

Chromosomal Instability Is Associated with Higher Expression of Genes Implicated in Epithelial-Mesenchymal Transition, Cancer Invasiveness, and Metastasis and with Lower Expression of Genes Involved in Cell Cycle Checkpoints, DNA Repair, and Chromatin Maintenance<sup>1</sup>

## Anna V. Roschke<sup>\*</sup>, Oleg K. Glebov<sup>\*</sup>, Samir Lababidi<sup>†</sup>, Kristen S. Gehlhaus<sup>\*</sup>, John N. Weinstein<sup>†</sup> and Ilan R. Kirsch<sup>\*</sup>

\*Genetics Branch, Center for Cancer Research, National Cancer Institute, Bethesda, MD 20889-5105, USA; <sup>†</sup>Laboratory of Molecular Pharmacology, Center for Cancer Research, National Cancer Institute, Bethesda, MD 20889-5105, USA

### Abstract

Chromosomal instability—a hallmark of epithelial cancers—is an ongoing process that results in aneuploidy and karyotypic heterogeneity of a cancer cell population. Previously, we stratified cancer cell lines in the NCI-60 drug discovery panel based on their karyotypic complexity and heterogeneity. Using this stratification in conjunction with drug response data for the cell lines allowed us to identify classes of chemical compounds whose growth-inhibitory activity correlates with karyotypic complexity and chromosomal instability. In this article, we asked the question: What are the biological processes, pathways, or genes associated with chromosomal instability of cancer cells? We found that increased instability of the chromosomal content in a cancer cell population, particularly, persistent gains and losses of chromosomes, is associated with elevated expression of genes involved with aggressive cellular behavior, including invasion- and metastasis-associated changes in cell communication, adhesion, motility, and migration. These same karyotypic features are negatively correlated with the expression of genes involved in cell cycle checkpoints, DNA repair, and chromatin maintenance.

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### Introduction

Most cancers have an abnormal chromosomal content characterized by changes in chromosomal structure and number. Chromosomal aberrations tend to be more numerous in malignant tumors than in benign ones [1,2], and karyotypic complexity is associated with aggressive clinical behavior of tumors and poor prognoses [3–5]. Cancers contain cells that not only possess an abnormal number of chromosomes but also often show population heterogeneity with regard to the exact chromosomal complement. That heterogeneity is a marker of ongoing chromosomal instability in cancers—accelerated rates of gains and losses of whole chromosomes or large portions of cancer cell genomes [6,7]. Chromosomal instability is a process that facilitates cancer cell evolution under selection pressure, and because of instability and selection, tumors most frequently acquire an aneuploid chromosomal content.

The NCI-60 cancer cell line panel was assembled by the Developmental Therapeutics Program of the National Cancer Institute for *in vitro* anticancer drug screening. It includes human cancer cell lines

Address all correspondence to: Anna V. Roschke, Genetics Branch, Center for Cancer Research, National Cancer Institute, NNMC, 8901 Wisconsin Avenue, Building 8, Room 5101, Bethesda, MD 20889-5105. E-mail: roschkea@mail.nih.gov

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Abbreviations: EMT, epithelial-mesenchymal transition; NH, numerical chromosomal heterogeneity; NC, numerical chromosomal complexity; SH, structural chromosomal heterogeneity; SC, structural chromosomal complexity; GO, Gene Ontology; SCC, Spearman correlation coefficient

of lung, renal, colorectal, ovarian, breast, prostate, central nervous system (CNS), melanocyte, and hematological origins [8]. Since 1990, the NCI-60 cells have been exposed to more than 100,000 compounds in short-term cytotoxicity assays (http://dtp.nci.nih.gov) [9], and they have been profiled more extensively at the DNA, RNA, protein, and functional levels than any other set of cell lines [10]. Previously, we defined and studied karyotypic complexity and heterogeneity (as markers of ongoing instability) in the NCI-60 [11] and used this stratification to identify groups and classes of chemical compounds with higher growth-inhibitory activity in the more karyotypically complex and chromosomally unstable lines [12–14]. In the present work, we ask the question: What biological processes, pathways, and genes are associated with karyotypic instability of cancer cells? To address that question, we analyzed the correlation between karyotypic parameters and expression of genes across the NCI-60 panel.

### **Materials and Methods**

## Karyotypic Parameters of the NCI-60 Panel of Cancer Cell Lines

The NCI-60 panel of cancer cell lines was developed by the National Cancer Institute for in vitro anticancer drug screening, and it included cell lineages derived from different tissues (lung, renal, colorectal, ovarian, breast, prostate, CNS, melanoma, and hematological malignancies). Every cell line in the NCI-60 panel carries karyotypic abnormalities with notable individual variations among the cell lines at the level of karyotypic complexity and heterogeneity [11]. Complexity of the karyotype was defined on the basis of numerical abnormalities and structural rearrangements. Numerical chromosomal complexity (NC) was expressed in relation to the cell line ploidy level, according to the International System for Human Cytogenetic Nomenclature convention, and was calculated as a sum of the number of deviations of each specific chromosome from the designated ploidy level. Structural chromosomal complexity (SC) was expressed as the number of different structurally rearranged chromosomes present in two or more metaphases. Numerical chromosomal heterogeneity (NH) corresponds to the number of cell-to-cell variations of similar chromosomes. Loss of a chromosome in only one or two cells or gain in only one cell was not considered in the calculation of numerical heterogeneity because of the possibility of mechanical loss or gain during preparation of the metaphase spreads. Any specific chromosome displaying a higher number of gains or losses was considered to show variability and tallied as "1 point" in the numerical heterogeneity index. Structural chromosomal heterogeneity (SH) was estimated as the number of nonclonal (i.e., present in only one metaphase, according to the International System for Human Cytogenetic Nomenclature convention) structurally abnormal chromosomes per metaphase.

## NCI-60 Gene Expression Data

We used mRNA expression databases for the NCI-60 cell lines from the HG-U95 and the HG-U133 Affymetrix sets. HG-U95A data set includes ~12,000 array features corresponding to 8978 genes. HG-U133 data set has ~22,000 array features corresponding to 13,032 genes [15]. Gene expression data for NCI-60 cell lines were generated by hybridization to U133A and U133B arrays (Affymetrix, Santa Clara, CA), and CEL files were downloaded from http://discover. nci.nih.gov/cellminer. Three cell lines were excluded from analysis for different reasons (MDA-N was not available for karyotypic analysis, NCI/ADR-RES was a derivative of OVCAR-8, and lung cancer cell line H23 had no gene expression data available).

#### Data Analysis

CEL files for 57 cell lines were imported into R-2.4.0 language and statistical computing environment [16] using the Affy package of BioConductor-1.8 [17]. Probe set summarization, convolution background correction, and quantile normalization were conducted using a robust multichip average method [18] separately for U133A and U133B array sets. Data were filtered to have expression measurements to be above 16 in at least 25% of the samples and the interquartile range across the samples to be at least 0.5 on log<sub>2</sub> scale. This nonspecific filtering leaves 7500 probe sets for the U133A array set and 4036 probe sets for the U133B array set. Probe set expression measurements (log<sub>2</sub>-transformed) were combined into one data matrix (11,536 probe sets) that was transposed and aligned with karyotypic characteristics of cell lines for analysis of Spearman's rank correlation between gene expression and karyotypic parameters.

To calculate the false discovery rate (FDR) for each Spearman correlation coefficients (SCCs), 1000 random permutations of the karyotypic characteristic value (NC, NH, SC, or SH) were performed, and SCCs were recalculated for all 11,536 probe sets for each permutation. The number of probe sets having an SCC with a *P* value  $\leq$  .001 per random permutation was used to estimate FDR as the number of such probe sets at 0.95 or 0.99 quantiles (corresponding percentiles were considered as confidence levels for FDR estimates).

Genes differentially expressed in cell lines depending on tissue of origin were identified separately for U133A and U133B arrays using univariate F test as it is implemented in BRB-Array Tools [19]. Genes were considered differentially expressed if their F test parametric P value was less than .001.

To identify the most relevant GO terms associated with gene lists, gene-GO term enrichment analysis was performed using the DAVID2007 Functional Annotation Tool with customized gene backgrounds [20,21].

### Results

## Correlation of Expression Profiles with Karyotypic Parameters

We obtained SCCs between karyotypic parameters (SC, SH, NC, and NH) and each of the 11,536 probe sets from HG-U133A and HG-U133B data set obtained after filtering. The highest number of statistically significant (P < .001) correlations was identified for NH (454 array elements corresponding to 360 genes), followed by SH (318 array elements corresponding to 264 genes), NC (278 array elements corresponding to 224 genes), and SC (54 array elements corresponding to 50 genes; Table W1). To estimate the proportion of false-positives, 1000 random permutations of NH, NC, SH, and SC values were performed, and for each permutation, SCCs were calculated for all 11,536 probe sets. The density distributions of the number of SCCs with *P* value  $\leq$  .001 for permuted sample were then analyzed. With 99% confidence, among 454 array elements correlated with NH for which SCCs have P values .001 or less, there were no more than 73 false-positive probe sets for which a positive or negative correlation of expression measurements with NH may be due to random variation in gene expression or NH (Table W1).

Because NH correlates with the highest number of gene expression profiles, and the number of possible false-positive results at P < .001 is the lowest for this parameter, correlations with gene expression profiles obtained for NH were chosen for further investigation.

Data for 454 probe sets for which the SCCs between NH and gene expression had *P* value .001, are presented in Table W2. Variability in SCCs for these 454 array elements was estimated by drawing 1000 bootstrap replicates and calculating the average bootstrap SCCs and corresponding quantiles as confidence intervals. For all 454 array elements, 99% bootstrap confidence intervals of SCCs do not include zero, remaining either positive or negative throughout.

## Top Genes Associated with NH

Table 1 shows the top 50 Affy IDs positively associated with NH. These 50 Affy IDs correspond to only 39 gene transcripts because 8 genes (*ABL2*, *ATP6V0E*, *CRTAP*, *FN1*, *GNG12*, *IL13RA1*, *TIMP2*, and *TNPO1*) had more than one Affy ID selected in the top 50 positive list. On the basis of the SCC and *P* value, the three top genes with expression positively associated with NH are *VEGFC*, *leprecan-like 1*, and *Ras-related GTP-binding C* (Table 1). The list of 50 positive top genes is significantly enriched with genes that control cell communication (15 genes) and signal transduction (14 genes), response to wounding and cell motility (6 genes), cytokine–cytokine receptor interaction (5 genes), and cell migration (4 genes).

The top 50 Affy IDs (corresponding to 46 genes) expression of which negatively correlated with NH are shown in the Table 1*B*. In this top 50 negative list, *NUP210* is represented by four Affy IDs and *BTBD16* is represented by two. Both are among the three top genes negatively associated with NH. The third is *MLLT6* (Table 1). Among all 46 gene transcripts, 26 are significantly associated with intracellular organelles, 22 have membrane-bound products, and 18 are related to the nucleus.

## Identification of Origin-Independent Transcriptional Changes Associated with NH

The NCI-60 panel includes cell lines derived from different tissues. It seems possible, therefore, that the differences in gene expression profiles that correlate with karyotype are actually determined by tissue of origin and that correlations with karyotypic parameters simply reflect that fact epiphenomenally. Indeed, cluster analysis (Supplementary Materials and Methods) shows that the main factor that affects pattern of gene expression in the NCI-60 cell lines is the tissue of origin of the cell line (Figures W1–W3). Even when we selected for this analysis the 454 probe sets whose expression correlates with NH, cell lines still tend to cluster according to the tissue of origin (Figure W4). However, in this case, there is also a correlation of the clustering pattern with NH (Supplementary Results).

To address this question of origin-independent transcriptional changes associated with NH, we used two approaches. First, to estimate possible biases imposed on karyotype correlations by tissue-of-origin groupings, we used a "jackknife" procedure: each tissue-of-origin was omitted in turn, and SCCs for the 454 probe sets that had SCCs between NH and gene expression with *P* values  $\leq$  .001 were calculated for the excluded subset of cell lines. For all 454, 99% jackknife confidence intervals of SCCs excluded zero and remained positive or negative throughout, confirming that correlation of the expression of these transcripts with NH is not associated with any specific tissue-of-origin (data not shown).

Second, univariate *F* test identifies 1579 and 1098 probe sets in U133A and U133B arrays, respectively, as differentially expressed between cell lines grouped according to their 9 tissues of origin. Among them, 241 array features (corresponding to 172 genes) overlap with the previously identified ones significantly associated with NH (P <.001). Consequently, among the 454 Affymetrix IDs associated with NH at P < .001, 213 IDs corresponding to 188 genes are not differentially expressed based on their tissue of origin (129 features/ 121 genes negative, 84 features/67 genes positive; Table W3).

### Discussion

Aneuploidy and chromosomal instability are common conditions for most epithelial cancer cells, but the relationships between those factors and cellular functions are not clear. We, therefore, used correlations between NH and gene expression profiles of the NCI-60 cell lines, followed by Gene Ontology (GO) categorization, to identify genes and cellular processes associated with the increase of chromosomal instability in cancer cells.

Gene Ontology analysis of the distribution of 360 genes correlated with NH (P < .001) indicated that cell communication and signal transduction, cell adhesion, motility, and migration, response to wounding and inflammatory response, negative regulation of cell proliferation, and DNA replication are the main biological processes associated with numerical heterogeneity of the chromosomal content in the cancer cells (Table 2). Moreover, when these genes were divided into two groups based on their positive or negative correlation coefficients, we saw a striking difference between these two groups. Genes, expression of which was positively correlated with NH, fell into GO categories such as cell communication and signal transduction, including cell surface receptor-linked signal transduction, cell adhesion, locomotion, motility, and migration, development, morphogenesis, and differentiation, response to wounding, and inflammatory response (Figure 1A). Products of these genes were associated with extracellular matrix and extracellular space, plasma membrane, and cytoskeleton and were involved in the focal adhesion pathway (HSA04510), cytokine-cytokine receptor interaction (HSA04060), regulation of actin cytoskeleton (HSA04810), JAK-STAT signaling pathways (HSA04630), cell communication (HSA01430), and ECM-receptor interaction pathways (HSA04512; Table 2).

Genes whose expression negatively correlated with NH fell into totally different GO categories: cellular metabolism, nucleic acid metabolism, regulation of transcription, DNA replication, response to DNA damage stimulus, DNA repair, chromosome organization and biogenesis, DNA packaging, unwinding and replication initiation, and base-excision repair (Figure 1*B* and Table 2). Products of those genes serve as transcription regulators, involved in nucleic acid binding, linked to ATP-ase activity, and associated with the cell cycle regulation pathway (HSA04110). They localize on intracellular organelles and are, for the most part, found in the nucleus, chromosome/ chromatin, or nuclear envelope.

Among the 454 Affy IDs associated with NH at P < .001, 213 of them (corresponding to 188 genes) are not differentially expressed based on their tissue of origin (see the Results section). When we examined distribution of 188 genes across GO categories, genes whose expression is negatively associated with NH (121 genes) again were significantly enriched within such categories as intracellular membrane–bound organelle, nuclear protein, nucleic acid, or protein binding, regulation of transcription, DNA replication initiation, cell Table 1. Top 50 Genes with Expression Profiles Correlated Positively (A) or Negatively (B) with NH across the NCI-60 Panel of Cancer Cell Lines.

Affy ID	Gene Symbol	Gene Name	ρ	Р
(A)				
209946_at	VEGFC	Vascular endothelial growth factor C	0.5817	2.08e-06
218717_s_at	LEPREL1	Leprecan-like 1	0.5763	2.72e-06
218088_s_at	RRAGC	Ras-related GTP binding C	0.5750	2.89e-06
204140_at	TPST1	Tyrosylprotein sulfotransferase 1	0.5549	7.48e-06
226656_at	CRTAP	Cartilage-associated protein	0.5501	9.31e-06
255086_at	I HBSI EN1	Ethernetic 1	0.5460	1.12e-05
212464_s_at	FINI ANTVD1	Fibronectin I Humenbarical protein El 110601	0.5428	1.29e-05
220092_s_at	VIM	Vimentin	0.5425	1.500-05
201420_s_at	V 11V1 II 8	Vinicitin Interleukin 8	0.5349	1.01e=05
201172 x at	ATP6V0E	ATPase. H+ transporting, lysosomal 9 kDa. V0 subunit E	0.5341	1.82e-05
211719 x at	FN1	Fibronectin 1	0.5331	1.96e-05
210495 x at	FN1	Fibronectin 1	0.5330	1.97e-05
201828_x_at	CXX1	CAAX BOX 1	0.5306	2.18e-05
201380_at	CRTAP	Cartilage-associated protein	0.5301	2.22e-05
237444_at		Unknown	0.5288	2.36e-05
205743_at	STAC	SH3 and cysteine-rich domain	0.5265	2.60e-05
201105_at	LGALS1	Lectin, galactoside-binding, soluble, 1 (galectin 1)	0.5257	2.67e-05
200096_s_at	ATP6V0E	ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit E	0.5257	2.68e-05
204214_s_at	RAB32	RAB32, member <i>ras</i> oncogene family	0.5248	2.78e-05
200885_at	RHOC	Ras homolog gene family, member C	0.5242	2.85e-05
231907_at	ABL2	V-abl Abelson murine leukemia viral oncogene homolog 2 (ARG, Abelson-related gene)	0.5225	3.05e-05
226955_at	FLJ36748	Hypothetical protein FLJ36748	0.5195	3.46e-05
216442_x_at	FN1	Fibronectin 1	0.5172	3.79e-05
212509_s_at	MXRA/	FLJ46603 protein	0.5144	4.26e-05
222834_s_at	GNG12 TIMD2	Guanine nucleotide binding protein (G protein), gamma 12	0.5130	4.50e-05
224360_at	1 11V11²2 11 12D 4 1	I IVIP metallopeptidase inhibitor 2 Interlaulin 13 recentor alpha 1	0.512/	4.30e-03
211012_s_at	CPER2	Ovtoplasmic polyadenylation element binding protein 2	0.5110	4.80e-05
202378 s at	LEPROT	Lentin receptor overlapping transcript	0.5107	4.00e=05
235072 s at	LEINOI	Unknown	0.5104	4 99e-05
209226 s at	TNPO1	Transportin 1	0.5086	5.36e-05
202733 at	P4HA2	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	0.5083	5.43e-05
220407_s_at	TGFB2	Transforming growth factor, beta 2	0.5074	5.62e-05
212294_at	GNG12	Guanine nucleotide binding protein (G protein), gamma 12	0.5073	5.64e-05
202377_at	LEPR	Leptin receptor	0.5064	5.85e-05
209278_s_at	TFPI2	Tissue factor pathway inhibitor 2	0.5056	6.02e-05
201887_at	IL13RA1	Interleukin 13 receptor, alpha 1	0.5048	6.23e-05
209225_x_at	TNPO1	Transportin 1	0.5047	6.23e-05
208924_at	RNF11	Ring finger protein 11	0.5044	6.31e-05
212658_at	LHFPL2	Lipoma HMGIC fusion partner-like 2	0.5044	6.31e-05
213696_s_at	MED8	Mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	0.5043	6.33e-05
229465_s_at	PIPRD	Protein tyrosine phosphatase, receptor type, D	0.5043	6.34e-05
203262_s_at	FAM50A	Family with sequence similarity 50, member A	0.503/	6.48e-05
209013_x_at	TNDO1	Triple functional domain (PTPRF interacting)	0.5034	6.56e-05
20/03/_x_at	TIMPOT	Transportin 1 TIMD motollonomidaes inhibiter 2	0.5026	7 120 05
200998 s at	CKAP4	Cytoskeleton-associated protein 4	0.5015	7.12e=05
200990_s_at	ANKRD28	Ankyrin repeat domain 28	0.5005	7.22e-05 7.45e-05
226893 at	ABL2	<i>V-abl</i> Abelson murine leukemia viral oncogene homolog 2 (ARG, Abelson-related gene)	0.5000	7.48e-05
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(B)				
226148_at	BTBD15	BTB (POZ) domain containing 15	-0.6236	2.20e-07
212316_at	NUP210	Nucleoporin 210 kDa	-0.6040	6.56e-07
224784_at	MLLT6	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	-0.5733	3.15e-06
200069_at	SART3	Squamous cell carcinoma antigen recognized by T cells 3	-0.5686	3.94e-06
212315_s_at	NUP210	Nucleoporin 210 kDa	-0.5666	4.35e-06
226482_s_at	F11R	F11 receptor	-0.5620	5.38e-06
206687_s_at	PTPN6	Protein tyrosine phosphatase, non-receptor type 6	-0.5518	8.60e-06
21394/_s_at	NUP210	Nucleoporin 210 kDa	-0.54/3	1.06e-05
212482_at	FLJ13910 SVTL1	Hypothetical protein FLJ15910	-0.5425	1.52e-05
$22/134_at$	STILI ENOSE1	Synaptotaginin-like 1 Englese superfamily member 1	-0.5405	1.42e-05
207172_at 224428_s_at	CDCA7	Cell division cycle-associated 7	-0.5376	1.020-05
201969 at	NASP	Nuclear autoantigenic sperm protein (histone-hinding)	-0 5354	1.780-05
225887 at	1 11 101	Chromosome 13 open reading frame 23	-0.5305	2.19e-05
218491 s at	THYN1	Thymocyte nuclear protein 1	-0.5300	2.24e-05
227560_at	SFXN2	Sideroflexin 2	-0.5288	2.35e-05
	MYB	V-myb myeloblastosis viral oncogene homolog (avian)	-0.5250	2.76e-05
212978_at	LRRC8B	Leucine-rich repeat containing 8 family, member B	-0.5218	3.15e-05
212446_s_at	LASS6	LAG1 longevity assurance homolog 6 (Saccharomyces cerevisiae)	-0.5215	3.18e-05
202107_s_at	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	-0.5202	3.36e-05

Affy ID	Gene Symbol	Gene Name	ρ	Р
212873_at	HMHA1	Histocompatibility (minor) HA-1	-0.5197	3.43e-05
227378_x_at	MGC13114	Hypothetical protein MGC13114	-0.5192	3.49e-05
213149_at	DLAT	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	-0.5189	3.55e-05
227586_at	LOC124491	LOC124491	-0.5188	3.55e-05
204767_s_at	FEN1	Flap structure-specific endonuclease 1	-0.5170	3.83e-05
201038_s_at	ANP32A	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-0.5166	3.90e-05
208901_s_at	TOP1	Topoisomerase (DNA) I	-0.5163	3.94e-05
219378_at	NARG1L	NMDA receptor-regulated 1-like	-0.5155	4.07e-05
225179_at	HIP2	Huntingtin interacting protein 2	-0.5151	4.13e-05
225716_at	BRI3BP	BRI3 binding protein	-0.5139	4.34e-05
217980_s_at	MRPL16	Mitochondrial ribosomal protein L16	-0.5125	4.59e-05
225845_at	BTBD15	BTB (POZ) domain containing 15	-0.5116	4.75e-05
213251_at	LOC441046	Hypothetical LOC 441046	-0.5101	5.04e-05
220035_at	NUP210	Nucleoporin 210 kDa	-0.5091	5.26e-05
223268_at	C110RF54	Chromosome 11 open reading frame 54	-0.5091	5.26e-05
210206_s_at	DDX11	Dead/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	-0.5079	5.52e-05
202778_s_at	ZNF198	Zinc finger protein 198	-0.5058	5.99e-05
201202_at	PCNA	Proliferating cell nuclear antigen	-0.5053	6.09e-05
212943_at	KIAA0528	KIAA0528	-0.5048	6.21e-05
219067_s_at	C100RF86	Chromosome 10 open reading frame 86	-0.5044	6.31e-05
219188_s_at	LRP16	LRP16 protein	-0.5020	6.94e-05
201401_s_at	ADRBK1	Adrenergic, beta, receptor kinase 1	-0.5014	7.10e-05
203375_s_at	TPP2	Tripeptidyl peptidase II	-0.4994	7.65e-05
200091_s_at	RPS25	Ribosomal protein S25	-0.4992	7.72e-05
224944_at	TMPO	Thymopoietin	-0.4982	8.01e-05
228992_at	MED28	Mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	-0.4970	8.39e-05
213626_at	CBR4	Carbonic reductase 4	-0.4966	8.54e-05
231887_s_at	KIAA1274	KIAA1274	-0.4926	9.91e-05
202163_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	-0.4906	1.07e-04
202163_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	-0.4906	1.07e-04

Table 2. Gene Ontology Categories Associated with Genes Whose Expression Profiles Correlated with NH (P < .001) Across the NCI-60 Panel of Cancer Cell Lines.

Category	GO Term		GO Terms Associated with 360 Gene Transcripts Correlated with NH, <i>P</i> < .001			GO Terms Associated with 189 Gene Transcripts Positively Correlated with NH, <i>P</i> < .001			GO Terms Associated with 171 Gene Transcript: Negatively Correlated with NH, P < .001		
		Count	%	Р	Count	%	Р	Count	%	Р	
GOTERM_BP_ALL	homophilic cell adhesion	22	5.76	1.14e-13	22	10.48	9.44e-19				
GOTERM_BP_ALL	cell-cell adhesion	23	6.02	4.25e-11	23	10.95	3.08e-16				
GOTERM_BP_ALL	cell adhesion	36	9.69	1.16e-08	36	17.14	2.35e-15				
GOTERM_BP_ALL	cell surface receptor-linked signal transduction	32	8.38	9.20e-04	27	12.86	3.65e-06				
GOTERM_BP_ALL	cell communication	70	18.32	4.48e-02	54	25.71	8.16e-05				
GOTERM_BP_ALL	signal transduction	65	17.02	6.08e-02	50	23.81	2.30e-04				
GOTERM_BP_ALL	response to wounding	13	3.40	7.31e-03	11	5.24	9.33e-04				
GOTERM_BP_ALL	response to external stimulus	16	4.19	7.84e-03	13	6.19	1.11e-03				
GOTERM_BP_ALL	development	41	10.80	2.80e-01	36	17.14	1.14e-03				
GOTERM_BP_ALL	locomotion	15	3.93	1.39e-03	11	5.24	1.33e-03				
GOTERM_BP_ALL	localization of cell	15	3.93	1.39e-03	11	5.24	1.33e-03				
GOTERM_BP_ALL	cell motility	15	3.93	1.39e-03	11	5.24	1.33e-03				
GOTERM_BP_ALL	cell migration	8	2.09	1.20e-02	7	3.33	2.88e-03				
GOTERM_BP_ALL	G-protein-coupled receptor protein signaling pathway	14	3.66	3.38e-03	10	4.76	4.18e-03				
GOTERM_BP_ALL	inflammatory response	9	2.36	5.25e-03	7	3.33	4.26e-03				
GOTERM_BP_ALL	cellular morphogenesis				10	4.76	1.75e-02				
GOTERM_BP_ALL	cell differentiation				12	5.71	2.68e-02				
GOTERM_BP_ALL	response to other organism	13	3.40	8.48e-02	10	4.76	3.16e-02				
GOTERM_BP_ALL	neurogenesis				5	2.38	3.17e-02				
GOTERM_BP_ALL	acute-phase response	3	0.79	8.75e-02	3	1.43	3.18e-02				
GOTERM_BP_ALL	morphogenesis	15	3.90	4.70e-01	14	6.67	4.30e-02				
GOTERM_BP_ALL	negative regulation of cell proliferation	10	2.62	2.49e-02	6	2.86	9.36e-02				
GOTERM_BP_ALL	neutrophil chemotaxis	3	0.79	2.30e-02							
GOTERM_BP_ALL	regulation of chemotaxis	3	0.79	2.30e-02							
GOTERM_BP_ALL	positive regulation of chemotaxis	3	0.79	2.30e-02							
GOTERM_BP_ALL	immune cell migration	3	0.79	3.33e-02							
GOTERM_BP_ALL	immune cell chemotaxis	3	0.79	3.33e-02							
GOTERM_CC_ALL	membrane	108	28.42	5.18e-02	85	40.48	1.83e-06				
GOTERM_CC_ALL	intrinsic to membrane	78	20.53	7.70e-02	64	30.48	1.77e-05				
GOTERM_CC_ALL	plasma membrane				29	13.81	6.32e-03				

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Category	GO Term		GO Terms Associated with 360 Gene Transcripts Correlated with NH, <i>P</i> < .001			GO Terms Associated with 189 Gene Transcripts Positively Correlated with NH, <i>P</i> < .001			GO Terms Associated with 171 Gene Transcripts Negatively Correlated with NH, <i>P</i> < .001		
		Count	%	Р	Count	%	Р	Count	%	Р	
GOTERM_CC_ALL	extracellular region	25	6.58	6.30e-03	25	11.90	1.75e-06				
GOTERM_CC_ALL	intrinsic to plasma membrane				20	9.52	1.24e-02				
GOTERM_CC_ALL	cytoskeleton	10	2 (2	( ) ( ) )	19	9.05	5.25e-02				
GOTERM_CC_ALL	extracellular matrix	10	2.63	4.36e-02	10	4.76	1.66e-03				
GOTERM CC ALL	heterotrimeric G-protein complex				3	1.43	4.23e-02				
GOTERM_CC_ALL	extrinsic to plasma membrane	4	1.05	2.63e-02	3	1.43	5.77e-02				
GOTERM_MF_ALL	calcium ion binding	35	9.21	6.86e-06	35	16.67	8.96e-13				
GOTERM_MF_ALL	metal ion binding				66	31.43	2.57e-06				
GOTERM_MF_ALL	cation binding	16	4.21	262002	59 16	28.10	1.48e-05				
GOTERM_MF_ALL	signal transducer activity	16	4.21	2.62e-02	39	18.57	1.52e-0.5				
GOTERM MF ALL	protein binding	135	35,53	3.29e-03	81	38.57	1.92c-04 1.45e-03				
GOTERM_MF_ALL	receptor activity				22	10.48	2.28e-03				
GOTERM_MF_ALL	actin binding	12	3.16	6.81e-02	10	4.76	1.06e-02				
GOTERM_MF_ALL	growth factor binding				4	1.90	2.60e-02				
GOTERM_MF_ALL	carbohydrate binding				6	2.86	3.63e-02				
GOTERM_MF_ALL	L-ascorbic acid binding				3	1.43	4.02e-02				
GOTERM_MF_ALL	enzyme regulator activity evtoskeletal protein binding				13	7.14 5.24	4.06e-02 4.17e-02				
GOTERM MF ALL	extracellular matrix structural constituent				4	1.90	4.64e-02				
GOTERM_MF_ALL	oncostatin-M receptor activity	2	0.53	9.61e-02	2	0.95	5.34e-02				
KEGG_PATHWAY	HSA04060: CYTOKINE-CYTOKINE RECEPTOR INTERACTION	10	2.63	2.17e-03	10	4.76	6.75e-05				
KEGG_PATHWAY	HSA04510: FOCAL ADHESION	12	3.16	3.43e-02	11	5.24	3.78e-03				
KEGG_PATHWAY	HSA04630: JAK-STAT SIGNALING PATHWAY	8	2.11	1.68e-02	7	3.33	6.57e-03				
KEGG_PATHWAY	HSA01430: CELL COMMUNICATION HSA04810: DECULATION OF ACTIN OVTOSVELETON	6	1.58	4.99e-02	2	2.38	3.85e-02				
KEGG_PATHWAY	HSA04512: ECM-RECEPTOR INTERACTION				0 5	2.38	4.3/e=02				
GOTERM BP ALL	DNA-dependent DNA replication	12	3.14	1.67e-04	2	2.50	9.130 02	12	7.02	3.70e-08	
GOTERM_BP_ALL	DNA replication	15	3.93	1.80e-03				15	8.77	1.08e-07	
GOTERM_BP_ALL	DNA replication initiation	7	1.83	1.74e-04				7	4.09	1.25e-06	
GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolism							57	33.33	3.65e-06	
GOTERM_BP_ALL	DNA metabolism							22	12.87	1.09e-05	
GOTERM_BP_ALL	regulation of cellular metabolism							28 36	22.22	1.05e-04	
GOTERM BP ALL	transcription							36	21.05	2.14e-04	
GOTERM_BP_ALL	regulation of transcription							34	19.88	3.73e-04	
GOTERM_BP_ALL	macromolecule metabolism							61	35.67	4.92e-03	
GOTERM_BP_ALL	cellular metabolism							85	49.71	5.44e-03	
GOTERM_BP_ALL	response to DNA damage stimulus							10	5.85	6.34e-03	
GOTERM_BP_ALL	response to endogenous stimulus	24	NT/A	NT/A				10	5.85	7.73e-03	
GOTERM_BP_ALL	cell cycle DNA unwinding during replication	24	N/A 0.79	IN/A 4 51e-02				18	10.55	8.62e-03	
GOTERM BP ALL	DNA tepair	5	0.79	4.910-02				9	5.26	9.74e-03	
GOTERM_BP_ALL	DNA packaging							7	4.09	3.44e-02	
GOTERM_BP_ALL	phosphoinositide-mediated signaling							4	2.34	3.78e-02	
GOTERM_BP_ALL	base-excision repair							3	1.75	3.96e-02	
GOTERM_BP_ALL	chromosome organization and biogenesis	2	0.52	0.05 02				8	4.68	4.19e-02	
GOTERM_BP_ALL	DINA ligation during DINA repair	2	0.52	9.85e-02				2	1.17	4.23e-02	
GOTERM CC ALL	nucleus	2	0.92	9.896-02				71	41.52	6.28e-10	
GOTERM_CC_ALL	intracellular organelle							92	53.80	2.32e-07	
GOTERM_CC_ALL	organelle							92	53.80	2.37e-07	
GOTERM_CC_ALL	intracellular membrane-bound organelle							85	49.71	4.34e-07	
GOTERM_CC_ALL	intracellular	15	2 (0	4 (5 02				100	58.48	1.88e-06	
GOTERM_CC_ALL	chromosome	15	5.68	4.65e-02				15	8.//	2.62e-06	
GOTERM_CC_ALL	intracellular non-membrane-bound organelle							25	14.62	4.08e-04	
GOTERM_CC_ALL	synaptic vesicle							3	1.75	2.53e-02	
GOTERM_CC_ALL	nuclear envelope							5	2.92	3.50e-02	
GOTERM_CC_ALL	condensed chromosome							3	1.75	4.36e-02	
GOTERM_MF_ALL	nucleic acid binding							55	32.16	4.48e-06	
GOTERM_MF_ALL	DNA dana dana ATDara antining	~	1.22	2.00 02				37	21.64	7.16e-05	
GOTERM_MF_ALL	DINA-dependent Al Pase activity	6	1.32	2.09e-02				6 16	5.51 0.26	9.65e-05	
GOTERM MF ALL	transcription regulator activity							22	12.87	9.78e-03	
GOTERM_MF_ALL	ATPase activity							9	5.26	2.13e-02	
GOTERM_MF_ALL	ATPase activity, coupled							8	4.68	3.19e-02	
KEGG_PATHWAY	HSA04110: CELL CYCLE	10	2.63	3.13e-02				10	5.85	1.64e-05	



Figure 1. Biological processes associated with expression of genes positively (A) and negatively (B) correlated with NH.

cycle, chromatin-related protein, and DNA repair. Genes whose expression correlated positively with NH (67 genes) again showed significant enrichment in such categories as cell communication and signal transduction, extracellular region, development and morphogenesis, response to wounding, cell migration, and motility. In summary, then, the GO classifications of genes positively and negatively associated with NH did not seem to depend on tissue of origin of the cancer cell.

Evaluation of 1122 genes whose expression correlated with NH at P < .01 (Table W4) revealed further enrichment of the same GO categories identified under stricter conditions (P < .001; data shown in the Table 2). That observation suggests that the essential findings are not sensitive to the P value cutoff used. Also reassuring with respect to robustness of the findings, analysis of the HG-U95A data showed similar GO category enrichments (data not shown).

Focusing on the negative correlations of expression with NH, we found enrichment of the following biological processes:

- 1) Cellular metabolism
- 2) Nucleic acid metabolism

- 3) Regulation of transcription
- 4) DNA replication
- 5) Response to DNA damage stimulus
- 6) DNA repair
- 7) Chromosome organization and biogenesis
- 8) DNA replication initiation
- 9) DNA packaging
- 10) Cell cycle regulation

The CIN phenotype has been associated with very rare mutations in the checkpoint genes [22–27] and with decreased protein levels of mitotic checkpoint components [25,27,28]. Deletion in mice of one allele of *Mad2*, *Bub1*, or *Bub3* compromises the mitotic checkpoint, yielding higher rates of chromosome missegregation [29–32]. In our study, regulators of mitotic cell cycle checkpoint (*MAD2* and *BUB3*), as well as a component of APC/C (*APC4*), are found among the genes whose expression is negatively correlated with NH. Correlations do not imply causative relationships; however, it would not be unreasonable to suggest that the decreased level of mitotic checkpoint components could be the basis of mitotic checkpoint relaxation leading to increased gains and losses of chromosomes. This supports already existing assumptions that a compromised mitotic checkpoint leads to accelerated rates of chromosomal instability in cancer cells [33].

The expression of genes involved in DNA damage checkpoints (CHK1, CHK2, H2AX, RAD21, XRCC5, DDB1) and DNA rereplication prevention (BCCIP, BRCA2, CDT1, MCM2-7, cyclin B2) negatively correlates with NH as well. The expression levels of genes involved in DNA packaging, chromosome condensation, and kinetochore formation (H3 histone, H1FX, H2AX, H2AZ, TOP1, RCC1, RCC2, SMARCA5, RCBTB1, CENPC1, ZWINT) are also relatively down-regulated in cancer cells with higher level of chromosomal instability compared to cancer cells with a lower level of instability.

Compromised cell cycle checkpoints give cancer cells an advantage in that they may be able to proliferate in a stressful environment with uncompleted DNA repair, perhaps with some level of unfinished chromatin condensation and/or individualization of chromatids, and perhaps with defects of mitotic chromosome organization. As a result, on-going gains and losses of chromosomes or their fragments can occur while cells are proliferating. We also found that chromosomal instability is associated with less effective cellular metabolism, DNA replication and transcription, DNA repair and packaging, weakness in proper chromatin condensation, and mitotic chromosome structural organization possibly owing to extensive imbalances in cellular protein composition of cells that undergo continuous gains and losses of parts of genome.

Gene Ontology's biological processes positively correlated with higher NH include the following:

- 1) Cell communication and signal transduction
- 2) Cell adhesion, including cell-cell adhesion
- 3) Cell surface receptor-linked signal transduction
- 4) Development and differentiation
- 5) Cell motility and migration
- 6) Response to wounding
- 7) Inflammatory response
- 8) G-protein-coupled receptor protein signaling
- 9) Cellular morphogenesis

A collective molecular portrait of numerical chromosomal heterogeneity in cancer cells includes relative up-regulation of genes that are associated with increased motility and migration, epithelialmesenchymal transition (EMT), and are critical for tumor invasion and metastasis: *RhoC, fibronectin, LOX, TWIST, SNAI2, EGFR, laminins, integrins, collagens, CDC42* effector protein (Rho GTPase binding), Rho family GTPase 3, *RAB, CXCL2, TGF-b2, VEGFC, IL-6, IL-8, CTGF, vimentin, N-cadherin, CD44, BCAR3, protocadherins, MMP2* and *MMP14, NOTCH2, SERPINE1, 2,* and *8, IGFBP3* and *7, TNFAIP3, TNFRSF12A* and *19, PLAUR,* and *SPARC.* Expression of several genes that promote cell proliferation and G<sub>1</sub> entry into cell cycle (*CCD1, EGFR, VEGFC*) correlate positively with the higher NH as well.

Advances in the molecular profiling of cancer using genome-wide approaches have revealed genes whose expression levels in primary tumors correlate strongly with the likelihood of metastatic recurrence [34–37]. In particular, genes that are involved in physiological programs of cellular response to tissue damage (inflammation, wound healing, tissue remodeling, and regeneration) and genes that participate in differentiation and morphogenesis during epithelial tissue development are involved in tumor invasiveness and metastasis [38–41]. Important to those processes is an EMT, which enables cells to undergo major changes in morphology, lose cellular contacts, and acquire motility and ability to migrate. Also an important part of those programs is stimulation of proliferation and differentiation of epithelial cells themselves, as well as angiogenesis and lymphangiogenesis. Our findings suggest a link, at least indirectly, between chromosomal instability and cancer proliferation, invasion, and metastasis.

Chromosomal instability can create both advantages and disadvantages for cancer cells. For instance, severe genomic damage due to losses or gains of whole chromosomes or their essential fragments can prevent cancer cells from further proliferation. At the same time, the program of response to tissue damage represents an advantageous feature for overall cancer progression. Release of chemokines and cytokines promotes a response from surrounding tumor and stromal cells leading to the EMT in cancer cells, changes in cell adhesion and motility, promoting epithelial cell proliferation, as well as angiogenesis and lymphangiogenesis. We suggest that gross instability of cancer cell genomes leads to evolution of cancer cell populations, which "internalize" various inducers of a tissue damage response, gradually making cancer cells more and more independent of environmental stimuli. These changes in the gene expression pattern persist in cancer-derived cell lines.

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## **Supplement: Cluster Analysis**

### Materials and Methods

For cluster analysis, U133A and U133B array data were processed separately as described (Materials and Methods, main text) with modifications. First, robust multichip average-transformed data were filtered to have expression measures higher than 64 at least in two cell lines, which is the minimum number of cell lines in a group. Two gene sets were selected: one for which the interquartile range in expression values was higher than 0.5 on log<sub>2</sub> scale (11,848 probe sets) and the second for which the interquartile range in expression values was higher than 1 on log<sub>2</sub> scale (this left 1667 and 682 probe sets for U133A and U133B array data sets, respectively). Gene expression matrixes were then additionally normalized by subtracting log<sub>2</sub>(median) expression value for each probe set. Gene expression matrixes for differentially expressed genes selected according to the F test (Materials and Methods, main text) and for 454 probe sets that show correlation with numerical heterogeneity (NH) level were also normalized by subtracting log<sub>2</sub>(median) expression value for each probe set. This normalization makes results more comparable when different distance measures are used. For Figures W2 to W4, clustering was done by Hierarchical Ordered Partitioning And Collapsing Hybrid (HOPACH) method as implemented in R package hopach [1] using cosine angle (uncentered correlation) and Euclidean distances for genes and arrays, respectively. For Figure W1, hierarchical clustering was performed by using function hclust (R package cluster), Euclidean distance, and average linkage. In the HOPACH algorithm, minimization of the median split silhouette value is used to choose the cluster number and cluster ordering. Compared with other clustering algorithms, the HOPACH method produces consistent cluster ordering regardless of the original ordering of the arrays in gene expression matrix [2]. Bootstrap resampling was done by selecting 10,000 sets of 57 arrays one array at a time with replacement. The proportion of resampled data sets in which each cell line falls into each of the clusters serves as an estimate of the membership of that cell line in each cluster. Bigger proportion of cell lines with consistent membership in a cluster indicates that cluster is well differentiated from other clusters and stable. Because we wanted to analyze mainly cell line characteristics (particularly karyotypic instability), the results are presented as ordered distance matrixes for cell lines together with bar plots of the bootstrap reappearance proportions for each cell line and each cluster. Additional details and results of cluster analysis are available on request.

### Results

Hierarchical clustering of the 57 cell lines from NCI-60 collection shows that cell lines are mostly grouped according to the presumptive tissue of origin when using 11,848 probe sets with moderate level in expression variability (Figure W1).

We observed such correspondence after using for hierarchical clustering of cell lines 2349 genes that were selected also nonspe-

cifically as displaying a higher (more than twofold difference between 25th and 75th percentiles) level of expression variability across cell lines (Figure W2). However, it can be seen that there are some similarities between cell lines unrelated to common tissue of origin: colon cell lines are similar to some prostate, renal, and ovarian cell lines and some colon cell lines are also similar to leukemia cell lines (Figure W2). Thus, though the tissue of origin seems to be a critical factor that influences gene expression pattern in the NCI-60 cell lines, there are additional variables that can be used to stratify cell lines if the gene set is selected appropriately (see also Ross et al. [3]).

For example, the correspondence of cell line gene expression patterns to tissue of origin can be enhanced if clustering is performed using a subset of genes that were selected according to an F test as differentially expressed between cell lines of different tissues of origin (Figure W3). Cell lines derived from leukemias, melanomas, colon tumors, renal tumors, CNS tumors, and, to a lesser extent, lung tumors form clusters that can be seen as separate blocks on the diagonal of the ordered dissimilarity matrix. This confirms the results obtained using spotted cDNA arrays [3] and illustrates that selection of genes changes the cluster analysis results: the clusters defined by differentially expressed genes are not only better separated but also are more stable than clusters obtained using nonspecifically selected genes, as follows from a bootstrap resampling analysis (compare Figures W2 and W3).

Impact of the tissue of origin of cell lines on gene expression pattern can still be traced after clustering using 454 probe sets whose expression correlates with NH index. However, the ordered dissimilarity matrix is quite different from the one based on genes differentially expressed among cell lines of different tissues of origin (Figure W4). Particularly, all cell lines derived from leukemia and colon tumors (together with two cell lines from breast tumors and one cell line from a lung tumor) form a tight cluster that is remarkably stable upon bootstrap resampling. Cell lines in this cluster have an average NH index of 0.27, whereas 21 cell lines in the biggest cluster that show maximal dissimilarity (denoted by the presence of a white color in the matrix) with the cluster of leukemia and colon cell lines have an average NH index 0.65.

Clustering analysis demonstrates that gene expression is influenced mainly by the tissue of origin, and at the same time, clustering of genes selected based on their correlation with NH is different, demonstrating an influence by NH as well.

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**Table W1.** Number of Gene Expression Array Elements and Corresponding Genes Correlatedwith Structural Complexity, Structural Heterogeneity, Numerical Complexity, and NumericalHeterogeneity with P < .01 and P < .001.

	P < .01		P < .001	.001	
	Array Elements	Genes	Array Elements	Genes	
SC-positive	190	165	20	18	
SC-negative	187	166	34	32	
SC total	377	331	54	50	
FP 0.95	279		38		
FP 0.99	430		75		
SH-positive	733	560	215	168	
SH-negative	398	352	103	96	
SH total	1131	912	318	264	
FP 0.95	271		36		
FP 0.99	446		82		
NC-positive	568	419	148	106	
NC-negative	479	407	130	118	
NC total	1047	826	278	224	
FP 0.95	306		44		
FP 0.99	484		98		
NH-positive	834	571	261	189	
NH-negative	640	551	193	171	
NH total	1474	1122	454	360	
FP 0.95	290		43		
FP 0.99	450		73		

FP indicates false-positive results.

## Table W2. List of 454 Array Features and Names of Corresponding Genes with Expression Profiles Correlated with NH (P < .001) Across the NCI-60 Panel of Cancer Cell Lines.

Affy ID	Gene Symbol	Description	ρ	Р
226148_at	BTBD15	BTB (POZ) domain containing 15	-0.6236	2.20e-07
212316_at	NUP210	nucleoporin 210 kDa	-0.6040	6.56e-07
209946_at	VEGFC	vascular endothelial growth factor C	0.5817	2.08e-06
218717_s_at	LEPREL1	leprecan-like 1	0.5763	2.72e-06
218088_s_at	RRAGC	Ras-related GTP binding C	0.5750	2.89e-06
224784_at	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	-0.5733	3.15e-06
200069_at	SART3	squamous cell carcinoma antigen recognized by T cells 3	-0.5686	3.94e-06
212315_s_at	NUP210	nucleoporin 210 kDa	-0.5666	4.35e-06
226482_s_at	F11R	F11 receptor	-0.5620	5.38e-06
204140_at	TPST1	tyrosylprotein sulfotransferase 1	0.5549	7.48e-06
206687_s_at	PTPN6	protein tyrosine phosphatase, non-receptor type 6	-0.5518	8.60e-06
226656_at	CRTAP	cartilage associated protein	0.5501	9.31e-06
213947_s_at	NUP210	nucleoporin 210 kDa	-0.5473	1.06e-05
235086_at	THBS1	Thrombospondin 1	0.5460	1.12e-05
212464_s_at	FN1	fibronectin 1	0.5428	1.29e-05
220092_s_at	ANTXR1	anthrax toxin receptor 1	0.5425	1.30e-05
212482_at	RMND5A	hypothetical protein FLJ13910	-0.5423	1.32e-05
227134_at	SYTL1	synaptotagmin-like 1	-0.5405	1.42e-05
201426_s_at	VIM	vimentin	0.5377	1.61e-05
204142_at	ENOSF1	enolase superfamily member 1	-0.5376	1.62e-05
224428_s_at	CDCA7	cell division cycle–associated 7	-0.5354	1.78e-05
201969_at	NASP	nuclear autoantigenic sperm protein (histone-binding)	-0.5354	1.78e-05
202859_x_at	IL8	interleukin 8	0.5349	1.82e-05
201172_x_at	ATP6V0E1	ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e	0.5341	1.88e-05
211719_x_at	FN1	fibronectin 1	0.5331	1.96e-05
210495_x_at	FN1	fibronectin 1	0.5330	1.97e-05
201828_x_at		CAAX box 1	0.5306	2.18e-05
225887_at	C13orf23	chromosome 13 open reading frame 23	-0.5305	2.19e-05
201380_at	CRTAP	cartilage-associated protein	0.5301	2.22e-05
218491_s_at	THYN1	thymocyte protein Thy28	-0.5300	2.24e-05
227560_at	SFXN2	sideroflexin 2	-0.5288	2.35e-05
237444_at		Transcribed locus	0.5288	2.36e-05
205743_at	STAC	SH3 and cysteine-rich domain	0.5265	2.60e-05
201105_at	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	0.5257	2.67e-05
200096_s_at	ATP6V0E	ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e	0.5257	2.68e-05
204798_at	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	-0.5250	2.76e-05
204214_s_at	RAB32	RAB32, member RAS oncogene family	0.5248	2.78e-05
200885_at	RHOC	ras homolog gene family, member C	0.5242	2.85e-05
231907_at	ABL2	V-abl Abelson murine leukemia viral oncogene homolog 2 (ARG, Abelson-related gene)	0.5225	3.05e-05
212978_at	LRRC8B	Leucine-rich repeat containing 8 family, member B	-0.5218	3.15e-05
212446_s_at	LASS6	LAG1 longevity assurance homolog 6 (S. cerevisiae)	-0.5215	3.18e-05

Affy ID	Gene Symbol	Description	ρ	Р
202107_s_at	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	-0.5202	3.36e-05
212873_at	HMHA1	minor histocompatibility antigen HA-1	-0.5197	3.43e-05
226955_at	FLJ36748	hypothetical protein FLJ36748	0.5195	3.46e-05
227378_x_at	MGC13114	hypothetical protein MGC13114	-0.5192	3.49e-05
213149_at	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	-0.5189	3.55e-05
227586_at	LOC124491	LOC124491	-0.5188	3.55e-05
216442_x_at	FN1	fibronectin 1	0.5172	3.79e-05
204767_s_at	FEN1	flap structure-specific endonuclease 1	-0.5170	3.83e-05
201038_s_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-0.5166	3.90e-05
208901_s_at	TOP1	topoisomerase (DNA) I	-0.5163	3.94e-05
219378_at	NARG1L	NMDA receptor regulated 1-like	-0.5155	4.07e-05
225179_at	HIP2	Huntingtin interacting protein 2	-0.5151	4.13e-05
212509_s_at	MXRA7	matrix-remodeling associated 7	0.5144	4.26e-05
225716_at	01/010	full-length cDNA clone CS0DK008Y109 of HeLa cells Cot 25-normalized of <i>Homo sapiens</i> (human)	-0.5139	4.34e-05
222834_s_at	GNG12	guanine nucleotide binding protein (G protein), gamma 12	0.5130	4.50e-05
224560_at	TIMP2	1 IMP metallopeptidase inhibitor 2	0.512/	4.56e-05
21/980_s_at	MRPL16	mitochondrial ribosomal protein L16	-0.5125	4.59e-05
225845_at	BIBDI5	B1B (POZ) domain containing 15	-0.5116	4./5e-05
211612_s_at	IL13RA1	interleukin 13 receptor, alpha l	0.5114	4.80e-05
226939_at	CPEB2	cytoplasmic polyadenylation element binding protein 2	0.5110	4.88e-05
2023/8_s_at	LEPROI	leptin receptor overlapping transcript	0.510/	4.93e-05
209153_s_at	ICF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E4/)	-0.5104	4.99e-05
2350/2_s_at		Iranscribed locus	0.5104	4.99e-05
213251_at	NULDO10	Hypothetical LOC 441046	-0.5101	5.04e-05
220035_at	NUP210	nucleoporin 210 kDa	-0.5091	5.26e-05
223268_at	PID012	PID012 protein	-0.5091	5.26e-05
209226_s_at		transportin I	0.5086	5.566-05
202/35_at	P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	0.5085	5.450-05
210206_s_at	DDXII	DEAD/H (Asp-Giu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, 5. cereviside)	-0.50/9	5.52e-05
22040/_s_at	IGFB2 CNC12	transforming growth factor, beta 2	0.50/4	5.62e-05
212294_at	GNG12	guanine nucleotide binding protein (G protein), gamma 12	0.50/5	5.64e-05
2025//_at	LEFR; LEFROI	ring Grade matching 100	0.5064	5.00- 05
202//8_s_at	Z.W11W12 TEDI2	zine foren nalmur inkilitar 2	-0.3038	5.99e-05
2092/8_s_at	IFP12 DCNA	tissue factor pathway inhibitor 2	0.5056	6.02e-05
201202_at	VTA 405 28	VIAA0528 cono product	-0.3033	6.096-05
212943_at	II 13DA1	interleulzin 13 recentor alpha 1	-0.3048	6.23e 05
20100/_at	TNDO1	transportin 1	0.5048	6.23e 05
209223_x_at	NSMCE44	chromosome 10 open reading frame 86	0.504/	6.31e.05
21900/_s_at	RNF11	ring finger protein 11	-0.5044	$6.31e_{-}05$
2005/24_at	I HEDI 2	linoma HMCIC fusion partner-like 2	0.5044	$6.31e_{-}05$
212090_at	MED8	mediator of RNA polymerase II transcription, subunit & homolog (vesst)	0.5043	6.33e_05
229465 s at	PTPRS	protein tyrosine phosphatase receptor type S	0.5043	6.34e=05
203262 s at	FAM50A	family with sequence similarity 50 member A	0.5037	6.48e=05
209013 x at	TRIO	triple functional domain (PTPRF interacting)	0.5034	6.56e=05
207657 x at	TNPO1	transportin 1	0.5026	6.78e-05
219188 s at	1111 01	LRP16 protein	-0.5020	6.94e-05
201401 s at	ADRBK1	adrenergic, beta, receptor kinase 1	-0.5014	7.10e-05
231579 s at	TIMP2	TIMP metallopeptidase inhibitor 2	0.5013	7.12e-05
200998 s at	CKAP4	cytoskeleton-associated protein 4	0.5009	7.22e-05
229307 at	ANKRD28	ankyrin repeat domain 28	0.5001	7.45e-05
226893 at	ABL2	V-abl Abelson murine leukemia viral oncogene homolog 2 (ARG, Abelson-related gene)	0.5000	7.48e-05
224796 at	DDEF1	development and differentiation enhancing factor 1	0.5000	7.49e-05
203375 s at	TPP2	tripeptidyl peptidase II	-0.4994	7.65e-05
238447 at	RBMS3	RNA binding motif, single-stranded interacting protein	0.4994	7.66e-05
200091_s_at	RPS25	ribosomal protein S25	-0.4992	7.72e-05
224944_at	ТМРО	Thymopoletin	-0.4982	8.01e-05
228234_at	TICAM2	toll-like receptor adaptor molecule 2	0.4974	8.27e-05
209019_s_at	PINK1	PTEN-induced putative kinase 1	0.4974	8.28e-05
200757_s_at	CALU	calumenin	0.4973	8.29e-05
228992_at	MED28	Mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	-0.4970	8.39e-05
213626_at	CBR4	carbonic reductase 4	-0.4966	8.54e-05
209263_x_at	TSPAN4	tetraspanin 4	0.4964	8.61e-05
225765_at	TNPO1	Transportin 1	0.4955	8.89e-05
203695_s_at	DFNA5	deafness, autosomal dominant 5	0.4952	8.99e-05
212470_at	SPAG9	sperm-associated antigen 9	0.4948	9.12e-05
213455_at		hypothetical LOC283677	0.4947	9.16e-05
204359_at	FLRT2	fibronectin leucine rich transmembrane protein 2	0.4945	9.25e-05
214696_at		hypothetical protein MGC14376	0.4937	9.53e-05
231887_s_at	KIAA1274	KIAA1274	-0.4926	9.91e-05
203773_x_at	BLVRA	biliverdin reductase A	0.4921	1.01055e-
200756	CALU	calumenin	0.4916	1.03041e-
200/56_x_at				

Affy ID	Gene Symbol	Description	ρ	Р
224790_at	DDEF1	development and differentiation enhancing factor 1	0.4908	1.06088e-
202163_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	-0.4906	1.07122e-
221771_s_at		M-phase phosphoprotein, mpp8	-0.4903	1.08198e-
218458_at	GMCL1	germ cell-less homolog 1 (Drosophila)	-0.4900	1.09481e-
212973_at	RPIA	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	-0.4900	1.09481e-
221/3/_at	GIVA12 MVO10	guanine nucleotide binding protein (G protein) alpha 12	0.4896	1.1094/e-
2019/6_s_at	SSH1	myösin A slingshot homolog 1 ( <i>Dragabila</i> )	0.4895	1.1094/e- 1.11215e-
212430 at	RBM38	RNA-hinding region (RNP1, RRM) containing 1	-0 4884	1.1121 <i>)</i> e=
200943 at	HMGN1	high-mobility group nucleosome binding domain 1	-0.4884	1.16009e-
222514_at	RRAGC	Ras-related GTP binding C	0.4881	1.17272e-
233888_s_at	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	0.4881	1.17555e-
223199_at	MKNK2	MAP kinase interacting serine/threonine kinase 2	-0.4877	1.19155e-
200990_at	TRIM28	tripartite motif-containing 28	-0.4871	1.21574e-
218980_at	FHOD3	formin homology 2 domain containing 3	0.4871	1.21719e-
209832_s_at	CDTT	DNA replication factor	-0.4865	1.24670e-
22/228_s_at	MCC12125	KIAAL309 hymothesical pyrotein MCC13125	-0.4865	1.25418e-
224304_s_at	WGC15125 VKT6	SNARE protein Vkr6	-0.4861	1.23/18e-
212607 at	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B. gamma)	0.4861	1.20170c=
200859 x at	FLNA	filamin A, alpha (actin binding protein 280)	0.4860	1.26774e-
210053_at	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100 kDa	-0.4853	1.29954e-
224791_at	DDEF1	development and differentiation enhancing factor 1	0.4848	1.32651e-
202555_s_at	MYLK	myosin, light polypeptide kinase	0.4845	1.34239e-
226651_at	HOMER1	homer homolog 1 ( <i>Drosophila</i> )	-0.4844	1.34718e-
201885_s_at	CYB5R3	cytochrome b5 reductase 3	0.4843	1.3520e-0
208549_x_at	PIMA	prothymosin, alpha (gene sequence 28); similar to prothymosin alpha; hypothetical gene supported by BC013859; hypothetical gene supported by BC013859; BC070480	-0.4839	1.36815e-
223625_at	DRCTNNB1A	down-regulated by Ctnnb1, a	0.4838	1.37629e-
205083_at	AUXI	aldehyde oxidase 1	0.4832	1.40/64e-
204141_at	CTSL1	cathensin I	0.4825	1.41203e-
202087_s_at	CAND1	cullin-associated and neddylation-dissociated 1	-0.4822	1.44505e-
224677 x at	C11orf31	chromosome 11 open reading frame 31	-0.4820	1.46756e-
206157_at	PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	0.4807	1.54150e-
209420_s_at	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	0.4806	1.54512e-
211066_x_at	PCDHG	protocadherin gamma subfamily	0.4806	1.54694e-
213746_s_at	FLNA	filamin A, alpha (actin binding protein 280)	0.4802	1.56889e-
215501_s_at	DUSP10	dual-specificity phosphatase 10	0.4797	1.59722e-
205/17_x_at	PCDHG	protocadherin gamma subfamily	0.4/96	1.59868e-
209012_at	COPO14	triple functional domain (PTPRF interacting)	0.4/86	1.66008e-
207085_at	ENOSE1	englase superfamily member 1	-0.4778	1.08071e=
225878 at	KIF1B	kinesin family member 1B	0.4773	1.74079e-
224610_at		full-length cDNA clone CL0BB014ZH04 of neuroblastoma of Homo sapiens (human)	-0.4772	1.74688e-
201930_at	МСМ6	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, <i>Schizosaccharomyces pombe</i> ) ( <i>S. cerevisiae</i> )	-0.4768	1.76935e-
201110_s_at	THBS1	thrombospondin 1	0.4755	1.85546e-
226099_at	ELL2	elongation factor, RNA polymerase II, 2	0.4749	1.89665e-
210547_x_at	ICA1	islet cell autoantigen 1, 69 kDa	-0.4746	1.91645e-
201051_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-0.4744	1.93198e-
201185_at	HTRAI	HtrA serine peptidase 1	0.4742	1.94315e-
224663_s_at	CFL2 MED 4	cotilin 2 (muscle)	0.4/35	1.99526e-
21/845_s_at	MED4 MVI K	mediator or KINA polymerase il transcription, subunit 4 nomolog (yeast)	-0.4/24	2.06/35e-
224025_at	MTLK MCM4	MCM4 minichromosome maintenance deficient 4 (S <i>cerevisiae</i> )	-0.4720	2.0841/e= 2.10334e=
214752 x at	FLNA	filamin A, alpha (actin binding protein 280)	0.4719	2.11121e-
200668_s_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-0.4718	2.11299e-
205207_at	IL6	interleukin 6 (interferon, beta 2)	0.4717	2.12268e-
211160_x_at	ACTN1	actinin, alpha 1	0.4713	2.15198e-
222880_at	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	0.4707	2.19914e-
229067_at		similar to Formin binding protein 2 (srGAP2)	0.4702	2.23957e-
218420_s_at	C130rf23	chromosome 13 open reading frame 23	-0.4697	2.27551e-
2205/4_at	DUSD10	paraspeckie component 1; 1111 and 1111N nomologous inositol lipid phosphatase pseudogene	-0.469/	2.2/331e-
221303_at	NAV1	neuron navigator 1	0.4690	.0002000 2 34631e
202074 s at	OPTN	optineurin	0.4686	2.3650e-0
211981_at	COL4A1	collagen, type IV, alpha 1	0.4682	2.40005e-
	SLC37A4	solute carrier family 37 (glycerol-6-phosphate transporter), member 4	-0.4681	2.40548e-
200788_s_at	PEA15	phosphoprotein enriched in astrocytes 15	0.4680	2.41912e-
205129_at	NPM3	nucleophosmin/nucleoplasmin, 3	-0.4678	2.43558e-
221829_s_at	TNPO1	transportin 1	0.4675	2.45842e-
233496_s_at	CFL2	cotilin 2 (muscle)	0.4661	2.58543e-

Display, and Suffareendame angeaendame angeaendame angeaendame angeaDisplay, and SuffareNational Compolition conting of a constant sector o	Affy ID	Gene Symbol	Description	ρ	Р
19907_sp     9177     attending 2 (Desc)dial)     4.663     2.0004       253.45     P10171     hypothesid provide P111643     -4.663     2.5037       253.45     P10170     hypothesid provide P111643     -4.663     2.5037       253.45     P10170     Hypothesid provide P111643     -4.663     2.5037       253.05     CM4     Constraint constraint of the p1011     -4.664     2.5037       253.05     CM4     constraint from p101 provide p101     -4.664     2.5038       253.05     CM4     constraint from p101 provide p101     -4.664     2.5038       253.05     CM4     constraint from p101 provide p101     -4.664     2.5038       253.05     CM4     constraint from p11 from p101     -4.664     2.5038       253.05     CM51     Nick from p11 from p11 from p101     -4.664     2.5038       253.05     CM51     Nick from p11 from p101     -4.664     2.5038       253.05     CM51     Nick from p11 from p11 from p11     -4.664     2.5038       253.05     CM51     Nick from p11 from p11 from p11     -4.66	205130_at	RAGE	renal tumor antigen	0.4659	2.59708e-
2020,     PRI/10     byoches janonic Fi [TRG4]     -0.666     2.509,       2020,     PRX504     PRX4 byoches constraints of constraints of -0.663     2.509,       2020,     PRX504     PRX4 byoches constraints of constraints of -0.663     2.609,       2020,     CAS1     CAS1     2.609,     2.609,       2020,     CAS1     CAS1     2.609,     2.609,       2020,     CAS1     CAS1     2.609,     2.609,       2020,     Lipolanding prop bo 2     -0.664     2.009,       2020,     Lipolanding prop bo 2     2.019,     2.0164,       2020,     Lipolanding prop bo 2     2.019,     4.623     2.239,       2020,     RTG1     Bit Comolg 1 (dw1Ah)     0.623     2.239,       2020,     RTG2     Bit Red	209897_s_at	SLIT2	slit homolog 2 ( <i>Drosophila</i> )	0.4658	2.60584e-
25464.m     FMM domin containing 6     60633     25000.m       25790.m     RVS 2501     RVS 2600.min containing 4     60633     25030.min       25700.m     CM     RVS 2600.min containing 4     60633     25030.min       25700.m     CM     RVS 2600.min containing 4     60633     25030.min       25700.m     CM     RVS 2600.min containing 4     20080.min     60643     25080.min       25700.m     CM     Recontaining 4 receptor period     60643     25080.min       2500.m     CM     Recontaining 4 receptor period     60643     25080.min       2500.m     TT     Hindram recontaining 2 dual     60643     25080.min       2500.m     TT     Hindram recontaining 2 dual     60643     25080.min       2500.m     TT     Hindram recontaining 1 dual     60643     25080.min       2500.m     TT     Hindram recontaining fram 30     60641     25080.min       2500.m     TT     Hindram recontaining fram 30     60641     50290.min       2500.m     TT     Hindram recontaining fram 30     6061     502	217872_at	PIH1D1	hypothetical protein FLJ20643	-0.4656	2.62935e-
25398 <i>PUNDY</i> PUNDY	225464_at	FRMD6	FERM domain containing 6	0.4653	2.65007e-
22708.p. <i>LMA1545</i> KAM1545     CDG ange inclusion 1 angen)     -0.663     2.0660.p.       32706.p. <i>CDG</i> CDG ange inclusion 1 angen)     0.664     2.0278.p.       32706.p. <i>CDG</i> CDG ange inclusion 1 angen)     0.664     2.0278.p.       32706.p. <i>LEPRI</i> 1     CDG angen inclusion 2 angen in	225398_at	RPUSD4	RNA pseudouridylate synthase domain containing 4	-0.4653	2.65304e-
20064     CASI miga (adamon) langed     0.609     2.0874-0.       20076     CM     absorption     0.609     2.0874-0.       20080     PMCR     big-molify group inr 2     0.608     2.0874-0.       20080     DOW     big-molify group inr 2     0.608     2.0874-0.       20080     DOW     big-molify group inr 2     0.606     2.0874-0.       20080     DOW     DOW     0.0616     2.0874-0.       20080     BAT     Bolinitin transformation of the properties of the second molify information of the second molify i	225703_at	KIAA1545	KIAA1545 protein	-0.4653	2.65602e-
25706C/Mcategorypidae M0.6692.622%-20073L/B/B21kaine-palae enfode protogy-an (lepran) 10.6482.009020073L/B/B21kaine-palae enfode protogy-an (lepran) 10.6482.009020073SY 50minum protogy-an (lepran) 10.6482.009020073SY 50minum protogy-an (lepran) 10.6452.257920043SY 50Minum randome-2 dapia0.6452.257920043IEEDIEED (lepran) 10.6422.557120043IEED (lepran) 1IEED (lepran) 10.6422.557120043IEED (lepran) 1IEED (lepran) 10.6422.557120043IEED (lepran) 1IEED (lepran) 10.6412.557120043IEED (lepran) 1IEED (lepran) 10.6412.557120043IEED (lepran) 1IEED (lepran) 10.6412.557120043IEED (lepran) 1IEED (lepran) 10.6412.557120043IEED (lepran) 1IEED (lepran) 10.6412.557220043IEED (lepran) 1IEED (lepran) 10.6412.557420043IEED (lepran) 1IEED (lepran) 10.6412.557420043IEED (lepran) 1IEED (lepran) 10.6412.557420043IEED (lepran) 1IEED (lepran) 10.6412.557420043IEED (lepran) 1IEED (lepran) 10.6413.557420045	200663_at	CD63	CD63 antigen (melanoma 1 antigen)	0.4650	2.68074e-
18408     18408     -0.4648     2.0888       20501     LMEPLI     Insiste profiles enclind proceedprom (leprenal)     -0.4648     2.0808       20501     CMM     constants M receptor     -0.453     2.2009       20501     CMM     constants M receptor     -0.453     2.2009       20501     FMT     fibration encodepart (leprenal)     -0.457     2.2007       20501     FMT     fibration encodepart (leprenal)     -0.461     2.2007       20501     FMT     HEG homolegal (leprenal)     -0.461     2.2007       20501     Pandle homolegal (laprenal)     -0.461     2.2007       20501     Pandle homolegal (laprenal)     -0.461     2.2007       20501     Pandle homolegal (laprenal)     -0.461     2.2007       20502     MCCG     bypodebal procein POLICicle denoma RNA holding proof: 0.371     -0.461     2.2007       20502     MCCG     bypodebal procein POLICicle denoma RNA holding proof: 0.371     -0.461     3.3027       20502     MCCG     bypodebal procein POLICicle	235706_at	CPM	carboxypeptidase M	0.4650	2.68294e-
22709	208808_s_at	HMGB2	high-mobility group box 2	-0.4648	2.6980e-0
22662	220750_s_at	LEPRE1	leucine-proline-enriched proteoglycan (leprecan) 1	0.4648	2.70102e-
20099	226621_at	OSMR	oncostatin M receptor	0.4639	2.78689e-
20094 g., mt     ST     follautin randomers 2 alpha     0.4615     2.2572- 2.2572- 2.2572-     0.4625     2.2572- 2.2572- 2.2572-     0.4625     2.2572- 2.2572- 2.2572-     0.4625     2.2572- 2.2572- 2.2572- 2.2572- 2.2572-     0.4625     2.2532- 2.2572- 2.2572- 2.2572- 2.2572-     0.4625     2.2532- 2.2572- 2.2572- 2.2572- 2.2572- 2.2572- 2.2572-     0.4625     2.2532- 2.2572- 2.2572- 2.2572- 2.2572-2.27       20072-1, at 20072-1, at 20	200099_s_at	RPS3A	ribosomal protein S3A	-0.4636	2.81501e-
2005 g.m.     -0.4627     2.8977.4.       2006 g.m.     /////.1000 g.m.     0.4613     2.9334.5.       2007 g.m.     ////.1000 g.m.     0.4614     2.9334.5.       2007 g.m.     ////.1000 g.m.     0.4614     2.9334.5.       2007 J.m.     Panulo booking 2.05mp/db.     0.4614     2.9354.5.       2007 J.m.     HNRPD     herespectore molar fibonal deprotein 1///.100.4.     0.4619     2.99354.2.       2007 J.m.     HNRPD     herespectore articlar fibonal deprotein 1/0001.500     0.4619     2.99354.2.       21006 J.m.     TACCO     hypoferical protein 1/001.500 molant     0.4611     5.017954.2.       21006 J.m.     TACON     hypoferical protein 1/001 sequence     0.4611     5.017954.2.       21026 J.m.     HOMBAN     Group and one of anima fibrical fibrical fibrical fibrical fibrical protein 1/001 sequence     0.4611     5.017954.2.       22023 J.m.     CAUPIT     GCN1 protein and yputhis 1-148.1 (year)     0.4611     5.017954.2.       22034 J.m.     MATTA     marrinoubles accontart and yputhis 1-148.1 (year)     0.4611     5.019954.2.       220361 J.m.     CAUPIT     marrinoublesa	204948_s_at	FST	follistatin transformer-2 alpha	0.4635	2.82529e-
21300# <i>HEGI</i> HEGI inondag 1 cabacitab)     0.4625     2.2335       25357# <i>HEMAS</i> ENA biolog notif, single-sound interacting protein     0.4624     2.9365       25370# <i>HOMD</i> -0.4624     2.9365     -0.4624     2.9365       25370# <i>HOMD</i> Biol CTDe activity growth and activity growth and activity growth and activity growth and activity growth activity g	204658_at			-0.4627	2.89772e-
23570_st <i>RNM</i> is     RNA binding-morie sugh-semanded interacting protein     0.6424     2.3536/ 2.3566/       23570_st     -0.4624     2.3566/st       23700_st     -0.4624     2.3666/st       23703_st     HDRPD     beterspreents nuclear ribonic/s ( <i>Umphphin</i> )     -0.4619     2.3966/st       234125_st <i>ABD(CMPA</i> Bio CTPase activating protein i     -0.4619     2.93554       234125_st <i>ABD(CMPA</i> Bio CTPase activating protein i     -0.4614     3.03527       23425_st <i>ABD(CMPA</i> Bio CTPase activating protein i     -0.4614     3.03527       23425_st <i>ABD(CMPA</i> beorer fromoles 3 ( <i>Umphphin</i> )     -0.4614     3.03527       23421_st <i>IDEANIT</i> BLD protein     -0.4614     3.03527       21421_st <i>IDEANIT</i> BLD protein     -0.4611     3.03527       21423_st <i>IDEANIT</i> BLD protein     -0.4611     3.03562       21435_st <i>IEEE IDEANIT</i> -0.4611     3.03652       21405_st <i>CEEE</i> -0.4611     3.03652       21405_st <i>CEEE</i>	213069_at	HEG1	HEG homolog 1 (zebrafish)	0.4625	2.92361e-
25313.g., More PUMB homolog ? (Domplék) -0.4624 2.53654   253705.g., MORCA HBRTO herengeneous molecopronein D (AU-fich densent RNA binding promein 1, 37 kDa) -0.4613 2.56284-   20073.g., MORCA RBGCAPW RBG CTP activiting protein 4 -0.4619 2.93634-   21094.g., MORCA RBGCAPW -0.4619 2.93634-   21095.g., MORCA Odd Morto Monolog 3 (Compare Intel) -0.4619 2.93634-   21094.g., MORCA Odd Morto Monolog 3 (Compare Intel) -0.4619 2.93634-   21094.g., MORCA Intermediate Internit PRO 1580 -0.6619 2.93654-   21094.g., MORCA Intermediate Internit PRO 1580 -0.6611 3.03274-   21094.g., MORCA Intermediate Internit PRO 1580 -0.6612 3.03274-   21094.g., MORCA MARIN microsoftal protein -0.6612 3.03274-   21094.g., MORCA MARIN -0.6610 3.1344-   20093.g. MORCA MARIN -0.6610 3.1092-   20094.g. MORCA	235570_at	RBMS3	RNA binding motif, single-stranded interacting protein	0.4624	2.93337e-
23705_ytt     —     —     0.4621     2.5058-1       20443_st     ARRCAPA     Blo CTPac activity protein 4     -0.6619     2.9058.1       20443_st     ARRCAPA     Blo CTPac activity protein 4     -0.6619     2.9058.1       21437_st     DK3     dicklorp henning 3 (Compu lenn)     -0.619     2.9058.2       21437_st     DK3     dicklorp henning 3 (Compu lenn)     -0.611     3.00379.5       21437_st     DK3     dicklorp henning 5 (Compu lenn)     -0.6161     3.00379.5       21437_st     DK3     dicklorp henning firme 3     -0.6161     3.00379.5       21432_st     DEEX     dicklorp hennin scalt synthesis Higk 1 (least)     -0.6161     3.00379.5       21238_st     GCNL1     GCN hennin scalt synthesis Higk 1 (least)     -0.6161     3.0069.5       22608_st     MAPPH     microstant =-strage tissine 2     -0.6611     3.0069.5       22608_st     MAPPH     microstant =-strage tissine 2     -0.6611     3.0069.5       22608_st     L/DNT     persotant actant =-strage tissine 2     -0.611     3.0069.5       226067_st <tdl <="" dnt<="" td=""><td>235138_at</td><td>PUM2</td><td>Pumilio homolog 2 (<i>Drosophila</i>)</td><td>-0.4624</td><td>2.93663e-</td></tdl>	235138_at	PUM2	Pumilio homolog 2 ( <i>Drosophila</i> )	-0.4624	2.93663e-
20072_1, 11     HTMRP     betrogenous node, monoclopoxia ID AU-tick denom: NAA binding protein 1, 37 MDA     -0.4612     2.9564.       21094.2, 14     RHCAIM     RhCAIM     RhCAIM     -0.4619     2.95854.       22109.2, 14     RHCAIM     ChCAID     ChCAID     0.4619     2.95854.       22120.2, 14     RHCAIM     ChCAID     0.4613     3.01794.       222224, 14     HOMARY     chammarmun 11 open randing firme 31     0.4613     3.03794.       21203.2, 14     GCN11     GCN1 promatine constanting, firme 31     0.4611     3.03294.       2203.2, 14     GCN11     GCN1 promatine constanting, firme 31     0.4611     3.03294.       2203.2, 14     GCN11     GCN11     GCN11     3.03294.       2203.2, 14     MAP18     microarbale sensitizer     3.0411     3.03294.       2003.2, 14     MAT24     athract anter anti-sensitizer sensitizer     3.0441.     3.0492.       2003.2, 14     MAT24     athract anter anti-sensitizer sensitizer     3.0461.     3.0492.       2003.2, 14     MAT24     athract anter anti-sensintizer sensintizer sensitizer sensitini athract sensitizer sens	235705_at			0.4621	2.96284e-
204425_xt     ABT(API     Rho CTPas activing procis 4     -0.4619     2.97335-       21405_xt     DACKS     bipOtolispo     -0.4619     2.98354-       214242_xt     DACKS     bipOtolispo     -0.4614     3.09320-       21424_xt     DACKS     bipOtolispo     -0.4614     3.09320-       21015_xt     Clugf1     phonts nonsome 11 opin rading farme 31     -0.4614     3.09320-       21783_xt     TAEMIT     30 bits prostim     -0.4614     3.09320-       21783_xt     TAEMIT     30 bits prostim     -0.4614     3.09320-       22694_xt     ALPR     changaine factors (strange rotation scale strange rot	200073_s_at	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37 kDa)	-0.4621	2.96613e-
21095_x, mt     7MC06     bppohnsical PRO1390     -0.6619     2.98266-       222224_x, mt     HOMEB     homes in forma of a 10 prophilal     -0.6614     3.03926-       22222_x, mt     HOMEB     homes in forma of a 10 prophilal     -0.6614     3.03926-       21421_x, mt     DEEMIT1     30 k12 protin     -0.6614     3.03927-       21422_x, mt     DEEMIT1     30 k12 protin     -0.6612     3.03246-       21035_x, mt     GCN11     GCN1 protin of anion acid symbia 1-like 1 (year)     -0.6612     3.0326-       21093_x, mt     GCN11     CCN1 protin of anion acid symbia 1-like 1 (year)     -0.6613     3.0326-       21093_x, mt     GCN11     constrain -scroing on resting to symbia     0.6611     3.0367-       21095_x, mt     GCN11     constrain -scroing resting to symbia     0.6610     3.0374-       21095_x, mt     GCN14     constrain -scroing resting to symbia     0.6691     3.1334-       21095_x, mt     GCN14     constrain -scroing resting to symbia     0.6691     3.1334-       21095_x, mt     GCN14     constrain -scroing resting to symbia     0.4693     3.2326	204425_at	ARHGAP4	Rho GTPase activating protein 4	-0.4619	2.97933e-
214307_xxt     DKK3     dickkopf homolog 3 ( <i>Kompur larini</i> )     0.4619     298994-       214057_xxt     C1146J1     bornsomen 1 open realing finare 31     -0.4614     3.02929-       214057_xxt     DKKH7     plckthich nondoge 3 ( <i>kompul larini</i> ) (' (vith FERM domain) member 1     0.4613     3.03937-       21788_xxt     TMEM11     GK kap vostin     -0.4614     3.03937-       22698_xt     MAP18     microtubule sociaciend protein 1B     -0.4614     3.03962-       22698_xt     EL/2     chagnin factor, RNA polymerash 1, 2     -0.4611     3.03962-       20403_xt     MAP18     microtubule sociaciend protein 1B     -0.4604     3.10072-       20403_xt     MAT2AI     antin-stoting resistance 3     -0.4604     3.1037-       20404_xt     MATAI     antin-stoting resistance 3     -0.4604     3.1037-       20405_xxt     LONAP     antin-stoting resistance 3     -0.4607     3.237-       20405_xxt     LONAP     antin-stoting resistance 3     -0.4607     3.237-       20405_xxt     LONAP     antin-stoting resistance 3     -0.4607     3.237-	221096_s_at	TMCO6	hypothetical protein PRO1580	-0.4619	2.98263e-
222222_uri     IOMERS     homer bronolog i Omophila     0.4615     3.01925-2       231645_x,ar     DEKKCI     pleckkrin konologi domain cuntaining, family C (with FEBM domain) member 1     0.4613     3.0927-2       214212_x,ar     DEKKCI     pleckkrin konologi domain cuntaining, family C (with FEBM domain) member 1     0.4613     3.0927-2       21623_x,ar     GCNU1     CCNI general control of amino scil synthols 1-like 1 (year)     -0.4612     3.0932-2       226084_x     MAPIB     best cancer and-recomport resistance 3     0.4611     3.0932-2       226091_x     ELL2     obagation factor, RNA polymexer II, 2     0.4603     3.1097-2       226091_x     AVTRA     canter atom ran receptor II     0.4600     3.1097-2       226091_x     LAVRA     canter atom ran receptor II     0.4600     3.1097-2       226091_x     LAVRA     canter atom ran receptor II     0.4600     3.1097-2       226091_x     LAVRA     attract tosin receptor II     0.4600     3.2098-2       226097_x     LOS2080     tporbrical protein factor binding to KCHM enhancer 3     0.4699     3.23320-2       226097_x     LOS2080	214247_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	0.4619	2.98594e-
231045_x.gt     C11e971     chomosone 10 open raining famic 31     -0.4614     3.0232-xt       21421_x.gt     TMEMT11     50 ADa protein     -0.4613     3.0432-xt       21782_x.gt     TMEMT11     50 ADa protein     -0.4613     3.0427-xt       21783_x.gt     TMEMT11     50 ADa protein     -0.4612     3.0528-xt       22684_st     MLP18     microtubel associated protein 18     -0.4612     3.0528-xt       22684_st     MLP18     microtubel associated protein 12     -0.4611     3.0598-xt       20032_x.gt     BCAR3     brast caner anti-ecrogen restance 3     -0.4611     3.0698-xt       20043_xt     ACTXN     antit caner inding to MMN     -0.4605     3.1345-xt       20052_xt     CHIR2     C11R2 checkpoint bonolog (5.pmR)     -0.4605     3.1345-xt       20053_xt     CDO25     ACTN1     attrait factor binding to HGHM enhancer 3     0.4601     3.1345-xt       21667_xt     CDO25     attrait factor binding to HGHM enhancer 3     0.4597     3.2358-xt       21677_xt     TFFS     attrait factor binding to HGHM enhancer 3     0.4597     3.3145-xt <	222222_s_at	HOMER3	homer homolog 3 (Drosophila)	0.4615	3.01950e-
21421_2,xt   PLEXIC:   pleckarin homology domain containing, family C (with FEEM domain) member 1   0.4613   3.03274-     21632_xt   GCVIII   GCN general control of amino acid synthesis 1-like 1 (year)   -0.4612   3.03526-     21632_xt   GCVIII   GCN general control of amino acid synthesis 1-like 1 (year)   -0.4611   3.0958-     22694_xt   MAPIB   bengriom factor, RNA polymezers II, 2   -0.4611   3.0958-     22694_xt   MAPIB   matrix cosin receptor 1   -0.4608   3.1052-     22664_xt   ANTXBI   anthrac tosin receptor 1   -0.4608   3.1052-     22665_xt   CHERC   CHERC   -0.4609   3.1076-     20653_xt   ICMPI   prophetical protein BC00106   -0.4597   3.21368-     22667_xt   LOCZ689   hypothetical protein BC00106   -0.4597   3.23168-     22667_xt   LOCZ689   hypothetical protein BC001206   -0.4587   3.33164-     23171_x_xt   HPGAEAA   -0.4587   3.33605-     23173_xt   PRADA   protein kinase, cAMIP-dependent, regulatory, type II, slpha   -0.4587   3.33602-     23173_xxt   PRGAEA   protein kinase, cAMIP-depen	231045_x_at	C11orf31	chromosome 11 open reading frame 31	-0.4614	3.02929e-
217882.nt   7M/M111   30 kDa promin   0.4612   3.0424- 3.0528     21632x   CXVIII   GCNIII   0.6612   3.05286- 3.05286- 3.05286- 2.0608.nt   0.4611   3.05286- 3.05286- 2.0608.nt     22608n   MAPIB   oncombub associated protein 1B   0.4611   3.05982- 3.0592     22608n   RCAB   broast concer anti-cerngen restance 3   0.4611   3.05926- 3.0592     22609n   RCAB   broast concer anti-cerngen restance 3   0.4601   3.1304- 3.0592     20205x   CHRZ   CHRZ   CHRZ   0.4609   3.1304- 3.1304- 2.12057     20205x   RLH4   emocisand-14   0.4601   3.1307- 3.1307- 2.23063.nt   1.0707   a.1304- 2.2305     20205x   RLH4   emocisand-14   0.4601   3.1307- 3.2339- 2.2305   0.4595   3.2339- 2.3208- 2.2305   0.4595   3.2339- 2.3208- 2.2305   0.4595   3.2339- 2.3208- 2.2305   0.4595   3.2339- 2.3208- 2.2305   0.4595   3.2339- 2.3339- 2.3339- 2.3339- 2.3305   0.4595   3.3410- 5.2320- 2.2316   0.4585   3.3410- 5.2320- 2.2316   0.4585   3.3410- 5.2320- 2.2316   0.4585   3.3410- 5.23205   0.4585   3.3410-	214212_x_at	PLEKHC1	pleckstrin homology domain containing, family C (with FERM domain) member 1	0.4613	3.03937e-
210232_xrt     CCNI general control of amino sid synthesis 1-like 1 (yeag)     -0.4612     3.05286- 3.05625.xr       226984_at     MLPI a     elongation facor, RNA polymerse II, 2     0.4611     3.05625- 3.05625.xr       226984_at     MCR8     breat cancer anti-crosgen resistance 3     0.4610     3.05625- 3.05625.xr       224694_at     MTXR1     anhza toxin receptor 1     0.4601     3.10524- 3.05625.xr       22663_xt     CLR2 chc2qbain brookeg (5 pmb)     0.4600     3.1077- 3.210862       22565_xt     LONPI     action in eceptor 1     0.4507     3.21308- 3.22668- 3.22669.xr       22565_xt     LONZ02009     bypochecial protein bilog to GCHM enhancer 3     0.4597     3.22308- 3.22669.xr       22565_xt     LONZ02009     bypochecial protein BCO01096     0.4598     3.31615- 3.23209- 3.23209- 3.23209- 3.23302.xr       22516_d_st     CAU     chromosome 7 open realing frame 25     0.4588     3.31615- 3.0505- 3.33070- 3.04582       21517_s_xst     PREAR2A     protein interacing protein 100019_xst     0.4585     3.34912- 3.34912       21517_s_xst     REAR2A     protein interacing protein 100019_xst     0.4585     3.34912- 3.34912       215	217882_at	TMEM111	30 kDa protein	0.4613	3.04274e-
22004.rt <i>MAPLB</i> nicronuble-sacciacel protein 1B     0.4612     3.05625-       22008.2. m <i>KLB</i> objetion factor, <i>RNA</i> polymenes 1, 2     0.4611     3.05926-       2409.4. at <i>AVTXB</i> metar cancer sarin-estroger restance 3     0.4611     3.05926-       21041.6.s.# <i>CHE2</i> CHE2 checkpoint homolog ( <i>S. psmb</i> )     0.4608     3.10926-       20205.2.s.# <i>CHE2</i> CHE2 checkpoint homolog ( <i>S. psmb</i> )     0.4600     3.1697e-       20265.3.m <i>LONPI</i> .     perosiomal LON process like     0.4001     3.1697e-       20265.7.s.# <i>ACTNI</i> perosiomal CON process like     0.4595     3.2332e-       20265.7.s.# <i>CAUU</i> calamenin     0.4591     3.2332e-       20254.6.at <i>COMUE</i> calamenin     0.4595     3.332e-       21373.3.s.# <i>Norobachia open realing fame</i> 25     0.4588     3.34516-       21375.2.s.# <i>PRAPLP</i> prophetical protein factor binding to DCMI sequence 1     0.4585     3.34516-       21375.2.s.# <i>PRAPLP</i> prophetical protein factor binding to DCMI sequence 28     3.36562-       213	216232_s_at	GCN1L1	GCN1 general control of amino acid synthesis 1–like 1 (yeast)	-0.4612	3.05286e-
22082.xt <i>FL2</i> elongation factor, RNA polymerse II, 2     0.4611     3.09906-       24002.xt     BCARB     bract accer anti-corgen resistance 3     0.4601     3.10906-       22404 f.x., xt     AVTXR1     antfrax torin receptor 1     0.4601     3.10926-       22005.2x, xt     RH4     retionic acidnduced 14     0.4601     3.10976-       22065.3x     LONR1     periodic aditnduced 14     0.4997     3.22086-       22067.3x     ACIN1     actionia global     0.4990     3.22618e-       22067.3x     LOX26809     hypochecial protein BC001006     0.4995     3.22302-       22075.5x, xt     CAUU     calamenin     0.4975     3.27630-       221416.3x     CAUF2     photehcical protein BC001026     0.4988     3.3105-       221405.2x     PRAD24     protein kings to E00326     0.4988     3.3600-       21313.2x, at     PRM24     protein kings to E00326     0.4988     3.3600-       21313.2x, at     PRM24     protein kings to E00326     0.4988     3.3600-       21313.2x, at     PRM24     protein instracting	226084_at	MAP1B	microtubule-associated protein 1B	0.4612	3.05625e-
20403.r. <i>BCMB</i> bears and entry usin restance 3     0.4611     3.00981c-       20404.r. <i>ANTXR CHEX</i> CHEX     0.4605     3.10925-       20404.r. <i>RAI14</i> reindia scid-indiance 14     0.4601     3.10975-       20563.r. <i>LONU</i> perosional LON proteac like     0.4600     3.10975-       20563.r. <i>ACTVI</i> perosional LON proteac like     0.4597     3.23068.       20667.r. <i>ACTVI</i> calumenin     0.4591     3.2328-       20667.r. <i>ILOC3268P</i> hypothetical protein BC01096     0.4591     3.2328-       21513.s#T <i>CHLU</i> calumenin     0.4591     3.2328-       21513.s#T     protein facase AMP dependent, regulary, type II, alpha     0.4587     3.33076-       21513.s#T <i>PRKM2A</i> protein intracting protein     0.4585     3.34516-       21513.s#T <i>RRKI</i> Protein intracting protein     0.4587     3.34516-       21513.s#T <i>RRKI</i> protein intracting in factor     0.4587     3.34516-       21513.s#T <i>RRKI RRKI</i> <td>226982_at</td> <td>ELL2</td> <td>elongation factor, RNA polymerase II, 2</td> <td>0.4611</td> <td>3.05963e-</td>	226982_at	ELL2	elongation factor, RNA polymerase II, 2	0.4611	3.05963e-
2464 xt     AVTXR1     andrax scoin receptor 1     0.4608     3.1052c-       20141 5_x xt     CHER2     CHER2     0.4601     3.1134c-       20205 2_x xt     RM14     retinois acid-induced 14     0.4601     3.1134c-       20205 2_x xt     LONNL     persistemil LON protests like     0.4601     3.1134c-       20205 7_x xt     ACTN1     actinia, alpha 1     0.4597     3.2230k-       20207 5_x xt     CALU     calumenin     0.4591     3.2230k-       20207 5_x xt     CALU     calumenin     0.4591     3.2261k-       2017 1_x xt     MVRP     persistemin RC08326     -0.4587     3.3307c-       2017 1_x xt     PKRRA     persistemin RC08326     -0.4587     3.3307c-       2017 1_x xt     SASTAI     persistemin RC08326     -0.4587     3.3307c-       2017 1_x xt     SASTAI     persistemin RC08326     -0.4587     3.3307c-       2017 1_x xt     SASTAI     persistemin RC08326     -0.4580     3.4307c-       2017 1_x xt     SASTAI     persistemin RC08326     -0.4580     3.4307c-	204032_at	BCAR3	breast cancer anti-estrogen resistance 3	0.4611	3.06981e-
210416_x, xtCHK2 heckpoint homolog (\$ ponkh)-0.46053.13246-220632_x, xtKM14retroinc acid-induced 140.46013.1697r-220637_xxtKATNperoxionul LON proteas like0.46003.1697r-220637_xxtTK3transcription factor binding to IGHM enhancer 30.45953.2398e-212457_xtTK3transcription factor binding to IGHM enhancer 30.45953.2332e-206697_xtLOC2269phytohetical protein BC0019060.45953.2332e-20755_xttCLUculumenin0.45973.2338e-21317_xxtValuephytohetical protein BC0089260.45953.33456-21317_xtPRKAR2Aprotein finance CAMP-dependent, regulatory, type II, alpha0.45853.34562-21305_xtPRKAR2Aprotein interacting protein0.45853.3490e-22306_xtRK2AHSCARG protein acucon avigaor 10.45853.4900e-22306_xtHSCARGHSCARG protein acucon avigaor 10.45853.4900e-22306_xtHSCARGHSCARG protein acucon avigaor 10.45853.4900e-22306_xtHSCARGHSCARG protein acucon avigaor 10.45853.4900e-22306_xtHSCARGHSCARG protein acucon avigaor 10.45873.4900e-22306_xtHSCARG protein acucon avigaor 10.45873.4900e-22306_xtHSCARG protein acucon avigaor 10.45873.4900e-23304_xtTHDPIchromosome 20 open rading frame 110.45873.4900e-23347_x_xt<	224694_at	ANTXR1	anthrax toxin receptor 1	0.4608	3.10052e-
202052_x at <i>RU14</i> erinoic acid-induced 14     0.6601     3.10377- 208637, x at     0.6601     3.10377- 208637, x at     0.6701     arcinin, alpha.1     0.4597     3.21908- 3.21908- 20075, x at     0.6202689     hypothetical protein BC001096     0.4595     3.23329- 3.23329- 20075, x at     0.0202689     hypothetical protein BC001096     0.4595     3.23329- 3.23529- 20075, x at     0.04591     3.23629- 3.23529- 20075, x at     0.4592     0.4588     3.31615c- 1.000324       213713, x at     Vince All     opticin BC0008326     -0.4587     3.3070c- 3.33070c- 20073, x BNR 20     0.4585     3.34542c- 3.34542c- 20003, x SNR 20     0.4585     3.34542c- 3.34542c- 20003, x SNR 20     0.4585     3.34542c- 3.38055c- 20003, x BNR 20     0.4585     3.34542c- 3.38055c- 20003, x BNR 20     -0.4582     3.38076c- 3.34542c- 20163, x BNR 20     -0.4580     3.4004c- 20072, x BNR 20     -0.4581     3.39721c- 3.38057c- 20163, x BNR 20     -0.4580     3.4004c- 20072, x BNR 20     -0.4580     3.4004c- 20072, x BNR 20     -0.4579     3.4837c- 20163, x 20064     -0.4570     3.4837c- 20163, x 20064     -0.4570     3.4837c- 20163, x 20064     -0.4570     3.53504 2.55604- 2.55604- 2.55604, x 20067, x BNR 20     -0.4560     3.50761c- 20164, x A     -0.4560	210416_s_at	CHEK2	CHK2 checkpoint homolog (S. pombe)	-0.4605	3.13244e-
22963, x, at     LONPL     peroxional LON porcess like     0.4600     3.1767-7       20563, x, at     ACTN1     exinin, alpha 1     0.4591     3.221908-       212647, x, at     TFE3     exinin, alpha 1     0.4591     3.23128-       22667, x, at     LOC22689     hypothetical protein BC001096     0.4595     3.23128-       225146, xt     Cowf25     chunnosome 9 open reading fame 25     -0.4588     3.31655-       213713, x, xt     PKRARA     protein BC00832, regulatory, type II, alpha     0.4587     3.330765-       21373, x, xt     PKNIP     protein interacting protein     0.4587     3.330765-       204009, x, xt     KMS     v.Ki-razk Xiten ex succons viral oncogene homolog     -0.4581     3.34902-       21374, x, xt     PKNIP     protein interacting protein     -0.4579     3.40086-       212374, x, xt     PKMA     protein interacting protein     -0.4579     3.40086-       212374, x, xt     PKMA     protein interacting protein interacting protein     -0.4570     3.53605-       212374, x, xt     PKMA     protein inforin for protein interacting protein infore 1000000000000000000000000	202052_s_at	RAI14	retinoic acid-induced 14	0.4601	3.16977e-
208637_xat     ACTVI     action, apha 1     0.4597     3.21096c.       212457_xat     TFE3     transcription factor binding to (GHM enhancer 3     0.4595     3.2236 lbc.       22607_xat     LOC20869     hypothenical provins BC001096     0.4591     3.2350c.       225146_xat     Olwg25     chunomiome 9 open reading frame 25     0.4588     3.31615c-       21517_13_xat     HPKAR2A     protein Kinasc. AMP-2dependent, regulatory, type II, alpha     0.4587     3.33076c-       20147_1_xat     SQSTM1     sequessoome 1     0.4588     3.34616c-       20206_xat     KRAS     v-Ki-raz Kisten rat surona viral oncogene homolog     -0.4581     3.33076c-       20206_xat     KKAS     v-Ki-raz Kisten rat surona viral oncogene homolog     -0.4581     3.34910e-       20400_x_xat     KKAS     v-Ki-raz Kisten rat surona viral oncogene homolog     -0.4581     3.34010e-       20400_x_xat     KKAS     v-Ki-raz Kisten rat surona viral oncogene homolog     -0.4570     3.44842c-       20404_x_xat     MV1     neuron navigator 1     -0.4570     3.44894c-       20474_x_xat     MV1     neuron avigator 1	229663_at	LONPL	peroxisomal LON protease like	0.4600	3.17677e-
212457.xt     7E83     transcription factor binding to IGHM enhancer 3     0.4596     3.22306-       206072.st_xt     COCUB90     hypothocial protein BC00036     0.4591     3.2330e-       20175.st_xt     CMU     calumenia     0.4591     3.2330e-       215116.gt_xt     Hypothocial protein BC008326     0.4587     3.001327       21307.st_xt     PRMRPA     protein kinase, cAMP-dependent, regulatory, type II, alpha     0.4587     3.33076-       20007.st_xt     PRMPP     pronotroin interacting protein     0.4585     3.34542e-       20007.st_xt     PRMPP     pronotroin interacting protein     0.4585     3.34602-       212474.st_xt     RKAS     v-Ki-xtz Kitters nat sarcona viral oncogene homolog     -0.4581     3.39076-       212306.st_xt     RKAS     v-Ki-xtz Kitter nat sarcona viral oncogene homolog     -0.4580     3.4004e-       212474.st_xt     RKAS     MVI     prothymosin, alpha (gene sequence 28)     -0.4580     3.4004e-       21250.st_xt     PTMA     prothymosin, alpha (gene sequence 28)     -0.4570     3.41837e-       212530.st_xt     ZBTR20     rinn finger and lift B domain con	208637_x_at	ACTN1	actinin, alpha 1	0.4597	3.21908e-
22667.xt     LOC32689     bypotherical procin BC001096     0.4595     3.23320-       225146.xt     CALU     calumentin     0.4591     3.276320-       225146.xt     CSw75.x, at     hypotherical procin BC008326     -0.4588     3.31615-       213713.x, at     PRKAR2A     protein Kinasc, AMP-dependent, regulatory, type II, alpha     0.4587     3.33076-       201471.x, at     SQSTM1     sequestosome 1     0.4587     3.34910e-       202005.y, at     RAKA     v-Ki-raz Kinsten rat surona viral oncogene homolog     -0.4581     3.36902e-       202005.y, at     HSCARG     WICAreaz Kinsten rat surona viral oncogene homolog     -0.4581     3.36902e-       202005.y, at     HSCARG protein     -0.4581     3.36902e-       20274.y, at     M/U     neuron navigator 1     -0.4581     3.40940e-       21848.gt,     TDOC6     WD repert domain 58     -0.04573     3.4887e-       21230.gt, at     TTBA1     chanecas A     -0.4570     3.51835e-       21230.gt, at     TDDF1     chanecas A     -0.4570     3.51835e-       21230.gt, at     TDDA1	212457_at	TFE3	transcription factor binding to IGHM enhancer 3	0.4596	3.22618e-
200755_s.at.     CLU     chromosome 9 open reading fame 25     0.4581     3.31615c       235146_atr     CS0rf25     chromosome 9 open reading fame 25     0.4588     3.31615c       213052_at     PRCM2A     protein kinase, cMP-dependent, regulatory, type II, alpha     0.4587     3.33076c       213052_at     PRCM2A     protein kinase, cMP-dependent, regulatory, type II, alpha     0.4585     3.34076c       208073_at     PRCM2P     pion protein interacting protein     0.4585     3.34010c       208073_at     PRCMP     pion protein interacting protein     0.4581     3.39721c       23806_st_at     HSCARG     HSCARG protein     -0.4581     3.39721c       23874_at     THOG     WD repeat domain 58     -0.4579     3.41877c       21848_at     THOG     WD repeat domain 52     -0.4579     3.41877c       21848_at     C20071     thormosome 20 open reading frame 11     -0.4579     3.41877c       218448_at     C20071     thormosome 20 open reading frame 12     -0.4579     3.51835c       21739_at     TDP1     transcription factor Dp-1     -0.4579     3.51835c <td>226697_at</td> <td>LOC92689</td> <td>hypothetical protein BC001096</td> <td>0.4595</td> <td>3.23329e-</td>	226697_at	LOC92689	hypothetical protein BC001096	0.4595	3.23329e-
225146_r     Cong25     chromosome 9 open reading frame 25     0.4588     3.31615c-       213713_s_at     hypothecial protein BC008326     -0.4587     0.003337       213713_s_at     SQSTM1     sequentsome 1     0.4585     3.33476c-       201471_s_at     SQSTM1     sequentsome 1     0.4585     3.34916c-       201471_s_at     RRNP1     prion protein interacting protein     0.4585     3.34910c-       20400_s_at     RKAS     vK-sna2 Kitsten att satooma viral oncogene homolog     -0.4581     3.33970c-       20400_s_at     KKAG     WIX     neuron navigator 1     -0.4581     3.34910c-       20474_s_at     MVI     neuron navigator 1     -0.4581     3.40840c-       20584_st     2060f1     chromosome 20 open reading frame 11     -0.4573     3.48887c-       21530_st     TFDP1     transcription factor Dp-1     -0.4573     3.53506-       2172_s_st     TFDV1     transcription factor Sp-1     -0.4573     3.53506-       2172_s_st     TFDV1     transcription factor Sp-1     -0.4573     3.53506-       2172_s_st     TFDV1	200755_s_at	CALU	calumenin	0.4591	3.27629e-
213713_s_at     bypothetical portein BC008326     -0.4587     .0003327       213052_at     PRKAR2A     portein kinase, cAMP-dependent, regulatory, type II, alpha     0.4587     3.30376-       213052_at     PRKAR2A     portein kinase, cAMP-dependent, regulatory, type II, alpha     0.4585     3.34916-       208973_at     PRKNPIP     prion protein intracting protein     0.4585     3.34910e-       204009_s_at     KRAS     v-Ki-raz Ziktsen at strearoma viral oncogene homolog     -0.4581     3.39721e-       212306_s_at     HSCARG     HSCARG protein     -0.4580     3.40094e-       218488_at     THOC6     WD repeat domain 58     -0.4580     3.40840e-       200772_s_at     PTMA     prodymosin, alpha (gene sequence 28)     -0.4570     3.58308-       218488_at     C20ef11     thorascription factor Dp-1     -0.4570     3.52608-       21730_x_at     PTM     prodymosin, alpha (gene sequence 28)     -0.4562     3.6173e-       21944_s_at     DIVA     prodymosin, alpha (gene sequence 28)     -0.4562     3.6173e-       21944_s_at     THD1     transcription factor Dp-1     -0.4562 <td< td=""><td>225146_at</td><td>C9orf25</td><td>chromosome 9 open reading frame 25</td><td>0.4588</td><td>3.31615e-</td></td<>	225146_at	C9orf25	chromosome 9 open reading frame 25	0.4588	3.31615e-
21305.at <i>PKkR2A</i> priorin kinase. cAMP-dependent, regulatory, type II, alpha   0.4587   3.33076e-     201471.g.,at <i>SQSTM1</i> sequestosome 1   0.4585   3.34516e-     204097.3_at <i>PRNPIP</i> priorin protein interacting protein   0.4585   3.34516e-     204009.g.,at <i>KRdS</i> v.K- <i>nac2</i> Kitsten rat sarcoma viral oncogene homolog   -0.4581   3.39076e-     20306.g.,at <i>KRdK</i> meuron navigaror 1   -0.4580   3.40046e-     21848.g.at <i>THOC6</i> WD repeat domain 58   -0.4570   3.40846e-     21230.g.,at <i>PTMA</i> protrymosin. alpha (gene sequence 28)   -0.4570   3.51838-     21230.g. at <i>TTDP1</i> thromosome 20 open reading frame 11   -0.4570   3.52638-     213230.g. at <i>TTDP1</i> thrasscription factor Dp-1   -0.4570   3.55638-     2137.g. at <i>BVRA</i> prothymosin. alpha (gene sequence 28)   -0.4558   3.56761e-     211921.g. at <i>PTMA</i> prothymosin. alpha (gene sequence 28)   -0.4558   3.66725e-     211821.g. at <i>TVRA</i> prothymosin. alpha (gene sequence 28)   -0.4551   3.5131e-     21416.g. at	213713_s_at	5	hypothetical protein BC008326	-0.4587	.0003327
201471_s.at     SQSTM1     sequestssome 1     Determination     0.4585     3.34542c       208973_at     PRNPIP     prion protein interacting protein     0.4582     3.34605e       203075_at     KKAS     v-Kinaz Kisten rat sarcoma viral oncogene homolog     -0.4582     3.36605e       22306_s.at     HSCARG     HSCARG     0.4580     3.40094e       22306_s.at     HSCARG     WD repert domain 58     -0.4580     3.40094e       200772_x.at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4570     3.48387e       21330_at     TTDP1     transcription factor Dp-1     -0.4570     3.52608e       21729_x.at     BVPA     biliverdin reducese A     0.4550     3.56071e       21921_x.at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4550     3.56071e       21921_x.at     BVPA     biliverdin reducese A     0.4550     3.56071e       21921_x.at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4552     3.66135e       211921_x.at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4559     3.66131e       <	213052_at	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	0.4587	3.33076e-
208973_art     PiNPIP     pin protein interacting protein     0.4585     3.34910c.       204009_s_att     KRAS     v-Ki-azd Xisten rat sarcoma vina loncogene homolog     -0.4581     3.38065c.       23206_s_att     HSCARG     HSCARG     0.4580     3.40906c.       23247_4_s_at     MAVI     neuron navigator I     -0.4581     3.40906c.       23247_4_s_at     THOC6     WD repeat domain 58     -0.4570     3.40846c.       20077_2_s_at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4570     3.48876c.       21230_s_at     ZBTB20     transcription factor Dp-1     -0.4570     3.51838c.       2172_9_x_at     ZBTB20     transcription factor Dp-1     -0.4560     3.56071c-       2172_9_x_at     ZBTB20     transcription factor     -0.4560     3.56071c-       2172_9_x_at     ZBTB20     prothymosin, alpha (gene sequence 28)     -0.4560     3.56072c-       2172_9_x_at     MEVA     bifwrdin reducase A     -0.4560     3.56072c-       2172_y_x_at     MEVA     bifwrdin reducase A     -0.4560     3.56072c-       2172_y_x_at	201471_s_at	SQSTM1	sequestosome 1	0.4585	3.34542e-
204099_s_at <i>KR4S</i> -KF-m2 Kister nat sarcoma viral oncogene homolog     -0.4581     3.38605c-       223206_s_at <i>HSCARG</i> protein     -0.4581     3.3721c-       223204 <i>NAV1</i> neuron navigator 1     -0.4580     3.40094c-       21848_at <i>THOCG</i> WD repeat domain 58     -0.4580     3.40894c-       200772_x_at <i>PTMA</i> prothymosin, alpha (gene sequence 28)     -0.4573     3.4837c-       21330_at <i>TEDP1</i> transcription factor Dp-1     -0.4570     3.51833c-       21330_at <i>ZBT20</i> zin finger and BTB domain containing 20     -0.4560     3.56971c-       21921_x_at <i>BLVRA</i> biliverdin reductase A     0.4569     3.5131c-       21921_x_at <i>PTMA</i> prothymosin, alpha (gene sequence 28)     -0.4566     3.6672c-       21921_x_at <i>PTMA</i> prothymosin, alpha (gene sequence 28)     -0.4556     3.6172c-       21921_x_at <i>PTMA</i> prothymosin, alpha (gene sequence 28)     -0.4556     3.6172c-       21921_x_at <i>PTMA</i> prothymosin, alpha (gene sequence 28)     -0.4553     3.72760c-	208973_at	PRNPIP	prion protein interacting protein	0.4585	3.34910e-
223306_sttHSCARGHSCARG protein-0.45813.39721e224774_s_atNAVIneuron navigator 10.45803.40094e-224774_s_atTHOC6WD repart domain 58-0.45803.40094e-200772_x_atPTMAprothymosin, alpha (gene sequence 28)-0.45793.41876-212330_atTFDP1thronsome 20 open reading frame 11-0.45733.48837e-212330_atTFDP1transcription factor Dp-1-0.45703.51833e-21530_stZBTR20zinc finger and BTB domain containing 200.45703.520046-21729_x_atBUVRAbil/verdin reductase A-0.45623.56071e-21010_s_atTFMAprothymosin, alpha (gene sequence 28)-0.45623.56071e-211921_x_atPTMAprothymosin, alpha (gene sequence 28)-0.45553.56725e-22416_s_atMED28mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)-0.45553.56725e-21180_x_atATP6V0E1ATPase, H+ transporting. lysosomal 9 kDa, VO subunit c-0.45553.50716e-21440_x_atACO79acyl-CoA thioseterase 90.45353.30986e-21445_s_atCALUcalumenin-0.45364.03122e-20773_x_atSFRS6splicing factor, arginine/srine-rich 6-0.45304.03102e-20773_x_atSFRS6splicing factor, arginine/srine-rich 6-0.45304.03102e-20330_s_atUNGuradi-DNA glycosylase-0.45254.04309e-20330_s_atUNGuradi-DNA glycosylase </td <td>204009_s_at</td> <td>KRAS</td> <td>v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog</td> <td>-0.4582</td> <td>3.38605e-</td>	204009_s_at	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	-0.4582	3.38605e-
224774_s_att     NAV1     neuron navigator 1     0.4580     3.400946-       218848_at     THOC6     WD repat domain 58     -0.4579     3.41877e-       218448_at     C20opf1     chromosome 20 open reading frame 11     -0.4579     3.48387e-       21330_at     TFDP1     chromosome 20 open reading frame 11     -0.4570     3.51835e-       21330_at     TFDP1     chromosome 20 open reading frame 11     -0.4570     3.52008e-       21330_at     TFDP1     chromosome 20 open reading frame 11     -0.4570     3.52008e-       21729_at     BUVRA     biliverdin reductase A     0.4560     3.5671e-       200047_s_at     YT     Y1 transcription factor     -0.4566     3.5671e-       201191_s_at     PTMA     prothynosin, alpha (gene sequence 28)     -0.4558     3.6672se-       23216_s_at     MED28     mediar of RNA polymerase II transcription, subunit 28 homolog. (yeast)     -0.4558     3.51316-       21416_s_s_at     MZFV     neuron-derived neurotophic factor     0.4553     3.27260e-       214415_s_at     MZPK     neuron-derived neurotophic factor     0.4553     3.2330e- </td <td>223206_s_at</td> <td>HSCARG</td> <td>HSCARG protein</td> <td>-0.4581</td> <td>3.39721e-</td>	223206_s_at	HSCARG	HSCARG protein	-0.4581	3.39721e-
21848_at   THOC6   WD repeat domain 58   -0.4580   3.40840c-     200772_x_at   PTMA   prothymosin, alpha (gene sequence 28)   -0.4579   3.4187c-     21230_at   TDDP1   transcription factor Dp-1   -0.4570   3.5183ac-     21330_at   ZBTB20   zinc finger and BTB domain containing 20   0.4570   3.5183ac-     21729_x_at   ZBTVA   bilverdin reductase A   0.4560   3.55761c-     200047_x_at   YI/1   Y11 transcription factor   -0.4560   3.56971c-     211729_x_at   PTMA   prothymosin, alpha (gene sequence 28)   -0.4560   3.56971c-     21101x_x_at   TTMS1   thrombospondin 1   -0.4550   3.5671sc-     21416_x_at   MED28   mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)   -0.4553   3.6672sc-     214150_x_at   ATDFVVDE1   ATDFAVEV1   ATDAM metallopeptidase domain 12 (metrin alpha)   -0.4554   3.82509c-     21641_x_at   ADZMI   DEAD/I (Asp-Glu-Ala-Asp/His) box polyperptide 11 (CHL1-like helicase homolog, S. errevisiae)   -0.4553   3.52760c-     21415_x_at   ADZMI   DEAD/I (Asp-Glu-Ala-Asp/His) box polyperptide 11 (CHL1-like helicase homolog, S. errev	224774_s_at	NAV1	neuron navigator 1	0.4580	3.40094e-
200772_x_at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4579     3.41877e-       218448_at     C20ofT1     chromosome 20 open reading frame 11     -0.4573     3.48887e-       21230_at     TEDP1     transcription factor Dp-1     -0.4500     3.51838e-       23508_at     ZBTB20     zinc finger and BTB domain containing 20     0.4550     3.52603e-       211729_x_at     BUVRA     billverdin reductase A     0.4560     3.53761e-       200047_s_at     YI     YI transcription factor     -0.4562     3.66173e-       2011921_x_at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4550     3.6672se-       201185_s.at     THBS1     thrombospondin 1     0.4559     3.6725e-       21416_s.at     MED28     mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)     -0.4553     3.72760e-       214416_s.at     ATPSVDE1     ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e     -0.4553     3.8308e-       214150_x_at     ATPGVDE1     ADAM metallopeptidase domain 12 (meltrin alpha)     -0.4553     3.8308e-       216777_at     ADAM12     ADAM metallopeptidase do	218848_at	THOC6	WD repeat domain 58	-0.4580	3.40840e-
218448_at     C20orf11     chromosome 20 open reading frame 11     -0.4573     3.48387e-       212330_at <i>TFDP1</i> transcription factor Dp-1     -0.4570     3.5183a-       235308_at <i>ZBT20</i> inc fnger and BTB domain containing 20     0.4570     3.5183a-       235308_at <i>ZBT20</i> inc fnger and BTB domain containing 20     0.4560     3.53761e-       200047_s_at <i>WTA</i> biliverdin reductase A     0.4560     3.5671e-       201191_s_at <i>PTMA</i> prohymosin, alpha (gene sequence 28)     -0.4556     3.6672s-       211845_s_at <i>MED28</i> mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)     -0.4558     3.6672s-       218465_s_at <i>MED28</i> mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)     -0.4558     3.72760e-       218407_s_at <i>ADM11</i> DAM metallopeptidase domain 12 (meltrin alpha)     0.4553     3.8208e-       21641_s_at <i>ACOT7</i> ayl-CoA thioesterase 9     0.4539     3.9098e-       218405_s_at <i>CAUU</i> calumenin     0.4537     3.93959e-       208804_s_at <i>SRRS</i> 6     splicing	200772_x_at	PTMA	prothymosin, alpha (gene sequence 28)	-0.4579	3.41877e-
212330_at <i>TFDP1</i> -0.4570   3.51833e-     235308_at <i>ZBTB20</i> zinc finger and BTB domain containing 20   0.4570   3.5203e-     235308_at <i>ZBTR20</i> inc finger and BTB domain containing 20   0.4560   3.53761e-     200047_s_at <i>W1A</i> bilverdin reductase A   0.4566   3.56971e-     21129_x.at <i>PTMA</i> prothymosin, alpha (gene sequence 28)   -0.4562   3.6117ae-     201108_s_at <i>THBS1</i> thrombospondin 1   0.4559   3.6573te-     232816_s_at <i>DDX11</i> DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, <i>S. cerevisiae</i> )   -0.4554   3.72760e-     218407_x.at <i>NENF</i> neuron-derived neurotrophic factor   0.4545   3.83018e-     221641_s_at <i>ACOT9</i> acyl-CoA thioesterase 9   0.4537   3.90986e-     214845_s_at <i>CALU</i> calumenin   0.4537   3.93959e-     202753_x.at <i>SFRS6</i> splicing factor, arginine/serine-rich 6   -0.4530   4.0302e-     20230_s_at <i>UNG</i> ucai-LDNA glycosylase   -0.4530   4.0302e-     202340_s_at <i>SFRS6</i> splicing factor, arginine/serine-ric	218448_at	C20orf11	chromosome 20 open reading frame 11	-0.4573	3.48387e-
235308_at     ZBTB20     zinc finger and BTB domain containing 20     0.4570     3.52603e-       211729_x_at     BLVRA     biliverdin reductase A     0.4560     3.53761e-       200047_s_att     YY1     YY1 transcription factor     -0.4566     3.650971e-       211921_x_at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4556     3.6173e-       211108_s_att     THBS1     thrombospondin 1     0.4559     3.66725e-       2232816_s_att     DDZV1     DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)     -0.4558     3.6725e-       214150_x_att     ATP6 VDE1     ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e     -0.4553     3.7260e-       21440_x_att     NENF     neuron-derived neurotrophic factor     0.4545     3.83018e-       221641_s_att     ADAM12     ADAM metallopeptidase domain 12 (meltrin alpha)     0.4553     3.93959e-       20884_s_att     SFRS6     splicing factor, arginine/serine-rich 6     -0.4530     4.03002e-       20230_s_att     UNG     uardi-DNA glycosylase     -0.4529     4.04309e-       20230_s_att     UNG	212330_at	TFDP1	transcription factor Dp-1	-0.4570	3.51833e-
211729_x_at     BLVRA     biliverdin reductase A     0.4569     3.53761e-       200047_s_at     YY1     YY1 transcription factor     -0.4566     3.56971e-       211921_x_at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4562     3.61173e-       21108_s_at     THBS1     thrombospondin 1     0.4559     3.66725e-       228416_s_at     MED28     mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)     -0.4558     3.66725e-       232816_s_at     DDX11     DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)     -0.4553     3.72760e-       214150_x_at     ATPKVDE1     ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e     0.4553     3.82509e-       226777_at     ADAM12     ADAM metallopeptidase domain 12 (meltrin alpha)     0.4553     3.83018e-       21641_s_at     ACOT9     acyl-CoA thioesterase 9     0.4530     3.93956e-       21845_s_at     SFRS6     splicing factor, arginine/serine-rich 6     -0.4530     4.02132e-       200753_x_at     SFRS2     splicing factor, arginine/serine-rich 2     -0.4530     4.02309-       20230_s_at	235308_at	ZBTB20	zinc finger and BTB domain containing 20	0.4570	3.52603e-
200047_s_att     YY1     YY1 transcription factor     -0.4566     3.56971e-       21192_x_at     PTMA     prothymosin, alpha (gene sequence 28)     -0.4562     3.61173e-       201108_s_att     THBS1     thrombospondin 1     0.4559     3.65131e-       224416_s_at     MED28     mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)     -0.4558     3.66725e-       232816_s_at     DDX11     DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)     -0.4553     3.72760e-       218450_x_at     ATP6V0E1     ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e     0.4545     3.83508e-       216477_at     NENF     neuron-derived neurotrophic factor     0.4545     3.83018e-       21641_s_at     ACOT9     acyl-CoA thioesterase 9     0.4530     3.93958e-       20845_s_s_at     CALU     calumenin     0.4533     3.93958e-       20845_s_s_at     FRS2     splicing factor, arginine/serine-rich 2     -0.4530     4.0012e-       202330_s_at     UNG     uracil-DNA glycosylase     -0.4529     4.04399e-       202330_s_at     UNG     uracil-DNA gl	211729_x_at	BLVRA	biliverdin reductase A	0.4569	3.53761e-
211921_x_atPTMAprothymosin, alpha (gene sequence 28)-0.45623.61173e-201108_s_atTHBS1thrombospondin 10.45593.65131e-224416_s_atMED28mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)-0.45583.66725e-232816_s_atDDX11DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)-0.45533.72760e-218407_x_atATP6V0E1ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e0.45533.72760e-216407_x_atNENFneuron-derived neurotrophic factor0.45453.83018e-221641_s_atACOT9axyl-CoA thioesterase 90.45393.90986e-218445_s_atCALUcalumenin0.45373.93959e-20804_s_atSFRS6splicing factor, arginine/serine-rich 6-0.45304.0012ae-202568_s_atPHLDB2plickstrin homology-like domain, family B, member 2-0.45294.04309e-202330_s_atUNGuracil-DNA glycosylase-0.45254.00694e-204400_s_atCDV4CD44CD44 antigen (homing function and India blood group system)0.45264.007374e-224840_atFKBP5FK506 binding protein 5-0.45234.1178e-20456_s_atDDX18DEAD (Asp-Glu-Ala-Asp box polypeptide 18-0.45234.1178e-204766_s_atDDX18DEAD (Asp-Glu-Ala-Asp box polypeptide 18-0.45214.1052e-20456_s_atFEN1flap structure-specific endonuclease 1-0.45154.10532e-202466_s_s	200047_s_at	YY1	YY1 transcription factor	-0.4566	3.56971e-
201108_s_atTHBS1thrombospondin 10.4559 $3.65131e-$ 224416_s_atMED28mediator of RNA polymerase II transcription, subunit 28 homolog (yeast) $-0.4558$ $3.66725e-$ 232816_s_atDDX11DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) $-0.4553$ $3.72760e-$ 2144150_x_atATP6V0E1ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e $0.4553$ $3.72760e-$ 218407_x_atNENFneuron-derived neurotrophic factor $0.4545$ $3.83018e-$ 226777_atADAM12ADAM metallopeptidase domain 12 (meltrin alpha) $0.4545$ $3.830986e-$ 216445_s_atACOT9acyl-CoA thioesterase 9 $0.4539$ $3.90986e-$ 208804_s_atSFRS6splicing factor, arginine/serine-rich 6 $-0.4530$ $4.02132e-$ 200753_x_atSFRS2splicing factor, arginine/serine-rich 2 $-0.4530$ $4.03002e-$ 20230_s_atUNGuracil-DNA glycosylase $-0.4527$ $4.06934e-$ 204490_s_atCD44CD44 antigen (homing function and Indian blood group system) $0.4526$ $4.0309e-$ 2023245_atSTRBPspermatid perinuclear RNA binding protein 5 $-0.4525$ $4.0007e-$ 202345_atDD4DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 $-0.4525$ $4.0007e-$ 20346_s_atFKBP5FK506 binding protein 5 $-0.4525$ $4.0007e-$ 20345_atSTRPspermatid perinuclear RNA binding protein $-0.4525$ $4.0007e-$ 20345_atDDX18DEAD (Asp-Glu-Ala-Asp) box p	211921_x_at	PTMA	prothymosin, alpha (gene sequence 28)	-0.4562	3.61173e-
224416_s_atMED28mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)-0.45583.66725e-232816_s_atDDX11DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)-0.45543.71858e-214150_x_atATP6VDE1ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e0.45533.72760e-218407_x_atNENFneuron-derived neurotrophic factor0.45453.83018e-220777_atADAM12ADAM metallopeptidase domain 12 (meltrin alpha)0.45453.83018e-21641_s_atACOT9acyl-CoA thioesterase 90.45333.90986e-21845_s_atCALUcalumenin0.45373.93959e-208804_s_atSFRS6splicing factor, arginine/serine-rich 2-0.45304.02132e-202330_s_atUNGuracil-DNA glycosylase-0.45254.04309e-202164_s_atCNOT8CCR4-NOT transcription complex, subunit 8-0.45254.06394e-202164_s_atFKBP5FK506 binding protein 5-0.45254.006394e-202440_atFKBP5FK506 binding protein 5-0.45254.00679e-22346_atDDX18DEAD (Asp-Glu-Ala-Asp) box polypeptide 18-0.45234.1017e-204768_s_atDDX18DEAD (Asp-Glu-Ala-Asp) box polypeptide 18-0.45234.1017e-204768_s_atFEN/Iflap structure-spcific endonuclease 1-0.45154.1017e-204768_s_atFEN/Iflap structure-spcific endonuclease 1-0.45234.1178be-204768_s_atFEN/Ifla	201108_s_at	THBS1	thrombospondin 1	0.4559	3.65131e-
232816_s_at     DDX11     DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, <i>S. cerevisiae</i> )     -0.4554     3.71858e-       214150_x_at     ATP6V0E1     ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e     0.4553     3.72760e-       218407_x_at     NENF     neuron-derived neurotrophic factor     0.4545     3.82509e-       226777_at     ADAM12     ADAM metallopeptidase domain 12 (meltrin alpha)     0.4545     3.8018e-       21641_s_at     ACOT9     acyl-CoA thioesterase 9     0.4539     3.90986e-       21845_s_at     CALU     calumenin     0.4533     3.93959e-       20804_s_at     SFRS6     splicing factor, arginine/serine-rich 2     -0.4530     4.03002e-       202330_s_at     UNG     uracil-DNA glycosylase     -0.4527     4.04309e-       202164_sat     CNO78     CCR4-NOT transcription complex, subunit 8     -0.4527     4.06394e-       204490_s_at     CD44     CD44 antigen (homing function and Indian blood group system)     0.4526     4.07374e-       224840_at     FKBP5     spermatid perinuclear RNA binding protein 5     -0.4525     4.06997e-       223245_at	224416_s_at	MED28	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	-0.4558	3.66725e-
214150_x_at   ATP6V0E1   ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e   0.4553   3.72760e-     218407_x_at   NENF   neuron-derived neurotrophic factor   0.4545   3.82509e-     226777_at   ADAM12   ADAM metallopeptidase domain 12 (meltrin alpha)   0.4545   3.83018e-     221641_s_at   ACO79   acyl-CoA thioesterase 9   0.4533   3.90986e-     218485_s_at   CALU   calumenin   0.4533   3.93959e-     208804_s_at   SFRS6   splicing factor, arginine/serine-rich 6   -0.4530   4.02132e-     205688_s_at   PHLDB2   pleckstrin homology-like domain, family B, member 2   0.4529   4.043009e-     20230_s_at   UNG   uracil-DNA glycosylase   -0.4520   4.04537     204490_s_at   CD44   CD44 antigen (homing function and Indian blood group system)   0.4526   4.07374e-     204840_at   FKBP5   FK506 binding protein 5   -0.4525   4.09697e-     223245_at   DZHA   DEAD (Asp-Gu-Ala-Asp) box polypeptide 18   -0.4525   4.09697e-     223245_at   DZHA   DEAD (Asp-Gu-Ala-Asp) box polypeptide 18   -0.4521   4.115782e-     204768_s_at	232816_s_at	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	-0.4554	3.71858e-
218407_x_at     NENF     neuron-derived neurorophic factor     0.4545     3.82509e-       226777_at     ADAM12     ADAM metallopeptidase domain 12 (meltrin alpha)     0.4545     3.83018e-       221641_s_at     ACOT9     acyl-CoA thioesterase 9     0.4537     3.93959e-       208804_s_at     SFRS6     splicing factor, arginine/serine-rich 6     0.4530     4.02132e-       200753_x_at     SFRS2     splicing factor, arginine/serine-rich 2     -0.4530     4.02132e-       203804_s_at     VING     uracil-DNA glycosylase     -0.4530     4.0300e-       202330_s_at     UNG     uracil-DNA glycosylase     -0.4527     4.06934e-       204490_s_at     CD44     CD44 antigen (homing function and Indian blood group system)     0.4525     4.09057e-       223425_at     STRBP     spermatid perinuclear RNA binding protein     -0.4525     4.09057e-       223425_at     STRBP     spermatid perinuclear RNA binding protein     -0.4525     4.0017e-       204768_s_at     DDX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4521     4.11789c-       214450_s_at     FEN1     flap structure-specific endonu	214150_x_at	ATP6V0E1	ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e	0.4553	3.72760e-
226777_at     ADAM12     ADAM metallopeptidase domain 12 (meltrin alpha)     0.4545     3.83018e-       221641_s_at     ACOT9     acyl-CoA thioesterase 9     0.4539     3.90986e-       214845_s_at     CALU     calumenin     0.4537     3.93959e-       208804_s_at     SFRS6     splicing factor, arginine/serine-rich 6     -0.4530     4.02132e-       200753_x_at     SFRS2     splicing factor, arginine/serine-rich 2     -0.4530     4.03002e-       20230_s_at     UNG     uracil-DNA glycosylase     -0.4520     4.04309e-       202164_s_at     CNO78     CCR4-NOT transcription complex, subunit 8     -0.4520     4.04309e-       20248_0_at     FKBP5     K506 binding protein 5     -0.4525     4.006934e-       20248_0_at     FKBP5     FK506 binding protein 5     -0.4525     4.00737e-       20248_0_at     JTRBP     spermatid perinuclear RNA binding protein     -0.4525     4.006934e-       208896_at     DDX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4525     4.00737e-       20230_s_at     FKBP5     spermatid perinuclear RNA binding protein     -0.4523     4	218407_x_at	NENF	neuron-derived neurotrophic factor	0.4545	3.82509e-
221641_s_attACOT9acyl-CoA thioesterase 90.45393.90986e-214845_s_attCALUcalumenin0.45373.93959e-208804_s_atSFRS6splicing factor, arginine/serine-rich 6 $-0.4530$ 4.02132e-200753_x_attSFRS2splicing factor, arginine/serine-rich 2 $-0.4530$ 4.03002e-225688_s_atPHLDB2pleckstrin homology-like domain, family B, member 2 $0.4529$ 4.04309e-20230_s_atUNGuracil-DNA glycosylase $-0.4520$ 4.04309e-202164_s_atCNO78CCR4-NOT transcription complex, subunit 8 $-0.4527$ 4.06934e-204490_s_attCD44CD44 antigen (homing function and Indian blood group system) $0.4526$ $4.07374e-$ 223245_attSTRBPspermatid perinuclear RNA binding protein $-0.4523$ $4.11789e-$ 208896_atDDX18DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 $-0.4521$ $4.15352e-$ 212593_s_atPDCD4programmed cell death 4 (neoplastic transformation inhibitor) $-0.4515$ $4.22562e-$	226777_at	ADAM12	ADAM metallopeptidase domain 12 (meltrin alpha)	0.4545	3.83018e-
214845_s_atCALUcalumenin0.45373.93959e-208804_s_atSFRS6splicing factor, arginine/serine-rich 6-0.45304.02132e-200753_x_atSFRS2splicing factor, arginine/serine-rich 2-0.45304.03002e-225688_s_atPHLDB2pleckstrin homology-like domain, family B, member 2-0.45304.03002e-20230_s_atUNGuracil-DNA glycosylase-0.45294.04309e-202164_s_atCNO78CCR4-NOT transcription complex, subunit 8-0.45274.06934e-204490_s_atCD44CD44 antigen (homing function and Indian blood group system)0.45264.07374e-223245_atSTRBPspermatid perinuclear RNA binding protein-0.45254.0007e-208896_atDDX18DEAD (Asp-Glu-Ala-Asp) box polypeptide 18-0.45214.15352e-212593_s_atFENIflap structure-specific endonuclease 1-0.45154.22562e-212593_atPDCD4programmed cell death 4 (neoplastic transformation inhibitor)-0.45154.22562e-	221641_s_at	ACOT9	acyl-CoA thioesterase 9	0.4539	3.90986e-
208804_s_at     SFRS6     splicing factor, arginine/serine-rich 6     -0.4530     4.02132e-       200753_x_at     SFRS2     splicing factor, arginine/serine-rich 2     -0.4530     4.03002e-       225688_s_at     PHLDB2     pleckstrin homology-like domain, family B, member 2     0.4529     4.04309e-       202330_s_at     UNG     uracil-DNA glycosylase     -0.4520     4.04309e-       202164_s_at     CNO78     CCR4-NOT transcription complex, subunit 8     -0.4527     4.06934e-       20440_s_at     FKBP5     CD44     CD44 antigen (homing function and Indian blood group system)     0.4526     4.07374e-       223245_at     STRBP     spermatid perinuclear RNA binding protein     -0.4525     4.0607e-       208896_at     DDX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4523     4.11789e-       204768_s_at     FENI     flap structure-specific endonuclease 1     -0.4515     4.2552e-       212593_s_at     PDCD4     programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	214845_s_at	CALU	calumenin	0.4537	3.93959e-
200753_x_atSFRS2splicing factor, arginine/serine-rich 2 $-0.4530$ $4.03002e-$ 225688_s_atPHLDB2pleckstrin homology-like domain, family B, member 2 $0.4529$ $4.04309e-$ 20230_s_atUNGuracil-DNA glycosylase $-0.4529$ $4.04309e-$ 202164_s_atCNOT8CCR4-NOT transcription complex, subunit 8 $-0.4527$ $4.06934e-$ 204490_s_atCD44CD44 antigen (homing function and Indian blood group system) $0.4526$ $4.07374e-$ 223245_atSTRBPspermatid perinuclear RNA binding protein $-0.4525$ $4.0007e-$ 204886_atDDX18DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 $-0.4521$ $4.15352e-$ 212593_s_atPDCD4programmed cell death 4 (neoplastic transformation inhibitor) $-0.4515$ $4.22562e-$	208804_s_at	SFRS6	splicing factor, arginine/serine-rich 6	-0.4530	4.02132e-
225688_s_at     PHLDB2     pleckstrin homology–like domain, family B, member 2     0.4529     4.04309e-       202330_s_at     UNG     uracil-DNA glycosylase     -0.4529     4.04309e-       202164_s_at     CNOT8     CCR4-NOT transcription complex, subunit 8     -0.4527     4.06934e-       204490_s_at     CD44     CD44 antigen (homing function and Indian blood group system)     0.4526     4.07374e-       224840_at     FKBP5     FK506 binding protein 5     -0.4525     4.09697e-       223245_at     STRBP     spermatid perinuclear RNA binding protein     -0.4525     4.10787e-       2048896_at     DX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4523     4.11789e-       204768_s_at     FEN1     flap structure-specific endonuclease 1     -0.451     4.15352e-       212593_s_at     PDCD4     programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	200753_x_at	SFRS2	splicing factor, arginine/serine-rich 2	-0.4530	4.03002e-
202330_s_at     UNG     uracil-DNA glycoylase     -0.4529     4.04309c-       202164_s_at     CNOT8     CCR4-NOT transcription complex, subunit 8     -0.4527     4.06934e-       204490_s_at     CD44     CD44 antigen (homing function and Indian blood group system)     0.4526     4.07374e-       224840_at     FKBP5     FK506 binding protein 5     -0.4525     4.09697e-       223245_at     STRBP     spermatid perinuclear RNA binding protein     -0.4525     4.10769-       2048896_at     DX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4521     4.11789e-       204768_s_at     FEN1     flap structure-specific endonuclease 1     -0.4511     4.12552e-       212593_s_at     PDCD4     programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	225688_s_at	PHLDB2	pleckstrin homology-like domain, family B, member 2	0.4529	4.04309e-
202164_s_at     CNOT8     CCR4-NOT transcription complex, subunit 8     -0.4527     4.06934e-       204490_s_at     CD44     CD44 antigen (homing function and Indian blood group system)     0.4526     4.07374e-       224840_at     FKBP5     FK506 binding protein 5     -0.4525     4.09697e-       223245_at     STRBP     spermatid perinuclear RNA binding protein     -0.4525     4.10017e-       208896_at     DDX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4523     4.11789e-       204768_s_at     FEN1     flap structure-specific endonuclease 1     -0.4521     4.15352e-       212593_s_at     PDCD4     programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	202330_s_at	UNG	uracil-DNA glycosylase	-0.4529	4.04309e-
204490_s_at     CD44     CD44 antigen (homing function and Indian blood group system)     0.4526     4.07374e-       224840_at     FKBP5     FK506 binding protein 5     -0.4525     4.09697e-       223245_at     STRBP     spermatid perinuclear RNA binding protein     -0.4525     4.10017e-       208896_at     DDX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4523     4.11789e-       204768_s_at     FEN1     flap structure-specific endonuclease 1     -0.4521     4.15352e-       212593_s_at     PDCD4     programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	202164_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	-0.4527	4.06934e-
224840_at <i>FKBP5</i> FK506 binding protein 5     -0.4525     4.09697e-       223245_at <i>STRBP</i> spermatid perinuclear RNA binding protein     -0.4525     4.10017e-       208896_at <i>DDX18</i> DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4523     4.11789e-       204768_s_at <i>FEN1</i> flap structure-specific endonuclease 1     -0.4521     4.15352e-       212593_s_at <i>PDCD4</i> programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	204490_s_at	CD44	CD44 antigen (homing function and Indian blood group system)	0.4526	4.07374e-
223245_at     STRBP     spermatid perinclear RNA binding protein     -0.4525     4.10017e-       208896_at     DDX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4523     4.11789e-       204768_s_at     FEN1     flap structure-specific endonuclease 1     -0.4521     4.15352e-       212593_s_at     PDCD4     programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	224840_at	FKBP5	FK506 binding protein 5	-0.4525	4.09697e-
208896_at     DDX18     DEAD (Asp-Glu-Ala-Asp) box polypeptide 18     -0.4523     4.11789e-       204768_s_at     FEN1     flap structure-specific endonuclease 1     -0.4521     4.15352e-       212593_s_at     PDCD4     programmed cell death 4 (neoplastic transformation inhibitor)     -0.4515     4.22562e-	223245_at	STRBP	spermatid perinuclear RNA binding protein	-0.4525	4.10017e-
204768_s_atFEN1flap structure-specific endonuclease 1-0.45214.15352e-212593_s_atPDCD4programmed cell death 4 (neoplastic transformation inhibitor)-0.45154.22562e-	208896_at	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-0.4523	4.11789e-
212593_s_at PDCD4 programmed cell death 4 (neoplastic transformation inhibitor) -0.4515 4.22562e-	204768_s_at	FEN1	flap structure-specific endonuclease 1	-0.4521	4.15352e-
	212593_s_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	-0.4515	4.22562e-

Affy ID	Gene Symbol	Description	ρ	Р
215446_s_at	LOX	lysyl oxidase	0.4514	4.24383e-
203167_at	TIMP2	TIMP metallopeptidase inhibitor 2	0.4512	4.27126e-
212419_at	C10orf56	chromosome 10 open reading frame 56	0.4512	4.27585e-
227771_at	LIFR	leukemia inhibitory factor receptor	0.4511	4.28504e-
214257_s_at	SEC22B	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)	0.4510	4.30348e-
225798_at	JAZF1	juxtaposed with another zinc finger gene 1	0.4509	4.31735e-
218069_at		XTP3-transactivated protein A	-0.4504	4.39203e-
221881_s_at	CLIC4	chloride intracellular channel 4	0.4499	4.45834e-
202303_x_at	SMARCA5	SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamily a, member 5	-0.4496	4.50625e-
201493_s_at	PUM2	pumilio homolog 2 ( <i>Drosophila</i> )	-0.4495	4.52072e-
213610_s_at	KLHL23	kelch-like 23 (Drosophila)	-0.4494	4.54007e-
226751_at	C2orf32	chromosome 2 open reading frame 32	0.4493	4.54978e-
209079_x_at	PCDHG	protocadherin gamma subfamily	0.4491	4.57900e-
219944_at	CLIP4	restin-like 2	0.4491	4.58389e-
227740_at	UHMK1	U2AF homology motif (UHM) kinase 1	0.4489	4.61332e-
212195_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	0.4488	4.62316e-
201376_s_at	HNRPF	heterogeneous nuclear ribonucleoprotein F	-0.4488	4.63303e-
210139_s_at	PMP22	peripheral myelin protein 22	0.4488	4.63303e-
201559_s_at	CLIC4	chloride intracellular channel 4	0.4486	4.65282e-
218067_s_at	1// 0700	hypothetical protein FLJ10154	-0.4485	4.66//le-
208682_s_at	MAGED2	melanoma antigen family D, 2	0.4484	4.68/63e-
5/163_at	ELOVLI	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)–like I	0.4483	4./0262e-
225563_at	PAN3	PABP1-dependent poly A-specific ribonuclease subunit PAN3	-0.4483	4./0262e-
202391_at	BASP1	brain-abundant, membrane-attached signal protein 1	0.4480	4./5291e-
200956_s_at	SSRP1	structure-specific recognition protein 1	-0.44/9	4./6505e-
215529_at	SKGAP2	SLIT-KOBO Kno G I Pase activating protein 2	0.4476	4.80369e-
2105/1_s_at	KBBP4 TMDO	retinoblastoma binding protein 4	-0.44/5	4.82414e-
209/34_s_at	IMPO	trymopoletin	-0.44/3	4.834396-
223391_at	LUC93622	SNADE protein DC000130	-0.44/4	4.849810-
21//04_at	SVDE1	survance proteini 1 Rho CTDess, homolog 1 (Cranenhabdini alagan)	0.44/1	4.076760
216262 c at	TCIE2	TCEB induced factor 2 (TALE family homeoboy)	0.4466	4.974760
210202_s_at	10/12	nbosnbonaformete immunoassociated protein 5	-0.4400	4.974/00-
2022))_3_at	$P \cap I F 2$	polymerase (DNA-directed), epcilon 2 (p59 subunit)	-0.4465	4.98531e-
203909_at	FGD1	FYVE. RhoGEF and PH domain containing 1 (faciogenital dysplasia)	0 4464	4 99587e-
225381 at	LOC399959	hypothetical gene supported by BX647608	0.4463	5.02768e-
218298 s at	C14orf159	chromosome 14 open reading frame 159	-0.4462	5.03833e-
215836 s at	PCDHG	protocadherin gamma subfamily	0.4461	5.04899e-
209750 at	NR1D2	nuclear receptor subfamily 1, group D, member 2	0.4459	5.08111e-
201035_s_at	HADH	L-3-hydroxyacyl–Coenzyme A dehydrogenase, short chain	-0.4458	5.10802e-
226342_at	SPTBN1	Spectrin, beta, non–erythrocytic 1	0.4458	5.10802e-
226934_at	CPSF6	Cleavage and polyadenylation specific factor 6, 68 kDa	-0.4449	5.25556e-
231810_at	BRI3BP	BRI3 binding protein	-0.4445	5.31677e-
219779_at	ZFHX4	zinc finger homeodomain 4	0.4443	5.36169e-
210904_s_at	IL13RA1	interleukin 13 receptor, alpha 1	0.4442	5.36733e-
202258_s_at		phosphonoformate-immunoassociated protein 5	-0.4441	5.38994e-
226912_at	ZDHHC23	zinc finger, DHHC-type containing 23	-0.4438	5.43542e-
218168_s_at	CABC1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	-0.4436	5.48125e-
203632_s_at	GPRC5B	G protein-coupled receptor, family C, group 5, member B	0.4435	5.49852e-
241879_at		Transcribed locus	0.4435	5.50429e-
200041_s_at	BAT1	HLA-B-associated transcript 1	-0.4437	5.53484e-
228174_at	GOLGA1	Golgi autoantigen, golgin subfamily a, 1	-0.4428	5.62083e-
219520_s_at	WWC3	KIAA1280 protein	0.4428	5.62083e-
228121_at	TGFB2	Transforming growth factor, beta 2	0.4423	5.70970e-
200957_s_at	SSRP1	structure-specific recognition protein 1	-0.4422	5.72763e-
201616_s_at	CALD1	caldesmon 1	0.4421	5.75762e-
232113_at		Hypothetical gene supported by BX64/608	0.4421	5./5/62e-
21/828_at	SLIM	modulator of estrogen induced transcription	-0.4420	5./6363e-
21955/_s_at	INRIP3	nuclear receptor interacting protein 3	0.4418	5./9984e-
223/11_s_at		thymocyte protein 1 hyz8	-0.4415	5.86065e-
218030_s_at	LHFP	IIpoma HMGIC tusion partner	0.4415	5.00512-
250150_at	NILID160	nucleonorin 160 kDe	0.4414	5.040560
212/07_at 202125_c_or	TRAKO	amvatranhic lateral sclerosis 2 (iuvenile) chromosome region, candidate 3	0.4410	5 9529/2
$202123_s_at$ 200679 x at	HMGB1	high-mobility group box 1	_0.4409	5 983000
2000/ J_x_at	1111(1)	CDNA ELI41690 fis clone HCASM2009405	0.4405	6.04654c
22/ 707_dl 222204_s_at	RRN3	RRN3 RNA polymerase I transcription factor homolog (veget)	_0 4403	6.08436e
214882 s at	SFRS2	splicing factor, arginine/serine_rich 2	-0 4403	6 08436
213836 s at	WIPI1	WD40 repeat protein interacting with phosphoinositides of 49 kDa	0.4401	6.12874e-
208178 x at	TRIO	triple functional domain (PTPRF interacting)	0.4401	6.14008e-
224856 at	FKBP5	FK506 binding protein 5	-0.4401	6.14148e-
213238 at	ATP10D	ATPase, class V, type 10D	0.4399	6.17983e-
201450_s_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	-0.4398	6.18624e-
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Affy ID	Gene Symbol	Description	ρ	Р
201712_s_at	RANBP2	RAN binding protein 2	-0.4395	6.24281e-
200977_s_at	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	0.4393	6.28315e-
225685_at	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	0.4390	6.34196e-
213139_at	SNAI2	snail homolog 2 (Drosophila)	0.4390	6.34196e-
202948_at	IL1R1	interleukin 1 receptor, type I	0.4390	6.34853e-
203317_at	PSD4	pleckstrin and Sec7 domain containing 4	-0.4387	6.40974e-
202238_s_at	NNMT	nicotinamide N-methyltransferase	0.4386	6.42778e-
208795_s_at	MCM7	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	-0.4386	6.43443e-
233364_s_at	DNIDO	Hypothetical gene supported by BX64/608	0.4386	6.43443e-
201848_s_at	DIVII'S ATVNI	bCL2/adenovirus E1B 19 kDa interacting protein 5	0.4384	6.50702°
203231_8_at	MAPIR	Alaxin 1 Microtubule-associated protein 1B: Hame capiens, clone IMACE:5535936, mRNA	0.4381	6.54159e-
208747 s at	C1S	complement component 1 s subcomponent	0.4380	6.56186e-
200999 s at	CKAP4	cytoskeleton-associated protein 4	0.4379	6.57541e-
214109 at	LRBA	LPS-responsive vesicle trafficking, beach and anchor containing	-0.4377	6.62302e-
213338 at	TMEM158	Ras-induced senescence 1	0.4374	6.67782e-
	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	0.4374	6.69158e-
207749_s_at	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	0.4372	6.72805e-
203856_at	VRK1	vaccinia-related kinase 1	-0.4371	6.74689e-
212603_at	MRPS31	mitochondrial ribosomal protein \$31	-0.4368	6.80261e-
236533_at	DDEF1	development and differentiation enhancing factor 1	0.4367	6.82909e-
212789_at	NCAPD3	KIAA0056 protein	-0.4366	6.85170e-
204647_at	HOMER3	homer homolog 3 (Drosophila)	0.4366	6.85874e-
203276_at	LMNB1	lamin B1	-0.4366	6.85874e-
201170_s_at	BHLHB2	basic helix-loop-helix domain containing, class B, 2	0.4364	6.90112e-
202302_s_at	RSRC2	similar to splicing factor, arginine/serine-rich 4	-0.4363	6.92239e-
212443_at	NBEAL2	neurobeachin-like 2	-0.4362	6.943/3e-
212418_at		E/4-like factor 1 (ets domain transcription factor)	-0.4361	6.95891e-
20/949_s_at	ICAI MSH2	isiet cell autoantigen 1, 69 kDa	-0.4360	7.00002
209421_at	D474D1	DAZ associated protein 1	-0.4339	7.000920-
21044 <u>9_3_</u> at	KTAA1280	KIAA1280 protein	0.4359	7.00809e-
203229 s at	CLK2	CDC-like kinase 2	-0.4356	7.0730e-0
213798 s at	CAPI	CAP, adenvlate cvclase-associated protein 1 (yeast)	0.4356	7.07504e-
216969_s_at	KIF22	kinesin family member 22	-0.4355	7.10202e-
204489_s_at	CD44	CD44 antigen (homing function and Indian blood group system)	0.4354	7.10929e-
208908_s_at	CAST	calpastatin	0.4353	7.13844e-
225481_at	FRMD6	FERM domain containing 6	0.4351	7.18237e-
203388_at	ARRB2	arrestin, beta 2	-0.4351	7.19707e-
212014_x_at	CD44	CD44 antigen (homing function and Indian blood group system)	0.4348	7.26355e-
218295_s_at	NUP50	nucleoporin 50 kDa	-0.4344	7.34556e-
214663_at	RIPK5	receptor interacting protein kinase 5	0.4343	7.36056e-
200770_s_at	LAMCI	laminin, gamma 1 (formerly LAMB2)	0.4343	7.36807e-
218/14_at	PRR14	hypothetical protein MGC3121	-0.4342	/.39818e-
212822_at 212920_at	negi	ricks nomolog 1 (zebransn)	0.4340	7 /0516e
212920_at	IIMA1	enithelial protein lost in peoplasm beta	-0.4337	7.51209e-
226425 at	RSNL2	restin-like 2	0.4337	7.51209e-
203358 s at	EZH2	enhancer of zeste homolog 2 ( <i>Drosophila</i> )	-0.4337	7.51974e-
200787 s at	PEA15	phosphoprotein enriched in astrocytes 15	0.4334	7.57348e-
215947_s_at		hypothetical protein FLJ14668	-0.4332	7.62202e-
232524_x_at	ANAPC4	anaphase promoting complex subunit 4	-0.4330	7.67422e-
39729_at	PRDX2	peroxiredoxin 2	-0.4328	7.71328e-
201849_at	BNIP3	BCL2/adenovirus E1B 19 kDa interacting protein 3	0.4327	7.75252e-
241418_at		Hypothetical LOC344887	0.4326	7.78405e-
200625_s_at	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	0.4324	7.81569e-
203729_at	EMP3	epithelial membrane protein 3	0.4323	7.85540e-
227846_at	GPR	putative G protein–coupled receptor	0.4322	7.87134e-
2228/2_x_at	FLJ22833	hypothetical protein FLJ22833	0.4321	/.8935/e-
201430_s_at	DPYSL3	dihydropyrimidinase-like 3 RCI 2 internation hiller (manazzini indusion)	0.4318	/.9/564e-
203/80_at	DIK USCARC	UCL2-interacting killer (apoptosis-inducing)	-0.4310	8.01009e-
2312/1_x_at 226405_s_at	ARRDC1	arrestin domain containing 1	-0.4315	8.042/06-
201560 at	CLIC4	chloride intracellular channel 4	0.4313	8.09753e-
223154 at	MRPL1	mitochondrial ribosomal protein L1	-0.4313	8.10572e-
211506 s at	IL8	interleukin 8	0.4311	8.14676e-
221081 s at	DENND2D	DENN/MADD domain containing 2D	-0.4310	8.16323e-
226281_at	DNER	delta-notch-like EGF repeat-containing transmembrane	0.4310	8.16323e-
211376_s_at	NSMCE4A	chromosome 10 open reading frame 86	-0.4308	8.21282e-
221191_at		DKFZp434A0131 protein	-0.4308	8.21282e-
205308_at	C8orf70	chromosome 8 open reading frame 70	0.4306	8.26267e-
206237_s_at	NRG1	neuregulin 1	0.4306	8.27101e-
200606_at	DSP	desmoplakin	-0.4305	8.30443e-

Affy ID	Gene Symbol	Description	ρ	Р
242673_at			-0.4303	8.35479e-
201865_x_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	0.4301	8.41389e-
226760_at	LOC203411	hypothetical protein LOC203411	0.4300	8.43933e-
212056_at	KIAA0182	KIAA0182 protein	-0.4296	8.54180e-
217788_s_at	GALNT2	UDP–N-acetyl- $\alpha$ -D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	0.4295	8.56575e-
214744_s_at	RPL23	ribosomal protein L23	-0.4294	8.58483e-
214446_at	ELL2	elongation factor, RNA polymerase II, 2	0.4291	8.67147e-
212267_at	WAPAL	KIAA0261	-0.4290	8.68017e-
228009_x_at	ZNRD1	zinc ribbon domain containing, 1	-0.4290	8.68889e-
211057_at	ROR1	receptor tyrosine kinase–like orphan receptor 1	0.4290	8.69574e-
214927_at	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	0.4290	8.69761e-
233167_at	SELO	selenoprotein O	-0.4288	8.75889e-
210757_x_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	0.4287	8.78528e-
210095_s_at	IGFBP3	insulin-like growth factor binding protein 3	0.4286	8.79409e-
204160_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	-0.4285	8.82056e-
234074_at		CDNA FLJ10946 fis, clone PLACE1000005	0.4284	8.84711e-
202013_s_at	EXT2	exostoses (multiple) 2	0.4281	8.92975e-
224886_at	LOC339123	hypothetical LOC339123	-0.4279	8.98993e-
202828_s_at	MMP14	matrix metallopeptidase 14 (membrane-inserted)	0.4279	8.98993e-
224942 at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	0.4279	8.99893e-
210212 x at	MTCP1	mature T-cell proliferation 1	0.4278	9.03499e-
204115 at	GNG11	guanine nucleotide binding protein (G protein), gamma 11	0.4277	9.04402e-
202532 s at	DHFR	dihydrofolate reductase	-0.4276	9.08024e-
202326 at	EHMT2	euchromatic histone-lysine N-methyltransferase 2	-0.4275	9.09646e-
202998 s at	LOXL2	lysyl oxidase–like 2	0.4274	9.12571e-
202822 at	LPP	LIM domain containing preferred translocation partner in lipoma	0.4274	9.13744e-
217762 s at	RAB31	RAB31, member RAS oncogene family	0.4273	9.15308e-
203441 s at	CDH2	cadherin 2, type 1, N-cadherin (neuronal)	0.4273	9.16222e-
204853 at	ORC2L	origin recognition complex, subunit 2-like (yeast)	-0.4273	9.16222e-
227561 at	DDR2	Discoidin domain receptor family, member 2	0.4271	9.22645e-
212077 at	CALD1	caldesmon 1	0.4268	9.30961e-
218170 at	ISOC1	isochorismatase domain containing 1	-0.4266	9.36543e-
241353 s at	LOC202775: LOC402617	hypothetical LOC202775: hypothetical LOC402617	0.4265	9.40281e-
232254 at	FBXO25	F-box protein 25	0.4260	9.54419e-
218688 at	DAK	dihydroxyacetone kinase 2 homolog (yeast)	-0.4259	9.57411e-
218028 at	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, veast)-like 1	0.4258	9.59174e-
212723 at	IMID6	phosphatidylserine receptor	0.4257	9.62037e-
209127 s at	SART3	squamous cell carcinoma antigen recognized by T cells 3	-0.4257	9.62037e-
202162 s at	CNOT8	CCR4-NOT transcription complex, subunit 8	-0.4256	9.63950e-
201069 at	MMP2	matrix metallopeptidase 2 (gelatinase A, 72-kDa gelatinase, 72-kDa type IV collagenase)	0.4256	9.65866e-
241763 s at			0.4255	9.66826e-
227129 x at	10C284701	hypothetical protein LOC284701	-0.4253	9.73566e-
209143 s at	CLNS1A: CLDND1	chloride channel, nucleotide-sensitive, 1A: chromosome 3 open reading frame 4	-0.4253	9.74533e-
212097 at	CAVI	caveolin 1. caveolae protein. 22 kDa	0.4251	9.79378e-
212077_at	NENE	neuron-derived neurotrophic factor	0.4249	9.85220e-
204341 at	TRIM16	tripartite motif-containing 16: similar to tripartite motif-containing 16: estrogen-responsive	0.4249	9.87175e-
a		B box protein		,, i, je-
215489_x_at	HOMER3	homer homolog 3 (Drosophila)	0.4248	9.88153e-
222900_at	NRIP3	nuclear receptor interacting protein 3	0.4248	9.89905e-
213793_s_at	HOMER1	homer homolog 1 (Drosophila)	-0.4246	9.94043e-
228297_at	CNN3	calponin 3, acidic	0.4245	9.97987e-



Figure W1. Hierarchical clustering of NCI-60 cell lines using Euclidean distance and average linkage (according to the expression of 11,848 genes).



**Figure W2.** HOPACH clustering of NCI-60 cell lines according to expression of 2349 genes selected unspecifically. Red color indicates small distance; white, large distance. Cell lines are ordered according to the final level of the cluster tree. The proportion of the estimated membership within a cluster is plotted on the right part of figure. Each cluster is represented by a different color. Dotted lines indicate the cluster boundaries at the tree level with minimum median split silhouette.



**Figure W3.** HOPACH clustering of NCI-60 cell lines according to genes differentially expressed between cell lines derived from different tissues. Red color indicates small distance; white, large distance. Cell lines are ordered according to the final level of the cluster tree. The proportion of the estimated membership within a cluster is plotted on the right part of figure. Each cluster is represented by a different color. Dotted lines indicate the cluster boundaries at the tree level with minimum median split silhouette.



**Figure W4.** HOPACH clustering of NCI-60 cell lines according to genes whose expression correlated with numerical heterogeneity index. Red color indicates small distance; white, large distance. Cell lines are ordered according to the final level of the cluster tree. The proportion of the estimated membership within a cluster is plotted on the right part of figure. Each cluster is represented by a different color. Dotted lines indicate the cluster boundaries at the tree level with minimum median split silhouette.

Table W3. List of 213 Array Features and Names of Corresponding Genes with Expression Profiles Correlated with NH (P < .001) Across the NCI-60 Panel of Cancer Cell Lines, After Exclusion of Array Elements Showing Differential Expression Based on Their Tissue of Origin.

Affy ID	Gene Symbol	Description	ρ	Р
226148_at	BTBD15	BTB (POZ) domain containing 15	-0.6236	2.2e-07
218088_s_at	RRAGC	Ras-related GTP binding C	0.5750	2.89e-06
200069_at	SART3	squamous cell carcinoma antigen recognized by T cells 3	-0.5686	3.94e-06
226482_s_at	F11R	F11 receptor	-0.5620	5.38e-06
220092_s_at	ANTXR1	anthrax toxin receptor 1	0.5425	1.3e-05
202859_x_at	IL8	interleukin 8	0.5349	1.82e-05
201172_x_at	ATP6V0E1	ATPase, H+ transporting, lysosomal 9 kDa, V0 subunit e	0.5341	1.88e-05
218491_s_at	THYN1	thymocyte protein Thy28	-0.5300	2.24e-05
227560_at	SFXN2	sideroflexin 2	-0.5288	2.35e-05
212978_at	LRRC8B	leucine-rich repeat containing 8 family, member B	-0.5218	3.15e-05
212446_s_at	LASS6	LAG1 longevity assurance homolog 6 (S.cerevisiae)	-0.5215	3.18e-05
213149_at	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	-0.5189	3.55e-05
204767_s_at	FEN1	flap structure–specific endonuclease 1	-0.5170	3.83e-05
208901_s_at	TOP1	topoisomerase (DNA) I	-0.5163	3.94e-05
219378_at	NARG1L	NMDA receptor regulated 1–like	-0.5155	4.07e-05
225179_at	HIP2	Huntingtin interacting protein 2	-0.5151	4.13e-05
225845_at	BTBD15	BTB (POZ) domain containing 15	-0.5116	4.75e-05
211612_s_at	IL13RA1	interleukin 13 receptor, alpha 1	0.5114	4.8e-05
213251_at		Hypothetical LOC 441046	-0.5101	5.04e-05
223268_at	P1D012	P1D012 protein	-0.5091	5.26e-05
202778_s_at	ZMYM2 KTA 40520	zinc finger protein 198	-0.5058	5.99e-05
212943_at	KIAA0528	KIAA0528 gene product	-0.5048	6.21e-05
20188/_at	ILI3RAI THEOL	interleukin 13 receptor, alpha 1	0.5048	6.23e-05
209225_x_at	INPOI	transportin 1	0.504/	6.23e-05
212658_at	LHFPL2 MED0	lipoma HMGIC tusion partner–like 2	0.5044	6.31e-05
213696_s_at	MED8 TRIO	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	0.5043	6.33e-05
209015_x_at	TMPO	There are inite	0.3034	0.300-03
224944_at	DINIKI	DTTEN in face d marrier binner 1	-0.4982	8.01e-05
209019_s_at	CPD4	P I EIN-induced putative kinase I	0.49/4	8.280-03
213020_at	SDAC0	carbonic reductase 4	-0.4900	0.120.05
20/350 at	FIDTO	fibronectin laucine rich transmembrane protein 2	0.4945	9.25e 05
2045552at	BIVRA	hiliverdin reductase A	0.4921	000101
202163 s at	CNOT8	CCR4-NOT transcription complex subunit 8	-0.4906	000107
218458 at	GMCL1	germ cell-less homolog 1 (Dresophila)	-0.4900	000109
221737 at	GNA12	guanine nucleotide binding protein (G protein) alpha12	0.4896	000111
221753 at	SSH1	slingshot homolog 1 ( <i>Drosophila</i> )	0.4895	.000111
212430 at	RBM38	RNA-binding region (RNP1, RRM) containing 1	-0.4884	.000116
200943 at	HMGN1	high-mobility group nucleosome binding domain 1	-0.4884	.000116
222514 at	RRAGC	Ras-related GTP binding C	0.4881	.000117
200990 at	TRIM28	tripartite motif-containing 28	-0.4871	.000122
209832_s_at	CDT1	DNA replication factor	-0.4865	.000125
224504_s_at	MGC13125	hypothetical protein MGC13125	-0.4862	.000126
217785_s_at	YKT6	SNARE protein Ykt6	0.4861	.000126
210053_at	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)–associated factor, 100 kDa	-0.4853	.00013
226651_at	HOMER1	homer homolog 1 (Drosophila)	-0.4844	.000135
201885_s_at	CYB5R3	cytochrome b5 reductase 3	0.4843	.000135
208549_x_at	PTMA	prothymosin, alpha (gene sequence 28); similar toprothymosin alpha; hypothetical gene supported	-0.4839	.000137
205092	40V1	aldahuda avidasa 1	0 / 922	0001/1
209085_at	CAND1	cullin-associated and neddylation-dissociated 1	-0.4822	.000141
200030_at	Cilorf31	chromosome 11 open reading frame 31	-0.4820	000140
206157 at	PTY3	pentravin-related gene rapidly induced by II-1 beta	0.4807	.00014/
2001)/_at	SMPD1	sphingomyelin phosphodiesterase 1 ocid lysosomal (ocid sphingomyelinase)	0.4806	000154
209420_3_at	51411 D 1	full-length cDNA clone CL0BB0147H04 of neuroblastoma of <i>Hama satiens</i> (human)	-0.4772	000175
201930_at	MCM6	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog <i>S pambe</i> ) ( <i>S cerevisiae</i> )	-0.4768	000177
226099_at	FII 2	elongation factor RNA polymerase II 2	0.4749	00019
201051 at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family member A	-0 4744	000193
201185 at	HTRA1	HtrA serine pentidase 1	0.4742	000195
217843 s at	MED4	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	-0.4724	.000207
222036 s at	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	-0.4720	.00021
200668 s at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-0.4718	.000211
205207 at	IL6	interleukin 6 (interferon, beta 2)	0.4717	.000212
218420 s at	C13orf23	chromosome 13 open reading frame 23	-0.4697	.000228
226574 at	PSPC1; LOC374491	paraspeckle component 1; TPTE and PTEN homologous inositol lipid phosphatase pseudogene	-0.4697	.000228
202830_s at	SLC37A4	solute carrier family 37 (glycerol-6-phosphatetransporter), member 4	-0.4681	.000241
205129 at	NPM3	nucleophosmin/nucleoplasmin, 3	-0.4678	.000244
209897 s at	SLIT2	slit homolog 2 ( <i>Drosophila</i> )	0.4658	.000261
217872_at	PIH1D1	hypothetical protein FLJ20643	-0.4656	.000263
	RPUSD4	RNA pseudouridylate synthase domain containing 4	-0.4653	.000265
235706_at	CPM	carboxypeptidase M	0.4650	.000268
220750_s_at	LEPRE1	leucine proline-enriched proteoglycan (leprecan) 1	0.4648	.00027

Affy ID	Gene Symbol	Description	ρ	Р
200099_s_at	RPS3A	ribosomal protein S3A	-0.4636	.000282
204948_s_at	FST	follistatin	0.4635	.000283
204658_at		transformer-2 alpha	-0.4627	.00029
235138_at	PUM2	Pumilio homolog 2 (Drosophila)	-0.4624	.000294
221096_s_at	TMCO6	hypothetical protein PRO1580	-0.4619	.000298
222222_s_at	HOMER3	homer homolog 3 (Drosophild)	0.4615	.000302
231043_x_at	DI FKHC1	pleckstrin homology domain containing, family C (with FERM domain) member 1	-0.4014	.000303
217212_x_at	TMEM111	30-kDa protein	0.4613	000304
216232 s at	GCN1L1	GCN1 general control of amino acid synthesis 1–like 1 (veast)	-0.4612	.000305
226982_at	ELL2	elongation factor, RNA polymerase II, 2	0.4611	.000306
210416_s_at	CHEK2	CHK2 checkpoint homolog (S. pombe)	-0.4605	.000313
229663_at	LONPL	peroxisomal LON protease like	0.4600	.000318
213052_at	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	0.4587	.000333
208973_at	PRNPIP	prion protein interacting protein	0.4585	.000335
204009_s_at	KRAS	v-Ki- <i>ras2</i> Kirsten rat sarcoma viral oncogene homolog	-0.4582	.000339
223206_s_at	HSCARG	HSCARG protein	-0.4581	.00034
218848_at	THOC6	WD repeat domain 58	-0.4580	.000341
218448_at	C20orf11	chromosome 20 open reading frame 11	-0.45/3	.000348
211/29_x_at	DDY11	DEAD/H (Asp Clu Ala Asp/His) hay polypoptide 11 (CHI 1 like beliegee homolog. S. cerevicia)	0.4369	.000534
214150 x at	ATP6V0F1	ATPase H $_{\pm}$ transporting lysosomal 9 kDa V0 subunit e	0.4553	.000372
218407 x at	NENF	neuron-derived neurotrophic factor	0.4545	.000383
221641 s at	ACOT9	acvl-CoA thioesterase 9	0.4539	.000391
208804_s_at	SFRS6	splicing factor, arginine/serine-rich 6	-0.4530	.000402
200753_x_at	SFRS2	splicing factor, arginine/serine-rich 2	-0.4530	.000403
202330_s_at	UNG	uracil-DNA glycosylase	-0.4529	.000404
202164_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	-0.4527	.000407
224840_at	FKBP5	FK506 binding protein 5	-0.4525	.00041
208896_at	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-0.4523	.000412
204768_s_at	FEN1	flap structure–specific endonuclease 1	-0.4521	.000415
212593_s_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	-0.4515	.000423
218069_at	0110/	X1P3-transactivated protein A	-0.4504	.000439
221881_s_at	CLIC4 SMARCA5	chloride intracellular channel 4 SWU/SNE related matrix associated actin dependent regulator of abromatin, subfamily a member 5	0.4499	.000446
202303_x_at	DUM2	s wi/sivr-related, matrix-associated, actin-dependent regulator of circomatin, subtaining a, memoer s	-0.4490	.000431
213610 s at	KLHL23	kelch-like 23 (Drosophila)	-0.4494	000452
227740 at	UHMK1	U2AF homology motif (UHM) kinase 1	0.4489	.000461
201376_s_at	HNRPF	heterogeneous nuclear ribonucleoprotein F	-0.4488	.000463
201559_s_at	CLIC4	chloride intracellular channel 4	0.4486	.000465
57163_at	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)–like 1	0.4483	.00047
225563_at	PAN3	PABP1-dependent poly A-specific ribonuclease subunit PAN3	-0.4483	.00047
200956_s_at	SSRP1	structure-specific recognition protein 1	-0.4479	.000476
213329_at	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	0.4476	.00048
225391_at	LOC93622	hypothetical protein BC006130	-0.4474	.000485
21//84_at	YK16 TCIE2	SNARE protein Ykto	0.44/1	.00049
216262_s_at	IGIF2	r GrB-induced factor 2 (TALE family homeobox)	-0.4466	.00049/
202239_8_at	$D \cap I = 2$	polymerese (DNA directed) encilon 2 (p50 cubunit)	-0.440)	.000498
204819 at	FGD1	FYVE. RhoGEF and PH domain containing 1 (faciogenital dysplasia)	0 4464	0005
218298 s at	C14orf159	chromosome 14 open reading frame 159	-0.4462	.000504
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	0.4459	.000508
201035_s_at	HADH	L-3-hydroxyacyl–Coenzyme A dehydrogenase, short chain	-0.4458	.000511
210904_s_at	IL13RA1	interleukin 13 receptor, alpha 1	0.4442	.000537
202258_s_at		phosphonoformate immuno-associated protein 5	-0.4441	.000539
226912_at	ZDHHC23	zinc finger, DHHC-type containing 23	-0.4438	.000544
218168_s_at	CABC1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	-0.4436	.000548
228174_at	GOLGA1	Golgi autoantigen, golgin subfamily a, 1	-0.4428	.000562
200957_s_at	SSRP1	structure-specific recognition protein 1	-0.4422	.0005/3
232113_at	NDID2	Hypothetical gene supported by BX64/608	0.4421	.0005/6
219337_s_at	THV28	thumocite protein Thy28	0.4418	.000586
22.3711_s_at 212709_at	NUP160	nucleonorin 160 kDa	-0.4411	000594
200679 x at	HMGB1	high-mobility group box 1	-0.4409	.000598
222204_s at	RRN3	RRN3 RNA polymerase I transcription factor homolog (veast)	-0.4403	.000608
214882_s_at	SFRS2	splicing factor, arginine/serine-rich 2	-0.4403	.000608
208178_x_at	TRIO	triple functional domain (PTPRF interacting)	0.4401	.000614
213238_at	ATP10D	ATPase, class V, type 10D	0.4399	.000618
201450_s_at	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	-0.4398	.000619
201712_s_at	RANBP2	RAN binding protein 2	-0.4395	.000624
200977_s_at	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	0.4393	.000628
202948_at	ILIRI DCD (	interleukin 1 receptor, type 1	0.4390	.000635
203317_at	PSD4	pleckstrin and Sec/ domain containing 4	-0.4387	.000641

Affy ID	Gene Symbol	Description	ρ	Р
233364_s_at		Hypothetical gene supported by BX647608	0.4386	.000643
208795_s_at	MCM7	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	-0.4386	.000643
203231_s_at	ATXN1	ataxin 1	0.4382	.000651
208747_s_at	C1S	complement component 1, s subcomponent	0.4380	.000656
214109_at	LRBA	LPS-responsive vesicle trafficking, beach and anchor containing	-0.4377	.000662
213338_at	TMEM158	Ras-induced senescence 1	0.4374	.000668
224940_s_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	0.4374	.000669
207749_s_at	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	0.4372	.000673
203856_at	VRK1	vaccinia-related kinase 1	-0.4371	.000675
212603_at	MRPS31	mitochondrial ribosomal protein S31	-0.4368	.00068
212789_at	NCAPD3	KIAA0056 protein	-0.4366	.000685
2011/0_s_at	BHLHB2	basic helix-loop-helix domain containing, class B, 2	0.4364	.00069
202302_s_at	KSKC2	similar to splicing factor, arginine/serine-rich 4	-0.4363	.000692
212445_at	INDEAL2	idet coll autoentigen 1 60 kDa	-0.4362	.000694
20/949_s_at	MSH2	isiet cell autoantigen 1, 69 kL/a	-0.4360	.000699
209421_at	D474D1	DAZ associated protein 1	-0.4359	.0007
203229 s at	CLK2	CDC-like kinse 2	-0.4355	000707
213798 s at	CAP1	CAP adenylate cyclase_associated protein 1 (yeast)	0.4356	000708
216969 s at	KIF22	kinesin family member 22	-0.4355	00071
208908 s at	CAST	calpastatin	0.4353	000714
203388 at	ARRB2	arrestin, beta 2	-0.4351	00072
218714 at	PRR14	hypothetical protein MGC3121	-0.4342	.00074
212920 at	110011		-0.4338	.00075
217892 s at	LIMA1	epithelial protein lost in neoplasm beta	0.4337	.000751
215947_s_at		hypothetical protein FLJ14668	-0.4332	.000762
232524_x_at	ANAPC4	anaphase promoting complex subunit 4	-0.4330	.000767
39729_at	PRDX2	peroxiredoxin 2	-0.4328	.000771
241418_at		Hypothetical LOC344887	0.4326	.000778
200625_s_at	CAP1	CAP, adenylate cyclase–associated protein 1 (yeast)	0.4324	.000782
203729_at	EMP3	epithelial membrane protein 3	0.4323	.000786
227846_at	GPR	putative G protein coupled receptor	0.4322	.000787
231271_x_at	HSCARG	HSCARG protein	-0.4315	.000804
226405_s_at	ARRDC1	arrestin domain containing 1	-0.4315	.000805
223154_at	MRPL1	mitochondrial ribosomal protein L1	-0.4313	.000811
211506_s_at	IL8	interleukin 8	0.4311	.000815
226281_at	DNER	delta-notch–like EGF repeat-containing transmembrane	0.4310	.000816
221191_at		DKFZp434A0131 protein	-0.4308	.000821
211376_s_at	NSMCE4A	chromosome 10 open reading frame 86	-0.4308	.000821
205308_at	C8orf70	chromosome 8 open reading frame 70	0.4306	.000826
20623/_s_at	NRGI	neuregulin 1	0.4306	.000827
2426/3_at	1214 40102	KIA 40102	-0.4303	.000835
212056_at	NIAA0182	KIAA0182 protein	-0.4296	.000854
214/44_s_at	KPL25 FUID	alongation factor DNA nolumerase II 2	-0.4294	.000838
214440_at	WAPAI	KIAA0261	-0.4291	.000868
212207_at	RORI	receptor tyrosine kinase–like orphan receptor 1	0.4290	00087
214927 at	ITGRL1	integrin, beta-like 1 (with EGE-like repeat domains)	0.4290	00087
233167 at	SELO	selenoprotein O	-0.4288	.000876
210095 s at	IGFBP3	insulin-like growth factor binding protein 3	0.4286	.000879
204160 s at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	-0.4285	.000882
202013_s_at	EXT2	exostoses (multiple) 2	0.4281	.000893
224886_at	LOC339123	hypothetical LOC339123	-0.4279	.000899
224942_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	0.4279	.0009
202532_s_at	DHFR	dihydrofolate reductase	-0.4276	.000908
202326_at	EHMT2	euchromatic histone-lysine N-methyltransferase 2	-0.4275	.00091
204853_at	ORC2L	origin recognition complex, subunit 2-like (yeast)	-0.4273	.000916
218170_at	ISOC1	isochorismatase domain containing 1	-0.4266	.000937
232254_at	FBXO25	F-box protein 25	0.4260	.000954
218688_at	DAK	dihydroxyacetone kinase 2 homolog (yeast)	-0.4259	.000957
218028_at	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0.4258	.000959
212723_at	JMJD6	phosphatidylserine receptor	0.4257	.000962
209127_s_at	SART3	squamous cell carcinoma antigen recognized by T cells 3	-0.4257	.000962
202162_s_at	CNOT8	CCR4-NOT transcription complex, subunit 8	-0.4256	.000964
227129_x_at	LOC284701	hypothetical protein LOC284701	-0.4253	.000974
209143_s_at	CLNSIA; CLDNDI	chloride channel, nucleotide-sensitive, 1A; chromosome 3 open reading frame 4	-0.4253	.000975
2140/5_at	IVEIVE NDID2	neuron-derived neurotrophic factor	0.4249	.000985
222900_at	IVKIPS HOMEP1	nuclear receptor interacting protein 5 homer homolog 1 (Dreathild)	0.4248	.00099
210/99_8_at	110MERI	nomer nomolog i (Drosophua)	-0.4240	.000994

Table W4. Gene Ontology Categories Associated with Genes Whose Expression Profiles Correlated with NH (P < .01) Across the NCI-60 Panel of Cancer Cell Lines.

Categories Associated with Expression of Genes Negatively Correlated with NH (P < .01) GO Term Count % Р Category GOTERM\_BP\_ALL cellular metabolism 275 49.73 4.80e-08 GOTERM\_BP\_ALL macromolecule metabolism 197 35.62 8.32e-08 GOTERM\_BP\_ALL nucleobase, nucleoside, nucleotide and nucleic acid metabolism 185 33.45 2.96e-19 149 26.94 GOTERM BP ALL biopolymier metabolism 4.01e-09 regulation of biological process GOTERM BP ALL 131 23.69 .0104873 GOTERM\_BP\_ALL regulation of cellular process 128 23.15 .0027890 GOTERM\_BP\_ALL regulation of physiological process 128 23.15 5.97e-04 22.78 GOTERM BP ALL regulation of cellular physiological process 126 5.81e-04 1.95e-04 GOTERM\_BP\_ALL regulation of metabolism 96 17.36 regulation of cellular metabolism 95 6.59e-05 GOTERM BP ALL 17.18 GOTERM\_BP\_ALL 92 16.64 5.53e-05 transcription GOTERM\_BP\_ALL regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism 90 16.27 5.56e-05 GOTERM BP ALL transcription, DNA-dependent 87 15.73 3.80e-05 GOTERM\_BP\_ALL 86 15.55 1.68e-04 regulation of transcription GOTERM BP ALL regulation of transcription, DNA-dependent 83 15.01 7.26e-05 GOTERM\_BP\_ALL DNA metabolism 58 10.49 1.87e-10 GOTERM\_BP\_ALL RNA metabolism 50 9.04 1.14e-08 GOTERM\_BP\_ALL cell cvcle 48 8 68 6.20e-04GOTERM\_BP\_ALL RNA processing 47 2.27e-10 8.50 GOTERM BP ALL mRNA metabolism 36 6.51 4.95e-10 GOTERM\_BP\_ALL mRNA processing 31 5.61 1.13e-08 GOTERM\_BP\_ALL DNA replication 26 4.70 1.46e-07 25 GOTERM\_BP\_ALL RNA splicing 4 52 4.15e-07 GOTERM\_BP\_ALL 24 4.34 6.50e-04 response to endogenous stimulus GOTERM BP ALL response to DNA damage stimulus 24 4.34 4.14e-04 GOTERM\_BP\_ALL DNA repair 23 4.16 1.82e-04 22 GOTERM\_BP\_ALL chromosome organization and biogenesis 3.98 .0013376 GOTERM BP ALL chromosome organization and biogenesis (sensu Eukaryota) 20 3.62 .0023155 GOTERM\_BP\_ALL nuclear mRNA splicing, through spliceosome 20 3.62 1.71e-05 GOTERM BP ALL RNA splicing, through transesterification reactions with bulged adenosine as nucleophile 20 3.62 1.71e-05 GOTERM\_BP\_ALL RNA splicing, through transesterification reactions 20 3.62 1.71e-05 GOTERM\_BP\_ALL DNA packaging 18 3.25 .0017667 protein complex assembly 2.89 GOTERM\_BP\_ALL 16 .0468127 GOTERM\_BP\_ALL 16 2.89 .0229671 M phase GOTERM BP ALL establishment and/or maintenance of chromatin architecture 2.89 .0075817 16 GOTERM\_BP\_ALL DNA-dependent DNA replication 15 2.71 3.74e-05 GOTERM\_BP\_ALL chromatin assembly or disassembly 9 1.63 .0425323 9 GOTERM BP ALL ribosome biogenesis and assembly 1.63 .0425323 GOTERM\_BP\_ALL DNA recombination 8 1.45 .0060408 GOTERM\_BP\_ALL transcription initiation 7 1.27 .0226955 GOTERM\_BP\_ALL DNA replication initiation 7 1 27 9.09e-04 GOTERM\_BP\_ALL M phase of meiotic cell cycle 5 0.90 .0438018 .0308043 GOTERM BP ALL mRNA catabolism 5 0.90 GOTERM\_BP\_ALL DNA unwinding during replication 0.72 .0090748 4 GOTERM\_CC\_ALL 304 54.97 2.02e-12 intracellular GOTERM\_CC\_ALL organelle 282 50.99 2.02e-17 1.90e-17 GOTERM\_CC\_ALL intracellular organelle 282 50.99 GOTERM CC ALL membrane-bound organelle 259 46.84 2.70e-16 GOTERM\_CC\_ALL intracellular membrane-bound organelle 259 46.84 2.61e-16 GOTERM\_CC\_ALL 202 36.53 2.54e-19 nucleus GOTERM CC ALL protein complex 93 16.82 9.34e-05 GOTERM\_CC\_ALL intracellular non-membrane-bound organelle 68 12.30 .0014360 GOTERM CC ALL non-membrane-bound organelle 68 12.30 .0014360 GOTERM\_CC\_ALL mitochondrion 39 7.05 .0217935 GOTERM\_CC\_ALL 35 6.33 1.77e-05 ribonucleoprotein complex GOTERM\_CC\_ALL membrane-enclosed lumen 31 5.61 .0266555 GOTERM\_CC\_ALL organelle lumen 31 5.61 .0266555 GOTERM\_CC ALL 31 5.61 3.74e - 08chromosome GOTERM\_CC\_ALL nuclear lumen 27 4.88 .005185 GOTERM\_CC\_ALL nucleoplasm 18 3.25 .0267792 2.53 .0304751 GOTERM CC ALL ribosome 14 GOTERM\_CC\_ALL 3.90e-04 chromatin 14 2.53 GOTERM CC ALL nuclear chromosome 7 1.27 .0300376 GOTERM\_CC\_ALL condensed chromosome 5 0.90 .0186952 GOTERM\_CC\_ALL synaptic vesicle 4 0.72 .0413124 GOTERM\_CC\_ALL obsolete cellular component 4 0.72 .0413124 GOTERM CC ALL delta-DNA polymerase cofactor complex 3 0.54 .0243645 nucleic acid binding GOTERM\_MF\_ALL 153 27.67 8.89e-11 GOTERM\_MF\_ALL nucleotide binding 92 16.64 .0023895 92 GOTERM\_MF\_ALL DNA binding 16.64 7.93e-06 55 9.95 .0049911 GOTERM MF ALL transcription regulator activity

55

9.95

6.23e-09

GOTERM\_MF\_ALL

RNA binding

Categories Associated with Expression of Genes Negatively Correlated with NH (P < .01)

Category	GO Term	Count	%	Р
GOTERM_MF_ALL	ATPase activity	20	3.62	.0098998
GOTERM_MF_ALL	transcriptional activator activity	17	3.07	.0134395
GOTERM_MF_ALL	ATPase activity, coupled	16	2.89	.0496740
GOTERM_MF_ALL	structural constituent of ribosome	15	2.71	.0339051
GOTERM_MF_ALL	mRNA binding	8	1.45	1.73e-04
GOTERM_MF_ALL	acetyltransferase activity	7	1.27	.0203796
GOTERM_MF_ALL	chromatin binding	7	1.27	.0149992
GOTERM_MF_ALL	DNA-dependent ATPase activity	7	1.27	.0030113
GOTERM_MF_ALL	double-stranded DNA binding	5	0.90	.0259470
BIOCARTA	h_prc2Pathway: The PRC2 Complex Sets Long-term Gene Silencing Through Modification of Histone Tails	4	0.72	.0301009

Categories Associated with Expression of Genes Positively Correlated with NH (P < .01)

Category	Term	Count	%	Р
GOTERM_BP_ALL	cell communication	136	23.01	3.55e-05
GOTERM_BP_ALL	signal transduction	127	21.49	4.00e-05
GOTERM_BP_ALL	localization	117	19.80	3.79e-04
GOTERM_BP_ALL	establishment of localization	117	19.80	3.08e-04
GOTERM_BP_ALL	development	97	16.41	1.75e-09
GOTERM_BP_ALL	cell organization and biogenesis	73	12.35	1.07e-05
GOTERM_BP_ALL	cell adhesion	68	11.51	1.39e-19
GOTERM_BP_ALL	intracellular signaling cascade	52	8.80	5.60e-04
GOTERM_BP_ALL	negative regulation of biological process	46	7.78	3.08e-06
GOTERM_BP_ALL	negative regulation of cellular process	45	7.61	1.03e-06
GOTERM_BP_ALL	phosphorus metabolism	42	7.11	.0049447
GOTERM_BP_ALL	phosphate metabolism	42	7.11	.0049447
GOTERM_BP_ALL	negative regulation of physiological process	41	6.94	6.83e-06
GOTERM_BP_ALL	negative regulation of cellular physiological process	40	6.77	7.04e-06
GOTERM_BP_ALL	morphogenesis	39	6.60	3.21e-06
GOTERM_BP_ALL	positive regulation of biological process	35	5.92	2.68e-04
GOTERM_BP_ALL	death	32	5.41	6.70e-04
GOTERM_BP_ALL	organ development	32	5.41	1.34e-04
GOTERM_BP_ALL	cell death	31	5.25	.0012428
GOTERM_BP_ALL	positive regulation of cellular process	31	5.25	3.58e-04
GOTERM BP ALL	cellular localization	30	5.08	.0056816
GOTERM_BP_ALL	programmed cell death	30	5.08	.0014543
GOTERM BP ALL	apoptosis	30	5.08	.0013914
GOTERM BP ALL	establishment of cellular localization	29	4.91	.0092904
GOTERM BP ALL	intracellular transport	29	4.91	.0078798
GOTERM BP ALL	response to external stimulus	29	4.91	8.90e-04
GOTERM BP ALL	cell proliferation	28	4.74	.0032481
GOTERM BP ALL	locomotion	28	4.74	8.90e-10
GOTERM BP ALL	localization of cell	28	4.74	8.90e-10
GOTERM BP ALL	cell motility	28	4.74	8.90e-10
GOTERM BP ALL	cell-cell adhesion	28	4.74	2.52e-10
GOTERM BP ALL	cell differentiation	26	4.40	.0054730
GOTERM BP ALL	cellular morphogenesis	25	4.23	1.16e-06
GOTERM BP ALL	homophilic cell adhesion	25	4.23	7.28e-13
GOTERM BP ALL	system development	22	3.72	.0328183
GOTERM BP ALL	nervous system development	22	3.72	.0306327
GOTERM BP ALL	regulation of cell cycle	21	3.55	.0464284
GOTERM BP ALL	regulation of progression through cell cycle	21	3.55	.0456837
GOTERM BP ALL	response to abiotic stimulus	21	3.55	.0336106
GOTERM BP ALL	vesicle-mediated transport	21	3.55	.0040294
GOTERM BP ALL	protein kinase cascade	21	3.55	1.70e-04
GOTERM BP ALL	cytoskeleton organization and biogenesis	20	3.38	.0207670
GOTERM BP ALL	response to wounding	20	3 38	0189762
GOTERM BP ALL	regulation of programmed cell death	20	3.38	.0066011
GOTERM BP ALL	regulation of apoptosis	20	3 38	0062443
GOTERM BP ALL	regulation of cell proliferation	20	3 38	9 79e=04
GOTERM BP ALL	regulation of signal transduction	20	3 38	2.33e-05
GOTERM BP ALL	response to chemical stimulus	19	3 21	0315919
GOTERM BP ALL	cell migration	16	2 71	2 07e=07
GOTERM BP ALL	small GTPase-mediated signal transduction	15	2.54	0288176
COTERM BP ALL	arowth	15	2.54	0013231
COTERM BP ALL	cell growth	14	2.54	5 31e-04
COTERM BP ALL	regulation of cell size	14	2.37	5.31e-04
COTEDM BD ALL	organ morphogenetic	14	2.37	0215042
COTERM BD ALL	enzyme_linked receptor protein signaling pathway	13	2.20	0070196
COTEDM BD ALL	L rB kinace/NE rB coccade	13	2.20	1 12 04
COTEDM DD ALL	I-KD KIII35C/INF-KD Cascaue	13	2.20	0261415
GOTEKWI_DP_ALL	nomeostasis	12	2.05	.0201415

Categories Associated with Expression of Genes Positively Correlated with NH (P < .01) Term Count % Р Category GOTERM\_BP\_ALL regulation of I-κB kinase/NF-κB cascade 12 2.03 2.82e-05 GOTERM\_BP\_ALL secretory pathway 11 1.86 .0439977 GOTERM\_BP\_ALL actin filament-based process 11 1.86 .0229747 GOTERM\_BP\_ALL 1.86 .0206056 inorganic anion transport 11 GOTERM BP ALL actin cytoskeleton organization and biogenesis 11 1.86 .0151636 GOTERM\_BP\_ALL negative regulation of progression through cell cycle 11 1.86 .0145675 GOTERM\_BP\_ALL negative regulation of cell proliferation 11 1.86 .0123569 GOTERM\_BP\_ALL 1.86 .0104091 dephosphorylation 11 GOTERM\_BP\_ALL negative regulation of programmed cell death .0079367 11 1.86 GOTERM\_BP\_ALL negative regulation of apoptosis 1.86 .0075730 11 GOTERM\_BP\_ALL protein amino acid dephosphorylation 11 1.86 .0072224 regulation of growth GOTERM\_BP\_ALL 11 1.86 .0041368 GOTERM\_BP\_ALL antiapoptosis 11 1.86 .0027945 GOTERM\_BP\_ALL positive regulation of signal transduction 111.86 4.31e-04 GOTERM\_BP\_ALL cell homeostasis 10 1.69 .0347712 GOTERM\_BP\_ALL positive regulation of cell proliferation 10 1.69 .0154140 GOTERM\_BP\_ALL regulation of cell growth 10 1.69 .0075542 wound healing GOTERM BP ALL 10 1 69 0023127 GOTERM\_BP\_ALL positive regulation of I-KB kinase/NF-KB cascade 10 1.69 4.02e-04 GOTERM\_BP\_ALL skeletal development 9 1.52 .0398567 GOTERM BP ALL transmembrane receptor protein tyrosine kinase signaling pathway 9 1.52 .0370367 GOTERM\_BP\_ALL locomotory behavior 9 1.52 .0318068 9 GOTERM\_BP\_ALL 0260108 chemotaxis 1 52 GOTERM\_BP\_ALL 9 1.52 .0260108 taxis cell development GOTERM BP ALL 9 1.52 .0191954 9 GOTERM\_BP\_ALL phosphate transport 1.52 .0095473 9 GOTERM\_BP\_ALL neurogenesis 1.52 .0095473 GOTERM\_BP\_ALL 9 1.52 .0076198 muscle development GOTERM\_BP\_ALL regulation of body fluids 8 1.35 .0342186 GOTERM\_BP\_ALL neuron differentiation 8 1.35 .0227081 GOTERM\_BP\_ALL hemostasis 8 1.35 .0205718 GOTERM\_BP\_ALL Golgi vesicle transport 8 1.35 .0195580 GOTERM\_BP\_ALL 8 1.35 .0167270 coagulation GOTERM\_BP\_ALL 8 1.35 .0150089 blood coagulation GOTERM BP ALL regulation of development 8 1.35 .0082556 GOTERM\_BP\_ALL cell cycle arrest 8 1.35 .0029397 .0022683 GOTERM BP ALL ER to Golgi vesicle-mediated transport 8 1.35 GOTERM BP ALL 7 .0309592 neuron development 1.18 7 GOTERM\_BP\_ALL integrin-mediated signaling pathway 1.18 .0167194 GOTERM\_BP\_ALL blood vessel morphogenesis 7 1.18 .0157055 7 .0157055 GOTERM\_BP\_ALL blood vessel development 1.18 7 GOTERM\_BP\_ALL vasculature development 1.18 .0157055 7 .0129206 GOTERM BP ALL angiogenesis 1.18 GOTERM\_BP\_ALL aminoglycan metabolism 5 0.85 .0275782 GOTERM\_BP\_ALL glycosaminoglycan metabolism 5 0.85 .0254349 GOTERM\_BP\_ALL regulation of locomotion 5 0.85 .0094927 GOTERM\_BP\_ALL regulation of cell motility 5 0.85 .0094927 GOTERM BP ALL regulation of cell migration 5 0.85 0094927 GOTERM\_BP\_ALL positive regulation of development 5 0.85 .0064945 GOTERM\_BP\_ALL regulation of axonogenesis 3 0.51 .0367302 GOTERM BP ALL regulation of Ras protein signal transduction 3 0.51 .0367302 regulation of epithelial cell proliferation .0109926 GOTERM\_BP\_ALL 3 0.51 GOTERM\_BP\_ALL epithelial cell proliferation 3 0.51 .0109926 GOTERM\_BP\_ALL copper ion homeostasis 3 0.51 .0074668 GOTERM\_BP\_ALL positive regulation of epithelial cell proliferation 0.51 .0074668 3 GOTERM\_CC\_ALL cytoplasm 128 21.66 .0153518 9.37e-05 GOTERM\_CC\_ALL plasma membrane 79 13.37 GOTERM CC ALL extracellular region 70 11.84 6.77e-07 cytoskeleton GOTERM\_CC\_ALL 58 9.81 6.81e-08 GOTERM\_CC\_ALL intrinsic to plasma membrane 49 8.29 .0269904 49 8 2 9 0246202 GOTERM CC ALL integral to plasma membrane GOTERM\_CC\_ALL extracellular matrix 5.92 9.43e-11 35 GOTERM CC ALL extracellular matrix (sensu Metazoa) 35 5.92 5.21e-11 GOTERM\_CC\_ALL endoplasmic reticulum 33 5.58 1.66e-04 GOTERM\_CC\_ALL Golgi apparatus 24 4.06 .0121383 24 GOTERM\_CC\_ALL extracellular space 4.06 .0076828 GOTERM CC ALL actin cytoskeleton 18 3.05 3.01e-04 .0054881 GOTERM\_CC\_ALL microtubule cytoskeleton 17 2.88 GOTERM\_CC\_ALL microtubule 13 2.20 .0076041 GOTERM\_CC\_ALL vacuole 10 1.69 .0220081 10 1.69 4.10e-05 GOTERM CC ALL basement membrane GOTERM\_CC\_ALL collagen 8 1.35 1.15e-04

Categories Associated with Expression of Genes Positively Correlated with NH (P < .01)

Category	Term	Count	%	Р
GOTERM_CC_ALL	extrinsic to membrane	6	1.02	.0104410
GOTERM_CC_ALL	basal lamina	5	0.85	.0106105
GOTERM_CC_ALL	heterotrimeric G-protein complex	4	0.68	.0425953
GOTERM_CC_ALL	laminin complex	3	0.51	.0265177
GOTERM_CC_ALL	anchoring collagen	3	0.51	.0265177
GOTERM_CC_ALL	sheet-forming collagen	3	0.51	.0160747
GOTERM_CC_ALL	laminin-1	3	0.51	.0160747
GOTERM_MF_ALL	cation binding	121	20.47	1.18e-04
GOTERM_MF_ALL	hydrolase activity	73	12.35	.0283996
GOTERM_MF_ALL		/2	12.18	.008843/
GOTERM_MF_ALL	calcium fon binding	67	11.31	1.916-13
COTERM ME ALL	adenvl nucleotide binding	50	8 46	0218535
GOTERM ME ALL	ATP binding	50 47	7 95	0382664
GOTERM MF ALL	structural molecule activity	43	7.28	7.94e-04
GOTERM MF ALL	enzyme regulator activity	40	6.77	1.49e-06
GOTERM_MF_ALL	kinase activity	38	6.43	.0151332
GOTERM_MF_ALL	phosphotransferase activity, alcohol group as acceptor	31	5.25	.0185969
GOTERM_MF_ALL	cytoskeletal protein binding	29	4.91	1.21e-07
GOTERM_MF_ALL	protein kinase activity	28	4.74	.0117125
GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides	26	4.40	.0143863
GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	26	4.40	.0119770
GOTERM_MF_ALL	pyrophosphatase activity	26	4.40	.0112973
GOTERM_MF_ALL	nucleoside-triphosphatase activity	25	4.23	.0120011
GOTERM_MF_ALL	actin binding	22	3.72	1.61e-06
GOTERM_MF_ALL	protein serine/threonine kinase activity	21	3.55	.0095445
GOTERM_MF_ALL	phosphoric ester hydrolase activity	19	3.21	.0024685
GOTERM_MF_ALL	guanyl nucleotide binding	18	3.05	.0328025
GOTERM_MF_ALL	CTD as a second se	1/	2.88	6.99e-04
COTERM ME ALL	G I Pase regulator activity	16	2.71	.0068181
COTERM ME ALL	absolete molecular function	10	2.71	.005510/
GOTERM ME ALL	magnesium ion binding	15	2.54	0145196
GOTERM ME ALL	enzyme inhibitor activity	15	2.54	0075281
GOTERM MF ALL	phosphoprotein phosphatase activity	14	2.37	6.78e-04
GOTERM_MF_ALL	GTPase activity	13	2.20	.0014018
GOTERM_MF_ALL	extracellular matrix structural constituent	13	2.20	1.44e-05
GOTERM_MF_ALL	small GTPase regulator activity	12	2.03	.0093352
GOTERM_MF_ALL	pattern binding	12	2.03	1.62e-04
GOTERM_MF_ALL	polysaccharide binding	12	2.03	6.74e-05
GOTERM_MF_ALL	glycosaminoglycan binding	12	2.03	4.76e-05
GOTERM_MF_ALL	cAMP-dependent protein kinase activity	11	1.86	.0325455
GOTERM_MF_ALL	cyclic nucleotide-dependent protein kinase activity	11	1.86	.0325455
GOTERM_MF_ALL	protein kinase CK2 activity	11	1.86	.0288109
GOTERM_MF_ALL	protease inhibitor activity	10	1.69	.0189656
GOTERM_MF_ALL	endopeptidase inhibitor activity	10	1.69	.0182981
COTERM ME ALL	camodum onding	10	1.09	.0040855
COTERM ME ALL	benarin binding	10	1.09	1.43e_04
GOTERM ME ALL	nbosholinid hinding	9	1.52	0194455
GOTERM MF ALL	structural constituent of cytoskeleton	9	1.52	.0021281
GOTERM MF ALL	copper ion binding	7	1.18	.0135518
GOTERM_MF_ALL	prenylated protein tyrosine phosphatase activity	7	1.18	.0067538
GOTERM_MF_ALL	growth factor binding	7	1.18	.0039932
GOTERM_MF_ALL	kinase regulator activity	6	1.02	.0347643
GOTERM_MF_ALL	tubulin binding	5	0.85	.0403221
GOTERM_MF_ALL	dioxygenase activity	5	0.85	.0134921
GOTERM_MF_ALL	insulin-like growth factor binding	5	0.85	.0029651
GOTERM_MF_ALL	L-ascorbic acid binding	5	0.85	5.08e-04
GOTERM_MF_ALL	integrin binding	4	0.68	.0426353
GOTERM_MF_ALL	actin filament binding	4	0.68	.0043206
GOTERM_MF_ALL	low-density lipoprotein binding	3	0.51	.0283400
GOTERM_MF_ALL	Ras G I Pase activator activity	3	0.51	.0283400
COTEDM ME ALL	npoprotein receptor activity	) 2	0.51	.0151426
COTERM ME ALL	opcostatin-M receptor activity	2	0.31	.0115423
BBID	12 IL 6 type cytok-signal-transduct	ے لا	0.54	0402738
BIOCARTA	h prionPathway: Prion Pathway	4	0.68	0103901
BIOCARTA	h il10Pathway: IL-10 Anti-inflammatory Signaling Pathway	4	0.68	.0080196
BIOCARTA	h_reckPathway: Inhibition of Matrix Metalloproteinases	4	0.68	.0060027
BIOCARTA	h_akap13Pathway: Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation	3	0.51	.0290874
COG_KOG_ONTO LOGY	Cell division and chromosome partitioning	12	2.03	.0107010