

**Differential Gene Expression in Explanted Human Retinal Pigment Epithelial Cells
12-hours Post-Exposure to 532 nm, 120 ps Pulsed Laser Light**

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Differential Gene Expression in Explanted Human Retinal Pigment Epithelial Cells 12 hours Post-Exposure to 532 nm, 120 ps Pulsed Laser-Light

ABSTRACT

The use of laser light for military and commercial applications has sharply increased the likelihood of personnel exposure to laser light during operations. The increased potential for human exposure highlights the fact that there is paucity of basic science at the cell and molecular level concerning the effects of laser exposure of human cells. Current safety standards are largely extrapolations of exposure limits using a minimal visible lesion endpoint in the Rhesus monkey retinal model. A non-animal model for assessing laser-light damage to tissue, particularly human, is quite desirable for obvious scientific, political, and fiduciary reasons. We assessed the sublethal insult to human retinal pigment epithelial cells using a cadaver organ donor explant system for genes differentially expressed 12 hours post-exposure using gene expression microarray technology (gene chip). It appears that pulses of laser light are sensed and markedly alter gene expression. The 64 pulses of 532 nm (green) light at 107 mJ per square centimeter appeared to induce the cells into cessation of cell cycling and a down-regulation of transcription related genes to include the genes involved in cytoskeletal metabolism, kinase activity, homeotic genes, and the production of transporters on a consortium of gene expression levels. Notably, several key genes involved in protein degradation, the inflammatory response, translation initiation, DNA metabolism (repair/replication) and a remarkable percentage of genes involved in ribosomal reconstruction were significantly up-regulated. Intriguingly, 37% of the first 100 genes up-regulated had to do with translational machinery reconstruction. That finding reflects an amazing metabolic investment in the machinery for protein synthesis, and also indicates that the ribosome may be the primary chromophore for damage in this exposure regime. Genes up-regulated approximately an order of magnitude are involved in prevention of oxidative damage (thioredoxin, 15 fold; glutathione metabolism, 8 fold). Up-regulated genes involved in the elimination of denatured proteins (UPP) provided strong evidence for the implication of intracellular oxygen-related damage indicating either the induction of hypoxia or oxidative damage or both. This investigative approach also showcases a global methodology for characterizing environmental stressors on a living system via genetic profiling and marks the first use of human explants as an experimental model for assessing laser-induced bioeffects at the cell and molecular level.

BACKGROUND

The use of laser light for targeting devices, blinders and weapons has sharply increased the likelihood of aircrew and support personnel exposure to laser light during operations. The advent of the airborne and space based laser defense systems potentially threatens inadvertent exposure to noncombatants due to backscatter and angle of attack. Expanded laser research efforts also may lead to excessive exposure of researchers and technicians. The increased potential for human exposure highlights the fact that there are no

scientifically based cell and molecular level safety standards for laser exposures at ultrashort pulse lengths. Current ANSI (American National Standards Institute) guidelines (revision in 2002) are extrapolations of exposure limits at longer pulse lengths or are based on a very limited number of data points. The great peak powers achieved at ultrashort pulse lengths suggest that the current standards may not be sufficient for protection. Additionally, safety standards are based on visible damage to tissues, and subsequent treatment of exposed persons ends when healing of such macroscopic damage (e.g., a retinal lesion) is complete. Consideration is not given to more subtle damage or to potential long-term sequelae, which are yet undefined. This study addresses the possibility of more subtle sub-lethal and long-term effects of irradiation, which may become manifest long after treatment ends. This work will identify cellular and molecular changes in cells, which survive irradiation but are not obviously damaged (lesioned). Earlier work in this laboratory compels us to think that previously unsuspected long-term effects should be considered, to include cancer and delayed loss of visual acuity.

There is a significant void in the current understanding of laser-tissue interaction at the cell and molecular level. Ocular laser-light damage has been primarily assessed by determining the Total Intraocular Energy (TIE) in Joules to cause retinal Minimal Visible Lesions (MVL) in 50% of exposures (ED50) (Cain, et al., 1994; Toth, et al., 1996; Zuchlich, et al., 1994, 1993). This criterion is also used to establish the American National Standards Institute (ANSI) and AF Surgeon General laser safety standard. The ANSI standard is a Maximum Permissible Exposure (MPE) 10-times less than the ED50 for the MVL energy for that laser-light wavelength and pulse width. This standard has obvious problems in that the MVL is based on the resolution power of the ophthalmoscope and operator. Further, the standard completely ignores the sublethal longer-term consequences of laser-light irradiation. This is especially important since the MVLs are scored usually at one or at 24 hours postexposure. Some biochemical studies have investigated free radical formation in the melanosomes of the retinal pigment epithelial (RPE), which are hypothesized to lead to oxidative damage (Glickman, et al., 1996a, 1996b, 1995, 1993, 1992; Lam, et al., 1992). Belkin and Schwartz (review, 1994) state that there is no known mechanism to explain the subthreshold effects of laser irradiation on ophthalmic tissue. More recently, Hall, (2001) et al, demonstrated the production of fragmented DNA in bovine RPE cells exposed to femtosecond pulses or continuous wave of 800 nm laser light using single cell electrophoresis (Hall R.M., et al., 2001). To date there remains a paucity of basic research on the cellular and molecular damage response caused by laser light at any dosage to eye or skin tissue.

Previous work in our laboratory has yielded three significant discoveries. (1) Irradiation with visible (532 nm) laser light was found to be more effective in damaging cultured mammalian cells than an equal irradiance of near-infrared (1064 nm) laser light (unpublished). This finding is consistent with others indicating that shorter wavelengths do more damage at equivalent energies. (2) A tenfold increase in mutation rate in mammalian cells was observed after irradiation with multiple laser pulses at 532 nm (Leavitt, et al., 1997). This finding would indicate that human eyes lased with high energy 532 nm light may subsequently develop cancer. (3) A transient increase in the expression of certain intracellular proteins was observed in irradiated cells (unpublished).

The function of most of these proteins in cellular damage, repair, or other responses to laser irradiation is unknown. However, matrix assisted laser-desorption ionization mass spectrometry identification of 7 protein spots recovered from on a 2D-PAGE gel resulted in 8 known proteins and 1 unknown being significantly altered by a sub-acute picosecond (ps) and nanosecond (ns) pulsed laser light exposure (Obringer, unpublished). The indication from this limited snapshot of the cellular protein-level response was that the cells had undergone some major perturbations to the electron transport system (energy production) and the cytoskeleton of the exposed RPE cells.

Using gene expression microarrays (GEM) with genes for DNA damage and repair as one possible cellular system to investigate, we investigated the effect of the 532 nm laser-light by repeating the approximate exposures used by Leavitt, et al. (1997) to attempt to validate the finding of mutagenesis in mammalian cells as mentioned above, but by introducing the human RPE cell as the model. This has significance in that mutagenic events are considered the genetic precursors to the development of most cancers. It could also demonstrate the existence in human cells of a mechanism of mutagenesis by green light (532 nm), which currently is hypothesized as being the phenomenon of multiple photon absorption and frequency up-conversion. The next higher harmonic of 532 nm light is 266 nm light which is in the ultra-violet (UV) range. The mutagenic effects of UV-light are well characterized as it causes pyrimidine dimer formation in DNA, the genetic material of life. The physical phenomenon for the laser induced DNA damage was first proposed by Cao, et al. (1993) stating that "exposure of thymine and DNA to high-intensity 532 nm pulsed radiation from a Nd:YAG laser resulted in the cyclobutylpyrimidine dimers, which were measured by the method of high performance liquid chromatography." They went on to suggest that the photochemistry was initiated by two-photon absorption by biomacromolecules. Their observation is further validated by Konig, et al. (1996), who observed pulsed beams at wavelengths less than 800 nm are capable of damaging cells through two-photon absorption. Other investigators have seen more gross forms of DNA damage from laser light such as sister chromatid exchanges (presumably the result of damage repair) from radiation at 632 nm (Quero, et al. 1997) and 810 nm light caused frank breakage of the DNA molecule (Both, et al. 1990, Shafirovich, et al. 1999). Previous work in our laboratory has yielded molecular biomarkers for DNA damage in a human liver cell reporter-gene system with the induction of p53 after exposure to mode locked 1064 nm, 37 picosecond (ps) as well as 3 nanosecond (ns) pulsewidth light (Obringer et al. 2000, Obringer, et al. 1999a) and the induction of the proto-oncogene *fos* after 532 nm, 37 ps exposure (Obringer, et al. 1999b). Therefore, we further explored these and other bioeffects of laser exposures of the above and other parameters in human RPE and skin cells using DNA microarray technology.

The recent development of DNA microarray or GEM technology now enables researchers to qualitatively and quantitatively examine the differential expression patterns of thousands of genes in one experiment (Hubin, et al. 2001, Schena, et al., 1996, Schena, et al, 1995). As the literature on laser induced bioeffects on the cells of the retinal pigment epithelium at the cell and molecular level is virtually nonexistent, there is an obvious need for basic science knowledge. DNA microarray methodology opens an

entirely new window for examining the perturbation of retinal tissue by laser exposure at the genetic level. By examining the differential gene expression patterns one can gain insight into the physiological state of the cells and, thereby, deduce the type and amount of damage/perturbation the tissue has undergone. A conceptual overview cartoon is presented in Figure 1. This strategy has proven successful in several other applications such as the investigation into human aging where mitotic misregulation seems to play a role (Danith, et al., 2000), *Drosophila* developmental regulation (White, et al., 1999), murine response to caloric restriction and age retardation (Lee, et al., 1999), transcriptional response of human fibroblasts to serum (Iyer, et al., 1999), and gene expression variation in human gliomas (Zhang, et al., 1997) to illustrate a few examples..

MATERIALS AND METHODS

Explant procurement and processing: General overview

Tissues were received as a tissue donor gift through the Rocky Mountain Lion's Eye Bank who accomplishes all of the donor consent paperwork. Posterior globes of both eyes were harvested 8 hours post time of death and put into a 50 ml vial with approx. 25 ml of buffered saline. The tissue was transported directly to tissue culture lab where the vitreous humor and retina were mechanically removed. Then the RPE still attached to the sclera were cut into 3-5 mm square pieces. The pieces were then placed into 96 well microtiter plates (1 per well) with 150 microliters (ul) of the media (DME/F12 with 10% FBS plus antibiotics) and cultured at 37 degrees C in 5% CO₂ until re-plated for exposure. In a fresh 96 well plate the pieces were placed RPE side up centered in the well, in 50 ul media (just covers the explant) to be exposed. Explants were kept at 37 degrees until they were transported in a pre-warmed insulated box to the laser lab and exposed at room temperature in the plates on an X-Y translation stage one well at a time as quickly as possible to minimize temperature fluctuations then returned to the incubator after stereoscopic examination and the additional 100 ul of warm media. At the desired time post exposure, RPE was mechanically removed from the sclera and collected in microcentrifuge tubes, labeled and frozen at -65 degrees C. Samples were shipped frozen to the vendor with approx. 10 lbs of dry ice via overnight delivery. We accepted donors age 65 years or younger, either sex, with no mitigating ocular or retinal pathology such as glaucoma, diabetic retinopathy, retinitis pigmentosa, etc.

Donor:

The RPE tissue donor was a 41 year old Caucasian, blue eyed, female that died of cancer. No ocular pathologies were noted.

Explant preparation:

Globes were removed 6 hr., 10 min. after death and stored for transport in neutral saline or media. The globes were removed from the transport liquid and processed for experimentation. Muscle and fatty tissue were removed from the outer globe surface

using scissors. The anterior segment was removed using a circumferential cut through the *pars plana* with iridectomy scissors. The globe was then hemisected with scissors passing through the edge of the optic disc. The optic nerve and disc were removed and the retina was peeled away from the RPE using fine forceps. The sclera with retinal pigment epithelium attached was cut into square pieces 3 mm on a side using a number 10 Proper carbon steel surgical blade. Each scleral piece was placed RPE side up, centered, in Falcon 96-well plates with in 100 ul media containing streptomycin and penicillin. Plates were labeled and wells labeled as to which eye the explant was derived from.

Laser: Equipment Used

Laser (Nd:YAG)	EKSPLA, model SL312T, serial number 017
Power Meter	Molelectron OM4001 power meter, serial number 136C
Detector Head	J50 Detector Head, with diffuser, serial number 1518B
Shutter	nmLaser model LS055S3W8
Shutter Controller	nmLaser model CX2450
Velmex XY Stage	model NF90-2

Figure 2 shows how the pulses were directed into each well of a 96 well microtiter culture plate. After a well was exposed to the laser, an x-y translation stage was used to bring the next well into position. A shaping lens was placed in the beam to match the beam diameter with the 6-mm diameter of a well entrance. Burn paper was used to verify that the beam neither under nor overfilled the cell. Prior to testing, a dish filled with water was placed on the x-y stage below the final turning mirror, and the angle of the mirror was adjusted until the reflection of the laser beam off the water's front surface returned along its incoming path. This ensured the pulses entered the wells at a ninety-degree angle with the horizontal.

Pulse energy was determined by placing a power meter on the x-y translation stage (the site of target exposure) and dividing the measured average power by the pulse repetition rate. This method was considered adequate since pulse-to-pulse energy typically varied less than 10%. The beam profile is a "top hat" with less than 5% variation across the wave front.

Laser-light exposure:

The explants were initially plated in flat bottomed 96 well microtiter plates and maintained in RPE growth medium until exposure. The diameter of the wells is 6 mm so the laser beam was focused to fill the well with light. Immediately prior to the experimental treatment the scleral/RPE sections were re-plated one per well in a fresh 96 well plate, RPE side up, centered in each well with 50 microliters of warmed fresh growth medium to reduce the amount of light absorbed by the medium and ensure an equal amount of medium in each well. Plates were kept in a 37 degrees C incubator until just prior to dosing. Then the plates were transported to the laser suite in an insulated warm box and then positioned onto the x-y translation stage and exposed in a sequential

fashion to the dose listed below. The measured temperature change of the fluid in the wells during the three minutes required for the exposure process was approximately one degree C. Control explants were treated identically, except they were sham exposed with the laser beam blocked. Explants from each eye were equally represented in each sample. The explant containing plates were then returned to the 37 degree C, 5% CO₂ incubator after the addition of 150 microliters of room temperature medium.

Wavelength (nm)	532
Average Power (mW)	505
Pulse Energy (mJ)	50.5 ± 3
Pulse Length (FWHM)	120 ps
Total Incident Energy (mJ)	3232
Peak Power (W)	4.21 x 10⁸
Fluence (mJ/cm ²)	107
Exposure Time (sec)	6.4
Laser Repetition Rate (Hz)	10
Beam Diameter (1/e ²)	6 mm
Irradiance (kW/m ²)	11.9

Total incident energy (TIE) is defined as the amount of laser-light energy that was delivered to the 6 mm well containing the RPE explants. Abbreviations: nm-nanometer; m-meter, mm-millimeter, ns-nanosecond; mJ-milliJoule; mW-milliWatt; FWHM-Full Width Half Max; Hz-Hertz; sec-second; W-watt; e-natural log.

Laser exposure of Human RPE Explants

The Nd:YAG laser light exposure regimen was based on empirical data (not shown) that established cell viability after a range of laser exposures. The exposure described above is calculated to be 1.2×10^{-7} J/cm² which is about 10% of the MVL value and approximately 20% above the MPE for the pulse width and wavelength considered (Sloney and Wolbarsht, 1980 and ANZI Z136.1-2000 Table 5a)

The cells were exposed to either 1) sham exposed to no laser-light (beam blocked upstream), or 2) 64 pulses of 532 nm visible laser-light. Each pulse containing 50.5 mJ ± 3 mJ (on average) of energy was delivered to a microtiter plate well 6 mm in diameter containing 50 microliters of medium. The 532 nm wavelength was chosen of the extreme damage possibilities of this common laser wavelength, and, more importantly, so as to provide a basis of comparison to the previous genomic experiments and subsequent genomic, proteomic and lipomic investigations using explants and 532 nm laser-light exposures. See Figure 2 for a general overview of the experimental procedures.

Exposed RPE collection

After the prescribed time post-exposure the RPE tissue was mechanically separated from the sclera using a sterilized forceps and probe, and collected in a pre-chilled 1.5 ml tube. The tubes were then immediately frozen and stored at -65 degrees C until further processing. The tissue was overnight shipped to NeuroLogic, Inc., Rockville, MD for mRNA isolation and differential gene expression (GeneChip) analysis as described below (personal communication, P. Manickam)

Oligonucleotide Microarray :

Total RNA was isolated using TRIZOL method (Invitrogen, Carlsbad, CA, USA) followed by Qiagen Rneasy Mini Column Cleanup.

The detailed protocol for the sample preparation and microarray processing is available from Affymetrix (Santa Clara, CA or as previously described- 2 References : Nature Biotechnology 14: 1675-1680 (1996); Physiol. Genomics 2: 143-147, 2000). Briefly, at least 10 ug total RNA was reverse transcribed by Superscript II reverse transcriptase (Invitrogen) using T7-(dT)24 primer (Geneset Oligos, La Jolla, CA, USA) containing T7 RNA polymerase promoter. After synthesis of the second complementary DNA (cDNA) strand, this product was used in an in vitro transcription reaction to generate biotinylated cRNA using a BioArray High Yield RNA Transcript Labeling Kit (Affymetrix). The biotinylated cRNA was cleaned with the Rneasy Mini Kit (Qiagen, Valencia, CA, USA).

Hybridization of RNA to High Density Oligonucleotide Microarrays :

Fifteen micrograms of fragmented cRNA was hybridized to a Human Genome arrays containing oligonucleotide probe sets representing approximately 24,000 known rat genes (GeneChip U133A array, Affymetrix). The hybridization mixture was incubated at 99 degree C for 5 min, followed by incubation at 45 degree C for 5 min. The hybridization was then carried out at 45 degree C for 16 hours with constant rotation at 60 rpm. Each microarray was used to assay a single sample. After hybridization, the microarray was washed and stained with streptavidin-phycoerythrin (Molecular Probes, Eugene, OR, USA) and amplified with biotinylated anti-streptavidin antibody (Vector Laboratories, Burlingame, CA, USA) on an Affymetrix fluidics station and scanned with an argon ion confocal laser (Agilent Gene Array Scanner, Affymetrix).

Data analysis/Bioinformatics :

The fluorescence intensity was measured for each microarray and normalized to global scaling to 500 and to the average fluorescence intensity for the entire microarray. This scale is automatically performed by the Affymetrix software to normalize the gene expression levels to allow comparison between any two samples. Data analysis was performed with the Affymetrix Data Mining Tool software version 3.0.

The software has the ability to provide hierarchical information concerning the type and functions of the known genes, which greatly aids in deciphering the functional genomics of laser-tissue interaction.

Gene Expression Microarray

We examined the differential gene expression profile of laser exposed tissue that will allow us to describe the resultant biological processes from a global genetic perspective. The cells of primary interest are those that are sublethally exposed to include those presumably at the margin of a laser induced lesion *in vivo*. These are obviously the cells that are of consequence to the organism post-exposure. The use of the DNA microarray will not only allow us to develop hypotheses that certain biomarkers might be useful for detecting and assessing laser induced tissue damage. It will also allow us to continue with gene-based biomarker discovery with both known and undescribed genes known to be expressed as part of the human transcriptome.

The DNA microarray that we used was the Affymetrix HG-U133A array that contains 14,593 human Unigene clusters, 513 additional potential full length sequences and 18,462 subclusters sequences from various other sources, which is generally comprised of totally unique genes or gene cluster sequences. Of these 13,049 are annotated genes/clusters, with the remainder being either annotated expressed sequence tags (ESTs) or unannotated ESTs. The annotation source is the UniGene *Homo sapiens* database which is updated quarterly. The build used for this array was #133, April 20, 2001. Several other sources of sequence were also used. The unannotated elements are clones of ESTs from complementary DNAs (cDNAs) produced from messenger RNA. Each probe is comprised of an oligonucleotide 25 bases in length (25-mer) with 11 probe pairs per sequence and the feature size of each probe spot is 18 microns. For a more complete listing of sequence sources and human array design the reader should visit Affymetrix's website at www.affymetrix.com, Technical Note: Array Design for the GeneChip Human Genome U133 Set. Figures 3, 4 and 5 are offered to familiarize the reader with the Affymetrix platform, general procedures for target preparation and the GeneChip array, respectively.

RESULTS

The results (Appendix A) of a gene expression microarray are expressed in fold change in expression for one gene in the control versus the experimental samples. For example, if gene YFG is expressed four times greater in the treated cells than in the sham exposed controls, it would show a fold change of positive four (4) in Appendix A that functionally means that gene YFG mRNA was found in 4 times greater concentration in the treated cells than in the controls. Thus, we conclude that the treatment induced the genetic expression of gene YFG four times greater in the experimentally treated cells than in the shame treated cells, presumably in response as the biological effect of the treatment. Conversely, if the YFG mRNA is 4 fold less in the experimental sample than in the control then a value of -4.0 fold is calculated. The assignment of the plus or minus

designations on Appendix A is a function of the algorithm in the software used to calculate the fold change. In the context of understanding the significance of fold change or fold induction of a gene, the analysis software calculates a 95% confidence level of fold change for each experiment. For this set of hybridizations the confidence was calculated to be +/- 1.8 fold.

Appendix A presents the most pertinent genes (at or above a 1.8 fold absolute value) listed in rank ordered by absolute fold change minus to plus at or above 1.8 fold change. To help clarify the interpretation of this appendix the following heading explanations are offered. Probe set: the listed name of the gene being probed. Control probe sets have been deleted from the data set in Appendix A. All signals in Appendix A have passed the quality control standards established by the manufacturer. The internal controls are used by Affymetrix to calibrate the array and as quality control elements. Control signal: the balanced (adjusted for background) signal strength for the control sample. Exptl Signal: the balanced (adjusted for background) signal strength for the experimental sample. Control vs Exptl Fold Change: the fold change based on the comparative signal strength of the control RPE sample as compared to the experimental. **This is the fold change value that is used as the endpoint value, and for further analysis in the interpretation of the differential gene expression microarray results for the designated genetic elements listed under "Probe set."** Description: a brief description of the gene or EST that is represented in the probe set. The appendix obviously contains only a portion of the total number of elements probed and only those whose absolute fold change was at least 1.8 or higher that has been calculated to be at or above the statistical significance of 95%.

A quick survey of the Differential Expression Scatter Plot (Figure 6) (internal controls are not in the graph data set) and Appendix A yields the observation that RPE mRNA was above 1.8 fold change in 607 of the approximately 22,000 (approximately 2.8%) probe elements on the GEM. Of those 397 (1.8% of the total possible elements and 65.4% of the significantly expressed elements) were up-regulated. The number of genes whose expression was down regulated was markedly less. 210 (1.0% of the total possible elements and 34.6% of the significantly expressed elements) genes were down-regulated at or above significant levels. In summary, the greatest number of significant changes in gene expression was in the up-regulated direction (nearly 2 times), and the greatest magnitude of change for single genes was also up-regulation with several above an order of magnitude fold change.

DISCUSSION

Selected genes and ESTs from Appendix A will be reviewed as to the physiological function and/or biological marker for which they are known whenever possible. Figures 7 and 8 illustrate several of the most differentially expressed genes/ESTs in both the positive and negative direction respectively. Figure 9 briefly capsulates the functional genomics of the differential gene expression profiles.

The number listed in the parenthesis is the reference to the source of the gene function in the "Gene References" section of the bibliography. Also note that Appendix A contains ESTs that were differentially regulated by the cells post laser exposure. As of the date of the experimental analysis, the functions of the genes related to the above ESTs were not known. But recently, with the latest update of the NCBI genomic database, several ESTs in Appendix A have been assigned genetic/physiologic functions and will be discussed below. However, other EST's that were differentially regulated functions remain unknown thus remain fertile ground for future exploration and analysis.

Turning our attention to the collection of differentially expressed genetic elements extracted from Appendix A whose function (at least one) and/or association is known, we will attempt to develop an analysis of cellular response 12 hours post exposure to the perturbation caused by green laser-light exposure. Once again referring to Appendix A, we can decipher the general pattern of the functional genomic response of cells treated with 532 nm laser light, 120 ps pulses, 51 mJ per pulse for 6.4 seconds at 10 Hz (3232 mJ total energy). It is evident that pulses of laser light are sensed and markedly alter gene expression in the model cells. The cellular physiological pattern that is evident from the analysis of the differential gene expression patterns is fundamentally that the treated cells are induced into cessation of cell cycling, but provide abundant indications of the reconstruction of the translational machinery as well as alterations in the macromolecular trafficking and response to oxygen stress. And an overall up-regulation of transcription is countered by the marked down-regulation of transcription of certain genes involved in cytoskeletal metabolism, cell cycling, anaerobic enzymes and kinase enzymes as well as specific cellular channel or receptor components. However, the most striking revelation of the gene profile is the apparent rebuilding of the translational machinery; most notably ribosome reconstruction with 37% of the first 100 up-regulated genes so involved. In the discussion to follow a few of the more significantly altered physiological systems that appear to be perturbed by the above laser exposure will be discussed in greater detail. Note: The number in [brackets] following a gene name indicates the fold change in that gene's expression.

Macromolecule Trafficking

As mentioned, several physiological systems appear to be induced at the transcriptional level. Not surprisingly, some processes for protein degradation were up-regulated as compared to the levels of the sham-exposed controls indicating a increase in protein degradation. Most notably up-regulated were the genes for the enzymes essential in the ubiquitin-proteasome pathway (UPP) shown to be up-regulated in response to oxidative stress in eye tissue (1). These were ubiquitin [2.0], 3 ubiquitin-conjugating enzyme genes E2 [2.3], E2D2 [2.3] and E2D3 [2.8]. Also up-regulated were two cathepsin genes (B [2.0] and L [3.7]) (2). It appears that the cells at the 12 hour point had indeed up-regulated the protein degradation machinery for cellular debridement; while the snapshot we viewed at 24 hours post exposure in USAFA-TR-2003-03 showed the contrary reflected the transcriptional rebound (return to homeostasis) of a system having possibly previously been induced (as described here) to deal with protein damage. As discussed in the previous publication, this conjecture is corroborated by Lykins, et al. (2002),

reporting that when epithelial cells were exposed to a similar laser-light treatment and examined 12 hours post-exposure at the protein level, the ubiquitination systems was markedly up-regulated implying that transcription of this system is early in the post-exposure gene-expression cascade. Also note that HSP 70 (3) is up-regulated >3-fold. As HSP 70 facilitates the removal of injured proteins by ubiquitin-mediated proteasomal degradation arguing for the prior activation of the UPP system despite the current state of expression of the above mentioned ubiquitin-activating enzyme E1. Furthermore, HSP 70 acts downstream to ubiquitination and is regarded as a chaperone driving a multi-protein degradation complex (3). Also HSPs 105 [4.9] and 60 (chaperonin) [5.4] were up-regulated. The induction of the chaperonin, as well as the induction of ubiquinol-cytochrome C reductase hinge protein [1.8] and its binding protein [2.7] indicates a mitochondrial involvement that will be further discussed in the oxygen-related metabolism discussion. Further examination of the additional genes involved in macromolecule trafficking reveals an increasingly intriguing picture. It appears that various tangential trafficking systems have been up-regulated such as the lysosomal degradation processes indicated by lysosomal-associated transmembrane 4-alpha protein [6.8] and lysosomal-associated membrane protein 1 [7.9]. It is also interesting to note the up-regulation of the annexins (A2 [10.5]; A2a [7.2]; A1 [6.0]) that are traditionally thought of as calcium-dependent phospholipid-binding proteins, but recent work suggests that they are responsible for distinct localizations and specialized functions of the protein through post-translational modification and binding to other proteins (4). The 11 fold induction of cofilin that has been shown to act in concert with HSP 105A, provides a strong indicator of actin metabolism in the cellular microtubular component (5).

Proliferation

In the context of cell cycling, the gene expression profile would indicate that the cells have ceased proliferation at 12 hours post-exposure, but showed signals for the genetic preamble for its resumption. For example, epidermal growth factor (EGF) receptor was down 2 fold, but substrate 8 of the EGF receptor synthesis pathway was up 2.5 fold. Other indicators such as GM2-activator protein, CDC 14 were both down-regulated over 2 fold. Two GADD genes were significantly up-regulated (A [3.9]; B [2.6]) indicating cessation of proliferation while S-phase kinase associated protein 1A [4.4], nucleoplasmin [5.7] and thrombomodulin [8.3] indicate the contrary. The gene expression pattern of the lasered cells indicates the cells had halted proliferation, but were preparing to resume cycling, possibly after recovery of whatever perturbation they may have suffered such as oxygen-related stress.

Oxygen-related Metabolism

The perturbation to the oxygen metabolism that the cells seemed to have responded to appears to have been a double edged sword; that is, there are indications of a laser induced hypoxic state and also a response to laser produced reactive oxygen species. The over 3.2 fold induction of the hypoxia-inducible factor-1 (6) provides strong indication of oxidative stress due to hypoxia. Likewise, supporting the oxygen stress theme is the 5.8 fold increase in cytochrome C production, the 2.7 fold induction of cytochrome c

reductase and the 3.0 and 2.8 fold increase in two components of cytochrome C oxidase. Also of note are numerous genes in the feeder pathways to oxidative phosphorylation that are down-regulated, such as glucose transporter protein 10 [-2.4] and aldehyde dehydrogenase 7 [-2.3]. Further corroboration of a laser induced hypoxic state is evidenced by a 3.4 fold up-regulation of mitochondrial ubiquinone-bind protein which has been shown to increase under hypoxic condition, and likewise with mitochondrial outer membrane translocase (2.2 fold increase). At this time I would like to point out the curious linkage between the aforementioned genes involved in oxygen metabolism and suggest a possible linkage to the processes involving molecular debridement and oxygen metabolic disruption probably at the mitochondrial level. The second edge of the oxygen metabolism sword is that of the production of reactive oxygen species (ROS) by laser light exposure, either directly and/or indirectly. Intracellular ROS has long been known for disruption of cellular function by the oxidative alteration of a whole host of biologically significant macromolecules. An incredible 14.5 fold induction of the thioredoxin gene flagships the lased tissues' response to this laser treatment closely followed by a 7.82 fold increase in glutathione transferase. Thioredoxin has been definitively shown to be up-regulated by oxygen stress and is a key component in the anti-oxidant defense system as well as glutathione. Other genetic indicators of ROS in the exposed tissue was the expression up-regulation of the following genes: HSP 70 [3.0], cytochrome P450, dioxin-inducible form [8.3] (the aromatic-compound inducible form was -2.7), HSP 105 [4.5] all previously shown to be up-regulated by ROS. Ironically, it has been found that cytochrome P450 (CYP) over-expression itself generates large amounts of ROS via the induction of CYP-dependent monooxygenases (7). Sapaone, et al. (7) further hypothesized that long-term CYP induction can have a co-carcinogenic and/or promoting potential. And finally, the over doubled [2.2] expression of metallothionein-III (MT-III) tissue inhibitor indicated the previous up-regulation of MT-III in the cells' attempt to protect themselves from either or both oxidants and/or hypoxia. MTs are metal binding proteins that are classically known to protect cells against metal toxicity and oxidants. MT, subtype III is brain-predominant and was shown by Tanji, et al., (8) to be induced in normal human astrocytes by hypoxia and that over expressed MT-III protects human cells from hypoxic damage. MT-III also could reasonably be expected to play its classic physiological role as an antioxidant against ROS and, in fact, was shown (9) to be involved in the protection from ROS-induced DNA damage, probably via direct interaction with ROS, and further that MT-III acts as a neuroprotective agent and has been shown to be involved in Sorsby fundus dystrophy. Its increased expression in RPE was most likely to fulfill a like physiological role. Overall, it appears that it can safely be said that laser-light exposure alters oxygen-metabolism in the context of energy production capability (hypoxia's impact on aerobic respiration) and macromolecule damage due to oxidative damage, most likely due to ROS production. Overall, it appears that the cells were on the mend and had up-regulated protective/restorative genetic responses at the transcriptional level.

Translation Initiation and Ribosome Reconstruction

Undoubtedly, the most striking result of this investigation is the number of genes up-regulated that have to do with the cell's translational machinery. Intriguingly, of the first

100 up-regulated genes 37 or 37% of them had to do with the some aspect of translation and most with the reconstruction of the ribosome and the trend continued throughout the remainder of the up-regulated genes. That finding reflects an amazing metabolic investment in the machinery for protein synthesis, and also indicates that the ribosome may be the primary target for damage from this treatment. From this observation we speculate that the ribosome may constitute a sub-organellar chromophore for this regime of laser-light exposure.

Transcription

Among the genes whose expression was altered at or above the 1.8 fold level, those involved in transcription would appear to have been globally up-regulated. Numerous oncogenes such as v-maf musculoaponeurotic fibrosarcoma oncogenes [12.7] and RAB1, a member of the ras oncogene family [8.8] and numerous others. These constitute transcriptional factors that originate from the nucleus, cytoplasm, and plasma membrane involving the signal transduction mechanisms associated with the extracellular matrix. Also noted was the down-regulation of numerous specific transcriptional factors and homeotic genes.

Inflammatory Response

Also prevalent in the gene expression profile of the laser-light treated cells was the dramatic up-regulation of a number of the immune system genes especially having to do with the inflammatory response. A few examples are prostaglandin-endoperoxide synthase 2 [12.5], interleukin 6 [12.0], thrombomodulin [8.3] and the list goes on. This reaction may provide an alternate explanation for the appearance of the late (24 hr) onset lesions in the primate MVL studies reviewed in the background section.

DNA Repair

Although it is known that the DNA damage/repair genes are always "on," it is interesting to note that several were significantly up-regulated in the exposed samples. The GADD45A, growth arrest and DNA-damage inducible, gene was up-regulated nearly 4 fold, while GADD45B was up-regulated 2.6 fold. Other DNA metabolism genes were also over expressed such as methyl CpG binding protein [2.7] and topoisomerase-related protein 4-1 [2.0] as well as others such as S-phase kinase associated protein 1A [4.4] and high mobility group (nonhistone chromosomal) protein 14 [4.1].

Summary

Taken together, global perturbations to the cellular metabolism is evidenced to have occurred during the 12 hours post-exposure given the numerous cellular systems affected. The picosecond pulses of 532 nm light appeared to induce the cells into cessation of cell cycling and a nearly global up-regulation of transcription include the genes involved in macromolecular trafficking, proliferation (mixed signals), oxygen-related metabolism

and various transcription-related regulatory genes. Additionally, numerous genes involved in neuronal development, cytoskeletal metabolism, transporter production and glycolysis were also generally up-regulated as well as the transcriptional up-regulation pattern of several key genes involved in the UPP system. Additionally, there appears to be little doubt that this laser-light treatment had a major impact on the oxygen-related metabolism of the cells either by the production of hypoxia or ROS or both. Once again we highlight the response of the translational machinery reconstruction efforts of the cell in response to the laser-light perturbation.

Closing

As a closing comment we offer the following observation: The gene profile seen in this experiment is very reminiscent of that seen in the experiment reported in USAFA-TR-2003-03 which was a picosecond 1064 nm 24 hour post-exposure. One of the notable differences is the reversed direction of expression seen in some of the genes especially in the UPP system, but since this is a 12 post-exposure experiment the difference is most likely due to the temporal considerations and actually aids in providing a timeline of cellular response to exposure. However, the most notable difference is the dramatic response of the laser-light treated cells is the amount of metabolic energy and resources expended in the reconstruction of the ribosome. This gene profile strongly suggests the occurrence of major damage to the ribosome as a result of the exposure. As this is written there is an electron microscopy project underway to visualize the putative structural damage to the ribosome in exposed tissue. These findings bode to be very telling as to the validity of the aforementioned genetic data.

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8. *Biochem Biophys Acta* 2002 Oct 10;1573(1):33-8
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Figure 1.

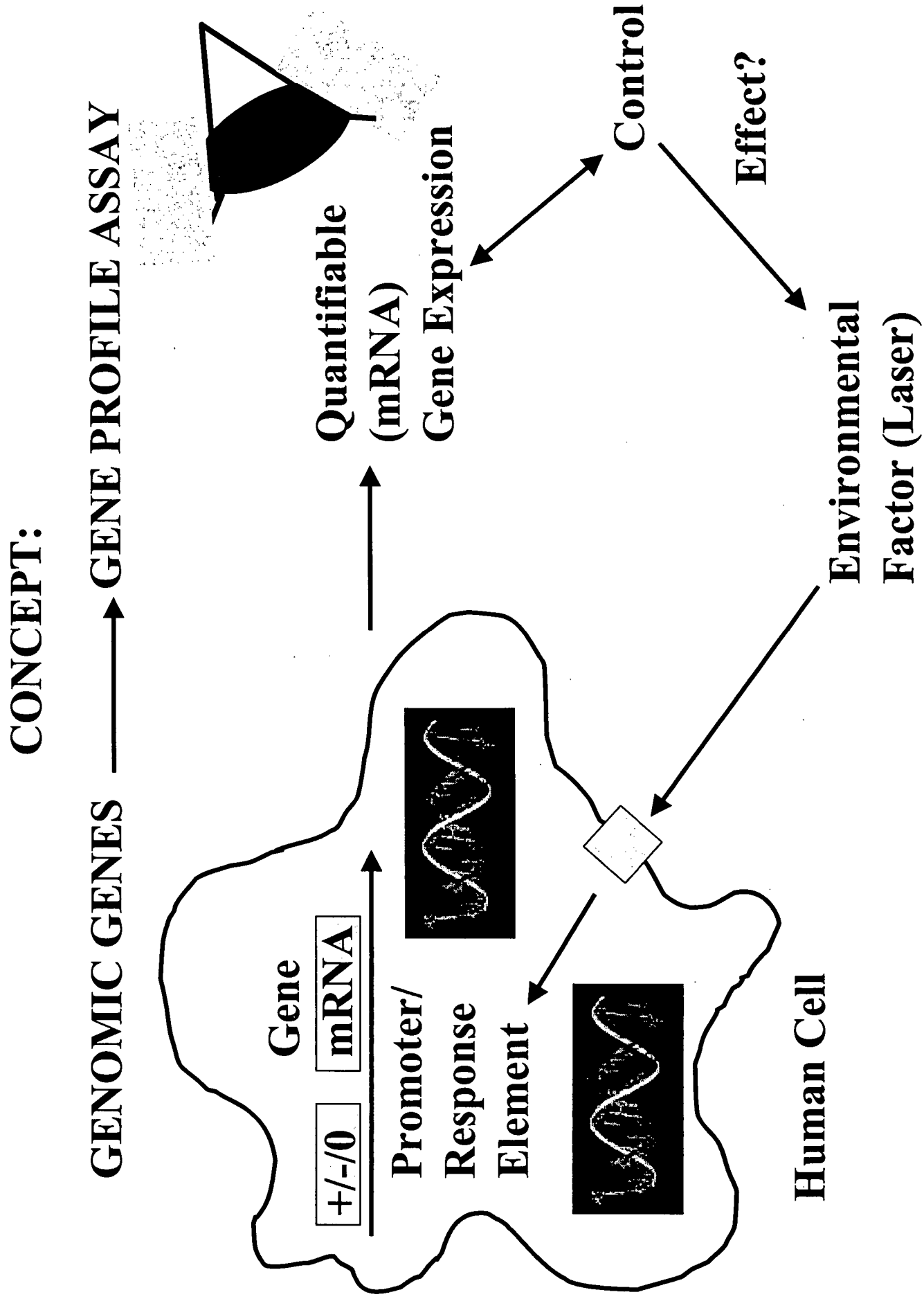
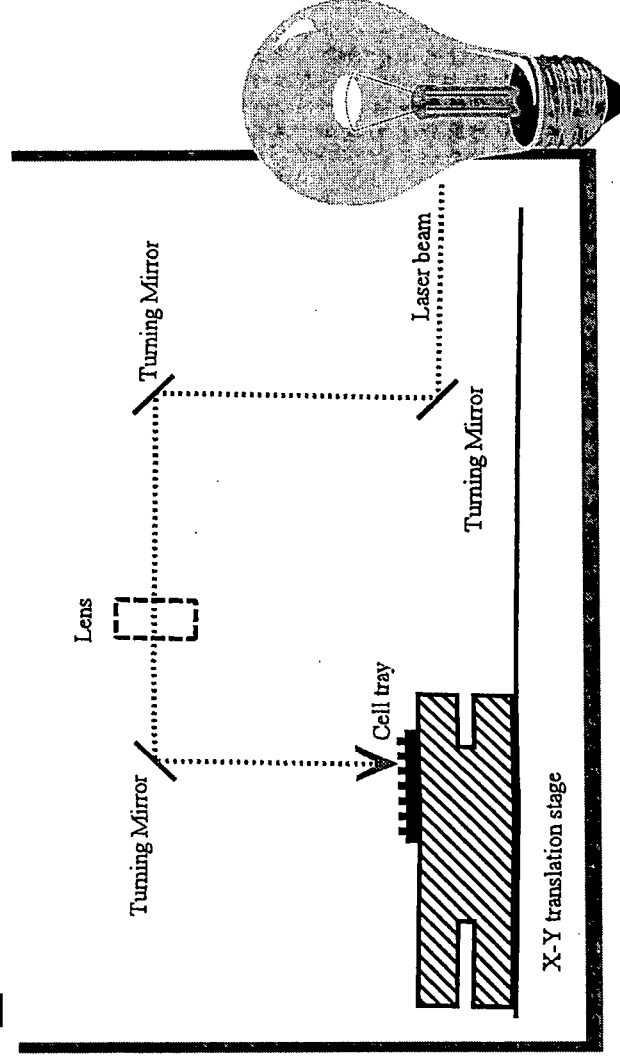


Figure 2.

Experimental Methods



RPE
Explants



Lyse



Differential Gene
(mRNA) Expression

Figure 3.

Affymetrix Platform

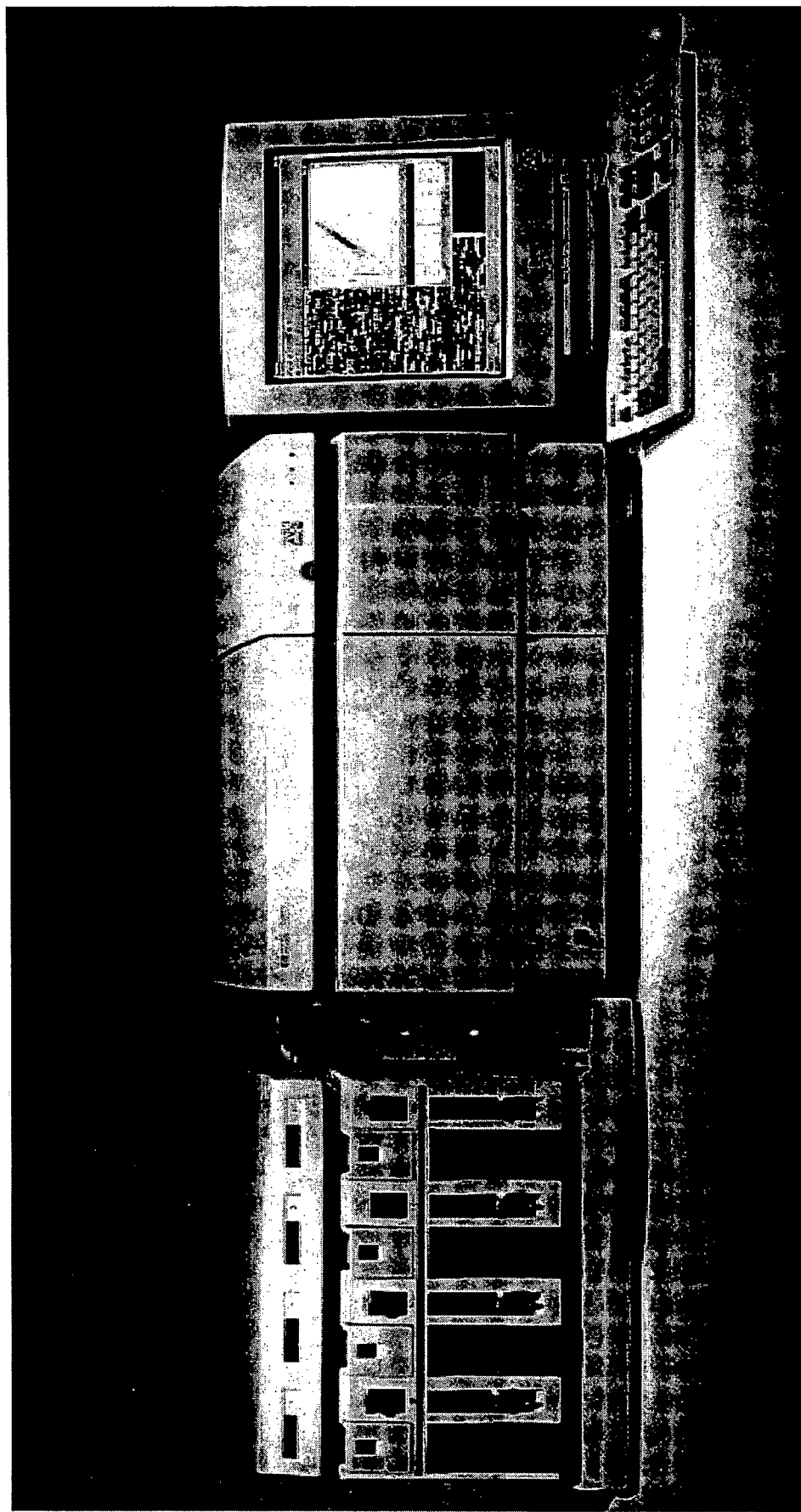


Figure 4.

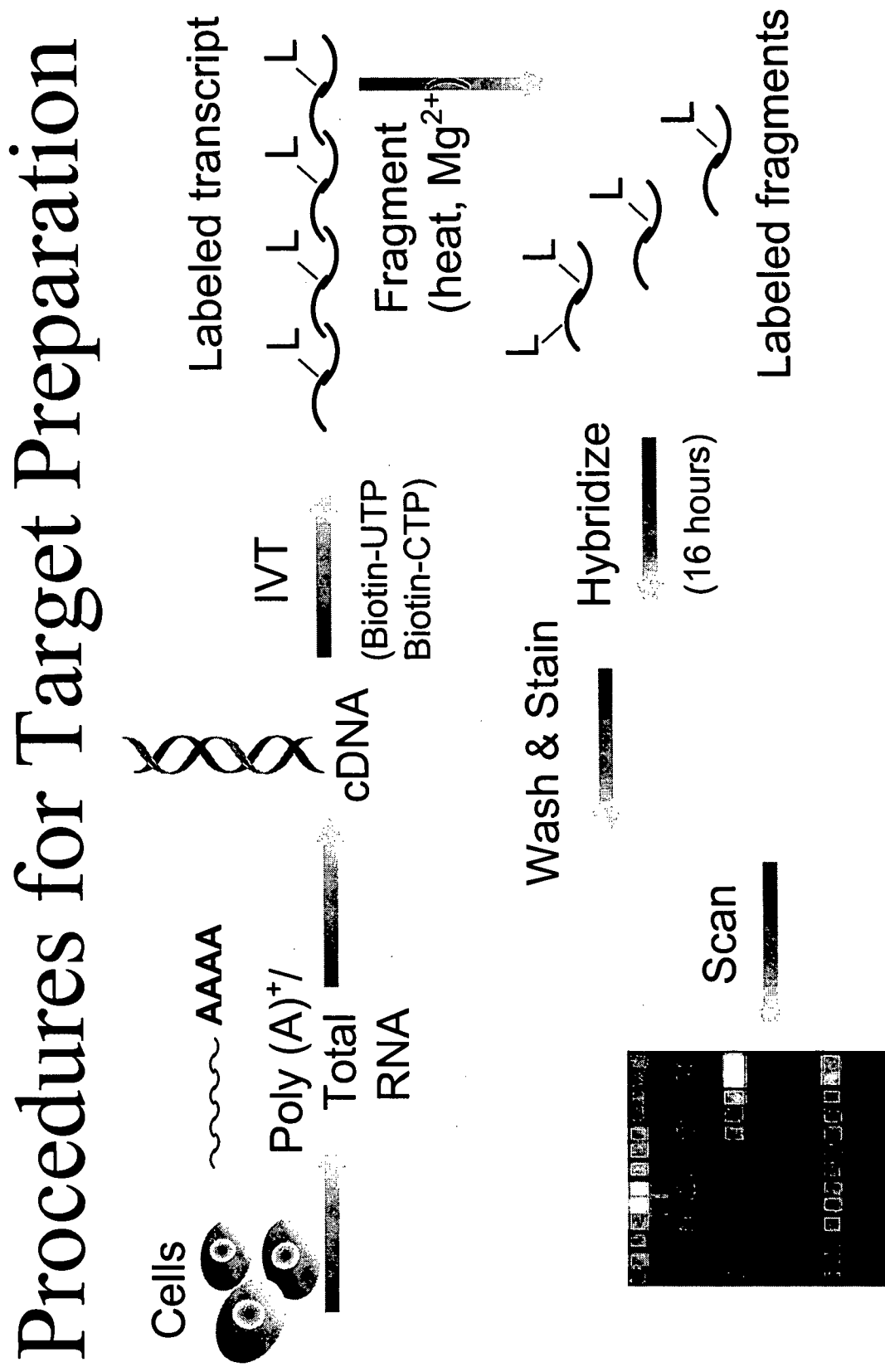


Figure 5.

GeneChip[®] Probe Arrays

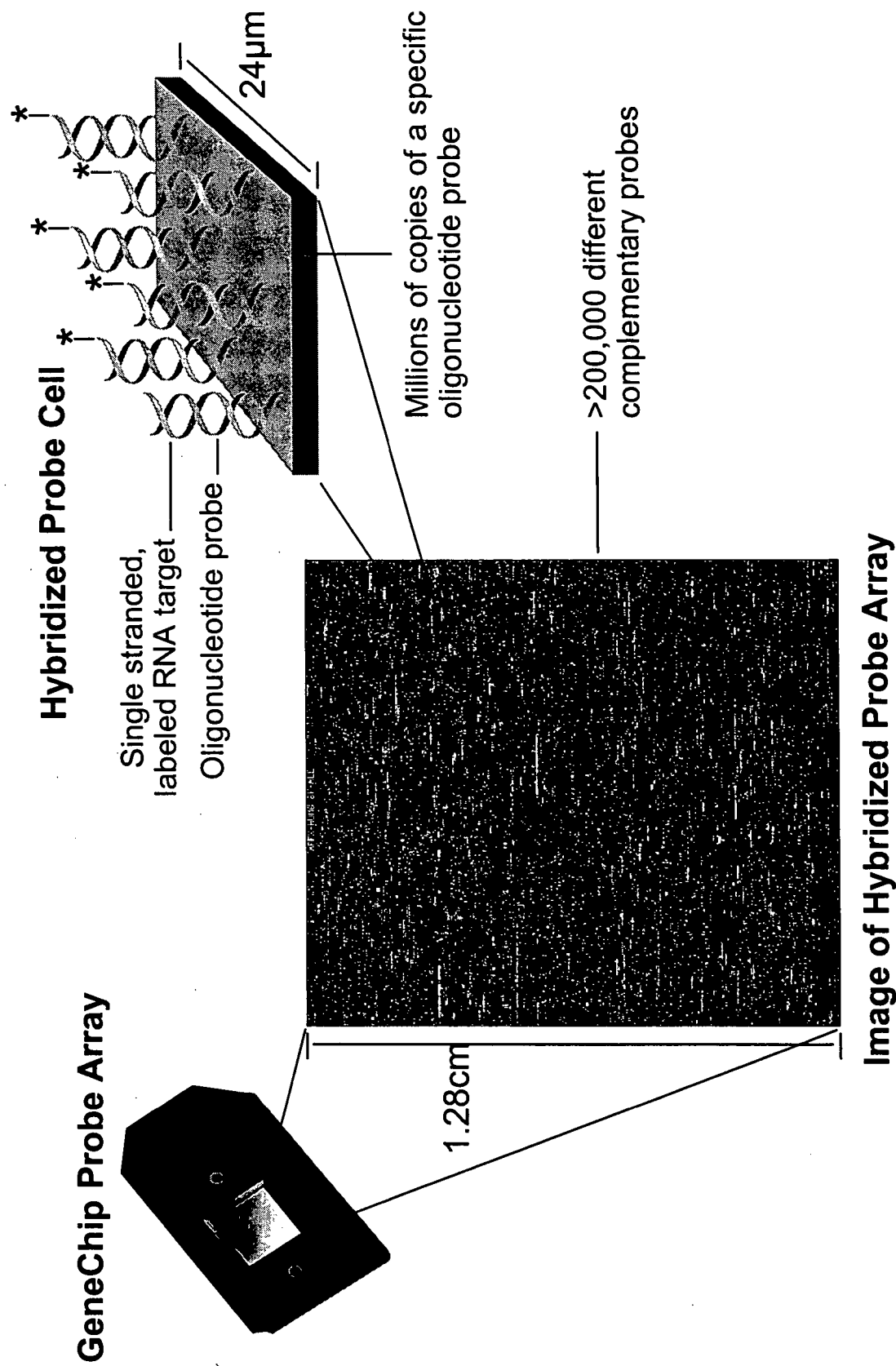


Figure 6.

DIFFERENTIAL GENE EXPRESSION (scatter plot)

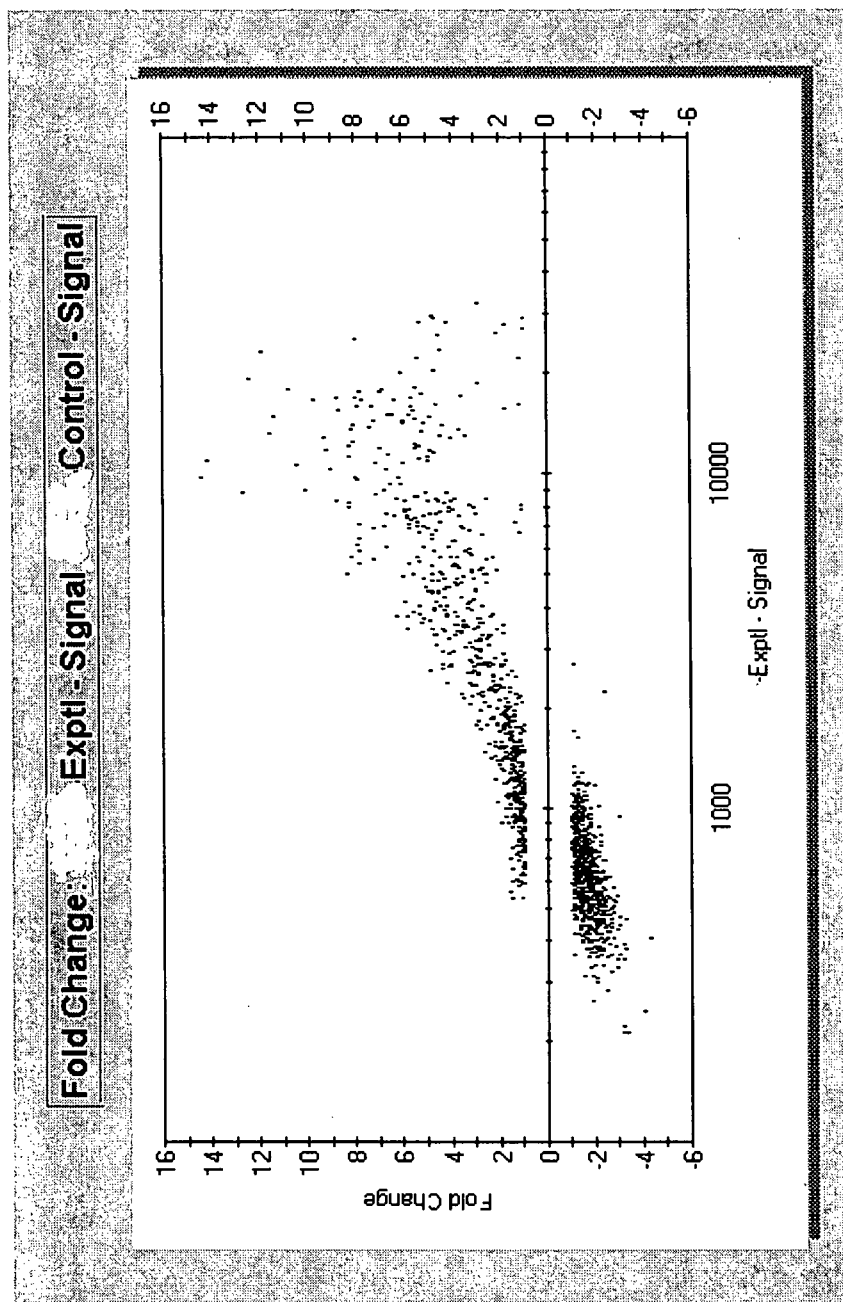


Figure 7.

RESULTS:P2HX12- DIFFERENTIAL GENE EXPRESSION		
Gene		Fold change
• Thioredoxin(anti-oxidant defense system)		14.5
• EST:oe90c01.s1		14.2
• V-maf (oncogene)		12.7
• Prostaglandin synthase		12.5
• Interleukin 6		12.0
• EST:we97d07.x1		11.6
• Ribosomal protein S17		11.4
• Cofilin(actin-depolymerization factor)		10.8
• Annexin A2(early marker of apoptosis)		10.5
• Ubiquitin		10.1
• Ribosomal proteins L13a and large		9.7 and 9.4
• ESTs:602565589F1 and 602340822F1		9.3 and 9.1
• Ras oncogene		8.8
• Ribosomal protein S24		8.8
• Cytochrome p450		8.3
• Thrombomodulin		8.3
• Histone H3.3		8.2
• Eukaryotic translation initiation factor		8.1

Figure 8.

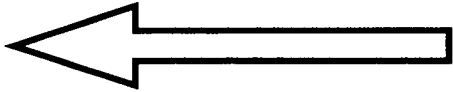
RESULTS:P2HX12- DIFFERENTIAL GENE EXPRESSION

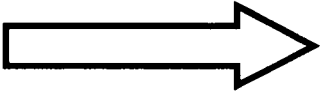
Gene	- Fold change
• Cyritestin (surface protein)	-4.3
• Ankyrin (repeats, protein-protein interaction, RPE)	-4.0
• Zinc finger protein	-3.6
• Leucine-rich repeat containing 2	-3.4
• Cofactor SP-1 transcriptional activation	-3.3
• Serum glucocorticoid regulated kinase 2	-3.2
• EST:wa95d04.x1	-3.1
• H.s. hypothetical protein	-3.1
• Src homolog 3/cysteine rich domain	-3.0
• Homeo box D3	-2.9

Figure 9.

FUNCTIONAL GENOMICS-

P2HX12

- 
- Protein degradation
 - Inflammatory response
 - Ribosomal reconstruction-35/94=37%
 - Translation initiation
 - DNA metabolism-repair/replication
 - ESTs- 41/135=30%

- 
- ESTs-20/118=17%
 - Transcriptional down regulation
 - Cell cycling
 - Protein kinase activity
 - Channel production

Appendix A.

Probe set	Control Signal	Exptl Signal	control vs Exptl Fold Change	Gene Description
216276_s_	1739.6	405.2	-4.29	Consensus includes gb:X89657.1 /DEF=H.sapiens mRNA for cyritestin protein (clone T6). /FEA=mRNA /DB_XR
221232_s_	978.1	245.9	-3.98	gb:Nm_020349.1 /DEF=Homo sapiens ankyrin repeat domain 2 (stretch responsive muscle) (ANKRD2), mRNA.
216279_at	763.9	211.7	-3.61	Consensus includes gb:X78931.1 /DEF=H.sapiens HZF8 mRNA for zinc finger protein. /FEA=mRNA /GEN=HZF
219949_at	730.7	212.6	-3.44	gb:Nm_024512.1 /DEF=Homo sapiens leucine-rich repeat-containing 2 (LRRRC2), mRNA. /FEA=mRNA /GEN=LR
204349_at	730	220.7	-3.31	gb:BC005250.1 /DEF=Homo sapiens, cofactor required for Sp1 transcriptional activation, subunit 9 (33kD), clo
220357_s_	1490.3	462.6	-3.22	gb:Nm_016276.1 /DEF=Homo sapiens serumglucocorticoid regulated kinase 2 (SGK2), mRNA. /FEA=mRNA /G
211804_s_	1216	379.5	-3.2	gb:AB012305.1 /DEF=Homo sapiens mRNA for d-HSCDK2, complete cds. /FEA=CDS /GEN=CDK2deltaT /PROD
203386_at	1097.6	349.3	-3.14	Consensus includes gb:AI650848 /FEA=EST /DB_XREF=gi:4734827 /DB_XREF=est:wa95d04.x1 /CLONE=IMAG
219792_at	1221.7	391.4	-3.12	gb:Nm_024758.1 /DEF=Homo sapiens hypothetical protein FLJ23384 (FLJ23384), mRNA. /FEA=mRNA /GEN=F
205743_at	1086	364.2	-2.98	gb:Nm_003149.1 /DEF=Homo sapiens src homology three (SH3) and cysteine rich domain (STAC), mRNA. /FE
216153_x_	2769.5	932.6	-2.97	Consensus includes gb:AK022897.1 /DEF=Homo sapiens cDNA FLJ12835 fis, clone NT2RP2003165. /FEA=mR
207330_at	1309.6	442.8	-2.96	gb:Nm_002864.1 /DEF=Homo sapiens pregnancy-zone protein (PZP), mRNA. /FEA=mRNA /GEN=PZP /PROD=p
214205_x_	1374.4	468	-2.94	Consensus includes gb:AK022131.1 /DEF=Homo sapiens cDNA FLJ12069 fis, clone HEMBB1002342, highly si
211173_at	1030.5	353.4	-2.92	Consensus includes gb:D85606 /DEF=Homo sapiens gene for cholecystokinin type-A receptor, complete cds
206601_s_	1248.4	429.9	-2.9	gb:BC005124.1 /DEF=Homo sapiens, homeo box D3, clone MGC:10470, mRNA, complete cds. /FEA=mRNA /PR
219923_at	951.5	329.6	-2.89	gb:Nm_025188.1 /DEF=Homo sapiens hypothetical protein FLJ13181 (FLJ13181), mRNA. /FEA=mRNA /GEN=F
221155_x_	1550.5	540.8	-2.87	gb:Nm_018603.1 /DEF=Homo sapiens hypothetical protein PRO1496 (PRO1496), mRNA. /FEA=mRNA /GEN=PR
213387_at	1462.3	521.7	-2.8	Consensus includes gb:AB033066.1 /DEF=Homo sapiens mRNA for KIAA1240 protein, partial cds. /FEA=mRN
222320_at	1055.5	381.5	-2.77	Consensus includes gb:AW970584 /FEA=EST /DB_XREF=gi:8160429 /DB_XREF=est:EST382665 /UG=Hs.29103
219169_s_	1109.9	408.4	-2.72	gb:Nm_016020.1 /DEF=Homo sapiens CGI-75 protein (LOC51106), mRNA. /FEA=mRNA /GEN=LOC51106 /PROD
210714_at	1444.9	530.6	-2.72	gb:BC001217.1 /DEF=Homo sapiens, Similar to KIAA0029 protein, clone MGC:767, mRNA, complete cds. /FEA
207608_x_	1295.1	480.5	-2.7	gb:Nm_000761.2 /DEF=Homo sapiens cytochrome P450, subfamily I (aromatic compound-inducible), polypept
207788_s_	1357.5	504	-2.69	gb:Nm_005775.1 /DEF=Homo sapiens vinexin beta (SH3-containing adaptor molecule-1) (SCAM-1), mRNA. /FE
205953_at	1537.6	572.6	-2.69	gb:Nm_014813.1 /DEF=Homo sapiens KIAA0806 gene product (KIAA0806), mRNA. /FEA=mRNA /GEN=KIAA080
216089_at	954.6	359.5	-2.66	Consensus includes gb:BE877397 /FEA=EST /DB_XREF=gi:10326173 /DB_XREF=est:601485434F1 /CLONE=IM
220699_s_	1224.2	464.2	-2.64	gb:Nm_018517.1 /DEF=Homo sapiens hypothetical protein PRO2214 (PRO2214), mRNA. /FEA=mRNA /GEN=PR
219472_at	848.3	323.4	-2.62	gb:Nm_024322.1 /DEF=Homo sapiens hypothetical protein MGC11266 (MGC11266), mRNA. /FEA=mRNA /GEN=F
220901_at	1135.9	437.5	-2.6	gb:Nm_024980.1 /DEF=Homo sapiens hypothetical protein FLJ12132 (FLJ12132), mRNA. /FEA=mRNA /GEN=F
219195_at	1290.4	495.7	-2.6	gb:Nm_013261.1 /DEF=Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1 (PPA
208365_s_	1173.3	452.6	-2.59	gb:Nm_005307.1 /DEF=Homo sapiens G protein-coupled receptor kinase 2 (Drosophila)-like (GPRK2L), mRNA
219636_s_	1085	421.7	-2.57	gb:Nm_025139.1 /DEF=Homo sapiens hypothetical protein FLJ12584 (FLJ12584), mRNA. /FEA=mRNA /GEN=F
217380_s_	1209.9	473	-2.56	Consensus includes gb:U92992.1 /DEF=Homo sapiens clone DT1P1A11 mRNA, CAG repeat region. /FEA=mRN

200751_s_	1357.2	532.9	-2.55	Consensus includes gb:BE898861 /FEA=EST /DB_XREF=gi:10365758 /DB_XREF=est:601682157F1 /CLONE=IM
204122_at	983.4	387.7	-2.54	gb:NM_003332.1 /DEF=Homo sapiens TYRO protein tyrosine kinase binding protein (TYROBP), mRNA. /FEA=
219501_at	1083.2	426.4	-2.54	gb:NM_017993.1 /DEF=Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA. /FEA=mRNA /GEN=F
220232_at	1565.6	620.5	-2.52	gb:NM_024906.1 /DEF=Homo sapiens hypothetical protein FLJ21032 (FLJ21032), mRNA. /FEA=mRNA /GEN=F
207439_s_	701.3	281.5	-2.49	gb:NM_005660.1 /DEF=Homo sapiens solute carrier family 35 (UDP-galactose transporter), member 2 (SLC35A
211655_at	1187.3	479.2	-2.48	gb:D01059.1 /DEF=Homo sapiens mRNA for immunoglobulin lambda light chain, complete cds. /FEA=mRNA /
214055_x_	887.5	359.1	-2.47	Consensus includes gb:AW238632 /FEA=EST /DB_XREF=gi:6571021 /DB_XREF=est:xp29d03.x1 /CLONE=IMA
215972_at	1191.8	487.3	-2.45	Consensus includes gb:AF070547.1 /DEF=Homo sapiens clone 24820 mRNA sequence. /FEA=mRNA /DB_XRE
214206_at	1336.2	544.8	-2.45	Consensus includes gb:AI739480 /FEA=EST /DB_XREF=gi:5101461 /DB_XREF=est:wi14a12.x1 /CLONE=IMAG
211617_at	1083.5	443.3	-2.44	gb:M21191.1 /DEF=Human aldolase pseudogene mRNA, complete cds. /FEA=mRNA /GEN=ALDOAP2 /DB_XRE
220801_s_	981	406.4	-2.41	gb:NM_016527.1 /DEF=Homo sapiens hydroxyacid oxidase 2 (long chain) (HAO2), mRNA. /FEA=mRNA /GEN=H
210034_s_	1027.8	425.7	-2.41	Consensus includes gb:AA582460 /FEA=EST /DB_XREF=gi:2359820 /DB_XREF=est:nn54e07.s1 /CLONE=IMAG
201886_at	1044.6	435.8	-2.4	gb:NM_025230.1 /DEF=Homo sapiens hypothetical protein PRO2389 (PRO2389), mRNA. /FEA=mRNA /GEN=PRO
219742_at	1180.5	492.9	-2.4	gb:NM_030567.1 /DEF=Homo sapiens hypothetical protein MGC10772 (MGC10772), mRNA. /FEA=mRNA /GEN=
205514_at	956.7	402.2	-2.38	gb:NM_018355.1 /DEF=Homo sapiens hypothetical protein FLJ11191 (FLJ11191), mRNA. /FEA=mRNA /GEN=F
214091_s_	1655.4	695.7	-2.38	Consensus includes gb:AW149846 /FEA=EST /DB_XREF=gi:6197742 /DB_XREF=est:xf42h12.x1 /CLONE=IMAG
206323_x_	535.8	2248.8	-2.38	gb:NM_002547.1 /DEF=Homo sapiens oligophrenin 1 (OPHN1), mRNA. /FEA=mRNA /GEN=OPHN1 /PROD=olig
208939_at	1250.6	530.6	-2.36	Consensus includes gb:AV682679 /FEA=EST /DB_XREF=gi:10284542 /DB_XREF=est:AV682679 /CLONE=GKB
221262_s_	1118.4	476.4	-2.35	gb:NM_030807.1 /DEF=Homo sapiens glucose transporter protein 10 (GLUT10), mRNA. /FEA=mRNA /GEN=GL
209320_at	1215.6	516.2	-2.35	gb:AF033861.1 /DEF=Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds. /FEA=mRNA /GEN=
206285_at	1319.1	565.4	-2.33	gb:NM_000272.1 /DEF=Homo sapiens nephronophthisis 1 (juvenile) (NPHP1), mRNA. /FEA=mRNA /GEN=NPHP
211004_s_	1421.3	610.3	-2.33	gb:BC002553.1 /DEF=Homo sapiens, Similar to aldehyde dehydrogenase 7, clone MGC:1805, mRNA, complete
214222_at	1429	613.9	-2.33	Consensus includes gb:AB023161.1 /DEF=Homo sapiens mRNA for KIAA0944 protein, partial cds. /FEA=mRN
205708_s_	1172	504.8	-2.32	Consensus includes gb:AI051254 /FEA=EST /DB_XREF=gi:3306788 /DB_XREF=est:oy49e07.x1 /CLONE=IMAG
202601_s_	1046	452.1	-2.31	Consensus includes gb:AI373539 /FEA=EST /DB_XREF=gi:4153405 /DB_XREF=est:qz46h02.x1 /CLONE=IMAG
207034_s_	1124.4	486	-2.31	gb:NM_030379.1 /DEF=Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 1, mRNA. /FE
207426_s_	853.5	370.6	-2.3	gb:NM_003326.1 /DEF=Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptona
221301_at	1145.6	503	-2.28	gb:NM_025258.1 /DEF=Homo sapiens NG37 protein (G7C), mRNA. /FEA=CDS /GEN=G7C /PROD=NG37 protein
201785_at	1161.1	509.2	-2.28	gb:NM_002933.1 /DEF=Homo sapiens RNase A family, 1 (pancreatic) (RNASE1), mRNA. /FEA=m
220409_at	1169.9	512.4	-2.28	gb:NM_018627.1 /DEF=Homo sapiens hypothetical protein PRO2405 (PRO2405), mRNA. /FEA=mRNA /GEN=PR
217715_x_	1208.7	532.3	-2.27	Consensus includes gb:BE045142 /FEA=EST /DB_XREF=gi:8362195 /DB_XREF=est:hn26h02.x1 /CLONE=IMAG
206773_at	894.8	396.8	-2.26	gb:NM_002347.1 /DEF=Homo sapiens lymphocyte antigen 6 complex, locus H (LY6H), mRNA. /FEA=mRNA /GE
210912_x_	1295.3	573.7	-2.26	gb:M99422.1 /DEF=Homo sapiens glutathione transferase (GST) mRNA, complete cds. /FEA=mRNA /GEN=GST
211619_s_	1449.8	640.8	-2.26	gb:M13077.1 /DEF=Human placental alkaline phosphatase mRNA, complete cds., /FEA=mRNA /GEN=ALPP /PR
206704_at	755.7	336.1	-2.25	gb:NM_000084.1 /DEF=Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5), m

210918_at	1424.7	633.3	-2.25	gb:AF130075.1 /DEF=Homo sapiens clone FLB9413 PRO2532 mRNA, complete cds. /FEA=mRNA /PROD=PRO
203077_s_s	840.6	375.9	-2.24	gb:NM_005901.1 /DEF=Homo sapiens MAD (mothers against decapentaplegic, Drosophila) homolog 2 (MADH2
218068_s_s	1038	464.3	-2.24	gb:NM_024836.1 /DEF=Homo sapiens hypothetical protein FLJ22301 (FLJ22301), mRNA. /FEA=mRNA /GEN=F
209347_s_s	1024.4	458.9	-2.23	Consensus includes gb:BF508646 /FEA=EST /DB_XREF=gi:11591944 /DB_XREF=est:UI-H-BI4-aop-b-03-0-UI.s1
204063_s_s	1069.7	479.2	-2.23	gb:NM_014683.1 /DEF=Homo sapiens KIAA0623 gene product (KIAA0623), mRNA. /FEA=mRNA /GEN=KIAA062
208020_s_s	1554.2	695.4	-2.23	gb:NM_000719.1 /DEF=Homo sapiens calcium channel, voltage-dependent, L type, alpha 1C subunit (CACNA1
51774_s_a	1774.1	795	-2.23	Cluster Incl. AW014299:UI-H-BI0p-aax-a-07-0-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2710573 /clone_
203685_at	998.4	450.4	-2.22	gb:NM_000633.1 /DEF=Homo sapiens B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial pr
215363_x_x	1135.2	511.8	-2.22	Consensus includes gb:AW168915 /FEA=EST /DB_XREF=gi:6400440 /DB_XREF=est:xj15b10.x1 /CLONE=IMAG
215300_s_s	797.4	360.1	-2.21	Consensus includes gb:AK022172.1 /DEF=Homo sapiens cDNA FLJ12110 fis, clone MAMMA1000020, highly s
213960_at	1110.5	502.9	-2.21	Consensus includes gb:T87225 /FEA=EST /DB_XREF=gi:715577 /DB_XREF=est:yc81f06.s1 /CLONE=IMAGE:22
202733_at	1218.1	552.1	-2.21	gb:NM_004199.1 /DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylas
823_at	1014.3	460.8	-2.2	U84487 /FEATURE= /DEFINITION=HSU84487 Human CX3C chemokine precursor, mRNA, alternatively spliced,
217097_s_s	1073.4	490.4	-2.19	Consensus includes gb:AC004990 /DEF=Homo sapiens PAC clone RP5-118517 from 7q11.23-q21 /FEA=CDS_1
208714_at	1694.6	772.7	-2.19	gb:AF092131.1 /DEF=Homo sapiens 51kDa subunit of NADH dehydrogenase mRNA, complete cds. /FEA=mRN
204718_at	907.9	415.8	-2.18	gb:NM_004445.1 /DEF=Homo sapiens EphB6 (EPHB6) mRNA. /FEA=mRNA /GEN=EPHB6 /PROD=EphB6 /DB_X
205235_s_s	1038.9	477.5	-2.18	gb:NM_016195.1 /DEF=Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA. /FEA=mRNA /GEN=MP
219980_at	876.9	403.9	-2.17	gb:NM_025097.1 /DEF=Homo sapiens hypothetical protein FLJ21106 (FLJ21106), mRNA. /FEA=mRNA /GEN=F
212951_at	976.5	449.1	-2.17	Consensus includes gb:N95226 /FEA=EST /DB_XREF=gi:1267507 /DB_XREF=est:zb53f09.s1 /CLONE=IMAGE:
204473_s_s	976.9	449.6	-2.17	gb:NM_014630.1 /DEF=Homo sapiens KIAA0211 gene product (KIAA0211), mRNA. /FEA=mRNA /GEN=KIAA021
32209_at	1173.4	540.8	-2.17	Cluster Incl. AF052151: Homo sapiens clone 24574 mRNA sequence /cds=UNKNOWN /gb=AF052151 /gi=33604
212144_at	1388.5	638.9	-2.17	Consensus includes gb:AL021707 /DEF=Human DNA sequence from clone RP3-508115 on chromosome 22q12
208096_s_s	997.4	461.7	-2.16	gb:NM_030820.1 /DEF=Homo sapiens hypothetical protein DKFZp564B052 (DKFZp564B052), mRNA. /FEA=mR
214349_at	1311.6	606.3	-2.16	Consensus includes gb:AV764378 /FEA=EST /DB_XREF=gi:10922226 /DB_XREF=est:AV764378 /CLONE=MDS
215218_s_s	1794.3	829.5	-2.16	Consensus includes gb:AC004144 /DEF=Homo sapiens chromosome 19, overlapping cosmid R28707 and R3
216227_at	976.1	455	-2.15	Consensus includes gb:X81001.1 /DEF=H.sapiens HCG II mRNA. /FEA=mRNA /DB_XREF=gi:531407 /UG=Hs.6
211795_s_s	1128.2	523.8	-2.15	gb:AF198052.1 /DEF=Homo sapiens EVH1 domain binding protein mRNA, complete cds. /FEA=CDS /PROD=EV
220059_at	1200.8	557.7	-2.15	gb:NM_012108.1 /DEF=Homo sapiens BCR downstream signaling 1 (BRDG1), mRNA. /FEA=mRNA /GEN=BRDG
221597_s_s	1262.2	588.4	-2.15	gb:BC003080.1 /DEF=Homo sapiens, Similar to HSPC171 protein, clone MGC:770, mRNA, complete cds. /FEA
215604_x_x	1285	596.5	-2.15	Consensus includes gb:AK023783.1 /DEF=Homo sapiens cDNA FLJ13721 fis, clone PLACE2000450. /FEA=mR
203735_x_x	1863.3	870.9	-2.14	Consensus includes gb:N35896 /FEA=EST /DB_XREF=gi:1157038 /DB_XREF=est:yy28c08.s1 /CLONE=IMAGE:
215801_at	967.3	453.3	-2.13	Consensus includes gb:AL133604.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434G1615 (from clone DKFZp43
213679_at	785.2	370.7	-2.12	Consensus includes gb:AL049329.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564G196 (from clone DKFZp564
206112_at	806	380.5	-2.12	gb:NM_019644.1 /DEF=Homo sapiens testis-specific ankyrin motif containing protein (LOC56311), mRNA. /FE
205351_at	1036.3	489.2	-2.12	gb:NM_000821.1 /DEF=Homo sapiens gamma-glutamyl carboxylase (GGCX), mRNA. /FEA=mRNA /GEN=GGCX

217203_at	1096.9	516.5	-2.12	Consensus includes gb:U08626 /DEF=Human glutamine synthetase pseudogene /FEA=CDS /DB_XREF=gi:551
217012_at	812.5	385.3	-2.11	Consensus includes gb:AL080233.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L111 (from clone DKFZp586
220927_s_	941.3	446	-2.11	gb:NM_021828.1 /DEF=Homo sapiens heparanase-like protein (HPA2), mRNA. /FEA=mRNA /GEN=HPA2 /PROD
221925_s_	1143	543.4	-2.1	Consensus includes gb:BE044503 /FEA=EST /DB_XREF=gi:8361556 /DB_XREF=est:ho46d12.x1 /CLONE=IMAG
206434_at	1276	611.5	-2.09	gb:NM_016950.1 /DEF=Homo sapiens testican 3 (HSAJ1454), mRNA. /FEA=mRNA /GEN=HSAJ1454 /PROD=tes
213914_s_	964.6	465.1	-2.07	Consensus includes gb:R85779 /FEA=EST /DB_XREF=gi:944185 /DB_XREF=est:yq23f07.s1 /CLONE=IMAGE:2
207804_s_	1474.2	712.7	-2.07	gb:NM_004108.1 /DEF=Homo sapiens ficolin (collagenfibrinogen domain-containing lectin) 2 (hucolin) (FCN2),
206839_at	1527.6	737	-2.07	gb:NM_015370.1 /DEF=Homo sapiens hypothetical protein (HS747E2A), mRNA. /FEA=mRNA /GEN=HS747E2A
44563_at	2086.5	1010.1	-2.07	Cluster Incl. AI858000:wj69b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2408049 /clone_end=3 /gb=AI85
218426_s_	1045.6	506.7	-2.06	gb:NM_019011.1 /DEF=Homo sapiens TRIAD3 protein (TRIAD3), mRNA. /FEA=mRNA /GEN=TRIAD3 /PROD=TR
212878_s_	1230	595.8	-2.06	Consensus includes gb:AA284075 /FEA=EST /DB_XREF=gi:1928356 /DB_XREF=est:zs49b01.s1 /CLONE=IMAG
204347_at	1318.9	639.9	-2.06	Consensus includes gb:AI653169 /FEA=EST /DB_XREF=gi:4737148 /DB_XREF=est:wb43g08.x1 /CLONE=IMAG
212382_at	1100.3	537.6	-2.05	Consensus includes gb:BF433429 /FEA=EST /DB_XREF=gi:11445592 /DB_XREF=est:7q53a12.x1 /CLONE=IMA
205355_at	925.3	453.1	-2.04	gb:NM_001609.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, shortbranched chain (ACADSB), nuc
218220_at	985.4	482.8	-2.04	gb:NM_021640.1 /DEF=Homo sapiens MYG1 protein (MYG1), mRNA. /FEA=mRNA /GEN=MYG1 /PROD=MYG1 p
222187_x_	1492.1	729.9	-2.04	Consensus includes gb:X78262.1 /DEF=H.sapiens mRNA for TRE5. /FEA=mRNA /DB_XREF=gi:587440 /UG=Hs
208002_s_	895.3	440.8	-2.03	gb:NM_007274.1 /DEF=Homo sapiens cytosolic acyl coenzyme A thioester hydrolase (HBACH), mRNA. /FEA=
33646_g_a	906.1	445.8	-2.03	Cluster Incl. X61094:H.sapiens RNA for GM2-activator protein (clone pGM2A) /cbs=(0,312) /gb=X61094 /gi=318
216997_x_	1342.9	660.6	-2.03	Consensus includes gb:AL358975 /DEF=Human DNA sequence from clone RP11-375O18 on chromosome 9 C
204918_s_	608.1	300.6	-2.02	gb:NM_004529.1 /DEF=Homo sapiens myeloidlymphoid or mixed-lineage leukemia (trithorax (Drosophila) hom
216025_x_	720.5	356.3	-2.02	Consensus includes gb:M21940.1 /DEF=Human cytochrome P-450 S-mephenytoin 4-hydroxylase (P-450mp) m
202959_at	1058.4	524.1	-2.02	Consensus includes gb:AI433712 /FEA=EST /DB_XREF=gi:4291098 /DB_XREF=est:ti88f08.x1 /CLONE=IMAGE
217573_at	770.8	383.9	-2.01	Consensus includes gb:AW138468 /FEA=EST /DB_XREF=gi:6142786 /DB_XREF=est:UI-H-BI1-adg-f-01-0-UI.s1
208022_s_	802	400	-2.01	gb:NM_003671.1 /DEF=Homo sapiens CDC14 (cell division cycle 14, S. cerevisiae) homolog B (CDC14B), mRN
217386_at	877.6	437.5	-2.01	Consensus includes gb:AL109953 /DEF=Human DNA sequence from clone RP4-746H2 on chromosome 20. Co
201715_s_	1032.5	513.3	-2.01	gb:NM_014977.1 /DEF=Homo sapiens KIAA0670 proteinacinus (KIAA0670), mRNA. /FEA=mRNA /GEN=KIAA06
204983_s_	1067.3	531.5	-2.01	gb:AF064826.1 /DEF=Homo sapiens glypican 4 (GPC4) mRNA, complete cds. /FEA=mRNA /GEN=GPC4 /PROD
215468_at	1089.8	541.4	-2.01	Consensus includes gb:AK001442.1 /DEF=Homo sapiens cDNA FLJ10580 fis, clone NT2RP2003533. /FEA=mR
209733_at	1126.6	561.4	-2.01	Consensus includes gb:AL034399 /DEF=Human DNA sequence from clone 191P20 on chromosome Xq23. Con
221745_at	1206.3	602.2	-2	Consensus includes gb:BE538424 /FEA=EST /DB_XREF=gi:9767069 /DB_XREF=est:601068256F1 /CLONE=IMA
209977_at	747.9	376.2	-1.99	gb:M74220.1 /DEF=Human plasminogen mRNA, complete cds. /FEA=mRNA /PROD=plasminogen /DB_XREF=g
204181_s_	832	417.4	-1.99	Consensus includes gb:T90308 /FEA=EST /DB_XREF=gi:718821 /DB_XREF=est:ye16a03.s1 /CLONE=IMAGE:1
219982_s_	892	448.8	-1.99	gb:NM_022978.1 /DEF=Homo sapiens small EDRK-rich factor 1B (centromeric) (SERF1B), mRNA. /FEA=mRNA
204362_at	997.8	500.8	-1.99	gb:NM_003930.1 /DEF=Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA. /FEA=mRNA /GEN=SKAP-HO
207466_at	1022.2	514.6	-1.99	gb:NM_015973.1 /DEF=Homo sapiens galanin-related peptide (LOC51083), mRNA. /FEA=mRNA /GEN=LOC510

214561_at	609.3	307.7	-1.98	Consensus includes gb:NM_024317.1 /DEF=Homo sapiens immunoglobulin-like transcript 10 (ILT10), mRNA. /
209719_x_	871.8	440.9	-1.98	gb:U19556.1 /DEF=Human squamous cell carcinoma antigen 1 (SCCA1) mRNA, complete cds. /FEA=mRNA /G
209199_s_	888.9	447.9	-1.98	Consensus includes gb:N22468 /FEA=EST /DB_XREF=gi:1128602 /DB_XREF=est:yw34e10.s1 /CLONE=IMAGE
204270_at	985.4	498.5	-1.98	Consensus includes gb:A1568728 /FEA=EST /DB_XREF=gi:4532102 /DB_XREF=est:th15a06.x1 /CLONE=IMAGE
204429_s_	1098.5	553.5	-1.98	Consensus includes gb:BE560461 /FEA=EST /DB_XREF=gi:9804181 /DB_XREF=est:601346729F1 /CLONE=IMA
218206_x_	1286.1	648.6	-1.98	gb:NM_016558.1 /DEF=Homo sapiens SCAN domain-containing 1 (SCAND1), mRNA. /FEA=mRNA /GEN=SCAN
215581_s_	942.6	478.5	-1.97	Consensus includes gb:AK022303.1 /DEF=Homo sapiens cDNA FLJ12241 fis, clone MAMMA1001274. /FEA=m
219504_s_	1168.5	594.4	-1.97	gb:NM_024813.1 /DEF=Homo sapiens hypothetical protein FLJ13150 (FLJ13150), mRNA. /FEA=mRNA /GEN=F
632_at	1226.8	621.9	-1.97	L40027 /FEATURE=mRNA /DEFINITION=HUMGLYSYN Homo sapiens glycogen synthase kinase 3 mRNA, com
217070_at	1253.4	637.1	-1.97	Consensus includes gb:AJ249275 /DEF=Homo sapiens partial MTHFR gene for methylenetetrahydrofolate red
215525_at	840.7	428	-1.96	Consensus includes gb:AL050185.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586A0423 (from clone DKFZp58
202990_at	1059.5	541.4	-1.96	gb:NM_002863.1 /DEF=Homo sapiens phosphatase, glycogen; liver (Hers disease, glycogen storage disease
215587_x_	1083.3	553.4	-1.96	Consensus includes gb:AK023891.1 /DEF=Homo sapiens cDNA FLJ13829 fis, clone THYRO1000625. /FEA=mR
222217_s_	1243	635.7	-1.96	Consensus includes gb:BC003654.1 /DEF=Homo sapiens, Similar to hypothetical protein MGC4365, clone IMA
217236_x_	1462.1	747.8	-1.96	Consensus includes gb:S74639.1 /DEF=lg VH4=lg heavy chain variable region {clone C20} human, systemic lu
216005_at	658.2	337.7	-1.95	Consensus includes gb:BF434846 /FEA=EST /DB_XREF=gi:11447134 /DB_XREF=est:7o74d07.x1 /CLONE=IMA
206433_s_	887.7	455.7	-1.95	gb:BC000460.1 /DEF=Homo sapiens, Similar to testican 3, clone MGC:8506, mRNA, complete cds. /FEA=mRN
203970_s_	1006.3	515	-1.95	gb:NM_003630.1 /DEF=Homo sapiens peroxisomal biogenesis factor 3 (PEX3), mRNA. /FEA=mRNA /GEN=PEX
210869_s_	1312.6	672.6	-1.95	gb:M29277.1 /DEF=Human aberrant (short) epidermal growth factor receptor mRNA (3 variant), complete cds. /FEA=mRNA /PR
211551_at	1363.1	700.1	-1.95	gb:K03193.1 /DEF=Human aberrant (short) epidermal growth factor receptor mRNA, complete cds. /FEA=mRN
206855_s_	1082.6	558.2	-1.94	gb:NM_003773.1 /DEF=Homo sapiens hyaluronoglucosaminidase 2 (HYAL2), mRNA. /FEA=mRNA /GEN=HYAL
210935_s_	1191.9	615.6	-1.94	gb:AF274954.1 /DEF=Homo sapiens PNAS-29 mRNA, complete cds. /FEA=mRNA /PROD=PNAS-29 /DB_XREF=
51200_at	1442.9	743	-1.94	Cluster Incl. A1744084:wc36b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2317233 /clone_end=3 /gb=A174
218055_s_	711.1	367.7	-1.93	gb:NM_018268.1 /DEF=Homo sapiens hypothetical protein FLJ10904 (FLJ10904), mRNA. /FEA=mRNA /GEN=F
205282_at	933.2	482.4	-1.93	gb:NM_004631.1 /DEF=Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e rece
208582_s_	735.2	382.6	-1.92	gb:NM_012148.1 /DEF=Homo sapiens double homeobox, 3 (DUX3), mRNA. /FEA=CDS /GEN=DUX3 /PROD=dou
222209_s_	815.8	424.7	-1.92	Consensus includes gb:AK000684.1 /DEF=Homo sapiens cDNA FLJ20677 fis, clone KAIA4183. /FEA=mRNA /D
207251_at	882.1	459.5	-1.92	gb:NM_005925.1 /DEF=Homo sapiens meprin A, beta (MEP1B), mRNA. /FEA=mRNA /GEN=MEP1B /PROD=mep
207593_at	1050.6	545.8	-1.92	gb:NM_022169.1 /DEF=Homo sapiens putative ABC transporter (WHITE2), mRNA. /FEA=mRNA /GEN=WHITE2
208176_at	1161.2	605.4	-1.92	gb:NM_012146.1 /DEF=Homo sapiens double homeobox, 1 (DUX1), mRNA. /FEA=mRNA /GEN=DUX1 /PROD=d
205132_at	1227	640.5	-1.92	gb:NM_005159.2 /DEF=Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA. /FEA=mRNA /GEN=ACTC /P
220725_x_	2247.2	1172.1	-1.92	gb:NM_025095.1 /DEF=Homo sapiens hypothetical protein FLJ23558 (FLJ23558), mRNA. /FEA=mRNA /GEN=F
202101_s_	1051	550.7	-1.91	gb:NM_002881.1 /DEF=Homo sapiens v-ral simian leukemia viral oncogene homolog B (ras related; GTP bindi
210786_s_	1135	594	-1.91	gb:M93255.1 /DEF=Human FLI-1 mRNA, complete cds for two alternate splicings. /FEA=mRNA /GEN=FLI-1; FL
213319_s_	764.3	402.9	-1.9	Consensus includes gb:AW170359 /FEA=EST /DB_XREF=gi:6401884 /DB_XREF=est:xn60c12.x1 /CLONE=IMA

207755_at	823.9	433.5	-1.9	gb:NM_025017.1 /DEF=Homo sapiens hypothetical protein FLJ13892 (FLJ13892), mRNA. /FEA=mRNA /GEN=F
208797_s_	922.3	484.7	-1.9	Consensus includes gb:AI829170 /FEA=EST /DB_XREF=gi:5449841 /DB_XREF=est:wk76b03.x1 /CLONE=IMAG
204816_s_	1024.7	538.5	-1.9	gb:NM_014681.1 /DEF=Homo sapiens KIAA0134 gene product (KIAA0134), mRNA. /FEA=mRNA /GEN=KIAA013
210882_s_	1210.7	637.2	-1.9	gb:U04811.1 /DEF=Human trophinin mRNA, complete cds. /FEA=mRNA /PROD=trophinin /DB_XREF=gi:90535
210799_at	1227.3	646.8	-1.9	gb:M81590.1 /DEF=Homo sapiens serotonin 1D receptor (5-HT1D~) mRNA, complete cds. /FEA=mRNA /GEN=5
204781_s_	1002.5	530.5	-1.89	gb:NM_000043.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRN
215766_at	1073.5	569.3	-1.89	Consensus includes gb:AL096729.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D044 (from clone DKFZp434
58900_at	1537.6	813.7	-1.89	Cluster Incl. AW025284:wu95h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990806 /clone_end=3 /gb=AW
50314_i_at	1090	581.1	-1.88	Cluster Incl. AI761506:wi61b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394717 /clone_end=3 /gb=AI76
211159_s_	1167.3	622.2	-1.88	gb:AB000635.1 /DEF=Homo sapiens mRNA for protein phosphatase 2A delta (B) regulatory subunit, delta3 iso
201974_s_	943.2	504.6	-1.87	gb:NM_015622.1 /DEF=Homo sapiens CGI-43 protein (LOC51622), mRNA. /FEA=mRNA /GEN=LOC51622 /PROD
213384_x_	1238.2	663.2	-1.87	Consensus includes gb:Z37544 /DEF=H.sapiens gene for phospholipase C beta 3, exon 1 /FEA=mRNA /DB_XR
217560_at	1253.5	669.9	-1.87	Consensus includes gb:AI879383 /FEA=EST /DB_XREF=gi:5553432 /DB_XREF=est:au50b05.x1 /CLONE=IMAG
216301_at	1481.8	791.3	-1.87	Consensus includes gb:AW405975 /FEA=EST /DB_XREF=gi:6925032 /DB_XREF=est:UI-HF-BL0-acv-a-05-0-JI.r
213130_at	859.4	461.7	-1.86	Consensus includes gb:AB032967.1 /DEF=Homo sapiens mRNA for KIAA1141 protein, partial cds. /FEA=mRNA
211918_x_	1286.1	692.9	-1.86	gb:AF311940.1 /DEF=Homo sapiens pregnancy-associated plasma preproprotein-A2 mRNA, complete cds. /F
210436_at	1359	731.2	-1.86	gb:BC005220.1 /DEF=Homo sapiens, Similar to chaperonin containing TCP1, subunit 8 (theta), clone MGC:122
202102_s_	982.2	529.8	-1.85	Consensus includes gb:BF718610 /FEA=EST /DB_XREF=gi:12019523 /DB_XREF=est:KEST81 /CLONE=S90413
64900_at	1195.2	646.9	-1.85	Cluster Incl. AA401703:zt60f09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-726761 /clone_end=5 /gb=AA401
210704_at	1269.4	685	-1.85	gb:L17328.1 /DEF=Human pre-TNK cell associated protein (3CI) mRNA, complete cds. /FEA=mRNA /GEN=3CI
204567_s_	576.3	313.9	-1.84	gb:NM_004915.2 /DEF=Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transc
205430_at	793.1	431.3	-1.84	Consensus includes gb:AL133386 /DEF=Human DNA sequence from clone RP1-181C24 on chromosome 6p11
218143_s_	1056	572.9	-1.84	gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FEA=mRNA /G
206993_at	1060.6	577.7	-1.84	gb:NM_015684.1 /DEF=Homo sapiens hypothetical protein (HSU79253), mRNA. /FEA=mRNA /GEN=HSU79253
211303_x_	478.9	262	-1.83	gb:AF261715.1 /DEF=Homo sapiens prostate-specific membrane antigen-like protein (PSMALGCP III) mRNA, c
211632_at	991.4	542	-1.83	gb:L34163.1 /DEF=Human Ig rearranged gamma-3 chain gene VH4-Dm1Dxp1-JH3 region, complete cds., polyr
206133_at	1086.3	594.1	-1.83	gb:NM_017523.1 /DEF=Homo sapiens XIAP associated factor-1 (HSXIAPAF1), mRNA. /FEA=mRNA /GEN=HSXI
212884_x_	1163.3	637	-1.83	Consensus includes gb:AI358867 /FEA=EST /DB_XREF=gi:4110488 /DB_XREF=est:qy24a09.x1 /CLONE=IMAG
205887_x_	1218.8	664.6	-1.83	gb:NM_002439.1 /DEF=Homo sapiens mutS (E. coli) homolog 3 (MSH3), mRNA. /FEA=mRNA /GEN=MSH3 /PRO
206368_at	1064.9	585.7	-1.82	gb:NM_006650.1 /DEF=Homo sapiens complexin 2 (CPLX2), mRNA. /FEA=mRNA /GEN=CPLX2 /PROD=comple
211722_s_	1124.1	616.8	-1.82	gb:BC005872.1 /DEF=Homo sapiens, clone MGC:4255, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (p
206477_s_	1240.7	682	-1.82	gb:NM_002516.1 /DEF=Homo sapiens neuro-oncological ventral antigen 2 (NOVA2), mRNA. /FEA=mRNA /GEN
218144_s_	1244	682	-1.82	gb:NM_022489.1 /DEF=Homo sapiens hypothetical protein FLJ22056 (FLJ22056), mRNA. /FEA=mRNA /GEN=F
220486_x_	1500.5	824.9	-1.82	gb:NM_017698.1 /DEF=Homo sapiens hypothetical protein FLJ20173 (FLJ20173), mRNA. /FEA=mRNA /GEN=F
206431_x_	1157	639.5	-1.81	gb:NM_015043.1 /DEF=Homo sapiens KIAA0676 protein (KIAA0676), mRNA. /FEA=mRNA /GEN=KIAA0676 /PR

212719_at	1270.8	701.5	-1.81	Consensus includes gb:AB011178.1 /DEF=Homo sapiens mRNA for KIAA0606 protein, partial cds. /FEA=mRNA
216070_at	658.6	366.5	-1.8	Consensus includes gb:AL049331.1 /DEF=Homo sapiens mRNA; cDNA DKFZp5641066 (from clone DKFZp5641
215203_at	1129.4	628.1	-1.8	Consensus includes gb:AW438464 /FEA=EST /DB_XREF=gi:6973770 /DB_XREF=est:xu43g07.x1 /CLONE=IMA
91682_at	1355.9	755.3	-1.8	Cluster Incl. AI571298:tn44e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2170492 /clone_end=3 /gb=AI571
202233_s_	1186.3	2141.1	1.8	gb:Nm_006004.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase hinge protein (UQCRH), mRNA. /FEA
210648_x_	1553.1	2795.5	1.8	gb:AB047360.1 /DEF=Homo sapiens SNX 3A mRNA for sorting nexin 3A, complete cds. /FEA=mRNA /GEN=SN
211943_x_	8723.1	15678.9	1.8	Consensus includes gb:AL565449 /FEA=EST /DB_XREF=gi:12916836 /DB_XREF=est:AL565449 /CLONE=CS0D
212590_at	656.1	1189	1.81	Consensus includes gb:AI431643 /FEA=EST /DB_XREF=gi:4304619 /DB_XREF=est:tg74f12.x1 /CLONE=IMAGE
202427_s_	927.5	1675.2	1.81	gb:Nm_015415.1 /DEF=Homo sapiens DKFZP564B167 protein (DKFZP564B167), mRNA. /FEA=mRNA /GEN=DK
213923_at	787.5	1433.7	1.82	Consensus includes gb:AW005535 /FEA=EST /DB_XREF=gi:5854313 /DB_XREF=est:wz87d04.x1 /CLONE=IMA
206792_x_	806.6	1471.9	1.82	gb:Nm_000923.1 /DEF=Homo sapiens phosphodiesterase 4C, cAMP-specific (dunce (Drosophila))-homolog ph
211097_s_	513.4	937.5	1.83	gb:BC003111.1 /DEF=Homo sapiens, Similar to pre-B-cell leukemia transcription factor 2, clone MGC:2174, mR
212038_s_	779.3	1424.6	1.83	Consensus includes gb:AL515918 /FEA=EST /DB_XREF=gi:12779411 /DB_XREF=est:AL515918 /CLONE=CS0D
221675_s_	760.4	1399.9	1.84	gb:AF195624.1 /DEF=Homo sapiens cholinephosphotransferase 1 beta mRNA, complete cds. /FEA=mRNA /PR
210825_s_	823.8	1519.4	1.84	gb:AF130103.1 /DEF=Homo sapiens clone FLB2914 PRO0720 mRNA, complete cds. /FEA=mRNA /PROD=PRO
201999_s_	1064.1	1954.2	1.84	gb:Nm_006519.1 /DEF=Homo sapiens t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA. /FEA=
222162_s_	929.9	1730.8	1.86	Consensus includes gb:AK023795.1 /DEF=Homo sapiens cDNA FLJ13733 fis, clone PLACE3000147, highly sim
203304_at	1039	1940.3	1.87	gb:Nm_012342.1 /DEF=Homo sapiens putative transmembrane protein (NMA), mRNA. /FEA=mRNA /GEN=NMA
201778_s_	1234	2309.3	1.87	gb:Nm_014774.1 /DEF=Homo sapiens KIAA0494 gene product (KIAA0494), mRNA. /FEA=mRNA /GEN=KIAA049
213249_at	632.6	1188.3	1.88	Consensus includes gb:AU145127 /FEA=EST /DB_XREF=gi:11006648 /DB_XREF=est:AU145127 /CLONE=HEM
204237_at	933.5	1758	1.88	gb:Nm_016315.1 /DEF=Homo sapiens CED-6 protein (CED-6), mRNA. /FEA=mRNA /GEN=CED-6 /PROD=CED-6
212646_at	1433.8	2689.7	1.88	Consensus includes gb:D42043.1 /DEF=Human mRNA for KIAA0084 gene, partial cds. /FEA=mRNA /GEN=KIA
203107_x_	1788.4	3364.9	1.88	gb:Nm_002952.1 /DEF=Homo sapiens ribosomal protein S2 (RPS2), mRNA. /FEA=mRNA /GEN=RPS2 /PROD=r
201893_x_	677	1281.9	1.89	Consensus includes gb:AF138300.1 /DEF=Homo sapiens decorin variant A mRNA, complete cds. /FEA=CDS /P
202464_s_	1867.4	3546	1.9	gb:Nm_004566.1 /DEF=Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 (PFKFB3), mRN
218696_at	617.6	1179.2	1.91	gb:Nm_004836.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRN
220939_s_	920.8	1766.9	1.92	gb:Nm_017743.1 /DEF=Homo sapiens hypothetical protein FLJ20283 (FLJ20283), mRNA. /FEA=mRNA /GEN=F
212581_x_	1506.2	2892.4	1.92	Consensus includes gb:BE561479 /FEA=EST /DB_XREF=gi:9805199 /DB_XREF=est:601346543F1 /CLONE=IMA
211937_at	675.9	1307.2	1.93	Consensus includes gb:Nm_001417.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), m
201586_s_	981.5	1896.7	1.93	gb:Nm_005066.1 /DEF=Homo sapiens splicing factor prolineglutamine rich (polypyrimidine tract-binding prote
212352_s_	1248.4	2433.5	1.95	Consensus includes gb:BE780075 /FEA=EST /DB_XREF=gi:10201273 /DB_XREF=est:601469954F1 /CLONE=IM
201225_s_	704	1388.7	1.97	gb:Nm_005839.1 /DEF=Homo sapiens SerArg-related nuclear matrix protein (plenty of prolines 101-like) (SRM1
201486_at	456.8	904.5	1.98	gb:Nm_002902.1 /DEF=Homo sapiens reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA. /FEA
212533_at	771.3	1527.6	1.98	Consensus includes gb:X62048.1 /DEF=H.sapiens Wee1 hu gene. /FEA=mRNA /GEN=Wee1 Hu /DB_XREF=gi:4
202466_at	1362.4	2693.3	1.98	gb:Nm_006999.2 /DEF=Homo sapiens topoisomerase-related function protein 4-1 (TRF4), mRNA. /FEA=mRNA

202077_at	1338.5	2670.1	1.99	gb:NM_005003.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1, alpha beta subcomplex, 1 (8kD, SD
208944_at	786.9	1571.8	2	gb:D50683.1 /DEF=Homo sapiens mRNA for TGF-beta1IR alpha, complete cds. /FEA=mRNA /PROD=TGF-beta1
217819_at	1143.2	2298	2.01	gb:NM_016099.1 /DEF=Homo sapiens HSPC041 protein (LOC51125), mRNA. /FEA=mRNA /GEN=LOC51125 /PR
200839_s_	1148.6	2318.2	2.02	gb:NM_001908.1 /DEF=Homo sapiens cathepsin B (CTSB), mRNA. /FEA=mRNA /GEN=CTSB /PROD=cathepsin
212509_s_	1139.8	2317.9	2.03	Consensus includes gb:BF98134 /FEA=EST /DB_XREF=gi:12335349 /DB_XREF=est:602269121F1 /CLONE=IM
218331_s_	746	1522.1	2.04	gb:NM_017782.1 /DEF=Homo sapiens hypothetical protein FLJ20360 (FLJ20360), mRNA. /FEA=mRNA /GEN=F
213491_x_	829.7	1700.5	2.05	Consensus includes gb:AL514285 /FEA=EST /DB_XREF=gi:12777779 /DB_XREF=est:AL514285 /CLONE=CL0B
213399_x_	1016	2098.5	2.07	Consensus includes gb:AI560720 /FEA=EST /DB_XREF=gi:4511061 /DB_XREF=est:tq55e12.x1 /CLONE=IMAGE
202034_x_	646.1	1343.2	2.08	gb:NM_014781.1 /DEF=Homo sapiens KIAA0203 gene product (KIAA0203), mRNA. /FEA=mRNA /GEN=KIAA020
201359_at	655.6	1386.3	2.11	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /G
212284_x_	12438.3	26281.7	2.11	Consensus includes gb:BG498776 /FEA=EST /DB_XREF=gi:13460293 /DB_XREF=est:602544416F1 /CLONE=IM
200080_s_	2420.1	5138.8	2.12	Consensus includes gb:AI955655 /FEA=EST /DB_XREF=gi:5747965 /DB_XREF=est:wt36f03.x1 /CLONE=IMAGE
205480_s_	648.9	1386.6	2.14	gb:NM_006759.2 /DEF=Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA. /FEA=mRNA /GEN=U
202949_s_	834.8	1784.9	2.14	gb:NM_001450.1 /DEF=Homo sapiens four and a half LIM domains 2 (FHL2), mRNA. /FEA=mRNA /GEN=FHL2 /
200662_s_	1600.6	3450.5	2.16	gb:NM_014765.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 20 (yeast) homolog (KIAA
201054_at	921.3	2001.5	2.17	Consensus includes gb:BE966599 /FEA=EST /DB_XREF=gi:11772191 /DB_XREF=est:601660283R1 /CLONE=IM
201772_at	480	1046.6	2.18	gb:NM_015878.1 /DEF=Homo sapiens antizyme inhibitor (LOC51582), mRNA. /FEA=mRNA /GEN=LOC51582 /P
213726_x_	824.6	1795.3	2.18	Consensus includes gb:AA515698 /FEA=EST /DB_XREF=gi:2255298 /DB_XREF=est:nf66f09.s1 /CLONE=IMAG
201922_at	1043.8	2274	2.18	gb:NM_014886.1 /DEF=Homo sapiens hypothetical protein (YR-29), mRNA. /FEA=mRNA /GEN=YR-29 /PROD=h
212205_at	646.9	1425.7	2.2	Consensus includes gb:AA534860 /FEA=EST /DB_XREF=gi:2279113 /DB_XREF=est:nf82a04.s1 /CLONE=IMAG
202347_s_	714.4	1576.6	2.21	gb:AB022435.1 /DEF=Homo sapiens LIG mRNA for E2 ubiquitin-conjugating enzyme, complete cds. /FEA=mR
213857_s_	1055.9	2340.4	2.22	Consensus includes gb:BG230614 /FEA=EST /DB_XREF=gi:12725656 /DB_XREF=est:naf41b12.x1 /CLONE=IM
201150_s_	1259.8	2809.7	2.23	gb:NM_000362.2 /DEF=Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseud
217742_s_	539.5	1212	2.25	gb:NM_016628.1 /DEF=Homo sapiens hypothetical protein (LOC51322), mRNA. /FEA=mRNA /GEN=LOC51322
212097_at	682	1537.3	2.25	Consensus includes gb:AU147399 /FEA=EST /DB_XREF=gi:11008920 /DB_XREF=est:AU147399 /CLONE=MAM
212245_at	980.2	2223.2	2.27	Consensus includes gb:AL567779 /FEA=EST /DB_XREF=gi:12921478 /DB_XREF=est:AL567779 /CLONE=CS0D
201334_s_	817.4	1866.6	2.28	Consensus includes gb:AB002380.1 /DEF=Human mRNA for KIAA0382 gene, partial cds. /FEA=mRNA /GEN=K
201653_at	994.2	2274.1	2.29	gb:NM_005776.1 /DEF=Homo sapiens cornichon-like (CNIL), mRNA. /FEA=mRNA /GEN=CNIL /PROD=cornicho
201443_s_	1182.7	2714.1	2.29	gb:AF248966.1 /DEF=Homo sapiens HT028 mRNA, complete cds. /FEA=mRNA /PROD=HT028 /DB_XREF=gi:12
201345_s_	807.6	1860	2.3	gb:NM_003339.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) (UBE
203455_s_	2452.9	5647.9	2.3	gb:NM_002970.1 /DEF=Homo sapiens spermidinespermine N1-acetyltransferase (SAT), mRNA. /FEA=mRNA /G
202776_at	1035.6	2404	2.32	gb:NM_014597.1 /DEF=Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA. /FEA=mRNA /GEN=HS-
201812_s_	1066.5	2470.9	2.32	gb:NM_019059.1 /DEF=Homo sapiens 6.2 kd protein (LOC54543), mRNA. /FEA=mRNA /GEN=LOC54543 /PROD
208718_at	1643.4	3827.6	2.33	Consensus includes gb:Z97056 /DEF=Human DNA sequence from clone RP3-434P1 on chromosome 22 Conta
200677_at	969.8	2266.4	2.34	gb:NM_004339.2 /DEF=Homo sapiens pituitary tumor-transforming 1 interacting protein (PTTG1IP), mRNA. /F

200023_s_	1080.2	2524.9	2.34	gb:NM_003754.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kd) (EIF3S
206924_at	797.6	1870.8	2.35	gb:NM_000641.1 /DEF=Homo sapiens interleukin 11 (IL11), mRNA. /FEA=mRNA /GEN=IL11 /PROD=interleukin
212297_at	779.2	1845.4	2.37	Consensus includes gb:BF218804 /FEA=EST /DB_XREF=gi:11112494 /DB_XREF=est:601882315F1 /CLONE=IM
208671_at	1593	3782.8	2.37	gb:AF164794.1 /DEF=Homo sapiens Diff33 protein homolog mRNA, complete cds. /FEA=mRNA /PROD=Diff33
212077_at	776.8	1858.1	2.39	Consensus includes gb:AL583520 /FEA=EST /DB_XREF=gi:12952562 /DB_XREF=est:AL583520 /CLONE=CS0D
209089_at	1374	3286.4	2.39	gb:BC001267.1 /DEF=Homo sapiens, RAB5A, member RAS oncogene family, clone MGC:5048, mRNA, comple
203324_s_	589	1415.3	2.4	gb:NM_001233.1 /DEF=Homo sapiens caveolin 2 (CAV2), mRNA. /FEA=mRNA /GEN=CAV2 /PROD=caveolin 2 /
212852_s_	963.9	2310.9	2.4	Consensus includes gb:AL538601 /FEA=EST /DB_XREF=gi:12867040 /DB_XREF=est:AL538601 /CLONE=CS0D
212434_at	816.8	2012.5	2.46	Consensus includes gb:AI984421 /FEA=EST /DB_XREF=gi:5811698 /DB_XREF=est:wr89a12.x1 /CLONE=IMAG
202609_at	629.1	1554.2	2.47	gb:NM_004447.1 /DEF=Homo sapiens epidermal growth factor receptor pathway substrate 8 (EPS8), mRNA. /F
202933_s_	1070.5	2656.4	2.48	gb:NM_005433.1 /DEF=Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), mRNA.
213932_x_	1311.9	3256.6	2.48	Consensus includes gb:AI923492 /FEA=EST /DB_XREF=gi:5659456 /DB_XREF=est:wn86a02.x1 /CLONE=IMAG
221479_s_	1224.8	3053.7	2.49	gb:AF060922.1 /DEF=Homo sapiens clone 016a05 My020 protein mRNA, complete cds. /FEA=mRNA /PROD=M
202228_s_	1094.5	2750.3	2.51	gb:NM_017455.1 /DEF=Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha,
207040_s_	904.4	2283.6	2.52	gb:NM_003932.1 /DEF=Homo sapiens suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-interacting
213687_s_	1314.4	3308.4	2.52	Consensus includes gb:BE968801 /FEA=EST /DB_XREF=gi:10579506 /DB_XREF=est:601649806F1 /CLONE=IM
205694_at	3322	8442.7	2.54	gb:NM_000550.1 /DEF=Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /FEA=mRNA /GEN=TYRP1
201738_at	1967.5	5019.9	2.55	gb:NM_005875.1 /DEF=Homo sapiens translation factor sui1 homolog (GC20), mRNA. /FEA=mRNA /GEN=GC2
221619_s_	1852	4738.3	2.56	gb:AF189289.1 /DEF=Homo sapiens presenilin-associated protein mRNA, complete cds. /FEA=mRNA /PROD=
211662_s_	1045.2	2692.3	2.58	gb:LO8666.1 /DEF=Homo sapiens porin (por) mRNA, complete cds and truncated cds. /FEA=mRNA /GEN=por;
216526_x_	2152.6	5561.3	2.58	Consensus includes gb:AK024836.1 /DEF=Homo sapiens cDNA: FLJ21183 fis, clone CAS11634, highly similar
210774_s_	678.4	1772.7	2.61	gb:AL162047.1 /DEF=Homo sapiens mRNA; cDNA DKFZp762E1112 (from clone DKFZp762E1112); complete cd
207574_s_	1228	3202.8	2.61	gb:NM_015675.1 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA. /FE
208394_x_	794.2	2085.2	2.63	gb:NM_007036.2 /DEF=Homo sapiens endothelial cell-specific molecule 1 (ESM1), mRNA. /FEA=mRNA /GEN=E
215691_x_	553.5	1460.2	2.64	Consensus includes gb:AV702994 /FEA=EST /DB_XREF=gi:10719324 /DB_XREF=est:AV702994 /CLONE=ADB
201842_s_	1894.4	5004.1	2.64	Consensus includes gb:AI826799 /FEA=EST /DB_XREF=gi:5447470 /DB_XREF=est:wk56d07.x1 /CLONE=IMAG
202484_s_	1011.6	2717.7	2.69	gb:AF072242.1 /DEF=Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds. /FEA=m
202130_at	1211.8	3296.6	2.72	Consensus includes gb:AA725102 /FEA=EST /DB_XREF=gi:2742809 /DB_XREF=est:ai08h05.s1 /CLONE=13422
205849_s_	1324	3617	2.73	gb:NM_006294.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA. /FE
202753_at	990	2715.2	2.74	gb:NM_014814.1 /DEF=Homo sapiens KIAA0107 gene product (KIAA0107), mRNA. /FEA=mRNA /GEN=KIAA010
200088_x_	2403.8	6581.6	2.74	Consensus includes gb:AK026491.1 /DEF=Homo sapiens cDNA: FLJ22838 fis, clone KAI44494, highly similar
200084_at	801	2220.6	2.77	Consensus includes gb:BE748698 /FEA=EST /DB_XREF=gi:10162690 /DB_XREF=est:601571740T1 /CLONE=IM
217801_at	1450.3	4014.2	2.77	gb:NM_006886.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subu
208405_s_	780.9	2173.7	2.78	gb:NM_006016.1 /DEF=Homo sapiens CD164 antigen, sialomucin (CD164), mRNA. /FEA=mRNA /GEN=CD164 /P
201090_x_	1875.4	5208.2	2.78	gb:NM_006082.1 /DEF=Homo sapiens tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA. /FEA=mRNA /GEN=K-AL

204396_s_	612.8	1715	2.8	gb:NM_005308.1 /DEF=Homo sapiens G protein-coupled receptor kinase 5 (GPRK5), mRNA. /FEA=mRNA /GEN=
201273_s_	1050.2	2936.5	2.8	gb:NM_003133.1 /DEF=Homo sapiens signal recognition particle 9kD (SRP9), mRNA. /FEA=mRNA /GEN=SRP9
201754_at	1334.2	3729.5	2.8	gb:NM_004374.1 /DEF=Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mito
209075_s_	1053.7	2964.6	2.81	gb:AY009128.1 /DEF=Homo sapiens ISCU2 (ISCU) mRNA, complete cds, alternatively spliced. /FEA=mRNA /G
200668_s_	1123.8	3155	2.81	gb:BC003395.1 /DEF=Homo sapiens, ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC45), clon
201200_at	991.4	2800.1	2.82	gb:NM_003851.1 /DEF=Homo sapiens cellular repressor of E1A-stimulated genes (CREG), mRNA. /FEA=mRNA
200701_at	698.3	1975.7	2.83	gb:NM_006432.1 /DEF=Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA. /FEA=mRNA /GEN=
214288_s_	1817.1	5144.9	2.83	Consensus includes gb:W86293 /FEA=EST /DB_XREF=gi:1398731 /DB_XREF=est:zh54c06.s1 /CLONE=IMAGE
205292_s_	1135.2	3221.7	2.84	gb:NM_002137.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein A2B1 (HNRPA2B1), mRNA. /F
213070_at	605.4	1734.2	2.86	Consensus includes gb:AV682436 /FEA=EST /DB_XREF=gi:10284299 /DB_XREF=est:AV682436 /CLONE=GKB
214334_x_	1245.1	3578.4	2.87	Consensus includes gb:N34846 /FEA=EST /DB_XREF=gi:1155988 /DB_XREF=est:yy45e11.s1 /CLONE=IMAGE:
208704_x_	970.4	2808.7	2.89	gb:BC000373.1 /DEF=Homo sapiens, Similar to amyloid beta (A4) precursor-like protein 2, clone MGC:8371, m
208742_s_	758.2	2201.9	2.9	gb:U78303.1 /DEF=Human 2HOR0202 mRNA, complete cds. /FEA=mRNA /PROD=2HOR0202 /DB_XREF=gi:664
211951_at	878.4	2543.1	2.9	Consensus includes gb:D21262.1 /DEF=Human mRNA for KIAA0035 gene, partial cds. /FEA=mRNA /GEN=KIA
212869_x_	11137.6	32265.8	2.9	Consensus includes gb:AI721229 /FEA=EST /DB_XREF=gi:5038485 /DB_XREF=est:as68c10.x1 /CLONE=IMAG
202854_at	628.1	1837.6	2.93	gb:NM_000194.1 /DEF=Homo sapiens hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) (H
213738_s_	860.8	2521.3	2.93	Consensus includes gb:AI587323 /FEA=EST /DB_XREF=gi:4573764 /DB_XREF=est:tq04h04.x1 /CLONE=IMAGE
211980_at	922.7	2715.5	2.94	Consensus includes gb:AI922605 /FEA=EST /DB_XREF=gi:5658569 /DB_XREF=est:wm90c05.x1 /CLONE=IMAG
211445_x_	1179.5	3482.4	2.95	gb:AF315951.1 /DEF=Homo sapiens FKSG17 (FKSG17) mRNA, complete cds. /FEA=mRNA /GEN=FKSG17 /PR
202859_x_	6377.2	18786.8	2.95	gb:NM_000584.1 /DEF=Homo sapiens interleukin 8 (IL8), mRNA. /FEA=mRNA /GEN=IL8 /PROD=interleukin 8 /D
202644_s_	856.2	2535.4	2.96	gb:NM_006290.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA. /FEA
208697_s_	953.6	2818.5	2.96	gb:BC000734.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 3, subunit 6 (48kD), clone MGC:20
212233_at	1250.3	3696.1	2.96	Consensus includes gb:AL523076 /FEA=EST /DB_XREF=gi:12786569 /DB_XREF=est:AL523076 /CLONE=CS0D
200007_at	1499.9	4454.6	2.97	gb:NM_003134.1 /DEF=Homo sapiens signal recognition particle 14kD (homologous Alu RNA-binding protein)
201134_x_	1508.5	4495.4	2.98	gb:NM_001867.1 /DEF=Homo sapiens cytochrome c oxidase subunit VIc (COX7C), mRNA. /FEA=mRNA /GEN=
201146_at	594.7	1775.9	2.99	gb:NM_006164.1 /DEF=Homo sapiens nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA. /FEA=mRNA
200692_s_	959.1	2866.6	2.99	gb:NM_004134.1 /DEF=Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B), mRNA. /FEA=mRNA
202932_at	774.3	2323.8	3	gb:NM_005433.1 /DEF=Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), mRNA.
200663_at	1056.1	3163.3	3	gb:NM_001780.1 /DEF=Homo sapiens CD63 antigen (melanoma 1 antigen) (CD63), mRNA. /FEA=mRNA /GEN=C
221748_s_	1511.6	4570.3	3.02	Consensus includes gb:AL046979 /FEA=EST /DB_XREF=gi:5435035 /DB_XREF=est:DKFZp586K0617_s1 /CLO
212230_at	2533.4	7655.8	3.02	Consensus includes gb:AV725664 /FEA=EST /DB_XREF=gi:10831279 /DB_XREF=est:AV725664 /CLONE=HTCA
212857_x_	982.6	2977.1	3.03	Consensus includes gb:BG231551 /FEA=EST /DB_XREF=gi:12726658 /DB_XREF=est:naf29h05.x1 /CLONE=IM
220960_x_	1604.7	4900	3.05	gb:NM_000983.1 /DEF=Homo sapiens ribosomal protein L22 (RPL22), mRNA. /FEA=mRNA /GEN=RPL22 /PROD
202076_at	838.3	2570.3	3.07	gb:NM_001166.2 /DEF=Homo sapiens baculoviral IAP repeat-containing 2 (BIRC2), mRNA. /FEA=mRNA /GEN=
201925_s_	2574.9	7994.3	3.1	gb:NM_000574.1 /DEF=Homo sapiens decay accelerating factor for complement (CD55, Cromer blood group s

200749_at	858	2669.6	3.11	Consensus includes gb:BF112006 /FEA=EST /DB_XREF=gi:10941619 /DB_XREF=est:7137e05.x1 /CLONE=IMAG
214039_s_	1104.4	3433.6	3.11	Consensus includes gb:T15777 /FEA=EST /DB_XREF=gi:517939 /DB_XREF=est:IB1875 /UG=Hs.296398 Homo
201599_at	1352.9	4214	3.11	gb:NM_000274.1 /DEF=Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encodi
202603_at	686.6	2165.8	3.15	Consensus includes gb:N51370 /FEA=EST /DB_XREF=gi:1192536 /DB_XREF=est:yz16d01.s1 /CLONE=IMAGE:
205788_s_	1247.6	3936.5	3.16	gb:NM_014827.1 /DEF=Homo sapiens KIAA0663 gene product (KIAA0663), mRNA. /FEA=mRNA /GEN=KIAA066
208942_s_	737.8	2337.9	3.17	Consensus includes gb:BE866511 /FEA=EST /DB_XREF=gi:10315287 /DB_XREF=est:601678885F1 /CLONE=IM
208812_x_	1613.4	5138.3	3.18	gb:BC004489.1 /DEF=Homo sapiens, major histocompatibility complex, class I, C, clone MGC:11039, mRNA, c
203667_at	795.6	2541.5	3.19	gb:NM_004607.1 /DEF=Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /FEA=mRNA /GEN=TBCA /
212296_at	948.2	3031.1	3.2	Consensus includes gb:NM_005805.1 /DEF=Homo sapiens 26S proteasome-associated pad1 homolog (POH1)
212639_x_	1781.3	5713.7	3.21	Consensus includes gb:AL581768 /FEA=EST /DB_XREF=gi:12949093 /DB_XREF=est:AL581768 /CLONE=CS0D
202061_s_	638.5	2058.9	3.22	Consensus includes gb:A1927770 /FEA=EST /DB_XREF=gi:5663734 /DB_XREF=est:wo08h07.x1 /CLONE=IMAG
200937_s_	855.4	2754.4	3.22	gb:NM_000969.1 /DEF=Homo sapiens ribosomal protein L5 (RPL5), mRNA. /FEA=mRNA /GEN=RPL5 /PROD=ri
200989_at	1593	5128.1	3.22	gb:NM_001530.1 /DEF=Homo sapiens hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcr
208766_s_	861.4	2780	3.23	gb:BC001449.1 /DEF=Homo sapiens, heterogeneous nuclear ribonucleoprotein R, clone MGC:2039, mRNA, co
200858_s_	1793.3	5785.3	3.23	gb:NM_001012.1 /DEF=Homo sapiens ribosomal protein S8 (RPS8), mRNA. /FEA=mRNA /GEN=RPS8 /PROD=r
200038_s_	2097.9	6787.8	3.24	gb:NM_000985.1 /DEF=Homo sapiens ribosomal protein L17 (RPL17), mRNA. /FEA=mRNA /GEN=RPL17 /PROD
217127_at	725.3	2357.4	3.25	Consensus includes gb:AL354872 /DEF=Human DNA sequence from clone RP11-42O15 on chromosome 1. Co
214211_at	1830.3	5956.4	3.25	Consensus includes gb:AA083483 /FEA=EST /DB_XREF=gi:1625544 /DB_XREF=est:zn32a06.s1 /CLONE=IMAG
201352_at	948.9	3115.2	3.28	gb:NM_014263.1 /DEF=Homo sapiens YME1 (S.cerevisiae)-like 1 (YME1L1), mRNA. /FEA=mRNA /GEN=YME1L1
200650_s_	2434.6	8041.6	3.3	gb:NM_005566.1 /DEF=Homo sapiens lactate dehydrogenase A (LDHA), mRNA. /FEA=mRNA /GEN=LDHA /PRO
203752_s_	1046	3476	3.32	gb:NM_005354.2 /DEF=Homo sapiens jun D proto-oncogene (JUND), mRNA. /FEA=mRNA /GEN=JUND /PROD=
209387_s_	1194.1	3972.7	3.33	gb:M90657.1 /DEF=Human tumor antigen (L6) mRNA, complete cds. /FEA=mRNA /GEN=L6 /DB_XREF=gi:1868
209066_x_	1228.4	4128.7	3.36	gb:M26700.1 /DEF=Human mitochondrial ubiquinone-binding protein mRNA, complete cds. /FEA=mRNA /GEN
200694_s_	751.2	2538.5	3.38	gb:NM_020414.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 24 (DDX24), mRNA. /FEA
222108_at	1047.2	3563.2	3.4	Consensus includes gb:AC004010 /DEF=Human BAC clone GS1-99H8 /FEA=CDS /DB_XREF=gi:2781385 /UG=
213524_s_	1730.1	5910.3	3.42	Consensus includes gb:NM_015714.1 /DEF=Homo sapiens putative lymphocyte G0G1 switch gene (G0S2), mR
201891_s_	3801.6	12994.7	3.42	gb:NM_004048.1 /DEF=Homo sapiens beta-2-microglobulin (B2M), mRNA. /FEA=mRNA /GEN=B2M /PROD=bet
200765_x_	884.5	3048.7	3.45	gb:NM_001903.1 /DEF=Homo sapiens catenin (cadherin-associated protein), alpha 1 (102kD) (CTNNA1), mRNA
212988_x_	1005.4	3521.5	3.5	Consensus includes gb:AL515810 /FEA=EST /DB_XREF=gi:12779303 /DB_XREF=est:AL515810 /CLONE=CS0D
209283_at	1974.2	6913.1	3.5	gb:AF007162.1 /DEF=Homo sapiens unknown mRNA, complete cds. /FEA=mRNA /PROD=unknown /DB_XREF
217883_at	1005	3545.7	3.53	gb:NM_015702.1 /DEF=Homo sapiens hypothetical protein (CL25022), mRNA. /FEA=mRNA /GEN=CL25022 /PR
215127_s_	600	2132.9	3.55	Consensus includes gb:AL517946 /FEA=EST /DB_XREF=gi:12781439 /DB_XREF=est:AL517946 /CLONE=CS0D
212071_s_	1029.2	3668.3	3.56	Consensus includes gb:BE968833 /FEA=EST /DB_XREF=gi:10579538 /DB_XREF=est:601649861F1 /CLONE=IM
203133_at	1392.2	4971.1	3.57	gb:NM_006808.1 /DEF=Homo sapiens protein translocation complex beta (SEC61B), mRNA. /FEA=mRNA /GEN
211765_x_	1961.3	7024.3	3.58	gb:BC005982.1 /DEF=Homo sapiens, peptidylprolyl isomerase A (cyclophilin A), clone MGC:14681, mRNA, com

218007_s_	931.8	3368	3.61	gb:NM_015920.1 /DEF=Homo sapiens 40S ribosomal protein S27 isoform (LOC51065), mRNA. /FEA=mRNA /GE
200788_s_	1181.6	4259.7	3.61	gb:NM_003768.1 /DEF=Homo sapiens phosphoprotein enriched in astrocytes 15 (PEA15), mRNA. /FEA=mRNA
202673_at	611.1	2215.2	3.62	gb:NM_003859.1 /DEF=Homo sapiens dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subun
201592_at	935.7	3401	3.63	gb:NM_003756.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S
216520_s_	4719.6	17174.4	3.64	Consensus includes gb:AF072098 /DEF=Homo sapiens HDCMB21P gene, complete cds /FEA=CDS /DB_XREF
208780_x_	1304	4760.5	3.65	gb:AF154847.1 /DEF=Homo sapiens 33 kDa Vamp-associated protein (VAMP) mRNA, complete cds. /FEA=mR
211978_x_	2053.2	7547.9	3.68	Consensus includes gb:A1708767 /FEA=EST /DB_XREF=gi:4998543 /DB_XREF=est:as35e01.x1 /CLONE=IMAG
213347_x_	3683.4	13603.3	3.69	Consensus includes gb:AW132023 /FEA=EST /DB_XREF=gi:6133630 /DB_XREF=est:xe71b05.x1 /CLONE=IMA
202087_s_	1417	5273.1	3.72	gb:NM_001912.1 /DEF=Homo sapiens cathepsin L (CTSL), mRNA. /FEA=mRNA /GEN=CTSL /PROD=cathepsin
200773_x_	936	3541.4	3.78	gb:NM_002823.1 /DEF=Homo sapiens prothymosin, alpha (gene sequence 28) (PTMA), mRNA. /FEA=mRNA /G
201666_at	1295.9	4896.7	3.78	gb:NM_003254.1 /DEF=Homo sapiens tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, co
217720_at	993.2	3772.8	3.8	gb:NM_016139.1 /DEF=Homo sapiens 16.7Kd protein (LOC51142), mRNA. /FEA=mRNA /GEN=LOC51142 /PROD
200912_s_	1400.8	5357.1	3.82	gb:NM_001967.2 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA. /F
217738_at	893.9	3423.3	3.83	Consensus includes gb:BF575514 /FEA=EST /DB_XREF=gi:11649318 /DB_XREF=est:602133090F1 /CLONE=IM
202391_at	1467.9	5619.1	3.83	gb:NM_006317.1 /DEF=Homo sapiens brain acid-soluble protein 1 (BASP1), mRNA. /FEA=mRNA /GEN=BASP1
200726_at	861.9	3322.6	3.85	gb:NM_002710.1 /DEF=Homo sapiens protein phosphatase 1, catalytic subunit, gamma isoform (PPP1CC), mR
200089_s_	1645.9	6358.8	3.86	Consensus includes gb:A1953886 /FEA=EST /DB_XREF=gi:5746196 /DB_XREF=est:wx70g02.x1 /CLONE=IMAG
217779_s_	923.3	3568.8	3.87	gb:NM_017761.1 /DEF=Homo sapiens hypothetical protein FLJ20312 (FLJ20312), mRNA. /FEA=mRNA /GEN=F
213864_s_	1221.	4732.9	3.88	Consensus includes gb:A1985751 /FEA=EST /DB_XREF=gi:5813028 /DB_XREF=est:wr76h07.x1 /CLONE=IMAG
201163_s_	1391.9	5399.7	3.88	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRN
212042_x_	2176.3	8438.6	3.88	Consensus includes gb:BG389744 /FEA=EST /DB_XREF=gi:13283180 /DB_XREF=est:602415111F1 /CLONE=IM
203725_at	989.9	3877.2	3.92	gb:NM_001924.2 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA. /F
200047_s_	747.4	2935.8	3.93	gb:NM_003403.2 /DEF=Homo sapiens YY1 transcription factor (YY1), mRNA. /FEA=mRNA /GEN=YY1 /PROD=Y
200795_at	1340.3	5296.1	3.95	gb:NM_004684.1 /DEF=Homo sapiens SPARC-like 1 (mast9, hev1n) (SPARCL1), mRNA. /FEA=mRNA /GEN=SPA
200817_x_	1593.3	6290.5	3.95	gb:NM_001014.1 /DEF=Homo sapiens ribosomal protein S10 (RPS10), mRNA. /FEA=mRNA /GEN=RPS10 /PRO
211542_x_	1991.6	7907.5	3.97	gb:BC004334.1 /DEF=Homo sapiens, ribosomal protein S10, clone MGC:10943, mRNA, complete cds. /FEA=m
200809_x_	1406.3	5638.6	4.01	gb:NM_000976.1 /DEF=Homo sapiens ribosomal protein L12 (RPL12), mRNA. /FEA=mRNA /GEN=RPL12 /PROD
211509_s_	2077.9	8340.6	4.01	gb:AB015639.1 /DEF=Homo sapiens ASY mRNA, complete cds. /FEA=mRNA /GEN=ASY /DB_XREF=gi:582113
200944_s_	656.1	2664.3	4.06	gb:NM_004965.1 /DEF=Homo sapiens high-mobility group (nonhistone chromosomal) protein 14 (HMG14), mR
212461_at	667	2714.9	4.07	Consensus includes gb:BF793951 /FEA=EST /DB_XREF=gi:12099005 /DB_XREF=est:602254576F1 /CLONE=IM
210517_s_	3147.1	12793.4	4.07	gb:AB003476.1 /DEF=Homo sapiens mRNA for gravin, complete cds. /FEA=mRNA /PROD=gravin /DB_XREF=g
208768_x_	2033.2	8304.3	4.08	gb:D17652.1 /DEF=Human mRNA for HBp15L22, complete cds. /FEA=mRNA /PROD=HBp15L22 /DB_XREF=gi:4
217232_x_	1473.8	6045.1	4.1	Consensus includes gb:AF059180 /DEF=Homo sapiens mutant beta-globin (HBB) gene, complete cds /FEA=m
200763_s_	1880.4	7707.3	4.1	gb:NM_001003.1 /DEF=Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA. /FEA=mRNA /GEN=RPLP1
216231_s	1931.4	7971.9	4.13	Consensus includes gb:AW188940 /FEA=EST /DB_XREF=gi:6463376 /DB_XREF=est:xk90f09.x1 /CLONE=IMAG

212764_at	638.6	2642.7	4.14	Consensus includes gb:A1806174 /FEA=EST /DB_XREF=gi:5392740 /DB_XREF=est:wf06h03.x1 /CLONE=IMAG
217722_s_	776.9	3212.7	4.14	gb:NM_016645.1 /DEF=Homo sapiens mesenchymal stem cell protein DSC92 (LOC51335), mRNA. /FEA=mRNA
201938_at	692.7	2884.6	4.16	gb:NM_004642.1 /DEF=Homo sapiens deleted in oral cancer (mouse, homolog) 1 (DOC1), mRNA. /FEA=mRNA
209277_at	1106.5	4599.2	4.16	Consensus includes gb:AL574096 /FEA=EST /DB_XREF=gi:12933969 /DB_XREF=est:AL574096 /CLONE=CS0D
207783_x_	6795.2	28609.4	4.21	gb:NM_017627.1 /DEF=Homo sapiens hypothetical protein FLJ20030 (FLJ20030), mRNA. /FEA=mRNA /GEN=F
221474_at	890.5	3757.8	4.22	gb:U26162.1 /DEF=Human myosin regulatory light chain mRNA, complete cds. /FEA=mRNA /PROD=myosin re
208845_at	909.7	3836.1	4.22	gb:BC002456.1 /DEF=Homo sapiens, voltage-dependent anion channel 3, clone MGC:1966, mRNA, complete c
200082_s_	1085.2	4585.3	4.23	Consensus includes gb:A1805587 /FEA=EST /DB_XREF=gi:5392153 /DB_XREF=est:tx97a02.x1 /CLONE=IMAGE
216342_x_	2080.3	8836.7	4.25	Consensus includes gb:AL121916 /DEF=Human DNA sequence from clone RP1-189G13 on chromosome 20. C
203885_at	558.7	2381.9	4.26	gb:NM_014999.1 /DEF=Homo sapiens KIAA0118 protein (KIAA0118), mRNA. /FEA=mRNA /GEN=KIAA0118 /PR
217739_s_	922.8	3934.7	4.26	gb:NM_005746.1 /DEF=Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA. /FEA=mRNA /GEN=P
211185_s_	942.6	4018.2	4.26	gb:AF130099.1 /DEF=Homo sapiens clone FLC1464 PRO3102 mRNA, complete cds. /FEA=mRNA /PROD=PRO
212967_x_	999.8	4265.7	4.27	Consensus includes gb:AW148801 /FEA=EST /DB_XREF=gi:6196697 /DB_XREF=est:xf04e10.x1 /CLONE=IMAG
211696_x_	1907.3	8177.2	4.29	gb:AF349114.1 /DEF=Homo sapiens beta globin chain variant (HBB) mRNA, complete cds. /FEA=mRNA /GEN=
201061_s_	783.7	3376.6	4.31	gb:M81635.1 /DEF=Homo sapiens erythrocyte membrane protein mRNA, complete cds. /FEA=mRNA /GEN=sto
201358_s_	1052.8	4541.7	4.31	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /G
200627_at	1125.7	4890.1	4.34	gb:BC003005.1 /DEF=Homo sapiens, inactive progesterone receptor, 23 kD, clone MGC:4004, mRNA, complet
207974_s_	601.7	2619.2	4.35	gb:NM_006930.1 /DEF=Homo sapiens S-phase kinase-associated protein 1A (p19A) (SKP1A), mRNA. /FEA=m
200018_at	3210.8	14089.3	4.39	gb:NM_001017.1 /DEF=Homo sapiens ribosomal protein S13 (RPS13), mRNA. /FEA=mRNA /GEN=RPS13 /PRO
208865_at	780.8	3453.4	4.42	Consensus includes gb:BG534245 /FEA=EST /DB_XREF=gi:13525785 /DB_XREF=est:602553366F1 /CLONE=IM
219293_s_	612.5	2714.9	4.43	gb:NM_013341.1 /DEF=Homo sapiens hypothetical protein (PTD004), mRNA. /FEA=mRNA /GEN=PTD004 /PRO
211430_s_	666.1	2947.7	4.43	gb:M87789.1 /DEF=Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complemen
208616_s_	1140	5057.2	4.44	gb:U48297.1 /DEF=Homo sapiens protein tyrosine phosphatase PTPCAAX2 (hPTPCAAX2) mRNA, complete cd
222229_x_	1143.7	5091.4	4.45	Consensus includes gb:AL121871 /DEF=Human DNA sequence from clone RP13-258O15 on chromosome Xq2
212661_x_	1610.9	7164.2	4.45	Consensus includes gb:BE731738 /FEA=EST /DB_XREF=gi:10145730 /DB_XREF=est:601568154F1 /CLONE=IM
217848_s_	1733.2	7779.7	4.49	gb:NM_021129.1 /DEF=Homo sapiens pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochondria
200738_s_	898.7	4040.9	4.5	gb:NM_000291.1 /DEF=Homo sapiens phosphoglycerate kinase 1 (PGK1), mRNA. /FEA=mRNA /GEN=PGK1 /PR
215001_s_	1247.3	5631	4.51	Consensus includes gb:AL161952.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M0813 (from clone DKFZp43
200926_at	5218.7	23548.9	4.51	gb:NM_001025.1 /DEF=Homo sapiens ribosomal protein S23 (RPS23), mRNA. /FEA=mRNA /GEN=RPS23 /PRO
200016_x_	2896.6	13083.8	4.52	gb:NM_002136.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), mRNA. /FEA=m
200097_s_	978.3	4429.8	4.53	Consensus includes gb:AI701949 /FEA=EST /DB_XREF=gi:4989849 /DB_XREF=est:tq09c07.x1 /CLONE=IMAGE
201318_s_	976.7	4446.8	4.55	gb:NM_006471.1 /DEF=Homo sapiens myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), m
211710_x_	1056.7	4805.7	4.55	gb:BC005817.1 /DEF=Homo sapiens, ribosomal protein L4, clone MGC:11073, mRNA, complete cds. /FEA=mR
216438_s_	1829.8	8328	4.55	Consensus includes gb:AL133228 /DEF=Human DNA sequence from clone RP5-1071L10 on chromosome 20 C
201429_s_	5689.1	26020	4.57	gb:NM_000998.1 /DEF=Homo sapiens ribosomal protein L37a (RPL37A), mRNA. /FEA=mRNA /GEN=RPL37A /P

200732_s_	667.3	3085.3	4.62	Consensus includes gb:AL578310 /FEA=EST /DB_XREF=gi:12942259 /DB_XREF=est:AL578310 /CLONE=CS0D
211956_s_	1473.7	6804.4	4.62	Consensus includes gb:BF246436 /FEA=EST /DB_XREF=gi:11160799 /DB_XREF=est:601854870F1 /CLONE=IM
211058_x_	1831.1	8451.5	4.62	gb:BC006379.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC:12832, mRNA, complete cds. /FEA=mRNA /PR
213477_x_	3505.4	16261.4	4.64	Consensus includes gb:AL515273 /FEA=EST /DB_XREF=gi:12778766 /DB_XREF=est:AL515273 /CLONE=CL0B
200716_x_	1640.7	7634.6	4.65	gb:NM_012423.1 /DEF=Homo sapiens ribosomal protein L13a (RPL13A), mRNA. /FEA=mRNA /GEN=RPL13A /P
202443_x_	712	3321.1	4.66	Consensus includes gb:AA291203 /FEA=EST /DB_XREF=gi:1939386 /DB_XREF=est:zt38h02.s1 /CLONE=IMAG
208752_x_	897.7	4178.8	4.66	Consensus includes gb:AI888672 /FEA=EST /DB_XREF=gi:5593836 /DB_XREF=est:wn34c03.x1 /CLONE=IMAG
200840_at	830.3	3904.2	4.7	gb:NM_005548.1 /DEF=Homo sapiens lysyl-tRNA synthetase (KARS), mRNA. /FEA=mRNA /GEN=KARS /PROD
215111_s_	1246.8	5862.4	4.7	Consensus includes gb:AK027071.1 /DEF=Homo sapiens cDNA: FLJ23418 fis, clone HEP21245, highly similar
201217_x_	2482.9	11677.7	4.7	gb:NM_000967.1 /DEF=Homo sapiens ribosomal protein L3 (RPL3), mRNA. /FEA=mRNA /GEN=RPL3 /PROD=ri
214150_x_	700	3305.8	4.72	Consensus includes gb:BE043477 /FEA=EST /DB_XREF=gi:8360530 /DB_XREF=est:hk39a01.y1 /CLONE=IMAG
210095_s_	843.2	3977.6	4.72	gb:M31159.1 /DEF=Human growth hormone-dependent insulin-like growth factor-binding protein mRNA, comp
208825_x_	6192.5	29374.2	4.74	gb:U43701.1 /DEF=Human ribosomal protein L23a mRNA, complete cds. /FEA=mRNA /PROD=ribosomal prote
203012_x_	4310.2	20452.4	4.75	gb:NM_000984.1 /DEF=Homo sapiens ribosomal protein L23a (RPL23A), mRNA. /FEA=mRNA /GEN=RPL23A /P
200819_s_	1107.4	5304.2	4.79	gb:NM_001018.1 /DEF=Homo sapiens ribosomal protein S15 (RPS15), mRNA. /FEA=mRNA /GEN=RPS15 /PRO
200748_s_	1372.6	6579.2	4.79	gb:NM_002032.1 /DEF=Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA. /FEA=mRNA /GEN=FTH1 /PR
201375_s_	1048.3	5028.1	4.8	gb:NM_004156.1 /DEF=Homo sapiens protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (PP
218353_at	716.6	3459.9	4.83	gb:NM_025226.1 /DEF=Homo sapiens MSTP032 protein (MSTP032), mRNA. /FEA=mRNA /GEN=MSTP032 /PRO
213646_x_	1327.7	6417.1	4.83	Consensus includes gb:BE300252 /FEA=EST /DB_XREF=gi:9184000 /DB_XREF=est:600944004T1 /CLONE=IMA
201071_x_	987.5	4789.1	4.85	gb:NM_012433.1 /DEF=Homo sapiens splicing factor 3b, subunit 1, 155kD (SF3B1), mRNA. /FEA=mRNA /GEN=
208834_x_	6152.3	29867.5	4.85	gb:BC001865.1 /DEF=Homo sapiens, Similar to cadherin 1, type 1, E-cadherin (epithelial), clone MGC:1151, mR
212687_at	923.3	4489	4.86	Consensus includes gb:AL110164.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586
212426_s_	912.5	4439.8	4.87	Consensus includes gb:BF033313 /FEA=EST /DB_XREF=gi:10741025 /DB_XREF=est:601458002F1 /CLONE=IM
209939_x_	747.3	3646.7	4.88	gb:AF005775.1 /DEF=Homo sapiens caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternatively sp
202912_at	1544.3	7603.9	4.92	gb:NM_001124.1 /DEF=Homo sapiens adrenomedullin (ADM), mRNA. /FEA=mRNA /GEN=ADM /PROD=adrenom
206976_s_	524.4	2583.7	4.93	gb:NM_006644.1 /DEF=Homo sapiens heat shock 105kD (HSP105B), mRNA. /FEA=mRNA /GEN=HSP105B /PRO
213583_x_	2390.5	11787.7	4.93	Consensus includes gb:BE964125 /FEA=EST /DB_XREF=gi:11767593 /DB_XREF=est:601657809R1 /CLONE=IM
202029_x_	2996.3	14760.2	4.93	gb:NM_000999.1 /DEF=Homo sapiens ribosomal protein L38 (RPL38), mRNA. /FEA=mRNA /GEN=RPL38 /PROD
212039_x_	2197.3	10894.9	4.96	Consensus includes gb:BG339228 /FEA=EST /DB_XREF=gi:13145666 /DB_XREF=est:602437093F1 /CLONE=IM
214938_x_	1671.5	8302.7	4.97	Consensus includes gb:AF283771.2 /DEF=Homo sapiens clone TCBAPO774 mRNA sequence. /FEA=mRNA /DB
213699_s_	1381.8	6882.6	4.98	Consensus includes gb:AA854017 /FEA=EST /DB_XREF=gi:2941555 /DB_XREF=est:aj52d02.s1 /CLONE=IMAG
213134_x_	895.2	4463.3	4.99	Consensus includes gb:AI765445 /FEA=EST /DB_XREF=gi:5231954 /DB_XREF=est:wi80b08.x1 /CLONE=IMAG
200958_s_	1664.9	8341.8	5.01	gb:NM_005625.1 /DEF=Homo sapiens syndecan binding protein (syntenin) (SDCBP), mRNA. /FEA=mRNA /GEN
211073_x_	2251.4	11306.7	5.02	gb:BC006483.1 /DEF=Homo sapiens, ribosomal protein L3, clone MGC:4393, mRNA, complete cds. /FEA=mRN
201254_x_	1748.7	8849.3	5.06	gb:NM_001010.1 /DEF=Homo sapiens ribosomal protein S6 (RPS6), mRNA. /FEA=mRNA /GEN=RPS6 /PROD=r

201031_s_	910.9	4628.9	5.08	gb:NM_005520.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA. /FE
211945_s_	1460.7	7529.9	5.15	Consensus includes gb:BG500301 /FEA=EST /DB_XREF=gi:13461818 /DB_XREF=est:602546969F1 /CLONE=IM
201807_at	714.8	3685.4	5.16	gb:NM_004896.1 /DEF=Homo sapiens vacuolar protein sorting 26 (yeast homolog) (VPS26), mRNA. /FEA=mRN
209134_s_	944.1	4868.1	5.16	gb:BC000524.1 /DEF=Homo sapiens, Similar to ribosomal protein S6, clone MGC:8597, mRNA, complete cds.
200032_s_	2762.7	14263.4	5.16	gb:NM_000661.1 /DEF=Homo sapiens ribosomal protein L9 (RPL9), mRNA. /FEA=mRNA /GEN=RPL9 /PROD=ri
208683_at	1353.6	7008	5.18	gb:M23254.1 /DEF=Human Ca2-activated neutral protease large subunit (CANP) mRNA, complete cds. /FEA=m
221478_at	1174.1	6098.8	5.19	Consensus includes gb:AL132665.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566E034 (from clone DKFZp566
212185_x_	3306.6	17323.4	5.24	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS /GEN
208680_at	682.9	3585.1	5.25	gb:L19184.1 /DEF=Human natural killer cell enhancing factor (NKEFA) mRNA, complete cds. /FEA=mRNA /GE
201406_at	2558.7	13421	5.25	gb:NM_021029.1 /DEF=Homo sapiens ribosomal protein L44 (RPL44), mRNA. /FEA=mRNA /GEN=RPL44 /PROD
200033_at	1032.8	5486.2	5.31	gb:NM_004396.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 5 (RNA helicase, 68kD) (D
213084_x_	5377	28544	5.31	Consensus includes gb:BF125158 /FEA=EST /DB_XREF=gi:10964198 /DB_XREF=est:601762392F1 /CLONE=IM
205644_s_	716.8	3812.7	5.32	gb:NM_003096.1 /DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA. /FEA=
208655_at	761.6	4051.7	5.32	Consensus includes gb:BG530368 /FEA=EST /DB_XREF=gi:13521905 /DB_XREF=est:602559112F1 /CLONE=IM
211959_at	2091.4	11166.8	5.34	Consensus includes gb:AW007532 /FEA=EST /DB_XREF=gi:5856310 /DB_XREF=est:ws52h07.x1 /CLONE=IMA
200807_s_	1256.1	6719.2	5.35	gb:NM_002156.1 /DEF=Homo sapiens heat shock 60kD protein 1 (chaperonin) (HSPD1), mRNA. /FEA=mRNA /G
200025_s_	2249.6	12099.1	5.38	gb:NM_000988.1 /DEF=Homo sapiens ribosomal protein L27 (RPL27), mRNA. /FEA=mRNA /GEN=RPL27 /PROD
201994_at	1574.8	8526.3	5.41	gb:NM_012286.1 /DEF=Homo sapiens MORF-related gene X (KIAA0026), mRNA. /FEA=mRNA /GEN=KIAA0026
204271_s_	1325.9	7187.9	5.42	gb:M74921.1 /DEF=Human endothelin receptor mRNA, complete cds. /FEA=mRNA /GEN=ETs /PROD=endothe
213356_x_	2222.8	12084.3	5.44	Consensus includes gb:AL568186 /FEA=EST /DB_XREF=gi:12922280 /DB_XREF=est:AL568186 /CLONE=CS0D
201492_s_	4058.9	22092.5	5.44	gb:NM_021104.1 /DEF=Homo sapiens ribosomal protein L41 (RPL41), mRNA. /FEA=mRNA /GEN=RPL41 /PROD
200718_s_	1291.8	7050	5.46	Consensus includes gb:AA927664 /FEA=EST /DB_XREF=gi:3076484 /DB_XREF=est:om71h10.s1 /CLONE=IMA
201097_s_	1031.9	5644.1	5.47	gb:NM_001660.2 /DEF=Homo sapiens ADP-ribosylation factor 4 (ARF4), mRNA. /FEA=mRNA /GEN=ARF4 /PRO
221476_s_	1343.8	7367.6	5.48	gb:AF279903.1 /DEF=Homo sapiens 60S ribosomal protein L15 (EC45) mRNA, complete cds. /FEA=mRNA /GE
211628_x_	2235.8	12327.1	5.51	gb:J04755.1 /DEF=Human ferritin H processed pseudogene, complete cds. /FEA=mRNA /GEN=FTHP1 /DB_XR
211072_x_	1553.9	8579.7	5.52	gb:BC006481.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC:4387, mRNA, complete cds. /FEA=mRNA /PR
200717_x_	2639.4	14556.3	5.52	gb:NM_000971.1 /DEF=Homo sapiens ribosomal protein L7 (RPL7), mRNA. /FEA=mRNA /GEN=RPL7 /PROD=ri
209278_s_	2144.3	11890.1	5.54	gb:L27624.1 /DEF=Homo sapiens tissue factor pathway inhibitor-2 mRNA, complete cds. /FEA=mRNA /PROD=
210592_s_	3290	18257.4	5.55	gb:M55580.1 /DEF=Human spermidinespermine N1-acetyltransferase mRNA, complete cds. /FEA=mRNA /GEN
213037_x_	694.5	3888.9	5.6	Consensus includes gb:AJ132258.1 /DEF=Homo sapiens mRNA for staufen protein, partial. /FEA=mRNA /GEN
213614_x_	2743.9	15420.1	5.62	Consensus includes gb:BE786672 /FEA=EST /DB_XREF=gi:10207870 /DB_XREF=est:601475022F1 /CLONE=IM
201154_x_	893.5	5032.9	5.63	gb:NM_000968.1 /DEF=Homo sapiens ribosomal protein L4 (RPL4), mRNA. /FEA=mRNA /GEN=RPL4 /PROD=ri
200063_s_	1295.6	7328.9	5.66	gb:BC002398.1 /DEF=Homo sapiens, nucleophosmin (nucleolar phosphoprotein B23, numatrin), clone MGC:8
208695_s_	2990	16933.7	5.66	gb:BC001019.1 /DEF=Homo sapiens, ribosomal protein L39, clone MGC:1636, mRNA, complete cds. /FEA=mR
208635_x_	2784.2	15936.2	5.72	Consensus includes gb:BF976260 /FEA=EST /DB_XREF=gi:12343475 /DB_XREF=est:602245139F1 /CLONE=IM

200031_s_	1200.6	6890.2	5.74	gb:NM_001015.1 /DEF=Homo sapiens ribosomal protein S11 (RPS11), mRNA. /FEA=mRNA /GEN=RPS11 /PROD
204595_s_	933.4	5386.4	5.77	Consensus includes gb:AI300520 /FEA=EST /DB_XREF=gi:3959866 /DB_XREF=est:qn55e06.x1 /CLONE=IMAG
200741_s_	2597.2	14982.4	5.77	gb:NM_001030.1 /DEF=Homo sapiens ribosomal protein S27 (metallopanstimulin 1) (RPS27), mRNA. /FEA=mR
200933_x_	2595.8	14994.9	5.78	gb:NM_001007.1 /DEF=Homo sapiens ribosomal protein S4, X-linked (RPS4X), mRNA. /FEA=mRNA /GEN=RPS
200888_s_	1223.1	7088.4	5.8	gb:NM_000978.1 /DEF=Homo sapiens ribosomal protein L23 (RPL23), mRNA. /FEA=mRNA /GEN=RPL23 /PROD
208905_at	1341.9	7811.4	5.82	gb:BC005299.1 /DEF=Homo sapiens, cytochrome c, clone MGC:12367, mRNA, complete cds. /FEA=mRNA /PR
217732_s_	647.2	3774.3	5.83	gb:AF092128.1 /DEF=Homo sapiens putative transmembrane protein E3-16 mRNA, complete cds. /FEA=mRNA
201926_s_	1279.2	7463.9	5.83	gb:BC001288.1 /DEF=Homo sapiens, Similar to decay accelerating factor for complement (CD55, Crmer blood
201669_s_	589.3	3452.1	5.86	gb:NM_002356.4 /DEF=Homo sapiens myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
201293_x_	1282.3	7524.4	5.87	gb:NM_021130.1 /DEF=Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA. /FEA=mRNA /
202291_s_	1312.2	7758.4	5.91	gb:NM_000900.1 /DEF=Homo sapiens matrix Gla protein (MGP), mRNA. /FEA=mRNA /GEN=MGP /PROD=matri
213619_at	704.9	4179.6	5.93	Consensus includes gb:AV753392 /FEA=EST /DB_XREF=gi:10911240 /DB_XREF=est:AV753392 /CLONE=NPDA
201012_at	1330.8	7915.8	5.95	gb:NM_000700.1 /DEF=Homo sapiens annexin A1 (ANXA1), mRNA. /FEA=mRNA /GEN=ANXA1 /PROD=annexin
212537_x_	1402.7	8385	5.98	Consensus includes gb:BE733979 /FEA=EST /DB_XREF=gi:10147971 /DB_XREF=est:601571007F1 /CLONE=IM
200017_at	1797.9	10866.6	6.04	gb:NM_002954.1 /DEF=Homo sapiens ribosomal protein S27a (RPS27A), mRNA. /FEA=mRNA /GEN=RPS27A /P
213881_x_	813.4	4919.9	6.05	Consensus includes gb:AI971724 /FEA=EST /DB_XREF=gi:5768550 /DB_XREF=est:wr07a04.x1 /CLONE=IMAG
209386_at	2362.5	14285.1	6.05	Consensus includes gb:AI346835 /FEA=EST /DB_XREF=gi:4084041 /DB_XREF=est:qp58g11.x1 /CLONE=IMAG
212391_x_	2390.6	14505.6	6.07	Consensus includes gb:AI925635 /FEA=EST /DB_XREF=gi:5661686 /DB_XREF=est:wo34f07.x1 /CLONE=IMAG
200963_x_	3282.6	20050.8	6.11	gb:NM_000993.1 /DEF=Homo sapiens ribosomal protein L31 (RPL31), mRNA. /FEA=mRNA /GEN=RPL31 /PROD
221798_x_	1525.4	9384.6	6.15	Consensus includes gb:AI183766 /FEA=EST /DB_XREF=gi:3734404 /DB_XREF=est:qe17g06.x1 /CLONE=IMAG
213890_x_	1573.6	9809.5	6.23	Consensus includes gb:AI200589 /FEA=EST /DB_XREF=gi:3753195 /DB_XREF=est:qf99c03.x1 /CLONE=IMAGE
200893_at	593.5	3747	6.31	gb:NM_004593.1 /DEF=Homo sapiens splicing factor, arginineserine-rich (transformer 2 Drosophila homolog)
201041_s_	1334	8446.8	6.33	gb:NM_004417.2 /DEF=Homo sapiens dual specificity phosphatase 1 (DUSP1), mRNA. /FEA=mRNA /GEN=DUS
201094_at	2604.7	16623	6.38	gb:NM_001032.1 /DEF=Homo sapiens ribosomal protein S29 (RPS29), mRNA. /FEA=mRNA /GEN=RPS29 /PRO
211458_s_	1167.4	7479.6	6.41	gb:AF180519.1 /DEF=Homo sapiens GABA-A receptor-associated protein mRNA, complete cds. /FEA=mRNA /
200949_x_	2331.4	15167.4	6.51	gb:NM_001023.1 /DEF=Homo sapiens ribosomal protein S20 (RPS20), mRNA. /FEA=mRNA /GEN=RPS20 /PRO
209122_at	1439.5	9394.1	6.53	gb:BC005127.1 /DEF=Homo sapiens, adipose differentiation-related protein, clone MGC:10598, mRNA, comple
213080_x_	2274.4	15043	6.61	Consensus includes gb:BF214492 /FEA=EST /DB_XREF=gi:11108078 /DB_XREF=est:601845736F1 /CLONE=IM
213941_x_	1723.4	11415.6	6.62	Consensus includes gb:AI970731 /FEA=EST /DB_XREF=gi:5767485 /DB_XREF=est:wr14b05.x1 /CLONE=IMAG
200012_x_	1535.8	10353.4	6.74	gb:NM_000982.1 /DEF=Homo sapiens ribosomal protein L21 (gene or pseudogene) (RPL21), mRNA. /FEA=mR
200092_s_	1126.4	7612.2	6.76	Consensus includes gb:BF216701 /FEA=EST /DB_XREF=gi:11110287 /DB_XREF=est:601884615F1 /CLONE=IM
213101_s_	892.8	6046.6	6.77	Consensus includes gb:Z78330 /FEA=EST /DB_XREF=gi:1495103 /DB_XREF=est:HSZ78330 /CLONE=2.49 (CEP
212110_at	1027.5	6978.9	6.79	Consensus includes gb:D31887.1 /DEF=Human mRNA for KIAA0062 gene, partial cds. /FEA=mRNA /GEN=KIA
200673_at	1310.7	8905.8	6.79	gb:NM_014713.2 /DEF=Homo sapiens lysosomal-associated protein transmembrane 4 alpha (MBNT), mRNA. /
200026_at	2608.5	17905	6.86	gb:NM_000995.1 /DEF=Homo sapiens ribosomal protein L34 (RPL34), mRNA. /FEA=mRNA /GEN=RPL34 /PROD

200834_s_	1712	11959.3	6.99	gb:NM_001024.1 /DEF=Homo sapiens ribosomal protein S21 (RPS21), mRNA. /FEA=mRNA /GEN=RPS21 /PRO
201257_x_	2530	17777.3	7.03	gb:NM_001006.1 /DEF=Homo sapiens ribosomal protein S3A (RPS3A), mRNA. /FEA=mRNA /GEN=RPS3A /PRO
221775_x_	1217	8747.5	7.19	Consensus includes gb:BG152979 /FEA=EST /DB_XREF=gi:12665009 /DB_XREF=est:nah24c06.y1 /CLONE=IM
201590_x_	1491.1	10736.7	7.2	gb:NM_004039.1 /DEF=Homo sapiens annexin A2 (ANXA2), mRNA. /FEA=mRNA /GEN=ANXA2 /PROD=annexin
211378_x_	951.4	6895.1	7.25	gb:BC001224.1 /DEF=Homo sapiens, clone MGC:982, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (pr
217982_s_	761.6	5540.2	7.27	gb:NM_006791.1 /DEF=Homo sapiens MORF-related gene 15 (MRG15), mRNA. /FEA=mRNA /GEN=MRG15 /PRO
200735_x_	1985.4	14468.1	7.29	gb:NM_005594.1 /DEF=Homo sapiens nascent-polypeptide-associated complex alpha polypeptide (NACA), mR
204892_x_	2177.8	15972.1	7.33	gb:NM_001402.1 /DEF=Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA. /FE
214328_s_	1876.1	13880.9	7.4	Consensus includes gb:R01140 /FEA=EST /DB_XREF=gi:750876 /DB_XREF=est:ye88e02.s1 /CLONE=IMAGE:1
200062_s_	2150.6	16776	7.8	gb:L05095.1 /DEF=Homo sapiens ribosomal protein L30 mRNA, complete cds. /FEA=mRNA /PROD=ribosomal
201470_at	819.2	6404.8	7.82	gb:NM_004832.1 /DEF=Homo sapiens glutathione-S-transferase like; glutathione transferase omega (GSTTLp2
201631_s_	2236.9	17534.4	7.84	gb:NM_003897.1 /DEF=Homo sapiens immediate early response 3 (IER3), mRNA. /FEA=mRNA /GEN=IER3 /PRO
213988_s_	902.9	7088.8	7.85	Consensus includes gb:BE971383 /FEA=EST /DB_XREF=gi:10584719 /DB_XREF=est:601651561F1 /CLONE=IM
200091_s_	680	5368.3	7.89	Consensus includes gb:AA888388 /FEA=EST /DB_XREF=gi:3004063 /DB_XREF=est:nw79f03.s1 /CLONE=IMAG
201553_s_	741.2	5847.4	7.89	gb:NM_005561.2 /DEF=Homo sapiens lysosomal-associated membrane protein 1 (LAMP1), mRNA. /FEA=mRNA
200674_s_	1217.3	9642.7	7.92	gb:NM_000994.1 /DEF=Homo sapiens ribosomal protein L32 (RPL32), mRNA. /FEA=mRNA /GEN=RPL32 /PROD
203034_s_	1999	15886.9	7.95	gb:NM_000990.1 /DEF=Homo sapiens ribosomal protein L27a (RPL27A), mRNA. /FEA=mRNA /GEN=RPL27A /P
200004_at	774.6	6164.1	7.96	gb:NM_001418.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA. /FE
200095_x_	2104.3	16874.1	8.02	Consensus includes gb:AA320764 /FEA=EST /DB_XREF=gi:1973113 /DB_XREF=est:EST23183 /UG=Hs.76230 r
213503_x_	1211.1	9753	8.05	Consensus includes gb:BE908217 /FEA=EST /DB_XREF=gi:10402569 /DB_XREF=est:601500477F1 /CLONE=IM
214003_x_	3134.7	25221.9	8.05	Consensus includes gb:BF184532 /FEA=EST /DB_XREF=gi:11062829 /DB_XREF=est:601842837F1 /CLONE=IM
212790_x_	1547.7	12511.9	8.08	Consensus includes gb:BF942308 /FEA=EST /DB_XREF=gi:12359628 /DB_XREF=est:nae9111.x1 /CLONE=IMA
206559_x_	1729.1	13978.6	8.08	gb:NM_001403.1 /DEF=Homo sapiens eukaryotic translation elongation factor 1 alpha 1-like 14 (EEF1A1L14), m
211999_at	690.6	5650.7	8.18	Consensus includes gb:Z48950 /DEF=H.sapiens hH3.3B gene for histone H3.3 /FEA=mRNA /DB_XREF=gi:7617
211487_x_	1658.6	13607	8.2	gb:BC004886.1 /DEF=Homo sapiens, ribosomal protein S17, clone MGC:11144, mRNA, complete cds. /FEA=m
211720_x_	1466.5	12164.6	8.29	gb:BC005863.1 /DEF=Homo sapiens, ribosomal protein, large, P0, clone MGC:3679, mRNA, complete cds. /FE
212190_at	954.6	7941.5	8.32	Consensus includes gb:AL541302 /FEA=EST /DB_XREF=gi:12872241 /DB_XREF=est:AL541302 /CLONE=CS0D
203887_s_	984.8	8190.6	8.32	gb:NM_000361.1 /DEF=Homo sapiens thrombomodulin (THBD), mRNA. /FEA=mRNA /GEN=THBD /PROD=throm
212578_x_	1352.8	11274.2	8.33	Consensus includes gb:BF026595 /FEA=EST /DB_XREF=gi:10734307 /DB_XREF=est:601672736F1 /CLONE=IM
202437_s_	600	5003.1	8.34	gb:NM_000104.2 /DEF=Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucom
214143_x_	1773.2	15411.2	8.69	Consensus includes gb:AL560573 /FEA=EST /DB_XREF=gi:4510914 /DB_XREF=est:tq49c03.x1 /CLONE=IMAGE
200061_s_	1920.7	16875.1	8.79	gb:BC000523.1 /DEF=Homo sapiens, Similar to ribosomal protein S24, clone MGC:8595, mRNA, complete cds.
208724_s_	940.4	8294.3	8.82	gb:BC000905.1 /DEF=Homo sapiens, RAB1, member RAS oncogene family, clone MGC:5233, mRNA, complete
212270_x_	1133.2	10284.4	9.08	Consensus includes gb:BG168283 /FEA=EST /DB_XREF=gi:12674986 /DB_XREF=est:602340822F1 /CLONE=IM
212788_x_	1263.5	11695.2	9.26	Consensus includes gb:BG537190 /FEA=EST /DB_XREF=gi:13528922 /DB_XREF=est:602565589F1 /CLONE=IM

208856_x_	1383.4	12928.9	9.35	gb:BC003655.1 /DEF=Homo sapiens, ribosomal protein, large, P0, clone MGC:4770, mRNA, complete cds. /FE
210646_x_	1707.8	16605.5	9.72	gb:BC001675.1 /DEF=Homo sapiens, ribosomal protein L13a, clone MGC:2546, mRNA, complete cds. /FEA=m
200019_s_	892.4	9007.9	10.09	gb:Nm_001997.1 /DEF=Homo sapiens Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously exp
210427_x_	1020.3	10703	10.49	gb:BC001388.1 /DEF=Homo sapiens, annexin A2, clone MGC:2257, mRNA, complete cds. /FEA=mRNA /PROD=
200021_at	1649.5	17811.9	10.8	gb:Nm_005507.1 /DEF=Homo sapiens cofilin 1 (non-muscle) (CFL1), mRNA. /FEA=mRNA /GEN=CFL1 /PROD=c
201665_x_	1295.2	14814.3	11.44	gb:Nm_001021.1 /DEF=Homo sapiens ribosomal protein S17 (RPS17), mRNA. /FEA=mRNA /GEN=RPS17 /PRO
213377_x_	1148	13261.5	11.55	Consensus includes gb:A1799007 /FEA=EST /DB_XREF=gi:5364479 /DB_XREF=est:we97d07.x1 /CLONE=IMAG
205207_at	1943.8	23225.5	11.95	gb:Nm_000600.1 /DEF=Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /FEA=mRNA /GEN=IL6 /PR
204748_at	1536.6	19127.7	12.45	gb:Nm_000963.1 /DEF=Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase an
36711_at	690.9	8765.9	12.69	Cluster Incl. AL021977:bK447C4.1 (novel MAFF (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene fa
213588_x_	772.8	10980.4	14.21	Consensus includes gb:AA838274 /FEA=EST /DB_XREF=gi:2913073 /DB_XREF=est:oe90c01.s1 /CLONE=IMAG
208864_s_	671.4	9722.7	14.48	gb:AF313911.1 /DEF=Homo sapiens thioredoxin mRNA, complete cds. /FEA=mRNA /PROD=thioredoxin /DB_X