring the levels of any of the genes as described hereinabove. Preferably the genes are attached to a support material or membrane such as nitrocellulose, or nylon or a plastic film or slide.

In a further preferred embodiment the present invention includes administration of an erbB receptor drug to a mammal selected according the methods described hereinabove.

According to another aspect of the invention there is provided a method of using the results of the methods described above in determining an appropriate dosage of an erbB receptor drug.

In a preferred embodiment the biological sample comprises either a single sample which may be tested for expression of any of the genes as described hereinabove, or multiple samples which may be tested for expression of one or more of the genes as described hereinabove.

The invention is illustrated by the following non-limiting examples in which:

Fig 1 illustrates a xenograft (A549 cell line) which when grown as a xenograft in athymic mice is sensitive to gefitinib. This involved oral dosing, once daily, at the dose indicated. Y axis = mean tumour volume in cm^3; x axis = days after treatment.

Fig 2 illustrates a xenograft (MKN45 cell line) which when grown as a xenograft in athymic mice is resistant to gefitinib. This involved oral dosing, once daily, at the dose indicated. Y axis = mean tumour volume in cm^3; x axis = days after treatment.

Figures 3, 4, 5 and 6 show examples of specific gene expression profiled across a wider panel of gefitinib sensitive and resistant lines, where definition of sensitivity is based on response to gefitinib when grown as a xenograft, to increase confidence that the expression profile of each gene is truly predictive. Iressa sensitivity is based on xenografts data. The cell lines and the tumours from which they are derived are as follows; KB – head and neck, HT29 - colon, BT474 – breast, DU145 – prostate, LoVo – colon, MCF7 – breast, GEO – colon, A549 – lung,

A431 - epidermoid, H322 – lung, HX147 – lung, RT112 – bladder, MiaPaCa2 – pancreas, MKN45 – gastric, MDAMB231 – breast, PC3 - prostate, Calu6 – lung, SW620 – colon. The legend key is S=sensitive, U=unknown and R=resistant.

Fig 3 shows EMP1 basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Fig 4 shows DAPK1 basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Fig 5 shows DAPK2 basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Fig 6 shows NES basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Example 1

Gene Expression in Gefitinib Resistant or Sensitive Tumour Cell Lines – Cell Culture and Xenograft Studies

We identified genes useful to predict response to erbB receptor drugs in the clinic. This is based on studies with gefitinib, but the findings are applicable to erbB receptor drugs in general.

The gene lists have been assembled by comparing tumour cell lines which have been demonstrated to be either sensitive to gefitinib or resistant to gefitinib. This definition is based on the response observed when the tumour cell line is implanted into nude mice and grown as a xenograft. This definition has been used for all the pre-clinical studies described herein.

Initially a small panel of six human tumour cell lines were assembled, three which are sensitive to gefitinib and three which are resistant to gefitinib in the xenograft setting defined above.

The sensitive cell lines were;

1. Lovo (ATCC[1] No. CCL-229) – colon tumour cell line
2. KB (ATCC No. CCL-17) – initially reported as a nasopharyngeal cell line (although more recently reported as Hela derived (cervical carcinoma)
3. HT29 (ATCC No. HTB-38) – colon tumour cell line

The resistant cell lines were;

1. MKN 45 (source - Nottingham University, UK) – gastric tumour cell line
2. Calu 6 (ATCC No. HTB-56) – lung tumour cell line
3. PC3 (ATCC No. CRL-1435) – prostate tumour cell line

[1]ATCC = American Type Culture Collection

The cell lines were grown both in cell culture and as xenografts, RNA prepared and the basal expression profiles determined by measuring RNA expression on the Affymetrix microarray platform. As part of our studies, the term 'basal' has been used to indicate constitutive or steady state expression levels (rather than expression levels which are modulated as a consequence of administration of an erbB ligand or gefitinib to the cells). Figure 1 illustrates the sensitivity of A549 xenografts (used in Example 3 below) to treatment with gefitinib. Figure 2 illustrates the resistance of MKN45 xenografts to gefitinib. See Example 2 below for analysis of results.

Example 2

Statistical analyses of cell culture and xenograft data sets

The following statistical analyses were performed separately for cell culture and xenograft data sets. Probe sets were eliminated if their signal was not distinguishable from background noise across all RNA samples in the set. Mixed ANOVA (see for example Scheffe, 1959) was applied separately to each remaining probe set to generate p values. The p values were then used to calculate Q values (Storey). The Q values indicate the expected proportion of genes in a gene list which are not truly differentially expressed but have been falsely discovered (False Discovery Rate or FDR). Q value cut-offs appropriate in the different studies were identified and applied, based on graphical examination of the p value and Q value results, in conjunction with fold change. The final genelists for each study were generated using Q value and fold change (FC) cut-offs. The different genelists were then combined to display an overall list of genes which showed consistent differences in expression profiles between the cell lines in the sensitive and resistant groups.

Further details of the analysis procedures are provided as follows. Fold change (FC) was calculated based on the mean of sensitive cells divided by the mean of resistant cells. To generate gene lists, FC cut-off of two-fold (2X) change in either direction was used in all cases. Furthermore FDR Q values were used to narrow down the lists and obtain the most significant gene changes across sensitive versus resistant cell lines. In the case of cell culture, Q value cut-off is 0.3. In the case of xenograft, Q value cut-off is 0.6. The different cut-offs used reflect the different design and variance values associated with each experiment.

In cell culture studies, lists were obtained based on the above criteria for cells grown either in full serum containing medium or in charcoal stripped serum. In the xenograft study, the same as above was performed for separate sets of tumours harvested at 18hr intervals. Gene lists contain some redundancy in genes where appropriate to illustrate consistency of results obtained for example with different probe sets.

Example 3

Identification of predictive genes

Genes which have not previously been identified as predictive of erbB receptor drug sensitivity are listed in Table 1. Other genes which we have identified to be optionally used in combination with Table 1 genes are listed in Table 2.

Key to Tables:

'Affymetrix ID' – the Affymetrix probe set identifier

'Sequence' – target sequence relating to the Affymetrix probe set indicated by 'Affymetrix ID'

"+ if up in sensitive" means that the gene is relatively highly expressed in sensitive cells. (Consequently, absence of a "+" means that the gene is relatively highly expressed in resistant cells).

'Gene Title'- The current annotation of the gene relating to 'Affymetrix ID' based on UniGene 133

'Gene Symbol' – shorthand synonym for the gene title

'Locus Link' & RefSeq Transcript ID' are provided for gene identification purposes.

Combining genes has the potential to generate an improved diagnostic over genes used in isolation. Collective gene expression profiles (at the RNA and/ or protein level) may be more likely to identify patients most likely to benefit from gefitinib rather than the expression level of one gene in isolation.

It may be more practical when developing a pre-treatment response prediction diagnostic to work with a truncated gene list from tables 1 and / or 2. A number of criteria have been used to shorten the gene list to identify those genes which are most predictive of response. Firstly the statistical (p values and Q values or FDR values) can indicate the statistical significance of a gene.

Secondly, the differential expression (fold change) between the sensitive and resistant groups indicates the potential sensitivity of a marker to be used in a diagnostic test (highest fold change between sensitive group and resistant group is preferred).

Thirdly, we have performed RT-PCR based expression profiling across a wider panel of gefitinib sensitive and resistant human tumour cell lines to increase confidence that the expression profile of each gene is truly predictive. Figs 3, 4, 5 and 6 show examples of specific gene expression profiled across a wider panel of cell lines as set out below.

The sensitive human tumour cell lines, where definition of sensitivity is based on response to Iressa when grown as a xenograft:

a. BT474 (ATCC No. HTB-20) – breast tumour cell line
b. DU145 (ATCC No. HTB-81) – colon tumour cell line

c. MCF7 (ATCC No. HTB-22, sourced from ICRF (now CR-UK), London), - breast tumour cell line

d. GEO colon tumour cell line. RNA obtained from Fortunato Ciardiello, Cattedra di Oncologia Medica, Dipartimento Medico-Chirurgico di Internistica Clinica e Sperimentale "F. Magrassi e A. Lanzara, " Seconda Universita delgi Studi di Napoli, Via S. Pansini, 5-80131, Naples, Italy.

e. A549 (ATCC No. CCL-185) – lung tumour cell line

f. A431 (ATCC No. CRL-155) – epidermoid cell line

The resistant human tumour cell lines, where definition of sensitivity is based on response to Iressa when grown as a xenograft:

1) HX147 - (source: ICRF (now CR-UK), London) – lung tumour cell line

2) RT112 - bladder tumour cell line (DSMZ No ACC 418)

3) MiaPac2 (ECACC 85062806, ref. no. 001611) pancreatic tumour cell line

4) MDAMB231 (ATCC No. HTB-26) – breast tumour cell line

5) SW620 (ECACC CCL-227) – colon tumour cell line

ATCC = American Type Culture Collection

DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (German Collection of Micro-organisms and Cell Cultures)

ECACC = European Collection of Cell Cultures

In isolation, each of these genes is reasonably predictive of gefitinib response, but collectively they can be applied to make predictions with a higher level of confidence.

The Affymetrix probe sets identifiers for the genes in the above diagnostic genelists are indicated in Tables 1 and 2. Current Affy IDs are based on Affy U133 chipset. For the avoidance of doubt, the target sequences of the Affymetrix probe sets which identified the listed genes are also provided in Tables 1 and 2.

Without wishing to be bound by theoretical considerations, it is contemplated that the specific sequences used to detect target genes in the Examples may define specific splice variants or sequences in homologous genes. Therefore in one embodiment, a listed gene for use in the method of the invention is defined by the specific sequence used in said Examples. In another embodiment, a gene for use in the method of the invention is not limited by the specific sequence used in these Examples. Indeed the fact that some genes in Tables 1 and 2 have been identified using different sequences (gene "redundancy") and confirmatory RT-PCR studies (see

Example 4) provides evidence that usefulness in the method of the invention is not generally limited to the specific sequences used to measure the target gene.

Note, in the event of a discrepancy in the sequence between Tables 1 and 2 and the Sequence Listing, the sequence as provided in the Tables is preferred.

Table 1: **as described in priority application US60/619027 filed on 18/10/2004.**

Gene Symbol	Gene Title	Affymetrix ID	+ up in sensitive	Sequence	LocusLink	RefSeq Transcript ID	SEQ ID NO.
ACOX2	"acyl-Coenzyme A oxidase 2, branched chain / acyl-Coenzyme A oxidase 2, branched chain"	205364_at		Gtgcagcatttacagaccctgacgcaatccggagctgaccagcacgaggcttgga accagaccactgtcatacacctccaggctgctaaggtgcactgctactatgtcactgtg aagggttttacagaagctctggagaaactagaaaatgaaccagcgattcagcaggt gctcaagcgcctctgtgacctccatgccatacatggaatcttgactaactcgggtgact ttctccatgacgccttcctgtctggtgcccaagtggacatggcaagaacagcctacctg gacctgctccgcctgatccggaaggatgccatcctgttaactgatgcttttgacttcacc gatcagtgtttaaattcagcccttggctgttatgatggaaacgtctacgaacgcctgttcc agtgggctcagaagtc	8309	NM_003500	SEQ ID NO:1
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	200729_s_at		gagcttaagatctggtgttttgttaatgcttctgtttattccagaagcattaaggtaacccat tgccaagtatcattcttgcaaattattcttttatataactgaccagtgcttaataaaacaag caggtacttacaaataattactggcagtaggttataattggtggtttaaaaataacattg gaatacaggacttgttgccaattgggtaattttcattagttgttttgtttgttttgatttgaaac ctggaaatacagtaaaatttgactgtttaaaatgttggccaaaaaaatcaagatttaatt ttttttatttgtactgaaaaactaatcataactgttaattctcagccatctttgaagcttgaaa gaagagtctttggtatttttgtaaacgttagcagactttcctgccagtgtcagaaaatccta tttatgaatcctgtcggtattccttggtatctgaaaaaaatataccaaatagtaccatacatg agttatttctaa	10097	NM_005722	SEQ ID NO:2
APOL1	"apolipoprotein L, 1 / apolipoprotein L, 1"	209546_s_at	+	agaatagagaggaggcttgaaggaaccagcaatgagaaggccaggaaaagaa agagctgaaaatggagaaagcccaagagttagaacagttggatacaggagaaga aacagcggctccactacagacccagccccaggttcaatgtcctccgaagaatgaag tctttccctggtgatggtcccctgccctgtctttccagcatccactctcccttgtcctcctgg gggcatatctcagtcaggcagcggcttcctgatgatggtcgttggggtggttgtcatgtg atgggtccctccaggttactaaagggtgcatgtcccctgcttgaacactgaagggcag gtggt	8542	NM_003661 / NM_145343 / NM_145344	SEQ ID NO:3
C10orf 10	chromosome 10 open reading frame 10 / chromosome 10 open reading frame 10	209183_s_at		aactcatacgtcctgtggtggcattgggagagttcccccatgatgagggccaagata gaatctgtaccactcagtgctaccatccccaccctacaccacttccacacaggggc ctcatggcatggtcagggtcccagctgtaggtgagagcagggcactgtccagctgtc cactggggaagtcaagatgtcctaaggcccaggtcagggcatctggagtctgaagg accctagttcctagaggcatctggcagcaagaaggtgaggcatcagggaacggga atcaggctgggactgatcagaggtgaagggacagagagaggagaggaggaaga ttgagctgggggcaacagccaagctcacctgggcaggtctctgccacctccttgctct gtgagctgtcagtctaggttattctctttttttgtggctatttttaattgctttggatttgttaaatg ttttctgtcttctgttaagtgtgttt	11067	NM_007021	SEQ ID NO:4

CALM1	"calmodulin 1 (phosphorylase kinase, delta)"	211984_at		tgaacggctgtgcagtaggcccagcgctgtgtctcgtcagaggaatagcttacca cgaaccctcagcatactgggaatctcttcctgaacaacgaatgtaaatttggtcaagt ctactcttccgttcattcaattatttaagcatttgaattatttattgtatatcctaaatatatttct ccttggcagtgactagatttccactaatgtgtcttaatctatcctccagctggcagttac tgttttttttaatcccctgaagttgtcctgtaggagacagaaattcttgctgtctgtatcccct ggagtaa	801	NM_006888	SEQ ID NO:5
CALM1	"calmodulin 1 (phosphorylase kinase, delta)"	211985_s_at		gaggcaaatggatctcgatatttcagatgggcttttgatgcactgttgccaaggaaggc ttttctgatttttttgacaaatgaatttttgcacacttcattggtgtcttcggcaacttacaca cattgaaaat	801	NM_006888	SEQ ID NO:6
CD44	CD44 antigen (homing function and Indian blood group system)	210916_s_at		caagtttggtggcacgcagctgggactctgcctcgtgccgctgagcctggcgca gatcgatttgaatataacctgccgcttgcaggtgtattccacgtggagaaaaatggtc gctacagcatctctggacggaggccgctgacctctgcaaggcttcaatagcacctt gcccacaatggccagatggagaaagctctgagcatcggatttgagacctgcagttt gcattgcagtcaacagtcgaagaaggtgtgggcagaagaaaaagctagtgatcaa cagtggcaatggagctgtggaggacagaaagccaagtggactcaacggagaggc cagcaagtctcaggaaatggtgcatttggtgaacaaggagtcgtcagaaactccag accagt	960	NM_000610	SEQ ID NO:7
CD44	CD44 antigen (homing function and Indian blood group system)	212063_at		attgtaaatcttttgtgtctcctgaagacttccctaaaattagctctgagtgaaaaatcaa aagagacaaaagacatctcgaatcatatttcaagcctggtagaattggcttttctag cagaaccttccaaaagtttatattgagattcataacaacaccaagaattgatttttgtag ccaacattcattcaatactgttatatcagaggagtaggagaggaaacatttgactta tctggaaaagcaaaatgtacttaagaataagaatacatggtccattcaccttatgtta tagatatgtcttgtgtaaatcatttgtttttgagtttcaaagaatagcccattgttcatttcttgt gctgtacaatgaccactgttattgttactttgacttttcagagcacaccc	960	NM_000610	SEQ ID NO:8
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	212864_at		ttctatgcatccacaccaaaatcctgcagaatgtaagtaagctctgcttataagatgg gttcaccttcatcgcagactgaaagttcagttttatttttttncagaaagcacgaaaaat tatttataatagtctggagaaaaaacacactgtaatatttcaagtgtatgcagtagaatg tactgtaactgagcccttcccacatgtctaggctccaatgtctccgtaggtccacctaa ctgtgtgtttcagggacaatgccatccatgtttgtgctgtagacttgctgctgctgaatcct ttctgggacttctcatcgggcagggagcagagggcttctcgttcatgcaccctttgcc tgaacaccatgtagctgctgttgtgtatatattactcttaagaggagtgtgtgtctgt gtttgtttaaaagtcacttatttctacagtgatttcaattgcaccatgacttctcactaaa accacaaagtcctgcttaaaactatggaaaacctaacctgattagagccttgac	8760	NM_003818	SEQ ID NO:9

CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 / carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	206756_at		ggcaatctgtcacactctcagagtctgggacttgacttgctaccaacaactgctgtgca attctgctgagcaggaatatcatgagctgttcaataatgacggacgcattggttgagat gaagtttccagtaaggaagtgacagtgcaatgtggatatttatggctgtaaaatagga agagctttagttcccaggctgaacctgccactgctggagccatttcaacaaggcatcc tcacaacaaagaagagatgtgatttggtaccatttcacaccagcaggtgtctggacg aaaacatcaatgtgaataagggccaagtgcagtcctgtcttgattaaattacttaataat attattaaataataataggtctgggcagtattgtttttaacctgactcatccagctgtccttc aaatagctccgtctccctctacccagaactgatttttaaaaagaagtaatttttctccctg ggctgggaaaaccctaatgaactgaaacacacttttactttaaaatttttctgtctggcgt ttttgtaatc	56548	NM_019886	SEQ ID NO:10
COMM D3	COMM domain containing 3	218048_at		gaattccctagaaatcctactgggaagtataggcagatctctccctcatataacggatg tttcttggcgcttggaatatcagataaagaccaatcaacttcataggatgtacagacct gcatatttggtgaccttaagtgtacagaacactgattccccatcctatccagagattagtt ttagttgcagcatggaacaattacaggacttggtggggaaacttaaagatgcttcgaa aagcctggaaagagcaactcagttgtaacttggggaagttaacgatccgcccgagt gcagaggaaaaccagaaacgccttgccttcagctgaaccaccgtttgtgcgagctg gatgtccttttcagtagaaaagaattttccttttgaatttataccattcatcaattttgacactt taaaaacgtgtgaaagggttaagagggaaagatactgcccaagtatttgaatcgttta gtagtaactgtccatttatcctat	23412	NM_012071	SEQ ID NO:11
CUL2	cullin 2 / cullin 2	203078_at		tataatacttcagtaaggcctttaaaaaatccacagtgatattattactcctaacaaaaa caataattacttagtatcatctaatatgtggttcatatttaaatttgttgttttgagatgggtctt acaattggtttattcaattgcattttttctaactcgtgtctcaagtgttttaaaaatctactgna cttataatgacttatataatgtatttctcattttacctttcttccaaaagaggaaataatggc aaaccatataatattgtacattcactgtcaaaaagcaaacccttgttttgataacttgt	8453	NM_003591	SEQ ID NO:12
DAPK1	death-associated protein kinase 1 / death-associated protein kinase 1	203139_at	+	cctcctccagggtgattttatgatcagtgttgttgctctaggaagacatttttccgtttgctttt gttccaatgtcaatgtgaacgtccacatgaaacctacacactgtcatgcttcatcattcc ctctcatctcaggtagaaggttgacacagttgtagggttacagagacctatgtaagaat tcagaagacccctgactcatcatttgtggcagtcccttataattggtgcatagcagatgg tttccacatttagatcctggtttcataacttcctgtacttgaagtctaaaagcagaaaata aaggaagcaagttttcttccatgattttaaattgtgatcgagttttaaattgataggaggg aacatgtcctaattcttctgtcctgagaa	1612	NM_004938	SEQ ID NO:13
DNAJC 3	"DnaJ (Hsp40) homolog, subfamily C, member 3"	208499_s_at		aggagaggatttgccactgcttttctaaggacgagaagcctgttgaagctattagggttt gttctgaagttttacagatggaacctgacaatgtgaatgccctgaaagatcgagctga ggcctatttgatagaggaaatgtatgatgaagctattcaggattatgaaactgctcagg aacacaatgaaaatgatcagcagattcgagaaggtctagagaaagcacaaagatt attgaaacagtcgcagaaacgagattattataaaatcttgggagtaaaaagaaatgc caaaaagcaagaaattattaaagcataccgaaaattagcactgcagtggcaccca gataacttccagaatgaagaagaaaagaaaaaagctgagaaaaagttcattgatat agcagctgctaaagaagtcctctctgatccagaaatgagaaagaagtttgacgacg gagaagatcctttggatgcagagagccagcaaggaggcggcggcaaccctttcca cagaagctggaactcatggcaagggttcaatcccttcagctcaggcggaccatttag a	5611	NM_006260	SEQ ID NO:14

DPYSL 3	dihydropyrimidinase-like 3 / dihydropyrimidinase-like 3	201431_s_at		tgagggccacgggcttggtagtggaaagggtgtttgggaaattgttaaatcagttac ccgtagtagagctatttcttgtactctaagtttctagaagtggaaggattgtagtcatcct gaaaatgggtttacttcaaaatcccctcagccttgttcttcacgactgtctatactgagagt gtcatgtttccacaaagggctgacacctgagcctgatttcactcatcctgagaagc cctttccagtagggtgggcaattcccaacttccttgccacaagcttcccaggctttctcc cctggaaaactccagcttgagtcccagatacactcatgggctgcctgggcagccag cattcattgtaagttcctcttgaaaactggtgtgtgggtgttcagttctgtgtctggtgggt atggacagacagtaatctcctgtgatctgtctagctgtgaggcagctctggaacgtg a	1809	NM_001387	SEQ ID NO:15
DUSP4	dual specificity phosphatase 4 / *dual specificity phosphatase 4*	204015_s_at		ggctcccagcaagggtaggacgggccgcatgcgggcagaaagttgggactgagc agctgggagcaggcgaccgagctccttcccaatcatttctcctggccaacgacgag gccagccagaatggcaataaggactccgaatacataataaagcaaacagaaca ctccaacttagagcaatacggctgccgcagcaggcaggaagacctggtttggttt atgtgtcagtttcactttccgatagaaatttcttacctcatttttttaagcagtaaggctga agtgatgaaacccacacagatcctagcaaatgtgcccaaccagctttactaaagggg aggaagggagggcaaagggatgagaagacaagtttcccagaagtgcctggttctg	1846	NM_001394 / NM_057158	SEQ ID NO:16
EIF3S4	"eukaryotic translation *initiation* factor 3, *subunit* 4 delta, 44kDa / eukaryotic translation initiation factor 3, subunit 4 delta, 44kDa"	208887_at		gatacgctgggccatgcagaaggagctggccgagcagctgggcctgtctactgg cgagaaggagaagctgccgggagagctagagccggtgcaggccacgcagaac aagacagggaagtatgtgccgccgagcctgcgcgacgggccagccgccgcgg ggagtccatgcagcccaaccgcagagccgacgacaacgccaccatccgtgtcac caactgtcagaggacacgcgtgagaccgacctgcaggagctcttccggccttcgg ctccatctcccgcatctacctggctaaggacaagaccactggccaatccaagggcttt gccttcatcagcttccaccgccgcgaggatgctgcgctgccattgccgggtgtccg gctttggctacgaccacctcatcctcaacgtcgagtgggccaagccgtccaccaact aagccagctgccactgtgtactcggtccgggaccctggcgacagaagacagcc	8666	NM_003755	SEQ ID NO:17
EIF5A	eukaryotic translation initiation factor 5A	213757_at		atgtgtcgggggagagagcccgcagggaagggtaaagcccannggggcagggcc ctcccagatgcctgaggagggggcaggtccccctcctcctcttcctcccat ctaaagggtttgggggagagacacaggcgaggcgagggggctggtccccagtctgtt ggggtggtgctcaggtaaagggctatnggcaacagggggaccagaccagggatg agtgggggagggcacaaggaccatttgccagaatccaccg	1984	NM_001970	SEQ ID NO:18
FADS2	fatty acid desaturase 2 / fatty acid desaturase 2	202218_s_at		ctgttgctccaggatgcattcgataggagggggcggcagggctgggccttgtgaca atctgcctttcaccacatggcctgcctgctggtgccctgactgtcaggggaggccagg gaggcagagcgggagggagtctcaggaggaggcttgccctgaggggctgggggag ggggtacctcatgaggaccagggtggagcttgagaagaggaggaggtgggggctt ggaggtgcttggtagctgaggggacgggcaagtgagaggggaggggaggaagtc ctgggaggatcctgagctgctgttgcagtctaacccactaatcagttcttagattcaggg gaagggcaggcaccaacaactcagaatgggggcttcgggggagggcgctagtcc aatggcatgccccccagctactgtatgcccccgacccccgcagaggcagaatgaa cccatagggagctgatcgtaat	9415	NM_004265	SEQ ID NO:19

FLJ12442	hypothetical protein FLJ12442	218051_s_at		gggaccacctctatagtgatctggcggatctcatgctgcggcacggctggcgcacag gcgccatcatcccggagctggagcgtgagatccgcatcatcaacacggagcagtac atgcactcgctgacgtggcagcaggcgctcacggggctgctggagcgcatgcaga cctatcaggacgcggagtcgaggcaggtgctggctgcctggatgaaagagcggca ggagctgaggtgcatcaccaaggccctgttcaatgcgcagttcggcagcatcttccg cacctccacaacccccacctactctcaaggcgcctcgtgcgctctctgacctctacat ggcctcctcagctgcctgctcaactaccgcgtggacttcacctctacccacgcccgta cgccgctgcagcacgaggcacccctctggatggaccagctctgcaccggctgcatg aagacccccttcctggtgacatggcccacatccgctgagggcaccttattgtctggg ac	64943	NM_022908	SEQ ID NO:20
FLJ22028	hypothetical protein FLJ22028	213878_at	+	tattcaaacggagtcctcccattccaagaaactggaaacccctagtttatgttaaaagg ccagtctaaattcttcacttacatcttacagaaaactatatttctctctccatacccag aaatctaatcagaaaaactgacttttctcatgttcaactggacctagggaatatgacag aaaagcatcccataggcttaatatactttttaaaatatataaaactgaaaattaatagc catttaccctgaaagagttctgcgtggacttgtcactgcatagtaatagcatgtgcctc attgttcagaagattagctttaggtcctatttttcaaatacgaaatggtagcataagctgta aaactgtagtcttctctgcagaaaataaaggccaacaataagaaagcttttgaagga atcacggaaaacaaatttataaaagaaataactatatgcgcagtaattcttaacacatt gac	79912	NM_024854	SEQ ID NO:21
FNTB	"farnesyltransferase, CAAX box, beta"	204764_at		gcaagtcgcgtgatttctaccacacctgctactgcctgagcggcctgtccatagccca gcacttcggcagcggagccatgttgcatgatgtggtcctgggtgtgcccgaaaacgct ctgcagcccactcacccagtgtacaacaattggaccagacaaggtgatccaggccac tacatacttctacagaagccagtccaggtttttgaggagcttaaggatgagacatcg gcagagcctgcaaccgactagaggaccttggtcccggcgcagctctttgctcacccatc tcccagtcagacaaggtttatacgttcaatacatactgcattctgtgctacacaagcc ttagcctcagtgggagctgtggttctctggtacttttctgtcaaacaaaaccaatggctctg ggtttggagaacacagtggctggttttaaaattctttccacacctgtcaa	2342	NM_002028	SEQ ID NO:22
GPRC5B	"G protein-coupled receptor, family C, group 5, member B / G protein-coupled receptor, family C, group 5, member B"	203632_s_at		tgatgtcacctagcagggcttcagggttcccactaggatgcagagatgacctctcgc tgcctcacaagcagtgacacctcgggtcctttccgttgctatggtgaaaattcctggatg gaatggatcacatgaggtttctgttgctttgggaggtgtgggggatatttgttttggtttt tctgcaggttccatgaaaacagccttttccaagccaattgtttctgtcatggttttccatct gtcctgagcaagtcattccttgtattagcatttcgaacatctcggccattcaaagccc ccatgttctctgcactgttggccagcataacctctagcatcgattcaaagcagagtttta acctgacggcatggaatgtataaatgagggtgggtcctctgcagatactctaatcact acattgctttttctataaaactacccataagccttaacctttaaagaaaaatgaaaaag gttagtgtttgggggccgggggaggactgaccgcttcataagccagtacgtctgagct gagta	51704	NM_016235	SEQ ID NO:23

GSPT2	G1 to S phase transition 2	205541_s_at		aagcaattttcttgatgcctctgcaagatactgtgaggagaattgacagcaaaagttca ccacctactcttatttactgcccattgattgacttttcttcatattttgcaaagagaaatttca cagcaaaaattcatgttttgtcagctttctcatgttgagatctgttatgtcactgatgaattta ccctcaagtttccttcctctgtaccactctgcttccttggacaatatcagtaatagctttgta agtgatgtggacgtaattgcctacagtaatgaaaaattaatgtactttaatttttcattttctt ttaggatatttagaccacccttgttccacgcaaaccagagtgtgtcagtgtttgtgtg	23708	NM_018094	SEQ ID NO:24
H2AFY 2	"H2A histone family, member Y2 / H2A histone family, member Y2"	218445_at		cagggatcggaggacgacccgagtcccaagagtggggttttgctttttaaaaggaga gaggaggggtgatggcaggggagtggagggtggccgggcaggtcctgccggcgc agggagccctctgcccttcacactctcctccaaaagagcctccatctgtaaggaagc aggtctccgcgaggggtttctttccatgtgttttcctcctgttgttaaaagaactttttaaaa aaacagacctcgttttagatttatagcattgacttttacacacattcacacaagaaaaa aatcctttcaaaattcttaaatcttctgttcctcctttttccaagggaagagggcaaaaag tggcctgggctctgttggtgtgcgtgttccgtggcggagagaagaaaatgggaaaga catctcactggtgcttttctcttttgttttagtgccccccgcccccatccctataatatctgta ac	55506	NM_018649	SEQ ID NO:25
HMGA 2	high mobility group AT-hook 2 / high mobility group AT-hook 2 / high mobility group AT-hook 2	208025_s_at		gaagcaattgctcatgttggccaaacatggtgcaccgagtgatttccatctctggtaaa gttacacttttatttcctgtatgttgtacaatcaaaacacactactacctcttaagtcccagt atacctcatttttcatactgaaaaaaaaagcttgtggccaatggaacagtaagaacat cataaaatttttatatatatagtttatttttgtgggagataaattttataggactgttctttgctgt tgttggtcgcagctaaataagactggacatttaacttttctaccatttctgcaagttaggta tgtttgccaggagaaaagtatcaagacgtttaactgcagttgactttctccctgttcctttg agtgtcttctaactttattctttgttctttatgtagaattgctgtctatgattgtactttgaatcgct tgacttgttgaaaatatttctctagtgtattatcactgtctgttctgcacaataaacataaca gcctctgtgatccc	8091	NM_003483	SEQ ID NO:26
IER2	immediate early response 2 / immediate early response 2	202081_at		gcgtttccaacctcggagaattccaggcactccccttccccctccgctgacatacttgta taagcggtcatcgttgcgtcatggggcaggcgtggggagcttcctgtcgccttggctgg gtgtgggcctggaggaaggtcctggggcgtgcactcgcctgggcagtggggagga gagtggcctgagttacttcacccccgcgtgctgctggttaatgtcccgcgtctctgcacc ttcgggtgggagcggggactgatctactttcacattctcaagtttttctcatctgcattaga ggtccccagtaggttcccaggttccagcgtgcccctccctcagacacacggacaca atcagccgagaagttcctggtctgaatcacgagaatgtggaggggtgggggtgtca gtggaaaggcataaggctgagctgagaccagttgctggtgaaactgggccaatctg gggaggggaacatccttgccagggagtttctgagggtctgctttgtttacctttcgtgcg gtggattctttttaactccgtctacctggcgttttgttaga	9592	NM_004907	SEQ ID NO:27
KIAA01 21	Vestigial-like 4	214004_s_at		ccacctgtgaccccgtggtggaggagcatttccgcaggagcctgggcaagaattac aaggagcccgagccggcacccaactccgtgtccatcacgggctccgtggacgacc actttgccaaagctctgggtgacacgtggctccagatcaaagcggccaaggacgga gcatccagcagccctgagtccgcctctcgcangggccagcccgccagcccctctgc ccacatggtcagccacagtcactccccctctgtggtctcctgaagggagcgcctcctc caacaacacgtggatctgcatggtttgcctgagctttgaacagtca	9686	NM_014667	SEQ ID NO:28

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KLHL7	kelch-like 7 (Drosophila)	220239_at		agttgatcagagccttccagagtgtggtatgcttttcactgtgtgatgatccttagtggcacatgaatgaacgtccagatgtttgtgcagtagcccacccttatctgcaggatacgttccaagacccccagtgaatgcctgaaactgcagatagtactgaatcctatatatactgtgttttttatgatacatacatgcctatgatgaagt	55975	NM_018846	SEQ ID NO:30
LAMC2	"laminin, gamma 2 / laminin, gamma 2"	202267_at		aagagaatgttcctactcacacttcagctgggtcacatccatccctccattcatccttccatccatctttccatccattacctccatccatccttccaacatatatttattgagtacctactgtgtgccaggggctggtgggacagtggtgacatagtctctgccctcatagagttgattgtctagtgaggaagacaagcatttttaaaaaataaatttaaacttacaaactttgtttgtcacaagtggtgtttattgcaataaccgcttggtttgcaacctctttgctcaacagaacatatgttgcaagaccctcccatgggggcacttgagttttggcaaggctgacagagctctgggttgtgcacatttctttgcattccagctgtcactctgtgcctttctacaactgattgcaacagactgttgagttatgataacaccagtgggaattgctggaggaaccagaggcacttccaccttggctgggaagactatggtgctgccttgc	3918	NM_005562 / NM_018891	SEQ ID NO:31
MLLT3	"myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 / myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3"	204918_s_at	+	aaggcattccacaggatcatcatttaaaaaaaaagaattctggtcctgttttctaaaaaaaaaaaactgttgtagaaattcttaatttggatctatttattagtcagagtttcagctttcttcagctgccagtgtgttactcatctttatcctaaaaatctggaatcagagatttttgtttgttcacatatgattctcttagacacttttatatttgaaaaaattaaaatctttctttggggaaaaattcttggttattctgccataacagattatgtattaacttgtagattcagtggttcaatacctgtttagttgcttgctaatatttccagaaggatttcttgtattggtgaaagacggttggggatgggggggatttttttgttcttgttgtacccttgttttgaaactagaaatctgtcctgtggcatgcaaaagaaagcaaattatttttaaaagaaaaaaaccaaagtacttttggtgtcattattccatcttctcca	4300	NM_004529	SEQ ID NO:32
MNAT1	menage a trois 1 (CAK assembly factor) / menage a trois 1 (CAK assembly factor)	203565_s_at		ccagccactgcagatagagacatatggaccacatgttcctgagcttgagatgctaggaagacttgggtatttaaaccatgtcagagctgcctcaccacaggaccttgctggaggctatacttcttctcttgcttgtcacagagcactacaggatgcattcagtgggcttttctggcagcccagttaaccatttataagatttggaccttggagctgaaccagggagctagcaaaagtaaagcagacttataaaattatagctatgtgcagctgcacaacacagtccttccactagcagctgtgttaa	4331	NM_002431	SEQ ID NO:33

MT1E	metallothionein 1E (functional)	212859_x_at	+	caccgcgcagagctcaggggtggtgcgcccggccctctgcggcgcacagccca gcccaggaacgcgggcggtgcggactcagcgggccgggtgcaggcgcggagct gggcctctgcgcccggcccgancctccgtctataaanagagcagccagttgcagggc tcnantctgctttccaactgcctgactgcttgttcgtctcactggtgtgagctccagcatcc cctttgctcgaaatggacccccaactgctcttgcgccactggnttggctcctgcacgtgcg ccggctcctgcaagtgcaaagagtgcaaatgcacctcctgcaagaagagctgctgtt cctgctncccctggnctgtgccaagtgtgcccagggctgcgtctgcaaagggcat cggagaagtgcagctgctgtgcctgatgtgggaacagctctctcccagatgtaaata gaacaacctgcacaacctggnatttttttaaaaatacaacactgagccatttgctgcatt tc	4493	NM_175617	SEQ ID NO:34
NES	nestin	218678_at		gcagcactcttaactacgatctcttgacatacggtttctggctgagaggcctggccg ctaaggtgaaaaggggtgtggcaaaggagcctactccaagaatggaggctgtagg aatataacctcccacccctgcaaagggaatctcttgcctgctctccatctcataggctaagt cagctgaatcccgatagtactaggtccccttcccttcccgcatcccgtcagctggaaaag gcctgtggcccagaggcttctccaaagggagggtgacatgctggctttgtgcccaag ctcaccagccctgcgccacctcactcagtagtgtgcaccatctcactgcagtagcacg ccctcctgggccgtctggcctgtggtaatggaggtgacggcactccatgtgctgact ccccccatcccctgccacgctgtggccctgccctggctagtccctgcctgaataaag	10763	NM_006617	SEQ ID NO:35
NPAS2	neuronal PAS domain protein 2	213462_at		gctacagattcacacttctggcctaaaccctaatgggatgaggctttcacccaggc catgctggtggtgatttttagcccctaaataaaacactggactatttcctgtttacttcatt gattgcaactacaaaggtggactcaaagcaaagcacacaatcatgccagccaacattc cagaattctgctgagaactccaagtctgtgagggggagaggtttacaagccagacag gcctgggggactgcagtcccccaaggagaccctgccacatgctggccctttgagtga gaatgctgcatctttctacatatcttcatgagaatactgagaatttggatttccttttcaaaa tgcactttgctttttttgtatgttttgttatgttgagatgtttctaaagaaaaagatttttatgtaatta taagatgaagcgtagtgtgaattgtacagctgttgtaataatgacctatttctatataaaata aaaattgtatggcttatgtgtaaattatttttgtatctgagataccagttccttttccc	4862	NM_002518 / NM_032235	SEQ ID NO:36
OSGEP	O-sialoglycoprotein endopeptidase	209450_at		aaagggatggacgtctcattctcagggatcctgtctttcattgaggatgtagcccatc ggatgctggccacaggcgagtgtactcctgaggatctgtgtttctcctgcaggaaact gtgtttgcaatgctggtagagatcacagagcggagccatggcacatttgtggctccag gaggccctcattgtgggaggagtgggtgtaatgtgaggctacaggagatgatggc aacaatgtgccaggaacgtgggagcccggcttttgctacagatgagagattctgtattg acaatggagcgatgatagcccaggctggctgggagatgtttcgggctggacacagg acccccactcagtgattctggg	55644	NM_017807	SEQ ID NO:37

PCDH GC3	"protocadherin gamma subfamily C, 3"	209079_x_at		cagaaagtctcagcccaggatgggcttcttcaacagggccctgccctcctgaagc ctcagtccttcacctgccaggtgccgtttctcttccgtgaaggccactgcccaggtccc cagtgcgccccctagtggccataggcctggttaaagttccccagtgcctccttgtgcata gaccttcttctccacccccttctgccctgggtccccggccatccagcgggggctgcca gagaacccagacctgccctacagtagtgtagcgccccctccctcttcggctgggtgt agaatagccagtagtgtagtgcggtgtgctttacgtgatggcgggtgggcagcgggc ggcgggctccgcgcagccgtctgtccttgatctgcccgcgggcggccgtgttgtgtttg tgctgtgtccacgcgctaaggcgaccccctcccccgtactgactctcctataagcgctt ctcttcgcatagtcacgtagtctcccaccccaacctcttcctgtgtctcacgcaagtttta	5098	NM_002588 / NM_032402 / NM_032403	SEQ ID NO:38
PCDH GC3	"protocadherin gamma subfamily C, 3 / protocadherin gamma subfamily C, 3"	211066_x_at		ggatgggggcttcttcaacagggccctgccctcctgaagcctcagtcttcaccttgcc aggtgccgtttctcttccgtgaaggccactgcccaggtcccctgcgcccctagtg gccatagcctggttaaagttcccagtgcctccttgtgcataggaccttctctcccaccc cttctgccctgggtcccccggccatccagcgggggctgccagagaacccagacctg ccttacagtagtgtagcgccccctccctcttcggctggtgtagaatagccagtagtgt agtgcggtgtgctttacgtgatggcgggtgggcagcgggcgggctcccgcgca gccgtctgtccttgatctgcccgcggcggcccgttgtgtttttgtgctgtgtccacgcgct aaggcgaccccctcccccgtactgactctcctataagcgctctcttcgcatagtcacg tagctcccaccccaccctcttcctgtgtctcacgcaagtttttatactctaatatttatatggc ttttttttcttcgacaa	5098	NM_002588 / NM_032402 / NM_032403	SEQ ID NO:39
PCDH GC3	"protocadherin gamma subfamily C, 3 / protocadherin gamma subfamily C, 3"	215836_s_at		gccagcttgggctgagctaacaggaccaatggattaaactggcatttcagtccaag gaagctcgaagcagtttaggaccaggtcccttgagaggtcagaggggcctctgt gggtgctgggtactccagaggtgccactggtggaaggtcagcggagcccagtgc ctccttgtgcatagacctcttctcccaccccttctgccctgggtcccggccatccag cgggctgccagagaaccccagacctgccttacagtagtgtagcgccccctcctc tttcggctggtgtagaatagccagtagtgtagtgcggtgtgctttacgtgatggcgggt gggcagcgggcgggcgggctccgcgcagccgtctgtccttgatctgcccgcgggcggc ccgtgttgtgtttttgtgctgtgtccacgcgctaaggcgaccccctcccccgtactgactctc tcctataagcgctctcctccgcatagtcacgtagctcccaccccaccctcttcctgtgtctc acgcaagtttta	5098	NM_002588 / NM_032402 / NM_032403	SEQ ID NO:40
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PEX3	peroxisomal biogenesis factor 3	203972_s_at		tggatccaaacctttattatgccattatatgatgccagatgaagaaactccattagcagt gcaggcctgtggactttctcctcgagacattaccactattaaacttctcaatgaaactag agacatgttggaaagcccagattttagtacagttttgaatacctgtttaaaccgaggtttt agtagacttctagacaatatggctgagttctttcgacctactgaacaggacctgcaaca tggtaactctatgaatagtctttccagtgtcagcctgcctttagctaagataattccaata gtaaacggacagatccattcagtttgcagtgaaacacctagtcattttgttcaggatctg ttgacaatggagcaagtgaaagactttgctgctaatgtgtatgaagcttttagtacccct cagcaactggagaaat	8504	NM_003630	SEQ ID NO:42
PIN1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 / protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	202927_at		agccatttgaagacgcctcgtttgcgctgcggacgggggagatgagcgggcccgtgt tcacggattccggcatccacatcatcctccgcactgagtgagggtggggagcccag gcctggcctcggggcagggcagggcggctaggccggccagctccccccttgcccgc cagccagtggccgaaccccccactccctgccaccgtcacacagtatttattgttccca caatggctgggagggggcccttccagattgggggccctggggtccccactccctgtc catccccagttggggctgcgaccgccagattctcccttaaggaattgacttcagcagg ggtgggaggctcccagacccagggcagtgtggtgggaggggtgttccaaagagaa ggcctggtcagcagagccgccccgtgtccccccaggtgctggaggcagactcgag ggccgaattgtttctagttaggccacgctcctctgttcagtcgcaaaggtgaacactcat gcggcagcc	5300	NM_006221	SEQ ID NO:43
PRKCA	"protein kinase C, alpha"	213093_at		gattaaacgactgtgtctttgtcacctctgcttaactttaggagtatccattcctgtgattgt agacntttgttgatattcttcctggaagaatatcattcttttcttgaagggttggtttactaga atattcaaaatcaatcatgaaggcagttactattttgagtctaaaggttttctaaaaatta acctcacatcccttctgttagggtctttcagaatatcttttataaacagaagcatttgaagt cattgcttttgctacatgatttgtgtgtgtgaaggacataccacgtttaaatcattaattgaa aaacatcatataagccccaactttgtttggaggaagagacggaggttgaggtttttcctt ctgtataagcacctactgacaaaatgtagaggccattcaaccgtcaaacaccatttgg ttatatcgcagaggagacggatgtgtaaattactgcattgctttttttttcagtttgtataacc tctaatctccgtttgcatgatacgctttgttagaa	5578	NM_002737	SEQ ID NO:44
RIOK3	RIO kinase 3 (yeast)	202129_s_at		tgaatgtacgcttgtccatgctgacctcagtgagtataacatgctgtggcatgctggaa aggtctggttgatcgatgtcagtcagtcagtagaacctacccaccctcacggcctgga gttcttgttccgggactgcaggaatgtctcgcagtttttccagaaaggaggagtcaagg aagcccttagtgaacgagaactcttcaatgctgtttcaggcttaaacatcacagcagat aatgaagctgattttttagctgagatagaagctttggagaaaatgaatgaagatcacgt tcagaagaatggaaggaaagctgcttcatttttgaaagatgatggagacccaccact actatatgatgaatagcactaatacccactgcttcagtgttaacacagcagtgattgtc agctgccaatagcaaatgaagttatgggtgacttgaaataccaaaacctgaggagtg ggcaatggtgcttctgtg	8780	NM_003831 / NM_145906	SEQ ID NO:45

SERPINB9	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9 / serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9"	209723_at	+	ttcgccacattggccgtgttggtcttgaactcctggcctcaagcaatccgcctacctcag cctcccaaagtgctaggattacaggcataagccactgagcccagccctagttcagta tcttttatgtaaattataaacatctgcaacattatgtatcatatgcagatacttattgcatttct tttattagtggtgaaagtgttctatgcatttattggctcttgaatttcctcatctatgaattgtca ttcacacacctacttttctgcttcgtttttacatatgtctttgcctattaaagatattatccctct gttttatattttctctcattcttgtattgccttttaa	5272	NM_004155	SEQ ID NO:46
SIX1	sine oculis homeobox homolog 1 (Drosophila) / sine oculis homeobox homolog 1 (Drosophila)	205817_at		ccggaggcaaagagaccgggccgcggaggccaaggaaagggagaacaccga aaacaataactcctcctccaacaagcagaaccaactctctcctctggaagggggca agccgctcatgtccagctcagaagaggaattctcacctccccaaagtccagaccag aactcggtccttctgctgcagggcaatatgggccacgccaggagctcaaactattctc tcccgggcttaacagcctcgcagcccagtcacggcctgcagacccaccagcatcag ctccaagactctctgctcggccccctcacctccagtctggtggacttggggtcctaagt ggggagggactggggcctcgaagggattcctggagcagcaaccactgcagcgact agggacacttgtaaatagaaatcaggaacatttttgcagcttgtttctggagttgtttgcg cataaaggaatggtggactttcacaaatatctttttaaaaatcaaaaccaacagcgat ctcaagcttaa	6495	NM_005982	SEQ ID NO:47
SLCO3A1	"solute carrier organic anion transporter family, member 3A1 / solute carrier organic anion transporter family, member 3A1"	219229_at		ggctgagcaccagtgagttctttgcctctactctgaccctagacaacctggggaggga ccctgtgcccgcaaaccagacacataggacaaagtttatctataacctggaagacc atgagtggtgtgaaaacatggagtccgttttatagtgactaaaggagggctgaactct gtattagtaatccaagggtcattttttcttaaaaaaagaaaaaaaggttccaaaaaaa accaaaactcagtacacacacacaggcacagatgcacacacacgcagacagac acaccgactttgtcctttttctcagcatcagagccagacaggattcagaataaggaga gaatgacatcgtgcggcagggtcctggaggccactcgcgcggctgggccacagag tctactttgaaggcacctcatggttttcaggatgctgacagctgcaagcaacaggcact gccaaattcagggaacagtggtggccagcttggaggatggac	28232	NM_013272	SEQ ID NO:48
SPINK1	"serine protease inhibitor, Kazal type 1 / serine protease inhibitor, Kazal type 1"	206239_s_at	+	gagacgtggtaagtgcggtgcagttttcaactgacctctggacgcagaacttcagcca tgaaggtaacaggcatctttcttctcagtgccttggccctgttgagtctatctggtaacact ggagctgactccctgggaagagaggccaaatgttacaatgaacttaatggatgcac caagatatatgaccctgtctgtgggactgatggaaatacttatcccaatgaatgcgtgtt atgttttgaaggtcggaaacgccagacttctatcctcattcaaaaatctgggccttgctg agaaccaaggttttgaaatcccatcaggtcaccgc	6690	NM_003122	SEQ ID NO:49

SPINK 5	"serine protease inhibitor, Kazal type 5 / serine protease inhibitor, Kazal type 5"	205185_at	+	agccatcccatgttagagcttctcaagaggaagacagcccagactctttcagttctctg gattctgagatgtgcaaagactaccgagtattgcccaggataggctatctttgtccaaa ggatttaaagcctgtctgtggtgacgatggccaaacctacaacaatccttgcatgctct gtcatgaaaacctgatacgccaaacaaatacacacatccgcagtacagggaagtgt gaggagagcagcaccccaggaaccaccgcagccagcatgcccccgtctgacga atgacaggaagattgttgaaagccatgagggaaaaaataaaccccagttctgaatc acctaccttcaccatctgtatatacaaagaattcttcggagcttgtcttatttgctatagaa aacaatacagagcttttgggaatggaatcactgattttcagtcttttccatttctttcctccta gaatctgtgatctgagggtataaagacatttccaccaagtttgagccctcaaaatgtcc tgattacaatgctgtctgtcc	11005	NM_006846	SEQ ID NO:50
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TAZ	transcriptional co-activator with PDZ-binding motif (TAZ)	202132_at		tgggggacttatttgttggggatcttaaataagattccttttgatctaccggaatatacatg tacagagtacattggatcatgttggaaagaaggcaagtgaaaaggtcagagatgaa gtagcgaagttatggaatatcgtggaaaggatactagttgtgaaatggaaagagaca agttatagtaccccaaaagcaaaacaagcaggagatgcaagagatgccccaaaa ggacaaagcaacaattttctgttgccacctttataccggaagactctgttgtagaagaa aagaaggctttggtgcaccttatgtgggaggaggaggggcagggcatgctgatgct gagcgtacaggcagacaagagcgtagcctgctgttgcctccatcactatgaaatgac ttattttacctgaaggacccatggtttatgttcctctaattcctttcactctccctaagccctct gagagagatg	25937	NM_015472	SEQ ID NO:52
TCEA2	"transcription elongation factor A (SII), 2 / transcription elongation factor A (SII), 2"	203919_at		gcctgtcggctcagatcgaggaatgcatcttccgggacgttggaaacacagacatga agtataagaaccgtgtacggagtcgtatctccaacctgaaggatgccaagaaccctg acctgcggcggaatgtgctgtgtggggccataacaccccagcagatcgctgtgatga cctcagaggagatggccagtgatgagctgaaggagatccgtaaggccatgaccaa ggaggccatccgagagcaccagatggcccgcactggcggcacgcagacagacct gttcacctgcggcaagtgcaggaaaaagaactgcacctacacacaggtgcagacc cgcagctctgatgagcccatgaccacctttgttgtctgcaacgagtgtggaaaccgct ggaagttctgctgacccctcgtgtagatgtgctgcagccttgggccctccccggccca cgtcctccgttgacacagcttctctggagaccctagaaggcggcatgtcc	6919	NM_003195 / NM_198723	SEQ ID NO:53

TNNC1	"troponin C, slow / troponin C, slow"	209904_at	+	tggatgacatctacaaggctgcggtagagcagctgacagaagagcagcagaaaaatga gttcaaggcagcctcgacatcttcgtgctgggcgctgaggatggctgcatcagcacc aaggagctgggcaaggtgatgaggatgctgggccagaacccacccctgaggag ctgcaggagatgatcgatgaggtggacgaggacggcagcggcacggtggacttg atgagttcctggtcatgatggttcggtgcatgaaggacgacagcaaagggaaatctg aggagctgtctgacctcttccgcatgtttgacaaaaatgctgatggctacatcgacctg gatgagctgaagataatgctgcaggctacaggcgagaccatcacggaggacgac atcgaggagctcatgaaggacggagacaagaacacgacggccgcatcgactat gatgagt	7134	NM_003280	SEQ ID NO:54
TRPM2	"transient receptor potential cation channel, subfamily M, member 2"	205708_s_at		acccttggccatcaggcgaggggctgggcctgtgcagctgggccttggccagagt ccactccttcctggctgtgtcacccggagcagctcatccaccatggaggtcattggcc tgaggcaagttcccccggagagtcgggntccctgtggcccctcaggcctatgtctgt gaggaagggcctgccactctcccccaagagggcctccatgttcgaggtgcctcaa catggagccttgcctggcctgggctagggcactgtctgaactcctgactgtcaggat aaactccgtgggggtacaggagcccagacaaagcccaggcctgtcaagagacgc agagggcccctgccagggttggccccagggacccttgggacgaggctgcagaagc tctccctcctactcccttgggagccactgctggccatgtggccagggacggcatga gcaggaggcgggggacgtgggggccttctggtttggtgtcaacagc	7226	NM_00100118 8 / NM_003307	SEQ ID NO:55
VAMP4	vesicle-associated membrane protein 4	213480_at		gaagccacaaagatgccacatgttagtatatcagtgagaggtgactccacagtgctc tctggagaagcaatatgagtgactgaagagtgtgggcctttgctttgcctggatatag gggtgctctctactgtaattgggtgtggaaaaactctggcttatggtattccattaggttc ttttcatttaaagtagtcttaaaatcaaagtatccaatatttttaaagccacaaagtagatt acataattagcagagatttttagtcagtaaaatgttagaaatcaaactataagaaaattc aagtccttatttttgtgtcttgggtatatgtcattatttttaaattccacactccttatttaatca ctttggtaagtgccttgatgttttgaaatgtatagtgtgggagatgagcaaatgtaaatgtc atgtgccctgttccctagcttctcaattcctcataacctcaaccatttttaccagtgttgcaaagttta gaccttttgttaatatcagaagtgtatttgtagcccctccatagtgaacaatga	8674	NM_003762 / NM_201994	SEQ ID NO:56
ZNF313	zinc finger protein 313	200868_s_at		gccgaagaagcctgtctgtgggtgtgtcgcagcgctctggcacctggcgtccggagc cgtggagctcgaggcggcagatcgagagcacagagacttcttgccatggctgccgta agaatttcttcctgtccaagatccggtcccacgtggctacttgttccaaatacccagaatt acatcatggaaggtgtgaaggccaccattaaggatgcatctcttcagccaaggaatg tcccaaaccgttacaccttccttgtcctactgtcctgagaagaacttgatcaggaag gacttgtggaacactgcaaattattccatagcacggatacccaaatctgtggttgtccg atatgtgcctcgatgcctggggagacccccaactaccgcagcgccaacttcagaga gcacatccagcgccggcaccggttttcttatgacacttttgtggattatgatgttgatgaa gaggacatgatgaatcaggtgttgcagcgcctccatcatcgaccagtgagcagagtcc gtgcttgctatc	55905	NM_018683	SEQ ID NO:57

Table 2: **as described in priority application US60/619027 filed on 18/10/2004.**

Gene Symbol	Gene Title	Affymetrix ID	+ up in *sensitive*	Sequence	Locus Link	RefSeq Transcript ID	SEQ ID NO.
AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1 / alanine-glyoxylate aminotransferase 2-like 1 / alanine-glyoxylate aminotransferase 2-like 1	221008_s_at	+	gctgaaagaagcccacatagaactgcttagggacagcaccactgactccaaa gaaaatcccagcagaaagagaaatggaatgtgcacggatacacattcactgct cagtaagaggctcaagacatgactgatttgcattttaaagcaagatgcgatgtcc agagttacagagaatgagtagatgtgtctcatcggttaatagctctattatacctct aaaggtggaattgtcagtttagattcataaatgaaaaggtaaatgagtaatcaga ataaaccaagtgataatcaaaccatgtcaagattattagttcagactctagcctgtt aattttcttagttgatttctgaagctacctgatttattctattaaattgtaagcttgcaaa ctcaaaataaattggcagatttacctctcatgttttaatgtgtcaaattagagagca aagtataacaggtgccttcacttttgagactt	64850	NM_031279	SEQ ID NO:58
AKAP12	A kinase (PRKA) anchor protein (gravin) 12 / A kinase (PRKA) anchor protein (gravin) 12	210517_s_at		gtgccatagtgcaggcttggggagctttaagcctcagttatataacccacgaaaa acagagcctcctagatgtaacattcctgatcaaggtacaattctttaaaattcacta atgattgaggtccatatttagtggtactctgaaattggtcactttcctattacacgga gtgtgctaaaactaaaaagcattttgaaacatacagaatgttctattgtcattggga aatttttctttctaacccagtggaggttagaaagaagttatattctggtagcaaatta actttacatccttttttcctacttgttatggttgtttggaccgataagtgtgcttaatcctga ggcaaagtagtgaatatgttttatatgttatgaagaaaagaattgttgtaagttttga ttctactcttatatgctggactgcattcacacatggcatgaaataagtcaggttcttta caaatggtattttgatagatactggattgtgtttgtgccatatttgtgccatt	9590	NM_005100 / NM_144497	SEQ ID NO:59
ANXA6	annexin A6 / annexin A6	200982_s_at		gggatgcatttgtggccattgttcaaagtgtcaagaacaagcctctcttctttgccg acaaacttacaaatccatgaagggtgctggcacagatgagaagactctgacc aggatcatggtatcccgcagtgagattgacctgctcaacatccggagggaattc attgagaaatatgacaagtctctccaccaagccattgagggtgacacctccgga gacttcctgaaggccttgctggctctctgtggtggtgaggactagggccacagctt tggcgggcacttctgccaagaaatggttatcagcaccagccgccatggccaag cctgattgttccagctccagagactaaggaaggggcaggggtgggggaggg gttgggttgggctcttatcttcatggagcttaggaaacgctcccactcccacgggc catcgagggccagcacggctgagcggtgaaaaaccgtagccatagatcctgt cc	309	NM_001155 / NM_004033	SEQ ID NO:60
AREG	amphiregulin (schwannoma-derived growth factor) / amphiregulin (schwannoma-derived growth factor)	205239_at	+	atttcaaaatttctgcattcacggagaatgcaaatatatagagcacctggaagca gtaacatgcaaatgtcagcaagaatatttcggtgaacggtgtggggaaaagtcc atgaaaactcacagcatgattgacagtagtttatcaaaaattgcattagcagcca tagctgcctttatgtctgctgtgatcctcacagctgttgctgttattacagtccagctta gaagacaatacgtcaggaaatatgaaggagaagctgaggaacgaaagaaa cttcgacaagagaatggaaatgtacatgctatagcataactgaagataaaatta caggatatcacattggagtcactgccaagtcatagccataaatgatgagtcggtc ctctttccagtggatcataagacaatggacccttttgttatgatggttttaaactttca attgtcacttttatgctatttctgtata	374	NM_001657	SEQ ID NO:61

BCAT1	"branched chain aminotransferase 1, cytosolic / branched chain aminotransferase 1, cytosolic"	214452_at	+	gacaacagccctggaggggaacagagtgagagagatgtttngctctggtaca gcctgtgttgtttgcccagtttctgatatactgtacaaaggcgagacaatacacatt ccaactatggagaatggtcctaagctggcaagccgcatcttgagcaaattaact gatatccagtatggaagagaagagagcgactggacaattgtgctatcctgaatg gaaaatagaggatacaatggaaaatagaggataccaactgtatgctactggga cagactgttgcatttgaattgtgatagatttctttggctacctgtgcataatgtagtttgt agtatcaatgtgttacaagagtgattgtttcttcatgccagagaaaatgaattgcaa tcatcaaatggtgtttcataacttggtagtagtaacttaccttaccttaccnanaaaa atattaatgtaagccatataacatgggattttcctcaannannnnannnnnncct tttgtacttcactcagatacta	586	NM_005504	SEQ ID NO:62
BCL3	B-cell CLL/lymphoma 3 / B-cell CLL/lymphoma 3	204908_s_at	+	gggcagatcttggactcatgaggaggggcccccctgcccagaggggtcaacc cttctggaaactgtgaagatctgacttcgcccccccccccccccatcttcgggac caggatttgcacagaagcacatgcacctacccatacacccccctcttctgagcgtc cctgttcccccatctcgctccctcccaggactctgaccccagcattctcaggcacc agtccctgtccggaatgccacccacatcttccatttccatgtcccctcccagagct ggtggacccagggaacagccactcccctccactctctaccagataactgagga ggggagaggtgggccgtaacgggcacggatcacgatgtaaattatt	602	NM_005178	SEQ ID NO:63
BST2	bone marrow stromal cell antigen 2 / bone marrow stromal cell antigen 2	201641_at	+	agcttcaggacgcgtctgcagaggtggagcgactgagaagagaaaaccagg tcttaagcgtgagaatcgcggacaagaagtactaccccagctcccaggactcc agctccgctgcggcgccccagctgctgattgtgctgctgggcctcagcgctctgct gcagtgagatcccaggaagctggcacatcttggaaggtccgtcctgctcggcttt tcgcttgaacattcccttgatctcatcagttctgagcgggtcatggggcaacacgg ttagcggggagagcacggggtagccggagaagggcctctggagcaggtctg gaggggccatggggcagtcctgggtgtggggacacagtcgggttgacccagg gctgtctccctccagagcctccctccggacaatgagtcccccctcttgtctcccac cctgagattgggcatggggtgcggtgtgggggggcatgtgctgcctgttgttatggg tttttttgcgggggggggttgctttttctggggtctttgagctccaaa	684	NM_004335	SEQ ID NO:64
C9orf16	chromosome 9 open reading frame 16	204480_s_at	+	catgctggaccagatcaactcctgtctggaccacctggaggagaagaatgacc acctccacgcccgcctccaggagctgctggagtccaaccggcagacacgcct ggagttccagcagcagctcggggaggcccccagtgatgccagcccctaggct ccaagagcccccaaccgggacccaaccctgcctccctgggctaggctctggc ctgggcactcaccccctggcttagacaccttctcaagggctggccttcagggacc cctggtgggtctgcctgcctgggccacccttcctgcctgggcctccccttggccta cctgggccagcccccaccacctggcatgccctcctggggccaagagtgggcct gcaacccacccacttgcctgcccacccaactcctgggcgctccccactctgccc aggccttgagtgtccacattaaatg	79095	NM_024112	SEQ ID NO:65
CAPZA2	"capping protein (actin filament) muscle Z-line, alpha 2"	201237_at		cacttaccagtgagcatatatattttaaaatactttctttggatattgtaattcttaactg gttgtaaattagaaaagctgggattacatatggtgtgcggttacagtctaaattttttc atcctcctatgcatcataagcatgtttgtaatattttcaaaaatagttctactgatgcta caggaatttcaagcctgtggtgaatgttagtatttaccatagggagtgaagtggag ttatggtttcattcaatagagtattgctgattatacttgagtggaatcctttcctcacgt actcccacagacgtctgggcctggaaa	830	NM_006136	SEQ ID NO:66

CCND1	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	208711_s_at		ggcggaggagaacaaacagatcatccgcaaacacgcgcagaccttcgttgcc ctctgtgccacagatgtgaagttcatttccaatccgccctccatggtggcagcggg gagcgtggtggccgcagtgcaaggcctgaacctgaggagccccaacaacttc ctgtcctactaccgcctcacacgcttcctctccagagtgatcaagtgtgacccgga ctgcctccgggcctgccaggagcagatcgaagccctgctggagtcaagcctgc gccaggcccagcagaacatggaccccaaggccgccgaggaggaggaaga ggaggaggaggaggtggacctggcttgcacacccaccgacgtgcgggacgt ggacatctgagggcgccaggcaggcgggcgccaccgccacccgcagcgag ggcggagccggccccaggtgctcccctgacagtccctcctctccggagcattttg ataccagaagggaaagcttcattctccttgttgttggttgttttttcctttgctctttcccc cttccatctctgacttaagcaaaa	595	NM_001758 / NM_053056	SEQ ID NO:67
CCND1	cyclin D1 (PRAD1: parathyroid adenomatosis 1) / cyclin D1 (PRAD1: parathyroid adenomatosis 1)	208712_at		gttttgggtatgtttaatctgttatgtactagtgttctgtttgttattgttttgttaattacacc ataatgctaatttaaagagactccaaatctcaatgaagccagctcacagtgctgt gtgccccggtcatctagcaagctgccgaaccaaaagaatttgcaccccgctgc gggcccacgtggttggggccctgccctggcagggtcatcctgtgctcggaggcc atctcgggcacaggcccaccccgccccacccctccagaacacggctcacgctt acctcaaccatcctggctgcggcgtctgtctgaaccacgcgggggccttgaggg acgctttgtctgtcgtgatggggcaagggcacaagtcctggatgttgtgtgtatcg agaggccaaaggctggtggcaagtgcacggggcacagcggagtctgtcctgt gacgcgcaagtctgagggtctgggcggcg	595	NM_001758 / NM_053056	SEQ ID NO:68
CDH1	"cadherin 1, type 1, E-cadherin (epithelial)"	201130_s_at		aattcctgccattctggggattcttggaggaattcttgctttgctaattctgattctgctg ctcttgctgtttcttcggaggagagcggtggtcaaagagcccttactgcccccaga ggatgacacccgggacaacgtttattactatgatgaagaaggaggcggagaa gaggaccaggactttgacttgagccagctgcacaggggcctggacgctcggcc tgaagtgactcgtaacgacgttgcaccaaccctcatgagtgtcccccggtatcttc cccgccctgccaatcccgatgaaattggaaattttattgatgaaaatctgaaagc ggctgatactgaccccacagccccgccttatgattctctgctcgtgtttgactatga aggaagcggttccgaagctgctagtctgagctccctgaactcctcagagtcaga caaagaccaggactatgactacttgaacgaatggggcaatccgttcaagaagc tggctgacatgtacggaggcg	999	NM_004360	SEQ ID NO:69
CDKN2A	"cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) / cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)"	207039_at	+	cttttcactgtgttggagttttctggagtgagcactcacgccctaagcgcacattcat gtgggcatttcttgcgagcctcgcagcctccggaagctgtcgacttcatgacaag cattttgtgaactagggaagctcagggggttactggcttctcttgagtcacactgc tagcaaatggca	1029	NM_000077 / NM_058195 / NM_058197	SEQ ID NO:70

CDKN2A	"cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)"	209644_x_at	+	tgaggagccagcgtctagggcagcagccgcttcctagaagaccaggtcatgat gatgggcagcgcccgagtggcggagctgctgctgctccacggcgcggaggccc aactgcgccgaccccgccactctcacctgaccgtgcacgacgctgcccggg agggcttcctggacacgctggtggtgctgcaccgggccgggggcgcggctggac gtgcgcgatgcctgggggccgtctgcccgtggacctggctgaggagctgggccat cgcgatgtcgcacggtacctgcgcgcggctgcgggggcaccagaggcagta accatgcccgcatagatgccacggaaggtccctcagacatcccccgatgaaag aaccagaggaggctctgagaaacctcgggaaacttagatcatcagtcaccgaa ggtcctacagggccacaactgccccgccacaacccaccgcttctgtagtttt catttagaaaataagagctttaaaaatgtcctgcctttaacgtagatatatgccttcc ccc	1029	NM_000077 / NM_058195 / NM_058197	SEQ ID NO:71
CEACAM 7	carcinoembryonic antigen-related cell adhesion molecule 7	206199_at	+	atattagttacctggtgtgctgtattctctaaaaccttaaatgtttgcatgcagccat tcgtcaaatgtcaaatattctctcttggctggaatgacaaaaactcaaataaatgt atgattaggaggacatcataacctatgaatgatggaagtccaaaaatgatggtaa ctgacagtagtgttaatgccttatgtttagtcaaactctcatttaggtgacagcctggt gactccagaatggagccagtcatgctaaatgccatatactcacactgaaacatg aggaagcaggtagatcccagaacagacaaaacttcctaaaaacatgagagt ccaggctgtctgagtcagcacagtaagaaagtccttctgctttaactcttagaaa aaagtaatatgaagtatctgaaattaaccaatcagtttatttaaatcaatttatttat attcttctgttcctggattccatttacaaaacccactgttctactgttgtattgccag t	1087	NM_006890	SEQ ID NO:72
CHORDC 1	"cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 / cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1"	218566_s_at		ggatttgtgttcttacagtactgaaaatatttaaggaagagatgaagctctgcagtt ttttctatgtgggatgattacttttttaaggaggattaattctgaggtagtatagtaact aaaggggaatatatgaattgtttaacaaattagaatttgtttacaactactgaatttt taaattatgtcaaaacttacattactgccaagcagtatgatgttataggaaacata aataagattacagaggtatcaattggttaaaattcaccatttttataagactaagca ataatcttaacaacctcttccctgaatatttaaatgtgttgtatggtgttatgactaatt gttactgatttagagactaagccctcttaaaacctttagttaaatataaaaagaaat tatatatatctttgcctccctgatggaaaactatataaaattgtagacttaaaaggttt gtggaaatacattaggatatcagaaaactaaatatatatggagttgctttatgactatt acatgt	26973	NM_012124	SEQ ID NO:73
CLU	"clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)"	208791_at	+	ggctgcctgcggatgaaggaccagtgtgacaagtgccgggagatcttgtctgtg gactgttccaccaacaacccctccaggctaagctgcggcgggagctcgacg aatccctccaggtcgctgagaggttgaccaggaaatataacgagctgctaaagt cctaccagtggaagatgtctcaacacctcctcctgtggagcagctgaacgagc agtttaactgggtgtccggctggcaaacctcacgcaaggcgaagaccagtac tatctgcgggtcaccacggtggctgaagcttttgactctgatcccatcactgtgacggttcct gtcactgaggtggtgtgaagctctttgactctgatcccatcactgtgacggttccct gtagaagtctccaggagaaccta	1191	NM_001831 / NM_203339	SEQ ID NO:74

CLU	"clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) / *clusterin (complement lysis inhibitor, SP-40,40,* sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)"	208792_s_at	+	agcagctgaacgagcagcagtttaactgggtgtcccggctggcaaacctcacgcaa ggcgaagaccagtactatctgcggtcaccacggtggctcccacactctgact cggacgttcctccggtgtcactgaggtggtcgtgaagctctttgactctgatccat cactgtgacggtccctgtagaagtctcaggaagaaccctaaatttatggagac cgtggcggagaaaagcgctgcaggaataccgcaaaaagcaccgggaggagt gagatgtggatgttgc	1191	NM_001831 / NM_203339	SEQ ID NO:75
COL4A1	"collagen, type IV, alpha 1"	211980_at		gaaagactgtgctgtccttaacatagtttttaaagactaggatattgaatgtgaa acatccgttttcattgttcacttctaaaccaaaaaattatgttgtgcaaaaaccaaac ccaggttcatgaatatggtgtctattatagtgaaacatgtacttgagcttattgttttta ttctgtattaaatatttttcaggtttttaaacactaatcacacaaactgaatgacttgactt caaaagcaacaacctaaaggccgtcatttcattagtattcctcattctgcatcctg gcttgaaaaacagctctgttgaatcacagtatcagtatttcacacgtaagcacatt cgggccatttccgtggtttctcatgagctgtgttcacagacctcagcagggcatcg catggaccgcaggagggcagattcggaccact	1282	NM_001845	SEQ ID NO:76
COL4A1	"collagen, type IV, alpha 1"	211981_at		tcggctactcttttgtgatgcacacaccagcgctggtgcagaaggctctggccaagc cctggcgtccccccggctcctgcctggaggagtttagaagtgcgccattcatcgag tgtcacggccgtgggacctgcaattactacgcaaacgcttacagctttggctcgc cacatagagaggaggagcgagatgttcaagaagcctacgccgtccaccttgaag gcagggagctgcgcacgcacgtcagccgctgccaagtctgtatgagaagaa cataatgaagcctgactcagctaatgtcacaacatggtgctacttcttctcttttgtt aacagcaacgaaccctagaaatatatcctgtgtacctcactgtccaatatgaaa accgtaaagtgccttataggaatttgccgtaactaacacacccctgc	1282	NM_001845	SEQ ID NO:77
CTSB	cathepsin B	200838_at		tccccctgtagactagtgccgtgggagtacctgctgcccagctgctgtggccccct ccgtgatccatccatctccagggagcaagacagagacgcaggatggaaagc ggagttcctaacaggatgaaagttccccccatcagttccccagtacctccaagc aagtagcttccacatttgtcacagaaatcagag	1508	NM_001908 / NM_147780 / NM_147781 / NM_147782 / NM_147783	SEQ ID NO:78
CTSB	cathepsin B / cathepsin B	200839_s_at		tggtgttgggagcccttggagaacgccagtctccaggtccccctgcatctatcga gtttgcaatgtcacaacctctctgatcttgtgctcagcatgattctttaatagaagtttt attttcgtgcactctgctaatcatgtgggtgagccagtggaacagcgggagcctg tgctggtttgcagattgcctcctaatgacgcggctcaaaggaaaccaagtggtc aggagttgtttctgacccactgatctctactaccacacaaggaaaatagtttaggaga aaccagctttactgttt	1508	NM_001908 / NM_147780 / NM_147781 / NM_147782 / NM_147783	SEQ ID NO:79

DAB2	"disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)"	201278_at		ggaaacgttcccagttcattttcagtcctgttgtgagcacagttctgaagggtttatta ttgtcaaaataagttttgttttgttttgtttatgttgggtttttaatgttgtctcttgacccttaa tgctcaggttcttgtgggagttaatcagccacatccaangttaccttgagggggaa gaagagggtgatgctcagaagctaaacaagacaggggccacatgaccctcta ttgattagccccaagtagaaagtcctgtggttttatgtttaatggtaatagttgatcat atatggcataattttctatcagcttcctactcagtcactataaacacagacttgaaat agtactttaaatgtccaaatacctaaatgtgctaaactggaggtaactatttctagg tagttgaatttttgaaagtcatgatcagccacacaactgttttgtacatact	1601	NM_001343	SEQ ID NO:80
DAB2	"disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)"	201280_s_at		aatccttattgttcagagttgtttgggggttctgtttcagagcataaaacctaaaggtt atagtagaacaaggcaccttcttaaaagaaatcttgcttcagaccatcagttaca gagaatttcctaaagtaaaattgaagcaactacaacttctccttagacactttgga atctaaccacttaaggacctttttaaagagatagcttctcttctttctgaagatcaattt ctcccaaggccaagattgtccttttctcccatttcttgctagctattgcaaatgaggg aagaacattattcatctctcctccccttttttttctgattctttttcagtcagttttgctcctg ggttcaagtagtattaccacccttcacaagcaacagactc	1601	NM_001343	SEQ ID NO:81
DIAPH2	diaphanous homolog 2 (Drosophila) / diaphanous homolog 2 (Drosophila)	205726_at	+	gctcactacactattcattgcacacaaatgaatttttcactttttaagatgcattcttgg tgctcaaaccagatcgaagtttgtctctnaaagctattgtctgcacaggctgctgc atgctctgttgttaaatggatggacaggctattctaaattttggttgatacttttgctact atgggcaattaacttgaaaaaaataatcgatcccaactctgtgctctgatgtacct cttctgccccttttatgacacctttgaccaaatgccttctatggttcacagtgcaggc acaaaactacctctgatacagaaggttctttacaagcttattttacataccgtgaat ccctcacctaaagggagaggtgaaagcaaagactgctttgaatgggtattgag ggagattgtgtccataccaagccaccctgaagaagtatttcacttgcagtagaac tgtggatttgtgctgtcatttcaccttggaataaacacctatctctaagcaggacca a	1730	NM_006729 / NM_007309	SEQ ID NO:82
EMP1	epithelial membrane protein 1 / epithelial membrane protein 1	201324_at		caccaaattacctaggctgaggttagagagattggccagcaaaaactgtggga agatgaactttgtcattatgatttcattatcacatgattatagaaggctgtcttagtgc aaaaaacatacttacatttcagacatatccaaagggaatactcacattttgttaag aagttgaactatgactggagtaaaccatgtattcccttatctttttactttttttctgtgac atttatgtctcatgtaatttgcattactctggtggattgttctagtactgtattgggcttctt cgttaat	2012	NM_001423	SEQ ID NO:83
EMP1	epithelial membrane protein 1	201325_s_at		ttatcgccctgagaagatctaccccagggagaatctgagacatcttgcctacttttc tttattagctttctcctcatccatttcttttataccttttcctttttggggagttgttatgccatg atttttggtatttatgtaaaaggattattactaattctatttctctatgtttattctagttaag gaaatgttgagggcaagccaccaaattacctag	2012	NM_001423	SEQ ID NO:84

EMP1	epithelial membrane protein 1	213895_at		aaggactggtatctttctgtgagcaataaggactggataaagactgcatatccttg tgtcnnnnncagcancnatacaataaggagggttttaatgtgaagcaggcaat ctnccagccccttctggtcttggatgaaatagttgcacagagtattgcaccaana atacacaatggaggctgaaaagttcaacatattttaagtcaattaatcaaattgca ttgattcttgatgctttcttagaggcctacatgatttcttagattgctctgataaactatc ataaggggtccacntcccctcatttagctcccccagggatttcttttcccccatgtca tacacccagtcctaaatcaacccccaaggctatccttccatcccttctgcagagg gaacttttgtcagactctgcaacaaactcctagctctatccagagtgtcctctgctg ctaagattggtatctttctcctcaaaagcctggatggtgaatgggggtgcattagtc agaattctcc	2012	NM_001423	SEQ ID NO:85
EREG	epiregulin / epiregulin	205767_at	+	taaaaacctgtatctgacccactttgtaatttttgctccaatatccattctgtagactttt gaaaaaaaagtttttaatttgatgcccaatatattctgaccgttaaaaaattcttgttc atatgggagaagggggagtaatgacttgtacaaacagtatttctggtgtatatttta atgtttttaaaaagagtaatttcatttaaatatctgttattcaaatttgatgatgttaaat gtaatataatgtattttctttttattttgcactctgtaattgcactttttaagtttgaagagc cattttggtaaacggtttttattaaagatgctatggaacataaagttgtattgcatgca atttaaagtaacttatttgactatgaatattatcggattactgaattgtatcaatttgttt gtgttcaatatcagctttgataattgtgtaccttaag	2069	NM_001432	SEQ ID NO:86
FGF2	fibroblast growth factor 2 (basic)	204421_s_at	+	gggatcctatttagctcttagtaccactaatcaaaagttcggcatgtagctcatgat ctatgctgtttctatgtcgtggaagcaccggatgggggtagtgagcaaatctgccc tgctcagcagtcaccatagcagctgactgaaaatcagcactgcctgagtagtttt gatcagtttaacttgaatcactaactgactgaaaattgaatgggcaaataagtgct tttgtctccagagtatgcgggagacccttccacctcaagatggatatttcttcccca aggatttcaagatgaattgaaatttttaatcaagatagtgtgctttattctgttg	2247	NM_002006	SEQ ID NO:87
FGF2	fibroblast growth factor 2 (basic) / fibroblast growth factor 2 (basic)	204422_s_at	+	atatcttcttcaggctctgacaggcctcctggaaacttccacatatttttcaactgca gtataaagtcagaaaataaagttaacataactttcactaacacacacatatgtag atttcacaaaatccacctataattggtcaaagtggttgagaatatattttttagtaatt gcatgcaaaatttttctagcttccatcctttctccctcgtttcttcttttttgggggagctg gtaactgatgaaatcttttcccaccttttctcttcaggaaatataagtggttttgtttggt taacgtgatacattctgtatgaatgaaacattggagggaaacatctactgaatttct gtaatttaaaatattttgctgctagttaactatgaacagatagaagaatcttacagat gctgctataaataagtagaaaatataaatttcatcactaaaatatgctattttaaaat ctatttcctatattgtatttctaatcagatgtattactcttattatttctat	2247	NM_002006	SEQ ID NO:88

FLJ22662	hypothetical protein FLJ22662	218454_at	+	gtggctatccactgttagttcagaagctgggcttggactactcttatgatttagctcc acgagccaaaatttccggcgtgaccaagggaaagtgactgatacggcatcca tgaaatatatcatgcgatacaacaaattataagaaggatcccttacagtagaggtga ccctgtaaataccatctgctgccgtgaggacctgaactcacctaacccaagttcct ggaggttgttatgacacaaaggtggcagatatctacctagcatctcagtacacat cctatgccataagtggtcccacagtacaaggtggcctccctgttttcgctgggac cgtttcaacaaaacctctacatcagggcatgccagaggtctacaacttgatttatt accatgaaaccaatttgaaactgatataaaatgaaggagggagatgacgga ctagaagactgtaaataagatacccaaaggcactatttagctatgttttcccatca gaat	79887	NM_024829	SEQ ID NO:89
GADD45 B	"growth arrest and DNA-damage-inducible, beta / growth arrest and DNA-damage-inducible, beta"	207574_s_at		ccccatcacggagaggtccagactgtccactcgggggtggagtgagactgactg caagccccacccttcttgagactggagctgagcgtctgcatcgagaccacacttgggacttgg ttgaaacttggttggtccttgtctgcacctctgcacaagaccacacttgggacttgg gagctgggggctgaagttgctctgtacccatgaactcccagtttgcgaattaataag agacaatctatttgttactgcacttgttatcgaaccactgagagcgagatgg	4616	NM_015675	SEQ ID NO:90
HIF1A	"hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) / hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)"	200989_at		tcatctgatgtttctatagtcacttgccagctcaaaagaaaacaatacccatatgta gttgtggaagtttatgctaatattgtgtaactgatattaaacctaaatgttctgcctac cctgttggtataaagatatttgagcagactgtaaacaagaaaaaaaaaaatcatg cattcttagcaaaattgcctagtatgtaatttgctcaaaatacaatgtttgatttatg cacttgtcgctattaacatccttttttcatgtagatttcaataattgagtaatttagaa gcattatttaggaatatatagttgtcacagtaaatatctttgttttctatgtacattgta caaatttttcattcctttttgtctttgtggttggatctaacactaactgt	3091	NM_001530 / NM_181054	SEQ ID NO:91
HOP	homeodomain-only protein / homeodomain-only protein	211597_s_at	+	aagctaigtgtatctctgtgtaaagcagtggcttcactggaaaaatggtgtggcta gcatttccttgagtcatgatgacagatggtgtgaaaaccatctaagtttgctttg accatcacctcccagtagcaatttgctttcataatccatttagcaatccaggcctct gttgaaaagatatatgagggagaaggaacacatttcctctgaacttacttcc ctaagtcacttcctatgtatcatctaatacaatgatggttgagtgaaaatacaga agggtgtttgagtattcagatttcataaaaacacttcctggaatatagctgcattaa cttggaaagaagcctgtgggccagaagacaga	84525	NM_032495 / NM_139211 / NM_139212	SEQ ID NO:92
HOXC10	homeo box C10 / homeo box C10	218959_at		gctggtgtgtgtgtcaaaccctcactcacccacgcactcacacacagcattctgtt ctccatgcaaagttaagatcgaatccatccgcttgtaggggaaaaaaaggaaa aaaattaaccagagagaggggtctgtaatctcgcagagcacaggcagaatcgttcct tccttgctgcatttcctccttagactaatagacgtttttggaaagttcggctagtgttcgt gtgtttgtcgtagcacccagagcctccaccaaaccctctccatgtctttacctccca gtcgctctaagatctgcttgaagtctcgtatttgtactgcttctgctttctcccaccc tcctagcacccccacatccccccatctagtaacatctcagaaatttcatccagagg aacaaaaaaattaaaaatagaacatagcaaagcaaagacagaatgcccccc cccaaatattgtccigtcccigtctgggagttgtgttatttaaagatattctgtatgttgt atctttigcatgtagttccttaat	3226	NM_017409	SEQ ID NO:93

ITGB2	"integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) / integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)"	202803_s_at		atctggaaggctctgatccacctgagcgacctccgggagtacaggcgctttgag aaggagaagctcaagtcccagtggaacaatgataatcccctttcaagagcgc caccacgacggtcatgaaccccaagtttgctgagagttaggagcacttggtgaa gacaaggccgtcaggacccaccatgtctgccccatcacgcggccgagacatg gcttggccacagctcttgaggatgtcaccaattaaccagaaatccagttattttcc gccctcaaaatgacagccatggccggccggtgcttctgggggctcgtcgggggg gacagctccactctgactggcacagtctttgcatggagacttgaggagggcttga ggttggtgaggttaggtgcgtgtttcctgtgcaagt	3689	NM_000211	SEQ ID NO:94
KHDRBS 3	"KH domain containing, RNA binding, signal transduction associated 3 / KH domain containing, RNA binding, signal transduction associated 3"	209781_s_at		cagcccggccagttggagttgtagtaccacgagggacgccaactcccagagg agtcctgtccacccgagggccagtgagtcggggaagaggacttctcactccca gagcaagaggagtccccccaactgggtacagacctccaccgccacccccga cacaagagacttatggagaatatgactatgatgatggatatggcactgcttatgat gaacagagttatgattcctatgataacagctatagcaccccagcccaaagtggt gctgattactatgattacggacatggactcagtgaggagacttatgattcctacgg gcaagaagagtggactaactcaagacacaaggcaccttcagcgaggacagc aaagggcgtctacagagaccagccatatggcagatactgattgtactgtctgatg ttgtgaaatagccaatctccaccagtcctgtatactg	10656	NM_006558	SEQ ID NO:95
KRT13	keratin 13 / keratin 13	207935_s_at	+	gagaacacggtggcagagacggagtgccgctatgccctgcagctgcagcag atccagggactcatcagcagcatcgaggcccagctgagcgagctccgcagtg agatggagtgccagaaccaagagtacaagatgctgctggacatcaagacacg tctggagcaggagatcgccacctaccgcagcctgctcgagggccaggacgcc aagaagcgtcagcccccgtagcacctctgttaccacgacttctagtgcctctgtta ccaccacctctaatgcctctggtcgccgcacttctgatgtccgtaggccttaaatct gcctggcgtcccctccctctgtcttcagcacccagaggaggagagagccggca gttccctgcaggagagaggaggggctgctggacccaaggctcagtccctctgct ctcaggacccccctgtcctgactctctcctgatggtgggccctctgtgctcttctcttcc ggtcggatctctctcctctctgacctggatacgctttggtttctcaacttc	3860	NM_002274 / NM_153490	SEQ ID NO:96
LASS6	LAG1 longevity assurance homolog 6 (S. cerevisiae)	212446_s_at	+	aactttaacttagagcttcattactttaagaatggaaaacaacctctgagtttgattt cccaaagtttcataaagcccctaagctcatgattttcatcaactctttgcccacata gtcatttacctccacagccgtttgttgtcatagaaggggtggtggtgtttggatttgat ttttttcaacttgcagtgagaaataggataggtgacaaaaccttacttgttttcttaag acaattcagtgcttgagcatctctgtcagaaatggaatgaaatactgttagccaat tagaattattttatgtattgttattgtgttttgctgatttttatatgaaaatataattattcatt cttgatctctggaagcaa	253782	NM_203463	SEQ ID NO:97

LTBP2	latent transforming growth factor beta binding protein 2 / latent transforming growth factor beta binding protein 2	204682_at		gggagccaaggctttatacgtctaaagaaaatattcagtagctgaatccgccca gtgatagcctgtgggcaccagcagcaagggctgccatgggatacagcaccca tctacaaagacctctattacataaacactgcttcttacaggaaacaaacctcttctg ggatctccttttgtgaaaaccagtttgatgtgctaaaagtaaaaagtctattttccag tgtggtcttgttcagaagcagccagatttccaatgttgtttttcccctccactcagaa acccctgccctttcccttcagaaaacgatggcaggcattcctctgagtttacaagc agagactcactccaacccaaactagctggg	4053	NM_000428 / NM_032035	SEQ ID NO:98
MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	203552_at		acacacacatgcaattttgcttaacaaaagtattttataatacagtttcatacagaa ttaccttaaaagggagtcttatgttttcaactacagatagttgtaagggatcntaca gaagatattgatgatagttgaaatattcttagaaggggtgtgtatgtctagctgtgtc taccatgtgtatgtattcttgacaagcagtataaaatacctgtgatttttctttacatta gggataatgcataaggaattaatcttcatatatattatcatccctaatgtagcaggg ggaagtatttaattgcccatgatatgtattttacttatactatgccagagaggaaact ataaagtaattacacatgtaatcttgggtttttcacatatgtaggtattcattttgagta ggttgaagaagaaaaaaaatatttaaatgaattgaattcctgatgggatagtatc aat	11183	NM_006575 / NM_198794	SEQ ID NO:99
MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	203553_s_at		gaactctgcatcttcatggtttacagaaattggtgcaggcagccagcagttagatt ccattcatgtaacacagttggagagagataccgttttagtgtgtttagacaaatttgt gaaaattgtaaatctacaaggaaaattaaaatcaagtaagaaactggcctctga gttaagttttgattttcgcattgaatctgtagtatgccttcaagacagtgtgttggctttc tggaaacatgggatgcagggtaaaagcttcaagtcagatgaggttacccagga gatttcagatgaaacaagagttttccgcttattaggatcagacagggttgtcgttttg gaaagtaggccaacagaaaatcctactgcacacagcaatctctacatcttggct ggacatgaaaatagttactaagcaacagaaactgatctcaaatgacaggaaa atgaatatactccattgaaagggaaaataaggaaattcaatacaaactgcacta tgatttgctttaact	11183	NM_006575 / NM_198794	SEQ ID NO:100
MMP2	"matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) / matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)"	201069_at		ctcagagccacccctaaagagatcctttgatattttcaacgcagccctgctttggg ctgccctggtgctgccacacttcaggctcttctcctttcacaaccttctgtggctcac agaacccttggagccaatggagactgtctcaagagggcactggtggcccgac agcctggcacagggcagtgggacagggcatggccaggtggccactccagac ccctggcttttcactgctggctgccttagaacctttcttacattagcagtttgctttgtat gcactttgtttttttctttgggtcttgtttttttttccacttagaaattgcatttcctgacaga aggactcaggttgtctgaagtcactgcacagtgcatctcagcccacatagtgatg gttcccctgttcactctacttagcatgtccctaccgagtctcttctccactggatgga ggaaaaccaagccgtggcttcccgctcagccctccctgcccctcccttcaaccat tccccatgggaaat	4313	NM_004530	SEQ ID NO:101

MYC	v-myc myelocytomatosis viral oncogene homolog (avian) / v-myc myelocytomatosis viral oncogene homolog (avian)	202431_s_at	+	gcaacaaccgaaaatgcaccagccccaggtcctcggacaccgaggagaatg tcaagaggcgaacacacaacgtcttgagcgccagaggaggaacgagctaa aacggagcttttttgcctgcgtgaccagatccggagttggaaaacaatgaaa aggccccaaggtagttatcctaaaaaagccacagcatacatcctgtccgtcc aagcagaggagcaaaagctcatttctgaagaggagttgttgcggaaacgacg agaacagttgaaacacaaactgaacagctacggaactctgtgcgtaaggaa aagtaaggaaaacgattcctctaacagaaatgtcctgagcaatcacctatgaa cttgtttcaaatgcatgatcaaatgcaacctcacaacctggctgagtc	4609	NM_002467	SEQ ID NO:102
NRP1	neuropilin 1	210510_s_at		aacatccgcctggtaaccagtcgctctggctgggcacttccacccgcacctcatt cctacatcaatgagtggctccaaatagacctgggggaggagaagatcgtgag gggcatcatcattcaggtgggaagcaccgagagcaccgaaggtgttcatgagg aagttcaagatcgggtacagcaacaacggctcggactggaagatgatcatgg atgacagcaaacgcaaggcgaagtctttgagggcaacaacactatgatcca cctgagctgcggacttttccagctctctccacgcgattcatcaggatctacccga gagagccactcatggcggactgggggctcagaatggagctgctgggctgtgaag tggaagccctacagctggaccgaccactccaacgggaacttggtggatgaa tgtgatgacgaccaggccaactgccacagtggaaca	8829	NM_003873	SEQ ID NO:103
NRP1	neuropilin 1	212298_at		gcaaatatcttaccaggcagcctatgaattaacccaaagaagctttggttgtttg gtggatttttatcatgccatgttggacatgagatttttttagatcttccttcccacattgct agacgtctcactcaaagacatttgttgggagtcacatttgcatcatagangagac agtccattcatcttagttaaattggattgaaatgccttttgtttccaggaaaatattg atcaccatgaaagaaagaatagttttttgtcccagagacatttcatttagttgatata atcctaccagaaggaaagcactaagaaacactcgttgttgttttaaaggcaac agacttaaagttgtcctcagccaagg	8829	NM_003873	SEQ ID NO:104
OLFM1	olfactomedin 1 / olfactomedin 1	205591_at	+	caggtgtatctgcacagtggtcgcccacagcagaccatgttcacgggatgc ccgcacaaaacagctgaggcagctactggagaaggtgcagaacatgtctcaa tccatagaggtcttggacaggcggacccagagagactgcagtacgtggagaa gatggagaaccaaatgaaaggactggagtccaagttcaaacaggtggagga gagtcataagcaacacctggccaggcagtttaagggctaacttaaaagagtttt tcaatgctgcagtgactgaagaagcagtccactcccatgtaaccatgaaagag agccagagagcttttgcaccatgcatttttactattatttccaatacttagcaccatt tcactaaggaaccttgaatacaaccaggatctcctttgcatgcgactgtagctgc	10439	NM_006334 / NM_014279 / NM_058199	SEQ ID NO:105
OLFM1	olfactomedin 1	213131_at	+	gcgggccacagacgtcggaagaaaactccgtatttgcagctggaactgcagcc cacggcgccccggtttctcccgccctgtcctctggtcaaacaacatacta aagaggcgaggcaatgactgttggccagttctcaccgggggaaaacccnact gttaggatggcatgaacatttccttagatcgtggtcagctccgaggaatgtggcn nccaggctctttgangagccatgggctgcacccngccgtaggcntagtgtaa ctcgcatcccattgcagtgccngtttcntigactgtgtgtctgtctcttagattaaccgt gctgaggctccnacatagctccntggacctgtgtcntagtacatactgaagcgat ggtcagagtgtgtagagtgaagttgctgtgcccacattgtttgaactcgcgtaccc cgtagatacattgtgcaacgttcttctgttattccctgaggtggtaacttcgtatgttc agt	10439	NM_006334 / NM_014279 / NM_058199	SEQ ID NO:106

OSMR	oncostatin M receptor / oncostatin M receptor	205729_at	+	ggagacttgagcttgacctaaggatatgcattaaccactctacagactcccactc agtactgtacagggtggctgtggtcctagaagttcagttttactgaggaaatatttc cattaacagcaattatattattgaaggcttaataaaggccacaggagacattact atagcatagattgtcaaatgtaaatttactgagcgtgtttataaaaaactcacagg tgtttgaggccaaaacagatttttagacttaccttgaacggataagaatctatagttc actgacacagtaaaattaactctgtgggtgggggcgggggcatagctctaatc taatatataaaatgtgtgatgaatcaacaagattccacaattctctgtcaagctta ctacagtgaaagaatgggattggcaagtaacttctgacttactgtcagttgtacttc tgctccatagacatcagtattctgccatcatttttgatgactacctcagaacataaa aaggaacgtatatcacataattccagtcacagttttttggttcctctt	9180	NM_003999	SEQ ID NO:107
PCDHAC 2	"protocadherin alpha subfamily C, 2 / protocadherin alpha subfamily C, 2"	210674_s_at		ctgacctcttgaagttgcagaatgcttgaaatctaatggtatctgaaatatcagc tcatagaaagtaacaaaatttgctgtcacctaaataagacatttaatttgttataa tgtacatttagaagtttgattaatatatatctatttaggcattaatataaaagaggt aggagtctgttatttaaaaaaaagcattaaatttaaaaaaaaactgtcttgtctacttt agcttcattctccatatttttgaaggtgtgtaacttcagctctgcaggattgcatgg ggtaaaacttgttaccaacacatgtgaaccattgctacattgtaggttgtgatcattt tgccccactgaagcccatgtatctgacctacgtgcctttgaactaggagaatcg ggctaatttattaatgatgataattataatgtatctgtacagcacttttacatttgcga agtgctttccaatccatgttagttactagttattacagctgtaaggataaaacacgtc atgtggattcatttga	56134	NM_018899 / NM_031883	SEQ ID NO:108
PDGFRA	"platelet-derived growth factor receptor, alpha polypeptide / platelet-derived growth factor receptor, alpha polypeptide"	203131_at		agaaaatttgccaatctttcctacttctatttttatgatgacaatcaaagccggcctg agaaacactatttgtgacttttaaacgattagtgatgtccttaaaatgtggtctgcc aatctgtacaaaatggtcctatttttgtgaagagggacataagatgaaatgatgtt atacatcaatatgtatatatgtatttctatatagactggagaatactgccaaaacat ttatgacaagctgtatcactgccttgtttatatttttttaactgtgataatcccccacag gcacattaactgttgcacttttgaatgtccaaaatttatatttttagaaatataataaaa gaaagatacttacatgttcccaaaacaatggtgtggtgaatgtgtgagaaaaact aacttgataggtctaccaatacaaaatgtattacgaatgccccctgttcatgtt	5156	NM_006206	SEQ ID NO:109
PDZK1	PDZ domain containing 1 / PDZ domain containing 1	205380_at		gtcaaaccatgactcgcacatggcaaaagaacgggccacagtacagcctca cattcttcttccaattctgaagatacagagatgtgatgaaaacaagtaatagcttg gctgtttattgatagctgtttctgggtatttaataggaatcctttctcaaggaatgagtt gtgaccgtttactgtctcttagaagaaaaactccactggaaaccattcaccatgt gtgactgtctctcgttatcatttgtcttacaggcggctattgcagacggctaatttatgc ttaacttaggaagagataaggcaagagctagatttttttcatgtgatctttccaagc ttcaacttaacttaactacatttctctgtatgatgatgtctctacttctacaggttccttg agcac	5174	NM_002614	SEQ ID NO:110

PEA15	phosphoprotein enriched in astrocytes 15 / phosphoprotein enriched in astrocytes 15	200788_s_at		taaattcacatgcagtctcagagactatttagacaaagttcaagttaggagctttta ggatgtgggagtaaaactttaatgggaggggagggctggctgctggaagaag gaagaagccagactggttagacagtactcttaactcctagcccagcctacgtgc cctgcccctctggccactgctgcagacacctgccttaacacacacacctctagg actccacagttttgccttaaaggaccttcccaagtctccctttccctgtctggcttctc ccttaagaagagagagatacttgtagaattgggtgggggaatgagcatgaac tgtccttccatttgggatatgttacattagagtgagagagagaataaggagcctttc ttatggaagaaatgggagaagagagacagggttcttttcagcagagtctagtag tttctctgtaaggcaaaataatctaaaaagactaacctgcccacccactccttatat tgctgtgagattgcccc	8682	NM_003768 / NM_013287	SEQ ID NO:111
PGM1	phosphoglucomutase 1 / phosphoglucomutase 1	201968_s_at		cggacccatccaagtcatctgattgaagagcatgacagaaacaaaatgtattca ccaagcattttaggatttgactttttcactaaccagttgacgagcagtgcatttacaa ggcactgccaaacaagatgcccttgggagctgtgagggaaagaggacctgcg ggcttagatcaatctcaattccttttcatgccctcctgcattgctgctgcgtgggtattt gtctccttagccatcaggtacagtttacactacaatgtaagctataggtggagcat cagcagtgagtgaggccattcttcatccttaggatgtggcaatgaaatgatggtg caagttcctttctcttttgtgaatctttccccccatttcctgtttacatgtaacccaacaa aatgcaatttctagtgccttctgtccaatcagttctttcctctgagtgagacgtacttg gctacagatttctgccttgttttgcgacattgtc	5236	NM_002633	SEQ ID NO:112
PI3	"protease inhibitor 3, skin-derived (SKALP)"	203691_at		gattggtatggccttagctcttagccaaacaccttcctgacaccatgagggccag cagcttcttgatcgtggtggtgttcctcatcgctgggacgctggttctagaggcagc tgtcacgggagttcctgttaaaggtcaagacactgtcaaaggccgtgttccattca atggacaagatcccgttaaaggacaagtttcagttaaaggtcaagataaagtca aagcgcaagagccagtcaaaggtccagtctccactaagcctggctcctgcccc attatcttgatccggtgcgccatgttgaatccccctaaccgctgcttgaaagatact gactgcccaggaatcaagaagtgctgtgaaggctcttgcgggatggcctgtttcg ttccccagtgaagggagccggtccttgct	5266	NM_002638	SEQ ID NO:113
PLAU	"plasminogen activator, urokinase / plasminogen activator, urokinase"	205479_s_at		cccgaccggtgggcatttgtgaggcccatggttgagaaatgaataatttcccaatt aggaagtgtaagcagctgaggtctcttgagggagcttagccaatgtgggagca gcggtttggggagcagagacactaacgacttcagggcagggctctgatattcca tgaatgtatcaggaaatatatatgtgtgtgtatgtttgcacacttgttgtgtgggctgt gagtgtaagtgtgagtaagagctggtgtctgattgttaagtctaaatatttccttaaa ctgtgtggactgtgatgccacacagagtggtctttctggagaggttataggtcactc ctggggcctcttgggtcccccacgtgacagtgcctgggaatgtacttattctgcag catgacctgtgaccagcactgtctcagtttcactttcacatagatgtccctttcttggc cagttatcccttccttttagcctagttcatccaatcctcactgggtgggg	5328	NM_002658	SEQ ID NO:114

PLAU	"plasminogen activator, urokinase / plasminogen activator, urokinase"	211668_s_at		accacaacgacattgccttgctgaagatccgttcaaggagggcaggtgtgcg cagccatccccggactatacagaccatctgcctgccctcgatgtataacgatcccc agtttggcacaagctgtgagatcactggcttgaaaagagaatttctaccgacta tctctatccggagcagctgaagatgactgttgtgaagctgatttccaccgggagt gtcagcagcccactactacggctctgaagtcaccaccaaaatgctgtgtgctg ctgacccacagtggaaaacagattcctgccagggagactcagggggaccct cgtctgttccctccaaggccgcatgacttgactggaattgtgagctgggccgtg gatgtgcctgaaggacaagccaggcgtctcacacgagagtctcacactt	5328	NM_002658	SEQ ID NO:115
PPIF	peptidylprolyl isomerase F (cyclophilin F) / peptidylprolyl isomerase F (cyclophilin F)	201489_at		gggttgccatccaagtgaaagtctttccttgaccaaggggacagtcagtttgc aaaaggactctaatacctgttaatattgtcttcctaatttgggataatttaatttaacaa gattgactagaagtgaaactgcaacactaacttcccgtgctgtggtgtgaccctg agttggtgacacaggccacagacccagagcttggctttgaaacacaactca gggctttgtgaaggttcccccgctgagatctttcctctggttactgtgaagcctgtt ggtttgctgctgcgttttgaggagggcccatgggggtaggagcagttgaacctg ggaacaaacctcacttgagctgtgcctagacaatgtgaatccctgttgctaaca gaagtggcctgtaagctcctgtgctccggagggaagcattcctggtaggctttg	10105	NM_005729	SEQ ID NO:116
PPIF	peptidylprolyl isomerase F (cyclophilin F)	201490_s_at		gctgaaggcagatgtcgtcccaaagacagctgagaacttcagagccctgtgca ctggtgagaagggcttcggctacaaaggctccacctccacaggtgatccctc cttcatgtgccaggcgggcgacttcaccaacaccacaatggcacaggcgggaagt ccatctacggaagccgctttcctgacgagaactttacactgaagcacgtgggc caggtgtcctgtccatggctaatgctggtcctaacaccaacggctcccagttcttc atctgcaccatcaaagacagactggttggatggcaagcatgttgttcggtcacgt caaagagggcatggacgtcgtgaagaaaatagaatcttcggctctaagagtg ggaggacatccaagaagattgtcatcacagactgtggccagttgagctaatctgt ggccagggtgctggcatggtggcagctgcaaatgtccatgcacccaggtggcc gcgttggctgtcagccaaggtgcctgaaacgatacgtgtgcccact	10105	NM_005729	SEQ ID NO:117
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) / prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	204748_at	+	ggttgaatgtttgtgtcttaggataggcctatgtgctagcccacaaagaatattgtctc attagccigaatgtgccataagactgaccttttaaaatgttttgagggatctgtggat gcttcgttaatttgttcagccacaatttattgagaaaaatatctgtgtcaagcactgtg ggttttaatatttttaaatcaaacgctgattacagataatagtatttatataaataatg aaaaaaatttctttttgggaagagggagaaaatgaaataaatatcatttaaagata actcaggagaatctctttacaatttttacgtttagaatgttaaggttaagaaagaaa tagtcaatatgcttgtataaaacactgttcactgttttttttaaaaaaaaaactgattt gttattaacattgatctgctgacaaaaacctgggaatttgggtgtgtatgcgaatgttt cagtgcctcagacaaat	5743	NM_000963	SEQ ID NO:118

RRM1	ribonucleotide reductase M1 polypeptide	201476_s_at	+	gaacaagcgtcctggggcatttgctatttacctggagccttggcatttagacatcttt gaattccttgatttaaagaagaacacaggaaaggaagagcagcgtgccagag atcttttctttgctctttggattccggatctcttcatgaaacgagtggagactaatcag gactggtctttgatgtgtccaaatgagtgtcctggtctggatgaggtttggggagag gaatttgagaaactatatgcaagttatgagaaacaaggtcgtgtccgcaaagttg taaaagctcagcagctttggtatgccatcattgagtctcagacggaaacaggca ccccgtatatgctctacaaagattcctgtaatcgaaagagcaaccagcagaacc tgggaaccatcaaatgcagcaacctgtgcacagaaatagtggagtacaccag caaagatgaggttgctgtttgtaatttggcttccctggccctgaatatgtatgt	6240	NM_001033	SEQ ID NO:119
SEMA3B	"sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B / sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B"	203071_at	+	gcccctggagtcgcggagaaagggccgtaaccggaggacccacgcccctga gcctcgcgctgagcgggggccgcgcagcgcaacgcactggtgaccagactgt ccccacgccgggaaccaagcaggagacgacaggcgagagaggagccag acagaccctgaaaagaaggacgggttggggccgggcacattgggggtcacc ggccgatggagacaccaaccgacaggccctggctgagggcagctgcgcggg cttatttattaacaggataacccttgaatgtagcagccccgggagggcggcaca ggtcgggcgcaggattcagccggagggaagggacggggaagccgagctcc agagcaacgaccagggccgaggaggtgcctggagtgcccaccctgggaga cagaccccacctccttgggtagtgagcagtg	7869	NM_004636	SEQ ID NO:120
SERPINE 1	"serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1"	202627_s_at		ggaactacggggcttacaggagcttttgtgtgcctggtagaaactatttctgttcca gtcacattgccatcactcttgtactgcctgccaccgcggaggaggctggtgacag gccnaaaggccagtggaagaaacaccctttcatctcagagtccactgtggcact ggccacccctccccagtacaggggtgctgcaggtggcagagtgaatgtccccc atcatgtggcccaactctcctggcctggccatctccctccccagaaacagtgtgc atgggttattttggagtgtaggtgacttgtttactcattgaagcagatttctgcttcctttt atttttataggaatagaggaagaaangtcagatgcgtgcccagctcttcaccccc caatctcttggtggggaggggtgtacctaaatatttatcatatccttgcccttgag	5054	NM_000602	SEQ ID NO:121
SERPINE 1	"serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1"	202628_s_at		aaattgaccatacaatttcatcctccttcaggggatcaaaaggacggagtgggg ggacagagactcagatgaggacagagtggtttccaatgtgttcaatagatttagg agcagaaatgcaaggggctgcatgacctaccaggacagaactttccccaatta cagggtgactcacagccgcattggtgactcacttcaatgtgtcatttccggctgctg tgtgtgagcagtggacacgtgagggggggtgggtgagagagacaggcagct cggattcaactaccttagataatatttctgaaaacctaccagccagagggta	5054	NM_000602	SEQ ID NO:122
SLC20A1	"solute carrier family 20 (phosphate transporter), member 1 / solute carrier family 20 (phosphate transporter), member 1"	201920_at		gtatcaggcttcaattccattatgttttaatgttgtctctgaagatgacttgtgatttttttt cttttttttaaaccatgaagagccgtttgacagagcatgctctgcgttgttggtttcac cagcttctgccctcacatgcacagggatttaacaacaaaaatataactacaactt cccttgtagtctcttatataagtagagtccttggtactctgccctcctgtcagtagtgg caggatctattggcatattcgggagcttcttagagggatgaggttctttgaacaca gtgaaaatttaaattagtaactttttgcaagcagtttattgactgttattgctaagaa gaagtaagaaagaaaaagcctgttggcaatcttggttatttctttaagatttctggc agtgtgggatggatgaatgaagtggaatgtgaactttgggcaagttaaatggga cagccttccatgttcatttgtctacctcttaactga	6574	NM_005415	SEQ ID NO:123

SPRY1	"sprouty homolog 1, antagonist of FGF signaling (Drosophila)"	212558_at		taatttttagattcgcctacaatgtaaatcttcacattggagataaatatggttggacc ttgccatcttcactctagccttcgtatttgtgaaggactcagccacctccttcttcac cccatgcttctcaccaaatttttgttgtcattgagggcacttggatactcaagttgat atttatagctgatcaatctatatgtgtcacagaactatgctgcctaaagtgatcttgg ctcctaatggtcctttggcccctggatagttaacagctgagtaattctaatctcttc tgtgttttccttgcctaaccacaaattgtgg	10252	NM_005841 / NM_199327	SEQ ID NO:124
SPRY2	sprouty homolog 2 (Drosophila) / sprouty homolog 2 (Drosophila)	204011_at		gagatacagaacttggtgacccatgtattgcataagctaaagcaacacagaca ctcctaggcaaagttttgttgtgaatagtacttgcaaaactgtaaattagcagat gacttttttccattgtttctccagagagaagaatgtgctatatttttgtatatacaataatatttt gcaactgtgaaaaacaaagttgtgccatactacatggcacagacacaaaaatatta tactaatatgttgtacattcggaagaatgtgaatcaatcagtatgttttagattgtatt ttgccttacagaaagccttattgtaagactctgatttcccttggactcatgtatattg tacagttacagtaaaattcaaccttatttctaatttttcaacatattgtttagtgtaaa gaatatttattgaagtttattattttataaaaaagaatatttattttaagaggcatctta caaatttgccccttt	10253	NM_005842	SEQ ID NO:125
SRPUL	sushi-repeat protein / sushi-repeat protein	205499_at		gcggcatgtgaccatcattgaactggtgggacagccacctcaggaggtggggc gcatccgggagcaacagctgtcagccaacatcatcgaggagctcaggcaattt cagcgcctcactcgctcctacttcaacatggtgttgattgacaagcagggtattga ccgagaccgctacatggaacctgtcaccccgaggaaatcttcacattcattgat gactacctactgagcaatcaggagttgacccagcgtcgggagcaaagggaca tatgcgagtgaacttgagccagggcatggttaaagtcaaggggaaaagctcctct agttagctgaaactgggacctaataaaaggagaggaaatgtttcccacagttctag ggacaggactctgaggtgggtgagtttgacaaatcctgcagtgtttccaggcatc cttttaggactgtgtaatagtttccctagaagctaggtagggactgaggacaggc cttgggcagtgggtt	27286	NM_014467	SEQ ID NO:126
TCF8	transcription factor 8 (represses interleukin 2 expression) / transcription factor 8 (represses interleukin 2 expression) / transcription factor 8 (represses interleukin 2 expression)	208078_s_at	+	agactgggcgcaaagggctgtccggagggcagaccaggtgccttgccgcagag aaaaacaccaaagtctcctgttcgctcataaagaagtttttgggatgggagagaat ccagaccatcttgggcagccaggccctgccttcatttttacagaggtagcaca actgattccaacacacaaaaccccttccctttttaaaatgatttctgttctaatgccata gatcaaaggcctcagaaaccattgtgtgtttcctcttgaagcaatgacaagcact ttacttcacggtggtgttttgttttcttattgctgtggaacctcttttggaggacgttaaa ggcgtgtttacttgttttttaagagtgtgtgatgtgtgtttgtagatttctgacagtgc tgtaatacagacggcaatgcaatagcctatttaa	6935	NM_030751	SEQ ID NO:127
TGFA	"transforming growth factor, alpha / transforming growth factor, alpha"	205016_at		cctgcctctagttggtctgggcttgatctcttccaacctgcccagtcacagaag gaggaatgactcaaatgcccaaaaccaagaacacattgcagaagtaagaca aacatgtatatttttaaatgttctaacataagacctgttctctagccattgatttacc aggctttctgaaagatctagtggttcacacagaggagagagaggagtactgaaaa agcaactcctcttctagtcttaataatttactaaaaatggtcaacttttcattatcttttatt ataataaacctgatgctttttttagaacicctactctgatgtctgtatatgttgcactg aaaaggttaatatttaatgtttaatttatttgtggtaagttaatttgatttctgtaaatg tgttaatgtgattagcagttatttccttaatatctgaattatactaaagagtagtgag caatataagacgcaattgtgttttcagt	7039	NM_003236	SEQ ID NO:128

TGFBR2	"transforming growth factor, beta receptor II (70/80kDa) / transforming growth factor, beta receptor II (70/80kDa)"	208944_at		gtttggatggtggaaggtctcattttattgagatttttaagatacatgcaaaggtttgg aaatagaacctctaggcaccctcctcagtgtgggtgggctgagagttaaagaca gtgtggctgcagtagcatagaggcgcctagaaattccacttgcaccgtagggca tgctgataccatcccaatagctgttgcccattgacctctagtggtgagtttctagaat actggtccattcatgagatattcaagattcaagagtattctcacttctgggttatcag cataaactggaatgtagtgtcagaggatactgtggctt	7048	NM_003242	SEQ ID NO:129
TIEG	TGFB inducible early growth response / TGFB inducible early growth response	202393_s_at		tttgcctgcagtttcttgtgtagatttgaaaattgtataccaatgtgttttctgtagactct aagatacactgcactttgtttagaaaaaaaactgaagatgaaatatatattgtaa agaagggatattaagaatcttagataacttcttgaaaaagatggcttatgtcatca gtaaagtacctttatgttatgaggatataatgtgtgctttattgaattagaaaattagt gaccattattcacaggtggacaaatgttgtcctgttaatttataggagttttttgggga tgtggaggtagttgggtagaaaaattattagaacattcacttttgttaacagtatttct cttttattctgttatatagtggatgatatacacagtggcaaaacaaaagtacattgct taaaatatatagtgaaaaatgtcactatatcttcccatttaacattgtttttgtatattgg gtgtagatttctgacatcaaaacttggacccttggaaaacaaaagttttaattaaa aaaaatccttgtgacttacaatttgcac	7071	NM_005655	SEQ ID NO:130
TIMP3	"tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)"	201147_s_at		gagtcggagatgatgcagcacacacacaattccccagcccagtgatgcttgtgt tgaccagatgttcctgagtctggagcaagcacccaggccagaataacagagct ttcttagttggtgaagacttaaacatctgcctgaggtcaggaggcaatttgcctgcc ttgtacaaaagctcaggtgaaagactgagatgaatgtctttcctctccctgcctccc accagacttcctcctggaaaacgctttggtagatttggccaggagctttcttttatgt aaattggataaatacacacaccatacactatccacagatatagccaagtagattt gggtagaggatactatttccagaatagtgtttagctcacctagggggatatgtttgt atacacatttgcatatacccacatgggg	7078	NM_000362	SEQ ID NO:131
TIMP3	"tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)"	201148_s_at		ttgttgtcgttgcttgtttgaagaaaatcatgacattccaagttgacattttttttttcatttt aattaaaatttgaaattctgaacaccgtcagcaccctctcttccctatcatgggtcat ctgacccctgtccgtctccttgtccctgcttcatgtttgggggcctttctttaactgcctt cctggcttagctcagatggcagatgagagtgtagtcaagggcctgggcacagg agggagagctgcagagtgtcctgcctgccttggctggagggacacctctcctgg gtgtggagacagcttggttccctttccctagctccctggtgggtgaatgccacctcc tgagatcctcacctcttggaattaaaattgttggtcactggggaaagcctgagtttg caaccagttg	7078	NM_000362	SEQ ID NO:132
TIMP3	"tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) / tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)"	201149_s_at		aggggctgaactatcggtatcacctgggttgtaactgcaagatcaagtcctgcta ctacctgccttgctttgtgacttccaagaacgagtgtctctggaccgacatgctctc caatttcggttaccctggctaccagtccaaacactacgcctgcatccggcagaa gggcggctactgcagctggtaccgaggatgggcccccccggataaaagcatc atcaatgccacagacccctgagcgccagaccctgccccacctcacttccctccc ttcccgctgagcttcccttggacactaactcttcccagatgatgacaatgaaattag tgcctgttttcttgcaaatttagcacttggaacatttaaagaaaggtctatgctgtcat atggggtttattgggaactatcctcctggcc	7078	NM_000362	SEQ ID NO:133

TIMP3	"tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)"	201150_s_at		gacttttggaataggccctgtctagggcaaactgtggccccaggagcactacc cttccatgcccagacctctgtcttgcatgtgacaattgacaatctggactacccc aagatggcacccaagttgttggctctggctacctaaggttaacatgtcactagag tatttttatgaggaggacaaacattataaaatctgatgtggcaaagcaaaacaaaat ggaaagtagggggaggtggatgtgacaacaacttccaaattggctctttggaggc gagaggaagggggaggaactggagaatagttttgcttgggggtagaggctctt agattctcccagcatccgcctttccctttagccagtctgctgtcctgtcaaacccagaa gtgatggagagaaaccaacaagagatctcgaacctgtctagaaggaatgtat ttgttgctaaatttcgtagcactgtttacagttttcctcatgttatttatg	7078	NM_000362	SEQ ID NO:134
TNFRSF6	"tumor necrosis factor receptor superfamily, member 6"	204781_s_at	+	gagtattactagagcttgccacctctccatttttgccttggtgctcatcttaatggcct aatgcaccccaaaacatggaaatatcaccaaaaaatacttaatagtccaccaa aaggcaagactgccttagaaattctagcctggtttggagatactaactgtctcta gagaaagtagcttgtgacatgtcatgaacccatgtttgcaatcaaagatgataa aatagattcttatttttccccacccccgaaaatgttcaataatgtccaatgtaaaac ctgctacaaatggcagcttatacatagcaatggtaaaatcatcatctggatttagg aattgtctgtcatacccccaagtttctaagatttaagatctcctactactatccta cgtttaaatatctttgaaagtttgtattaaatgtgaatttaagaaataatatatttataittc tgtaaatgtaaactgtgaagatagttataaactgaagcagatacctggaaccac ctaaagaacttccatttatggaggatttttttgcccctgtgtttggaatttat	355	NM_000043 / NM_152871 / NM_152872 / NM_152873 / NM_152874 / NM_152875 / NM_152876 / NM_152877	SEQ ID NO:135
TNFRSF6	"tumor necrosis factor receptor superfamily, member 6"	215719_x_at	+	accaaggttctcatgaatctccaacctaaatcctgaaacagtggcaataaatta tctgatgttgacttgagtaaatatatcaccactattgctggagtcatgacactaagtc aagttaaaggcttttgttcgaaagaatggtgtcaatgaagccaaaatagatgaga tcaagaatgacaatgtccaagacacacagcagaacagaaagttcaactgcttcgt aattggcatcaacttcatggaaagaaagaagcgtatgacacattgattaaagat ctcaaaaaagccaatcttttgtactcttgcagagaaaattcaaacttcagaaatgaaatccaaagctt ggacatactagtgactcagaaaaattcaaacttcagttctgagtatatgcaattagtgttgan ggtctagagtgtgaaaaacaacaaaattcagttctgagtatatgcaattagtgttgan aagattcttaatagctggctgtaaatactgcttggttt	355	NM_000043 / NM_152871 / NM_152872 / NM_152873 / NM_152874 / NM_152875 / NM_152876 / NM_152877	SEQ ID NO:136
TNFSF10	"tumor necrosis factor (ligand) superfamily, member 10"	202687_s_at	+	gtagcagctcacataactgggaccagaggaagaagcaacacattgtctctcc aaactccaagaatgaaaaggctctgggccgcaaaataaactcctgggaatcat caaggagtgggcattcatcctgagcaacttgcacttgaggaatggtgaactggt catccatgaaaaaaggtttactacatcatattcccaaacatacttcgatttcagga ggaaataaaagaaaacacaaagaacgacacaaacaaatggtccaatatatttac aaatacacaagttatcctgaccctatattgttgatgaaaagtgctagaaatagttgt tggtctaaagatgcagaatatggactctatttccatctatcaagggggaatatttga gcttaaggaaaatgacagaatttttgttctgtaacaaatgagcacttgatagacat ggaccatgaagccagttttttcgggggccttttagttggctaactgacct	8743	NM_003810	SEQ ID NO:137
TNFSF10	"tumor necrosis factor (ligand) superfamily, member 10 / tumor necrosis factor (ligand) superfamily, member 10"	202688_at	+	ctctacctcatatcagttgctagcagaaatctagaagactgtcagcttccaaaca ttaatgcaatggttaacatcttctgtcttataatctactcctgtaaagactgtagaa gaaagcgcaacaatccatctctcaagtagtgtatcacagtagtgcctccaggtt tcctaagggacaacatcctaagtcaaaagagagaagaggcaccactaaaa gatcgcagtttgcctggtgcagtggc	8743	NM_003810	SEQ ID NO:138

TUBB4	"tubulin, beta, 4"	213476_x_at		gctcacccagcagatgttcgatgccaagaacatgatggccgcctgcgacccgc gccacggccgnctanctgacggtggccaccgtgttccggggccgcatgtccat gaaggaggtggacgagcagatgctggccatccagagcaagaacagcagcta cttcgtggagtggatccccaacaacgtgaaggtggccgtgtgtgacatcccgcc ccgcggcctcaagatgtcctccaccttcatcgggaacagcacggccatccagg agctgttcaagcgcatctccgagcagttcacggccatgttccggcgcaaggcctt cctgcactggtacacgggcgagggcatggacgagatggagttcaccgaggcc gagagcaacatgaacgacctggtgtccgagtacc	10381	NM_006086	SEQ ID NO:139
TUSC3	tumor suppressor candidate 3	209227_at		gatgcctaaccaaggactagagctccttcttgagatctaaatctaaagtaaatgtg cattaaagcagtgtgcttcaaaggcatcagacgatgaaagcaacataccacaa ctaggagttatttctcaaacttaaatgtcctctgggaatccagacttaaaaataag agcaaacttaacacactatccattttcgagcaaacttaacccactatatccattttg ctcatgtgttttatgcaaccagctttccatcaaatcctcaatccttgaatccaggtaa aaggttaattatcctaggattagtgaatgattcaatgaagctttcttgaaaacaaac ataggagtgtaatgtactattatgtttgtatcctgttttagtttataaagcactttcacat acattatgg	7991	NM_006765 / NM_178234	SEQ ID NO:140
TUSC3	tumor suppressor candidate 3	209228_x_at		acccaactactctggtaccattgctttggccctgttagtgtcgcttgttggaggtttgc tttatttgagaaggaacaacttggagttcatctataacaagactggttgggccatg gtgtctctgtgtatagtctttgctatgacttctggccagatgtggaaccatatccgtgg acctccatatgctcataagaacccacacaatggacaagtgagctacattcatgg gagcagccaggctcagtttgtggcagaatcacacattattctggtactgaatgcc gctatcaccatggggatggttcttctaaatgaagcagcaacttcgaaaggcgatg ttggaaaaagacggataatttgcctagtgggattgggcctggtggtcttcttcttca gttttctactttcaatatttcgttccaagtaccacggctatccttatagtgatctggactt tgagtgagaagatgtgatttggaccatggcacttaaaaactctataacctcagcct tttaat	7991	NM_006765 / NM_178234	SEQ ID NO:141
TUSC3	tumor suppressor candidate 3	213423_x_at		ctttgctatgacttctggccagatgtggaaccatatccgtggacctccatatgctcat aagaacccacacaatggacaagtgagctacattcatgggagcagccaggctc agtttgtggcagaatcacacattattctggtactgaatgccgctatcaccatgggg atggttcttctaaatgaagcagcaacttcgaaaggcgatgttggaaaaagacgg ataatttgcctagtgggattgggcctggtggtcttcttcttcagttttctactttcaatattt cgttccaagtaccacggctatccttatagctttttaattaaatgaagccaagtggga tttgcataaagtgaatgtttaccatgaagataaactgttcctgactttatactattttga attcattcatttcattgtgatcagctagcttattcttgtgtac	7991	NM_006765 / NM_178234	SEQ ID NO:142

Example 4

RT-PCR Confirmation Studies

In addition, the sequence of the RT-PCR primers used in the confirmatory follow up studies as highlighted in Figs 3, 4, 5 and 6 are listed in Table 3. Note that DAPK2 was not identified by Affymetrix analysis, only via follow up of the DAPK gene family by RT-PCR following discovery of predictivity of DAPK1. Hence no Affymetrix ID or Affymetrix ID sequence is provided for DAPK2.

Table 3

Sequences relevant to genes followed up by RT-PCR (see Figs 3, 4, 5 & 6)

(all sequences written 5'-3')

Gene	affy id	affy probe seq	Taqman Forward Primer	Taqman Reverse Primer	Taqman probe
EMP1	201324_at	CACCAAATTACCTAGGCTGAGGTTAGAGAGATTGGCCAGCAAA AACTGTGGGAAGATGAACTTTGTCATTATGATTTCATTTATCAC ATGATTATAGAAGGCTGTCTTAGTGCAAAAAACATACTTACATT TCAGACATATCCAAAGGGAATACTCACATTTTTGTTAAGAAGTT GAACTATGACTGGAGTAAACCATGTATTCCCTTATCTTTTACTT TTTTTCTGTGACATTTATGTCCTCATGTAATTTGCATTACTCTG GTGGATTGTTCTAGTACTGTATTGGGCTTCTTCGTTAAT	AGCCATCCTG CCCTTCTGA	ACCTTACAAAC TCTCTTTCC	CAAAGCA AAACATC ACATTCC AGTC
NES	218678_at	GCAGCACTCTTAACTTACGATCTCTTGACATACGGTTTCTGGC TGAGAGGCCTGGCCCGCTAAGGTGAAAAGGGGTGTGGGCAA AGGAGCCTACTCCAAGAATGGAGGCTGTAGGAATATAACCTC CCACCCTGCAAAGGGAATCTCTTGCCTGCTCCATTCTCATAGG CTAAGTCAGCTGAATCCCGATAGTACTAGGTCCCCTTCCCTCC GCATCCCGTCAGCTGGAAAAGGCCTGTGGGCCCAGAGGCTTC TCCAAAGGGAGGGTGACATGCTGGCTTTTGTGCCCAAGCTCA CCAGCCCTGCGCCACCTCACTGCAAGTAGTGCACCATCTCAC TGCAGTAGCACGCCCTCCTGGGCCGTCTGGCCTGTGGCTAAT GGAGGTGACGGCACTCCCATTGTGCTGACTCCCCCCATCCCT GCCACGCTGTGGCCCTGCCTGGCTAGTCCCTGCCTGAATAAA G	GCCCCTTTCA GGAGGAGGA	AGTGCCGGGG AGATGGTCTT	AGTGCTC TGAAGAC CTCTTGG GC
DAPK1	203139_at	CCTCCTCCAGGGTGATTTTATGATCAGTGTTGTTGCTCTAGGA AGACATTTTTCCGTTTGCTTTTGTTCCAATGTCAATGGTGAACG TCCACATGAAACCTACACACTGTCATGCTTCATCATTCCCTCTC ATCTCAGGTAGAAGGTTGACACAGTTGTAAGGGTTACAGAGAC CTATGTAAGAATTCAGAAGACCCCTGACTCATCATTTGTGGCA GTCCCTTATAATTGGTGCATAGCCAGATGGTTTCCACATTTAG ATCCTGGTTTCATAACTTCCTGTACTTGAAGTCTAAAAGCAGAA AATAAAGGAAGCAAGTTTTTCTTCCATGATTTTAAATTGTGATC GAGTTTTAAATTGATAGGAGGGAACATGTCCTAATTCTTCTGT CCTGAGAA	AGGAAACGCT ACCTCTCTGT	CTGGAGGAGG ATTCCCTTCT	CTTGCTG TATGCTG ATCATCG CC
DAPK2	Not applicable	Not applicable	GGGTAGGCAC CTGGCATC	AGTGCAGTGG CGTGATCTC	TACTCCA GGGGCT GAGGTGA CA

Example 5

Diagnostic test for Clinical Studies

The predictive gene lists above have been generated using the preclinical studies described. The following approach is employed to develop a diagnostic test for the clinical setting based on this data.

a) Identify patients which represent the population of individuals whom we would expect to derive benefit from a diagnostic test, and for which pre-treatment tumour samples and outcome of gefitinib treatment are known or will be available. For each sample the expression level for our genes of interest is evaluated, using for example the RNA signal from RT-PCR. QC procedures are applied to identify the set of samples and genes to take forward to step b).

a) Identify a subset of the genes which together are able to distinguish between patients showing different responses to gefitinib. There are a variety of methods which are useful to select the subset of genes and combine their expression values to provide a prediction, possibly a predictive value and a corresponding threshold which distinguishes between different patient groups. An example is stepwise Linear Discriminant Analysis where genes that distinguish well between patient groups are successively added to a linear combination until addition of a further gene does not provide additional predictive power (Mardia et al.). The threshold value of the linear combination is then selected to give the appropriate sensitivity and specificity properties.

d) Tool validation would partly be carried out during development in step 2, for example using cross validation and permutation tests. In addition, the finally developed diagnostic procedure (gene subset and method of combining to generate a prediction and a platform for biological analysis) is tested and validated in its entirety using an independent set of samples not used within tool development in step b).

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CLAIMS

1. A method of selecting a mammal having or suspected of having a tumour for treatment with an erbB receptor drug which comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 1 or DAPK2, whereby to predict an increased likelihood of response to the erbB receptor drug.

2. A method according to claim 1 comprising testing a biological sample from the mammal for expression of any one of NPAS2, NES, CHST7, DAPK1, ACOX2, GSPT2, TNNC1 or DAPK2.

3. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of any one of NPAS2, NES, CHST7 or DAPK1.

4. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of at least two of NPAS2, NES, CHST7 or DAPK1.

5. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of at least three of NPAS2, NES, CHST7 or DAPK1.

6. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of NPAS2, NES, CHST7 and DAPK1.

7. A method according to any preceding claims additionally comprising testing a biological sample from the mammal for expression of any gene listed in Table 2 as defined herein.

8. A method according to claim 7 comprising testing a biological sample from the mammal for expression of any one of EMP1, SLC20A1, SPRY2 or PGM1.

9. A method according to any one of claims 7-8 comprising testing a biological sample from the mammal for expression of EMP1.

10. A method according to any preceding claim wherein the tumour is selected from the group consisting of leukaemia, multiple myeloma, lymphoma, bile duct, bone, bladder, brain, CNS, glioblastoma, breast, colorectal, cervical, endometrial, gastric, head, neck, hepatic, lung, muscle, neuronal, oesophageal, ovarian, pancreatic, pleural membrane, peritoneal membrane, prostate, renal, skin, testicular, thyroid, uterine and vulval.

11. A method according to claim 10 wherein the tumour is selected from one of non-small cell lung, pancreatic, head or neck.

12. A method according to any preceding claim wherein the erbB receptor drug is selected from any one of gefitinib, erlotinib, PKI-166, EKB-569, HKI-272, lapatinib, canertinib, AEE788, XL647, BMS 5599626, cetuximab, matuzumab, panitumumab, MR1-1, IMC-11F8 or EGFRL11.

13. A method according to claim 12 wherein the erbB receptor drug is gefitinib.

14. A method according to any preceding claim wherein the mammal is a human and in which the method comprises testing a biological sample from the human for increased expression of DAPK1 and decreased expression of NPAS2, NES, CHST7 and EMP1 whereby to predict an increased likelihood of response to gefitinib.