

**Differential Gene Expression in Explanted Human Retinal Pigment Epithelial Cells
24-hours Post-Exposure to 532 nm, 3.0 ns Pulsed Laser Light and 1064 nm, 170 ps
Pulsed Laser Light 12-hours Post-Exposure: Results Compendium**

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Differential Gene Expression in Explanted Human Retinal Pigment Epithelial Cells 24 hours Post-Exposure to 532 nm, 3.0 ns Pulsed Laser-Light and 1064 nm, 170 ps Pulsed Laser-Light 12 hours Post-Exposure: Results Compendium

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 and 24 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 two experiments presented herein are intended to add to the database of laser-tissue interaction at the molecular level using gene expression profiling as the assessment endpoint. This investigative approach also showcases a global methodology for characterizing environmental stressors on a living system via genetic profiling and hallmarks the use of human explants as an experimental model for assessing laser-induced bioeffects at the cell and molecular level. Additionally, we offer 3 conceptual cartoons outlining our vision for the future progress of laser bioeffects research, metabonomic risk assessment modeling and knowledge building from laser bioeffects data.

BACKGROUND

In the interest of brevity the reader is referred to USAFA-TR 2004-01 for the background.

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.

This report provides the results of two gene expression experiments. The first was a 532 nm, nanosecond pulse width exposure designated as N2. The second was a 1064 nm, picosecond pulse width exposure designated as P4.

Donor:

The RPE tissue donor for N2 was a 65 year old Caucasian, blue eyed, male that died of cancer. The RPE tissue donor for P4 was a 41 year old Caucasian, blue eyed, female that died of cancer. No ocular pathologies were noted.

Explant preparation: See USAFA-TR-2004-01

Laser: Equipment Used for N2

Laser (Nd:YAG)	Coherent Infinity XPO Laser
Power Meter	Scientech Power Meter model S310
Detector Head	Scientech model PHDX50
Shutter	nmLaser model LS055S3W8
Shutter Controller	nmLaser model CX2450
Velmex XY Stage	model NF90-2

Laser: Equipment Used for P4

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

In both exposures the 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:

For procedures see USAFA-TR-2004-01. In the table below are the exposure parameters for the experiments reported herein.

Treatment	N2	P4
Wavelength (nm)	532	1064
Average Power (mW)	508	1150
Pulse Energy (mJ)	50.8 ± 1.2	115 ± 5
Pulse Length (FWHM)	3.0 ns	170 ps
Total Incident Energy (mJ)	3251	3220
Peak Power (W)	1.69 x 10 ⁷	6.76 x 10 ⁸
Fluence (mJ/cm ²)	108	244
Exposure Time (sec)	6.4	2.8
Laser Repetition Rate (Hz)	10	10
Beam Diameter (1/e ²)	6 mm	6 mm
Irradiance (kW/m ²)	18.0	40.7

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 for treatment N2 was calculated to be 1.8 kJ/m² which is about 10% of the MVL value and approximately 65% above the MPE for the pulse width and wavelength considered (Sloney and Wolbarsht, 1980 and ANZI Z136.1-2000 Table 5a). The exposure described above for treatment P4 was calculated to be 4.1 kJ/m² which is about 16% 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).

In experiment N2 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 50.8 mJ ± 1.2 mJ (on average) of energy was delivered to a microtiter plate well 6 mm in diameter containing 50 microliters of medium. In experiment P4 the cells were exposed to either 1) sham exposed to no laser-light (beam blocked upstream), or 2) 28 pulses of 1064 nm visible laser-light. Each pulse containing 115.5 mJ ± 5 mJ (on

average) of energy was delivered to a microtiter plate well 6 mm in diameter containing 50 microliters of medium. See Figure 2 in USAFA-TR-2004-01 for a general overview of the experimental procedures.

Exposed RPE collection

Sample N2 was harvested 24 hours post-exposure for gene chip analysis; while sample P4 was harvested at 12 hours post-exposure. A "C" beginning the sample designation (i.e. CP4 or CN2) indicates the control sample for comparison. The "HX" designation indicates the use of human explanted tissue as the experimental model. See USAFA-TR-2004-01 for further procedural details.

Oligonucleotide Microarray Description Protocol and Analysis:

See USAFA-TR-2004-01.

For a 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.

RESULTS

The results (Appendix A and B) 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 labeled N2 and P4 the confidence was calculated to be +/- 1.2 for both.

Appendices A and B presents the most pertinent genes (at or above the absolute value for significance) listed in rank ordered by absolute fold change minus to plus at or above the significance value. 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 at the minimum significance level or higher that has been calculated to be at or above the statistical significance of 95%.

For experiment N2 a quick survey of the Fold Change (Figure 1), Variable Bin Histogram (Figure 2) and Differential Expression Scatter Plot (Figure 3) (internal controls are not in the graph data set) and Appendix A yields the observation that RPE mRNA was above 1.2 absolute fold change in 146 of the approximately 22, 000 (approximately 0.7%) probe elements on the GEM. Of those 77 (0.4% of the total possible elements and 52.7% of the significantly expressed elements) were up-regulated. The number of genes whose expression was down regulated was markedly less. 68 (0.3% of the total possible elements and 46.6% of the significantly expressed elements) genes were down-regulated at or above significant levels. In summary, the number of significant changes in gene expression was approximately equal in the up-regulated direction versus down-regulated direction, but the greatest magnitude of change for single genes was up-regulation with over two times greater fold change.

For experiment P4 a quick survey of the Differential Expression Scatter Plot (Figure 4) (internal controls are not in the graph data set) and Appendix B yields the observation that RPE mRNA was above 1.2 absolute fold change in 408 of the approximately 22, 000 (approximately 1.9%) probe elements on the GEM. Of those 324 (1.5% of the total possible elements and 79.4% of the significantly expressed elements) were up-regulated. The number of genes whose expression was down regulated was markedly less. 83 (0.4% of the total possible elements and 20.3% 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 4 times), and the greatest magnitude of change for single genes (over 2 times) was also up-regulation.

DISCUSSION

Selected genes and ESTs from Appendices A and B can be reviewed as to the physiological function and/or biological marker for which they are known whenever possible. Also note that the appendices contain 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 recent updates of the NCBI genomic database, several ESTs in the appendices have been assigned

genetic/physiologic functions. However, other EST's that were differentially regulated functions remain unknown thus remain fertile ground for future exploration and analysis. Gene functions can easily be located through a PubMed query in the NCBI searchable database format found in the appendices.

These two experimental data sets are offered as a contribution to the continuing efforts in understanding the response of RPE to the exposure of high energy pulsed laser-light exposure using gene expression profiling 12 hours and 24 hours post-exposure. In the multi-dimensional hyper-volume of laser settings versus various tissues' response and time of response post-exposure, these can provide insights at specific matrix data points to possible perturbation to cellular physiology to include aspects of damage, repair and decreased/absent/rescued function.

Closing

As a closing comment we offer the following observation: These are the last gene expression profile experiments using Affymetrix GeneChip technology done in the Laser and Optics Research Center, Department of Physics, United States Air Force Academy. We highly recommend that this type of work, started here, be continued to aid in understanding the effect of laser-light exposure on affected human tissue. This use of living human cadaver donor tissue marks a major step forward toward assessing the cellular perturbation to be expected in the human organism and should be strongly considered as an experimental model until such time as the tissue microarray and organotypic model technologies more closely approximate the *in vivo* human response. We also suggest the employment of various statistical modeling techniques such as Taguchi's to establish the relevant orthogonal contrasts in the multi-dimensional hypervolume of laser settings versus biological response endpoints to rationally define the pertinent experimental data points to appropriately model laser-tissue interaction. In the context of more in depth analysis of the gene expression data, numerous higher order software platforms offer advance analyses, some employing artificial intelligence capabilities. As a closing thought we are attaching our concepts of future laser bioeffects research directions (Figure 5), a metabonomic risk assessment model of laser tissue interaction (Figure 6), and some suggestions for the transition to knowledge building/modeling from data collection (Figure 7) in laser bioeffects research.

Figure 1.

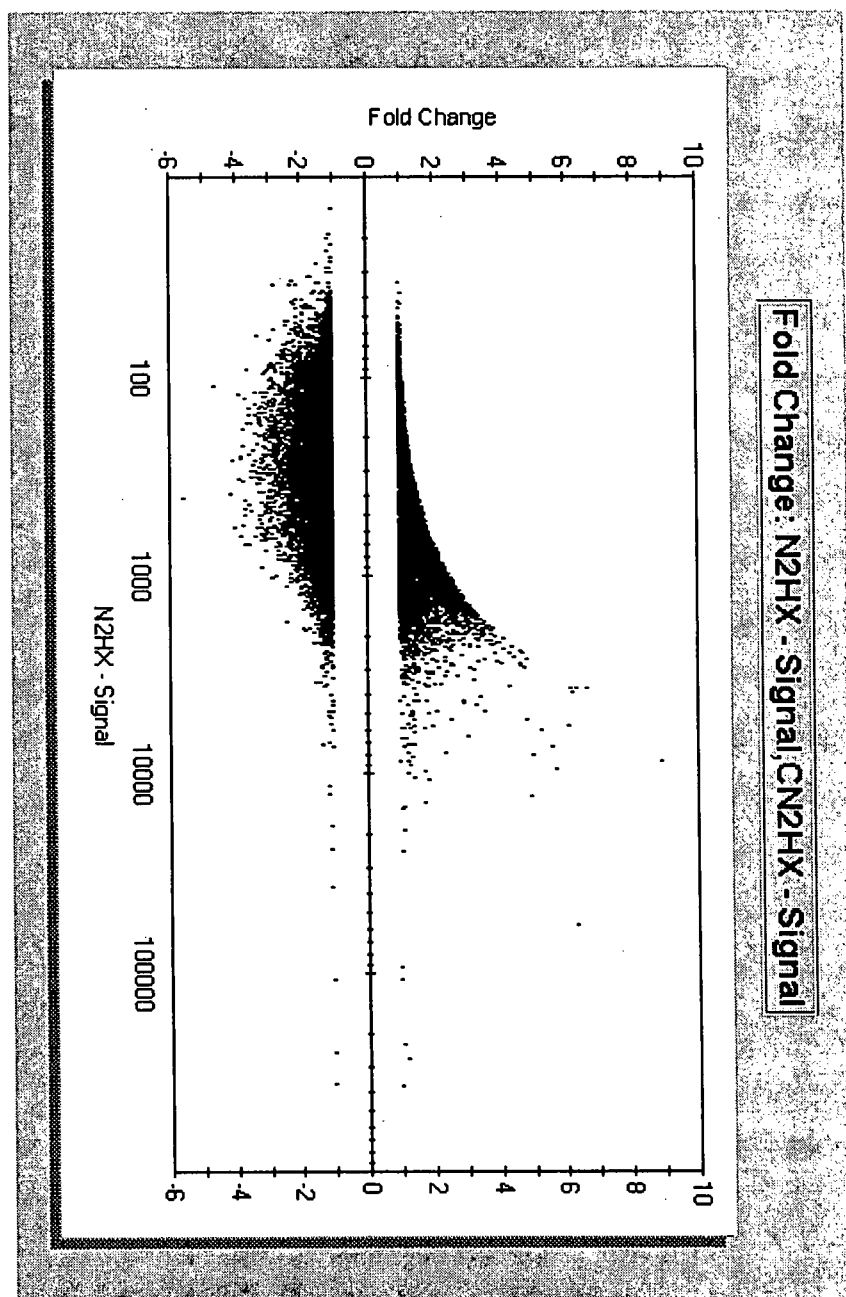


Figure 2.

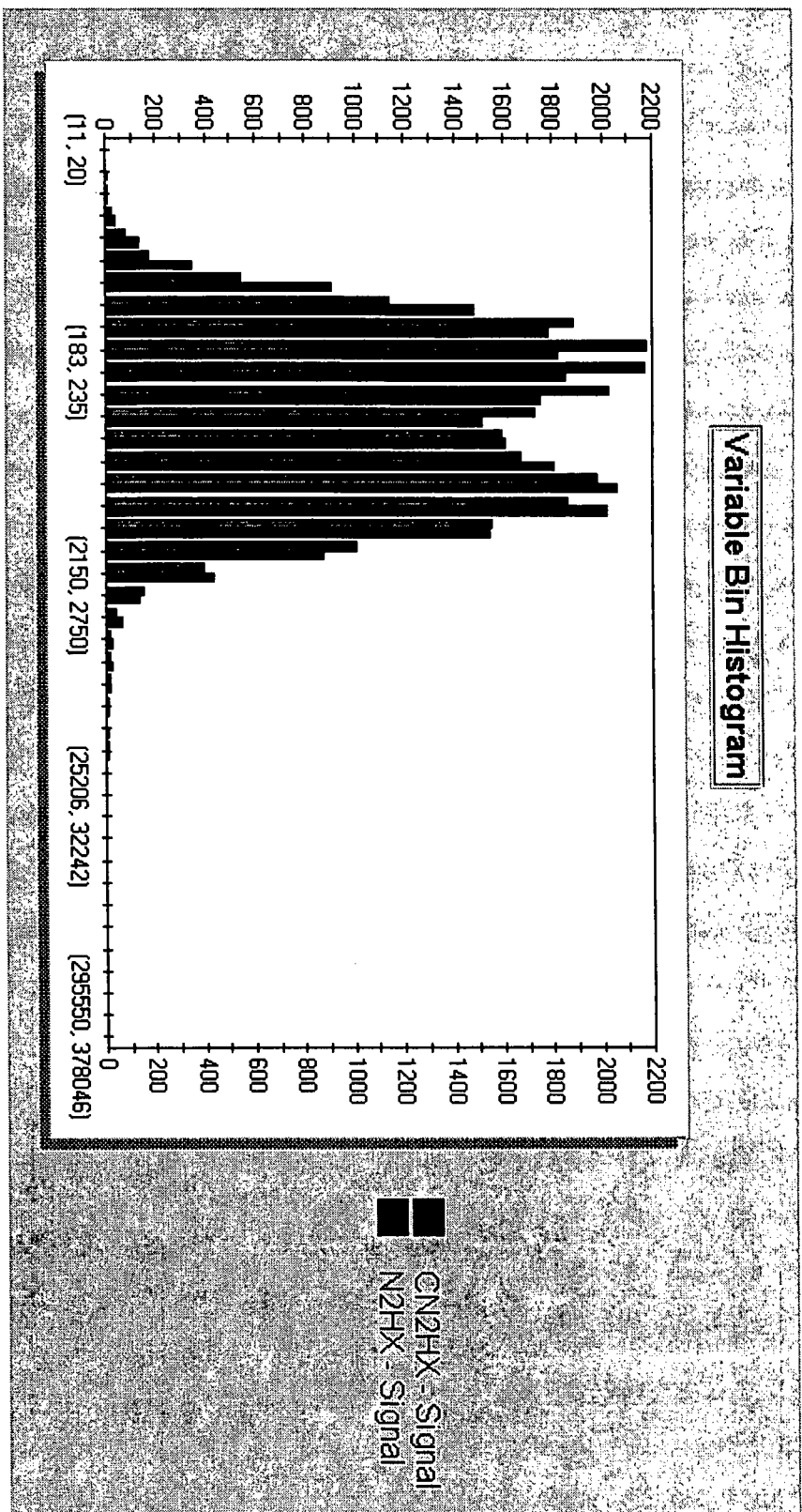


Figure 3.

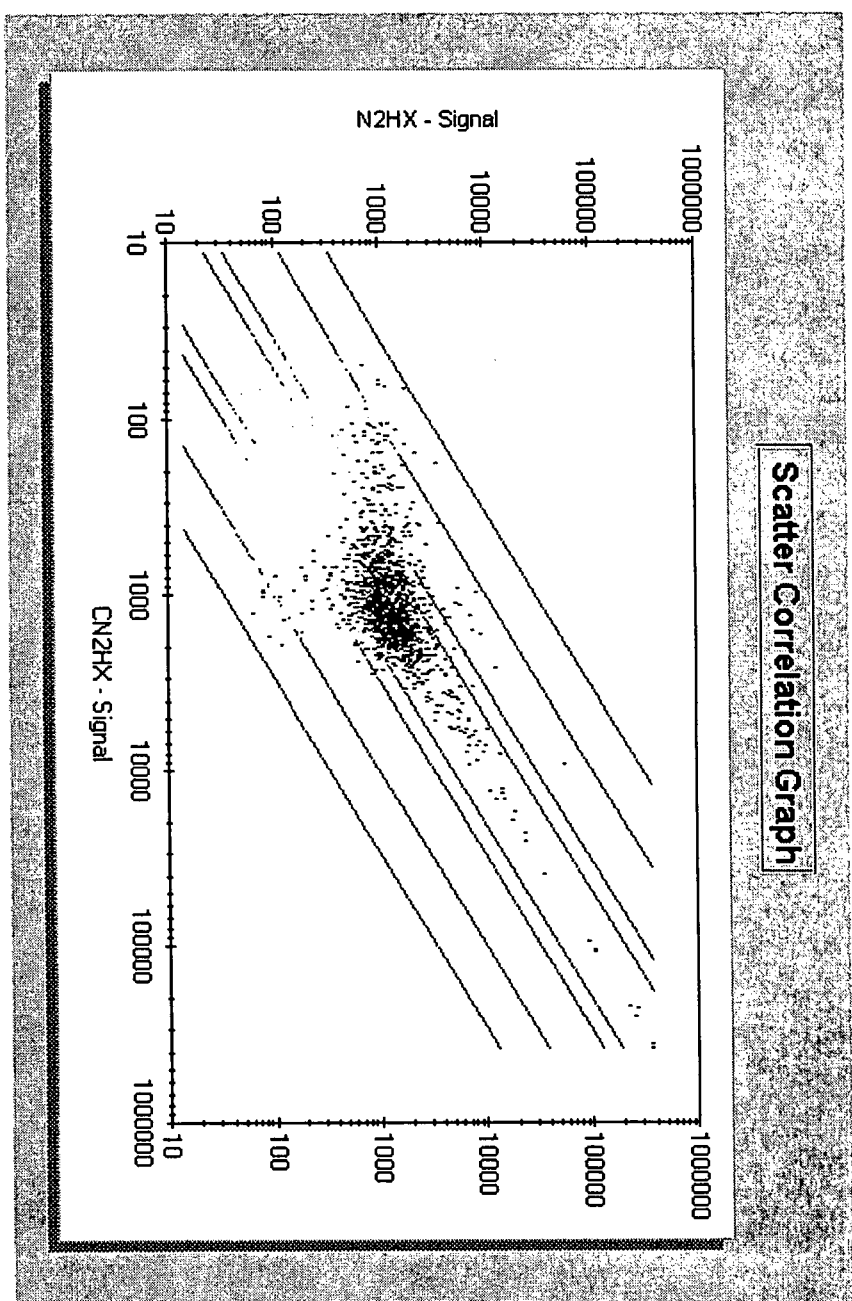


Figure 4.

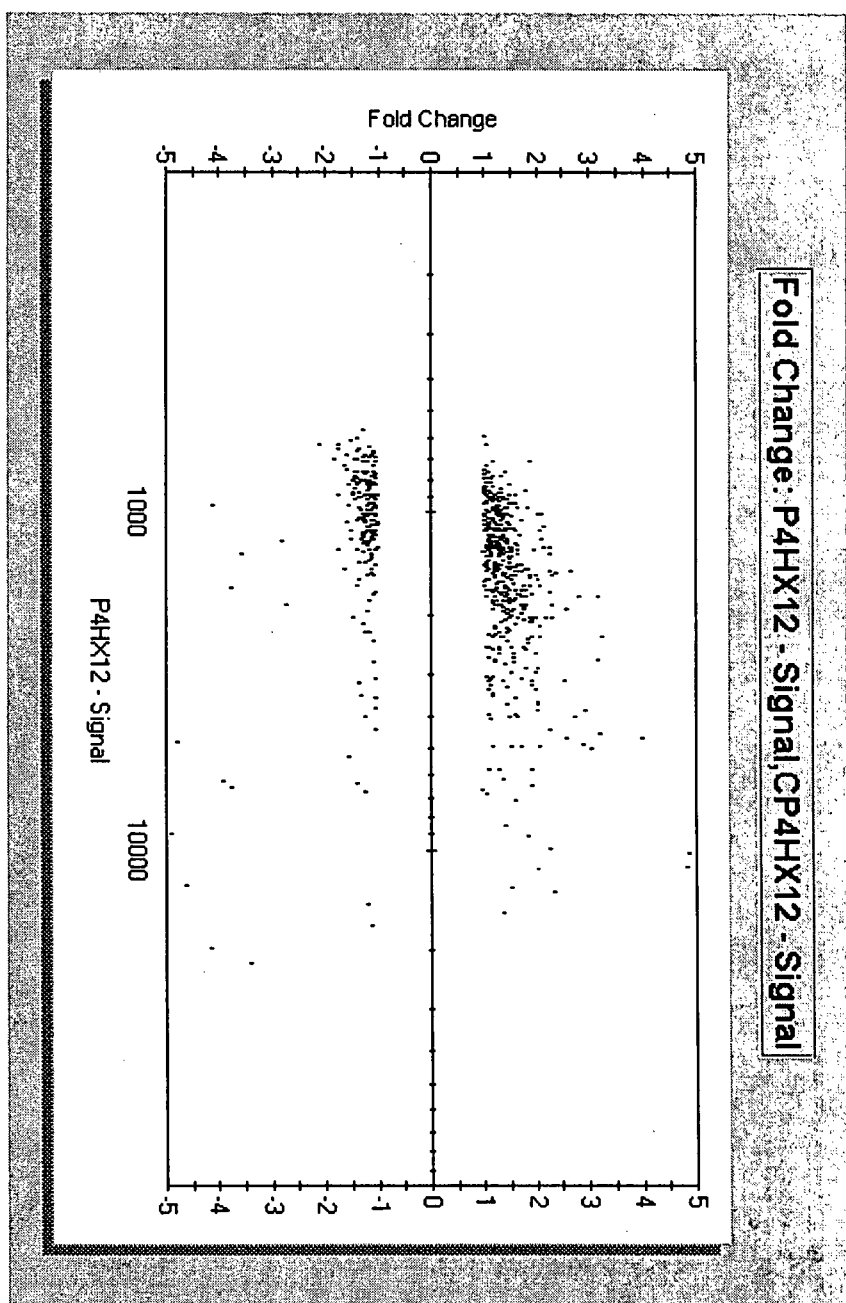


Figure 5.

LASER BIOEFFECTS

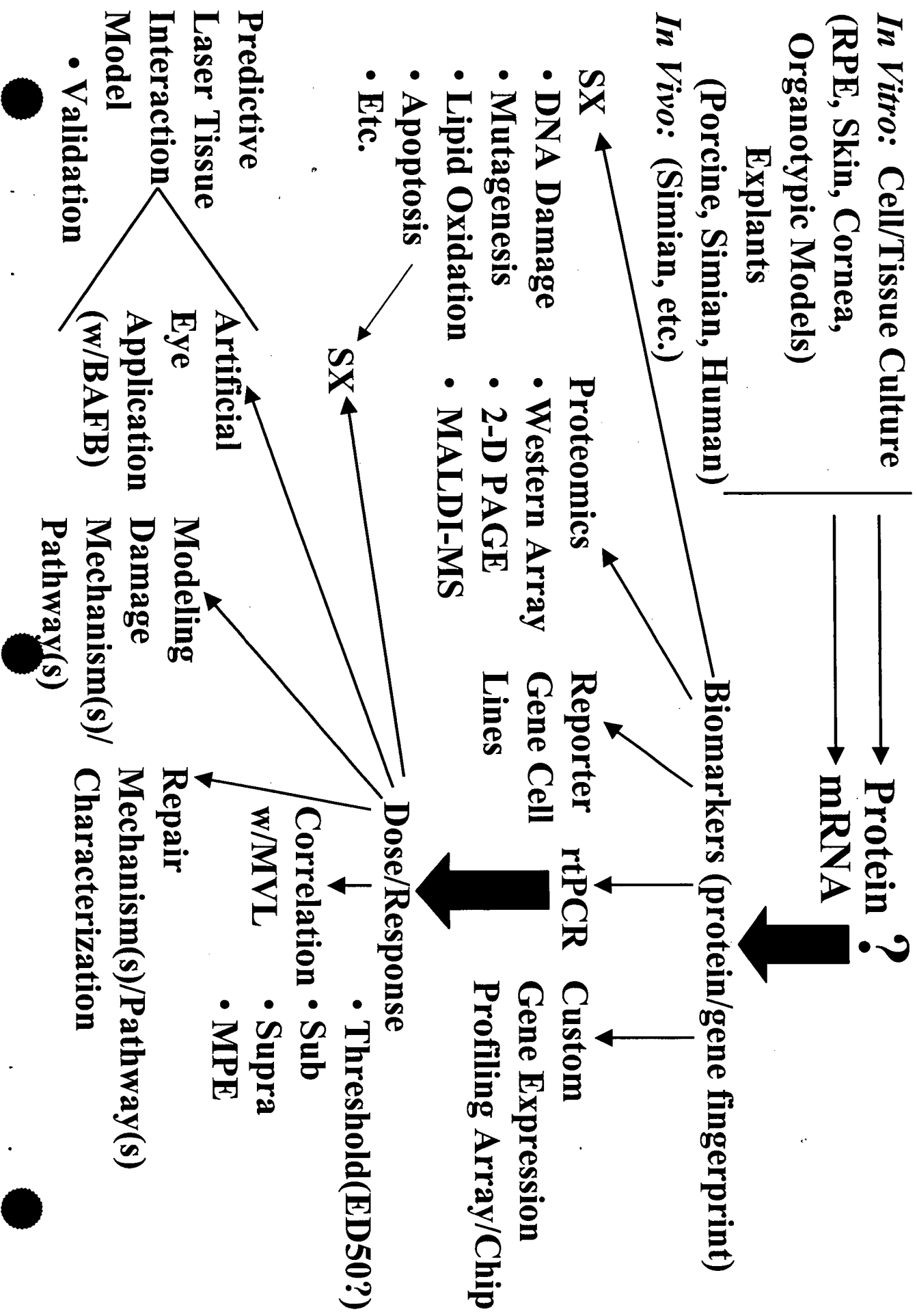


Figure 6.

METABONOMIC RISK ASSESSMENT

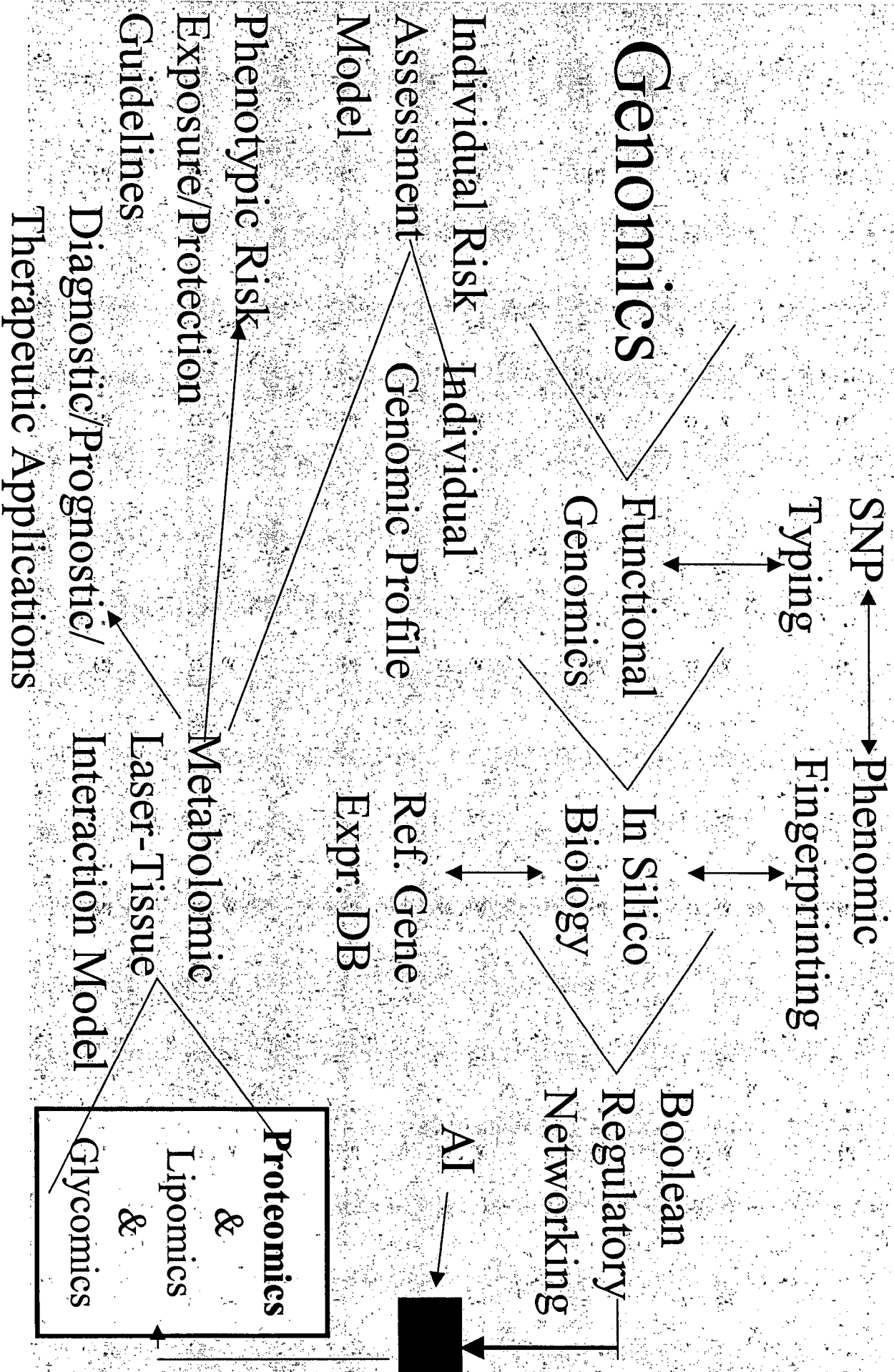


Figure 7.

KNOWLEDGE BUILDING

(Transition from data collection)

- Statistical Design
 - Multi-Dimensional Hyper-Volume (laser settings)
 - Orthogonal Contrasts Drive Experimental Design
 - Biological Endpoints
- Bioinformatics
 - Integrative Platform (data mining)
 - Central Repository
 - Biomarker Discovery/Validation
- Retrospective Analysis-MVL
 - Clinical data correlated to histo/cell/molecular data
 - Exposures/Metabolic Homology/Bridging Experiments
- Collaboration=Max. Efficiency/Integration/Holism

Appendix A.

Probe set	CN2HX Signal	N2HX Signal	CN2 vs N2 Fold Change	Description
212917_x_at	922.1	325.2	-2.84	Consensus includes gb:A1814728 /FEA=EST /DB_XREF=gi:5425943 /DB_XREF=est:wk66h11.x1 /CL
217715_x_at	2715.5	989	-2.75	Consensus includes gb:BE045142 /FEA=EST /DB_XREF=gi:8362195 /DB_XREF=est:hn26h02.x1 /C
220625_s_at	2057.1	822.4	-2.5	gb:AF115403.1 /DEF=Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds. /FEA=m
214421_x_at	2212.3	980.6	-2.26	Consensus includes gb:AV652420 /FEA=EST /DB_XREF=gi:3873434 /DB_XREF=est:AV652420 /CLO
215823_x_at	1145.2	527.9	-2.17	Consensus includes gb:U64661 /DEF=Human poly(A)-binding protein processed pseudogene3 /FE
201060_x_at	2178.8	1033.6	-2.11	Consensus includes gb:A1537887 /FEA=EST /DB_XREF=gi:4452022 /DB_XREF=est:tp32g06.x1 /CLO
218807_at	2276.8	1078	-2.11	gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mRNA /GEN=VAV3 /PR
211504_x_at	1971.2	1023.7	-1.93	gb:D87931.1 /DEF=Homo sapiens mRNA for Rho kinase, complete cds. /FEA=mRNA /PROD=Rho k
207684_at	1584.6	837.8	-1.89	gb:NM_004608.1 /DEF=Homo sapiens T-box 6 (TBX6), mRNA. /FEA=mRNA /GEN=TBX6 /PROD=T-b
203758_at	1343.5	714.1	-1.88	Consensus includes gb:AV729484 /FEA=EST /DB_XREF=gi:10838905 /DB_XREF=est:AV729484 /CL
215112_x_at	932.7	519.2	-1.8	Consensus includes gb:AB020668.1 /DEF=Homo sapiens mRNA for KIAA0861 protein, partial cds.
208114_s_at	2260.9	1268.9	-1.78	gb:NM_030980.1 /DEF=Homo sapiens hypothetical protein FLJ12671 (FLJ12671), mRNA. /FEA=mR
213881_x_at	2545.9	1440.9	-1.77	Consensus includes gb:A1971724 /FEA=EST /DB_XREF=gi:5768550 /DB_XREF=est:wr07a04.x1 /CL
206434_at	1636.1	962.6	-1.7	gb:NM_016950.1 /DEF=Homo sapiens testican 3 (HSAJ1454), mRNA. /FEA=mRNA /GEN=HSAJ1454
202594_at	1182.6	699.7	-1.69	gb:NM_015344.1 /DEF=Homo sapiens MY047 protein (MY047), mRNA. /FEA=mRNA /GEN=MY047 /P
204252_at	1613.4	970.3	-1.66	gb:M68520.1 /DEF=Human cdc2-related protein kinase mRNA, complete cds. /FEA=mRNA /PROD=c
217097_s_at	1040.5	629.3	-1.65	Consensus includes gb:AC004990 /DEF=Homo sapiens PAC clone RPS-118517 from 7q11.23-q21 /F
216801_at	2056.3	1258	-1.63	Consensus includes gb:AK026910.1 /DEF=Homo sapiens cDNA: FLJ23257 fts, clone COL05579. /FE
49327_at	3438.9	2176.6	-1.58	Cluster incl. A1492888:th78c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2124784 /clone_end=
212749_s_at	1527.2	971.5	-1.57	Consensus includes gb:A1096477 /FEA=EST /DB_XREF=gi:3445971 /DB_XREF=est:qa03c06.x1 /CL
222252_x_at	3007.9	1920	-1.57	Consensus includes gb:AK023354.1 /DEF=Homo sapiens cDNA FLJ13292 fts, clone OVARC100118
207788_s_at	1566.8	1025.8	-1.53	gb:NM_005775.1 /DEF=Homo sapiens vinexin beta (SH3-containing adaptor molecule-1) (SCAM-1),
65635_at	5209.2	3401.8	-1.53	Cluster incl. AL044097:DKFZp434M1928_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434M1928 /c
207265_s_at	2283	1502.5	-1.52	gb:NM_016657.1 /DEF=Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein rete
214222_at	1673.7	1132.2	-1.48	Consensus includes gb:AB023161.1 /DEF=Homo sapiens mRNA for KIAA0944 protein, partial cds.
214902_x_at	2298	1556.6	-1.48	Consensus includes gb:AL080232.1 /DEF=Homo sapiens mRNA: cDNA DKFZp586A061 (from clone
49878_at	3230.3	2181.2	-1.48	Cluster incl. AA523441:ng30d08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-936303 /clone_end=
212896_at	879.8	612.4	-1.44	Consensus includes gb:D29641.2 /DEF=Homo sapiens mRNA for KIAA0052 protein, partial cds. /FE
209130_at	1213.7	845.8	-1.43	gb:BC003686.1 /DEF=Homo sapiens, synaposomal-associated protein, 23kD, clone MGC:5155, mR
218374_s_at	1580.8	1110.2	-1.42	gb:NM_020374.1 /DEF=Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA. /F
200630_x_at	2728.4	1919.4	-1.42	Consensus includes gb:AV702810 /FEA=EST /DB_XREF=gi:10719140 /DB_XREF=est:AV702810 /CL
220290_at	1399.6	997.9	-1.4	gb:NM_017977.1 /DEF=Homo sapiens hypothetical protein FLJ10040 (FLJ10040), mRNA. /FEA=mR

218020_s_at	1899	1358.6	-1.4	gb:NM_021943.1/DEF=Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA. /FEA=mR
211918_x_at	2309.7	1654.7	-1.4	gb:AF311940.1/DEF=Homo sapiens pregnancy-associated plasma preproprotein-A2 mRNA, compl
200662_s_at	2076.6	1499	-1.39	gb:NM_014765.1/DEF=Homo sapiens translocase of outer mitochondrial membrane 20 (yeast) hom
208020_s_at	1272	923.7	-1.38	gb:NM_000719.1/DEF=Homo sapiens calcium channel, voltage-dependent, L type, alpha 1C subun
212261_at	2753.3	2006.7	-1.37	Consensus includes gb:AB014542.1/DEF=Homo sapiens mRNA for KIAA0642 protein, partial cds.
200012_x_at	1571.5	1155.6	-1.36	gb:NM_000982.1/DEF=Homo sapiens ribosomal protein L21 (gene or pseudogene) (RPL21), mRNA
222370_x_at	1986.5	1458.4	-1.36	Consensus includes gb:N57781/FEA=EST/DB_XREF=gi:1201671/DB_XREF=est:vv56g05.s1/CLO
56197_at	3832.8	2838.1	-1.35	Cluster Incl. A1783924:tr30e11.x1 Homo sapiens cDNA, 3 end/clone=IMAGE-2219852/clone_end=3
217497_at	1261.3	943.1	-1.34	Consensus includes gb:AW613387/FEA=EST/DB_XREF=gi:7318573/DB_XREF=est:hh71e04.x1/C
213226_at	1237.6	930.3	-1.33	Consensus includes gb:A1346350/FEA=EST/DB_XREF=gi:4083556/DB_XREF=est:qp50c06.x1/CL
213798_s_at	2376.8	1780.5	-1.33	Consensus includes gb:AA806142/FEA=EST/DB_XREF=gi:2874892/DB_XREF=est:oe29d06.s1/C
200763_s_at	2612.7	1974.5	-1.32	gb:NM_001003.1/DEF=Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA. /FEA=mRNA/G
220015_at	2899.9	2204.7	-1.32	gb:NM_017766.1/DEF=Homo sapiens hypothetical protein FLJ20321 (FLJ20321), mRNA. /FEA=mR
216187_x_at	9297	7096.3	-1.31	Consensus includes gb:AF222691.1/DEF=Homo sapiens Alu repeat (LNX1) mRNA sequence. /FEA
215019_x_at	3189.9	2462.1	-1.3	Consensus includes gb:AW474158/FEA=EST/DB_XREF=gi:7044264/DB_XREF=est:xy11f01.x1/CL
222329_x_at	4701.1	3629.1	-1.3	Consensus includes gb:AW974816/FEA=EST/DB_XREF=gi:8166019/DB_XREF=est:EST386921/U
219938_s_at	1194.6	922.6	-1.29	gb:NM_024430.1/DEF=Homo sapiens proline-serine-threonine phosphatase interacting protein 2 (P
218143_s_at	2299.2	1781.5	-1.29	gb:NM_005697.2/DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FE
206916_x_at	2861.6	2235.8	-1.28	gb:NM_000353.1/DEF=Homo sapiens tyrosine aminotransferase (TAT), nuclear gene encoding mit
214034_at	1326.9	1046.8	-1.27	Consensus includes gb:AB011097.1/DEF=Homo sapiens mRNA for KIAA0525 protein, partial cds.
201143_s_at	1136.1	901.9	-1.26	gb:BC002513.1/DEF=Homo sapiens, eukaryotic translation initiation factor 2, subunit 1 (alpha, 35k
210927_x_at	1777.1	1412.7	-1.26	gb:BC004239.1/DEF=Homo sapiens, jumping translocation breakpoint, clone MGC:10274, mRNA, c
215478_at	1388.9	1111.4	-1.25	Consensus includes gb:AF007156.1/DEF=Homo sapiens clone 23617 unknown mRNA, partial cds.
217406_at	1932.6	1548.7	-1.25	Consensus includes gb:AL021937/DEF=Human DNA sequence from clone RP1-149A16 on chromo
215607_x_at	2606	2076.8	-1.25	Consensus includes gb:AU144530/FEA=EST/DB_XREF=gi:11006051/DB_XREF=est:AU144530/CL
214869_x_at	1127.2	910	-1.24	Consensus includes gb:AK021533.1/DEF=Homo sapiens cDNA FLJ11471 f1s, clone HEMBA100167
210840_s_at	1563.4	1269.9	-1.23	gb:D29640.1/DEF=Human mRNA for KIAA0051 gene, complete cds. /FEA=mRNA/GEN=KIAA0051
214135_at	1740.1	1417.9	-1.23	Consensus includes gb:BE551219/FEA=EST/DB_XREF=gi:9792911/DB_XREF=est:7b56b11.x1/CL
203899_s_at	1780.4	1448.8	-1.23	gb:NM_014478.1/DEF=Homo sapiens calcitonin gene-related peptide-receptor component protein
213612_x_at	2957.5	2397.5	-1.23	Consensus includes gb:A1800419/FEA=EST/DB_XREF=gi:5365891/DB_XREF=est:tf14b09.x1/CLO
35150_at	3243.7	2635.7	-1.23	Cluster Incl. X60592:Human CDw40 mRNA for nerve growth factor receptor-related B-lymphocyte a
206336_at	1133.4	932.4	-1.22	gb:NM_002993.1/DEF=Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 6
216993_s_at	3147.8	2583.4	-1.22	Consensus includes gb:U32169/DEF=Human pro-a2 chain of collagen type XI (COL11A2) gene, co
211115_x_at	1285	1064.1	-1.21	gb:AB037703.1/DEF=Homo sapiens SIP1-delta mRNA for SMN interacting protein 1-delta, complet
217484_at	1593.5	1326.5	-1.2	Consensus includes gb:X14362.1/DEF=Human CR1 mRNA for C3bC4b receptor secreted form. /FE

203297_s_at	2019.8	1685.1	-1.2	Consensus includes gb:BG029530 /FEA=EST /DB_XREF=gi:12418626 /DB_XREF=est:602297090F1
36888_at	4267.1	3560.4	-1.2	Cluster Incl. AB020648:Homo sapiens mRNA for KIAA0841 protein, partial cds /cds=(0,1925) /gb=A
216220_s_at	1209.3	1462.8	1.21	Consensus includes gb:X68485.1 /DEF=H.sapiens mRNA for A1 adenosine receptor. /FEA=mRNA /
201649_at	1602.4	1937.1	1.21	gb:NM_004223.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2L 6 (UBE2L6), mRNA. /FEA=
218269_at	1044.9	1269.9	1.22	gb:NM_013235.1 /DEF=Homo sapiens putative ribonuclease III (RNASE3L), mRNA. /FEA=mRNA /GE
204517_at	1136.1	1388.4	1.22	Consensus includes gb:BE962749 /FEA=EST /DB_XREF=gi:11765968 /DB_XREF=est:601656143R1
219410_at	1165.6	1426.8	1.22	gb:NM_018004.1 /DEF=Homo sapiens hypothetical protein FLJ10134 (FLJ10134), mRNA. /FEA=mR
221158_at	1402.6	1708.3	1.22	gb:NM_013329.1 /DEF=Homo sapiens GC-rich sequence DNA-binding factor candidate (GCFC), mR
215383_x_at	3715.8	4515.3	1.22	Consensus includes gb:AL137312.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761K23121 (from clo
217810_x_at	2031.2	2504.9	1.23	gb:NM_020117.1 /DEF=Homo sapiens hypothetical protein FLJ10595 (FLJ10595), mRNA. /FEA=mR
216159_s_at	1206.8	1512.8	1.25	Consensus includes gb:AK023757.1 /DEF=Homo sapiens cDNA FLJ13695 fts, clone PLACE2000124
208591_s_at	1688.9	2110.3	1.25	gb:NM_000922.1 /DEF=Homo sapiens phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA. /FE
200989_at	1704	2154.2	1.26	gb:NM_001530.1 /DEF=Homo sapiens hypoxia-inducible factor 1, alpha subunit (basic helix-loop-h
201404_x_at	4464.7	5656.3	1.27	gb:BC000268.1 /DEF=Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 2, cion
206792_x_at	7879.1	9990	1.27	gb:NM_000923.1 /DEF=Homo sapiens phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-h
212208_at	1460.7	1877.9	1.29	Consensus includes gb:AK023837.1 /DEF=Homo sapiens cDNA FLJ13775 fts, clone PLACE4000369
220352_x_at	1469.7	1925.3	1.31	gb:NM_024305.1 /DEF=Homo sapiens hypothetical protein MGC4278 (MGC4278), mRNA. /FEA=mR
212607_at	2235.8	2928.8	1.31	Consensus includes gb:N32526 /FEA=EST /DB_XREF=gi:1152925 /DB_XREF=est:yy11f04.s1 /CLON
215588_x_at	3831.3	5021.2	1.31	Consensus includes gb:AK024958.1 /DEF=Homo sapiens cDNA: FLJ21305 fts, clone COL02124. /FE
220796_x_at	6875.1	8986.1	1.31	gb:NM_024881.1 /DEF=Homo sapiens hypothetical protein FLJ14251 (FLJ14251), mRNA. /FEA=mR
207783_x_at	1864.1	2466.5	1.32	gb:NM_017627.1 /DEF=Homo sapiens hypothetical protein FLJ20030 (FLJ20030), mRNA. /FEA=mR
213030_s_at	666.3	899.9	1.35	Consensus includes gb:A1688418 /FEA=EST /DB_XREF=gi:4899712 /DB_XREF=est:wc94h03.x1 /CL
40420_at	991.1	1337.6	1.35	Cluster Incl. AB015718:Homo sapiens lok mRNA for protein kinase, complete cds /cds=(50,2956) /g
213507_s_at	1552	2096.6	1.35	Consensus includes gb:BG249565 /FEA=EST /DB_XREF=gi:12759381 /DB_XREF=est:602319636F1
214672_at	1262.1	1714.5	1.36	Consensus includes gb:AB023215.1 /DEF=Homo sapiens mRNA for KIAA0998 protein, partial cds.
209927_s_at	1374.9	1872.5	1.36	gb:AF261137.1 /DEF=Homo sapiens HT031 mRNA, complete cds. /FEA=mRNA /PROD=HT031 /DB_
215604_x_at	1875.3	2557.5	1.36	Consensus includes gb:AK023783.1 /DEF=Homo sapiens cDNA FLJ13721 fts, clone PLACE2000450
214022_s_at	5238.3	7138	1.36	Consensus includes gb:AA749101 /FEA=EST /DB_XREF=gi:2789059 /DB_XREF=est:ny11d02.s1 /C
121_at	3601.5	4958.8	1.38	X69699 /FEATURE= /DEFINITION=HSPAX8A H.sapiens Pax8 mRNA
215303_at	666.4	925	1.39	Consensus includes gb:BE046461 /FEA=EST /DB_XREF=gi:8363514 /DB_XREF=est:hn47g05.x2 /C
215179_x_at	3502.6	4858.3	1.39	Consensus includes gb:AK023843.1 /DEF=Homo sapiens cDNA FLJ13781 fts, clone PLACE4000465
208120_x_at	5959.6	8319.7	1.4	gb:NM_031221.1 /DEF=Homo sapiens hypothetical protein FKSG63 (FKSG63), mRNA. /FEA=mRNA
211040_x_at	2034.3	2862.8	1.41	gb:BC006325.1 /DEF=Homo sapiens, G-2 and S-phase expressed 1, clone MGC:12560, mRNA, com
214473_x_at	1096.5	1561.5	1.42	Consensus includes gb:NM_005395.1 /DEF=Homo sapiens postmeiotic segregation increased 2-lik
55705_at	3787.7	5368.6	1.42	Cluster Incl. W07773:zb03g04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-301014 /clone_end=5

214715_x_at	5050.3	7190	1.42	Consensus includes gb:AK024789.1/DEF=Homo sapiens cDNA: FLJ21136 fts, clone CAS07469./FE
210686_x_at	3960.6	5675.8	1.43	gb:BC001407.1/DEF=Homo sapiens, Similar to cytochrome c-like antigen, clone MGC:2960, mRNA
209057_x_at	7271.8	10405.8	1.43	gb:AB007892.1/DEF=Homo sapiens KIAA0432 mRNA, complete cds./FEA=mRNA/GEN=KIAA0432
215726_s_at	1179.8	1693.4	1.44	Consensus includes gb:M22976.1/DEF=Human cytochrome b5 mRNA, 3 end./FEA=mRNA/GEN=C
219206_x_at	1491.5	2145.1	1.44	gb:NM_016056.1/DEF=Homo sapiens CGI-119 protein (LOC51643), mRNA./FEA=mRNA/GEN=LOC
215628_x_at	4210.6	6154.8	1.46	Consensus includes gb:AL049285.1/DEF=Homo sapiens mRNA; cDNA DKFZp564M193 (from clone
206936_x_at	2925.9	4313.7	1.47	gb:NM_022335.1/DEF=Homo sapiens hypothetical protein PRO2849 (PRO2849), mRNA./FEA=mRN
211600_at	2704.1	4012.4	1.48	gb:U20489.1/DEF=Human glomerular epithelial protein 1 (GLEPP1) mRNA, complete cds./FEA=mR
204246_s_at	1387.3	2091.5	1.51	gb:NM_007234.2/DEF=Homo sapiens dynactin 3 (p22) (DCTN3), transcript variant 1, mRNA./FEA=m
203406_at	1483.7	2252.8	1.52	gb:NM_005926.1/DEF=Homo sapiens microfilillar-associated protein 1 (MFAP1), mRNA./FEA=mR
212639_x_at	2227.4	3412.4	1.53	Consensus includes gb:AL581768/FEA=EST/DB_XREF=gi:12949093/DB_XREF=est:AL581768/CL
216054_x_at	1106.7	1706.5	1.54	Consensus includes gb:X58851/DEF=Human MLC1emb gene for embryonic myosin alkaline light c
212735_at	1180.3	1817.6	1.54	Consensus includes gb:BF448041/FEA=EST/DB_XREF=gi:11513102/DB_XREF=est:7q97f09.x1/C
201922_at	1634.7	2536	1.55	gb:NM_014886.1/DEF=Homo sapiens hypothetical protein (YR-29), mRNA./FEA=mRNA/GEN=YR-2
212284_x_at	1858.2	2899.4	1.56	Consensus includes gb:BG498776/FEA=EST/DB_XREF=gi:13460293/DB_XREF=est:602544416F1
206940_s_at	1046.6	1648.6	1.58	gb:NM_006237.1/DEF=Homo sapiens POU domain, class 4, transcription factor 1 (POU4F1), mRNA
218171_at	909	1449.5	1.59	gb:AF195514.1/DEF=Homo sapiens VPS4-2 ATPase (VPS42) mRNA, complete cds./FEA=mRNA/G
203480_s_at	1245.5	1976.3	1.59	gb:NM_014928.1/DEF=Homo sapiens KIAA1046 protein (KIAA1046), mRNA./FEA=mRNA/GEN=KIA
207990_x_at	1146.1	1838.9	1.6	gb:NM_020114.1/DEF=Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 9, mR
221435_x_at	881.7	1427.6	1.62	gb:NM_031207.1/DEF=Homo sapiens hypothetical protein HT036 (HT036), mRNA./FEA=CDS/GEN
203504_s_at	603.2	1002.4	1.66	gb:NM_005502.1/DEF=Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABC
208780_x_at	1121.1	1930.1	1.72	gb:AF154847.1/DEF=Homo sapiens 33 kDa Vamp-associated protein (VAMP) mRNA, complete cds
210739_x_at	2020.1	3496	1.73	gb:AF069510.1/DEF=Homo sapiens sodium bicarbonate cotransporter (NBC) mRNA, complete cds
205370_x_at	8100.3	14071.5	1.74	gb:NM_001918.1/DEF=Homo sapiens dihydrolipoamide branched chain transacylase (E2 compone
201575_at	1246.3	2182.3	1.75	gb:NM_012245.1/DEF=Homo sapiens SKI-INTERACTING PROTEIN (SNW1), mRNA./FEA=mRNA/G
208246_x_at	3369.8	5918.3	1.76	gb:NM_017618.1/DEF=Homo sapiens hypothetical protein FLJ20006 (FLJ20006), mRNA./FEA=mR
211452_x_at	2358.7	4248.9	1.8	gb:AF130054.1/DEF=Homo sapiens clone FLB4816 PRO1252 mRNA, complete cds./FEA=mRNA/P
217918_at	1771.8	3279.7	1.85	gb:NM_014183.1/DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA./FEA=mRNA/GEN=HSP
220071_x_at	2615.6	4959.7	1.9	gb:NM_018097.1/DEF=Homo sapiens hypothetical protein FLJ10460 (FLJ10460), mRNA./FEA=mR
220232_at	5702.1	10811.6	1.9	gb:NM_024906.1/DEF=Homo sapiens hypothetical protein FLJ21032 (FLJ21032), mRNA./FEA=mR
213382_at	783.7	1516.9	1.94	Consensus includes gb:AL137798/DEF=Human DNA sequence from clone RP5-1182A14 on chrom
213835_x_at	2887.1	5764.6	2	Consensus includes gb:AL524262/FEA=EST/DB_XREF=gi:12787755/DB_XREF=est:AL524262/CL
210319_x_at	746.5	1500	2.01	gb:D89377.1/DEF=Homo sapiens mRNA for MSX-2, complete cds./FEA=mRNA/PROD=MSX-2/DB
208869_s_at	690.2	1436.2	2.08	gb:AF087847.1/DEF=Homo sapiens GABA-A receptor-associated protein like 1 (GABARAPL1) mR
213936_x_at	997.9	2086	2.09	Consensus includes gb:AW276646/FEA=EST/DB_XREF=gi:6663676/DB_XREF=est:xr17f12.x1/CL

44783_s_at	2252.2	4775.3	2.12	Cluster Incl. R61374:yh15e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-37665 /clone_end=3 /g
216989_at	685	1601.8	2.34	Consensus includes gb:L13779.1 /DEF=Homo sapiens (clone H16) sperm surface protein PH-20 mR
208855_s_at	904.2	2179.2	2.41	gb:AF083420.1 /DEF=Homo sapiens brain-specific STE20-like protein kinase 3 (STK3) mRNA, comp
200759_x_at	2062.8	5302	2.57	gb:NM_003204.1 /DEF=Homo sapiens nuclear factor (erythroid-derived 2)-like 1 (NFE2L1), mRNA.
200095_x_at	2102.2	6436.5	3.06	Consensus includes gb:AA320764 /FEA=EST /DB_XREF=gi:1973113 /DB_XREF=est:EST23183 /UG
35201_at	1196.1	4106.8	3.43	Cluster Incl. X16135:Human mRNA for novel heterogeneous nuclear RNP protein, L protein /cds=(2
201429_s_at	2608.6	12987.4	4.98	gb:NM_000998.1 /DEF=Homo sapiens ribosomal protein L37a (RPL37A), mRNA. /FEA=mRNA /GEN
208845_at	1136.5	6016.2	5.29	gb:BC002456.1 /DEF=Homo sapiens, voltage-dependent anion channel 3, clone MGC:1966, mRNA,
201358_s_at	1664.1	9562.7	5.75	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FE
214041_x_at	9133.1	57937.9	6.34	Consensus includes gb:BE857772 /FEA=EST /DB_XREF=gi:10372131 /DB_XREF=est:7d62a11.x1 /C

Appendix B.

Probe set	CP4HX12		P4HX12		CP4 vs P4		Description
	Signal	Signal	Fold Change	Signal	Signal	Fold Change	
205430_at	1308.1	628.6	-2.08				Consensus includes gb:AL133386/DEF=Human DNA sequence from clone RP1-181C24 on chromosome 6
201742_x_at	1249	697	-1.79				gb:Nm_006924.1/DEF=Homo sapiens splicing factor, arginineserine-rich 1 (splicing factor 2, alternate spl
206247_at	1119.8	644.7	-1.74				gb:Nm_005931.1/DEF=Homo sapiens MHC class I polypeptide-related sequence B (MICB), mRNA. /FEA=m
213031_s_at	1537.9	886.6	-1.73				Consensus includes gb:AF161382.1/DEF=Homo sapiens HSPC264 mRNA, partial cds. /FEA=mRNA/PROD
214321_at	1076.1	624.6	-1.72				Consensus includes gb:BF440025/FEA=EST/DB_XREF=gi:11452542/DB_XREF=est:nac52c12.x1/CLONE
201540_at	2224.9	1296.5	-1.72				gb:Nm_001449.1/DEF=Homo sapiens four and a half LIM domains 1 (FHL1), mRNA. /FEA=mRNA/GEN=FH
205549_at	2372.6	1470.7	-1.61				gb:Nm_006198.1/DEF=Homo sapiens Purkinje cell protein 4 (PCP4), mRNA. /FEA=mRNA/GEN=PCP4/PR
201427_s_at	1154	723.3	-1.6				gb:Nm_005410.1/DEF=Homo sapiens selenoprotein P, plasma, 1 (SEPP1), mRNA. /FEA=mRNA/GEN=SEP
206297_at	1678.6	1062.2	-1.58				gb:Nm_007272.1/DEF=Homo sapiens chymotrypsin C (caldecrin) (CTRC), mRNA. /FEA=mRNA/GEN=CTR
205506_at	1056.1	676.8	-1.56				gb:Nm_007127.1/DEF=Homo sapiens villin 1 (VIL1), mRNA. /FEA=mRNA/GEN=VIL1/PROD=villin 1/DB_X
205006_s_at	1159	741.8	-1.56				gb:Nm_004808.1/DEF=Homo sapiens N-myristoyltransferase 2 (NMT2), mRNA. /FEA=mRNA/GEN=NMT2/P
200018_at	8197	5297.4	-1.55				gb:Nm_001017.1/DEF=Homo sapiens ribosomal protein S13 (RPS13), mRNA. /FEA=mRNA/GEN=RPS13/P
213513_x_at	1480.6	959.2	-1.54				Consensus includes gb:BG034239/FEA=EST/DB_XREF=gi:12427339/DB_XREF=est:602302301F1/CLON
210448_s_at	1254.8	826.5	-1.52				gb:U49396.1/DEF=Human ionotropic ATP receptor P2X5b mRNA, complete cds. /FEA=mRNA/PROD=P2X
201592_at	1686.1	1131.9	-1.49				gb:Nm_003756.1/DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (E
213878_at	907	613.9	-1.48				Consensus includes gb:AL685944/FEA=EST/DB_XREF=gi:4897238/DB_XREF=est:tu38g02.x1/CLONE=IM
200799_at	1778.3	1200.2	-1.48				gb:Nm_005345.3/DEF=Homo sapiens heat shock 70kD protein 1A (HSPA1A), mRNA. /FEA=mRNA/GEN=H
202787_s_at	1181.7	805.5	-1.47				gb:U43784.1/DEF=Human mitogen activated protein kinase activated protein kinase-3 mRNA, complete cd
203278_s_at	1275.2	871.8	-1.46				gb:Nm_016621.1/DEF=Homo sapiens hypothetical protein (LOC51317), mRNA. /FEA=mRNA/GEN=LOC51
203885_at	1299.4	889.3	-1.46				gb:Nm_014999.1/DEF=Homo sapiens KIAA0118 protein (KIAA0118), mRNA. /FEA=mRNA/GEN=KIAA0118
208405_s_at	2947.3	2049.2	-1.44				gb:Nm_006016.1/DEF=Homo sapiens CD164 antigen, sialomucin (CD164), mRNA. /FEA=mRNA/GEN=CD1
215203_at	993.6	693.1	-1.43				Consensus includes gb:AW438464/FEA=EST/DB_XREF=gi:6973770/DB_XREF=est:xu43g07.x1/CLONE=
201200_at	1078.7	759.5	-1.42				gb:Nm_003851.1/DEF=Homo sapiens cellular repressor of E1A-stimulated genes (CREG), mRNA. /FEA=m
202388_at	1118.4	786.8	-1.42				gb:Nm_002923.1/DEF=Homo sapiens regulator of G-protein signalling 2, 24kD (RGS2), mRNA. /FEA=mRN
213319_s_at	1191	844.3	-1.41				Consensus includes gb:AW170359/FEA=EST/DB_XREF=gi:6401884/DB_XREF=est:xn60c12.x1/CLONE=
208116_s_at	1066.9	759.8	-1.4				gb:Nm_005907.1/DEF=Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /FEA=m
221435_x_at	1087.8	776.4	-1.4				gb:Nm_031207.1/DEF=Homo sapiens hypothetical protein HT036 (HT036), mRNA. /FEA=CDS/GEN=HT036
203563_at	1279.2	915	-1.4				gb:Nm_021638.1/DEF=Homo sapiens actin filament associated protein (AFAP), mRNA. /FEA=mRNA/GEN
204234_s_at	835	602.8	-1.39				Consensus includes gb:AL476267/FEA=EST/DB_XREF=gi:4329312/DB_XREF=est:tt172g01.x1/CLONE=IM
220059_at	910.6	656.2	-1.39				gb:Nm_012108.1/DEF=Homo sapiens BCR downstream signaling 1 (BRDG1), mRNA. /FEA=mRNA/GEN=B
207719_x_at	959.6	692.8	-1.39				gb:Nm_014812.1/DEF=Homo sapiens KIAA0470 gene product (KIAA0470), mRNA. /FEA=mRNA/GEN=KIA
204372_s_at	1119.3	810.5	-1.38				gb:Nm_003685.1/DEF=Homo sapiens KH-type splicing regulatory protein (FUSE binding protein 2) (KHSR

212181_s_at	2279.7	1650.7	-1.38	Consensus includes gb:AF191654.2 /DEF=Homo sapiens diphosphoinositol polyphosphate phosphohydr
211395_x_at	1040	759.1	-1.37	gb:U90940.1 /DEF=Homo sapiens cell-type natural killer cells Fc gamma receptor IIc3 (Fc-gammaRIIc) mR
218323_at	1087.6	795.2	-1.37	gb:NM_018307.1 /DEF=Homo sapiens hypothetical protein FLJ11040 (FLJ11040), mRNA. /FEA=mRNA /GE
206833_s_at	1124.2	820.9	-1.37	gb:NM_001108.1 /DEF=Homo sapiens acylphosphatase 2, muscle type (ACYP2), mRNA. /FEA=mRNA /GEN
218312_s_at	1448.4	1058.5	-1.37	gb:NM_023926.1 /DEF=Homo sapiens hypothetical protein FLJ12895 (FLJ12895), mRNA. /FEA=mRNA /GE
208942_s_at	1752.5	1285	-1.36	Consensus includes gb:BE86511 /FEA=EST /DB_XREF=gi:10315287 /DB_XREF=est:60167885F1 /CLON
205694_at	8659.9	6373.5	-1.36	gb:NM_000550.1 /DEF=Homo sapiens tyrosinase-related protein 1 (TYRPP1), mRNA. /FEA=mRNA /GEN=TY
218502_s_at	869.2	643.3	-1.35	gb:NM_014112.1 /DEF=Homo sapiens trichorhinophalangeal syndrome I gene (TRPS1), mRNA. /FEA=mRN
212149_at	1181.2	873.3	-1.35	Consensus includes gb:AW470003 /FEA=EST /DB_XREF=gi:7040109 /DB_XREF=est:xr2705.x1 /CLONE=I
44563_at	1890.1	1396.1	-1.35	Cluster Incl. A1858000:wj69b05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2408049 /clone_end=3 /gb=
222339_x_at	1090.7	813.7	-1.34	Consensus includes gb:A1054381 /FEA=EST /DB_XREF=gi:3322168 /DB_XREF=est:q164d09.x1 /CLONE=IM
203455_s_at	4309.5	3206.2	-1.34	gb:NM_002970.1 /DEF=Homo sapiens spermidinespermine N1-acetyltransferase (SAT), mRNA. /FEA=mRN
206279_at	1172.2	879.7	-1.33	gb:NM_002760.1 /DEF=Homo sapiens protein kinase, Y-linked (PRKY), mRNA. /FEA=mRNA /GEN=PRKY /P
209293_x_at	1191.3	894.8	-1.33	gb:U16153.1 /DEF=Human Id-4H protein mRNA, complete cds. /FEA=mRNA /PROD=Id-4H protein /DB_XRE
219489_s_at	1288.2	972.4	-1.32	gb:NM_017821.1 /DEF=Homo sapiens hypothetical protein FLJ20435 (FLJ20435), mRNA. /FEA=mRNA /GE
201588_at	1377.6	1039.7	-1.32	gb:NM_004786.1 /DEF=Homo sapiens thioredoxin-like, 32kD (TXNL), mRNA. /FEA=mRNA /GEN=TXNL /PR
221478_at	2075.5	1569	-1.32	Consensus includes gb:AL132665.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566E034 (from clone DKFZ
222230_s_at	1182.9	902.9	-1.31	Consensus includes gb:AK022248.1 /DEF=Homo sapiens cDNA FLJ12186 fls, clone MAMMA1000824, wea
201143_s_at	1045.1	802.7	-1.3	gb:BC002513.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD), clo
217731_s_at	4498.4	3453.3	-1.3	gb:NM_021999.1 /DEF=Homo sapiens integral membrane protein 2B (ITM2B), mRNA. /FEA=mRNA /GEN=IT
203445_s_at	1260.4	980.1	-1.29	gb:NM_005730.1 /DEF=Homo sapiens conserved gene amplified in osteosarcoma (OS4), mRNA. /FEA=mR
214041_x_at	1480.3	1159.4	-1.28	Consensus includes gb:BE857772 /FEA=EST /DB_XREF=gi:10372131 /DB_XREF=est:7d62a11.x1 /CLONE=
218456_at	1508.6	1180.2	-1.28	gb:NM_023925.1 /DEF=Homo sapiens hypothetical protein FLJ22569 (FLJ22569), mRNA. /FEA=mRNA /GE
201860_s_at	1531.3	1195	-1.28	gb:NM_000930.1 /DEF=Homo sapiens plasminogen activator, tissue (PLAT), mRNA. /FEA=mRNA /GEN=PL
211740_at	959.7	758.1	-1.27	gb:BC005922.1 /DEF=Homo sapiens, Similar to islet cell autoantigen 1 (69kD), clone MGC:14523, mRNA, c
38447_at	1331.4	1049.4	-1.27	Cluster Incl. U08438:Human beta-adrenergic receptor kinase (ADRBK1) gene /cds=(40,2109) /gb=U08438 /g
202379_s_at	1646.6	1298.2	-1.27	Consensus includes gb:AL361805 /FEA=EST /DB_XREF=gi:4113426 /DB_XREF=est:qz24g07.x1 /CLONE=IM
216557_x_at	866.4	686.8	-1.26	Consensus includes gb:U92706 /DEF=Human rearranged immunoglobulin heavy chain (A1VH3) gene, par
216976_s_at	884.9	703.7	-1.26	Consensus includes gb:X96588.1 /DEF=H.sapiens mRNA for H-RYK receptor tyrosine kinase. /FEA=mRNA
209108_at	890.7	709	-1.26	gb:AF053453.1 /DEF=Homo sapiens tetraspan TM4SF (TSPAN-6) mRNA, complete cds. /FEA=mRNA /GEN
202732_at	1565.6	1241.8	-1.26	gb:NM_007066.1 /DEF=Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor gamma (PKIG)
213064_at	1259.4	1008.1	-1.25	Consensus includes gb:N64802 /FEA=EST /DB_XREF=gi:1212631 /DB_XREF=est:yz31b05.s1 /CLONE=IMA
201345_s_at	1290	1033.1	-1.25	gb:NM_003339.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45)
217958_at	1316	1053.4	-1.25	gb:NM_016146.1 /DEF=Homo sapiens PTD009 protein (PTD009), mRNA. /FEA=mRNA /GEN=PTD009 /PROD
207804_s_at	1429.3	1144.2	-1.25	gb:NM_004108.1 /DEF=Homo sapiens ficollin (collagenfibrinogen domain-containing lectin) 2 (huclolin) (FC

221392_at	704.8	567.7	-1.24	gb:NM_016944.1/DEF=Homo sapiens taste receptor, type 2, member 4 (TAS2R4), mRNA./FEA=CDS/GEN
202371_at	1322.2	1070.3	-1.24	gb:NM_024863.1/DEF=Homo sapiens hypothetical protein FLJ21174 (FLJ21174), mRNA./FEA=mRNA/GE
209028_s_at	1330.1	1075.1	-1.24	gb:AF006516.1/DEF=Homo sapiens eps8 binding protein e3b1 mRNA, complete cds./FEA=mRNA/PROD
201163_s_at	2634.1	2120.6	-1.24	gb:NM_001553.1/DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA./FEA=
217094_s_at	833.3	679.9	-1.23	Consensus includes gb:AL109923/DEF=Human DNA sequence from clone RP3-46801 on chromosome 2
221975_s_at	1251.9	1018.5	-1.23	Consensus includes gb:A1539305/FEA=EST/DB_XREF=gi:4453440/DB_XREF=est:te50h12.x1/CLONE=IM
201885_s_at	1491.4	1216.3	-1.23	gb:NM_000398.3/DEF=Homo sapiens diaphorase (NADH) (cytochrome b-5 reductase) (DIA1), nuclear gen
201358_s_at	4906.6	4002.2	-1.23	gb:NM_016451.1/DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA./FEA=mRN
205255_x_at	1084.3	887.1	-1.22	gb:NM_003202.1/DEF=Homo sapiens transcription factor 7 (T-cell specific, HMG-box) (TCF7), mRNA./FE
AFFX-hum_alu_at	8222.3	6745.5	-1.22	U14573 Human Alu-Sq subfamily consensus sequence.
205647_at	939.1	773.3	-1.21	gb:NM_002879.1/DEF=Homo sapiens RAD52 (S. cerevisiae) homolog (RAD52), mRNA./FEA=mRNA/GEN=
212932_at	975.3	806	-1.21	Consensus includes gb:AK022494.1/DEF=Homo sapiens cDNA FLJ12432 fis, clone NT2RM1000018, highl
44617_at	1273.4	1048.3	-1.21	Cluster Incl. A1431902:ti26e07.x1 Homo sapiens cDNA, 3 end/clone=IMAGE-2131620/clone_end=3/ gb=A
202001_s_at	1383.4	1146.6	-1.21	gb:NM_002490.1/DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B
210704_at	1701.2	1404.6	-1.21	gb:L17328.1/DEF=Human pre-TNK cell associated protein (3C1) mRNA, complete cds./FEA=mRNA/GEN=
214892_x_at	1087.8	908.1	-1.2	Consensus includes gb:BC004262.1/DEF=Homo sapiens, Similar to cactin, clone IMAGE:3609158, mRNA
211458_s_at	2696.4	2244.7	-1.2	gb:AF180519.1/DEF=Homo sapiens GABA-A receptor-associated protein mRNA, complete cds./FEA=mR
209787_s_at	944.3	1135.1	1.2	gb:BC001282.1/DEF=Homo sapiens, high-mobility group (nonhistone chromosomal) protein 17-like 3, clo
203067_at	978.7	1170.7	1.2	gb:NM_003477.1/DEF=Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X;
221607_x_at	1542.4	1844.7	1.2	gb:BC001920.1/DEF=Homo sapiens, actin, gamma 1, clone MGC:3728, mRNA, complete cds./FEA=mRNA
200749_at	1558.5	1877.4	1.2	Consensus includes gb:BF112006/FEA=EST/DB_XREF=gi:10941619/DB_XREF=est:7137e05.x1/CLONE=
210563_x_at	728.4	881.3	1.21	gb:U97075.1/DEF=Homo sapiens FLICE-like inhibitory protein short form mRNA, complete cds./FEA=mR
210652_s_at	930.7	1128.2	1.21	gb:BC004399.1/DEF=Homo sapiens, clone MGC:10985, mRNA, complete cds./FEA=mRNA/PROD=Unkno
205711_x_at	933.2	1127.7	1.21	gb:NM_005174.1/DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, gamma
202609_at	1008.3	1216	1.21	gb:NM_004447.1/DEF=Homo sapiens epidermal growth factor receptor pathway substrate 8 (EPs8), mRN
203887_s_at	1184.7	1432	1.21	gb:NM_000361.1/DEF=Homo sapiens thrombomodulin (THBD), mRNA./FEA=mRNA/GEN=THBD/PROD=
203011_at	1198.1	1447.7	1.21	gb:NM_005536.2/DEF=Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA./FEA=mR
208808_s_at	1218.8	1471.5	1.21	gb:BC000903.1/DEF=Homo sapiens, high-mobility group (nonhistone chromosomal) protein 2, clone MGC
212297_at	1232.1	1488.3	1.21	Consensus includes gb:BF218804/FEA=EST/DB_XREF=gi:11112494/DB_XREF=est:601882315F1/CLON
202090_s_at	1265.9	1529.2	1.21	gb:NM_006830.1/DEF=Homo sapiens ubiquinol-cytochrome c reductase (6.4kD) subunit (UQCR), mRNA.
208274_at	1279.6	1546.8	1.21	gb:NM_022375.1/DEF=Homo sapiens oculomedin (OCLM), mRNA./FEA=mRNA/GEN=OCLM/PROD=ocul
218388_at	795.9	968.5	1.22	gb:NM_012088.1/DEF=Homo sapiens 6-phosphogluconolactonase (PGLS), mRNA./FEA=mRNA/GEN=PG
202034_x_at	879.2	1073.3	1.22	gb:NM_014781.1/DEF=Homo sapiens KIAA0203 gene product (KIAA0203), mRNA./FEA=mRNA/GEN=KIA
219771_at	914.2	1116.3	1.22	gb:NM_017752.1/DEF=Homo sapiens hypothetical protein FLJ20298 (FLJ20298), mRNA./FEA=mRNA/GE
212774_at	974.8	1190.7	1.22	Consensus includes gb:AJ223321/DEF=Homo sapiens RP58 gene, complete CDS/FEA=mRNA/DB_XREF

211929_at	1445.7	1763.9	1.22	Consensus includes gb:AA527502 /FEA=EST /DB_XREF=gi:2269571 /DB_XREF=est:ng41f10.s1 /CLONE=I
214022_s_at	1771.3	2152.7	1.22	Consensus includes gb:AA749101 /FEA=EST /DB_XREF=gi:2789059 /DB_XREF=est:ny11d02.s1 /CLONE=
213588_x_at	2240	2734.2	1.22	Consensus includes gb:AA836274 /FEA=EST /DB_XREF=gi:2913073 /DB_XREF=est:oe90c01.s1 /CLONE=
203480_s_at	1138.4	1396	1.23	gb:NM_014928.1 /DEF=Homo sapiens KIAA1046 protein (KIAA1046), mRNA. /FEA=mRNA /GEN=KIAA1046
209921_at	1381.1	1693.9	1.23	gb:AB040875.1 /DEF=Homo sapiens hxCt mRNA for cystineglutamate exchanger, complete cds. /FEA=m
209067_s_at	1481.5	1826.3	1.23	gb:D89092.1 /DEF=Homo sapiens hnRNP JKTBP mRNA, complete cds. /FEA=mRNA /GEN=hnRNP JKTBP
208768_x_at	1771	2185.9	1.23	gb:D17652.1 /DEF=Human mRNA for HBP15L22, complete cds. /FEA=mRNA /PROD=HBP15L22 /DB_XREF
208881_x_at	876.9	1088.7	1.24	gb:BC005247.1 /DEF=Homo sapiens, isopentenyl-diphosphate delta isomerase, clone MGC:12281, mRNA,
204440_at	1161.4	1436.5	1.24	gb:NM_004233.1 /DEF=Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfam
201217_x_at	1202.9	1491.9	1.24	gb:NM_000967.1 /DEF=Homo sapiens ribosomal protein L3 (RPL3), mRNA. /FEA=mRNA /GEN=RPL3 /PRO
205849_s_at	1456.4	1812.5	1.24	gb:NM_006294.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase binding protein (UQCRCB), mRNA
216526_x_at	1847	2282	1.24	Consensus includes gb:AK024836.1 /DEF=Homo sapiens cDNA: FLJ21183 fts, clone CAS11634, highly sim
217848_s_at	2233.8	2766	1.24	gb:NM_021129.1 /DEF=Homo sapiens pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochon
217127_at	766.9	961.3	1.25	Consensus includes gb:AL354872 /DEF=Human DNA sequence from clone RP11-42015 on chromosome
201843_s_at	862.9	1082.6	1.25	gb:NM_004105.2 /DEF=Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1),
213583_x_at	1342.8	1674.6	1.25	Consensus includes gb:BE964125 /FEA=EST /DB_XREF=gi:11767593 /DB_XREF=est:601657809R1 /CLON
209277_at	1483.8	1861.3	1.25	Consensus includes gb:AL574096 /FEA=EST /DB_XREF=gi:12933969 /DB_XREF=est:AL574096 /CLONE=C
203935_at	753.7	949.3	1.26	gb:NM_001105.2 /DEF=Homo sapiens activin A receptor, type I (ACVR1), mRNA. /FEA=mRNA /GEN=ACVR
35201_at	790.6	995.7	1.26	Cluster Incl. X16135: Human mRNA for novel heterogeneous nuclear RNP protein, L protein /cds=(28,1704
219805_at	971.7	1225.3	1.26	gb:NM_022101.1 /DEF=Homo sapiens hypothetical protein FLJ22965 (FLJ22965), mRNA. /FEA=mRNA /GE
203753_at	988.9	1247.5	1.26	gb:NM_003199.1 /DEF=Homo sapiens transcription factor 4 (TCF4), mRNA. /FEA=mRNA /GEN=TCF4 /PRO
212183_at	1149.4	1448.6	1.26	Consensus includes gb:AW511135 /FEA=EST /DB_XREF=gi:7149213 /DB_XREF=est:hd43g08.x1 /CLONE=
201772_at	717.2	909.2	1.27	gb:NM_015878.1 /DEF=Homo sapiens antizyme inhibitor (LOC51582), mRNA. /FEA=mRNA /GEN=LOC5158
218864_at	767.1	976.2	1.27	gb:AF116610.1 /DEF=Homo sapiens PRO0929 mRNA, complete cds. /FEA=mRNA /PROD=PRO0929 /DB_X
213300_at	797.7	1010.6	1.27	Consensus includes gb:AW168132 /FEA=EST /DB_XREF=gi:6399657 /DB_XREF=est:xg60c11.x1 /CLONE=
218350_s_at	850.7	1082.9	1.27	gb:NM_015895.1 /DEF=Homo sapiens geminin (LOC51053), mRNA. /FEA=mRNA /GEN=LOC51053 /PROD=
210689_at	928.6	1177.7	1.27	gb:AF314090.1 /DEF=Homo sapiens claudin 14 (CLDN14) mRNA, complete cds. /FEA=mRNA /GEN=CLDN1
201215_at	987.9	1255.9	1.27	gb:NM_005032.2 /DEF=Homo sapiens plastin 3 (T isoform) (PLS3), mRNA. /FEA=mRNA /GEN=PLS3 /PROD
213961_s_at	995.1	1265.1	1.27	Consensus includes gb:AI077556 /FEA=EST /DB_XREF=gi:3411964 /DB_XREF=est:oz33f08.x1 /CLONE=IM
213009_s_at	722	924.8	1.28	Consensus includes gb:AK022701.1 /DEF=Homo sapiens cDNA FLJ12639 fts, clone NT2RM4001938, highl
218171_at	757.5	966.8	1.28	gb:AF195514.1 /DEF=Homo sapiens VPS4-2 ATPase (VPS42) mRNA, complete cds. /FEA=mRNA /GEN=VP
202194_at	881	1129.6	1.28	Consensus includes gb:AL117354 /DEF=Human DNA sequence from clone RP5-976013 on chromosome
213712_at	963.2	1232.1	1.28	Consensus includes gb:BF508639 /FEA=EST /DB_XREF=gi:11591937 /DB_XREF=est:UL-H-B14-aop-a-07-0-
204685_s_at	969.3	1240.6	1.28	Consensus includes gb:R52647 /FEA=EST /DB_XREF=gi:814549 /DB_XREF=est:y82f05.s1 /CLONE=IMAG
208020_s_at	1161.5	1483.2	1.28	gb:NM_000719.1 /DEF=Homo sapiens calcium channel, voltage-dependent, L type, alpha 1C subunit (CAC

200043_at	1271.2	1625.4	1.28	gb:NM_004450.1/DEF=Homo sapiens enhancer of rudimentary (Drosophila) homolog (ERH), mRNA. /FEA=
211983_x_at	1944.2	2494	1.28	Consensus includes gb:BE741683 /FEA=EST /DB_XREF=gi:10155675 /DB_XREF=est:601594740F1 /CLON
210303_at	694	897.4	1.29	gb:AF262032.1 /DEF=Homo sapiens MAB21L2 protein (MAB21L2) mRNA, complete cds. /FEA=mRNA /GEN
204135_at	770.6	990.5	1.29	gb:NM_014890.1 /DEF=Homo sapiens downregulated in ovarian cancer 1 (DOC1), mRNA. /FEA=mRNA /GE
208939_at	836.2	1078.1	1.29	Consensus includes gb:AV682679 /FEA=EST /DB_XREF=gi:10284542 /DB_XREF=est:AV682679 /CLONE=G
222112_at	971.6	1254.1	1.29	Consensus includes gb:AV710549 /FEA=EST /DB_XREF=gi:10729178 /DB_XREF=est:AV710549 /CLONE=C
201761_at	995.2	1288	1.29	gb:NM_006636.2 /DEF=Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), met
209927_s_at	1033.5	1333.5	1.29	gb:AF261137.1 /DEF=Homo sapiens HT031 mRNA, complete cds. /FEA=mRNA /PROD=HT031 /DB_XREF=
200994_at	1110.6	1433.5	1.29	Consensus includes gb:BG291787 /FEA=EST /DB_XREF=gi:13050002 /DB_XREF=est:602386007F1 /CLON
201553_s_at	1743.8	2251.4	1.29	gb:NM_005561.2 /DEF=Homo sapiens lysosomal-associated membrane protein 1 (LAMP1), mRNA. /FEA=m
202842_s_at	1969.5	2544.2	1.29	gb:AL080081.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564F1862 (from clone DKFZp564F1862); comple
208625_s_at	673.9	874.4	1.3	gb:AF104913.1 /DEF=Homo sapiens eukaryotic protein synthesis initiation factor mRNA, complete cds. /F
208652_at	735.5	958.3	1.3	gb:BC000400.1 /DEF=Homo sapiens, protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
202657_s_at	784.2	1017.9	1.3	gb:NM_014755.1 /DEF=Homo sapiens KIAA0127 gene product (KIAA0127), mRNA. /FEA=mRNA /GEN=KIA
220439_at	862.9	1120.9	1.3	gb:NM_024892.1 /DEF=Homo sapiens hypothetical protein FLJ11700 (FLJ11700), mRNA. /FEA=mRNA /GE
203613_s_at	1029.9	1340.6	1.3	gb:NM_002493.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B1
208870_x_at	1134.7	1474.8	1.3	gb:BC000931.2 /DEF=Homo sapiens, ATP synthase, H+ transporting, mitochondrial F1 complex, gamma p
222297_x_at	2003.5	2598.8	1.3	Consensus includes gb:AV738806 /FEA=EST /DB_XREF=gi:10856387 /DB_XREF=est:AV738806 /CLONE=C
201891_s_at	4410.8	5746.1	1.3	gb:NM_004048.1 /DEF=Homo sapiens beta-2-microglobulin (B2M), mRNA. /FEA=mRNA /GEN=B2M /PROD
200733_s_at	829.2	1087.4	1.31	gb:U48296.1 /DEF=Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, comple
221471_at	857	1126.7	1.31	Consensus includes gb:AW173623 /FEA=EST /DB_XREF=gi:6439571 /DB_XREF=est:xj10a08.x1 /CLONE=I
215691_x_at	984.1	1289.6	1.31	Consensus includes gb:AV702994 /FEA=EST /DB_XREF=gi:10719324 /DB_XREF=est:AV702994 /CLONE=A
219410_at	816.3	1078.8	1.32	gb:NM_018004.1 /DEF=Homo sapiens hypothetical protein FLJ10134 (FLJ10134), mRNA. /FEA=mRNA /GE
201128_s_at	855.5	1130	1.32	gb:NM_001096.1 /DEF=Homo sapiens ATP citrate lyase (ACLY), mRNA. /FEA=mRNA /GEN=ACLY /PROD=
218283_at	1072.4	1416	1.32	gb:NM_016305.1 /DEF=Homo sapiens kina-iso protein (LOC51188), mRNA. /FEA=mRNA /GEN=LOC51188 /
213134_x_at	1205.3	1588.8	1.32	Consensus includes gb:AI765445 /FEA=EST /DB_XREF=gi:5231954 /DB_XREF=est:w180b08.x1 /CLONE=IM
200088_x_at	1304.4	1718.3	1.32	Consensus includes gb:AK026491.1 /DEF=Homo sapiens cDNA. FLJ22838 fts, clone KIAA4494, highly sim
209075_s_at	1315.1	1739.3	1.32	gb:AY009128.1 /DEF=Homo sapiens ISCU2 (ISCU) mRNA, complete cds, alternatively spliced. /FEA=mRN
203837_at	789.8	1050.4	1.33	gb:NM_005923.2 /DEF=Homo sapiens mitogen-activated protein kinase kinase 5 (MAP3K5), mRNA.
202854_at	890.1	1183.4	1.33	gb:NM_000194.1 /DEF=Homo sapiens hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrom
201715_s_at	959	1274.8	1.33	gb:NM_014977.1 /DEF=Homo sapiens KIAA0670 proteinacinus (KIAA0670), mRNA. /FEA=mRNA /GEN=KIA
202422_s_at	1001.6	1331.2	1.33	gb:NM_022977.1 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript varia
208180_s_at	633.7	846.9	1.34	gb:NM_003543.2 /DEF=Homo sapiens H4 histone family, member H (H4FH), mRNA. /FEA=mRNA /GEN=H4
202693_s_at	653.4	878.3	1.34	Consensus includes gb:AW194730 /FEA=EST /DB_XREF=gi:6473630 /DB_XREF=est:xn43d11.x1 /CLONE=
211452_x_at	735.8	987.9	1.34	gb:AF130054.1 /DEF=Homo sapiens clone FLB4816 PRO1252 mRNA, complete cds. /FEA=mRNA /PROD=P

205655_at	752	1009.9	1.34	gb:NM_002393.1 /DEF=Homo sapiens mouse double minute 4, human homolog of; p53-binding protein (M
200761_s_at	1063.1	1421.5	1.34	gb:NM_006407.2 /DEF=Homo sapiens vitamin A responsive; cytoskeleton related (JWA), mRNA. /FEA=mR
210933_s_at	575.7	780	1.35	gb:BC004908.1 /DEF=Homo sapiens, clone MGC:4655, mRNA, complete cds. /FEA=mRNA /PROD=Unknow
217052_x_at	887.9	1203.1	1.35	Consensus includes gb:AK024108.1 /DEF=Homo sapiens cDNA FLJ14046 fts, clone HEMBA1006461. /FEA
209186_at	948.5	1280.1	1.35	gb:M2314.1 /DEF=Homo sapiens calcium-ATPase (HK1) mRNA, complete cds. /FEA=mRNA /GEN=HK1 /D
200027_at	966	1308	1.35	gb:NM_004539.2 /DEF=Homo sapiens asparaginyl-tRNA synthetase (NARS), mRNA. /FEA=mRNA /GEN=NA
200602_at	1390.8	1884.5	1.35	gb:NM_000484.1 /DEF=Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer di
209089_at	1726.1	2328	1.35	gb:BC001267.1 /DEF=Homo sapiens, RAB5A, member RAS oncogene family, clone MGC:5048, mRNA, com
202032_s_at	762.8	1038.7	1.36	gb:NM_006122.1 /DEF=Homo sapiens mannosidase, alpha, class 2A, member 2 (MAN2A2), mRNA. /FEA=m
222209_s_at	825.7	1125	1.36	Consensus includes gb:AK000684.1 /DEF=Homo sapiens cDNA FLJ20677 fts, clone KAI4183. /FEA=mRN
208073_x_at	835.1	1139.7	1.36	gb:NM_003316.1 /DEF=Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA. /FEA=mRNA /GEN
202324_s_at	1253.9	1711.4	1.36	gb:NM_022735.1 /DEF=Homo sapiens golgi resident protein GCP60 (GCP60), mRNA. /FEA=mRNA /GEN=G
200958_s_at	1545.1	2094.3	1.36	gb:NM_005625.1 /DEF=Homo sapiens syndecan binding protein (syntenin) (SDCBP), mRNA. /FEA=mRNA
200092_s_at	1710.3	2332.8	1.36	Consensus includes gb:BF216701 /FEA=EST /DB_XREF=gi:11110287 /DB_XREF=est:601884615f1 /CLON
220978_at	670.3	918.9	1.37	gb:NM_030966.1 /DEF=Homo sapiens keratin associated protein 1.3 (KRTAP1.3), mRNA. /FEA=mRNA /GE
200694_s_at	947.1	1294.2	1.37	gb:NM_020414.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 24 (DDX24), mRNA.
207507_s_at	1006.1	1378.2	1.37	gb:NM_001689.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit
50314_l_at	1007.9	1380.1	1.37	Cluster Incl. A1761506:w61b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394717 /clone_end=3 /gb=
214327_x_at	4489.1	6143.6	1.37	Consensus includes gb:A1888178 /FEA=EST /DB_XREF=gi:5593342 /DB_XREF=est:wm40b09.x1 /CLONE=
210528_at	655.3	905.7	1.38	gb:AF010447.1 /DEF=Homo sapiens MHC class I related protein 1 isoform C (MR1C) mRNA, complete cds
218445_at	749	1031.5	1.38	gb:NM_018649.1 /DEF=Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA. /FEA=mRNA /GE
209022_at	915	1265.6	1.38	Consensus includes gb:AK026678.1 /DEF=Homo sapiens cDNA: FLJ23025 fts, clone LNG01702, highly sim
211487_x_at	1100.2	1521.5	1.38	gb:BC004886.1 /DEF=Homo sapiens, ribosomal protein S17, clone MGC:11144, mRNA, complete cds. /FE
201662_s_at	1105.8	1520.7	1.38	gb:DB9053.1 /DEF=Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds. /FEA=mRNA /PROD=A
205788_s_at	1152.8	1590	1.38	gb:NM_014827.1 /DEF=Homo sapiens KIAA0663 gene product (KIAA0663), mRNA. /FEA=mRNA /GEN=KIA
213857_s_at	1317.6	1824	1.38	Consensus includes gb:BG230614 /FEA=EST /DB_XREF=gi:12725656 /DB_XREF=est:naf41b12.x1 /CLONE
217883_at	661.1	919.4	1.39	gb:NM_015702.1 /DEF=Homo sapiens hypothetical protein (CL25022), mRNA. /FEA=mRNA /GEN=CL25022
214972_at	812.9	1129.6	1.39	Consensus includes gb:AU144791 /FEA=EST /DB_XREF=gi:11006312 /DB_XREF=est:AU144791 /CLONE=
206133_at	835	1160.1	1.39	gb:NM_017523.1 /DEF=Homo sapiens XIAP associated factor-1 (HSXIAPAF1), mRNA. /FEA=mRNA /GEN=H
204686_at	845.7	1174.6	1.39	gb:NM_005544.1 /DEF=Homo sapiens insulin receptor substrate 1 (IRS1), mRNA. /FEA=mRNA /GEN=IRS1
208855_s_at	1361.2	1886.8	1.39	gb:AF083420.1 /DEF=Homo sapiens brain-specific STE20-like protein kinase 3 (STK3) mRNA, complete cd
212852_s_at	1406.7	1957.7	1.39	Consensus includes gb:AL538601 /FEA=EST /DB_XREF=gi:12867040 /DB_XREF=est:AL538601 /CLONE=C
209122_at	2259	3138.9	1.39	gb:BC005127.1 /DEF=Homo sapiens, adipose differentiation-related protein, clone MGC:10598, mRNA, com
212869_x_at	11100.7	15395	1.39	Consensus includes gb:A1721229 /FEA=EST /DB_XREF=gi:5038485 /DB_XREF=est:as68c10.x1 /CLONE=IM
212588_at	793.9	1113.1	1.4	Consensus includes gb:Y00062.1 /DEF=Human mRNA for T200 leukocyte common antigen (CD45, L-C-A).

204681_s_at	864.4	1212.5	1.4	gb:NM_012294.1/DEF=Homo sapiens guanine nucleotide exchange factor for Rap1; M-Ras-regulated GEF
217741_s_at	947.8	1333.2	1.4	Consensus includes gb:AW471220 /FEA=EST /DB_XREF=gi:7041326 /DB_XREF=est:xv13g08.x1 /CLONE=
201071_x_at	1080.1	1508.7	1.4	gb:NM_012433.1/DEF=Homo sapiens splicing factor 3b, subunit 1, 155kD (SF3B1), mRNA. /FEA=mRNA /G
202391_at	1231	1729.4	1.4	gb:NM_006317.1/DEF=Homo sapiens brain acid-soluble protein 1 (BASP1), mRNA. /FEA=mRNA /GEN=BA
221773_at	1257.6	1764.6	1.4	Consensus includes gb:AW575374 /FEA=EST /DB_XREF=gi:7246913 /DB_XREF=est:U1-HF-BL0-adc-c-12-0
219077_s_at	798.1	1124.8	1.41	gb:NM_016373.1/DEF=Homo sapiens WW domain-containing oxidoreductase (WWOX), mRNA. /FEA=mRNA
201975_at	801.1	1126	1.41	gb:NM_002956.1/DEF=Homo sapiens retin (Reed-Steinberg cell-expressed intermediate filament-associat
212974_at	803.9	1134.2	1.41	Consensus includes gb:AI808958 /FEA=EST /DB_XREF=gi:5395524 /DB_XREF=est:wf67a09.x1 /CLONE=IM
209541_at	680.8	969.5	1.42	Consensus includes gb:AI972496 /FEA=EST /DB_XREF=gi:5769242 /DB_XREF=est:wr38c02.x1 /CLONE=IM
221626_at	705.8	1004.6	1.42	gb:AL136548.1/DEF=Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); com
217845_x_at	1154.5	1638.6	1.42	gb:NM_014056.1/DEF=Homo sapiens DKFZP564K247 protein (DKFZP564K247), mRNA. /FEA=mRNA /GEN
200014_s_at	531.4	760.4	1.43	gb:NM_004500.1/DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1C2) (HNRPC), mRNA
213102_at	1053	1504.3	1.43	Consensus includes gb:Z78330 /FEA=EST /DB_XREF=gi:1495103 /DB_XREF=est:HSZ78330 /CLONE=2.49
201366_at	1159.1	1658.7	1.43	gb:NM_004034.1/DEF=Homo sapiens annexin A7 (ANXA7), transcript variant 2, mRNA. /FEA=mRNA /GEN
200077_s_at	1274.2	1826	1.43	gb:DB7914.1/DEF=Human mRNA for ornithine decarboxylase antizyme, complete cds. /FEA=mRNA /GEN=
200834_s_at	1443.2	2062.6	1.43	gb:NM_001024.1/DEF=Homo sapiens ribosomal protein S21 (RPS21), mRNA. /FEA=mRNA /GEN=RPS21 /P
216342_x_at	1948.4	2782.9	1.43	Consensus includes gb:AL121916/DEF=Human DNA sequence from clone RP1-189G13 on chromosome
214003_x_at	5953.6	8516	1.43	Consensus includes gb:BF184532 /FEA=EST /DB_XREF=gi:11062829 /DB_XREF=est:601842837F1 /CLON
203080_s_at	697.8	1007.4	1.44	gb:NM_013450.1/DEF=Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA.
203423_at	855.1	1230.5	1.44	gb:NM_002899.2/DEF=Homo sapiens retinol-binding protein 1, cellular (RBP1), mRNA. /FEA=mRNA /GEN
213037_x_at	1158.4	1670.4	1.44	Consensus includes gb:AJ132258.1/DEF=Homo sapiens mRNA for staufen protein, partial. /FEA=mRNA /
208724_s_at	1261.5	1811.2	1.44	gb:BC000905.1/DEF=Homo sapiens, RAB1, member RAS oncogene family, clone MGC:5233, mRNA, com
218213_s_at	1344.3	1940.3	1.44	gb:NM_014206.1/DEF=Homo sapiens chromosome 11 open reading frame 10 (C11orf10), mRNA. /FEA=mR
208691_at	1660.6	2397.6	1.44	gb:BC001188.1/DEF=Homo sapiens, transferrin receptor (p90, CD71), clone MGC:3151, mRNA, complete c
211509_s_at	2270.4	3279	1.44	gb:AB015639.1/DEF=Homo sapiens ASY mRNA, complete cds. /FEA=mRNA /GEN=ASY /DB_XREF=gi:582
210705_s_at	669.4	970.2	1.45	gb:AF220028.1/DEF=Homo sapiens tripartite motif protein TRIM5 isoform delta (TRIM5) mRNA, complete
213017_at	1002.2	1450.4	1.45	Consensus includes gb:AL534702 /FEA=EST /DB_XREF=gi:12798195 /DB_XREF=est:AL534702 /CLONE=C
211073_x_at	1324.5	1923.8	1.45	gb:BC006483.1/DEF=Homo sapiens, ribosomal protein L3, clone MGC:4393, mRNA, complete cds. /FEA=
200627_at	726.7	1061.7	1.46	gb:BC003005.1/DEF=Homo sapiens, inactive progesterone receptor, 23 kD, clone MGC:4004, mRNA, com
207854_at	834.6	1221.6	1.46	gb:NM_002102.1/DEF=Homo sapiens glycophorin E (GYPE), mRNA. /FEA=mRNA /GEN=GYPE /PROD=gly
206424_at	1073.3	1564.3	1.46	gb:NM_000783.1/DEF=Homo sapiens cytochrome P450, subfamily XXVIA, polypeptide 1 (CYP26A1), mRN
221775_x_at	1363.1	1995.8	1.46	Consensus includes gb:BG152979 /FEA=EST /DB_XREF=gi:12665009 /DB_XREF=est:nah24c06.y1 /CLONE
41220_at	1497.5	2189.4	1.46	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB0
204595_s_at	1546.3	2261.5	1.46	Consensus includes gb:AI300520 /FEA=EST /DB_XREF=gi:3959866 /DB_XREF=est:qn55e06.x1 /CLONE=IM
205434_s_at	619	912.6	1.47	Consensus includes gb:AW451954 /FEA=EST /DB_XREF=gi:6992730 /DB_XREF=est:U1-H-BI3-alt-h-06-0-U

213960_s_at	821.4	1205	1.47	Consensus includes gb:T87225 /FEA=EST /DB_XREF=gi:715577 /DB_XREF=est:yc81f06.s1 /CLONE=IMAG
200738_s_at	897	1315.1	1.47	gb:NM_000291.1 /DEF=Homo sapiens phosphoglycerate kinase 1 (PGK1), mRNA. /FEA=mRNA /GEN=PGK
36888_at	976.5	1435.6	1.47	Cluster Incl. AB020648:Homo sapiens mRNA for KIAA0841 protein, partial cds /cds=(0,1925) /gb=AB02064
203752_s_at	1192.4	1752.8	1.47	gb:NM_005354.2 /DEF=Homo sapiens jun D proto-oncogene (JUND), mRNA. /FEA=mRNA /GEN=JUND /PR
218007_s_at	1237.8	1821.1	1.47	gb:NM_015920.1 /DEF=Homo sapiens 40S ribosomal protein S27 isoform (LOC51065), mRNA. /FEA=mRNA
214211_at	2495.1	3657.2	1.47	Consensus includes gb:AA083483 /FEA=EST /DB_XREF=gi:1625544 /DB_XREF=est:zn32a06.s1 /CLONE=I
206087_x_at	860.4	1273.6	1.48	gb:NM_000410.1 /DEF=Homo sapiens hemochromatosis (HFE), mRNA. /FEA=mRNA /GEN=HFE /PROD=he
203725_at	929.5	1374.6	1.48	gb:NM_001924.2 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA
207473_at	995.2	1472.9	1.48	gb:NM_002418.1 /DEF=Homo sapiens motilin (MLN), mRNA. /FEA=mRNA /GEN=MLN /PROD=motilin /DB_
210095_s_at	1213.3	1793.5	1.48	gb:M31159.1 /DEF=Human growth hormone-dependent insulin-like growth factor-binding protein mRNA, c
219454_at	1241.7	1836.1	1.48	gb:NM_015507.2 /DEF=Homo sapiens EGF-like domain, multiple 6 (EGFL6), mRNA. /FEA=mRNA /GEN=EG
201606_s_at	555	827.5	1.49	Consensus includes gb:BE796924 /FEA=EST /DB_XREF=gi:10218031 /DB_XREF=est:601587284F1 /CLON
211149_at	592.5	882.3	1.49	gb:AF000994.1 /DEF=Homo sapiens ubiquitous TPR motif, Y isoform (UTY), mRNA, alternative transcript 3
219803_at	745.2	1109.9	1.49	gb:NM_014495.1 /DEF=Homo sapiens angiopoietin-like 3 (ANGPTL3), mRNA. /FEA=mRNA /GEN=ANGPTL
213864_s_at	1371.3	2043.5	1.49	Consensus includes gb:AI985751 /FEA=EST /DB_XREF=gi:5613028 /DB_XREF=est:wr76h07.x1 /CLONE=IM
202029_x_at	2695.6	4029.9	1.49	gb:NM_000999.1 /DEF=Homo sapiens ribosomal protein L38 (RPL38), mRNA. /FEA=mRNA /GEN=RPL38 /P
212006_at	722.4	1080.4	1.5	Consensus includes gb:AUI49908 /FEA=EST /DB_XREF=gi:11011429 /DB_XREF=est:AUI49908 /CLONE=
211207_s_at	907.1	1364.7	1.5	gb:AF129166.1 /DEF=Homo sapiens long-chain acyl-CoA synthetase 5 (LACS5), mRNA, complete cds. /FE
202690_s_at	941.3	1412.2	1.5	gb:BC001721.1 /DEF=Homo sapiens, small nuclear ribonucleoprotein D1 polypeptide (16kD), clone MGC:2
201012_at	1121.9	1687.5	1.5	gb:NM_000700.1 /DEF=Homo sapiens annexin A1 (ANXA1), mRNA. /FEA=mRNA /GEN=ANXA1 /PROD=ann
208616_s_at	1476.4	2219.6	1.5	gb:U48297.1 /DEF=Homo sapiens protein tyrosine phosphatase PTPCAAX2 (nPTPCAAX2), mRNA, comple
214672_at	617.9	936	1.51	Consensus includes gb:AB023215.1 /DEF=Homo sapiens mRNA for KIAA0998 protein, partial cds. /FEA=m
207458_at	837.1	1267.7	1.51	gb:NM_024035.1 /DEF=Homo sapiens hypothetical protein MGC3113 (MGC3113), mRNA. /FEA=mRNA /GE
218226_s_at	890	1341.4	1.51	gb:NM_004547.2 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD), B1
200004_at	668.4	1018.2	1.52	gb:NM_001418.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA.
204470_at	877.6	1336.7	1.52	gb:NM_001511.1 /DEF=Homo sapiens GRO1 oncogene (melanoma growth stimulating activity, alpha) (GR
214179_s_at	951.6	1445.2	1.52	Consensus includes gb:H93013 /FEA=EST /DB_XREF=gi:1099341 /DB_XREF=est:yv07g07.s1 /CLONE=IMA
200912_s_at	1002.7	1526.1	1.52	gb:NM_001967.2 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA
213214_x_at	1289.6	1963.7	1.52	Consensus includes gb:AW190090 /FEA=EST /DB_XREF=gi:6464570 /DB_XREF=est:xl59a03.x1 /CLONE=I
210592_s_at	1939.2	2944.8	1.52	gb:M55580.1 /DEF=Human spermidinespermine N1-acetyltransferase mRNA, complete cds. /FEA=mRNA /
209123_at	670.4	1023.3	1.53	gb:BC000576.1 /DEF=Homo sapiens, quinoid dihydropyridine reductase, clone MGC:1657, mRNA, comple
201059_at	855.2	1305	1.53	gb:NM_005231.1 /DEF=Homo sapiens ems1 sequence (mammary tumor and squamous cell carcinoma-as
210779_x_at	879.7	1342.9	1.53	gb:AB037701.1 /DEF=Homo sapiens SIP1-beta mRNA for SMN interacting protein1-beta, complete cds. /F
222108_at	1647	2512	1.53	Consensus includes gb:AC004010 /DEF=Human BAC clone GS1-99H8 /FEA=CDS /DB_XREF=gi:2781385 /
221748_s_at	3191.3	4867.2	1.53	Consensus includes gb:AL046979 /FEA=EST /DB_XREF=gi:5435035 /DB_XREF=est:DKFZp586K0617_s1 /

203738_at	605.8	933	1.54	Consensus includes gb:AL421192 /FEA=EST /DB_XREF=gi:4267123 /DB_XREF=est:tt24e12.x1 /CLONE=IM
202289_s_at	820.2	1265.2	1.54	gb:NM_006997.1 /DEF=Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA
221368_at	1184.2	1823.4	1.54	gb:NM_005383.1 /DEF=Homo sapiens stailidase 2 (cytosolic stailidase) (NEU2), mRNA. /FEA=CDS /GEN=NE
212687_at	1312.1	2022.2	1.54	Consensus includes gb:AL110164.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586i0324 (from clone DKFZ
207720_at	829.2	1287	1.55	gb:NM_000427.1 /DEF=Homo sapiens loricrin (LOR), mRNA. /FEA=mRNA /GEN=LOR /PROD=loricrin /DB_
213151_s_at	1012.7	1568	1.55	Consensus includes gb:AU157515 /FEA=EST /DB_XREF=gi:11019036 /DB_XREF=est:AU157515 /CLONE=
201429_s_at	8390.7	13018	1.55	gb:NM_000998.1 /DEF=Homo sapiens ribosomal protein L37a (RPL37A), mRNA. /FEA=mRNA /GEN=RPL37
221505_at	713	1109	1.56	Consensus includes gb:AW612574 /FEA=EST /DB_XREF=gi:7317760 /DB_XREF=est:hh05b12.x1 /CLONE=
206050_s_at	923.2	1436.2	1.56	gb:NM_002939.1 /DEF=Homo sapiens ribonucleaseangiogenin inhibitor (RNHI), mRNA. /FEA=mRNA /GEN=
201352_at	1668.1	2597.9	1.56	gb:NM_014263.1 /DEF=Homo sapiens YME1 (S.cerevisiae)-like 1 (YME1L1), mRNA. /FEA=mRNA /GEN=YM
207574_s_at	1693.8	2663.8	1.57	gb:NM_015675.1 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA.
201502_s_at	1752.1	2766.1	1.58	Consensus includes gb:AI078167 /FEA=EST /DB_XREF=gi:3412575 /DB_XREF=est:oz30d08.x1 /CLONE=IM
203324_s_at	1021.4	1622.2	1.59	gb:NM_001233.1 /DEF=Homo sapiens caveolin 2 (CAV2), mRNA. /FEA=mRNA /GEN=CAV2 /PROD=caveoli
201922_at	1151.5	1828.4	1.59	gb:NM_014886.1 /DEF=Homo sapiens hypothetical protein (YR-29), mRNA. /FEA=mRNA /GEN=YR-29 /PRO
200662_s_at	1207.9	1919.1	1.59	gb:NM_014765.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 20 (yeast) homolog (K
202786_at	590	942	1.6	gb:NM_013233.1 /DEF=Homo sapiens Ste-20 related kinase (SPAK), mRNA. /FEA=mRNA /GEN=SPAK /PRO
211946_s_at	1057.1	1696.4	1.6	Consensus includes gb:AL096857.1 /DEF=Novel human mRNA from chromosome 1, which has similaritie
212230_at	2196.1	3509.5	1.6	Consensus includes gb:AV725664 /FEA=EST /DB_XREF=gi:10831279 /DB_XREF=est:AV725664 /CLONE=H
209397_at	551.4	887.6	1.61	gb:BC000147.1 /DEF=Homo sapiens, Similar to malic enzyme 2, NAD(+)-dependent, mitochondrial, clone M
206157_at	770.3	1239.3	1.61	gb:NM_002852.1 /DEF=Homo sapiens pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA.
65635_at	922.6	1482.8	1.61	Cluster Incl. AL044097:DKFZp434M1928_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434M1928 /clone_e
220044_x_at	947.8	1523.4	1.61	gb:NM_016424.1 /DEF=Homo sapiens cisplatin resistance-associated overexpressed protein (LUC7A), mR
213347_x_at	4440.7	7156.5	1.61	Consensus includes gb:AW132023 /FEA=EST /DB_XREF=gi:6133630 /DB_XREF=est:xe71b05.x1 /CLONE=
212386_at	695.8	1127.6	1.62	Consensus includes gb:BF592782 /FEA=EST /DB_XREF=gi:11685106 /DB_XREF=est:7j94d06.x1 /CLONE=
222229_x_at	887.8	1438.1	1.62	Consensus includes gb:AL121871 /DEF=Human DNA sequence from clone RP13-258O15 on chromosome
211628_x_at	1306.8	2116.7	1.62	gb:J04755.1 /DEF=Human ferritin H processed pseudogene, complete cds. /FEA=mRNA /GEN=FTHP1 /DB
200718_s_at	2433.8	3951.9	1.62	Consensus includes gb:AA927664 /FEA=EST /DB_XREF=gi:3076484 /DB_XREF=est:om71h10.s1 /CLONE=
200891_s_at	1070.4	1748.9	1.63	gb:NM_003144.2 /DEF=Homo sapiens signal sequence receptor, alpha (translocon-associated protein alph
200840_at	1103.4	1796.6	1.63	gb:NM_005548.1 /DEF=Homo sapiens lysyl-tRNA synthetase (KARS), mRNA. /FEA=mRNA /GEN=KARS /PR
200026_at	2436.3	3981.2	1.63	gb:NM_000995.1 /DEF=Homo sapiens ribosomal protein L34 (RPL34), mRNA. /FEA=mRNA /GEN=RPL34 /P
203621_at	788.3	1292.2	1.64	gb:NM_002492.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SG
201665_x_at	1237.2	2026.2	1.64	gb:NM_001021.1 /DEF=Homo sapiens ribosomal protein S17 (RPS17), mRNA. /FEA=mRNA /GEN=RPS17 /P
200069_at	761.1	1255.9	1.65	Consensus includes gb:AI656011 /FEA=EST /DB_XREF=gi:4739990 /DB_XREF=est:tt42e08.x1 /CLONE=IM
208645_s_at	857.6	1418.9	1.65	gb:AF116710.1 /DEF=Homo sapiens PRO2640 mRNA, complete cds. /FEA=mRNA /PROD=PRO2640 /DB_X
207594_s_at	584.1	967.9	1.66	gb:NM_003895.1 /DEF=Homo sapiens synaptotagmin 1 (SYNJ1), mRNA. /FEA=mRNA /GEN=SYNJ1 /PROD=s

207268_x_at	800	1335.2	1.67	gb:NM_005759.1 /DEF=Homo sapiens abi-interactor 12 (SH3-containing protein) (AIP-1), mRNA. /FEA=mR
212426_s_at	1040.3	1747.8	1.68	Consensus includes gb:BF033313 /FEA=EST /DB_XREF=gi:10741025 /DB_XREF=est:601458002F1 /CLON
213020_at	687.8	1164.2	1.69	Consensus includes gb:A1814252 /FEA=EST /DB_XREF=gi:5425467 /DB_XREF=est:wj70g04.x1 /CLONE=IM
221301_at	883.1	1492.6	1.69	gb:NM_025258.1 /DEF=Homo sapiens NG37 protein (G7C), mRNA. /FEA=CDS /GEN=G7C /PROD=NG37 pro
201738_at	1818.7	3115.5	1.71	gb:NM_005875.1 /DEF=Homo sapiens translation factor sui1 homolog (GC20), mRNA. /FEA=mRNA /GEN=
208780_x_at	989.6	1703.7	1.72	gb:AF154847.1 /DEF=Homo sapiens 33 kDa Vamp-associated protein (VAMP) mRNA, complete cds. /FEA
200963_x_at	2844.6	4902.4	1.72	gb:NM_000993.1 /DEF=Homo sapiens ribosomal protein L31 (RPL31), mRNA. /FEA=mRNA /GEN=RPL31 /P
201166_s_at	609.4	1056	1.73	gb:NM_014676.1 /DEF=Homo sapiens pumilio (Drosophila) homolog 1 (PUM1), mRNA. /FEA=mRNA /GEN=
215127_s_at	859.7	1484.5	1.73	Consensus includes gb:AL517946 /FEA=EST /DB_XREF=gi:12781439 /DB_XREF=est:AL517946 /CLONE=C
200817_x_at	1151.7	1992.4	1.73	gb:NM_001014.1 /DEF=Homo sapiens ribosomal protein S10 (RPS10), mRNA. /FEA=mRNA /GEN=RPS10 /P
208394_x_at	1022.8	1780.2	1.74	gb:NM_007036.2 /DEF=Homo sapiens endothelial cell-specific molecule 1 (ESM1), mRNA. /FEA=mRNA /GE
200765_x_at	813.6	1420.1	1.75	gb:NM_001903.1 /DEF=Homo sapiens catenin (cadherin-associated protein), alpha 1 (102KD) (CTNNA1), m
208671_at	1071.4	1872.8	1.75	gb:AF164794.1 /DEF=Homo sapiens Diff33 protein homolog mRNA, complete cds. /FEA=mRNA /PROD=DI
209339_x_at	937	1654.1	1.77	gb:AF005775.1 /DEF=Homo sapiens caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternative
202325_s_at	1089.2	1925.1	1.77	gb:NM_001685.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit
201599_at	1162.8	2062.9	1.77	gb:NM_000274.1 /DEF=Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene en
200726_at	1060.9	1890.6	1.78	gb:NM_002710.1 /DEF=Homo sapiens protein phosphatase 1, catalytic subunit, gamma isoform (PPP1C)
204271_s_at	1388.4	2482.4	1.79	gb:M74921.1 /DEF=Human endothelin receptor mRNA, complete cds. /FEA=mRNA /GEN=ETs /PROD=endo
201061_s_at	980.1	1762.8	1.8	gb:M81635.1 /DEF=Homo sapiens erythrocyte membrane protein mRNA, complete cds. /FEA=mRNA /GEN
213356_x_at	1607.4	2895.7	1.8	Consensus includes gb:AL568186 /FEA=EST /DB_XREF=gi:12922280 /DB_XREF=est:AL568186 /CLONE=C
217720_at	939.3	1699.8	1.81	gb:NM_016139.1 /DEF=Homo sapiens 16.7Kd protein (LOC51142), mRNA. /FEA=mRNA /GEN=LOC51142 /P
211072_x_at	1034	1875.4	1.81	gb:BC006481.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC-4387, mRNA, complete cds. /FEA=mRNA
218319_at	1401.8	2535.9	1.81	gb:NM_020651.2 /DEF=Homo sapiens pellino (Drosophila) homolog 1 (PEL1), mRNA. /FEA=mRNA /GEN=
213165_at	470.8	856.1	1.82	Consensus includes gb:A1041204 /FEA=EST /DB_XREF=gi:3280398 /DB_XREF=est:ov77g06.x1 /CLONE=IM
202466_at	796.9	1458.3	1.83	gb:NM_006999.2 /DEF=Homo sapiens topoisomerase-related function protein 4-1 (TRF4), mRNA. /FEA=m
208864_s_at	1284.6	2369.3	1.84	gb:AF313911.1 /DEF=Homo sapiens thioredoxin mRNA, complete cds. /FEA=mRNA /PROD=thioredoxin /D
204744_s_at	796.2	1475.9	1.85	gb:NM_013417.1 /DEF=Homo sapiens isoleucine-tRNA synthetase (IARS), transcript variant long, mRNA.
210512_s_at	1309	2425.1	1.85	gb:AF022375.1 /DEF=Homo sapiens vascular endothelial growth factor mRNA, complete cds. /FEA=mRNA
205003_at	521.8	971.5	1.86	gb:NM_014705.1 /DEF=Homo sapiens KIAA0716 gene product (KIAA0716), mRNA. /FEA=mRNA /GEN=KIA
201492_s_at	4873	9066.3	1.86	gb:NM_021104.1 /DEF=Homo sapiens ribosomal protein L41 (RPL41), mRNA. /FEA=mRNA /GEN=RPL41 /P
212814_at	812.3	1527.1	1.88	Consensus includes gb:AB020635.1 /DEF=Homo sapiens mRNA for KIAA0828 protein, partial cds. /FEA=m
214039_s_at	826.1	1553.8	1.88	Consensus includes gb:T15777 /FEA=EST /DB_XREF=gi:517939 /DB_XREF=est:IB1875 /UG=Hs.296398 Ho
213320_at	372.6	705.6	1.89	Consensus includes gb:AL551971 /FEA=EST /DB_XREF=gi:12890422 /DB_XREF=est:AL551971 /CLONE=C
211945_s_at	1121.2	2114.1	1.89	Consensus includes gb:BG500301 /FEA=EST /DB_XREF=gi:13461818 /DB_XREF=est:602546969F1 /CLON
212391_x_at	862.9	1637.2	1.9	Consensus includes gb:A1925635 /FEA=EST /DB_XREF=gi:5661686 /DB_XREF=est:wo34f07.x1 /CLONE=IM

219293_s_at	1063.7	2030.4	1.91	gb:NM_013341.1/DEF=Homo sapiens hypothetical protein (PTD004), mRNA. /FEA=mRNA /GEN=PTD004 /P
202130_at	1103.9	2110	1.91	Consensus includes gb:AA725102 /FEA=EST /DB_XREF=gi:2742809 /DB_XREF=est:al08n05.s1 /CLONE=1
201667_at	1642.1	3142.6	1.91	gb:NM_000165.2 /DEF=Homo sapiens gap junction protein, alpha 1, 43kD (connexin 43) (GJA1), mRNA. /F
208905_at	1692.1	3248.8	1.92	gb:BC005299.1 /DEF=Homo sapiens, cytochrome c, clone MGC:12367, mRNA, complete cds. /FEA=mRNA
200926_at	2997.9	5750.3	1.92	gb:NM_001025.1 /DEF=Homo sapiens ribosomal protein S23 (RPS23), mRNA. /FEA=mRNA /GEN=RPS23 /P
202644_s_at	900.9	1735.9	1.93	gb:NM_006290.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA. /
212788_x_at	1074.3	2077.9	1.93	Consensus includes gb:BG537190 /FEA=EST /DB_XREF=gi:1352892 /DB_XREF=est:602565589F1 /CLON
211959_at	3320.9	6398.2	1.93	Consensus includes gb:AW007532 /FEA=EST /DB_XREF=gi:5856310 /DB_XREF=est:ws52h07.x1 /CLONE=
200063_s_at	1186.6	2305.7	1.94	gb:BC002398.1 /DEF=Homo sapiens, nucleophosmin (nucleolar phosphoprotein B23, numatrin), clone MG
200061_s_at	1051.5	2055.2	1.95	gb:BC000523.1 /DEF=Homo sapiens, Similar to ribosomal protein S24, clone MGC:8595, mRNA, complete
217824_at	647.7	1283.7	1.98	Consensus includes gb:AW500009 /FEA=EST /DB_XREF=gi:7112213 /DB_XREF=est:U1-HF-BN0-aki-e-09-0
201842_s_at	1026	2041	1.99	Consensus includes gb:A1826799 /FEA=EST /DB_XREF=gi:5447470 /DB_XREF=est:wk56d07.x1 /CLONE=1
201266_at	1298.5	2599	2	gb:NM_003330.1 /DEF=Homo sapiens thioredoxin reductase 1 (TXNRD1), mRNA. /FEA=mRNA /GEN=TXNR
200062_s_at	1489.1	2983.5	2	gb:L05095.1 /DEF=Homo sapiens ribosomal protein L30 mRNA, complete cds. /FEA=mRNA /PROD=riboso
200777_x_at	1676.7	3349	2	gb:NM_000971.1 /DEF=Homo sapiens ribosomal protein L7 (RPL7), mRNA. /FEA=mRNA /GEN=RPL7 /PRO
203414_at	765.7	1536.2	2.01	gb:NM_012329.1 /DEF=Homo sapiens monocyte to macrophage differentiation-associated (MMD), mRNA.
208896_at	496.3	1011.5	2.04	Consensus includes gb:X98743.1 /DEF=H. sapiens mRNA for RNA helicase (Myc-regulated dead box prote
208635_x_at	1804.2	3674.5	2.04	Consensus includes gb:BF976260 /FEA=EST /DB_XREF=gi:12343475 /DB_XREF=est:602245139F1 /CLON
212185_x_at	1875.1	3822.5	2.04	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS
200735_x_at	1773.5	3635.4	2.05	gb:NM_005594.1 /DEF=Homo sapiens nascent-polypeptide-associated complex alpha polypeptide (NACA
212578_x_at	769	1581.2	2.06	Consensus includes gb:BF026595 /FEA=EST /DB_XREF=gi:10734307 /DB_XREF=est:601672736F1 /CLON
213084_x_at	5532.5	11421.8	2.06	Consensus includes gb:BF125158 /FEA=EST /DB_XREF=gi:10964198 /DB_XREF=est:601762392F1 /CLON
55065_at	799.2	1655.1	2.07	Cluster Incl. AL120554:DKFZp761B169_s1 Homo sapiens cDNA, 3 end /clone=DKFZp761B169 /clone_end
220960_x_at	1047.8	2166.4	2.07	gb:NM_000983.1 /DEF=Homo sapiens ribosomal protein L22 (RPL22), mRNA. /FEA=mRNA /GEN=RPL22 /P
201994_at	1398	2887	2.07	gb:NM_012286.1 /DEF=Homo sapiens MORF-related gene X (KIAA0026), mRNA. /FEA=mRNA /GEN=KIAA0
202692_s_at	536.8	1126.6	2.1	gb:NM_014233.1 /DEF=Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), m
209066_x_at	1107.6	2328.6	2.1	gb:M26700.1 /DEF=Human mitochondrial ubiquinone-binding protein mRNA, complete cds. /FEA=mRNA /
200095_x_at	2342.5	4908.5	2.1	Consensus includes gb:AA320764 /FEA=EST /DB_XREF=gi:1973113 /DB_XREF=est:EST23183 /UG=Hs.76
201064_s_at	568.3	1198.8	2.11	gb:NM_003819.2 /DEF=Homo sapiens poly(A)-binding protein, cytoplasmic 4 (inducible form) (PABPC4), m
201031_s_at	477.7	1015.3	2.13	gb:NM_005520.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA.
213478_at	595.6	1278.9	2.15	Consensus includes gb:AB028949.1 /DEF=Homo sapiens mRNA for KIAA1026 protein, partial cds. /FEA=m
202347_s_at	507.3	1100.8	2.17	gb:AB022435.1 /DEF=Homo sapiens LIG mRNA for E2 ubiquitin-conjugating enzyme, complete cds. /FEA
217739_s_at	929.6	2042.9	2.2	gb:NM_005746.1 /DEF=Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA. /FEA=mRNA /GE
200032_s_at	1928.9	4380.1	2.27	gb:NM_000661.1 /DEF=Homo sapiens ribosomal protein L9 (RPL9), mRNA. /FEA=mRNA /GEN=RPL9 /PRO
203405_at	581.2	1323.4	2.28	gb:NM_003720.1 /DEF=Homo sapiens Down syndrome critical region gene 2 (DSCR2), mRNA. /FEA=mRNA

204108_at	754.9	1721.3	2.28
207783_x_at	4353.8	9942.1	2.28
204651_at	555.9	1273.9	2.29
213477_x_at	648.1	1484.2	2.29
205061_s_at	659.8	1540	2.33
217975_at	800	1867.3	2.33
203282_at	875.1	2042	2.33
208825_x_at	5728.7	13420	2.34
208834_x_at	5712.9	13418.7	2.35
200893_at	635.9	1516.9	2.39
213101_s_at	1221.2	3121	2.56
201257_x_at	743.2	1916.6	2.58
221619_s_at	1786.9	4643.6	2.6
221474_at	553.2	1487.2	2.69
200933_x_at	1461.7	4005.2	2.74
212724_at	623.7	1779.6	2.85
209386_at	1668.9	4862.3	2.91
216438_s_at	1293	3817.8	2.95
201406_at	1612.2	4954	3.07
201590_x_at	855.9	2724.9	3.18
214938_x_at	553.3	1774.2	3.21
201631_s_at	1404.5	4524.6	3.22
211185_s_at	704	2311.5	3.28
204748_at	1150	4628	4.02
205207_at	2308.6	11218.4	4.86
211943_x_at	2098.5	10217.5	4.87

Consensus includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1
 gb:NM_017627.1 /DEF=Homo sapiens hypothetical protein FLJ20030 (FLJ20030), mRNA. /FEA=mRNA /GE
 Consensus includes gb:AW003022 /FEA=EST /DB_XREF=gi:5849860 /DB_XREF=est:wq61d03.x1 /CLONE=
 Consensus includes gb:AL515273 /FEA=EST /DB_XREF=gi:12778766 /DB_XREF=est:AL515273 /CLONE=C
 gb:NM_005033.1 /DEF=Homo sapiens polymyositiscleroderma autoantigen 1 (75kd) (PMSCL1), mRNA. /
 gb:NM_016303.1 /DEF=Homo sapiens pp21 homolog (LOC51186), mRNA. /FEA=mRNA /GEN=LOC51186 /P
 gb:NM_000158.1 /DEF=Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzym
 gb:U43701.1 /DEF=Human ribosomal protein L23a mRNA, complete cds. /FEA=mRNA /PROD=ribosomal p
 gb:BC001865.1 /DEF=Homo sapiens, Similar to cadherin 1, type 1, E-cadherin (epithelial), clone MGC:1151
 gb:NM_004593.1 /DEF=Homo sapiens splicing factor, arginineserine-rich (transformer 2 Drosophila homo
 Consensus includes gb:Z78330 /FEA=EST /DB_XREF=gi:1495103 /DB_XREF=est:HSZ78330 /CLONE=2.49
 gb:NM_001006.1 /DEF=Homo sapiens ribosomal protein S3A (RPS3A), mRNA. /FEA=mRNA /GEN=RPS3A
 gb:AF189289.1 /DEF=Homo sapiens presentin-associated protein mRNA, complete cds. /FEA=mRNA /PRO
 gb:U26162.1 /DEF=Human myosin regulatory light chain mRNA, complete cds. /FEA=mRNA /PROD=mys
 gb:NM_001007.1 /DEF=Homo sapiens ribosomal protein S4, X-linked (RPS4X), mRNA. /FEA=mRNA /GEN=
 Consensus includes gb:BG054844 /FEA=EST /DB_XREF=gi:12511973 /DB_XREF=est:qp58g11.x1 /CLONE=IM
 Consensus includes gb:AL346835 /FEA=EST /DB_XREF=gi:4084041 /DB_XREF=est:nac90f11.x1 /CLONE=IM
 Consensus includes gb:AL133228 /DEF=Human DNA sequence from clone RP5-1071L10 on chromosome
 gb:NM_021029.1 /DEF=Homo sapiens ribosomal protein L44 (RPL44), mRNA. /FEA=mRNA /GEN=RPL44 /P
 gb:NM_004039.1 /DEF=Homo sapiens annexin A2 (ANXA2), mRNA. /FEA=mRNA /GEN=ANXA2 /PROD=ann
 Consensus includes gb:AF283771.2 /DEF=Homo sapiens clone TCBAPO774 mRNA sequence. /FEA=mRNA
 gb:NM_003897.1 /DEF=Homo sapiens immediate early response 3 (IER3), mRNA. /FEA=mRNA /GEN=IER3
 gb:AF130099.1 /DEF=Homo sapiens clone FLC1464 PRO3102 mRNA, complete cds. /FEA=mRNA /PROD=P
 gb:NM_000963.1 /DEF=Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthas
 gb:NM_000600.1 /DEF=Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /FEA=mRNA /GEN=IL6
 Consensus includes gb:AL565449 /FEA=EST /DB_XREF=gi:12916836 /DB_XREF=est:AL565449 /CLONE=C