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Global Comparative Gene Expression Analysis of Melanoma Patient Samples, Derived Cell Lines and Corresponding Tumor Xenografts

YAGUANG XI[1], **ADAM RIKER**[1], **LALITA SHEVDE-SAMANT**[1], **RAJEEV SAMANT**[1], **CHRISTOPHER MORRIS**[1], **ELAINE GAVIN**[1], **OYSTEIN FODSTAD**[1,2], and **JINGFANG JU**[1]

[1]Mitchell Cancer Institute-USA, Mobile, AL, 36688, U.S.A.

[2]Department of Tumor Biology, Norwegian Radium Hospital, Oslo, Norway

Abstract

Various in vitro and in vivo experimental models have been used for the discovery of genes and pathways involved in melanoma and other types of cancer. However, in many cases, the results from various tumor models failed to be validated successfully in clinical studies. Limited information is available on how closely these models reflect the in vivo physiological conditions. In this study, a comprehensive genomics approach was used to systematically compare the expression patterns of snap frozen samples obtained from patients with primary melanoma, lymph node metastasis, and distant metastases, and compare these patterns to those of their corresponding cell lines and tumor xenografts in nude mice. The GE Healthcare 20k human genome array was used and the expression data was normalized and analyzed using GeneSpring 7.2 software. Based on the expression analysis, the correlation rate between the snap frozen primary patient samples vs. derived cell lines was 66%, with 1687 differentially expressed genes. The correlation rate between the snap frozen primary patient samples and the tumor xenografts was 75%, with 1,374 differentially expressed genes, and the correlation rate comparing tumor xenografts to derived cell lines ranged between 58% and 84%. These results demonstrated significant gene expression differences between tumor materials with different in vitro and in vivo growth microenvironments. Such studies can help us to distinguish between genes up- or down-regulated as a result of the microenvironment and those stably expressed independently of the tumor milieu. With the extensive use of cell lines and xenografts in cancer research, the information obtained using our approach may help to better interpret results generated from different tumor models by understanding common differences, as well as similarities at the gene expression level, information that may have important practical and biological implications.

Keywords

Melanoma; expression profiling; connexin 43; metastasis

The mortality rate of melanoma patients is still on the rise despite extensive research efforts. Recent technologies applying high throughput genomics to cancer research have been successfully utilized in melanoma research, identifying key molecular gene targets such as microphthalmia-associated transcription factor (MITF), v-raf murine sarcoma viral oncogene homolog B1(BRAF), and neural precursor cell expressed, developmentally down-

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Correspondence to: Jingfang Ju, Ph.D., Head, Cancer Genomics Laboratory, Assistant Professor of Pharmacology and Medicine, Mitchell Cancer Institute, MSB2316, 307 N. University Blvd., Mobile, AL 36688, U.S.A. Tel: +1 251 460 7393, Fax: +1 251 460 6994, jju@usouthal.edu.

regulated 9 (NEDD9) (1-5). The molecular and cellular mechanisms of many genes have been successfully validated *in vivo*. However, in other cases, the functional significance of such targets has failed to be confirmed *in vivo*, despite a strong *in vitro* phenotype. This may reflect the intrinsic and/or extrinsic differences in some tumor models used for such studies. In the case of melanoma, it is known that the disease development not only involves genetic and epigenetic changes that take place within the cell, but also involves processes determined collectively by tumor micro-environmental factors, including cell-cell interactions with a plethora of surrounding stromal elements. Currently, very limited information is available in regard to the distinct genetic and epigenetic mechanisms of gene regulation and expression in these models.

Over the years, cancer biologists have utilized many different tumor models in order to gain an improved understanding of the processes involved in human cancer. One of the most important sources of *in vitro* models that is still in use today is the NCI-60 cell line panel, used for drug screening, target discovery and validation (6-13). However, in many cases, the functional significance of these genes found *in vitro* is poorly consistent with those identified in *in vivo* models. It is well-known that the tumor micro-environment can have a tremendous influence upon gene expression (14). Culture conditions and long-term cell passaging are known to greatly change the gene expression patterns for such artificial environments (15, 16). Currently, there is a lack of systematic analysis of the differences among the available research models that are in use. In many cases, the desired phenotype cannot be replicated *in vivo* due to the intrinsic differences in the model system. Therefore, it is important to understand the fundamental differences of tumor models in different situations in order to inform and guide gene targets and validation efforts.

To systematically address this issue, a comprehensive gene expression profiling-based analysis was employed to investigate the gene expression differences utilizing melanoma as a model system. This is an ideal system for such examination due to the extensive biobanking efforts of the surgical oncologists in obtaining freshly procured samples followed by immediate cryopreservation. Additionally, an attempt was made to grow and expand daughter melanoma cell lines *in vitro* whenever enough tissue was available. Utilizing these cell lines, further experiments were performed in several xenograft models, comparing the results of each of these tissue samples for evidence of differences in gene expression. In addition, to further validate this approach, a well characterized pair of melanoma cell lines (FEMX-1 and FEMX-V) with different *in vivo* metastatic potentials and their corresponding tumor xenografts were also used (17).

Materials and Methods

Tumor specimens

Surgically procured tumor samples from patients with primary cutaneous and metastatic melanoma were obtained under an Investigational Review Board (IRB) approved tissue procurement protocol (MCC#13448, IRB#101751; PSM# 990914-JM, 020318-JM). The tumor specimens were macrodissected and cryopreserved within 5 minutes, being careful to avoid any surrounding, non-neoplastic stromal tissue. All the samples were cryopreserved in liquid nitrogen and stored within the Tissue Procurement Laboratory of the Moffitt Cancer Center, securely de-identified through a centralized database.

Cell lines and tissue culture

Freshly excised melanoma samples were placed into culture media RPMI 1640 with 5% FCS. The expansion of daughter cell lines was performed utilizing previously published techniques (18, 19). All the cell lines were split and serially passaged less than 10 times and characterized by flow cytometry and/or cytospin preparation for cellular confirmation of melanoma cell purity (data not shown). Three cell lines were used in this study, one was derived from a primary melanoma, one from a brain metastasis and one from a distant subcutaneous leg metastasis. One of the best characterized melanoma cell lines, FEMX-I, and its derivative, FEMX-V. which were established and described previously were subsequently investigated (17). These paired cell lines were derived a decade ago from the same patient with lymphnode metastatic melanoma. FEMX-I was the first generation of the clonal variants selected by *in vivo* experiments that exhibited a strongly aggressive capability of metastasis. FEMX-V was derived from the fifth consecutive generation of metastases developing after injection of isolated cells into a recipient mouse. The FEMX-V cells have no metastatic potential (17). The molecular and cellular mechanisms underlying this change in metastatic capacity have not been systematically investigated, but with high throughput gene expression analysis this is now possible. A comprehensive gene expression analysis of the FEMX-I and FEMX-V cells grown *in vitro* and xenografts in nude mice was performed. These cell lines were incubated at 37°C in a humidified atmosphere of 5% CO_2, in RPMI 1640 (Invitrogen Inc. Carlsbad, CA, USA) supplemented with 10% fetal bovine serum (HyClone. Logan, UT, USA). The xenografts were grown as described previously (20). In brief, the cells were detached at 80-90% confluence with 2 mM EDTA or trypsin-EDTA (0.1% trypsin and 2mM EDTA) solution, washed with calcium- and magnesium-free Dulbecco's phosphate-buffered saline solution (CMF-DPBS), counted using a hemacytometer and resuspended in ice-cold Hank's balanced salt solution (HBSS) to a final concentration of 10^7 cells/ml. The cells, 1×10^6 (0.1 ml), were injected subcutaneously into the scapular region of 3 weeks old, female athymic mice (Harlan Sprague-Dawley, Indianapolis, IN, USA), using a 27 gauge needle affixed to a 1 cc syringe. The tumor size was measured weekly by Vernier calipers. After the mean tumor diameter reached 10 mm, the mice were euthanized and the tumors were removed for further analysis. The animals were maintained under the guidelines of the National Institute of Health and the University of South Alabama. All the protocols were approved by the Institutional Animal Care and Use Committee of the University of South Alabama. Food and water were provided *ad libitum*.

RNA isolation and purification

The samples were homogenized in Trizol (Invitrogen Inc.). The 100 Ìl of 1-bromo-3-chloropropane (BCP) solution (Molecular Research Center, Inc., Cincinnati, OH, USA) was added to the samples. After 2 minutes vortexing, the samples were incubated for 3 minutes at room temperature. The upper aqueous phase containing the RNA from each sample was transferred to a new tube and centrifuged at 14,000 rpm for 7 minutes. Equal volume of 100% isopropanol (Sigma, St. Louis, MO, USA) was added and precipitation was performed at −80°C for 60 minutes. After centrifuging at 14,000 rpm for 7 minutes at 4°C, the supernatant was removed and 1 ml of 75% ethanol was added for washing. The pellet of each sample was air dried and eluted with nuclease-free water. The samples were treated with DNase to avoid potential DNA contamination, 15 Ìl DNase treatment mix (2 Ìl RQ1 RNase-Free DNase, 11 Ìl RQ1 DNase 10X Reaction Buffer and 2 Ìl RNasin Plus RNase Inhibitor, Promega, Madison, WI, USA) was incubated with each sample in 100 Ìl volume at 37°C for 30 minutes. Then 115 Ìl UltraPureì phenol: chloroform: isoamyl alcohol (25:24:1, Invitrogen Inc.) was added. After 2 minutes of vortexing, the samples were centrifuged at 14,000 rpm for 7 minutes. The upper aqueous phase was carefully taken out and mixed with 2 volumes of 100% ethanol and 1/10 volume of 3M sodium scetate pH 5.5 (Ambion Inc., Austin, TX, USA). The samples were held at room temperature for 15-30 minutes, then centrifuged at 14,000 rpm for 7 minutes. After removing the supernatant, 1 ml of 75% ethanol was added for washing, centrifuging was repeated and then the pellets were air dried. The samples were dissolved in nuclease-free water. A NanoDrop ND-100 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA) was used to determine the concentration of all the samples.

Gene expression analysis via microarray

The CodeLink UniSet Human 20 K Oligo Bioarray (Amersham Biosciences, NJ, USA), containing approximately 20,289 gene probes, was used to generate the gene expression profiles for all the samples examined. The procedure has been described in detail previously (21, 22). In brief, double-stranded cDNAs were generated using 2 Ìg of total RNA from each sample. All the reagents and protocols were provided by GE Healthcare/Amersham Biosciences except for special indication. After purification, the double-stranded cDNAs were used as templates to generate cRNA *via* an *in vitro* transcription reaction using T7 RNA polymerase and biotin-11-UTP (Perkin-Elmer, Boston, MA, USA). The biotin-labeled cRNA (10 Ìg) was fragmented and hybridized to the CodeLink UniSet Human 20 K Oligo Bioarray. The arrays were stained with Cy5-streptavadin. After washing, the dried slides were scanned by Axon GenePix Professional 4200A microarray scanner under Genepix Pro 5.1 software (Molecular Devices Corporation, Sunnyvale, CA, USA). The images were grided by Codelink 4.1 software (GE-Healthcare/Amersham Biosciences) and exported to GeneSpring Software 7.2 (Agilent, Palo Alto, CA, USA).

GeneSpring software allows multifilter comparisons using data from different experiments to perform the normalization, the generation of restriction lists and the functional classification of the differentially expressed genes. Utilizing the Cross-Gene Error Model, normalization was applied in two steps: “per chip normalization” in which each measurement was divided by the 50th percentile of all measurements in its array and “per gene normalization” in which all the samples were normalized against the specific samples (controls). The data was filtered by flags. The expression profiles of the different groups were compared using one-way ANOVA with cut-off $p<0.05$. Comparisons of the gene lists across the different groups were performed using Venn diagrams and clustering function using Genespring.

Statistical analysis

All the statistical analyses were performed by JMP 6.0 software (SAS Institute Inc. Cary, NC, USA). All the normalized data from tumor tissue, cell lines and tumor xenografts were analyzed to determine the correlation coefficient of expression. P-values of <0.05 were interpreted as statistically significant.

Results

Clustering analysis of expression profiles among three sets of melanoma models

The genes clustered from the primary melanoma models (snap frozen, xenograft and cell line) are shown in Figure 1A. Gene clustering analysis showed that the expression profiles of the melanoma cells and those from human xenografts had more similarities in gene expression compared to the freshly procured tumor samples. Venn diagram analysis (Figure 1B) was utilized to discover the overlapping and unique gene sets among the three samples. Between the melanoma xenografts and the snap frozen tissues 5,135 overlapping genes were found and between the melanoma tumor xenografts and the cell lines8,412 overlapping genes were found. The clustering analysis of the models generated from the brain melanoma metastasis (Figure 2A) and Venn diagram analysis (Figure 2B) were also obtained. The clustering analysis showed that the cell lines and the xenografts had more similarities than the original tumor sample. There were 8,151 overlapping genes between the melanoma xenograft and the snap frozen tissues and 8,347 overlapping genes between melanoma tumor xenografts and cell lines. With the models from the distant (leg) metastasis, the clustering analysis (Figure 3A) showed a close similarity between the cell lines and the xenografts compared to the profiles of the melanoma tissue samples. The Venn diagram analysis (Figure 3B) with the distant metastasis model (snap frozen tissue, derived cell line and xenograft) showed 7,737 overlapping genes between the melanoma xenografts and the snap frozen tissues and 7,404 overlapping genes between the melanoma tumor xenografts and the cell lines.

Correlations analysis based on global gene expression profiles

Next, the expression profiles were compared between the snap frozen surgical samples and their derived cell lines and the tumor xenografts based on global gene expression profiles. The weakest correlation was observed with the cell lines and snap frozen surgical tissue samples, having an overall correlation coefficient of r^2=0.59 (Figure 4A). The expression profiles between the cell lines and the corresponding tumor xenografts had a correlation coefficient of r^2=0.75, based upon the global gene expression profiles, which was the strongest correlation among the different comparisons (Figure 4B). The correlation between the expression profiles of the snap frozen tissue and the xenograft was r^2=0.64 (Figure 4C).

Correlations analysis based on overlapping gene expression profiles

Correlation analysis was also performed based on all the overlapping genes (Figure 5). The correlation coefficient between the melanoma snap frozen tissues and its derived cell lines was r^2=0.61 (Figure 5A). The correlation coefficient between the xenograft and the cell line was r^2=0.77 (Figure 5B). The correlation coefficient between the tissue and the cell line was r^2=0.67 (Figure 5C).

Validation of prediction models using cell lines and xenografts

Clustering analysis was performed between the FEMX-I and FEMX-V cell lines and their xenografts (Figure 6A and 6B). Venn diagram analysis was conducted and showed that there were 367 differentially regulated genes in the FEMX-I and FEMX-V cells (Table II). In contrast, 763 genes were altered in the corresponding tumor xenografts. A Venn diagram shows 110 overlapping genes (Figure 6B, Table I). Among these, the tumor susceptibility gene 101 (TSG101) was up-regulated in both model systems. There were 653 non-overlapping genes in the xenografts that were uniquely expressed (Table III). Among these, gap junction protein, alpha 1 (connexin 43), was over-expressed >400-fold in the FEMX-I tumor xenografts compared to the FEMX-V tumor xenografts. However, this gene was not found to be significantly different in gene expression for the daughter cell lines.

Discussion

In this study, melanoma was used as a model system to systematically investigate the expression differences among snap frozen melanoma specimens, its derived primary culture cell lines and tumor xenografts by high throughput gene expression profiling analysis. Some genes those were concordant in all the models and many other genes that were differentially regulated were identified. Based on the clustering analysis, the expression profiles of the melanoma cell lines and the xenografts had more similarities than the profile of the snap frozen tumor tissue (Figures 1-3). It may be due to the heterogeneity of the tumor tissue despite the fact that over 90% of the cells were confirmed to be melanoma. This may also reflect the true intrinsic differences of gene expression between *in vitro* and *in vivo* models. Correlation analysis revealed that the best correlation was between the cell lines and the xenografts (Figures 4B and 5B). The correlation between the cell lines and the tumor tissues was the weakest among the three comparisons (Figures 4A and 5A). A fairly high degree of gene concordance was identified between the samples, ranging from 50-80% which may provide a selection of genes for careful examination in the future for clinical correlation with patient outcomes.

To further validate this approach, a pair of well characterized melanoma cell lines FEMX-I and FEMX-V were involved this study (17). The comparison of genes expression levels between their cultured cell lines and established corresponding tumor xenografts were analyzed base on the genes profiling. No significant differences in cellular proliferation, motility, migration or invasive capacity were identified under normal culture conditions. This may reflect differences of the influence of the tumor microenvironment *in vivo* and the unique properties of intercellular communication during the process of tumor cell proliferation and metastasis. In order to discover genes that may be responsible for such differences, the expression profiles of the melanoma cells and the tumor xenografts. Our data revealed that there were only 101 overlapping genes between the xenografts and the cell lines (Table I), with 239 differentially expressed genes in the cell lines (Table II) and 553 uniquely expressed genes in the xenografts (Table III). Many of these genes function as cell adhesion molecules such as JAM3, connexin-43 and growth factor binding proteins such as FIBP and IGFBP-5. Someof these genes may contribute to the phenotypic differences *in vivo* in terms of metastatic potential. Among these genes, connexin-43 expression was found to be no different between the two cell lines, however, it was over expressed over 400-fold in the metastatic tumor xenografts (Table III). Adhesion to vascular endothelium is a crucial first step in the colonization of select target organs by blood-borne cancer cells, and connexin-43 appears to represent an important gap junction protein, having a possible further function in angiogenesis and metastasis in melanoma, glioma, colon, lung and breast cancer (23-28). It has also been suggested that gap junction proteins such as connexin-43 may contribute to a more aggressive tumor cell phenotype *via* the loss of normal homeostatic growth regulation. A further understanding of this mechanism may provide new insights into the pathogenesis of human melanoma (29, 30). Thus, the high *in vivo* expression of connexin-43 in FEMX-I compared to FEMX-V tumors may reflect the differences in metastatic capacity. These examples demonstrate how such models may be used for gene profiling studies to identify progression-associated genes in melanoma. Furthermore it may help us to distinguish between genes expressed as a result of interactions within the microenvironment in which the cells grow. In this regard, novel genomic approaches provide a unique platform to explore genes that may play a key role in melanoma tumorigenesis and metastasis, possibly leading to targeted therapeutic approaches and gene discovery in melanoma research.

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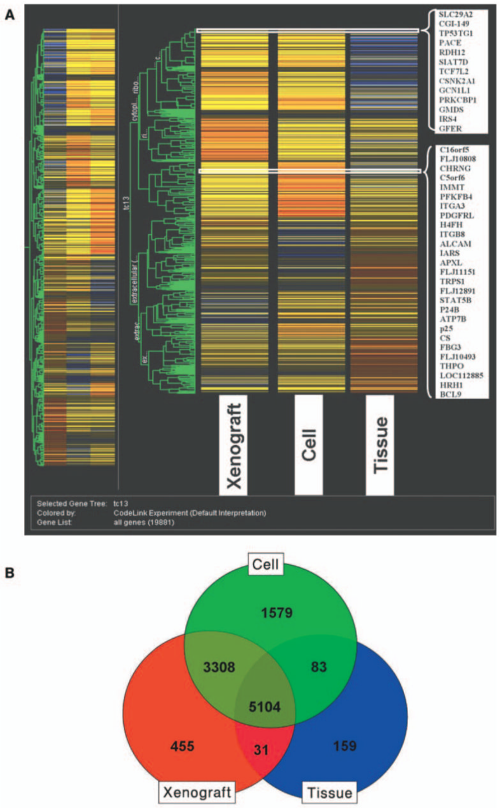


Figure 1.

Clustering analysis of expression of snap frozen primary melanoma, its derived cell line and tumor xenograft (A). The data was filtered by flags. The expression profiles of the different groups were compared using one-way ANOVA with cut-off p<0.05. Comparisons of gene lists across different groups were performed using Venn diagrams and clustering function using Genespring 7.2 (B).

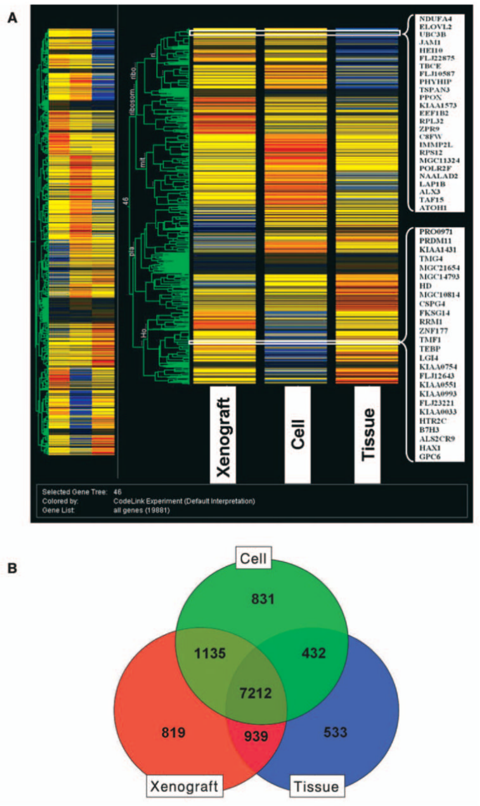


Figure 2.

Clustering analysis of expression of snap frozen brain metastatic melanoma, its derived cell line and tumor xenograft (A). The data was filtered by flags. The expression profiles of the different groups were compared using one-way ANOVA with cut-off p<0.05. Comparisons of gene lists across different groups were performed using Venn diagrams and clustering function using Genespring 7.2 (B).

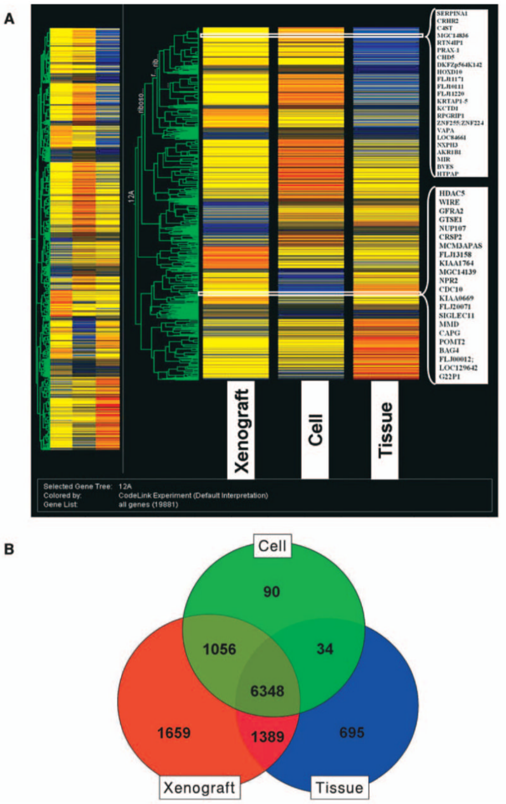


Figure 3.

Clustering analysis of expression of snap frozen distant (leg) metastatic melanoma, its derived cell line and tumor xenograft (A). The data was filtered by flags. The expression profiles of the different groups were compared using one-way ANOVA with cut-off $p<0.05$. Comparisons of gene lists across different groups were performed using Venn diagrams and clustering function using Genespring 7.2 (B).

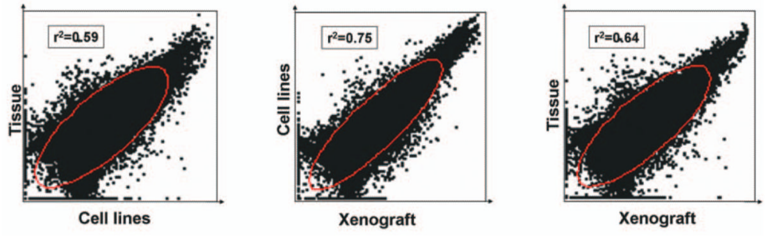


Figure 4.
Correlation coefficient analysis of the expression of all normalized data from tumor tissue, cell lines and tumor xenografts. Statistical analysis was performed using JMP 6.0 software (SAS Institute Inc. Cary, NC, USA). P-values of <0.05 were interpreted as statistically significant.

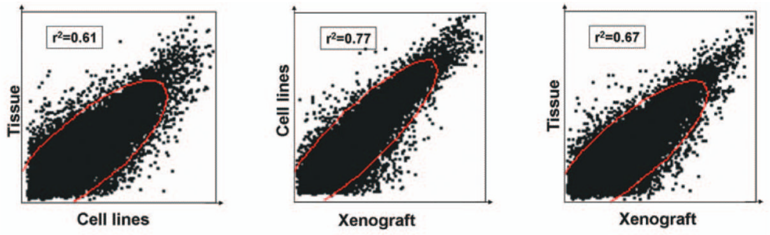
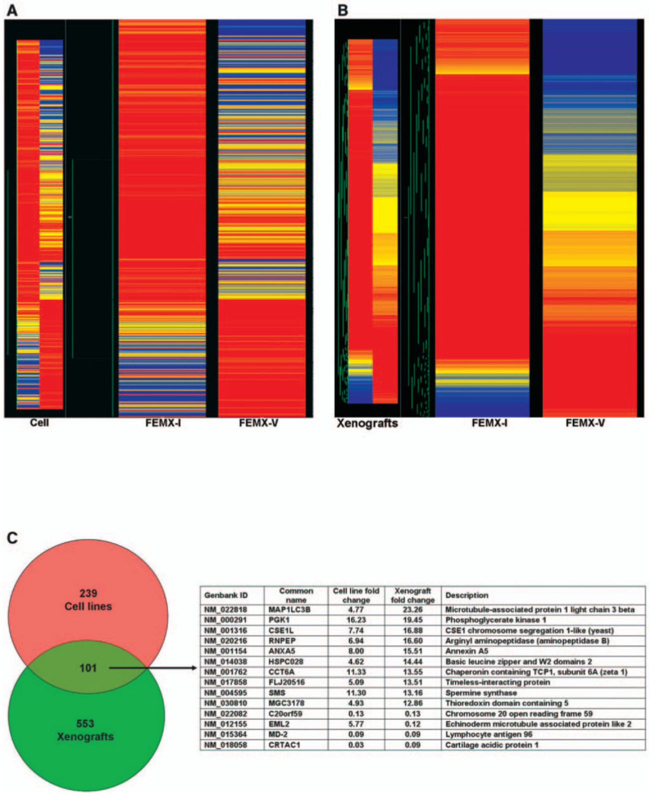


Figure 5.

Correlation coefficient analysis of the expression of all over-lapping genes from tumor tissue, cell lines and tumor xenografts. Statistical analysis was performed using JMP 6.0 software (SAS Institute Inc. Cary, NC, USA). P-values of <0.05 were interpreted as statistically significant.



Genbank ID	Common name	Cell line fold change	Xenograft fold change	Description
NM_022818	MAP1LC3B	4.77	23.26	Microtubule-associated protein 1 light chain 3 beta
NM_000291	PGK1	16.23	19.45	Phosphoglycerate kinase 1
NM_001316	CSE1L	7.74	16.88	CSE1 chromosome segregation 1-like (yeast)
NM_020216	RNPEP	6.94	16.60	Arginyl aminopeptidase (aminopeptidase B)
NM_001154	ANXA5	8.00	15.51	Annexin A5
NM_014038	HSPC028	4.62	14.44	Basic leucine zipper and W2 domains 2
NM_001762	CCT6A	11.33	13.55	Chaperonin containing TCP1, subunit 6A (zeta 1)
NM_017858	FLJ20516	5.09	13.51	Timeless-interacting protein
NM_004595	SMS	11.30	13.16	Spermine synthase
NM_030810	MGC3178	4.93	12.86	Thioredoxin domain containing 5
NM_022082	C20orf59	0.13	0.13	Chromosome 20 open reading frame 59
NM_012155	EML2	5.77	0.12	Echinoderm microtubule associated protein like 2
NM_015364	MD-2	0.09	0.09	Lymphocyte antigen 96
NM_018058	CRTAC1	0.03	0.09	Cartilage acidic protein 1

Figure 6.

Clustering analysis of expression of melanoma cell lines FEMX-I and FEMX-V and their derived tumor xenografts (A). The data was filtered by flags. The expression profiles of the different groups were compared using one-way ANOVA with cut-off $p<0.05$. Comparisons of gene lists across different groups were performed using Venn diagrams and clustering function using Genespring 7.2 (B).

Table I

Overlapping differentially regulated genes, FEMX-I and FEMX-V vs. the derived tumor xenografts

GenBank ID	Common name	Xenograft fold change	Cell line fold change	Description
Up-regulated				
NM_003752	EIF3S8	51.96	53.86	Eukaryotic translation initiation factor 3, subunit 8, 110 kDa
NM_000181	GUSB	47.20	11.92	Glucuronidase, beta
NM_006111	ACAA2	40.84	11.94	Acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)
NM_001416	EIF4A1	32.61	5.60	Eukaryotic translation initiation factor 4A, isoform 1
AB014540	KIAA0640	31.32	4.98	SWAP-70 protein
NM_000967	RPL3	31.15	6.48	Ribosomal protein L3
NM_004559	NSEP1	30.48	5.75	Nuclease sensitive element binding protein 1
NM_003405	YWHAH	29.89	15.51	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
NM_002136	HNRPA1	25.64	12.66	Heterogeneous nuclear ribonucleoprotein A1
NM_001402	EEF1A1	23.53	23.74	Eukaryotic translation elongation factor 1 alpha 1
NM_022818	MAP1LC3B	23.26	4.77	Microtubule-associated protein 1 light chain 3 beta
NM_024057	MGC5585	22.39	4.94	Nucleoporin Nup37
NM_017812	FLJ20420	20.99	5.42	Coiled-coil-helix-coiled-coil-helix domain containing 3
NM_000291	PGK1	19.45	16.23	Phosphoglycerate kinase 1
NM_003418	ZNF9	19.43	5.46	Zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)
NM_001316	CSE1L	16.88	7.74	CSE1 chromosome segregation 1-like (yeast)
NM_020216	RNPEP	16.60	6.94	Arginyl aminopeptidase (aminopeptidase B)
BC008861	ATP6D	16.24	4.77	Atpase, H+ transporting, lysosomal 38 kDa, V0 subunit d isoform 1
NM_000183	HADHB	15.98	6.03	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
NM_001154	ANXA5	15.51	8.00	Annexin A5
AL137681	EIF4A2	14.67	10.06	Eukaryotic initiation factor 4AII, unspliced; *Homo sapiens* mrna; cdna dkfzp434m0326 (from clone dkfzp434m0326); partial cds.
BC021714	PPFIBP2	14.47	6.97	PTPRF interacting protein, binding protein 2 (liprin beta 2)
NM_014038	HSPC028	14.44	4.62	Basic leucine zipper and W2 domains 2
NM_006070	TFG	14.43	10.61	TRK-fused gene
NM_001762	CCT6A	13.55	11.33	Chaperonin containing TCP1, subunit 6A (zeta 1)

GenBank ID	Common name	Xenograft fold change	Cell line fold change	Description
NM_017858	FLJ20516	13.51	5.09	Timeless-interacting protein
NM_004595	SMS	13.16	11.30	Spermine synthase
NM_030810	MGC3178	12.86	4.93	Thioredoxin domain containing 5
AF134802	CFL2	12.40	5.21	Cofilin 2 (muscle)
NM_000182	HADHA	12.38	6.62	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
NM_016359	ANKT	12.36	11.72	Nucleolar and spindle associated protein 1
NM_003142	SSB	11.98	5.77	Sjogren syndrome antigen B (autoantigen La)
NM_014309	RBM9	11.73	9.41	RNA binding motif protein 9
NM_002847	PTPRN2	11.72	6.16	Protein tyrosine phosphatase, receptor type, N polypeptide 2
NM_033317	ZD52F10	11.50	6.69	Hypothetical gene ZD52F10
NM_006743	RBM3	10.81	5.46	RNA binding motif protein 3
NM_015679	CLONE24922	10.55	6.87	Trub pseudouridine (psi) synthase homolog 2 (*E. Coli*)
NM_003819	PABPC4	9.93	6.50	Poly(A) binding protein, cytoplasmic 4 (inducible form)
NM_001634	AMD1	9.77	5.63	Adenosylmethionine decarboxylase 1
NM_006904	PRKDC	9.51	5.94	Protein kinase, DNA-activated, catalytic polypeptide
NM_022874	SMN1;SMN2	9.44	4.57	Survival of motor neuron 1, telomeric
NM_014062	ART-4	9.40	9.49	Likely ortholog of mouse nin one binding protein
NM_018472	HT011	9.38	5.65	Uncharacterized hypothalamus protein HT011
NM_022337	RAB38	9.19	5.37	RAB38, member RAS oncogene family
NM_012470	TRN-SR	9.06	4.52	Transportin 3
NM_014713	LAPTM4A	8.91	4.85	Lysosomal-associated protein transmembrane 4 alpha
AB037716	KIAA1295;FLJ20831	8.87	5.63	KIAA1295 protein
NM_018206	VPS35	8.83	11.36	Vacuolar protein sorting 35 (yeast)
NM_004125	GNG10	8.76	5.07	Guanine nucleotide binding protein (G protein), gamma 10
NM_006017	PROML1	8.73	9.62	Prominin 1
NM_021105	PLSCR1	8.41	9.49	Phospholipid scramblase 1
NM_031844	HNRPU	8.14	7.20	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
NM_002080	GOT2	8.10	25.65	Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
NM_016308	UMP-CMPK	7.68	5.82	UMP-CMP kinase
NM_000520	HEXA	7.29	7.95	Hexosaminidase A (alpha polypeptide)

GenBank ID	Common name	Xenograft fold change	Cell line fold change	Description
NM_004046	ATP5A1	7.14	19.12	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
NM_004868	GPSN2	6.98	5.79	Glycoprotein, synaptic 2
NM_001418	EIF4G2	6.82	24.72	Eukaryotic translation initiation factor 4 gamma, 2
NM_016397	TH1L	6.77	5.82	TH1-like (Drosophila)
AK098818	FLJ25952	6.75	15.21	Hypothetical protein FLJ25952
NM_005704	PTPRU	6.53	14.41	Protein tyrosine phosphatase, receptor type, U
L29065		6.51	5.78	Human DNA-binding protein A gene, exon 2.
NM_024666	FLJ11506	6.46	11.13	Hypothetical protein FLJ11506
NM_001881	CREM	6.44	8.66	Camp responsive element modulator
NM_005348	HSPCA	6.19	18.43	Heat shock 90 kDa protein 1, alpha
AB037723	ODZ4	6.15	6.52	Odd Oz/ten-m homolog 4
NM_022145	FKSG14	6.00	6.91	Leucine zipper protein FKSG14
NM_002079	GOT1	5.96	7.19	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
NM_019006	AWP1	5.87	8.21	Protein associated with PRK1
NM_024306	FAAH	5.86	12.89	Fatty acid 2-hydroxylase
NM_001908	CTSB	5.46	4.93	Cathepsin B
Down-regulated				
NM_017863	FLJ20527	−100.00	−46.08	Hypothetical protein FLJ20527
AB011538	SLIT3	−99.01	−7.75	Slit homolog 3 (Drosophila)
NM_004106	FCER1G	−90.91	−75.19	Fc fragment of ige, high affinity I, receptor for; gamma polypeptide
NM_003592	CUL1	−71.43	10.92	Cullin 1
NM_016608	ALEX1	−48.54	−38.91	ALEX1 protein
NM_002961	S100A4	−45.25	−6.06	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
NM_033292	CASP1;COP	−28.25	−100.00	Caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
NM_017590	RoXaN	−27.32	−9.09	Ubiquitous tetratricopeptide containing protein roxan
NM_014909	KIAA1036	−25.45	−20.53	Kiaa1036
X07109	PRKCB1	−24.88	−7.09	Protein kinase C, beta 1
BC011739	APOBEC3C	−23.09	−19.05	Apolipoprotein B mrna editing enzyme, catalytic polypeptide-like 3C
NM_001803	CDW52	−20.96	−9.09	CDW52 antigen (CAMPATH-1 antigen)

GenBank ID	Common name	Xenograft fold change	Cell line fold change	Description
NM_001778	CD48	−17.70	−99.01	CD48 antigen (B-cell membrane protein)
NM_000237	LPL	−16.29	−10.38	Lipoprotein lipase
NM_018659	C17	−14.79	−45.25	Cytokine-like protein C17
AK025833	CD33L3	−11.09	−25.13	CD33 antigen-like 3
NM_018058	CRTAC1	−10.99	−33.44	Cartilage acidic protein 1
NM_015364	MD-2	−10.93	−10.67	Lymphocyte antigen 96
D10537	MPZ	−10.41	−47.62	Myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)
AL390147	DKFZp547D065	−10.07	−86.21	Family with sequence similarity 20, member C
AF401235	SLC29A2	−9.62	−15.48	Solute carrier family 29 (nucleoside transporters), member 2
BC015510	RGS1	−8.85	−34.13	Regulator of G-protein signalling 1
NM_012155	EML2	−8.13	5.77	Echinoderm microtubule associated protein like 2
AK026966	AK3	−7.81	−11.93	Adenylate kinase 3
NM_030801	MAGE-E1	−7.63	−20.88	Melanoma antigen, family D, 4
NM_022082	C20orf59	−7.58	−7.81	Chromosome 20 open reading frame 59
NM_000483	APOC2	−6.94	−26.74	Apolipoprotein C-II
NM_012253	TKTL1	−5.95	−17.01	Transketolase-like 1
NM_001553	IGFBP7	−5.62	−17.79	Insulin-like growth factor binding protein 7
NM_004369	COL6A3	−5.32	−5.38	Collagen, type VI, alpha 3

Table II

Non-overlapping differentially regulated genes comparison between FEMX-I and FEMX-V cell lines

GenBank ID	Common name	Fold change	Description	Function
Up-regulated				
NM_032380	EFG2	36.70	Mitochondrial elongation factor G2	Protein biosynthesis; translational elongation
NM_000175	GPI	36.50	Glucose phosphate isomerase	Carbohydrate metabolism; gluconeogenesis; glycolysis; hemostasis; humoral immune response; neurogenesis
NM_006297	XRCC1	34.50	X-ray repair complementing defective repair in Chinese hamster cells 1	Single strand break repair
D42045	DCLRE1A	33.33	DNA cross-link repair 1A (PSO2 homolog, *S. cerevisiae*)	
NM_001990	EYA3	31.14	Eyes absent homolog 3 (Drosophila)	Development; metabolism; morphogenesis; visual perception
NM_016478	HSPC216	28.97	Nuclear interacting partner of anaplastic lymphoma kinase (ALK)	
NM_016355	LOC51202	26.51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	RNA metabolism
AL137581	FLJ34497	25.16	Hypothetical protein FLJ34497	
D83781	NUP160	25.01	Nucleoporin 160 kDa	Mrna-nucleus export; transport
NM_018412	ST7	24.89	Suppression of tumorigenicity 7	
NM_016343	CENPF	23.73	Centromere protein F, 350/400ka (mitosin)	DNA replication and chromosome cycle; regulation of mitosis
NM_002627	PFKP	23.39	Phosphofructokinase, platelet	Glycolysis
NM_016292	TRAP1	23.35	Heat shock protein 75	Protein folding
NM_021078	GCN5L2	19.94	GCN5 general control of amino-acid synthesis 5-like 2 (yeast)	Chromatin remodeling; protein amino acid acetylation; regulation of transcription from Pol II promoter
NM_006819	STIP1	19.65	Stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	Response to stress
NM_020998	MST1	19.49	Macrophage stimulating 1 (hepatocyte growth factor-like)	Blood coagulation; proteolysis and peptidolysis
NM_004922	SEC24C	19.41	SEC24 related gene family, member C (*S. cerevisiae*)	ER to Golgi transport; intracellular protein transport
NM_005381	NCL	19.22	Nucleolin	Nuclear mrna splicing, *via* spliceosome
NM_006746	SCML1	18.47	Sex comb on midleg-like 1 (Drosophila)	Morphogenesis
NM_018255	ELP2	17.94	Signal transducer and activator of transcription 3 interacting protein 1	
NM_058179	PSA	16.20	Phosphoserine aminotransferase 1	L-serine biosynthesis; metabolism;

GenBank ID	Common name	Fold change	Description	Function
				pyridoxine biosynthesis
NM_015954	LOC51071	15.69	Unr-interacting protein	
AW293890	THRAP3	14.71	Thyroid hormone receptor associated protein 3	
NM_006796	AFG3L2	14.56	AFG3 atpase family gene 3-like 2 (yeast)	Proteolysis and peptidolysis
NM_007355	HSPCB	14.18	Heat shock 90 kDa protein 1, beta	Positive regulation of nitric oxide biosynthesis; protein folding; response to unfolded protein
NM_016223	PACSIN3	12.76	Protein kinase C and casein kinase substrate in neurons 3	Endocytosis; negative regulation of endocytosis
NM_002902	RCN2	12.58	Reticulocalbin 2, EF-hand calcium binding domain	
NM_014390	p100	11.98	Staphylococcal nuclease domain containing 1	Regulation of transcription, DNA-dependent
NM_013436	NCKAP1	11.88	NCK-associated protein 1	Apoptosis; central nervous system development
NM_019005	FLJ20323	11.71	Hypothetical protein FLJ20323	
NM_004315	ASAH	11.63	N-acylsphingosine amidohydrolase (acid ceramidase) 1	Ceramide metabolism; fatty acid metabolism
NM_000918	P4HB	11.54	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	Electron transport
NM_021149	COTL1	11.50	Coactosin-like 1 (Dictyostelium)	Biological_process unknown
NM_000108	DLD	11.47	Dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	Electron transport; energy pathways; glycolysis
NM_016026	ARSDR1	11.24	Retinol dehydrogenase 11 (all-trans and 9-cis)	Metabolism; photoreceptor maintenance; retinol metabolism
NM_003100	SNX2	11.19	Sorting nexin 2	Endocytosis; intracellular protein transport; intracellular signaling cascade
NM_007178	UNRIP	11.19	Unr-interacting protein	
NM_016238	APC7	11.11	Anaphase promoting complex subunit 7	Cytokinesis; mitosis; regulation of cell cycle
NM_006621	AHCYL1	10.74	S-adenosylhomocysteine hydrolase-like 1	One-carbon compound metabolism
BM460564	BAG4	10.71	BCL2-associated athanogene 4	
NM_013236	E46L	10.61	Like mouse brain protein E46	Biological_process unknown
NM_001798	CDK2	10.56	Cyclin-dependent kinase 2	G_2/M transition of mitotic cell cycle; cytokinesis; mitosis; positive regulation of cell proliferation; protein amino acid phosphorylation; regulation of DNA replication; traversing start control point of mitotic cell cycle

GenBank ID	Common name	Fold change	Description	Function
NM_018899	PCDHAC2	10.48	Protocadherin alpha 5	Cell adhesion; homophilic cell adhesion; neurogenesis
NM_003472	DEK	10.4	DEK oncogene (DNA binding)	SRP-dependent cotranslational membrane targeting; cell growth and/or maintenance; regulation of transcription from Pol II promoter; signal transduction; viral genome replication
NM_001415	EIF2S3	10.4	Eukaryotic translation initiation factor 2, subunit 3 gamma, 52 kDa	Protein biosynthesis
NM_024586	OSBPL9	10.4	Oxysterol binding protein-like 9	Lipid transport; steroid metabolism
AK056156	TMP21	10.36	Transmembrane trafficking protein	ER to Golgi transport; intracellular protein transport
NM_015361	R3HDM	10.35	R3H domain (binds single-stranded nucleic acids) containing	
AL050143	DKFZP586B2420	10.30	FLJ00133 protein	
NM_015367	MIL1	10.26	BCL2-like 13 (apoptosis facilitator)	Caspase activation; induction of apoptosis; regulation of apoptosis
NM_006337	MCRS1	10.13	Microspherule protein 1	
AL136807	SERP1	10.06	Stress-associated endoplasmic reticulum protein 1	Plasma membrane organization and biogenesis; protein amino acid glycosylation; response to stress
NM_152374	FLJ38984	10.03	Hypothetical protein FLJ38984	
NM_001070	TUBG1;TUBG2	9.89	Tubulin, gamma 1	Microtubule cytoskeleton organization and biogenesis; microtubule-based movement
NM_018356	FLJ11193	9.76	Hypothetical protein FLJ11193	
AL117616	SRI	9.58	Sorcin	Heart development; intracellular iron ion storage; muscle development; regulation of action potential; regulation of heart rate; regulation of striated muscle contraction; transport
NM_018985	HCGIV.9	9.50	HLA complex group 4	
NM_002950	RPN1	9.50	Ribophorin I	Protein amino acid glycosylation
NM_000271	NPC1	9.44	Niemann-Pick disease, type C1	Cholesterol transport; intracellular protein transport
NM_052940	MGC8974	9.36	Hypothetical protein MGC8974	
NM_000687	AHCY	9.17	S-adenosylhomocysteine hydrolase	One-carbon compound metabolism
NM_005973	PRCC	9.14	Papillary renal cell carcinoma (translocation-associated)	Cell growth and/or maintenance
NM_017819	FLJ20432	9.14	RNA (guanine-9-) methyltransferase domain containing 1	
NM_002510	GPNMB	9.03	Glycoprotein (transmembrane) nmb	Negative regulation of cell proliferation
NM_016129	COPS4	8.91	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	

GenBank ID	Common name	Fold change	Description	Function
AB032261	SCD	8.85	Stearoyl-coa desaturase (delta-9-desaturase)	Fatty acid biosynthesis
AK055297	LSM11	8.82	U7 snrna-associated Sm-like protein	
L12711	TKT	8.63	Transketolase (Wernicke-Korsakoff syndrome)	
NM_001325	CSTF2	8.61	Cleavage stimulation factor, 3′ pre-RNA, subunit 2, 64 kDa	Mrna cleavage; mrna polyadenylation
U06863	FSTL1	8.60	Follistatin-like 1	
NM_006644	HSP105B	8.55	Heat shock 105 kDa/110 kDa protein 1	Protein folding; response to unfolded protein
NM_005494	DNAJB6	8.50	Dnaj (Hsp40) homolog, subfamily B, member 6	Biological_process unknown
NM_001881	CREM	8.48	Camp responsive element modulator	Regulation of transcription, DNA-dependent; signal transduction
NM_005313	GRP58	8.20	Glucose regulated protein, 58 kDa	Electron transport; protein-ER retention; protein-nucleus import; signal transduction
NM_004414	DSCR1	8.19	Down syndrome critical region gene 1	Calcium-mediated signaling; central nervous system development; circulation; signal transduction
NM_014992	DAAM1	8.05	Dishevelled associated activator of morphogenesis 1	Actin cytoskeleton organization and biogenesis; cell organization and biogenesis
NM_006876	B3GNT6	8.02	UDP-glcnac:betagal beta-1,3-N-acetylglucosaminyltransferase 6	Poly-N-acetyllactosamine biosynthesis
NM_016230	b5&b5R	7.92	NADPH cytochrome B5 oxidoreductase	Electron transport; energy pathways; sensory perception of chemical stimulus
D83778	KIAA0194	7.86	KIAA0194 protein	Regulation of transcription, DNA-dependent
NM_014720	SLK	7.85	SNF1 sucrose nonfermenting like kinase (yeast)	Nucleotide-excision repair; protein amino acid phosphorylation
NM_005146	SART1	7.82	Squamous cell carcinoma antigen recognised by T cells	
NM_005134	PPP4R1	7.81	Protein phosphatase 4, regulatory subunit 1	
NM_004127	GPS1	7.76	G protein pathway suppressor 1	JNK cascade; cell cycle; inactivation of MAPK
AK055491	DNCI2	7.68	Dynein, cytoplasmic, intermediate polypeptide 2	Microtubule-based movement
NM_016229	LOC51700	7.64	Cytochrome b5 reductase b5r.2	Electron transport
NM_000178	GSS	7.59	Glutathione synthetase	Amino acid metabolism; glutathione biosynthesis; neurogenesis; response to oxidative stress
NM_005565	LCP2	7.56	Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76 kDa)	Immune response; intracellular signaling cascade; transmembrane receptor protein tyrosine kinase signaling pathway
NM_014287	PM5	7.41	Hypothetical protein LOC283820	Biological_process unknown
NM_033657	DAP3	7.33	Death associated protein 3	Apoptosis; induction of apoptosis by

GenBank ID	Common name	Fold change	Description	Function
				extracellular signals
NM_012413	QPCT	7.28	Glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	Protein modification
NM_031304	MGC4293	7.26	Hypothetical protein MGC4293	
NM_013390	TMEM2	7.26	Transmembrane protein 2	
NM_012164	FBXW2	7.22	F-box and WD-40 domain protein 2	Ubiquitin cycle
NM_032737	LMNB2	7.22	Lamin B2	Biological_process unknown
NM_000788	DCK	7.19	Deoxycytidine kinase	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism; pyrimidine nucleotide metabolism
NM_003146	SSRP1	7.12	Structure specific recognition protein 1	Regulation of transcription, DNA-dependent
NM_001695	ATP6C	7.08	Atpase, H+ transporting, lysosomal 42 kDa, V1 subunit C, isoform 1	ATP synthesis coupled proton transport; cell surface receptor linked signal transduction; development
NM_018050	FLJ10298	7.02	Hypothetical protein FLJ10298	
BC033103	INPP5E	6.99	Peptidase (mitochondrial processing) alpha	Proteolysis and peptidolysis
NM_031216	SEC13L	6.99	Sec13-like protein	Intracellular protein transport
AB032973	LCHN	6.94	LCHN protein	
NM_007002	ADRM1	6.90	Adhesion regulating molecule 1	Cell adhesion
NM_015922	H105E3	6.86	NAD(P) dependent steroid dehydrogenase-like	Cholesterol biosynthesis; steroid biosynthesis
NM_003171	SUPV3L1	6.77	Suppressor of var1, 3-like 1 (*S. cerevisiae*)	
NM_004184	WARS	6.75	Tryptophanyl-trna synthetase	Negative regulation of cell proliferation; protein biosynthesis; tryptophanyl-trna aminoacylation
NM_005826	HNRPR	6.69	Heterogeneous nuclear ribonucleoprotein R	Mrna processing
NM_003915	CPNE1	6.66	Copine I	Lipid metabolism; vesicle-mediated transport
NM_032179	FLJ20542	6.66	Hypothetical protein FLJ20542	
NM_001315	MAPK14	6.66	Mitogen-activated protein kinase 14	Antimicrobial humoral response (sensu Vertebrata); cell motility; cell surface receptor linked signal transduction; chemotaxis; protein amino acid phosphorylation; protein kinase cascade; response to stress
NM_018142	FLJ10569	6.61	Hypothetical protein FLJ10569	
BC006427	KIAA1279	6.61	Kiaa1279	
NM_004749	CPR2	6.53	Transforming growth factor beta regulator 4	G1 phase of mitotic cell cycle; cell cycle arrest; positive regulation of cell proliferation
NM_005765	ATP6IP2	6.45	Atpase, H+ transporting, lysosomal accessory protein 2	

GenBank ID	Common name	Fold change	Description	Function
NM_005499	UBA2	6.45	SUMO-1 activating enzyme subunit 2	Ubiquitin cycle
NM_002767	PRPSAP2	6.43	Phosphoribosyl pyrophosphate synthetase-associated protein 2	Nucleoside metabolism; nucleotide biosynthesis
NM_003338	UBE2D1	6.28	Ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	Ubiquitin cycle; ubiquitin-dependent protein catabolism
NM_133436	ASNS	6.27	Asparagine synthetase	Asparagine biosynthesis; glutamine metabolism
AK057548	LOC154790	6.26	CDNA FLJ32986 fis, clone THYMU1000029	
NM_001105	ACVR1	6.15	Activin A receptor, type I	Protein amino acid phosphorylation; transmembrane receptor protein serine/threonine kinase signaling pathway
NM_002444	MSN	6.12	Moesin	Cell motility
NM_017982	FLJ10052	6.11	Hypothetical protein FLJ10052	
NM_000304	PMP22	6.10	Peripheral myelin protein 22	Mechanosensory behavior; negative regulation of cell proliferation; perception of sound; peripheral nervous system development; synaptic transmission
NM_000274	OAT	6.08	Ornithine aminotransferase (gyrate atrophy)	Amino acid metabolism; ornithine metabolism; visual perception
NM_002835	PTPN12	6.02	Protein tyrosine phosphatase, non-receptor type 12	Protein amino acid dephosphorylation
NM_022758	FLJ22195	6.00	Chromosome 6 open reading frame 106	
NM_015646	RAP1B	5.98	RAP1B, member of RAS oncogene family	Small gtpase mediated signal transduction
NM_003300	TRAF3	5.97	TNF receptor-associated factor 3	Apoptosis; induction of apoptosis; signal transduction
NM_017613	DONSON	5.95	Downstream neighbor of SON	Biological_process unknown
BC023525	C6orf69	5.92	Chromosome 6 open reading frame 69	
AF155110	NY-REN-45	5.90	Similar to potassium channel proteins; Homo sapiens NY-REN-45 antigen mrna, complete cds.	
NM_032333	MGC4248	5.84	Hypothetical protein MGC4248	
NM_005745	BCAP31	5.80	B-cell receptor-associated protein 31	Apoptosis; immune response; intracellular protein transport
AK022632	UAP1L1	5.70	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Metabolism
NM_002532	NUP88	5.69	Nucleoporin 88 kDa	Transport
NM_007158	D1S155E	5.66	NRAS-related gene	Male gonad development; regulation of transcription, DNA-dependent
NM_004317	ASNA1	5.59	Arsa arsenite transporter, ATP-binding, homolog 1 (bacterial)	Anion transport; response to arsenate

GenBank ID	Common name	Fold change	Description	Function
NM_001877	CR2	5.59	Complement component (3d/Epstein Barr virus) receptor 2	Complement activation, classical pathway; immune response
AL834171	MGC16733	5.58	Hypothetical gene MGC16733 similar to CG12113	
NM_004060	CCNG1	5.56	Cyclin G1	Cell cycle; cytokinesis; mitosis; regulation of cyclin dependent protein kinase activity
NM_014847	KIAA0144	5.54	NICE-4 protein	
NM_003600	STK15;STK6	5.51	Serine/threonine kinase 6	Cell cycle; mitosis; protein amino acid phosphorylation
NM_006559	KHDRBS1	5.46	KH domain containing, RNA binding, signal transduction associated 1	G_1/S transition of mitotic cell cycle; RAS protein signal transduction; cell cycle arrest; cell proliferation; mrna processing
NM_012113	CA14	5.45	Carbonic anhydrase XIV	One-carbon compound metabolism
NM_005805	POH1	5.21	Synonyms: PAD1, POH1, rpn11; go_component: 26S proteasome [goid 0005837] [evidence TAS] [pmid 9374539]; go_component: cytosol [goid 0005829] [evidence IEA]; go_component: proteasome complex (sensu Eukarya) [goid 0000502] [evidence TAS]; go_process: ubiquitin-dependent protein catabolism [goid 0006511] [evidence TAS] [pmid 9374539]; Homo sapiens proteasome (prosome, macropain) 26S subunit, non-atpase, 14 (PSMD14), mrna.	Ubiquitin-dependent protein catabolism
NM_018312	C11orf23	5.19	Chromosome 11 open reading frame 23	
AF222345	SUFU	5.19	Suppressor of fused homolog (Drosophila)	Regulation of transcription, DNA-dependent
NM_014321	ORC6L	5.16	Origin recognition complex, subunit 6 homolog-like (yeast)	DNA replication
NM_004600	SSA2	5.16	Sjogren syndrome antigen A2 (60 kDa, ribonucleoprotein autoantigen SS-A/Ro)	Transcription from Pol III promoter
NM_006400	DCTN2	5.15	Dynactin 2 (p50)	Cell proliferation; microtubule-based process; mitosis
AL832599	STARD4;	5.12	START domain containing 4, sterol regulated	Lipid transport; steroid biosynthesis
AB033023	FLJ10201	5.11	Hypothetical protein FLJ10201	Regulation of transcription, DNA-dependent
NM_021824	NIF3L1	5.10	NIF3 NGG1 interacting factor 3-like 1 (S. Pombe)	
NM_003896	SIAT9	5.07	Sialyltransferase 9 (CMP-neuac:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase)	Ganglioside biosynthesis; protein amino acid glycosylation
NM_004568	SERPINB6	5.06	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	
NM_020151	STARD7	5.02	START domain containing 7	
NM_004368	CNN2	5.00	Calponin 2	Cytoskeleton organization and biogenesis; smooth muscle contraction

GenBank ID	Common name	Fold change	Description	Function
AJ251973	NAV1; POMFIL3; FLJ12560; FLJ14203; KIAA1151; MGC14961; steerin-1	5.00	*Homo sapiens* partial steerin-1 gene.	DNA methylation
NM_000819	GART	4.97	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	‘*De novo*’ IMP biosynthesis; purine base biosynthesis; purine nucleotide biosynthesis
U03851	CAPZA2	4.96	Capping protein (actin filament) muscle Z-line, alpha 2	Actin cytoskeleton organization and biogenesis; cell motility; protein complex assembly
U03851	CAPZA2	4.75	Capping protein (actin filament) muscle Z-line, alpha 2	Actin cytoskeleton organization and biogenesis; cell motility; protein complex assembly
NM_021129	PP	4.69	Pyrophosphatase (inorganic)	Metabolism; phosphate metabolism
NM_007217	PDCD10	4.68	Programmed cell death 10	
AK055660	MTPN	4.56	Myotrophin	
Down-regulated				
NM_000800	FGF1	−100.00	Fibroblast growth factor 1 (acidic)	Angiogenesis; cell proliferation; cell-cell signaling; morphogenesis; regulation of cell cycle; signal transduction
NM_020411	GAGED2	−100.00	G antigen, family D, 2	
AL120032	GABRB3	−100.00	Gamma-aminobutyric acid (GABA) A receptor, beta 3	
NM_024736	FLJ12150	−100.00	Hypothetical protein FLJ12150	
NM_006158	NEFL	−100.00	Neurofilament, light polypeptide 68 kDa	
BC008915	SERPINA3	−68.97	Serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	
NM_025181	FLJ22004	−59.17	Solute carrier family 35, member F5	
NM_002050	GATA2	−57.47	Synonyms: NFE1B, MGC2306; GATA-binding protein 2; go_component: nucleus [goid 0005634] [evidence TAS] [pmid 1370462]; go_function: transcription activating factor [goid 0003710] [evidence E] [pmid 1370462]; go_function: transcription factor activity [goid 0003700] [evidence TAS] [pmid 8078582]; go_function: translation regulator activity [goid 0045182] [evidence IEA]; go_process: cell growth and/or maintenance [goid 0008151] [evidence TAS] [pmid 8078582]; go_process: transcription from Pol II promoter [goid 0006366] [evidence TAS] [pmid 1370462]; go_process: regulation of transcription, DNA-dependent [goid 0006355]	

GenBank ID	Common name	Fold change	Description	Function
			[evidence IEA]; Homo sapiens GATA binding protein 2 (GATA2), mrna.	
NM_002922	RGS1	−44.05	Regulator of G-protein signalling 1	B-cell activation; G-protein signaling, adenylate cyclase inhibiting pathway; immune response; signal transduction
NM_004335	BST2	−27.40	Bone marrow stromal cell antigen 2	Cell proliferation; cell-cell signaling; development; humoral immune response; positive regulation of I-kappab kinase/NF-kappab cascade
NM_007283	MGLL	−26.81	Monoglyceride lipase	Aromatic compound metabolism; inflammatory response; lipid metabolism
NM_021992	TMSNB	−25.00	Thymosin, beta, identified in neuroblastoma cells	Cytoskeleton organization and biogenesis
AL137259	DKFZp434D0513	−23.98	Hydrocephalus inducing	
NM_024600	FLJ20898	−21.32	Hypothetical protein FLJ20898	
NM_152773	MGC33212	−16.67	Hypothetical protein MGC33212	
NM_018476	BEX1	−16.50	Brain expressed, X-linked 1	
NM_001187	BAGE	−16.34	B melanoma antigen	
NM_001266	CES1	−15.97	Carboxylesterase 1 (monocyte/ macrophage serine esterase 1)	Metabolism; response to toxin
NM_000170	GLDC	−15.75	Glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)	Glycine catabolism
NM_139177	C17orf26	−14.95	Solute carrier family 39 (metal ion transporter), member 11	Metal ion transport
NM_001869	CPA2	−14.18	Carboxypeptidase A2 (pancreatic)	Proteolysis and peptidolysis; vacuolar protein catabolism
U83115	AIM1	−12.77	Absent in melanoma 1	
NM_001719	BMP7	−12.32	Bone morphogenetic protein 7 (osteogenic protein 1)	Growth; skeletal development
NM_005574	LMO2	−12.02	LIM domain only 2 (rhombotin-like 1)	Cell growth and/or maintenance; development
NM_004609	TCF15	−11.89	Transcription factor 15 (basic helix-loop-helix)	Development; mesoderm development; regulation of transcription from Pol II promoter
NM_003227	TFR2	−11.82	Transferrin receptor 2	Iron ion transport; proteolysis and peptidolysis
AF288741	OSBP2	−11.81	Oxysterol binding protein 2	Lipid transport; steroid metabolism
NM_016429	COPZ2	−11.52	Coatomer protein complex, subunit zeta 2	Intracellular protein transport
NM_002250	KCNN4	−11.27	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	Defense response; ion transport; potassium ion transport

GenBank ID	Common name	Fold change	Description	Function
BC015794	FLJ10097	−10.47	Hypothetical protein FLJ10097	
NM_005712	HHLA1	−9.90	HERV-H LTR-associating 1	
NM_005978	S100A2	−9.90	S100 calcium binding protein A2	Biological_process unknown
NM_002928	RGS16	−9.80	Regulator of G-protein signalling 16	Regulation of G-protein coupled receptor protein signaling pathway; signal transduction; visual perception
NM_032638	MGC2306	−9.35	GATA binding protein 2	Cell growth and/or maintenance; regulation of transcription, DNA-dependent; transcription from Pol II promoter
BF344649	MGC8685	−8.85	Tubulin, beta polypeptide paralog	
NM_004078	CSRP1	−8.47	Cysteine and glycine-rich protein 1	
NM_003733	OASL	−8.40	2′-5′-oligoadenylate synthetase-like	Immune response
NM_006417	MTAP44	−8.40	Interferon-induced protein 44	Response to virus
NM006169	NNMT	−8.20	Nicotinamide N-methyltransferase	
AL834409	DKFZp547J144	−8.20	Reticulon 4 receptor-like 1	
AF399547	OR1N1; OR1N3; OR1-26	−7.52	Contains transmembrane regions 2-7; Homo sapiens clone OR1N3 olfactory receptor gene, partial cds.	G-protein coupled receptor protein signaling pathway; perception of smell
NM_001175	ARHGDIB	−7.25	Rho GDP dissociation inhibitor (GDI) beta	Rho protein signal transduction; actin cytoskeleton organization and biogenesis; development; immune response; negative regulation of cell adhesion
AK074703	LOC89944	−7.09	Hypothetical protein BC008326	Carbohydrate metabolism
NM_004924	ACTN4	−7.04	Actinin, alpha 4	Cell motility
AI123815	FLJ21963	−7.04	FLJ21963 protein	
NM_032261	DKFZp434N0650	−6.90	Chromosome 21 open reading frame 56	
NM_006993	NPM3	−6.85	Nucleophosmin/nucleoplasmin, 3	Protein folding
BC009033	LOC253982	−6.80	Hypothetical protein LOC253982	Peptidyl-amino acid modification
NM_005794	HEP27	−6.76	Dehydrogenase/reductase (SDR family) member 2	Metabolism
NM_012219	MRAS	−6.71	Muscle RAS oncogene homolog	RAS protein signal transduction; actin cytoskeleton organization and biogenesis; development; muscle development
AB067508	KIAA1921	−6.58	Start codon is not identified.; *Homo sapiens* mrna for KIAA1921 protein, partial cds.	
NM_004711	SYNGR1	−6.49	Synaptogyrin 1	
NM_020169	LXN	−6.29	Latexin protein	

GenBank ID	Common name	Fold change	Description	Function
NM_018170	FLJ10656	−6.21	Hypothetical protein FLJ10656	
NM_004107	FCGRT	−6.13	Fc fragment of igg, receptor, transporter, alpha	Immune response; pregnancy
NM_018265	FLJ10901	−6.10	Hypothetical protein FLJ10901	
NM_006302	GCS1	−6.06	Glucosidase I	N-linked glycosylation; carbohydrate metabolism; oligosaccharide metabolism
NM_003633	ENC1	−5.85	Ectodermal-neural cortex (with BTB-like domain)	Development; neurogenesis
NM_004583	RAB5C	−5.81	RAB5C, member RAS oncogene family	Intracellular protein transport; small gtpase mediated signal transduction
AK074859	LOC147808	−5.71	Similar to zinc finger protein	
BE615983	STUB1	−5.71	STIP1 homology and U-Box containing protein 1	
NM_018022	FLJ10199	−5.59	Hypothetical protein FLJ10199	
NM_024710	FLJ23469	−5.49	Hypothetical protein FLJ23469	Metabolism
NM_016202	LOC51157	−5.46	Zinc finger protein 580	Regulation of transcription, DNA-dependent
AJ011713	TNNT1	−5.38	Homo sapiens TNNT1 gene, exons 12-14.	Muscle development; regulation of muscle contraction
NM_003283	TNNT1	−5.35	Troponin T1, skeletal, slow	Muscle development; regulation of muscle contraction
NM_032488	LOC84518	−5.15	Protein related with psoriasis	
AK055959	TOM1L2	−5.08	Target of myb1-like 2 (chicken)	Intra-Golgi transport; intracellular protein transport
NM_001060	TBXA2R	−4.98	Thromboxane A2 receptor	G-protein coupled receptor protein signaling pathway; muscle contraction; respiratory gaseous exchange
NM_002514	NOV	−4.88	Nephroblastoma overexpressed gene	Regulation of cell growth
NM_000117	EMD	−4.83	Emerin (Emery-Dreifuss muscular dystrophy)	Muscle contraction; muscle development
NM_007286	KIAA1029	−4.72	Synaptopodin	
NM_018956	C9orf9	−4.67	Chromosome 9 open reading frame 9	
NM_032603	LOXL3	−4.67	Lysyl oxidase-like 3	Biological_process unknown
NM_015681	B9	−4.65	B9 protein	
NM_014849	SV2	−4.63	Synaptic vesicle glycoprotein 2A	Transport

Table III

Unique differentially regulated genes comparison between FEMX-I and FEMX-V tumor xenografts

GenBank ID	Common name	Fold change	Description	Function
Up-regulated				
NM_004214	FIBP	507.00	Fibroblast growth factor (acidic) intracellular binding protein	Fibroblast growth factor receptor signaling pathway
NM_000165	GJA1	439.00	Gap junction protein, alpha 1, 43 kDa (connexin 43)	Cell-cell signaling; heart development; muscle contraction; perception of sound; positive regulation of I-kappab kinase/NF-kappab cascade; transport
NM_014640	KIAA0173	237.00	Tubulin tyrosine ligase-like family, member 4	Protein modification
NM_021979	HSPA2	229.00	Heat shock 70 kDa protein 2	Male meiosis; spermatid development
AF300796	CSE-C	164.00	Cytosolic sialic acid 9-*O*-acetylesterase homolog	
NM_012311	KIN	96.38	KIN, antigenic determinant of reca protein homolog (mouse)	
NM_000188	HK1	93.04	Hexokinase 1	Glycolysis
NM_016113	TRPV2	69.01	Transient receptor potential cation channel, subfamily V, member 2	Cation transport; sensory perception
NM_015610	DKFZP434J154	62.59	DKFZP434J154 protein	
NM_001099	ACPP	62.51	Acid phosphatase, prostate	Regulation of cell cycle
NM_007017	SOX30	60.01	SRY (sex determining region Y)-box 30	Regulation of transcription from Pol II promoter; spermatogenesis
NM_000167	GK	51.31	Glycerol kinase	Carbohydrate metabolism; glycerol-3-phosphate metabolism
NM_003750	EIF3S10	49.46	Eukaryotic translation initiation factor 3, subunit 10 theta, 150/170 kDa	Protein biosynthesis; regulation of translational initiation
NM_018702	ADAR3	48.50	Adenosine deaminase, RNA-specific, B2 (RED2 homolog rat)	Mrna editing; mrna processing
NM_000308	PPGB	48.29	Protective protein for beta-galactosidase (galactosialidosis)	Intracellular protein transport; proteolysis and peptidolysis
NM_014065	HT001	44.69	HT001 protein	
NM_003367	USF2	43.19	Upstream transcription factor 2, c-fos interacting	Regulation of transcription, DNA-dependent
AK024450	ARHT2	43.05	Ras homolog gene family, member T2	Small gtpase mediated signal transduction
NM_000375	UROS	41.01	Uroporphyrinogen III synthase (congenital erythropoietic porphyria)	Heme biosynthesis; uroporphyrinogen III biosynthesis
NM_024689	FLJ14103	37.77	Hypothetical protein FLJ14103	

GenBank ID	Common name	Fold change	Description	Function
NM_005412	SHMT2	36.17	Serine hydroxymethyltransferase 2 (mitochondrial)	L-serine metabolism; glycine metabolism; one-carbon compound metabolism
NM_004862	PIG7	36.14	Lipopolysaccharide-induced TNF factor	Positive regulation of I-kappab kinase/NF-kappab cascade; regulation of transcription from Pol II promoter
BC002980	SCRN2	34.47	Secernin 2	Proteolysis and peptidolysis
NM_018410	DKFZp762E1312	33.04	Hypothetical protein dkfzp762e1312	
NM_032801	JAM3	32.75	Junctional adhesion molecule 3	
NM_003681	PDXK	32.05	Pyridoxal (pyridoxine, vitamin B6) kinase	
NM_022449	RAB17	30.90	RAB17, member RAS oncogene family	Intracellular protein transport; small gtpase mediated signal transduction
NM_002046	GAPD	29.98	Glyceraldehyde-3-phosphate dehydrogenase	Glucose metabolism; glycolysis
NM_003900	SQSTM1	28.30	Sequestosome 1	Endosome transport; intracellular signaling cascade; positive regulation of transcription from Pol II promoter; protein localization; regulation of I-kappab kinase/NF-kappab cascade; response to stress
L09674	SLC2A2; GLUT2	26.57	Human glucose transporter 2 (GLUT2) gene, exon 1.	Carbohydrate metabolism; carbohydrate transport; glucose transport
NM_145792	MGST1	26.39	Microsomal glutathione S-transferase 1	
AK054993	RAC1	26.38	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	Cell adhesion; cell motility; inflammatory response; morphogenesis; small gtpase mediated signal transduction
NM_002300	LDHB	26.03	Lactate dehydrogenase B	Glycolysis; tricarboxylic acid cycle intermediate metabolism
NM_002629	PGAM1	25.26	Phosphoglycerate mutase 1 (brain)	Glycolysis; metabolism
NM_002077	GOLGA1	24.72	Golgi autoantigen, golgin subfamily a, 1	
NM_015640	PAI-RBP1	24.27	PAI-1 mrna-binding protein	
NM_005418	ST5	24.19	Suppression of tumorigenicity 5	
NM_005968	HNRPM	23.87	Heterogeneous nuclear ribonucleoprotein M	
NM_001968	EIF4E	23.69	Eukaryotic translation initiation factor 4E	Regulation of protein biosynthesis; regulation of translation; translational initiation
NM_001496	GFRA3	23.51	GDNF family receptor alpha 3	Peripheral nervous system development; signal transduction
NM_001679	ATP1B3	23.42	Atpase, Na+/K+ transporting, beta 3 polypeptide	Potassium ion transport; sodium ion transport
NM_000041	APOE	23.30	Apolipoprotein E	Cholesterol homeostasis; circulation; cytoskeleton organization and biogenesis; induction of apoptosis; intracellular transport; learning and/or memory;

GenBank ID	Common name	Fold change	Description	Function
				lipid transport; lipoprotein metabolism; regulation of axon extension; regulation of neuronal synaptic plasticity; response to reactive oxygen species; synaptic transmission, cholinergic
AA933967	SPRY3	23.30	Sprouty homolog 3 (Drosophila)	
NM_005507	CFL1	22.71	Cofilin 1 (non-muscle)	Rho protein signal transduction; actin cytoskeleton organization and biogenesis
NM_000403	GALE	22.55	Galactose-4-epimerase, UDP-	Carbohydrate metabolism; galactose metabolism; nucleotide-sugar metabolism
NM_020162	DDX33	22.48	DEAH (Asp-Glu-Ala-His) box polypeptide 33	
NM_006170	NOL1	22.35	HOM-TES-103 tumor antigen-like	Positive regulation of cell proliferation; regulation of cell cycle
NM_004570	PIK3C2G	22.18	Phosphoinositide-3-kinase, class 2, gamma polypeptide	Intracellular signaling cascade
NM_018223	CHFR	21.83	Checkpoint with forkhead and ring finger domains	
AK057343	ZNF131	21.32	Zinc finger protein 131 (clone phz-10)	Regulation of transcription, DNA-dependent
NM_001469	G22P1	21.30	Thyroid autoantigen 70 kDa (Ku antigen)	DNA ligation; double-strand break repair *via* nonhomologous end-joining
NM_016372	TPRA40	20.85	Seven transmembrane domain orphan receptor	Aging; lipid metabolism
NM_006098	GNB2L1	20.34	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	Protein kinase C activation; signal transduction
NM_005216	DDOST	20.27	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase	N-linked glycosylation *via* asparagine
AB002376	KIAA0378	19.92	CAZ-associated structural protein	
NM_006821	ZAP128	19.79	Peroxisomal long-chain acyl-coa thioesterase	Acyl-coa metabolism; lipid metabolism
NM_000874	IFNAR2	19.42	Interferon (alpha, beta and omega) receptor 2	JAK-STAT cascade; cell surface receptor linked signal transduction; response to virus
AB011173	KIAA0601	19.08	Amine oxidase (flavin containing) domain 2	Electron transport
NM_002087	GRN	18.86	Granulin	Cell proliferation; cell-cell signaling; positive regulation of cell proliferation; signal transduction
NM_006088	TUBB2	18.38	Tubulin, beta, 2	Microtubule polymerization; microtubule-based movement
NM_016180	MATP	18.35	Membrane associated transporter	Melanin biosynthesis from tyrosine; visual perception
NM_000447	PSEN2	18.26	Presenilin 2 (Alzheimer disease 4)	Apoptotic program; chromosome organization and biogenesis (sensu Eukarya); chromosome segregation; intracellular signaling cascade
NM_005083	U2AF1RS1; U2AF1RS2	18.21	Signal recognition particle 19 kDa	Biological_process unknown

GenBank ID	Common name	Fold change	Description	Function
NM_002455	MTX1	18.13	Metaxin 1	Protein transport
NM_006791	MRG15	17.90	Mortality factor 4 like 1	Chromatin assembly/disassembly; regulation of cell growth
NM_015966	SDBCAG84	17.43	Serologically defined breast cancer antigen 84	
NM_005720	ARPC1B	17.41	Actin related protein 2/3 complex, subunit 1B, 41 kDa	Cell motility
BC014110	LOC132241	17.41	Hypothetical protein LOC132241	Protein biosynthesis
NM_004592	SFRS8	17.18	Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	Mrna splice site selection; nuclear mrna splicing, *via* spliceosome; regulation of transcription, DNA-dependent
NM_004279	PMPCB	17.02	Peptidase (mitochondrial processing) beta	Proteolysis and peptidolysis
NM_000143	FH	16.98	Fumarate hydratase	Fumarate metabolism; negative regulation of cell cycle; tricarboxylic acid cycle
NM_002265	KPNB1	16.97	Karyopherin (importin) beta 1	NLS-bearing substrate-nucleus import; intracellular protein transport; protein-nucleus import, docking; protein-nucleus import, translocation
NM_004147	DRG1	16.90	Developmentally regulated GTP binding protein 1	Development; transcription
AJ223353	H2BFB	16.81	Histone 1, h2bd	Chromosome organization and biogenesis (sensu Eukarya); nucleosome assembly
NM_005956	MTHFD1	16.09	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	Amino acid biosynthesis; folic acid and derivative biosynthesis; histidine biosynthesis; methionine biosynthesis; one-carbon compound metabolism; purine nucleotide biosynthesis
AL049365	MGC50853	16.03	MRNA; cdna dkfzp586a0618 (from clone dkfzp586a0618)	
AB007856	FEM1B	15.97	Fem-1 homolog b (*C. elegans*)	Induction of apoptosis
NM_000701	ATP1A1	15.93	Atpase, Na+/K+ transporting, alpha 1 polypeptide sodium ion transport; sperm motility	ATP hydrolysis coupled proton transport; hydrogen ion homeostasis; metabolism; potassium ion transport;
NM_004988	MAGEA1	15.84	Melanoma antigen, family A, 1 (directs expression of antigen MZ2-E)	
BC030618	LOC196463	15.75	Hypothetical protein LOC196463	
NM_004637	RAB7	15.61	RAB7, member RAS oncogene family	Endocytosis; intracellular protein transport; small gtpase mediated signal transduction
NM_001122	ADFP	15.54	Adipose differentiation-related protein	
NM_014677	RIMS2	15.28	Regulating synaptic membrane exocytosis 2	Intracellular protein transport
NM_004596	SNRPA	15.23	Small nuclear ribonucleoprotein polypeptide A	
AF204171	POP3	15.13	Popeye domain containing 3	Biological_process unknown

GenBank ID	Common name	Fold change	Description	Function
NM_016001	LOC51096	14.93	CGI-48 protein	
NM_022157	GTR2	14.89	Ras-related GTP binding C	RNA splicing; apoptosis; cell growth; cell growth and/or maintenance; small gtpase mediated signal transduction; transcription
AK057545	PLDN	14.87	Pallidin homolog (mouse)	Synaptic vesicle docking
NM_000248	MITF	14.71	Microphthalmia-associated transcription factor	Development; melanocyte differentiation; perception of sound; regulation of transcription, DNA-dependent
NM_005273	GNB2	14.66	Guanine nucleotide binding protein (G protein), beta polypeptide 2	G-protein coupled receptor protein signaling pathway; signal transduction
NM_032558	FLJ14753	14.59	Hypothetical protein FLJ14753	Tetracycline transport
NM_012067	AKR7A3	14.46	Aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	Aldehyde metabolism
NM_005637	SS18	14.28	Synovial sarcoma translocation, chromosome 18	Cell growth and/or maintenance
NM_016535	HSPC189	14.07	Zinc finger protein 581	Regulation of transcription, DNA-dependent
NM_020357	PCNP	14.05	PEST-containing nuclear protein	
NM_005466	MED6	14.01	Mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	Regulation of transcription, DNA-dependent
AB037843	KIAA1422	13.89	Potassium channel, subfamily T, member 1	Ion transport; potassium ion transport
NM_004159	PSMB8	13.81	Proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)	Immune response; proteolysis and peptidolysis; ubiquitin-dependent protein catabolism
X53305	STMN1	13.76	Stathmin 1/oncoprotein 18	Cell growth and/or maintenance; intracellular signaling cascade
NM_003831	SUDD	13.72	RIO kinase 3 (yeast)	Chromosome segregation
NM_002817	PSMD13	13.67	Proteasome (prosome, macropain) 26S subunit, non-atpase, 13	
BC007195	NCK2	13.64	NCK adaptor protein 2	T-cell activation; intracellular signaling cascade; negative regulation of cell proliferation; positive regulation of T-cell proliferation; positive regulation of actin filament polymerization; regulation of epidermal growth factor receptor activity; signal complex formation
BC019236	HLA-A	13.47	Major histocompatibility complex, class I, A	Antigen presentation, endogenous antigen; antigen processing, endogenous antigen *via* MHC class I; immune response
NM_024663	NPEPL1	13.45	Aminopeptidase-like 1	Proteolysis and peptidolysis
NM_003883	HDAC3	13.44	Histone deacetylase 3	Anti-apoptosis; chromatin modification; histone deacetylation; regulation of cell cycle; regulation of transcription, DNA-dependent
NM_023016	FLJ21870	13.43	Septin 10	

GenBank ID	Common name	Fold change	Description	Function
NM_005569	LIMK2	13.21	LIM domain kinase 2	Protein amino acid phosphorylation
NM_002574	PRDX1	13.21	Peroxiredoxin 1	Cell proliferation; skeletal development
NM_002914	RFC2	13.16	Replication factor C (activator 1) 2, 40 kDa	DNA replication
NM_004071	CLK1	13.08	CDC-like kinase 1	Cell proliferation; protein amino acid phosphorylation; regulation of cell cycle
NM_012173	FBXO25	13.01	F-box only protein 25	Ubiquitin cycle
NM_001975	ENO2	12.84	Enolase 2 (gamma, neuronal)	Glycolysis
NM_017920	URG4	12.80	Up-regulated gene 4	
NM_018380	DDX28	12.69	Hypothetical protein FLJ20399	
NM_013379	DPP7	12.66	Dipeptidylpeptidase 7	Proteolysis and peptidolysis
NM_012179	FBXO7	12.66	F-box only protein 7	Ubiquitin-dependent protein catabolism
NM_033133	CNP	12.62	2′,3′-Cyclic nucleotide 3′ phosphodiesterase	Cyclic nucleotide catabolism; synaptic transmission
NM_014575	SCHIP1	12.58	Schwannomin interacting protein 1	Biological_process unknown
NM_012079	DGAT1	12.54	Diacylglycerol *O*-acyltransferase homolog 1 (mouse)	Fat body development; triacylglycerol metabolism
NM_006397	RNASEHI	12.47	Jun B proto-oncogene	DNA replication; RNA catabolism
BC002971	CCT5	12.44	Chaperonin containing TCP1, subunit 5 (epsilon)	Protein folding
NM_000018	ACADVL	12.43	Acyl-coenzyme A dehydrogenase, very long chain	Electron transport; energy derivation by oxidation of organic compounds; fatty acid beta-oxidation; fatty acid metabolism
NM_002266	KPNA2	12.41	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	DNA metabolism; G2 phase of mitotic cell cycle; M phase specific microtubule process; NLS-bearing substrate-nucleus import; intracellular protein transport; regulation of DNA recombination
NM_006913	RNF5	12.41	Ring finger protein 5	Protein ubiquitination
BE737594	RBPSUH	12.39	Recombining binding protein suppressor of hairless (Drosophila)	
NM_006367	CAP	12.38	CAP, adenylate cyclase-associated protein 1 (yeast)	Adenylate cyclase activation; establishment and/or maintenance of cell polarity; signal transduction
NM_012111	C14orf3	12.31	AHA1, activator of heat shock 90 kDa protein atpase homolog 1 (yeast)	Protein folding; response to stress
NM_003299	TRA1	12.28	Tumor rejection antigen (gp96) 1	Protein folding; response to stress
AF154121	SLC13A3	12.14	Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	Sodium ion transport
NM_006115	PRAME	12.11	Preferentially expressed antigen in melanoma	
AK027480	ZNF266; HZF1	12.07	Unnamed protein product; *Homo sapiens* cdna	Regulation of transcription, DNA-dependent

GenBank ID	Common name	Fold change	Description	Function
			FLJ14574 fis, clone NT2RM4000751, moderately similar to ZINC FINGER PROTEIN 184.	
NM_006758	U2AF1	11.99	U2(RNU2) small nuclear RNA auxiliary factor 1	RNA splicing; nuclear mrna splicing, *via* spliceosome
NM_020187	DC12	11.98	DC12 protein	
NM_000895	LTA4H	11.95	Leukotriene A4 hydrolase	Inflammatory response; leukotriene biosynthesis; proteolysis and peptidolysis
NM_003288	TPD52L2	11.87	Tumor protein D52-like 2	Cell proliferation
NM_014501	E2-EPF	11.85	Ubiquitin-conjugating enzyme E2S	Ubiquitin cycle
NM_022036	GPRC5C	11.84	G protein-coupled receptor, family C, group 5, member C	G-protein coupled receptor protein signaling pathway
NM_002643	PIGF	11.7	Phosphatidylinositol glycan, class F (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	GPI anchor biosynthesis
NM_006111	ACAA2	11.63	Acetyl-Coenzyme A acyltransferase 2	Fatty acid metabolism
NM_018955	UBB	11.58	Ubiquitin B	
NM_004642	CDK2AP1	11.56	CDK2-associated protein 1	DNA-dependent DNA replication; S phase of mitotic cell cycle; negative regulation of cell cycle; protein amino acid phosphorylation
BE967375	RANBP9	11.51	RAN binding protein 9	
NM_012103	AUP1	11.48	Ancient ubiquitous protein 1	Metabolism
U86453	PIK3CD	11.39	Phosphoinositide-3-kinase, catalytic, delta polypeptide	Protein amino acid phosphorylation; signal transduction
AK025586	SPATA13	11.31	Spermatogenesis associated 13	
NM_015908	ARS2	11.25	Arsenate resistance protein ARS2	Response to arsenic
NM_021178	HEI10	11.25	Cyclin B1 interacting protein 1	Ubiquitin cycle
NM_016615	SLC6A13	11.23	Solute carrier family 6 (neurotransmitter transporter, GABA), member 13	Neurotransmitter transport
M94345	CAPG	11.17	Capping protein (actin filament), gelsolin-like	Protein complex assembly; response to pest/pathogen/parasite
NM_017710	FLJ20203	11.17	Synonyms: FLJ12923, FLJ23040, KIAA1606, dkfzp761i241; Homo sapiens hypothetical protein FLJ20203 (FLJ20203), mrna.	
NM_052861	MGC21675	11.05	Hypothetical protein MGC21675	
S68616	SLC9A1	11.03	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)	Regulation of ph; sodium ion transport
NM_018845	LOC55974	11.03	Stromal cell protein	

GenBank ID	Common name	Fold change	Description	Function
AL117440	PDPR	11.01	Pyruvate dehydrogenase phosphatase regulatory subunit	Electron transport
BM467642	SNTB2	10.91	Syntrophin, beta 2 (dystrophin-associated protein A1, 59 kDa, basic component 2)	
NM_003968	UBE1C	10.90	Ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)	Proteolysis and peptidolysis; ubiquitin cycle
NM_003916	AP1S2	10.88	Adaptor-related protein complex 1, sigma 2 subunit	Endocytosis; intracellular protein transport
NM_001799	CDK7	10.88	Cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	DNA repair; cytokinesis; protein amino acid phosphorylation; regulation of cyclin dependent protein kinase activity; regulation of transcription, DNA-dependent; transcription initiation from Pol II promoter
NM_005596	NFIB	10.85	Nuclear factor I/B	DNA replication; regulation of transcription, DNA-dependent
AL834255	DKFZp586M1819	10.84	Putative lysophosphatidic acid acyltransferase	Metabolism
NM_018482	DDEF1	10.77	Synonyms: PAP, PAG2, ASAP1, ZG14P, KIAA1249; Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mrna.	Regulation of gtpase activity
NM_030577	MGC10993	10.71	Hypothetical protein MGC10993	
NM_022095	ZNF335	10.69	Zinc finger protein 335	Regulation of transcription, DNA-dependent
NM_006410	HTATIP2	10.66	HIV-1 Tat interactive protein 2, 30 kDa	Anti-apoptosis; induction of apoptosis; regulation of transcription from Pol II promoter
NM_015332	KIAA1068	10.63	KIAA1068 protein	
NM_080820	HARS2	10.48	Histidyl-trna synthetase 2	D-amino acid catabolism
M23161	MCFD2; F5F8D; SDNSF; LMAN1IP	10.48	Human transposon-like element mrna.	Protein transport
NM_015510	DKFZp566O084	10.47	DKFZP566O084 protein	Metabolism
NM_014186	HSPC166	10.46	COMM domain containing 9	
NM_001515	GTF2H2	10.46	General transcription factor IIH, polypeptide 2, 44 kDa	DNA repair; regulation of transcription, DNA-dependent
NM_003021	SGT	10.44	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Biological_process unknown
L48722	PTP4A2	10.40	Homo sapiens (clone hh18) protein tyrosine phosphatase (ptp-IV1r) gene, 5′ end of cds.	Protein amino acid dephosphorylation
NM_013393	FTSJ2	10.38	Ftsj homolog 2 (*E. Coli*)	Rrna processing
NM_006191	PA2G4	10.33	Proliferation-associated 2G4, 38 kDa	Cell cycle arrest; cell proliferation; proteolysis

GenBank ID	Common name	Fold change	Description	Function
				and peptidolysis
NM_016628	WAC	10.29	WW domain containing adaptor with coiled-coil	
NM_007269	STXBP3	10.26	Syntaxin binding protein 3	Intracellular protein transport; protein secretion
NM_018091	ELP3	10.24	Elongation protein 3 homolog (*S. cerevisiae*)	ATP synthesis coupled proton transport
NM_018182	FLJ10700	10.22	Hypothetical protein FLJ10700	
NM_032689	MGC13071	10.22	Hypothetical protein MGC13071	DNA metabolism; regulation of transcription, DNA-dependent
NM_003759	SLC4A4	10.20	Solute carrier family 4, sodium bicarbonate cotransporter, member 4	Anion transport
NM_032025	CDA02	10.14	Eukaryotic translation initiation factor (eif) 2A	Regulation of protein biosynthesis; ribosome assembly
NM_052935	MGC20781	10.14	Hypothetical protein MGC20781	
BC014130	FBXW5	10.12	F-box and WD-40 domain protein 5	Ubiquitin cycle
NM_022039	SHFM3	10.11	Split hand/foot malformation (ectrodactyly) type 3	Wnt receptor signaling pathway; development; embryonic limb morphogenesis; ubiquitin-dependent protein catabolism
NM_024868	FLJ14124	10.10	Hypothetical protein FLJ14124	
NM_024033	MGC5242	10.09	Hypothetical protein MGC5242	
NM_001640	APEH	10.06	N-acylaminoacyl-peptide hydrolase	Proteolysis and peptidolysis
NM_000528	MAN2B1	10.05	Mannosidase, alpha, class 2B, member 1	Carbohydrate metabolism; protein deglycosylation; protein modification
M93718	NOS3	10.01	Nitric oxide synthase 3 (endothelial cell)	Amino acid metabolism; cell motility; electron transport; nitric oxide biosynthesis
NM_016930	STX18	9.98	Syntaxin 18	ER to Golgi transport; intracellular protein transport; vesicle docking during the process of exocytosis
NM_014311	SMUG1	9.96	Single-strand selective monofunctional uracil DNA glycosylase	DNA repair
NM_003187	TAF9	9.94	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32 kDa	Regulation of transcription, DNA-dependent; transcription from Pol II promoter; transcription initiation
BC004170	POLE3	9.92	Polymerase (DNA directed), epsilon 3 (p17 subunit)	DNA replication
NM_014323	ZNF278	9.89	Zinc finger protein 278	Cell growth and/or maintenance; regulation of transcription, DNA-dependent
NM_003678	PK1.3	9.88	Synonyms: Fmip, PK1.3; gene from NF2/ meningioma region of 22q12; placental protein 39.2; go_function: tumor suppressor [goid 0008181] [evidence TAS] [pmid 8242058]; *Homo sapiens* chromosome 22 open reading	

GenBank ID	Common name	Fold change	Description	Function
			frame 19 (c22orf19), mrna.	
NM_013232	PDCD6	9.85	Programmed cell death 6	Apoptosis; induction of apoptosis by extracellular signals
NM_003782	B3GALT4	9.79	UDP-Gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 4	Protein amino acid glycosylation
NM_014920	KIAA0936	9.72	Intestinal cell (MAK-like) kinase	Protein amino acid phosphorylation
NM_018106	FLJ10479	9.71	Zinc finger, DHHC domain containing 4	
NM_003849	SUCLG1	9.70	Succinate-coa ligase, GDP-forming, alpha subunit	Glycolysis; metabolism; tricarboxylic acid cycle
NM_032907	MGC14421	9.69	Bone marrow stromal cell-derived ubiquitin-like	Protein modification
NM_005726	TSFM	9.66	Ts translation elongation factor, mitochondrial	Protein biosynthesis; translational elongation
NM_014046	MRPS18B	9.63	Mitochondrial ribosomal protein S18B	Protein biosynthesis
NM_003364	UP	9.61	Uridine phosphorylase 1	Nucleoside metabolism
NM_003017	SFRS3	9.49	Splicing factor, arginine/serine-rich 3	Nuclear mrna splicing, *via* spliceosome
NM_006570	RAGA	9.47	Ras-related GTP binding A	Cell death; cell growth and/or maintenance; cell surface receptor linked signal transduction
NM_006339	HMG20B	9.36	High-mobility group 20B	Establishment and/or maintenance of chromatin architecture; regulation of transcription, DNA-dependent
AB058716	KIAA1813	9.36	Start codon is not identified.; *Homo sapiens* mrna for KIAA1813 protein, partial cds.	Superoxide metabolism
NM_020199	HTGN29	9.35	HTGN29 protein	
AK021789	LOC146174	9.33	Hypothetical protein LOC146174	
NM_007008	RTN4	9.32	Reticulon 4	Negative regulation of anti-apoptosis; negative regulation of axon extension; regulation of apoptosis
NM_001205	BNIP1	9.27	BCL2/adenovirus E1B 19 kDa interacting protein 1	Anti-apoptosis
NM_005057	RBBP5	9.22	Retinoblastoma binding protein 5	
BF698884	DC2	9.21	DC2 protein	
NM_004728	DDX21	9.20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	
NM_014341	MTCH1	9.20	Mitochondrial carrier homolog 1 (*C. elegans*)	Caspase activation; ion channel clustering; positive regulation of apoptosis; regulation of signal transduction; transport
NM_006325	RAN	9.20	RAN, member RAS oncogene family	DNA metabolism; RNA-nucleus export; intracellular protein transport; mitotic spindle assembly; protein-nucleus export; regulation of cell cycle; signal transduction; small gtpase mediated signal transduction

GenBank ID	Common name	Fold change	Description	Function
NM_018107	FLJ10482	9.18	RNA-binding region (RNP1, RRM) containing 4	Mrna processing
BC012795	CAMK2G	9.15	Calcium/calmodulin-dependent protein kinase (cam kinase) II gamma	Insulin secretion; protein amino acid phosphorylation
NM_001424	EMP2	9.15	Epithelial membrane protein 2	Cell death; cell proliferation; development
BQ889085	KIAA1164	9.15	Hypothetical protein KIAA1164	
NM_006917	RXRG	9.10	Retinoid X receptor, gamma	Regulation of transcription, DNA-dependent
NM_005167	ARHC	9.04	Ras homolog gene family, member C	
NM_002694	POLR2C	8.98	Polymerase (RNA) II (DNA directed) polypeptide C, 33 kDa	Transcription; transcription from Pol II promoter
NM_017582	HSA243666	8.95	Ubiquitin-conjugating enzyme E2Q (putative)	Ubiquitin cycle
NM_005141	FGB	8.93	Fibrinogen, B beta polypeptide	Blood coagulation; positive regulation of cell proliferation; regulation of blood pressure
NM_001631	ALPI	8.91	Alkaline phosphatase, intestinal	Metabolism; phosphorylation
NM_014371	NAKAP95	8.87	A kinase (PRKA) anchor protein 8-like	Biological_process unknown
NM_032280	DKFZp761J139	8.86	Zinc finger, CCHC domain containing 9	
NM_004128	GTF2F2	8.81	General transcription factor IIF, polypeptide 2, 30 kDa	RNA elongation from Pol II promoter; regulation of transcription, DNA-dependent; transcription initiation from Pol II promoter
NM_017542	KIAA1513	8.79	Pogo transposable element with KRAB domain	Anti-apoptosis
NM_004725	BUB3	8.75	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	Cell proliferation; mitosis; mitotic spindle checkpoint
NM_006868	RAB31	8.75	RAB31, member RAS oncogene family	Small gtpase mediated signal transduction
NM_025267	MGC2744	8.73	Hypothetical protein MGC2744	Alanyl-trna aminoacylation
AL137398	DKFZp434P162	8.73	Similar to hypothetical protein (LOC388094), mrna	
AB033041	VANGL2	8.73	Vang-like 2 (van gogh, Drosophila)	
NM_006357	UBE2E3	8.72	Ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	Ubiquitin cycle
AK056862	MPHOSPH10	8.70	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	Rrna processing
NM_018235	FLJ10830	8.67	Cytosolic nonspecific dipeptidase (EC 3.4.13.18)	Proteolysis and peptidolysis
NM_006925	SFRS5	8.64	Splicing factor, arginine/serine-rich 5	Mrna splice site selection; nuclear mrna splicing, *via* spliceosome
AJ224162	LIAS	8.63	Lipoic acid synthetase	Lipoate biosynthesis
NM_001069	TUBB	8.62	Tubulin, beta polypeptide	

GenBank ID	Common name	Fold change	Description	Function
NM_013989	DIO2	8.61	Deiodinase, iodothyronine, type II	Thyroid hormone generation
NM_152417	FLJ32370	8.60	Hypothetical protein FLJ32370	Metabolism
NM_016943	TAS2R3	8.59	Taste receptor, type 2, member 3	G-protein coupled receptor protein signaling pathway; perception of taste; signal transduction
NM_014335	CRI1	8.55	CREBBP/EP300 inhibitory protein 1	Biological_process unknown
NM_018842	LOC55971	8.55	Insulin receptor tyrosine kinase substrate	
NM_021826	FLJ13149	8.48	Homo sapiens hypothetical protein FLJ13149 (FLJ13149), mrna.	Apoptosis
AL832304	SLC9A9	8.48	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	Regulation of ph; sodium ion transport
NM_002027	FNTA	8.47	Farnesyltransferase, CAAX box, alpha	Protein amino acid farnesylation; protein amino acid geranylgeranylation; protein amino acid prenylation; transforming growth factor beta receptor signaling pathway
NM_005102	FEZ2	8.46	Fasciculation and elongation protein zeta 2 (zygin II)	Axon guidance; hemopoiesis; neurogenesis; signal transduction
NM_030798	WBSCR16	8.46	Williams-Beuren syndrome chromosome region 16	Biological_process unknown
NM_003213	TEAD4	8.44	TEA domain family member 4	Regulation of transcription, DNA-dependent
NM_002431	MNAT1	8.40	Menage a trois 1 (CAK assembly factor)	DNA repair; cell cycle; protein complex assembly; regulation of cyclin dependent protein kinase activity; regulation of transcription from Pol II promoter
NM_002015	FOXO1A	8.38	Forkhead box O1A (rhabdomyosarcoma)	Anti-apoptosis; cell growth and/or maintenance; regulation of transcription from Pol II promoter
NM_002221	ITPKB	8.37	Inositol 1,4,5-trisphosphate 3-kinase B	Signal transduction
NM_017832	FLJ20457	8.35	Hypothetical protein FLJ20457	
NM_002808	PSMD2	8.30	Proteasome (prosome, macropain) 26S subunit, non-atpase, 2	Regulation of cell cycle
AB002313	PLXNB2	8.26	Plexin B2	Development
NM_004462	FDFT1	8.23	Farnesyl-diphosphate farnesyltransferase 1	Biosynthesis; cholesterol biosynthesis; isoprenoid biosynthesis; steroid biosynthesis
NM_002109	HARS	8.23	Histidyl-trna synthetase	Histidyl-trna aminoacylation; protein biosynthesis
NM_024330	SLC27A3	8.22	Solute carrier family 27 (fatty acid transporter), member 3	Metabolism
NM_020350	AGTRAP	8.15	Angiotensin II receptor-associated protein	
NM_001288	CLIC1	8.15	Chloride intracellular channel 1	Chloride transport; ion transport
N28741	HIPK2	8.15	Homeodomain interacting protein kinase 2	

GenBank ID	Common name	Fold change	Description	Function
NM_004044	ATIC	8.09	5-Aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism; purine nucleotide biosynthesis
AF052148	G22P1	8.09	Thyroid autoantigen 70 kDa (Ku antigen)	
AL050205	LOC113251	8.08	C-Mpl binding protein	
AF250920	FOXP1	8.08	Forkhead box P1	Regulation of transcription, DNA-dependent
BC001855	WASF2	8.08	WAS protein family, member 2	
NM_003311	TSSC3	8.07	Pleckstrin homology-like domain, family A, member 2	Apoptosis; imprinting
AV650362	SFRS6	8.01	Splicing factor, arginine/serine-rich 6	
NM_018492	TOPK	8.00	T-LAK cell-originated protein kinase	Protein amino acid phosphorylation
X80199	MLN51	7.98	Cancer susceptibility candidate 3	Biological_process unknown
NM_007031	HSF2BP	7.94	Heat shock transcription factor 2 binding protein	Spermatogenesis; transcription from Pol II promoter
NM_002254	KIF3C	7.88	Kinesin family member 3C	Microtubule-based movement
NM_002481	PPP1R12B	7.88	Protein phosphatase 1, regulatory (inhibitor) subunit 12B	Regulation of muscle contraction; signal transduction
NM_004701	CCNB2	7.83	Cyclin B2	Cytokinesis; mitosis; regulation of cell cycle
NM_001722	BN51T	7.79	Polymerase (RNA) III (DNA directed) polypeptide D, 44 kDa	Regulation of cell cycle; trna metabolism; transcription
NM_004356	CD81	7.78	CD81 antigen (target of antiproliferative antibody 1)	Activation of MAPK; phosphatidylinositol biosynthesis; phosphoinositide metabolism; positive regulation of 1-phosphatidylinositol 4-kinase activity; positive regulation of B-cell proliferation; positive regulation of cell proliferation; positive regulation of peptidyl-tyrosine phosphorylation; protein localization; viral entry into host cell; virion attachment, binding of host cell surface receptor
NM_018983	NOLA1	7.77	Nucleolar protein family A, member 1 (H/ACA small nucleolar rnps)	Rrna processing
NM_003091	SNRPB	7.74	Small nuclear ribonucleoprotein polypeptides B and B1	RNA splicing; nuclear mrna splicing, *via* spliceosome
NM_022831	FLJ12806	7.72	Hypothetical protein FLJ12806	
NM_005701	RNUT1	7.72	RNA, U transporter 1	
NM_138443	LOC115106	7.7	Coiled-coil domain containing 5 (spindle associated)	Cell cycle; cytokinesis; mitosis
AL157442	GRINA	7.69	Glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	
NM_004269	CRSP8	7.68	Cofactor required for Sp1 transcriptional activation, subunit 8, 34 kDa	Regulation of transcription from Pol II promoter; transcription initiation from Pol II promoter

GenBank ID	Common name	Fold change	Description	Function
NM_002149	HPCAL1	7.67	Hippocalcin-like 1	Vesicle-mediated transport
NM_016033	CGI-90	7.64	CGI-90 protein	
NM_001398	ECH1	7.64	Enoyl Coenzyme A hydratase 1, peroxisomal	Energy pathways; fatty acid beta-oxidation; fatty acid metabolism
NM_001513	GSTZ1	7.64	Glutathione transferase zeta 1 (maleylacetoacetate isomerase)	Aromatic amino acid family metabolism; phenylalanine catabolism; tyrosine catabolism
NM_024662	FLJ10774	7.64	N-acetyltransferase-like protein	Biological_process unknown
BC015882	EZH1;HGS	7.62	Enhancer of zeste homolog 1 (Drosophila)	Morphogenesis; regulation of transcription, DNA-dependent
NM_024619	FLJ12171	7.58	Fructosamine-3-kinase-related protein	
NM_002911	RENT1	7.57	Regulator of nonsense transcripts 1	Mrna catabolism, nonsense-mediated; regulation of translational termination
AJ005866	SQV7L	7.55	Solute carrier family 35, member D2	Biological_process unknown
AL834255	DKFZp586M1819	7.53	Putative lysophosphatidic acid acyltransferase	Metabolism
NM_016491	MRPL37	7.50	Mitochondrial ribosomal protein L37	Electron transport; response to oxidative stress
NM_000070	CAPN3	7.49	Calpain 3, (p94)	Muscle development; proteolysis and peptidolysis
NM_003642	HAT1	7.48	Histone acetyltransferase 1	DNA packaging; internal protein amino acid acetylation
NM_006561	CUGBP2	7.47	CUG triplet repeat, RNA binding protein 2	RNA processing; neuromuscular junction development; regulation of heart rate
NM_020117	FLJ10595	7.44	Leucyl-trna synthetase	Protein biosynthesis; trna aminoacylation for protein translation
NM_006590	SAD1	7.43	Ubiquitin specific protease 39	RNA splicing; mrna processing; spliceosome assembly; ubiquitin-dependent protein catabolism
NM_006349	CG1I	7.40	Zinc finger, HIT domain containing 1	
NM_014251	SLC25A13	7.39	Solute carrier family 25, member 13 (citrin)	Transport
NM_018706	KIAA1630	7.36	Dehydrogenase E1 and transketolase domain containing 1	Metabolism
NM_032361	MGC5469	7.34	THO complex 3	Mrna-nucleus export; nuclear mrna splicing, *via* spliceosome; transport
BC003353	MGC5309	7.33	Hypothetical protein MGC5309	
NM_057158	DUSP4	7.30	Dual specificity phosphatase 4	MAPKKK cascade; protein amino acid dephosphorylation; regulation of cell cycle
NM_006451	PAIP1	7.29	Poly(A) binding protein interacting protein 1	Protein biosynthesis
NM_030813	SKD3	7.29	Suppressor of potassium transport defect 3	
NM_001098	ACO2	7.27	Aconitase 2, mitochondrial	Citrate metabolism; energy pathways; tricarboxylic

GenBank ID	Common name	Fold change	Description	Function
				acid cycle
NM_032527	KIAA1847	7.26	Kiaa1847	
M96739	NHLH1	7.20	Nescient helix loop helix 1	Cell differentiation; central nervous system development; regulation of transcription, DNA-dependent
NM_013374	PDCD6IP	7.19	Programmed cell death 6 interacting protein	Apoptosis; signal transduction
NM_005572	LMNA	7.18	Lamin A/C	Muscle development
NM_016447	LOC51678	7.16	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	Protein complex assembly
NM_004132	HABP2	7.15	Hyaluronan binding protein 2	Cell adhesion; proteolysis and peptidolysis
NM_002814	PSMD10	7.14	Proteasome (prosome, macropain) 26S subunit, non-atpase, 10	
NM_014629	ARHGEF10	7.14	Rho guanine nucleotide exchange factor (GEF) 10	
NM_003707	RUVBL1	7.14	Ruvb-like 1 (*E. Coli*)	DNA recombination; regulation of transcription from Pol II promoter; spermatogenesis
NM_014551	384D8-2	7.13	Hypothetical protein 384D8_6	
AL365410	LOC56930	7.12	Clone IMAGE:4441633, mrna	
NM_024863	FLJ21174	7.08	Hypothetical protein FLJ21174	
NM_001358	DDX15	7.07	DEAH (Asp-Glu-Ala-His) box polypeptide 15	Nuclear mrna splicing, *via* spliceosome
NM_138615	DDX30	7.04	DEAH (Asp-Glu-Ala-His) box polypeptide 30	
BG497672	CD44	7.03	CD44 antigen (homing function and Indian blood group system)	
AB020626	KIAA0819	6.98	KIAA0819 protein	
BE818483	ATP1B3	6.96	Atpase, Na+/K+ transporting, beta 3 polypeptide	
NM_032122	DTNBP1	6.95	Dystrobrevin binding protein 1	Visual perception
BC021565	SNX8	6.94	Sorting nexin 8	Intracellular protein transport; intracellular signaling cascade
NM_025199	FLJ20886	6.94	Synonyms: ASH, Grb3-3, EGFRBP-GRB2; isoform 1 is encoded by transcript variant 1; HT027; growth factor receptor-bound protein 3; epidermal growth factor receptor-binding protein GRB2; abundant SRC homology; go_function: SH3/SH2 adaptor protein activity [goid 0005070] [evidence TAS] [pmid 8253073]; go_process: epidermal growth factor receptor signaling pathway [goid 0007173] [evidence TAS] [pmid 1322798]; go_process: RAS protein signal transduction [goid 0007265] [evidence TAS] [pmid 8253073]; go_process: cell shape and cell size control [goid 0007148] [evidence E];	

GenBank ID	Common name	Fold change	Description	Function
			go_process: cell-cell signaling [goid 0007267] [evidence TAS] [pmid 8253073]; go_process: intracellular signaling cascade [goid 0007242] [evidence IEA]; Homo sapiens growth factor receptor-bound protein 2 (GRB2), transcript variant 1, mrna.	
NM_021639	SP192	6.92	Hypothetical protein SP192	
NM_001333	CTSL2	6.87	Cathepsin L2	Proteolysis and peptidolysis
D29641	KIAA0052	6.86	KIAA0052 protein	
AK094458	WBP2	6.86	Unnamed protein product; Homo sapiens cdna FLJ37139 fis, clone BRACE2023727, weakly similar to Human WW domain binding protein-2 mrna.	
NM_014468	VENTX2	6.86	VENT-like homeobox 2	Regulation of transcription, DNA-dependent
NM_001769	CD9	6.84	CD9 antigen (p24)	Cell adhesion; cell motility; fusion of sperm to egg plasma membrane; paranodal junction formation; platelet activation
NM_002980	SCTR	6.83	Secretin receptor	G-protein coupled receptor protein signaling pathway; digestion; excretion
NM_014907	KIAA0967	6.79	FERM and PDZ domain containing 1	
NM_030673	SEC13L1	6.79	SEC13-like 1 (*S. cerevisiae*)	Intracellular protein transport
NM_007126	VCP	6.78	Valosin-containing protein	Transport
NM_017957	FLJ20778	6.77	Epsin 3	
NM_004741	NOLC1	6.77	Nucleolar and coiled-body phosphoprotein 1	Cell cycle; mitosis; rrna processing
NM_012321	LSM4	6.75	LSM4 homolog, U6 small nuclear RNA associated (*S. cerevisiae*)	RNA splicing; nuclear mrna splicing, *via* spliceosome
NM_015638	C20orf188	6.74	Transient receptor potential cation channel, subfamily C, member 4 associated protein	Antigen presentation, endogenous peptide antigen; antigen processing, endogenous antigen *via* MHC class I; cytosol to ER transport; intracellular protein transport; peptide transport; protein complex assembly
NM_024960	PANK2	6.73	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	Coenzyme A biosynthesis
NM_000392	ABCC2	6.72	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	Transport
NM_005918	MDH2	6.72	Malate dehydrogenase 2, NAD (mitochondrial)	Tricarboxylic acid cycle
NM_003795	SNX3	6.71	Sorting nexin 3	Endocytosis; intracellular protein transport; intracellular signaling cascade
AK025687	JRK	6.70	Jerky homolog (mouse)	Biological_process unknown
AK056268	SHD	6.69	Src homology 2 domain-containing	Intracellular signaling cascade

GenBank ID	Common name	Fold change	Description	Function
			transforming protein D	
NM_022839	MRPS11	6.64	Mitochondrial ribosomal protein S11	Protein biosynthesis
NM_004896	VPS26	6.62	Vacuolar protein sorting 26 (yeast)	Intracellular protein transport; retrograde transport, endosome to Golgi
NM_017907	FLJ20625	6.57	Hypothetical protein FLJ20625	Regulation of transcription, DNA-dependent
NM_023080	FLJ20989	6.57	Hypothetical protein FLJ20989	
NM_032038	LOC83985	6.57	Spinster-like	Transport
NM_003754	EIF3S5	6.55	Eukaryotic translation initiation factor 3, subunit 5 epsilon, 47 kDa	Protein biosynthesis; regulation of translational initiation
AB002360	MCF2L	6.54	MCF.2 cell line derived transforming sequence-like	Cell growth and/or maintenance; intracellular signaling cascade
AB033001	FLJ10209	6.54	Phosphofurin acidic cluster sorting protein 1	
AK093442	ZNF596	6.54	Zinc finger protein 596	
NM_005444	RQCD1	6.53	RCD1 required for cell differentiation1 homolog (S. Pombe)	Sex differentiation
NM_015994	ATP6M	6.49	Atpase, H+ transporting, lysosomal 34 kDa, V1 subunit D	ATP synthesis coupled proton transport
BF984906	LOC199800	6.44	Hypothetical protein LOC199800	
NM_001102	ACTN1	6.43	Actinin, alpha 1	
NM_005032	PLS3	6.42	Plastin 3 (T isoform)	
NM_017934	PHIP	6.42	Pleckstrin homology domain interacting protein	Insulin receptor signaling pathway
U40271	PTK7	6.42	PTK7 protein tyrosine kinase 7	Cell adhesion; protein amino acid phosphorylation; signal transduction
NM_007103	NDUFV1	6.40	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51 kDa	Energy pathways; mitochondrial electron transport, NADH to ubiquinone
NM_004716	PCSK7	6.40	Proprotein convertase subtilisin/kexin type 7	Peptide hormone processing; proteolysis and peptidolysis
NM_000116	TAZ	6.39	Tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	Heart development; metabolism; muscle contraction; muscle development
NM_000137	FAH	6.38	Fumarylacetoacetate hydrolase (fumarylacetoacetase)	Aromatic amino acid family metabolism; phenylalanine catabolism; tyrosine catabolism
NM_001611	ACP5	6.36	Acid phosphatase 5, tartrate resistant	
NM_001130	AES	6.36	Amino-terminal enhancer of split	Wnt receptor signaling pathway; development; organogenesis; regulation of transcription, DNA-dependent
NM_020410	CGI-152	6.35	Atpase type 13A	Cation transport; metabolism

GenBank ID	Common name	Fold change	Description	Function
NM_006838	METAP2	6.35	Methionyl aminopeptidase 2	Protein modification; proteolysis and peptidolysis; regulation of translation
NM_014254	TMEM5	6.32	Transmembrane protein 5	
NM_024960	PANK2	6.30	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	Coenzyme A biosynthesis
NM_016016	CGI-69	6.29	CGI-69 protein	Transport
NM_001662	ARF5	6.28	ADP-ribosylation factor 5	Intracellular protein transport; small gtpase mediated signal transduction
NM_080476	CDC91L1	6.27	CDC91 cell division cycle 91-like 1 (*S. cerevisiae*)	GPI anchor biosynthesis
NM_002887	RARS	6.26	Arginyl-trna synthetase	Arginyl-trna aminoacylation; protein biosynthesis
NM_002414	MIC2	6.26	CD99 antigen	Cell adhesion
AF183421	RAB31	6.26	RAB31, member RAS oncogene family	Small gtpase mediated signal transduction
NM_002571	PAEP	6.24	Progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin, alpha uterine protein)	Development; transport
NM_003574	VAPA	6.22	VAMP (vesicle-associated membrane protein)-associated protein A, 33 kDa	Positive regulation of I-kappab kinase/NF-kappab cascade
NM_006523	XPNPEPL	6.20	Synonyms: SAMP, XPNPEP, XPNPEPL; X-prolyl aminopeptidase (aminopeptidase P)-like; go_function: aminopeptidase activity [goid 0004177] [evidence P]; Homo sapiens X-prolyl aminopeptidase (aminopeptidase P) 1, soluble (XPNPEP1), mrna.	
NM_018263	FLJ10898	6.17	Additional sex combs like 2 (Drosophila)	
Z70703	LOC166994	6.17	Similar to ba110h4.2 (similar to membrane protein) (LOC389281), mrna	
NM_003077	SMARCD2	6.16	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	Chromatin remodeling; regulation of transcription from Pol II promoter
NM_003977	AIP	6.15	Aryl hydrocarbon receptor interacting protein	Protein folding
AK027249	CAPN3	6.15	Calpain 3, (p94)	Muscle development; proteolysis and peptidolysis
AB018297	KIAA0754	6.15	KIAA0754 protein	
AK000300	ATP2A2	6.14	Atpase, Ca++ transporting, cardiac muscle, slow twitch 2	
NM_004229	CRSP2	6.14	Cofactor required for Sp1 transcriptional	Androgen receptor signaling pathway; regulation of transcription from Pol II promoter;

GenBank ID	Common name	Fold change	Description	Function
			activation, subunit 2, 150 kDa	transcription initiation from Pol II promoter
AB051469	3-PAP	6.14	Phosphatidylinositol-3-phosphate associated protein	Phospholipid dephosphorylation
NM_020533	MCOLN1	6.12	Mucolipin 1	Cation transport
NM_005865	PRSS16	6.12	Protease, serine, 16 (thymus)	Proteolysis and peptidolysis
NM_004461	FARSL	6.11	Phenylalanine-trna synthetase-like, alpha subunit	Phenylalanyl-trna aminoacylation; protein biosynthesis
NM_021198	NLI-IF	6.10	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	Biological_process unknown
AL833978	HP1-BP74	6.10	Hp1-bp74	Nucleosome assembly
BC000050	ART-4	6.10	Likely ortholog of mouse nin one binding protein	
NM_000126	ETFA	6.09	Electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	Electron transport
NM_003295	TPT1	6.08	Tumor protein, translationally-controlled 1	
NM_002319	LRRN1	6.06	Leucine rich repeat neuronal 4	Neurogenesis
NM_014932	NLGN1	6.02	Neuroligin 1	Calcium-dependent cell-cell adhesion; ion channel clustering; protein targeting; regulation of neuron differentiation; synaptic vesicle targeting; synaptogenesis
NM_013241	FHOD1	6.01	Formin homology 2 domain containing 1	Cell organization and biogenesis
NM_007032	HRIHFB2122	6.01	Tara-like protein	Actin modification
NM_001765	CD1C	6.00	CD1C antigen, c polypeptide	Antimicrobial humoral response (sensu Vertebrata)
AB051535	DKFZP586K0524	6.00	Zinc finger, DHHC domain containing 5	
AA316117	MACF1	5.98	Microtubule-actin crosslinking factor 1	
NM_014275	MGAT4B	5.97	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B	Carbohydrate metabolism
NM_004549	NDUFC2	5.97	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5 kDa	Mitochondrial electron transport, NADH to ubiquinone
NM_021141	XRCC5	5.97	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80 kDa)	DNA recombination; double-strand break repair *via* nonhomologous end-joining; regulation of DNA repair
NM_138777	LOC92399	5.96	Mitochondrial ribosome recycling factor	Protein biosynthesis
AB007960	SH3GLB1	5.95	SH3-domain GRB2-like endophilin B1	Apoptosis
NM_016059	PPIL1	5.93	Peptidylprolyl isomerase (cyclophilin)-like 1	Protein folding
NM_002768	PCOLN3	5.93	Procollagen (type III) N-endopeptidase	Gene silencing; mitotic chromosome condensation; negative regulation of S phase of mitotic cell cycle; negative regulation of transcription by glucose; negative regulation of transcription, DNA-dependent;

GenBank ID	Common name	Fold change	Description	Function
				vesicle-mediated transport
NM_000930	PLAT	5.92	Plasminogen activator, tissue	Blood coagulation; protein modification; proteolysis and peptidolysis
NM_003002	SDHD	5.89	Succinate dehydrogenase complex, subunit D, integral membrane protein	Electron transport; tricarboxylic acid cycle
NM_000581	GPX1	5.86	Glutathione peroxidase 1	Response to oxidative stress
AK075559	MGC20446;	5.86	Hypothetical protein MGC20446	Electron transport
NM_016553	NUP62	5.86	Nucleoporin 62 kDa	Transport
AK023373	GTR2;	5.84	Ras-related GTP binding C	RNA splicing; apoptosis; cell growth; cell growth and/or maintenance; small gtpase mediated signal transduction; transcription
NM_005626	SFRS4	5.84	Splicing factor, arginine/serine-rich 4	RNA splicing; nuclear mrna splicing, *via* spliceosome
AJ237724	SLC19A2	5.82	Solute carrier family 19 (thiamine transporter), member 2	Perception of sound; thiamin transport
NM_014730	KIAA0152	5.81	Go_component: integral to membrane [goid 0016021] [evidence IEA]; *Homo sapiens* KIAA0152 gene product (KIAA0152), mrna.	
NM_006164	NFE2L2	5.80	Nuclear factor (erythroid-derived 2)-like 2	Regulation of transcription, DNA-dependent; transcription from Pol II promoter
NM_006196	PCBP1	5.77	Poly(rc) binding protein 1	Mrna metabolism
NM_139178	DEPC-1	5.76	Prostate cancer antigen-1	
AK026920	MYO1D	5.75	Myosin ID	
NM_004814	HPRP8BP	5.75	U5 snrnp-specific 40 kDa protein (hprp8-binding) RNA splicing; nuclear mrna splicing, *via* spliceosome	
AK026373	HNRPA2B1	5.74	Heterogeneous nuclear ribonucleoprotein A2/B1	
NM_002123	HLA-DQB1	5.73	Major histocompatibility complex, class II, DQ beta 1	Antigen presentation, exogenous antigen; antigen processing, exogenous antigen *via* MHC class II; immune response
AB046815	KIAA1595;	5.72	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	
AA318395	MRLC2	5.72	Myosin regulatory light chain MRLC2	
NM_003562	SLC25A11	5.70	Solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	Transport
NM_003485	GPR68	5.69	G protein-coupled receptor 68	G-protein coupled receptor protein signaling pathway; inflammatory response
NM_001731	BTG1	5.68	B-cell translocation gene 1, anti-proliferative	Cell proliferation; negative regulation of cell proliferation
NM_003145	SSR2	5.67	Signal sequence receptor, beta	Cotranslational membrane targeting

GenBank ID	Common name	Fold change	Description	Function
			(translocon-associated protein beta)	
NM_019100	DMAP1	5.66	DNA methyltransferase 1 associated protein 1	DNA methylation; chromatin modification; negative regulation of transcription; regulation of cell growth; regulation of transcription, DNA-dependent
NM_006811	TDE1	5.66	Tumor differentially expressed 1	
AB023166	CIT	5.65	Citron (rho-interacting, serine/threonine kinase 21)	Intracellular signaling cascade; protein amino acid phosphorylation
NM_003769	SFRS9	5.65	Splicing factor, arginine/serine-rich 9	Mrna splice site selection; nuclear mrna splicing, *via* spliceosome
NM_031213	MGC:5244	5.63	Hypothetical protein MGC5244	
NM_001757	CBR1	5.62	Carbonyl reductase 1	Metabolism
NM_003364	UP	5.62	Uridine phosphorylase 1	Nucleoside metabolism
BC020243	SSH1	5.58	Slingshot 1	
NM_015957	LOC51074	5.57	Likely ortholog of mouse monocyte macrophage 19	
NM_016038	CGI-97	5.56	Shwachman-Bodian-Diamond syndrome	
NM_004904	H_GS165L15.1	5.55	Camp responsive element binding protein 5	Positive regulation of transcription, DNA-dependent; transcription from Pol II promoter
NM_023077	FLJ12439	5.55	Hypothetical protein FLJ12439	
NM_014369	PTPN18	5.55	Protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	Protein amino acid dephosphorylation
AF212303	GSTTLp28	5.54	Glutathione S-transferase omega 1	Metabolism
NM_004070	CLCNKA	5.52	Chloride channel Ka	Chloride transport; excretion; ion transport
U47077	PRKDC	5.52	Protein kinase, DNA-activated, catalytic polypeptide	DNA recombination; double-strand break repair; protein modification
NM_006809	TOMM34	5.51	Translocase of outer mitochondrial membrane 34	Protein-mitochondrial targeting
NM_004053	BYSL	5.50	Bystin-like	Cell adhesion; pregnancy
NM_014370	STK23	5.49	Serine/threonine kinase 23	Protein amino acid phosphorylation
NM_004517	ILK	5.46	Integrin-linked kinase	Cell-matrix adhesion; integrin-mediated signaling pathway; protein amino acid phosphorylation
NM_145255	MRPL10	5.46	Mitochondrial ribosomal protein L10	
D43948	KIAA0097	5.45	KIAA0097 gene product	Biological_process unknown
NM_032772	MGC2555	5.43	Zinc finger protein 503	
NM_003904	ZNF259	5.42	Zinc finger protein 259	Cell proliferation; signal transduction

GenBank ID	Common name	Fold change	Description	Function
NM_030782	CRR9	5.41	Cisplatin resistance related protein CRR9p	
NM_001532	SLC29A2	5.41	Solute carrier family 29 (nucleoside transporters), member 2	Cell proliferation; nucleobase, nucleoside, nucleotide and nucleic acid metabolism; nucleoside transport
NM_022827	FLJ21347	5.40	Hypothetical protein FLJ21347	Carbohydrate metabolism
NM_006303	JTV1	5.39	JTV1 gene	Protein biosynthesis
NM_017455	SDFR1	5.33	Stromal cell derived factor receptor 1	
NM_018413	C4ST	5.27	Carbohydrate (chondroitin 4) sulfotransferase 11	
NM_004582	RABGGTB	5.27	Rab geranylgeranyltransferase, beta subunit	Protein modification; visual perception
NM_004550	NDUFS2	5.25	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49 kDa (NADH-coenzyme Q reductase)	Electron transport; mitochondrial electron transport, NADH to ubiquinone
AK023089	SLC30A7	5.21	Solute carrier family 30 (zinc transporter), member 7	Cation transport
NM_033301	RPL8	5.20	Ribosomal protein L8	Protein biosynthesis
NM_015524	C6orf5	5.20	Synonyms: ACT1, CIKS, c6orf5, c6orf6, MGC3581, DKFZP586G0522; isoform 2 is encoded by transcript variant 2; chromosome 6 open reading frame 6; chromosome 6 open reading frame 5; connection to IKK and SAPK/JNK; nfkb-activating protein ACT1; go_component: cellular_component unknown [goid 0008372] [evidence ND]; go_function: molecular_function unknown [goid 0005554] [evidence ND]; go_process: intracellular signaling cascade [goid 0007242] [evidence NAS] [pmid 10962033]; Homo sapiens chromosome 6 open reading frame 4 (c6orf4), transcript variant 2, mrna.	
NM_004134	HSPA9B	5.18	Heat shock 70 kDa protein 9B (mortalin-2)	Protein folding
Down-regulated				
AB040935	CerCAM	−100.00	Cerebral endothelial cell adhesion molecule 1	Lipopolysaccharide biosynthesis
NM_001482	GATM	−100.00	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Creatine biosynthesis
X07263	MYCL1; LMYC	−100.00	Human l-myc gene exon 3 and 3′-flanking region.	Cell growth and/or maintenance; regulation of transcription, DNA-dependent
L27560	IGFBP5	−100.00	Insulin-like growth factor binding protein 5	Cell growth and/or maintenance; regulation of cell growth; signal transduction
AB037804	KIAA1383	−100.00	KIAA1383 protein	
NM_002357	MAD	−100.00	MAX dimerization protein 1	Cell proliferation; development; regulation of transcription, DNA-dependent

GenBank ID	Common name	Fold change	Description	Function
NM_139136	KCNC2	−100.00	Potassium voltage-gated channel, Shaw-related subfamily, member 2	Cation transport; potassium ion transport
NM_000962	PTGS1	−100.00	Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	Lipid metabolism; physiological process; prostaglandin biosynthesis
AK000416	SLC16A5	−100.00	Solute carrier family 16 (monocarboxylic acid transporters), member 5	Monocarboxylic acid transport
NM_000543	SMPD1	−100.00	Sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	Carbohydrate metabolism; neurogenesis; signal transduction; sphingomyelin metabolism
NM_016525	UBAP	−100.00	Ubiquitin associated protein 1	
NM_005263	GFI1	−87.72	Growth factor independent 1	G1/S-specific transcription in mitotic cell cycle; viral life cycle
NM_001276	CHI3L1	−84.75	Chitinase 3-like 1 (cartilage glycoprotein-39)	Metabolism
AB033076	KIDINS220	−80.00	Likely homolog of rat kinase D-interacting substance of 220 kDa	
Y10183	ALCAM	−66.23	Activated leukocyte cell adhesion molecule	Antimicrobial humoral response (sensu Vertebrata); cell adhesion; signal transduction
NM_052944	KST1	−62.89	Sodium/myo-inositol cotransporter 2	Transport
AL080094	RPESP	−60.98	RPE-spondin	
NM_013448	BAZ1A	−48.78	Bromodomain adjacent to zinc finger domain, 1A	Protein ubiquitination; regulation of transcription, DNA-dependent
NM_017936	FLJ20707	−45.87	Kiaa2010	ATP synthesis coupled proton transport; phosphate transport
NM_013357	PURG	−39.37	Werner syndrome	
NM_017884	PINX1	−35.21	PIN2-interacting protein 1	Negative regulation of cell cycle; negative regulation of cell proliferation; telomerase-dependent telomere maintenance
NM_005900	MADH1; DKFZP586M0622	−30.67	MAD, mothers against decapentaplegic homolog 1 (Drosophila)	Regulation of transcription, DNA-dependent; signal transduction; transforming growth factor beta receptor signaling pathway
X75489	LIPA	−29.24	H.sapiens LIPA gene, exon 1.	
M97496	GUCA2A	−28.41	Guanylate cyclase activator 2A (guanylin)	Signal transduction
AK000462	OCIA	−26.74	Ovarian carcinoma immunoreactive antigen	
NM_000756	CRH	−25.77	Corticotropin releasing hormone	Immune response; learning and/or memory; parturition; pregnancy; signal transduction; synaptic transmission
NM_130467	PAGE-5	−25.77	PAGE-5 protein	
NM_030973	TCBAP0758	−23.70	Hypothetical protein TCBAP0758	

GenBank ID	Common name	Fold change	Description	Function
NM_018324	FLJ11106	−21.51	Hypothetical protein FLJ11106	Biosynthesis
NM_000961	PTGIS	−19.46	Prostaglandin I2 (prostacyclin) synthase	Electron transport; lipid metabolism; prostaglandin biosynthesis
NM_002363	MAGEB1	−16.75	Melanoma antigen, family B, 1	
NM_003940	USP13	−16.67	Ubiquitin specific protease 13 (isopeptidase T-3)	Ubiquitin-dependent protein catabolism
NM_004284	CHD1L	−16.23	Synonyms: CHDL, FLJ22530; go_function: ATP binding [goid 0005524] [evidence IEA]; go_function: DNA binding [goid 0003677] [evidence IEA]; go_function: ATP-dependent helicase activity [goid 0008026] [evidence IEA]; go_function: hydrolase activity [goid 0016787] [evidence IEA]; Homo sapiens chromodomain helicase DNA binding protein 1-like (CHD1L), mrna.	
NM_030642	APOL5	−15.77	Apolipoprotein L, 5	Lipid metabolism; lipid transport
AK001640	KIAA0738	−15.77	KIAA0738 gene product	
NM_016270	KLF2	−14.53	Kruppel-like factor 2 (lung)	Regulation of transcription, DNA-dependent
NM_002390	ADAM11	−13.93	A disintegrin and metalloproteinase domain 11	Integrin-mediated signaling pathway; proteolysis and peptidolysis
NM_006651	CPLX1	−13.83	Complexin 1	Exocytosis; neurotransmitter transport; synaptic transmission
NM_006350	FST	−13.72	Follistatin	Development; negative regulation of follicle-stimulating hormone secretion
NM_004245	TGM5	−13.40	Transglutaminase 5	Epidermis development; peptide cross-linking
AL512713	DKFZp762K222	−13.25	Similar to hypothetical protein dkfzp762k222 (LOC401163), mrna	
NM_032649	CPGL2	−13.18	Carnosinase 1	Proteolysis and peptidolysis
NM_022817	PER2	−12.79	Period homolog 2 (Drosophila)	Circadian rhythm; regulation of transcription, DNA-dependent; signal transduction
NM_012453	TBL2	−11.59	Transducin (beta)-like 2	Biological_process unknown
NM_025019	TUBA4	−11.55	Tubulin, alpha 4	Microtubule-based movement
AL133096	DNAJA4	−11.42	Dnaj (Hsp40) homolog, subfamily A, member 4	Protein folding
AK000470	LOC286434	−11.14	Homo sapiens cdna FLJ20463 fis, clone KAT06143.	
NM_024410	ODF1	−10.95	Outer dense fiber of sperm tails 1	Spermatogenesis
NM_000448	RAG1	−10.81	Recombination activating gene 1	DNA recombination; hemocyte development; immune response
AB075834	KIAA1954;	−10.75	Zinc finger protein 90 homolog (mouse)	

GenBank ID	Common name	Fold change	Description	Function
NM_003635	NDST2	−10.26	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	
BF089733	NRXN3	−10.01	Neurexin 3	
NM_000451	SHOX	−9.90	Short stature homeobox	Development; regulation of transcription, DNA-dependent; skeletal development; transcription from Pol II promoter
BC005107	LOC90625	−9.71	Chromosome 21 open reading frame 105	
NM_001215	CA6	−9.62	Carbonic anhydrase VI	One-carbon compound metabolism
NM_001917	DAO	−9.52	D-amino-acid oxidase	Electron transport
NM_138569	MGC18257	−9.43	Chromosome 6 open reading frame 142	
NM_024727	FLJ23259	−9.43	Hypothetical protein FLJ23259	
NM_021946	FLJ11362	−9.35	Hypothetical protein FLJ11362	
NM_001170	AQP7	−9.26	Aquaporin 7	Energy pathways; excretion; glycerol transport; water transport
BC007251	MGC15504	−8.26	Chromosome 14 open reading frame 128	
NM_005013	NUCB2	−7.94	Nucleobindin 2	
NM_000328	RPGR	−7.81	Retinitis pigmentosa gtpase regulator	Intracellular protein transport; perception of sound; visual perception
AL137763	LOC57822	−7.19	Sister-of-mammalian grainyhead	
AY008283	PORIMIN	−7.09	Pro-oncosis receptor inducing membrane injury gene	
NM_000700	ANXA1	−6.99	Annexin A1	Cell motility; cell surface receptor linked signal transduction; inflammatory response; lipid metabolism
NM_014244	ADAMTS2	−6.49	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2	Collagen catabolism
NM_000602	SERPINE1	−6.29	Serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	Blood coagulation
X05299	CENPB	−6.25	Centromere protein B, 80 kDa	Centromere/kinetochore complex maturation
NM_002559	P2RX3	−6.02	Purinergic receptor P2X, ligand-gated ion channel, 3	Ion transport; signal transduction
NM_015900	PS-PLA1	−5.95	Phospholipase A1 member A	Lipid metabolism; phosphatidylserine metabolism
NM_016629	LOC51323	−5.81	Synonyms: DR6, BM-018; death receptor 6; TNFR-related death receptor 6; Homo sapiens tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), mrna.	

GenBank ID	Common name	Fold change	Description	Function
NM_018641	C4S2	−5.59	Carbohydrate (chondroitin 4) sulfotransferase 12	Dermatan sulfate biosynthesis
NM_024106	MGC2663	−5.59	Zinc finger protein 426	Regulation of transcription, DNA-dependent
AK055449	FLJ11588	−5.49	Hypothetical protein FLJ11588	
NM_001615	ACTG2	−5.43	Actin, gamma 2, smooth muscle, enteric	Muscle development
NM_003287	TPD52L1	−5.29	Tumor protein D52-like 1	Biological_process unknown