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Cellular processes involved in human epidermal cells exposed to extremely low frequency electric fields

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Abstract

We observed on different tissues and organisms a biological response after exposure to pulsed low frequency and low amplitude electric or electromagnetic fields but the precise mechanism of cell response remains unknown. The aim of this publication is to understand, using bioinformatics, the biological relevance of processes involved in the modification of gene expression. The list of genes analyzed was obtained after microarray protocol realized on cultures of human epidermal explants growing on deepidermized human skin exposed to a pulsed low frequency electric field. The directed acyclic graph on a WebGestalt Gene Ontology module shows six categories under the biological process root: “biological regulation”, “cellular process”, “cell proliferation”, “death”, “metabolic process” and “response to stimulus”. Enriched derived categories are coherent with the type of in vitro culture, the stimulation protocol or with the previous results showing a decrease of cell proliferation and an increase of differentiation. The Kegg module on WebGestalt has highlighted “cell cycle” and “p53 signaling pathway” as significantly involved. The Kegg website brings out interactions between FoxO, MAPK, JNK, p53, p38, PI3K/Akt, Wnt, mTor or NF-KappaB. Some genes expressed by the stimulation are known to have an exclusive function on these pathways. Analyses performed with Pathway Studio linked cell proliferation, cell differentiation, apoptosis, cell cycle, mitosis, cell death etc. with our microarrays results. Medline citation generated by the software and the fold change variation confirms a diminution of the proliferation, activation of the differentiation and a less well-defined role of apoptosis or wound healing. Wnt and DKK functional classes, DKK1, MACF1, ATF3, MME, TXNRD1, and BMP-2 genes proposed in previous publications after a manual analysis are also highlighted with other genes after Pathway Studio automatic procedure. Finally, an analysis conducted on a list of genes characterized by an accelerated regulation after extremely low frequency pulsed stimulation also confirms their role in the processes of cell proliferation and differentiation. Bioinformatics approach allows in-depth research, without the bias of pre-selection, on cellular processes involved in a huge gene list.

1. Introduction

We observed in our laboratory a biological response after exposure of the following different tissues to low frequency and low amplitude electric or electromagnetic fields:

- bones of mouse embryos in vitro [1],
- bones of chicken embryos in vivo [2],
- bones of quail embryo in vivo [3],
- human epidermal explant culture in vitro [4,5].

Considering the very coherent response of our biological models to specific low frequencies and low-amplitude asymmetric charge balanced pulse-train modulated electric or electromagnetic fields, we tried to identify the mechanism involved at the cell level through microarray screening.

An analysis of potential metabolic networks and potential changes in cellular functions of all the up- and down-regulated data from microarray studies is a very useful method to maximize information. In 2006, Leszczynski [6] explained the interest on a screening approach using high-throughput transcriptomics techniques to determine the molecular targets of an electromagnetic field (EMF) on the sub-cellular level. He is convinced that a systematic screening will generate a large database that will allow scientists to formulate more accurate hypotheses concerning the mechanisms of biological effects of EMF.

To achieve our goal, we used a model of human epidermal explants cultured on deepidermized and devitalized human skin close to physiologic conditions [4,5]. Screening of gene expression variation on our biological model after electrical stimulation was realized with microarray chips U133 Plus 2.0 [5].

The amount of data obtained by microarray screening techniques is so huge that many analyses can be considered and published with the same data set [7]. We published in 2011 our first observations obtained after a manual analysis conducted on microarrays results [5,8] and in 2013, an original statistical approach allowed us to validate an hypothesis on the acceleration of the differentiation after extremely low frequency (ELF) stimulation [9]. It is still possible to find more information on these microarray screening data sets and bioinformatics can help generate a significant amount of results such as active links between genes or highlighted biological processes expressed by our stimulation.

The aim of this publication is to understand, with the help of bioinformatics, the biological relevance of the processes expressed by the modification of gene expression in our data set obtained in 2011.

WebGestalt (WEB-based GENE SeT ANALYSIS Toolkit) [10] was used as an interface for a functional enrichment analysis using GeneOntology (GO) [11] and Kyoto Encyclopedia of Genes and Genomes (KEGG) [12, 13]. GO project provides a structured representation of a

set of concepts and their relationships with defined terms representing gene properties. The analysis call “Gene-set enrichment” can be used to functionally profile a large set of genes and to determine which GO terms appear more frequently than would be expected by chance. This technique finds functionally coherent gene-sets, such as pathways, that are statistically over-represented in a given gene list. KEGG is a database resource for understanding high-level functions and utilities of the biological system from large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies. Pathway Studio software (Ariadne Genomics) [14] allowed the characterization of a biological association network supported by Medline publications related to the differentially expressed genes.

2. Materials and methods

2.1. Biological model

Human epidermal explants were cultured on deepidermized and devitalized human skin close to physiologic conditions. Strips of skin were obtained from abdominoplasty after plastic surgery. Epidermal and hypodermal layers from the harvested skin were removed and cells contained in the dermal layer were destroyed by freeze–thaw cycles and gamma radiation. Finally, this dermis, which will served as culture support, is cut into a 60 mm × 30 mm rectangle. For epidermis explants, a thin layer of epidermis is removed from the skin with a Wagner's dermatome and a punch biopsy is used to cut a 3 mm circle from this harvested epidermis thin layer. Six epidermal explants are placed on the dermal support itself lying on foam. The model is completed by the culture medium. The explant culture was repeated on three different subjects. Eighty-four explants per subjects were divided into control and exposed groups and distributed in 14 Petri dishes. The details for the biological model and culture protocol are explained in Collard et al. [5].

2.2. Electrical stimulation

After 3 days, when the explants are attached to the dermal support, two platinum electrodes are placed on each side of the dermal support and are used to apply the electric signal. Stimulation is realized with a generator producing a pulsed biphasic, asymmetric, charge-balanced current signal with a carrier frequency of 40 Hz and peak current amplitude of 20 mA. The stimulus is repeated during 4 s followed by a 4 s break, for 40 min/day for 11 days. The control group will not be connected to the generator and did not receive stimulation. The electrical stimulation pattern details are explained in Collard et al. [5].

2.3. RNA extraction, microarray and real-time rtPCR

Samplings for microarray analysis were done at days 1, 4, 7 and 12 (Fig. 1). After sampling, the total RNA was extracted from a pool of 12 explants in each sampling condition.

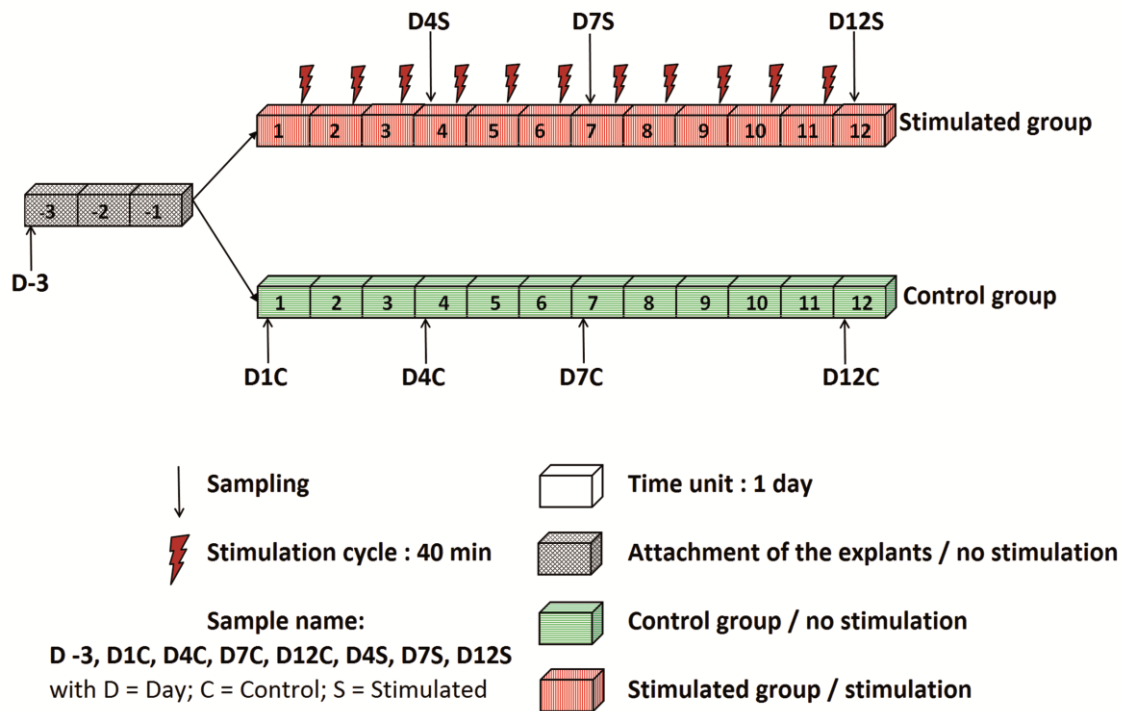


Fig. 1. Study design and sampling time. Control explants: D-3: sampling just after the punch biopsies, D1C: sampling after the period of explant attachment and before the first stimulation, D4C, D7C, D12C: sampling at days 4, 7 and 12 in the control group. Stimulated explants: D4S, D7S, D12S: sampling at days 4, 7 and 12 in the stimulated group after 3, 6 and 11 periods of stimulation.

Total RNA of each pool was extracted using a Qiagen RNeasyMini Kit (Dusseldorf, Germany) after homogenization by a rotor-stator. RNA quality and quantities were measured respectively with the capillary electrophoresis system of Agilent Technologies (Santa Clara, CA) and the spectrometry system of NanoDrop Technologies (Wilmington, DE).

The gene expressions are analyzed following the procedure recommended by Affymetrix (Santa Clara, CA) using Affymetrix microarray U133 Plus 2.0 chips. Quality control was assessed based on 3'/5' ratios of glyceraldehyde 3-phosphate dehydrogenase and b-actin control probe sets. Normalization and statistical analysis of microarray data were performed using ArrayAssist1 Expression Software (Agilent Technologies-Stratagene Products, La Jolla, CA) for the analysis of variance (ANOVA) and k-means analysis. For Student's t-tests, p-values were performed individually for each sampling time comparison.

To validate the microarray results, real-time rtPCR was performed using an Applied Biosystems 7500 Fast Real-Time PCR System and Power SYBR Green PCR MasterMix (Foster City, CA) to evaluate the expression of five transcripts in all of the RNA samples used for

microarray analyses. The results showed similar expression in control and stimulated samples as microarray data.

The details for RNA extraction, microarray and real-time rtPCR are explained in Collard et al. [5].

2.4. Bioinformatics

For this analysis, we used the entire list of probes differentially expressed found in D4S vs. D4C and D7S vs. D7C and D12S vs. D12C comparisons in order to have all genes having their expression modified by the stimulation in early and later times to highlight a maximum metabolic interaction. The complete list was presented in “Supplementary Table 1” with the denomination “List A”.

Probe sets were defined as differentially expressed if the fold change (FC) was ≥ 2 or ≤ -2 and the p-value was ≤ 0.05 after unpaired Student's t-test for one of the following ratio: D(4, 7, or 12)stimulated versus D(4, 7, or 12)control time points.

Different tools were used to analyze “List A”: GO module on WebGestalt, KEGG module on WebGestalt, KEGG website and Pathway Studio.

To facilitate reading, the various analyses performed on “List A” with bioinformatics tools (GO module on WebGestalt, KEGG module on WebGestalt, KEGG website and Pathway Studio) will be presented just before each result.

3. Results

3.1. WebGestalt

WebGestalt website is designed for large-scale genetic studies from which high-throughput datasets are generated. A gene can be visualized and organized by a user-selected method (GO, KEGG etc.). He can also perform a statistical analysis to suggest areas of interest with respect to the set of genes selected.

Parameters introduced in the WebGestalt stating page analysis are “List A” for the Data, “hsapiens” for Organism, the Id Type was “affy_hg_u133_plus_2”, the Ref Set was “affy_hg_u133a_plus_2”, “Hypergeometric” for Statistic, the level of significance was fixed to 0.01, the multiple test adjustment was set to “Benjamini & Hochberg (1995)” and the minimum number of genes for a category was fixed at “2”.

The analysis, using these parameters, generated the following output: the total number of IDs in “List A” was 836; 622 IDs can unambiguously map to 613 unique “Entrez Gene IDs” and 214 IDs could not be mapped to any Entrez Gene ID.

3.1.1. GO module on WebGestalt

WebGestalt plots “directed acyclic graph” (DAG) structure for enriched GO biological processes. The red label represents enriched categories (terms appear in our results more frequently than would be expected by chance) and nodes with a black label represent their non-enriched parents. The enriched nodes show the name of the GO category, number of genes in the category and the adjusted p-value.

As the DAG generated was too large to be displayed correctly in the publication, it can be viewed in “Supplementary Fig. 1”. Nevertheless, analysis described in the Discussion remains clear without viewing the figure.

3.1.2. KEGG module on WebGestalt

The pathway database of KEGG records networks of molecular interactions in cells and connects them with a gene set. We have identified “Cell cycle” and “p53 signaling pathway” as biological pathways proposed by KEGG and revealed by statistics conducted on WebGestalt.

For “Cell cycle”, the number of genes shared by the gene set and by the category was 16; the number of referenced genes in the category, 122; the expected number in the category, 3; the ratio of enrichment, 4.19; the p-value from hypergeometric test, $1.32e-06$ and the p-value adjusted by the multiple test adjustment, 0.0002. The 16 genes identified in “Cell cycle” are presented with their FC obtained in our results in “Supplementary Table 2”.

For “p53 signaling pathway”, the number of genes shared by the gene set and by the category was 11; the number of reference genes in the category, 68; the expected number in the category, 2.13; the ratio of enrichment, 5.17; the p-value from hypergeometric test, $7.78e-06$ and the p-value adjusted by the multiple test adjustment, 0.0005. The 11 genes identified in “p53 signaling pathway” are presented with their FC obtained in our results in “Supplementary Table 3”.

3.2. KEGG website manual analysis

The “List A” allows with the KEGG module on WebGestalt to select statistically “Cell cycle” and “p53 signaling pathway”. Starting from these two pathways, a manual analysis on the KEGG website identifies other related pathways (Table 1) including also genes from “List A”. The goal is to find out the cascade of pathways triggered by ELF stimulation and the pathways including genes known to have an exclusive function on a unique pathway (Table 2).

KEGG pathway name	Number of genes from "List A" included in the pathway	The KEGG pathway is linked to	The KEGG pathway uses
Cell cycle	16	MAPK signaling pathway	
FoxO signaling pathway	13	Apoptosis Cell cycle	MAPK signaling pathway PI3K/Akt signaling pathway TGF- β signaling pathway
MAPK signaling pathway	12	Apoptosis Cell cycle p53 signaling pathway Phosphatidylinositol (PI3K) signaling system Wnt signaling pathway	Calcium signaling pathway
Cytokine-cytokine receptor interaction	12	Adherens junction Apoptosis Focal adhesion Jak-STAT signaling pathway	
p53 signaling pathway	11	Apoptosis Cell cycle	
PI3K/Akt signaling pathway	11	Apoptosis B Cell receptor signaling pathway Cell cycle Focal adhesion Jak-STAT signaling pathway NF-Kappa B signaling pathway p53 signaling pathway	MAPK signaling pathway mTOR signaling pathway
Regulation of Actin cytoskeleton	11	Adherens junction Focal adhesion MAPK signaling pathway	
Focal adhesion	9	Cell cycle PI3K/Akt signaling pathway	Cytokine-cytokine Receptor Interaction ECM-Receptor Interaction MAPK signaling pathway Phosphatidylinositol signaling system Regulation of Actin cytoskeleton Wnt signaling Pathway
Wnt signaling pathway	9	Adherens junction Cell cycle Focal adhesion MAPK signaling pathway TGF- β signaling pathway	
Apoptosis	7	Cell cycle	Cytokine-cytokine Receptor Interaction NF-Kappa B signaling pathway p53 signaling pathway PI3K/Akt signaling pathway
Calcium signaling pathway	6	Apoptosis MAPK signaling pathway	
Jak-STAT signaling	6	Apoptosis	Cytokine-cytokine Receptor Interaction

pathway		Cell cycle	MAPK signaling pathway PI3K/Akt signaling pathway
Tight junction	6	Adherens junction Regulation of Actin cytoskeleton	Phosphatidylinositol signaling system
Complement and coagulation cascades	5	B Cell receptor signaling pathway	
Adherens junction	4	Tight junction Wnt signaling pathway	Cytokine-cytokine Receptor Interaction MAPK signaling pathway TGF- β signaling pathway
B Cell receptor signaling pathway	4	Complement and coagulation cascades Regulation of Actin cytoskeleton	Calcium signaling pathway MAPK signaling pathway NF-Kappa B signaling Ppathway PI3K/Akt signaling pathway
ErbB signaling pathway	4	Cell cycle	Calcium signaling pathway MAPK signaling pathway mTOR signaling pathway PI3K/Akt signaling pathway
T-cell receptor signaling pathway	4	Regulation of Actin cytoskeleton	Calcium signaling pathway Cell adhesion molecules MAPK signaling pathway NF-Kappa B signaling pathway PI3K/Akt signaling pathway
ECM-Receptor Interaction	3	Focal adhesion	
mTOR signaling pathway	3		MAPK signaling pathway
NF-Kappa B signaling Pathway	3		Apoptosis B Cell receptor signaling pathway Calcium signaling pathway T-cell receptor signaling pathway
Phosphatidylinositol signaling system	3	Focal adhesion	
TGF- β signaling pathway	3	Apoptosis Cell cycle MAPK signaling pathway	

Table 1 KEGG website manual analysis. This list contains the pathways linked to “Cell cycle” or “p53 signaling pathway” (obtained from the WebGestalt KEGG module) and including some genes from “List A”.

3.3. Pathway Studio

The first analysis was performed with genes from “List A” to identify the biological processes where the majority of the 836 genes of the list interact. The list of cell processes with more than 100 local connections with genes from “List A” is presented on Fig. 2. The complete list of genes involved in the local connections is presented in “Supplementary Table 4”.

The second analysis was realized with the genes from “List A” having a $FC \geq 10$ or ≤ -10 . With this analysis, we looked for biological processes containing these genes with a very important change in their expression. The left side of Table 3 shows the list of genes from our “List A” with a $FC \geq 10$ or ≤ -10 used for analyses. The central part of the table is a list of accessory genes added by the software during the research of cell processes and having some local connectivity. The right part of the table shows the results of the analysis, and gives a table of biological processes having at least 5 local connections with genes of “List A” having a $FC \geq 10$ or ≤ -10 . We have developed in details the results for the biological processes having at least 7 genes connected (with a $FC \geq 10$ or ≤ -10). “Supplementary Table 5” presented these genes, their FC, Medline citation justifying the connection and all Medline reference numbers.

Probe with $FC \geq 10$ or ≤ -10 selected from List A			Selected by Software Yes/No	Results Number of Local Connectivity	Gene added by Software present in list A		Results Number of Local Connectivity	Results	
Probe	Name	FC Value			Name	FC Value		List of Cell Processes with Local Connectivity > 5	Number of Local Connectivity
204595_s_at	STC1	23.3541	Yes	64	PTGER4	7.7085	2	cell proliferation	11
203434_s_at	MME	20.2766	Yes	100	BRAF	3.0284	1	apoptosis	11
203131_at	PDGFRA	15.0401	Yes	68	BAX	2.9361	1	cell growth	9
202672_s_at	ATF3	13.4129	Yes	71	BMP2	2.8173	1	cell differentiation	9
242809_at	IL1RL1	12.6018	Yes	30	CCL22	2.5772	2	wound healing	7
202157_s_at	CELF2	10.4316	Yes	24	MDM2	2.5016	1	cell migration	6
225975_at	PCDH18	10.2059	Yes	2	HSP90B1	2.4634	1	cell adhesion	6
226084_at	MAP1B	10.1488	Yes	45	FAS	2.4535	2	cell death	6
215704_at	FLG	-11.5147	Yes	23	IL6ST	2.0350	1	inflammatory response	6
213933_at	PTGER3	-11.8960	Yes	81	CHEK1	-2.1364	1	vascularization	6
220414_at	CALML5	-12.4239	Yes	6	CYP2R1	-2.2817	1	endothelial cell function	5
1552544_at	SERPINA12	-22.0370	Yes	10	CDK1	-2.3588	1	translation	5
1569410_at	RP1-14N1.3	-32.8168	Yes	1	KNG1	-2.4975	1	Cell Cycle	5
207908_at	KRT2	-50.0784	Yes	1	KIAA0101	-2.6139	2	regeneration	5
206177_s_at	ARG1	-80.3099	Yes	44	CD44	-2.8185	2	cytokine production	5
229733_s_at	---	11.8369	No		EGFR	-3.0511	4	oxidative stress	5
240248_at	C10orf46	-10.1538	No		SERPINE1	-3.0534	1		
240420_at	AADACL2	-11.4116	No		LYNX1	-4.3924	1		
1553454_at	RPTN	-15.6725	No						
206643_at	HAL	-17.4474	No						
217521_at	---	-18.2340	No						

Results after Software analysis

Table 3 Pathway Studio second analysis. Table of biological processes having at least 5 local connections with genes of List A having a $FC \geq 10$ or ≤ -10 .

The third analysis was made with genes from “List A” having a $FC \geq 4$ or ≤ -4 . Pathway Studio was set to analyze the direct link between genes and the link with the biological processes

having at least 10 local connections with the linked genes. Table 4 presents cell processes, functional classes and proteins linked together or with a cell process.

A cell processes			B Functional Classes			C proteins		
Cell process name	Fold Change	Local Connectivity	Name	Fold Change	Local Connectivity	Gene name	Fold Change	Local Connectivity
cell differentiation		34	WNT		32	MME	20.2766	24
cell proliferation		33	DKK	4.4211	9	PDGFRA	15.0401	22
apoptosis		29				ATF3	13.4129	23
cell growth		25				TFPI2	9.5950	9
cell migration		20				UCHL1	9.5583	17
vascularization		20				PTGER4	7.7085	25
cell death		19				NOV	5.2515	15
cell adhesion		17				ACTA2	5.0869	14
Cell Cycle		15				ADAMTS1	4.9705	10
pregnancy		15				CTGF	4.6389	32
cell motility		14				DKK1	4.4211	27
cell survival		14				PGF	4.1359	24
embryonal development		14				DUSP4	4.0811	10
regeneration		14				TXNRD1	3.2171	15
contraction		13				BMP2	2.8173	29
wound healing		13				SFRP1	-2.3446	21
cell invasion		12				PLD1	-2.5277	16
chemotaxis		12				IFNK	-4.1843	3
DNA replication	-2.0063	12				MACF1	-4.3308	5
inflammatory response		12				LYNX1	-4.3924	3
osteogeneses		12				DLX2	-4.7061	12
oxidative stress		12				MX1	-4.8258	7
morphogenesis		11				HPGD	-4.9080	13
cell fate		10				CXCL14	-5.4770	10
immune response		10				IFIT1	-7.1063	5
neurogenesis		10				MMP9	-8.9066	44
ROS generation		10				TCHH	-9.6763	3
translation	3.6274	10				FLG	-11.5147	10
						PTGER3	-11.8960	22
						RPTN	-15.6725	1
						FLG2	-32.8168	1
						ARG1	-80.3099	11

Table 4 Pathway Studio third analysis. Genes ($FC \geq 4$ or ≤ -4) having links between them and at least 10 local connections with the linked genes. A presents the cell processes, B the functional classes and C the protein linked together or with a cell process.

The fourth analysis was performed on a gene list generated during a study conducted in 2013 [9]. This study showed with an original analysis of statistical triangulation that pulsed extremely low frequency electrical stimulation accelerates the up or down-regulation of some genes which in normal circumstances (control group not stimulated) will follow the same trend (up- or down-regulation) but in a slower manner. The gene list was obtained after a triangulation analysis at sampling time D4S, D4C and D7C. Gene list, with a FC ≥ 2 or ≤ -2 and the p-value ≤ 0.05 , was analyzed with Pathway Studio to research the biological processes concerned with acceleration. Fig. 3 represents links between cell processes and genes from the list of genes showing an acceleration of their regulation after the ELF stimulation.

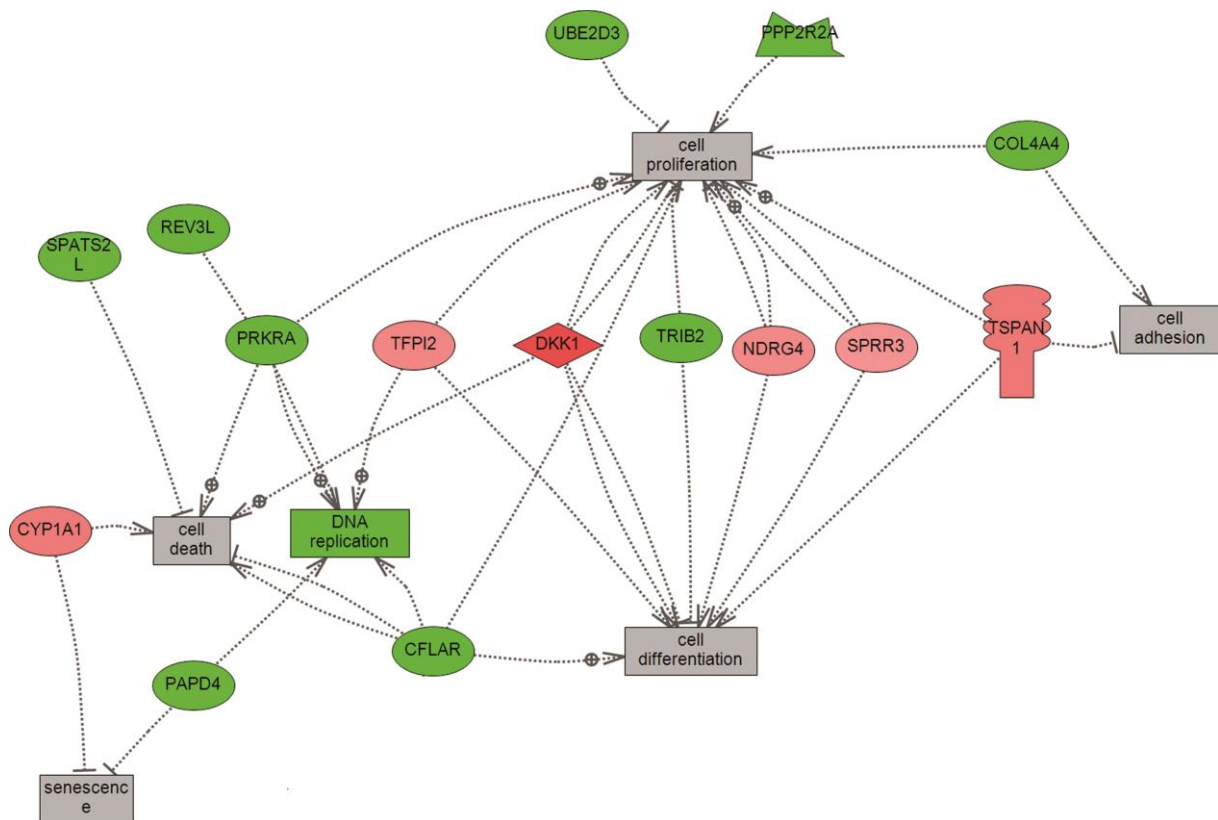


Fig. 3. Pathway Studio fourth analysis. Links between cell processes and genes from a list of genes showing an acceleration of their regulation after the ELF stimulation. Green color is for down-regulated genes or processes and red color for the up-regulated.

4. Discussion

Exploitation of the huge amount of data generated by the microarray screening chip U133 Plus 2.0 is complex, however this technique constitutes one of the best tools to help to understand the mechanisms of the biological effects of EMF [6].

Manual analysis of the results, published in 2011 and 2013, is an interesting step to make the first observations [5,8] or to validate specific hypothesis [9]. Nevertheless, bioinformatics

can generate a significant amount of results linking genes expressed by a stimulus to biological processes.

4.1. WebGestalt GO module

The first bioinformatics approach, using online tools, was made with WebGestalt and the GO module. Enriched GO categories are brought together and visualized on a DAG ("Supplementary Fig. 1"). The "Biological Process" term forms the root and six children categories are highlighted. By clicking on any of the enriched cell processes in red, the gene list for each object can be obtained.

The first child process, non-enriched, is "biological regulation" arising by enriched categories as "positive (or negative) regulation of biological processes" defined as "any process that activates or increases (or stops, prevents, or reduces) the frequency, rate or extent of a biological process" [15]. This way connects the regulation at the "cellular level" and ends at the "nuclear division process" with a second link to "cellular processes". This first category path is quite general but essential for cell mechanisms in which cell is activated and modified in its expression, function or maturation.

The second child process, linked with the first one is "cellular process". Categories enriched from this way mainly have a role in cell cycle and cell division. It should be noted that the "negative regulation of cellular process" followed by the "negative regulation of cell cycle" is present but not the positive category. The "regulation of cell cycle arrest" was also highlighted as "M phase of the mitosis cell cycle" and "mitosis". For this second category, the absence of "positive regulation for the cell cycle" and the presence of "cell cycle arrest" seems to highlight a decrease in cell proliferation.

The third child process enriched and linked to the root is "cell proliferation". This category which is defined as "the multiplication or reproduction of cells, resulting in the expansion of a cell population" [15] is not integrated to the "cellular process" because it is a cell population level process, and cellular processes are restricted to those processes that involve individual cells. The presence of this category confirms the observation of the second category about the decrease of cell proliferation.

The fourth child process is "death" followed by the enriched processes "apoptotic process" and "regulation of programmed cell death". Apoptosis was maybe highlighted owing to a similar part in the molecular mechanisms involved in apoptosis and epidermal terminal differentiation [16]. It is probable that the terminal differentiation of keratinocytes is included in this category. It is also conceivable that the natural apoptosis appears during the time of cell culture.

The fifth child process, "metabolic process" includes macromolecular processes such as DNA repair and replication, and protein synthesis and degradation. The only enriched process in this category is "DNA metabolic process". This process can be explained by the functions

stimulated by the first three categories that require cell division or protein synthesis. For its part, Table 4 indicates “DNA replication” as down-regulated which is also consistent with the decrease of the proliferation highlighted in the second and the third child processes.

The last child process is “response to stimulus” with enriched categories “cellular response to stress”, “response to external stimulus”, “response to wounding”, “response to chemical stimulus” followed by “response to organic cyclic compound”. The cellular response to stress and the response to external stimulus can be easily explained by the ELF stimulation. For the “response to wounding”, we think that it could be explained by the processes involved in the repair of skin injury: the proliferation and the differentiation are mainly activated and it is also clearly the case in our model.

Results and observations from a DAG, automatically generated with a list of an 836 probe set (“List A”), are identical and consistent with the previous observations.

4.2. Kegg module on WebGestalt

The Kegg module on WebGestalt has highlighted statistically two biological pathways. “Cell cycle” contains 16 genes from our “List A” on 122 in the pathway and “p53 signaling pathway” contains 11 genes on 68. The lists with the 16 and 11 genes are presented in “Supplementary Table 2” and “Supplementary Table 3”. It can be noted that the p53 gene is not part of “Supplementary Table 3”.

4.3. Manual analysis with KEGG website

The manual analysis with the KEGG website highlights some biological pathways, arising from “cell cycle” and “p53 signaling pathways”, including genes present in our “List A”. Table 1 presents the list of these biological pathways, the number of genes from “List A” included in the pathway, their links with others pathways including genes present in our “List A” and pathways (including genes present in our “List A”) having a function inside the pathways.

Some genes active in pathways listed on Table 1 and present in “List A” are found in a unique pathway (Table 2) [12,13]. If a gene is known to work exclusively in a specific pathway and if expression of this gene is modified by ELF stimulation, there is a good chance that this pathway is indeed active in the biological process activated by the stimulation.

Forkhead box O (FoxO) is a key regulator of cell growth with the ability to limit cell proliferation by promoting cell cycle arrest, quiescence or apoptosis. He allows an adaptive response to stress, and translates environmental stimuli in the modification of gene expression to coordinate organism reaction [19]. A central regulatory mechanism of FoxO proteins is his phosphorylation by the serine–threonine kinase (Akt) [17]. The FoxO factors are involved in mediating the proliferative effect of Akt on cell survival and growth [18]. Greer and Brunet [19] noticed that c-Jun N-terminal kinases (JNK), a mitogen-activated protein kinases (MAPK) family member activated by stress stimuli, is responsible of FoxO

regulation in several organisms. FoxO are negatively regulated by PKB/Akt and involved in the regulation of cell cycle and cell death [20]. It was also explained by Ponugoti [21] that FoxO1 is required for keratinocyte transition to a wound-healing phenotype that involves increased migration and up-regulation of transforming growth factor β 1 (TGF- β 1) which together promote migration and decrease of apoptosis. The TGF- β s are a group of multifunctional growth factors which inhibit cell cycle progression in many cell types. A mediator of TGF- β , Smad4 induces apoptosis through the JNK pathway [22].

Pathway name	Gene Symbol	EntrezGene
Regulation of actin cytoskeleton	ARHGEF7	8874
	SSH1	54434
	ENAH	55740
	IQGAP3	128239
Wnt signaling pathway	SFRP1	6422
	DKK1	22943
	DAAM1	23002
	TBL1XR1	79718
Complement and coagulation cascades	F12	2161
	KNG1	3827
	THBD	7056
Cell Cycle	CDC6	990
	TTK	7272
FoxO	PRMT1	3276
	PLK4	10733
MAPK	DUSP4	1846
	MAP4K4	9448
Adherens junction	SSX2IP	117178
Calcium signaling pathway	ORAI2	80228
ECM-Receptor Interaction	HMMR	3161
ErbB signaling pathway	NRG1	3084
Focal adhesion	PARVA	55742
Jak-STAT signaling pathway	SPRY4	81848
TGF-beta signaling pathway	FST	10468
Tight junction	EPB41L3	23136

Table 2 List of pathways including gene from "List A". These genes are known to have only function in one pathway.

P53 signaling pathway has a fundamental function in live cells and is associated with many cellular processes such as differentiation, DNA repair, cell cycle, and apoptosis. In response to various stress signals, p53 initiates cell cycle arrest, apoptosis or senescence to maintain cell integrity with the help of Akt and mTor pathways [23,24]. Chen demonstrated [25] the relationship among p53, checkpoint kinase 2 (Chk2) and p38 MAPK in cell cycle arrest mediated by an anticancer drug.

There are many parallels in the mode of regulations of FoxO and p53 to mediate cell cycle arrest, cell death and cellular oxidative stress [26].

MAPKs transduce signals as growth factors and stress from the cell membrane to the transcription factors in the nucleus in response to stimuli as stress [27]. MAPK pathways modulate gene expression for apoptosis, cell cycle, mitosis, proliferation, differentiation or mobility regulations [28,29]. It is also recognized that MAPK and phosphatidylinositol 3-kinase (PI3K) pathways do not function in isolation but as a part of an interconnected signaling network to control a wide range of fundamental cellular functions such as cell growth, survival, and differentiation [30]. p38 MAPK is generally considered to take part in stress response but it also plays a role in cell cycle regulation [25]. The group of Chao [31] indicates that there are at least two independent pathways for stimulation of MAP kinase: one that is dependent on intracellular calcium mobilization, and one that is mediated by tyrosine kinase epidermal growth factor receptor and is calcium independent.

The cytokine–cytokine receptor interaction pathway used also 12 genes of our “LIST A”. Different authors [32,33] underline that cellular responses to the majority of cytokines and growth factors are mediated by Janus kinase/signal transducers and activators of transcription (Jak/STAT) signaling pathway. These responses include proliferation, differentiation, migration, apoptosis and cell survival.

Akt has emerged as a critical signaling node within all cells and as one of the most important protein kinase in eukaryote physiology and disease. Akt is regulated mainly following the activation of PI3K. PI3K/Akt signaling regulated cell proliferation and survival in part by phosphorylating FoxO [26]. Activated PI3K generates several phosphoinositols leading to Akt activation considered as a key survival factor by stimulating cell proliferation and inhibiting apoptosis [34]. When PI3K activation is required for G1/S progression, its inhibition leads G1 arrest in many cell types [35]. PI3K/Akt is a signal transduction pathway and is stimulated by different cytokines, growth factors, and cell–matrix interactions and it controls many biological functions including survival, cell proliferation, cell cycle progression and apoptosis with interaction with Ras and PTEN or DNA synthesis [36]. Akt controls cell growth via mTor complex 1 (mTorC1) pathway which is itself regulated by growth factor signaling [18,37]. The interactions between PI3K/Akt and MAPK/ERK (also known as Raf/Mek/ERK) are important for the regulation of cell cycle progression and apoptosis [38]. The stress-activated MAPKs JNK and p38 have also been shown to be inhibited by Akt signaling. Therefore, a balance between PI3K/Akt survival signaling and JNK/p38 apoptotic signaling can be established through such crosstalk [37]. Another direct or indirect upstream regulator of Akt is focal adhesion kinase (FAK) with a direct bind of Akt1 and FAK and a potentiation of each other's activation [39]. Focal adhesion kinase (FAK) plays a role in the coordinate regulation of cell proliferation and migration in response to integrin-mediated cell adhesion [40]. It is also observed by Lu [41] that an inhibition of Akt by a PI3K inhibitor reduces active NF-KappaB and STAT3 expression when his activation caused the opposite effects. On the other hand,

inhibition of STAT3 activity diminished Akt expression. This observation shows a crosstalk between PI3K/Akt/NF-KappaB and Jak2/STAT3 pathways with a protective effect against apoptosis. He also underlines that PI3K/Akt plays a role in the phosphorylation of STAT via a tyrosine kinase that links cytokine receptors to PI3K through Jak. Cascades of reactions between Jak/STAT or Jak/PI3K/Akt/mTOR with a joint action on proliferation was also analyzed by Yamada [42]. The group of Dan [43] indicates the role of Akt to promote NF-KappaB activation via mTor. PI3K/Akt has also interactions with Tight junction physiology but no generalizations can be made as opposite effects have been observed [44]. Besides the role in immune response of NF-KappaB signaling pathway, there is evidence for his active function in cell cycle and proliferation [45,46] and apoptosis [47].

Tight junctions and adherens junctions are two junctional complexes of epithelial cell–cell adhesion. Adherens junction initiates and stabilizes cell–cell adhesion and regulates actin cytoskeleton or intracellular signaling. Tight junctions have a fence function to prevent some movement of proteins membrane and a gate function for passage of ions and molecules in-between the cells. Tight may link to adherens junction and actin-cytoskeleton via associated cytoplasmic proteins [48,49]. p38 MAPK seems to interact with actin cytoskeleton and modulated actin filament rearrangement during differentiation [50]. Wnt pathway was also studied and it destabilizes adherens junctions and promotes cell migration [51]. Growth factor receptor is active in the membranous phase of this signaling pathway and is followed by the activation of several cytoplasmic kinases known as MAPK. Different groups of MAPs exist: one is activated by growth factors and regulates cell proliferation and differentiation is integrated by the extracellular signal-regulated kinases (ERKs); another group, JNK and p38, is activated by stress stimuli and is involved in cell differentiation and apoptosis. Another way has been found to be activated by growth factors and stress stimuli and participates in cell proliferation [44,52]. MAPK signaling pathway relates to Tight junction by modulating the expression of several Tight junction proteins and by the interactions of Tight junction integral proteins with others for the activation of ERK signaling pathway [44].

Wnt pathway regulates cell proliferation, mobility and differentiation. The activity of Wnt allows the precise control of the cell cycle [53]. Bikkavilli [54] observed the regulation of canonical Wnt signaling by p38 MAPK. The team of Nishita [55] proposes a model of interaction between Wnt and TGF-B signaling pathways. For Peng [56], Wnt regulated the proliferation and the differentiation of mesenchymal progenitor cells through the p53 pathway.

In summary, this analysis allowed us to list different pathways and their interactions which include genes reacting to electrical stimulation. Some of these pathways include genes expressed by ELF stimulation and having only the role of a unique pathway. FoxO is a key regulator of cell growth allowing an adaptive response to stress with the action of Akt and JNK as a regulatory mechanism. FoxO is known to participate in the wound healing of keratinocyte. Akt, another critical node, phosphorylates FoxO and is regulated following

activation of PI3K, JNK, FAK or p38. The cytokines and growth factors have an important function as an activator of Jak/STAT or PI3K/Akt. MAPK and PI3K pathway is an interconnected network and important for the regulation of cell growth or differentiation. p38 MAPK or p53 signaling with the help of Akt under the control of mTor and NF-KappaB, also takes part in stress response. Tight junctions and adherens junctions are also associated with proliferation and differentiation. Actin cytoskeleton interacts with p38 MAPK and Wnt pathway destabilizes the adherens junction. After the activation of membranous growth factor receptor, the different MAPKs signaling are activated. p38 MAPK regulated canonical Wnt pathway allowing a precise control of cell cycle. An interaction between Wnt and TGF-B is also possible. p53 and Wnt are also interconnected.

4.4. Pathway Studio

The first analysis made with Pathway Studio is presented on Fig. 2. The cell processes, the most significant in our complete list of genes, correspond to the results obtained with the GO module on WebGestalt. These results are consistent with our previous observations on cell proliferation and cell differentiation [1–4].

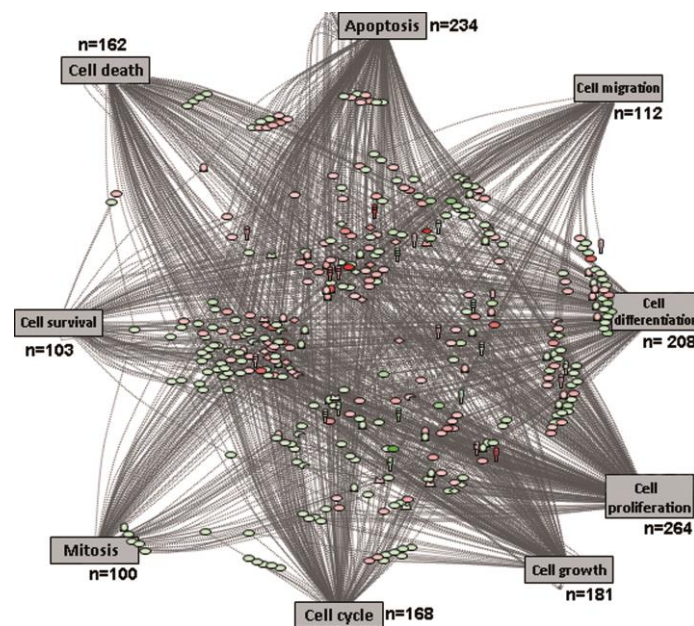


Fig. 2. Pathway Studio first analysis. Pathway Studio representation of the cell processes having more than 100 local connections with genes from “List A”. n = number of local connections of the cell processes.

The second analysis with Pathway Studio is focused on the list of genes with the most important expression variation of our results ($FC \geq 10$ or $\leq -$) (Table 3). We see that the genes whose expression was very highly modified play roles in cell processes previously identified: cell proliferation, apoptosis, cell growth, cell differentiation, wound healing etc. If we analyze the Medline citation proposed by the software of the 11 genes having a local connection with the “cell proliferation” process (“Supplementary Table 5A”), we see for the

upregulated genes: STC1 inhibits longitudinal bone growth by suppressing growth plate chondrocyte proliferation [57]; MME inhibits the growth of hormone-refractory CaP cells [58]; ATF3 can alter proliferation in fibroblasts [59] etc. and for down-regulated genes: blockade of ARG1 blocked the increase in cell proliferation [60]; up-regulation of SERPINA12 promoted the proliferation [61] but we observe a downregulation; up-regulation of FLG promoted the proliferation [62] but we have a down-regulation etc. Only the up-regulation of PDGFRA was not totally coherent with the idea of a decrease of the proliferation [63] but as a receptor, he needs to be activated to promote the proliferation.

“Supplementary Table 5B”, presenting the genes linked with apoptosis, shows that the regulation of the 10 genes is in favor of apoptosis. Nevertheless, results obtained by Law et al. support the notion that STC1 is a pro-apoptotic factor [64] but in the results of Block et al. STC1 [65] mediates the antiapoptotic effects of multipotent stromal cells; MME reduces β -cell apoptosis [66]; PDGFRalpha signaling has a protective role in preventing apoptosis in early development [67]. We see that the apoptosis mechanisms are complex and may depend on the cell type and the level of differentiation. As indicated above, apoptosis was maybe highlighted owing to the sharing in some molecular mechanisms involved in epidermal terminal differentiation [16] and apoptosis and it is also conceivable that apoptosis appears naturally during our cell culture.

Medline information shown in “Supplementary Table 5C” does not allow seeing the direction taken by the process “cell growth” in our results. This process is defined as “the process in which a cell irreversibly increases in size over time by accretion and biosynthetic production of matter similar to that already present” [15]. This process should be perhaps studied sampling time by sampling time.

In contrast, it is clear that the process “cell differentiation” (“Supplementary Table 5D”) is activated: STC1 is expressed in chondrocytic and osteoblastic cells during murine development and can enhance differentiation of calvarial cell culture [68]; MME plays a specific role in the control of growth and differentiation of many cell types [69] and markers of myoepithelial lineage (MME/Cd10) increased strongly during differentiation [70]; ATF3 induction appears to facilitate cell cycle exit and terminal differentiation of chondrocytes [71] etc. The downregulation of filaggrin may seem abnormal especially since filaggrin is used as a marker of cell differentiation but Bernerd et al. published that “some differentiation proteins (i.e., K10, loricrin, filaggrin) were found to be altered in vitro reconstructed epidermis xeroderma pigmentosum” [72] which could confirm the absence of fillagrin in our results. This down-regulation is also consistent with results (unpublished) of a study realized on our keratinocyte explants with the inability to assay the filaggrin at late sampling time.

For genes and FC highlighted in the process “wound healing” (“Supplementary Table 5E”), we suggest that this process should be activated with our culture model showing healing and growing characteristics with and activation of proliferation and differentiation as during the

repair of a skin injury. Our previous observations [73,74] suggest that cells have to be in healing or in growing phases to be sensitive to electrical stimulation. This process should be studied sampling time by sampling time.

The cell processes highlighted on the third analysis with genes ($FC \geq 4$ or ≤ -4) having links between them and at least 10 local connections with the linked genes (Table 4A) are the same as presented above. However, this analysis is interesting because she highlights two functional classes (Table 4B): Wnt, not directly connected to a probe of the Affymetrix chip and DKK, which is connected by the software with the DKK1 probe (FC 4.4211). These pathways are already proposed after a manual analysis [5]. DKK1 plays a role in the down-regulation of Wnt receptor signaling pathway [75] with the effect of a reduction of cell proliferation [76] and an induction of terminal cell differentiation [75,77]. It is also interesting to note that all genes cited in the 2011 publications [5,8] (DKK1, MACF1, ATF3, MME, TXNRD1, and BMP-2) were also found in Table 4C. The process "DNA replication" that the software has integrated with the down-regulated gene MCM4 (FC -2.0063) (Table 4A, Fig. 3) is coherent with previous observations of a diminution of the [3H]-thymidine incorporation in the stimulated samples [4].

For the fourth analysis, Fig. 3 shows cell proliferation and differentiation as main processes involved with genes concerned by the acceleration of their regulation after ELF stimulation.

5. Conclusion

The bioinformatics approach allows in-depth research without preselection bias of the cellular processes highlighted in a microarray screening gene list. New results obtained by this analysis at the molecular level are consistent with previous macroscopic, histologic and histochemical observations [3,4] but also results in animal models [1,2] and clinical studies. This analysis helped to draw the complete list of genes involved in the cell processes which would be very difficult manually. These lists shall be analyzed to determine protein localizations and their interactions to understand the cellular mechanisms activated by an electromagnetic field.

In this analysis of the biological processes on a microarray expression profile in human epidermal cells exposed to extremely low frequency electric fields, different biological pathways and their interactions are highlighted. All these pathways and their interactions have a significant function in cell cycle regulation, proliferation, differentiation, mitoses, apoptosis or stress regulation and include genes from our microarray results ("List A")

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Supplementary Table1:

List A. Entire list of probes differentially expressed in our microarray results for sampling time comparison D4S vs. D4C and D7S vs. D7C and D12S vs. D12C.

Probe Set ID	Gene Symbol	Gene Title	Fold Change
204595_s_at	STC1	stanniocalcin 1	23.3541
203434_s_at	MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	20.2766
203131_at	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	15.0401
202672_s_at	ATF3	activating transcription factor 3	13.4129
242809_at	IL1RL1	Interleukin 1 receptor-like 1	12.6018
229733_s_at	---	Transcribed locus, strongly similar to NP_055107.3 chromobox homolog 6 [Homo sapiens]	11.8369
202157_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	10.4316
225975_at	PCDH18	protocadherin 18	10.2059
226084_at	MAP1B	microtubule-associated protein 1B	10.1488
209278_s_at	TFPI2	tissue factor pathway inhibitor 2	9.5950
201387_s_at	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	9.5583
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	7.7085
201438_at	COL6A3	collagen, type VI, alpha 3	7.4881
208134_x_at	PSG2	pregnancy specific beta-1-glycoprotein 2 /// pregnancy specific beta-1-glycoprotein 2	6.1802
201596_x_at	KRT18	keratin 18	6.1400
206498_at	OCA2	oculocutaneous albinism II (pink-eye dilution homolog, mouse)	6.0356
205083_at	AOX1	aldehyde oxidase 1	6.0162
234994_at	KIAA1913	KIAA1913	5.8534
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	5.4524
206157_at	PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	5.3981
214321_at	NOV	nephroblastoma overexpressed gene	5.2515
200974_at	ACTA2	actin, alpha 2, smooth muscle, aorta	5.0869
222162_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	4.9705
227792_at	LOC162073	Hypothetical protein LOC162073	4.8992
212188_at	KCTD12	potassium channel tetramerisation domain containing 12 /// potassium channel tetramerisation domain containing 12	4.8056
226145_s_at	FRAS1	Fraser syndrome 1	4.6439
209101_at	CTGF	connective tissue growth factor	4.6389
204602_at	DKK1	dickkopf homolog 1 (Xenopus laevis)	4.4211
202047_s_at	CBX6	chromobox homolog 6	4.3214
1559449_a_at	ZNF539	Zinc finger protein 539	4.2012
1555742_at	---	---	4.1799
209652_s_at	PGF	placental growth factor, vascular endothelial growth factor-related protein	4.1359
224461_s_at	AMID	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death /// apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death	4.0929
226034_at	---	Homo sapiens, clone IMAGE:3881549, mRNA	4.0811
1562102_at	AKR1C2	Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase,	4.0718

type III)

1555854_at	---	---	4.0109
227458_at	---	---	3.9876
211924_s_at	PLAUR	plasminogen activator, urokinase receptor /// plasminogen activator, urokinase receptor	3.9476
227295_at	IKIP	IKK interacting protein	3.9393
204720_s_at	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	3.9200
224583_at	COTL1	coactosin-like 1 (Dictyostelium)	3.8309
213943_at	TWIST1	twist homolog 1 (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)	3.7244
1553861_at	TCP11L2	t-complex 11 (mouse) like 2	3.7175
219985_at	HS3ST3A1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	3.7072
209286_at	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	3.6782
1556773_at	PTH1H	Parathyroid hormone-like hormone	3.6707
227345_at	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	3.6573
235296_at	EIF5A2	eukaryotic translation initiation factor 5A2	3.6274
228562_at	---	Transcribed locus	3.5911
202888_s_at	ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	3.5880
203939_at	NT5E	5'-nucleotidase, ecto (CD73)	3.5699
235412_at	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	3.5433
213187_x_at	FTL	ferritin, light polypeptide	3.4496
226955_at	FLJ36748	hypothetical protein FLJ36748	3.4368
217553_at	MGC87042	similar to Six transmembrane epithelial antigen of prostate	3.4358
212099_at	RHOB	ras homolog gene family, member B	3.3820
207719_x_at	CEP170	centrosomal protein 170kDa	3.3662
201028_s_at	CD99	CD99 molecule	3.3469
230528_s_at	MGC2752	hypothetical protein MGC2752	3.3153
200736_s_at	GPX1	glutathione peroxidase 1	3.2702
227534_at	C9orf21	chromosome 9 open reading frame 21	3.2272
201289_at	CYR61	cysteine-rich, angiogenic inducer, 61	3.2192
205694_at	TYRP1	tyrosinase-related protein 1	3.2174
201266_at	TXNRD1	thioredoxin reductase 1	3.2171
204830_x_at	PSG5	pregnancy specific beta-1-glycoprotein 5	3.2168
235456_at	---	CDNA clone IMAGE:4819084	3.1343
202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	3.1341
217890_s_at	PARVA	parvin, alpha	3.1305
231259_s_at	---	Transcribed locus	3.1084
202759_s_at	AKAP2 /// PALM2-AKAP2	A kinase (PRKA) anchor protein 2 /// PALM2- AKAP2 protein	3.0924
223132_s_at	TRIM8	tripartite motif-containing 8	3.0585
225820_at	---	Full-length cDNA clone CS0DB001YB20 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	3.0563
208025_s_at	HMGA2	high mobility group AT-hook 2 /// high mobility group AT-hook 2	3.0474
217858_s_at	ARMCX3	armadillo repeat containing, X-linked 3	3.0447
221985_at	KLHL24	kelch-like 24 (Drosophila)	3.0374
236402_at	---	CDNA FLJ42263 fis, clone TKIDN2014570	3.0284
202497_x_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	3.0075

204015_s_at	DUSP4	dual specificity phosphatase 4	2.9941
200649_at	NUCB1	nucleobindin 1	2.9839
227769_at	---	Transcribed locus, strongly similar to NP_061844.1 G protein-coupled receptor 27; super conserved receptor expressed in brain 1 [Homo sapiens]	2.9821
232434_at	DIRC3	disrupted in renal carcinoma 3	2.9809
224911_s_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	2.9576
219702_at	PLAC1	placenta-specific 1	2.9510
226847_at	FST	follistatin	2.9464
211833_s_at	BAX	BCL2-associated X protein	2.9361
224663_s_at	CFL2	cofilin 2 (muscle)	2.9125
1564630_at	EDN1	endothelin 1	2.9051
226017_at	CMTM7	CKLF-like MARVEL transmembrane domain containing 7	2.8889
239250_at	ZNF542	zinc finger protein 542	2.8878
209276_s_at	GLRX	glutaredoxin (thioltransferase)	2.8731
221752_at	SSH1	Slingshot homolog 1 (Drosophila)	2.8380
223120_at	FUCA2	fucosidase, alpha-L- 2, plasma	2.8303
205290_s_at	BMP2	bone morphogenetic protein 2	2.8173
209114_at	TSPAN1	tetraspanin 1	2.8135
205122_at	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	2.8106
218517_at	PHF17	PHD finger protein 17	2.8104
220477_s_at	C20orf30	chromosome 20 open reading frame 30	2.7949
220178_at	C19orf28	chromosome 19 open reading frame 28	2.7908
205180_s_at	ADAM8	ADAM metallopeptidase domain 8 /// ADAM metallopeptidase domain 8	2.7673
201467_s_at	NQO1	NAD(P)H dehydrogenase, quinone 1	2.7579
201559_s_at	CLIC4	chloride intracellular channel 4	2.7512
205749_at	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	2.7346
203562_at	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	2.7213
209184_s_at	IRS2	insulin receptor substrate 2	2.7157
201540_at	FHL1	four and a half LIM domains 1	2.6863
205602_x_at	PSG7	pregnancy specific beta-1-glycoprotein 7	2.6778
218066_at	SLC12A7	solute carrier family 12 (potassium/chloride transporters), member 7	2.6750
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	2.6594
226725_at	---	Transcribed locus	2.6433
218309_at	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	2.6407
201325_s_at	EMP1	epithelial membrane protein 1	2.6234
209120_at	NR2F2	nuclear receptor subfamily 2, group F, member 2	2.6150
224916_at	LOC340061	hypothetical protein LOC340061	2.6114
37028_at	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	2.6056
200919_at	PHC2	polyhomeotic-like 2 (Drosophila)	2.5913
228234_at	TICAM2	toll-like receptor adaptor molecule 2	2.5910
207861_at	CCL22	chemokine (C-C motif) ligand 22	2.5772
203857_s_at	PDIA5	protein disulfide isomerase family A, member 5	2.5628
201272_at	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	2.5519
201050_at	PLD3	phospholipase D family, member 3	2.5288
234986_at	---	Full-length cDNA clone CS0CAP007YJ17 of Thymus of Homo sapiens (human)	2.5196
225160_x_at	MGC5370	hypothetical protein MGC5370	2.5016

215913_s_at	GULP1	GULP, engulfment adaptor PTB domain containing 1	2.4921
200748_s_at	FTH1	ferritin, heavy polypeptide 1	2.4905
213112_s_at	SQSTM1	sequestosome 1	2.4834
205668_at	LY75	lymphocyte antigen 75	2.4798
224346_at	RNPS1	RNA binding protein S1, serine-rich domain /// RNA binding protein S1, serine-rich domain	2.4797
212233_at	---	3'UTR of hypothetical protein (ORF1)	2.4707
216450_x_at	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	2.4634
225442_at	---	Clone DPDP-3 dental pulp-derived protein 3, mRNA sequence	2.4551
204780_s_at	FAS	Fas (TNF receptor superfamily, member 6)	2.4535
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	2.4501
224927_at	KIAA1949	KIAA1949	2.4450
206307_s_at	FOXD1	forkhead box D1	2.4303
213262_at	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	2.4184
230795_at	---	Transcribed locus	2.4125
217771_at	GOLPH2	golgi phosphoprotein 2	2.4092
1568609_s_at	FAM91A2 /// FLJ39739 /// LOC440685 /// LOC644642 /// LOC644677 /// LOC645052 /// LOC653496	family with sequence similarity 91, member A2 /// FLJ39739 protein /// hypothetical gene supported by AK124550 /// hypothetical protein LOC644642 /// hypothetical protein LOC644677 /// similar to poly (ADP-ribose) polymerase family, member 8 /// similar to hypothetical gene supported by AK123662	2.4065
221773_at	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	2.4040
208814_at	HSPA4	Heat shock 70kDa protein 4	2.4028
204743_at	TAGLN3	transgelin 3	2.4018
201631_s_at	IER3	immediate early response 3	2.3989
219210_s_at	RAB8B	RAB8B, member RAS oncogene family	2.3789
210719_s_at	HMG20B	high-mobility group 20B	2.3762
219655_at	C7orf10	chromosome 7 open reading frame 10	2.3718
208669_s_at	CR11	CREBBP/EP300 inhibitor 1	2.3706
1552277_a_at	C9orf30	chromosome 9 open reading frame 30	2.3643
209298_s_at	ITSN1	intersectin 1 (SH3 domain protein)	2.3634
1566342_at	SOD2	Superoxide dismutase 2, mitochondrial	2.3579
231907_at	---	CDNA FLJ31718 fis, clone NT2RI2006647	2.3559
218056_at	BFAR	bifunctional apoptosis regulator	2.3461
224707_at	ORF1-FL49	putative nuclear protein ORF1-FL49	2.3277
225842_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	2.3260
227418_at	KIAA1826	KIAA1826	2.3242
1553413_at	---	---	2.3234
209159_s_at	NDRG4	NDRG family member 4	2.3176
221004_s_at	ITM2C	integral membrane protein 2C /// integral membrane protein 2C	2.3143
204346_s_at	RASSF1	Ras association (RalGDS/AF-6) domain family 1	2.3056
226337_at	SCYL1BP1	SCY1-like 1 binding protein 1	2.3034
223027_at	SNX9	sorting nexin 9	2.2975
209758_s_at	MFAP5	microfibrillar associated protein 5	2.2919
221489_s_at	SPRY4 /// LOC653170	sprouty homolog 4 (Drosophila) /// similar to sprouty homolog 4 (Drosophila)	2.2764
207528_s_at	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	2.2741
228745_at	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	2.2681
224716_at	SLC35B2	solute carrier family 35, member B2	2.2671

222619_at	ZNF281	zinc finger protein 281	2.2638
202211_at	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3	2.2603
207233_s_at	MITF	microphthalmia-associated transcription factor	2.2524
214455_at	HIST1H2BC	histone 1, H2bc	2.2459
204493_at	BID	BH3 interacting domain death agonist	2.2411
201462_at	SCRN1	secernin 1	2.2341
219390_at	FKBP14	FK506 binding protein 14, 22 kDa	2.2293
204472_at	GEM	GTP binding protein overexpressed in skeletal muscle	2.2266
226773_at	---	MRNA (clone ICRFp50711077)	2.2213
228754_at	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	2.2204
225331_at	CCDC50	coiled-coil domain containing 50	2.2147
64900_at	CHST5 /// ABHD14B	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5 /// abhydrolase domain containing 14B	2.2043
229865_at	FNDC3B	fibronectin type III domain containing 3B	2.2016
221900_at	COL8A2	collagen, type VIII, alpha 2	2.2006
207000_s_at	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	2.1972
1555841_at	---	---	2.1965
205372_at	PLAG1	pleiomorphic adenoma gene 1	2.1820
232035_at	HIST1H4H /// HIST2H4A /// H4/o	histone 1, H4h /// histone 2, H4a /// histone H4/o	2.1713
242293_at	ING3	inhibitor of growth family, member 3	2.1673
225102_at	MGLL	monoglyceride lipase	2.1658
202075_s_at	ITGAV /// PLTP	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) /// phospholipid transfer protein	2.1651
206445_s_at	PRMT1	protein arginine methyltransferase 1	2.1625
225688_s_at	PHLDB2	pleckstrin homology-like domain, family B, member 2	2.1527
204944_at	PTPRG	protein tyrosine phosphatase, receptor type, G	2.1514
209383_at	DDIT3	DNA-damage-inducible transcript 3	2.1452
226479_at	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	2.1438
203349_s_at	ETV5	ets variant gene 5 (ets-related molecule)	2.1394
201525_at	APOD	apolipoprotein D	2.1354
200885_at	RHOC	ras homolog gene family, member C	2.1343
208699_x_at	TKT	transketolase (Wernicke-Korsakoff syndrome)	2.1333
218276_s_at	SAV1	salvador homolog 1 (Drosophila)	2.1330
225609_at	GSR	glutathione reductase	2.1323
203925_at	GCLM	glutamate-cysteine ligase, modifier subunit	2.1314
200787_s_at	PEA15	phosphoprotein enriched in astrocytes 15	2.1308
201393_s_at	IGF2R	insulin-like growth factor 2 receptor	2.1262
226264_at	SUSD1	sushi domain containing 1	2.1256
228073_at	NANP	N-acetylneuraminic acid phosphatase	2.1246
200958_s_at	SDCBP	syndecan binding protein (syntenin)	2.1246
219502_at	NEIL3	nei endonuclease VIII-like 3 (E. coli)	2.1223
200867_at	ZNF313	zinc finger protein 313	2.1201
201889_at	FAM3C	family with sequence similarity 3, member C	2.1186
225447_at	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	2.1124
202260_s_at	STXBP1	syntaxin binding protein 1	2.1094
202912_at	ADM	adrenomedullin	2.1088
226886_at	---	Clone 114 tumor rejection antigen	2.0984
242979_at	---	Transcribed locus	2.0974
242277_at	PHACTR2	Phosphatase and actin regulator 2	2.0955

242191_at	NBPF11 /// NBPF9 /// NBPF10	neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 9 /// neuroblastoma breakpoint family, member 10	2.0942
226893_at	---	CDNA FLJ31718 fis, clone NT2RI2006647	2.0921
225598_at	SLC45A4	solute carrier family 45, member 4	2.0884
221039_s_at	DDEF1	development and differentiation enhancing factor 1	2.0872
227013_at	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	2.0872
222212_s_at	LASS2	LAG1 longevity assurance homolog 2 (S. cerevisiae)	2.0854
218990_s_at	SPRR3	small proline-rich protein 3	2.0839
1558693_s_at	C1orf85	chromosome 1 open reading frame 85	2.0780
217988_at	CCNB1IP1	cyclin B1 interacting protein 1	2.0765
224833_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2.0764
225665_at	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	2.0745
212274_at	LPIN1	lipin 1	2.0738
231576_at	ETNK1	Ethanolamine kinase 1	2.0633
227037_at	LOC201164	similar to CG12314 gene product	2.0611
233406_at	KIAA0256	KIAA0256 gene product	2.0579
217294_s_at	ENO1	enolase 1, (alpha)	2.0512
212894_at	SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)	2.0509
200615_s_at	AP2B1	adaptor-related protein complex 2, beta 1 subunit	2.0480
210896_s_at	ASPH	aspartate beta-hydroxylase	2.0445
239231_at	---	CDNA FLJ41910 fis, clone PEBLM2007834	2.0443
233888_s_at	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	2.0443
241418_at	---	MRNA; cDNA DKFZp686B14224 (from clone DKFZp686B14224)	2.0433
223370_at	PLEKHA3	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	2.0431
211372_s_at	IL1R2	interleukin 1 receptor, type II	2.0403
203103_s_at	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	2.0379
212196_at	IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	2.0350
201751_at	JOSD1	Josephin domain containing 1	2.0312
203093_s_at	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	2.0201
224951_at	LASS5	LAG1 longevity assurance homolog 5 (S. cerevisiae)	2.0177
227279_at	TCEAL3	transcription elongation factor A (SII)-like 3	2.0166
222547_at	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	2.0165
209385_s_at	PROSC	proline synthetase co-transcribed homolog (bacterial)	2.0144
228933_at	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	2.0137
206683_at	ZNF165	zinc finger protein 165	2.0131
239804_at	CCNI	Cyclin I	2.0117
206343_s_at	NRG1	neuregulin 1	2.0087
219155_at	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	2.0073
201619_at	PRDX3	peroxiredoxin 3	2.0066
225055_at	AMZ2	Archaeometzincins-2	2.0008
236297_at	---	CDNA FLJ45742 fis, clone KIDNE2016327	-2.0020
232931_at	ASCC3L1	activating signal cointegrator 1 complex subunit 3- like 1	-2.0025

237232_at	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	-2.0035
1559232_a_at	SLC33A1	Solute carrier family 33 (acetyl-CoA transporter), member 1	-2.0035
227211_at	PHF19	PHD finger protein 19	-2.0058
222037_at	MCM4	MCM4 minichromosome maintenance deficient 4 (<i>S. cerevisiae</i>)	-2.0063
209512_at	HSDL2	hydroxysteroid dehydrogenase like 2	-2.0065
222016_s_at	ZNF323	zinc finger protein 323	-2.0080
214807_at	---	MRNA; cDNA DKFZp564O0862 (from clone DKFZp564O0862)	-2.0088
204033_at	TRIP13	thyroid hormone receptor interactor 13	-2.0092
1569157_s_at	LOC162993	hypothetical protein LOC162993	-2.0098
240242_at	---	Transcribed locus	-2.0101
228708_at	RAB27B	RAB27B, member RAS oncogene family	-2.0112
224771_at	NAV1	neuron navigator 1	-2.0125
236781_at	ANKS1A	Ankyrin repeat and sterile alpha motif domain containing 1A	-2.0138
1565976_at	FCHO2	FCH domain only 2	-2.0203
235660_at	---	MRNA; cDNA DKFZp667E0114 (from clone DKFZp667E0114)	-2.0226
242560_at	FANCD2	Fanconi anemia, complementation group D2	-2.0241
1559204_x_at	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	-2.0242
213995_at	ATP5S	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit s (factor B)	-2.0269
243330_at	CTNNA2	Catenin (cadherin-associated protein), alpha 2	-2.0290
213603_s_at	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	-2.0304
238902_at	PCMTD1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-2.0317
1568706_s_at	AVIL	Advillin	-2.0333
228032_s_at	---	CDNA FLJ36663 fis, clone UTERU2002826	-2.0336
231722_at	CASP14	caspace 14, apoptosis-related cysteine peptidase	-2.0337
243793_at	AHDC1	AT hook, DNA binding motif, containing 1	-2.0341
237238_at	WWC1	WW, C2 and coiled-coil domain containing 1	-2.0377
214594_x_at	ATP8B1	ATPase, Class I, type 8B, member 1	-2.0386
1560199_x_at	FLJ11903	similar to hypothetical protein MGC40405	-2.0386
236492_at	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	-2.0392
235247_at	---	Full-length cDNA clone CS0DI029YM01 of Placenta Cot 25-normalized of Homo sapiens (human)	-2.0397
227510_x_at	PRO1073	PRO1073 protein	-2.0404
222039_at	SLC35E1 /// LOC146909	solute carrier family 35, member E1 /// hypothetical protein LOC146909	-2.0425
242932_at	FARP2	FERM, RhoGEF and pleckstrin domain protein 2	-2.0429
242146_at	SNRPA1	Small nuclear ribonucleoprotein polypeptide A'	-2.0429
241832_at	FAM98A	family with sequence similarity 98, member A	-2.0435
244663_at	---	Transcribed locus	-2.0450
206277_at	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	-2.0452
203554_x_at	PTTG1	pituitary tumor-transforming 1	-2.0485
230312_at	---	Transcribed locus	-2.0488
211776_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3 /// erythrocyte membrane protein band 4.1-like 3	-2.0545
233867_at	---	CDNA FLJ20112 fis, clone COL05405	-2.0562
229457_at	ANKHD1	ankyrin repeat and KH domain containing 1	-2.0562
1563130_a_at	IREB2	Iron-responsive element binding protein 2	-2.0572

240240_at	UBE2J2	Ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	-2.0597
232865_at	AFF4	AF4/FMR2 family, member 4	-2.0600
232529_at	SP3	Sp3 transcription factor	-2.0605
215203_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	-2.0620
226259_at	EXOC6	exocyst complex component 6	-2.0623
233824_at	LPP	LIM domain containing preferred translocation partner in lipoma	-2.0629
222889_at	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, <i>S. cerevisiae</i>)	-2.0635
209754_s_at	TMPO	thymopoietin	-2.0637
242476_at	---	Transcribed locus	-2.0646
239629_at	CFLAR	CASP8 and FADD-like apoptosis regulator	-2.0651
206364_at	KIF14	kinesin family member 14	-2.0663
244766_at	SMG1 /// LOC23117 /// LOC440345 /// LOC440354 /// LOC595101	PI-3-kinase-related kinase SMG-1 /// KIAA0220-like protein /// hypothetical protein LOC440345 /// PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1 pseudogene	-2.0666
205206_at	KAL1	Kallmann syndrome 1 sequence	-2.0696
216237_s_at	MCM5	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (<i>S. cerevisiae</i>)	-2.0701
237216_at	GARNL1	GTPase activating Rap/RanGAP domain-like 1	-2.0705
204300_at	PET112L	PET112-like (yeast)	-2.0709
239780_at	KIF1B	Kinesin family member 1B	-2.0712
240262_at	CTNNA1	Catenin (cadherin-associated protein), alpha 1, 102kDa	-2.0718
243301_at	COL22A1	collagen, type XXII, alpha 1	-2.0751
205339_at	STIL	SCL/TAL1 interrupting locus	-2.0756
240165_at	---	Transcribed locus, weakly similar to XP_209041.2 PREDICTED: similar to KIAA1503 protein [<i>Homo sapiens</i>]	-2.0766
225067_at	ULK3	unc-51-like kinase 3 (<i>C. elegans</i>)	-2.0772
221666_s_at	PYCARD	PYD and CARD domain containing	-2.0796
215726_s_at	CYB5A	cytochrome b5 type A (microsomal)	-2.0822
213517_at	PCBP2	Poly(rC) binding protein 2	-2.0850
219494_at	RAD54B	RAD54 homolog B (<i>S. cerevisiae</i>)	-2.0853
222634_s_at	TBL1XR1	transducin (beta)-like 1X-linked receptor 1	-2.0876
205909_at	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	-2.0887
227955_s_at	---	CDNA: FLJ22256 fis, clone HRC02860	-2.0953
237262_at	---	Full length insert cDNA clone ZE05E03	-2.0956
231449_at	---	Transcribed locus	-2.1010
1552619_a_at	ANLN	anillin, actin binding protein	-2.1015
244822_at	GART	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	-2.1040
218726_at	DKFZp762E1312	hypothetical protein DKFZp762E1312	-2.1041
1558515_at	---	CDNA clone IMAGE:4328048	-2.1047
1564308_a_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-2.1068
241768_at	BCCIP	BRCA2 and CDKN1A interacting protein	-2.1083
225239_at	---	CDNA FLJ26120 fis, clone SYN00419	-2.1101
202338_at	TK1	thymidine kinase 1, soluble	-2.1114
232094_at	C15orf29	Chromosome 15 open reading frame 29	-2.1115
242642_at	NDEL1	NudE nuclear distribution gene E homolog like 1 (<i>A. nidulans</i>)	-2.1129
244659_at	TRIP12	Thyroid hormone receptor interactor 12	-2.1135

229327_s_at	---	Transcribed locus, strongly similar to NP_005351.2 v-maf musculoaponeurotic fibrosarcoma oncogene homolog; Avian musculoaponeurotic fibrosarcoma (MAF) protooncogene; v-maf musculoaponeurotic fibrosarcoma (avian) oncogene homolog [Homo sapiens]	-2.1137
227891_s_at	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	-2.1139
234326_at	N4BP1	Nedd4 binding protein 1	-2.1150
226936_at	C6orf173	chromosome 6 open reading frame 173	-2.1152
201896_s_at	PSRC1	proline/serine-rich coiled-coil 1	-2.1164
201506_at	TGFBI	transforming growth factor, beta-induced, 68kDa	-2.1171
232552_at	DAAM1	Dishevelled associated activator of morphogenesis 1	-2.1175
242369_x_at	NCOA2	Nuclear receptor coactivator 2	-2.1179
237713_at	TACC2	Transforming, acidic coiled-coil containing protein 2	-2.1196
1557963_at	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	-2.1200
212570_at	ENDOD1	endonuclease domain containing 1	-2.1229
233254_x_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-2.1231
205933_at	SETBP1	SET binding protein 1	-2.1249
236462_at	YEATS2	YEATS domain containing 2	-2.1274
227678_at	XRCC6BP1	XRCC6 binding protein 1	-2.1288
235626_at	CAMK1D	calcium/calmodulin-dependent protein kinase ID	-2.1305
221861_at	---	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	-2.1309
219250_s_at	FLRT3	fibronectin leucine rich transmembrane protein 3	-2.1322
1554486_a_at	C6orf114	chromosome 6 open reading frame 114	-2.1346
229070_at	C6orf105	chromosome 6 open reading frame 105	-2.1347
205394_at	CHEK1	CHK1 checkpoint homolog (S. pombe)	-2.1364
236951_at	NSFL1C	NSFL1 (p97) cofactor (p47)	-2.1367
226875_at	DOCK11	dedicator of cytokinesis 11	-2.1369
1557586_s_at	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	-2.1382
240282_at	WDR1	WD repeat domain 1	-2.1383
228729_at	CCNB1	cyclin B1	-2.1390
213454_at	APITD1	apoptosis-inducing, TAF9-like domain 1	-2.1395
234762_x_at	NLN	Neurolysin (metallopeptidase M3 family)	-2.1399
226223_at	PAWR	PRKC, apoptosis, WT1, regulator	-2.1407
244610_x_at	UBE2E2	Ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	-2.1421
235716_at	---	Transcribed locus	-2.1427
1556373_a_at	MGC35361	Hypothetical protein MGC35361	-2.1441
233388_at	CA12	Carbonic anhydrase XII	-2.1478
204092_s_at	AURKA	aurora kinase A	-2.1483
228320_x_at	CCDC64	coiled-coil domain containing 64	-2.1501
225904_at	C1orf96	chromosome 1 open reading frame 96	-2.1504
210868_s_at	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	-2.1511
237868_x_at	KIAA0674	KIAA0674	-2.1523
213701_at	C12orf29	chromosome 12 open reading frame 29	-2.1529
243384_at	---	---	-2.1543
234552_at	---	CDNA FLJ20083 fis, clone COL03440	-2.1559
1562416_at	FLNB	Filamin B, beta (actin binding protein 278)	-2.1598
243647_at	---	---	-2.1613
226365_at	SMA3 /// LOC643998	SMA3 /// Similar to cadherin 12, type 2 preproprotein	-2.1619

243004_at	---	Transcribed locus	-2.1627
243769_at	---	---	-2.1647
239536_at	C1orf56	Chromosome 1 open reading frame 56	-2.1667
237107_at	PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	-2.1669
243660_at	CHD9	Chromodomain helicase DNA binding protein 9	-2.1768
219428_s_at	PXMP4	peroxisomal membrane protein 4, 24kDa	-2.1786
231540_at	DKFZp451M2119	hypothetical protein DKFZp451M2119	-2.1791
203178_at	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	-2.1812
218662_s_at	HCAP-G	chromosome condensation protein G	-2.1829
204887_s_at	PLK4	polo-like kinase 4 (Drosophila)	-2.1853
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	-2.1854
213007_at	KIAA1794	KIAA1794	-2.1864
201008_s_at	TXNIP	thioredoxin interacting protein	-2.1865
239551_at	TMED3	Transmembrane emp24 protein transport domain containing 3	-2.1902
224428_s_at	CDCA7	cell division cycle associated 7 /// cell division cycle associated 7	-2.1903
1559023_a_at	---	---	-2.1917
225299_at	MYO5B	myosin VB	-2.1924
202705_at	CCNB2	cyclin B2	-2.1935
243499_at	---	Transcribed locus	-2.1939
206642_at	DSG1	desmoglein 1	-2.1940
232890_at	C14orf135	Chromosome 14 open reading frame 135	-2.1972
229566_at	LOC645638 /// LOC650626	similar to WDNM1 homolog /// similar to WDNM1 homolog	-2.2005
47571_at	ZNF236	zinc finger protein 236	-2.2009
216392_s_at	SEC23IP	SEC23 interacting protein	-2.2044
240991_at	NDRG1	N-myc downstream regulated gene 1	-2.2047
1553718_at	ZNF548	zinc finger protein 548	-2.2083
236752_at	PKP4	Plakophilin 4	-2.2085
238534_at	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	-2.2091
244665_at	ITGA6	Integrin, alpha 6	-2.2099
219316_s_at	C14orf58	chromosome 14 open reading frame 58	-2.2109
229966_at	EWSR1	Ewing sarcoma breakpoint region 1	-2.2149
236524_at	TM2D1	TM2 domain containing 1	-2.2154
240008_at	ARID1B	AT rich interactive domain 1B (SWI1-like)	-2.2189
216211_at	C10orf18	Chromosome 10 open reading frame 18	-2.2222
221698_s_at	CLEC7A	C-type lectin domain family 7, member A /// C-type lectin domain family 7, member A	-2.2245
240499_at	KIAA1128	KIAA1128	-2.2271
236470_at	---	Transcribed locus	-2.2276
202954_at	PAK3 /// UBE2C	p21 (CDKN1A)-activated kinase 3 /// ubiquitin-conjugating enzyme E2C	-2.2289
239486_at	---	---	-2.2294
218349_s_at	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	-2.2301
1553672_at	ENAH	enabled homolog (Drosophila)	-2.2322
243828_at	KATNAL1	Katanin p60 subunit A-like 1	-2.2350
205627_at	CDA	cytidine deaminase	-2.2352
1557996_at	---	---	-2.2352
202575_at	CRABP2	cellular retinoic acid binding protein 2	-2.2381
238774_at	KIAA1267	KIAA1267	-2.2381
214199_at	SFTPD	surfactant, pulmonary-associated protein D	-2.2418
213067_at	MYH10	myosin, heavy polypeptide 10, non-muscle	-2.2443
232511_at	---	CDNA clone IMAGE:5310744	-2.2476

223126_s_at	C1orf21	chromosome 1 open reading frame 21	-2.2527
1773_at	FNTB	farnesyltransferase, CAAX box, beta	-2.2527
239571_at	MEF2A	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)	-2.2600
1552621_at	POLR2J2	DNA directed RNA polymerase II polypeptide J-related gene	-2.2613
1560926_at	PPP4R2	Protein phosphatase 4, regulatory subunit 2	-2.2632
1560680_at	EEA1	Early endosome antigen 1, 162kD	-2.2646
239954_at	ZNF160	zinc finger protein 160	-2.2646
205024_s_at	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	-2.2647
231925_at	P2RY1	Purinergic receptor P2Y, G-protein coupled, 1	-2.2659
233674_at	FOXO3A	Forkhead box O3A	-2.2674
232489_at	CCDC76	coiled-coil domain containing 76	-2.2678
216858_x_at	---	---	-2.2691
220066_at	CARD15	caspase recruitment domain family, member 15	-2.2710
1554287_at	TRIM4	tripartite motif-containing 4	-2.2718
227209_at	CNTN1	Contactin 1	-2.2722
241837_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	-2.2724
1557384_at	ZNF131	Zinc finger protein 131 (clone pHZ-10)	-2.2738
1557270_at	ZNF69	Zinc finger protein 69	-2.2740
1553333_at	C1orf161	chromosome 1 open reading frame 161	-2.2748
1552622_s_at	POLR2J2 /// LOC441259	DNA directed RNA polymerase II polypeptide J-related gene /// similar to postmeiotic segregation increased 2-like 2	-2.2780
229538_s_at	IQGAP3	IQ motif containing GTPase activating protein 3	-2.2799
227109_at	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	-2.2817
1563900_at	FAM83B	family with sequence similarity 83, member B	-2.2818
242972_at	HCG18	HLA complex group 18	-2.2833
236379_at	EPB41	Erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	-2.2864
233931_at	ELF1	E74-like factor 1 (ets domain transcription factor)	-2.2868
201996_s_at	SPEN	spen homolog, transcriptional regulator (Drosophila)	-2.2882
1562378_s_at	PROM2	prominin 2	-2.2895
240314_at	NCOR1	Nuclear receptor co-repressor 1	-2.2917
205363_at	BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	-2.2929
236613_at	RBM25	RNA binding motif protein 25	-2.2953
243031_at	RTN4	Reticulon 4	-2.2964
207414_s_at	PCSK6	proprotein convertase subtilisin/kexin type 6	-2.2971
215191_at	---	CDNA FLJ14085 fis, clone HEMBB1002534	-2.2973
201930_at	MCM6	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	-2.2974
204400_at	EFS	embryonal Fyn-associated substrate	-2.2987
212022_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	-2.2992
206023_at	NMU	neuromedin U	-2.3020
227759_at	PCSK9	proprotein convertase subtilisin/kexin type 9	-2.3134
225911_at	NPNT	nephronectin	-2.3176
205774_at	F12	coagulation factor XII (Hageman factor)	-2.3185
244674_at	RBM6	RNA binding motif protein 6	-2.3206
226959_at	---	---	-2.3215
218806_s_at	VAV3	vav 3 oncogene	-2.3234
214753_at	PFAAP5	Phosphonoformate immuno-associated protein 5	-2.3318
212949_at	BRRN1	barren homolog 1 (Drosophila)	-2.3321
1556950_s_at	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6	-2.3341

238880_at	GTF3A	general transcription factor IIIA	-2.3378
210397_at	DEFB1	defensin, beta 1	-2.3405
209762_x_at	SP110	SP110 nuclear body protein	-2.3411
237768_x_at	---	---	-2.3411
223229_at	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	-2.3441
202037_s_at	SFRP1	secreted frizzled-related protein 1	-2.3446
237690_at	GPR115	G protein-coupled receptor 115	-2.3450
238982_at	DENR	density-regulated protein	-2.3488
232278_s_at	DEPDC1	DEP domain containing 1	-2.3498
217586_x_at	---	---	-2.3498
242225_at	MON2	MON2 homolog (<i>S. cerevisiae</i>)	-2.3569
203213_at	CDC2	cell division cycle 2, G1 to S and G2 to M	-2.3588
218802_at	CCDC109B	coiled-coil domain containing 109B	-2.3602
235730_at	LOC642351	hypothetical protein LOC642351	-2.3608
203755_at	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	-2.3623
215206_at	EXT1	Exostoses (multiple) 1	-2.3639
203742_s_at	TDG	thymine-DNA glycosylase	-2.3664
226877_at	RPL32P3	ribosomal protein L32 pseudogene 3	-2.3677
225687_at	FAM83D	family with sequence similarity 83, member D	-2.3699
236474_at	ZNF395	Zinc finger protein 395	-2.3722
240636_at	---	Transcribed locus	-2.3771
221768_at	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	-2.3887
235493_at	ZNF638	Zinc finger protein 638	-2.3926
1556277_a_at	PAPD4	PAP associated domain containing 4	-2.3960
238812_at	ZA20D3	Zinc finger, A20 domain containing 3	-2.3962
244145_at	FYCO1	FYVE and coiled-coil domain containing 1	-2.3975
244801_at	PSMB7	Proteasome (prosome, macropain) subunit, beta type, 7	-2.3983
205421_at	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	-2.3986
239238_at	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	-2.3998
242550_at	EIF3S9	eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa	-2.4005
222104_x_at	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	-2.4022
232141_at	U2AF1	U2 small nuclear RNA auxiliary factor 1	-2.4025
1555019_at	PCDH21	protocadherin 21	-2.4107
242859_at	TFCP2	Transcription factor CP2	-2.4212
203968_s_at	CDC6	CDC6 cell division cycle 6 homolog (<i>S. cerevisiae</i>)	-2.4227
235138_at	VPS35	Vacuolar protein sorting 35 (yeast)	-2.4239
242413_at	ITSN2	Intersectin 2	-2.4260
222348_at	---	---	-2.4287
1558714_at	ROBO1	Roundabout, axon guidance receptor, homolog 1 (<i>Drosophila</i>)	-2.4302
215268_at	KIAA0754	hypothetical LOC643314	-2.4320
244185_at	METAP2	Methionyl aminopeptidase 2	-2.4351
219510_at	POLQ	polymerase (DNA directed), theta	-2.4362
205442_at	MFAP3L	microfibrillar-associated protein 3-like	-2.4369
1557360_at	LRPPRC	leucine-rich PPR-motif containing	-2.4379
229674_at	SERTAD4	SERTA domain containing 4	-2.4389
226663_at	ANKRD10	ankyrin repeat domain 10	-2.4405
218953_s_at	PCYOX1L	prenylcysteine oxidase 1 like	-2.4409
1564248_at	VIL2	Villin 2 (ezrin)	-2.4412

228483_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	-2.4426
223822_at	SUSD4	sushi domain containing 4	-2.4458
215252_at	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	-2.4469
214079_at	DHRS2	dehydrogenase/reductase (SDR family) member 2	-2.4470
207192_at	DNASE1L2	deoxyribonuclease I-like 2	-2.4483
239348_at	USP31	Ubiquitin specific peptidase 31	-2.4512
239635_at	TMEM137	transmembrane protein 137	-2.4520
201890_at	RRM2	ribonucleotide reductase M2 polypeptide	-2.4525
202871_at	TRAF4	TNF receptor-associated factor 4	-2.4546
236907_at	PABPC1	Poly(A) binding protein, cytoplasmic 1	-2.4566
240155_x_at	ZNF738 /// ZNF493	zinc finger protein 738 /// zinc finger protein 493	-2.4619
1557352_at	SQLE	Squalene epoxidase	-2.4711
204796_at	EML1	echinoderm microtubule associated protein like 1	-2.4752
223701_s_at	USP47	ubiquitin specific peptidase 47	-2.4765
240238_at	TBC1D22A	TBC1 domain family, member 22A	-2.4816
1558695_at	PLEKHA5	Pleckstrin homology domain containing, family A member 5	-2.4827
231235_at	NKTR	natural killer-tumor recognition sequence	-2.4847
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	-2.4871
243562_at	---	---	-2.4975
223381_at	CDCA1	cell division cycle associated 1	-2.4982
223878_at	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-2.5029
219306_at	KIF15 /// C7orf9	kinesin family member 15 /// chromosome 7 open reading frame 9	-2.5034
239597_at	PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-2.5062
236496_at	DEGS2	degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)	-2.5131
244605_at	---	---	-2.5166
214805_at	EIF4A1	Eukaryotic translation initiation factor 4A, isoform 1	-2.5181
208955_at	DUT	dUTP pyrophosphatase	-2.5199
242673_at	UBE3C	Ubiquitin protein ligase E3C	-2.5270
215723_s_at	PLD1	phospholipase D1, phosphatidylcholine-specific	-2.5277
218542_at	CEP55	centrosomal protein 55kDa	-2.5278
214295_at	KIAA0485	KIAA0485 protein	-2.5287
240458_at	ITPR2	Inositol 1,4,5-triphosphate receptor, type 2	-2.5311
230792_at	AMDD	amidase domain containing	-2.5332
225834_at	LOC652689 /// FAM72A /// LOC653594 /// LOC653820	hypothetical protein LOC652689 /// family with sequence similarity 72, member A /// similar to family with sequence similarity 72, member A /// similar to family with sequence similarity 72, member A	-2.5336
226279_at	PRSS23	protease, serine, 23	-2.5337
1562063_x_at	NBPF1 /// NBPF3 /// NBPF11 /// NBPF20 /// NBPF9 /// NBPF10 /// NBPF8	neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 9 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 8	-2.5344
220521_s_at	ATG16L1	ATG16 autophagy related 16-like 1 (S. cerevisiae)	-2.5350
224555_x_at	IL1F7	interleukin 1 family, member 7 (zeta)	-2.5385
204162_at	KNTC2	kinetochore associated 2	-2.5439
225655_at	UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1	-2.5545

217653_x_at	LOC653468 /// LOC653471	hypothetical protein LOC653468 /// similar to Ribosome biogenesis protein BMS1 homolog	-2.5560
242055_at	C6orf85	Chromosome 6 open reading frame 85	-2.5599
215062_at	FMNL2	Formin-like 2	-2.5611
204962_s_at	CENPA	centromere protein A	-2.5650
236313_at	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-2.5690
226649_at	PANK1	pantothenate kinase 1	-2.5702
235575_at	LOC440993	Hypothetical gene supported by AK128346	-2.5705
242712_x_at	LOC653086 /// LOC653489 /// LOC653596	similar to RAN-binding protein 2-like 1 isoform 2 /// similar to Ran-binding protein 2 (RanBP2) (Nuclear pore complex protein Nup358) (Nucleoporin Nup358) (358 kDa nucleoporin) (P270) /// similar to RAN-binding protein 2-like 1 isoform 2	-2.5780
242836_at	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	-2.5786
204072_s_at	FRY	furry homolog (Drosophila)	-2.5825
227450_at	C12orf46	chromosome 12 open reading frame 46	-2.5857
226789_at	---	CDNA FLJ46881 fis, clone UTERU3015647, moderately similar to Embigin precursor	-2.5901
242572_at	GAB1	GRB2-associated binding protein 1	-2.5903
237252_at	THBD	thrombomodulin	-2.5906
229765_at	ZNF207	Zinc finger protein 207	-2.5911
203961_at	NEBL	nebullette	-2.5924
213805_at	ABHD5	abhydrolase domain containing 5	-2.5928
229899_s_at	HSUP1	Similar to RPE-spondin	-2.5929
244780_at	SGPP2	sphingosine-1-phosphate phosphatase 2	-2.5951
242271_at	SLC26A9	solute carrier family 26, member 9	-2.6001
227062_at	TncRNA	trophoblast-derived noncoding RNA	-2.6018
228323_at	CASC5	cancer susceptibility candidate 5	-2.6072
242008_at	AGTPBP1	ATP/GTP binding protein 1	-2.6074
203889_at	SCG5	secretogranin V (7B2 protein)	-2.6091
243583_at	TCF7L2	Transcription factor 7-like 2 (T-cell specific, HMG-box)	-2.6094
202503_s_at	KIAA0101	KIAA0101	-2.6139
211788_s_at	TREX2	three prime repair exonuclease 2	-2.6191
238755_at	LOC644943	Similar to peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor	-2.6199
218585_s_at	DTL	denticleless homolog (Drosophila)	-2.6215
223316_at	CCDC3	coiled-coil domain containing 3	-2.6230
220651_s_at	MCM10	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)	-2.6242
205651_x_at	RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4	-2.6281
211906_s_at	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4 /// serpin peptidase inhibitor, clade B (ovalbumin), member 4	-2.6321
205685_at	CD86	CD86 molecule	-2.6329
232264_at	EDD1	E3 ubiquitin protein ligase, HECT domain containing, 1	-2.6340
1558732_at	---	---	-2.6428
242829_x_at	FBXL3	F-box and leucine-rich repeat protein 3	-2.6469
241339_at	C9orf52	Chromosome 9 open reading frame 52	-2.6484
1566191_at	SUZ12	Suppressor of zeste 12 homolog (Drosophila)	-2.6528
1556551_s_at	SLC39A6	solute carrier family 39 (zinc transporter), member 6	-2.6577
226617_at	ARL5A	ADP-ribosylation factor-like 5A	-2.6582
219259_at	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	-2.6583

217602_at	PPIA	peptidylprolyl isomerase A (cyclophilin A)	-2.6587
219918_s_at	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	-2.6615
233595_at	USP34	ubiquitin specific peptidase 34	-2.6620
1552777_a_at	RAET1E	retinoic acid early transcript 1E	-2.6622
230000_at	C17orf27	chromosome 17 open reading frame 27	-2.6631
227276_at	PLXDC2	plexin domain containing 2	-2.6636
222809_x_at	C14orf65	chromosome 14 open reading frame 65	-2.6665
203767_s_at	STS	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	-2.6681
232266_x_at	CDC2L5	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	-2.6689
242710_at	RSNL2	Restin-like 2	-2.6699
213707_s_at	DLX5	distal-less homeobox 5	-2.6712
235592_at	ELL2	Elongation factor, RNA polymerase II, 2	-2.6718
242903_at	IFNGR1	interferon gamma receptor 1	-2.6784
215012_at	ZNF451	zinc finger protein 451	-2.6810
236322_at	FLJ31951	Hypothetical protein FLJ31951	-2.6817
238883_at	THRAP2	Thyroid hormone receptor associated protein 2	-2.6823
235701_at	R3HDM2	R3H domain containing 2	-2.6827
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	-2.6852
221521_s_at	GINS2	GINS complex subunit 2 (Psf2 homolog)	-2.6875
226999_at	RNPC3	RNA-binding region (RNP1, RRM) containing 3	-2.6881
206400_at	LGALS7	lectin, galactoside-binding, soluble, 7 (galectin 7)	-2.6884
203016_s_at	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	-2.6911
240066_at	LOC168850	Hypothetical protein LOC168850	-2.6975
240690_at	DKFZp761P0423	Hypothetical protein DKFZp761P0423	-2.7087
238455_at	---	CDNA FLJ45742 fis, clone KIDNE2016327	-2.7199
223307_at	CDCA3	cell division cycle associated 3	-2.7204
220221_at	VPS13D /// LOC654256	vacuolar protein sorting 13 homolog D (S. cerevisiae) /// similar to vacuolar protein sorting 13D isoform 1	-2.7237
235847_at	ZFAND3	Zinc finger, AN1-type domain 3	-2.7426
1559078_at	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-2.7449
204718_at	EPHB6	EPH receptor B6	-2.7475
233350_s_at	TEX264	testis expressed sequence 264	-2.7535
238342_at	---	---	-2.7538
243752_s_at	PSCD3	pleckstrin homology, Sec7 and coiled-coil domains 3	-2.7549
207078_at	MED6	mediator of RNA polymerase II transcription, subunit 6 homolog (S. cerevisiae)	-2.7560
207828_s_at	CENPF	centromere protein F, 350/400ka (mitosin)	-2.7587
234331_s_at	---	---	-2.7689
1569519_at	NBPF1 /// NBPF11 /// NBPF20 /// NBPF9 /// NBPF10 /// NBPF8	neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 9 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 8	-2.7700
242059_at	ETNK1	Ethanolamine kinase 1	-2.7732
242695_at	---	Transcribed locus	-2.7869
220085_at	HELLS	helicase, lymphoid-specific	-2.7894
218355_at	KIF4A	kinesin family member 4A	-2.7943
1556658_a_at	MBNL1	Muscleblind-like (Drosophila)	-2.7946
240673_at	---	Transcribed locus	-2.7955
232170_at	S100A7L1	S100 calcium binding protein A7-like 1	-2.7978
209681_at	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-2.8017

218755_at	KIF20A	kinesin family member 20A	-2.8042
228623_at	---	Transcribed locus, weakly similar to XP_517454.1 PREDICTED: similar to hypothetical protein MGC45438 [Pan troglodytes]	-2.8079
203418_at	CCNA2	cyclin A2	-2.8117
206539_s_at	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	-2.8173
217523_at	CD44	CD44 molecule (Indian blood group)	-2.8185
243073_at	C6orf153	Chromosome 6 open reading frame 153	-2.8297
202095_s_at	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	-2.8354
242871_at	PAQR5	progesterone and adiponectin receptor family member V	-2.8419
243993_at	PCTK2	PCTAIRE protein kinase 2	-2.8453
219990_at	E2F8	E2F transcription factor 8	-2.8464
206363_at	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	-2.8529
236966_at	ARMC8	armadillo repeat containing 8	-2.8586
239660_at	C20orf74	chromosome 20 open reading frame 74	-2.8730
1564424_at	FAM62B	Family with sequence similarity 62 (C2 domain containing) member B	-2.8825
209891_at	SPBC25	spindle pole body component 25 homolog (S. cerevisiae)	-2.8870
201310_s_at	C5orf13	chromosome 5 open reading frame 13	-2.8923
205197_s_at	ATP7A /// LOC644732	ATPase, Cu ⁺⁺ transporting, alpha polypeptide (Menkes syndrome) /// similar to ATPase, Cu ⁺⁺ transporting, alpha polypeptide	-2.8988
241242_at	C9orf10	Chromosome 9 open reading frame 10	-2.9114
236514_at	ACOT8	Acyl-CoA thioesterase 8	-2.9157
240046_at	---	---	-2.9198
241954_at	FDFT1	Farnesyl-diphosphate farnesyltransferase 1	-2.9208
213832_at	---	MRNA; cDNA DKFZp547P042 (from clone DKFZp547P042)	-2.9283
243319_at	MED31	Mediator of RNA polymerase II transcription, subunit 31 homolog (S. cerevisiae)	-2.9317
243179_at	---	CDNA FLJ33993 fis, clone DFNES2007757	-2.9326
1563088_a_at	LOC284837	hypothetical protein LOC284837	-2.9336
236201_at	---	Transcribed locus	-2.9343
231108_at	FUS	Fusion (involved in t(12;16) in malignant liposarcoma)	-2.9343
240383_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-2.9389
232169_x_at	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	-2.9405
232344_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	-2.9413
242352_at	NIPBL	Nipped-B homolog (Drosophila)	-2.9489
233405_at	FIP1L1	FIP1 like 1 (S. cerevisiae)	-2.9678
242074_at	PITPNB	Phosphatidylinositol transfer protein, beta	-2.9705
242732_at	MTSS1	Metastasis suppressor 1	-2.9736
203423_at	RBP1	retinol binding protein 1, cellular	-2.9751
231148_at	IGFL2	IGF-like family member 2	-2.9829
236985_at	EIF4B	Eukaryotic translation initiation factor 4B	-3.0014
210701_at	CFDP1	craniofacial development protein 1	-3.0070
204709_s_at	KIF23	kinesin family member 23	-3.0218
204822_at	TTK	TTK protein kinase	-3.0231
207018_s_at	RAB27B /// SH3BGR	RAB27B, member RAS oncogene family /// SH3 domain binding glutamic acid-rich protein	-3.0275
239272_at	MMP28	matrix metalloproteinase 28	-3.0362

1565483_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	-3.0511
202627_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	-3.0534
1553982_a_at	RAB7B	RAB7B, member RAS oncogene family	-3.0534
238736_at	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	-3.0566
213624_at	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	-3.0813
219148_at	PBK	PDZ binding kinase	-3.0825
241702_at	HNRPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-3.0885
224839_s_at	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	-3.0909
207254_at	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	-3.0949
232597_x_at	SFRS2IP	Splicing factor, arginine/serine-rich 2, interacting protein	-3.0963
238431_at	---	Transcribed locus	-3.1013
1563468_at	ZAK	Sterile alpha motif and leucine zipper containing kinase AZK	-3.1025
213256_at	39144	membrane-associated ring finger (C3HC4) 3	-3.1043
232958_at	PYGL	Phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	-3.1045
236700_at	LOC653352	similar to eukaryotic translation initiation factor 3, subunit 8	-3.1122
204942_s_at	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	-3.1321
210052_s_at	TPX2	TPX2, microtubule-associated, homolog (<i>Xenopus laevis</i>)	-3.1531
204444_at	KIF11	kinesin family member 11	-3.1660
236678_at	JAG1	Jagged 1 (Alagille syndrome)	-3.1691
235405_at	GSTA4	glutathione S-transferase A4	-3.1691
237689_at	SARS	Seryl-tRNA synthetase	-3.1698
1557987_at	LOC641298	PI-3-kinase-related kinase SMG-1 - like locus	-3.1817
235805_at	ACSS2	Acyl-CoA synthetase short-chain family member 2	-3.1999
1559360_at	EFNA5	Ephrin-A5	-3.2070
240180_at	---	MRNA full length insert cDNA clone EUROIMAGE 1090207	-3.2081
235409_at	MGA	MAX gene associated	-3.2274
1569312_at	ZNF146	Zinc finger protein 146	-3.2288
209642_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	-3.2352
240361_at	---	---	-3.2594
221081_s_at	DENND2D	DENN/MADD domain containing 2D	-3.2633
215314_at	ANK3	Ankyrin 3, node of Ranvier (ankyrin G)	-3.2698
234032_at	ZCCHC7	Zinc finger, CCHC domain containing 7	-3.2701
203798_s_at	VSNL1	visinin-like 1	-3.2776
243206_at	CCDC45	Coiled-coil domain containing 45	-3.2914
235798_at	---	---	-3.2915
239022_at	SDHAL1	Succinate dehydrogenase complex, subunit A, flavoprotein-like 1	-3.2919
215029_at	---	---	-3.2935
232527_at	---	CDNA FLJ13309 fis, clone OVARC1001442	-3.3177
222034_at	GNB2L1	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	-3.3262
225354_s_at	SH3BGR2	SH3 domain binding glutamic acid-rich protein like 2	-3.3318
207109_at	POU2F3	POU domain, class 2, transcription factor 3	-3.3335
235144_at	---	CDNA FLJ32320 fis, clone PROST2003537	-3.3382

203764_at	DLG7	discs, large homolog 7 (Drosophila)	-3.4421
219978_s_at	NUSAP1	nucleolar and spindle associated protein 1	-3.4521
202687_s_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10 /// tumor necrosis factor (ligand) superfamily, member 10	-3.4603
1566232_at	LOC126917	Hypothetical protein LOC126917	-3.4810
229740_at	LOC643008	PP12104	-3.4840
232304_at	PELI1	Pellino homolog 1 (Drosophila)	-3.4926
243171_at	---	---	-3.5052
230053_at	---	Transcribed locus	-3.5137
1553906_s_at	FGD2	FYVE, RhoGEF and PH domain containing 2	-3.5585
202870_s_at	CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	-3.5709
230599_at	RNF19	Ring finger protein 19	-3.5953
218986_s_at	FLJ20035	hypothetical protein FLJ20035	-3.5965
235651_at	---	---	-3.6240
244597_at	DNAPTP6	DNA polymerase-transactivated protein 6	-3.6378
223940_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	-3.6857
238142_at	KCTD13	Potassium channel tetramerisation domain containing 13	-3.7052
1556007_s_at	CSNK1A1	Casein kinase 1, alpha 1	-3.7180
1556361_s_at	ANKRD13C	ankyrin repeat domain 13C	-3.7276
229546_at	LOC653602	hypothetical LOC653602	-3.7366
206465_at	ACSBG1	acyl-CoA synthetase bubblegum family member 1	-3.7543
209446_s_at	C7orf44	chromosome 7 open reading frame 44	-3.7589
220413_at	SLC39A2	solute carrier family 39 (zinc transporter), member 2	-3.7906
1555773_at	BPIL2	bactericidal/permeability-increasing protein-like 2	-3.8309
243544_at	ADH1C	Alcohol dehydrogenase 1C (class I), gamma polypeptide	-3.8425
227238_at	MUC15	mucin 15, cell surface associated	-3.8625
206605_at	P11	26 serine protease	-3.8929
1558426_x_at	TMEM142B	transmembrane protein 142B	-3.8934
205249_at	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	-3.9374
208188_at	KRT9	keratin 9 (epidermolytic palmoplantar keratoderma)	-3.9451
233874_at	KIAA1458	KIAA1458	-4.0320
232530_at	LOC652226	hypothetical protein LOC652226	-4.0428
243740_at	---	Transcribed locus	-4.1165
243177_at	C6orf117	Chromosome 6 open reading frame 117	-4.1290
209714_s_at	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	-4.1583
226382_at	LOC283070	hypothetical protein LOC283070	-4.1647
217014_s_at	AZGP1	alpha-2-glycoprotein 1, zinc	-4.1651
224093_at	IFNK	interferon, kappa	-4.1843
208246_x_at	---	CDNA FLJ20006 fis, clone ADKA02694	-4.2011
1564333_a_at	SORCS2	Sortilin-related VPS10 domain containing receptor 2	-4.2156
219300_s_at	CNTNAP2	contactin associated protein-like 2	-4.2502
236350_at	---	Transcribed locus	-4.2659
236266_at	LOC283666	Hypothetical protein LOC283666	-4.2757
229374_at	EPHA4	EPH receptor A4	-4.3010
1562529_s_at	RORA	RAR-related orphan receptor A	-4.3122
1553407_at	MACF1	microtubule-actin crosslinking factor 1	-4.3308
242998_at	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	-4.3381
1554179_s_at	LYNX1	Ly6/neurotoxin 1	-4.3924
229596_at	AMDHD1	amidohydrolase domain containing 1	-4.4176
1553986_at	RASEF	RAS and EF-hand domain containing	-4.4527

1554565_x_at	UNQ1887	signal peptide peptidase 3	-4.4724
238827_at	SH3RF2	SH3 domain containing ring finger 2	-4.5778
239771_at	CAND1	cullin-associated and neddylation-dissociated 1	-4.5790
231930_at	ELMOD1	ELMO/CED-12 domain containing 1	-4.6531
207147_at	DLX2	distal-less homeobox 2	-4.7061
207730_x_at	HDGF2	Hepatoma-derived growth factor-related protein 2	-4.7804
228538_at	ZNF662	zinc finger protein 662	-4.7805
203328_x_at	IDE	insulin-degrading enzyme	-4.8145
202086_at	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) /// myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	-4.8258
203913_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-4.9080
227725_at	ST6GALNAC1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1	-4.9467
211712_s_at	ANXA9	annexin A9 /// annexin A9	-4.9757
235514_at	FLJ25084	Skin ASpartic Protease	-5.0316
210130_s_at	TM7SF2	transmembrane 7 superfamily member 2	-5.0340
214070_s_at	ATP10B	ATPase, Class V, type 10B	-5.0435
202179_at	BLMH	bleomycin hydrolase	-5.0938
218002_s_at	CXCL14	chemokine (C-X-C motif) ligand 14	-5.4770
205513_at	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	-5.5351
1552532_a_at	ATP6V1C2	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	-5.5408
220432_s_at	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	-5.5901
205054_at	NEB	nebulin	-5.7908
1554195_a_at	MGC23985	similar to AVLV472	-5.9873
242559_at	C20orf38	Chromosome 20 open reading frame 38	-6.2197
239787_at	KCTD4	potassium channel tetramerisation domain containing 4	-6.4315
205590_at	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	-6.6097
229125_at	ANKRD38	ankyrin repeat domain 38	-6.6611
226064_s_at	DGAT2	diacylglycerol O-acyltransferase homolog 2 (mouse)	-6.8606
203153_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1 /// interferon-induced protein with tetratricopeptide repeats 1	-7.1063
227736_at	C10orf99	chromosome 10 open reading frame 99	-7.3007
215123_at	LOC440345	hypothetical protein LOC440345	-7.4296
214382_at	UNC93A	unc-93 homolog A (C. elegans)	-7.5546
210096_at	CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	-7.9935
244197_x_at	CNOT2	CCR4-NOT transcription complex, subunit 2	-8.7575
207324_s_at	DSC1	desmocollin 1	-8.8212
203936_s_at	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	-8.9066
214536_at	SLURP1	secreted LY6/PLAUR domain containing 1	-9.4176
217087_at	C1orf68	chromosome 1 open reading frame 68	-9.4579
213780_at	TCHH	trichohyalin	-9.6763
240248_at	C10orf46	Chromosome 10 open reading frame 46	-10.1538
240420_at	AADACL2	arylacetamide deacetylase-like 2	-11.4116
215704_at	FLG	filaggrin	-11.5147
213933_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	-11.8960
220414_at	CALML5	calmodulin-like 5	-12.4239

1553454_at	RPTN	repetin	-15.6725
206643_at	HAL	histidine ammonia-lyase	-17.4474
217521_at	---	Transcribed locus	-18.2340
1552544_at	SERPINA12	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12	-22.0370
1569410_at	RP1-14N1.3	filaggrin 2	-32.8168
207908_at	KRT2	keratin 2 (epidermal ichthyosis bullosa of Siemens)	-50.0784
206177_s_at	ARG1	arginase, liver	-80.3099

Supplementary Table 2:

Table of genes from List A highlighted with the KEGG module on WebGestalt and included in “cell cycle”.

UserID	Gene Symbol	Gene Name	Fold Change	Entrez Gene	Ensembl
209642_at	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	-3.2352	699	ENSG00000169679
203755_at	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	-2.3623	701	ENSG00000156970
203418_at	CCNA2	cyclin A2	-2.8117	890	ENSG00000145386
228729_at	CCNB1	cyclin B1	-2.1390	891	ENSG00000134057
231259_s_at	CCND2	cyclin D2	3.1084	894	ENSG00000118971
203213_at	CDK1	cyclin-dependent kinase 1	-2.3588	983	ENSG00000170312
203968_s_at	CDC6	cell division cycle 6 homolog (S. cerevisiae)	-2.4227	990	ENSG00000094804
202870_s_at	CDC20	cell division cycle 20 homolog (S. cerevisiae)	-3.5709	991	ENSG00000117399
236313_at	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-2.5690	1030	ENSG00000147883
205394_at	CHEK1	checkpoint kinase 1	-2.1364	1111	ENSG00000149554
222037_at	MCM4	minichromosome maintenance complex component 4	-2.0063	4173	ENSG00000104738
216237_s_at	MCM5	minichromosome maintenance complex component 5	-2.0701	4174	ENSG00000100297
201930_at	MCM6	minichromosome maintenance complex component 6	-2.2974	4175	ENSG00000076003
204822_at	TTK	TTK protein kinase	-3.0231	7272	ENSG00000112742
202705_at	CCNB2	cyclin B2	-2.1935	9133	ENSG00000157456
203554_x_at	PTTG1	pituitary tumor-transforming 1	-2.0485	9232	ENSG00000164611

Supplementary Table 3:

Table of genes from List A highlighted with the KEGG module on WebGestalt and included in “p53 signaling pathway”.

UserID	Gene Symbol	Gene Name	Fold Change	Entrez Gene	Ensembl
204780_s_at	FAS	Fas (TNF receptor superfamily, member 6)	2.4535	355	ENSG00000026103
211833_s_at	BAX	BCL2-associated X protein	2.9361	581	ENSG00000087088
204493_at	BID	BH3 interacting domain death agonist	2.2411	637	ENSG00000015475
228729_at	CCNB1	cyclin B1	-2.1390	891	ENSG00000134057
231259_s_at	CCND2	cyclin D2	3.1084	894	ENSG00000118971
203213_at	CDK1	cyclin-dependent kinase 1	-2.3588	983	ENSG00000170312
205394_at	CHEK1	checkpoint kinase 1	-2.1364	1111	ENSG00000149554
202627_s_at	SERPINE1	serpin peptidase inhibitor, clade E, member 1	-3.0534	5054	ENSG00000106366
233254_x_at	PTEN	phosphatase and tensin homolog	-2.1231	5728	ENSG00000171862
201890_at	RRM2	ribonucleotide reductase M2	-2.4525	6241	ENSG00000171848
202705_at	CCNB2	cyclin B2	-2.1935	9133	ENSG00000157456

Supplementary Table 4: List of genes involved in more than 100 local connections with cell processes highlighted in the first analysis realized with Pathway Studio.

Name of the cell process	Number of local connectivity with the cell process	Gene name with local connectivity											
cell proliferation	264	ABL2	CCNB2	DCLRE1B	EPHB6	HS3ST3A1	LGALS7	NR2F2	PRDX3	SERPINE1	TNFRSF10D		
		ACTA2	CD274	DDIT3	ETS1	HSP90B1	LRRFIP1	NRG1	PRKRA	SETBP1	TNFSF10		
		ADAMTS1	CD44	DDR2	ETV5	HSPA4	LY75	NT5E	PRMT1	SFRP1	TOP2A		
		ADM	CD86	DEFB1	EWSR1	IDE	MACF1	NUF2	PRPF19	SFTPD	TPX2		
		AKR1C1	CD99	DENND2D	F12	IER3	MAF	NUSAP1	PTEN	SLC12A7	TREX2		
		ANKHD1	CDC20	DKK1	FAM3C	IFIT1	MALAT1	P2RY2	PTGER3	SLC7A11	TSPAN1		
		ANLN	CDC6	DLGAP5	FAM59A	IFNGR1	MAP1B	PARVA	PTGER4	SLURP1	TTK		
		ANPEP	CDK1	DLX2	FAS	IGF2R	MAP4K4	PBK	PTGS2	SMG1	TWIST1		
		APOD	CDKN2B	DLX5	FDFT1	IL1RL1	MCM10	PCBP2	PTPRG	SOD2	TXNIP		
		ARG1	CDKN3	DTL	FHL1	IL6ST	MCM4	PCSK6	PTTG1	SP3	TXNRD1		
		ARHGEF7	CELF2	DUSP4	FLG	INPP4B	MCM5	PCSK9	PTX3	SPRR3	TYRP1		
		ASPH	CENPA	DUT	FLRT3	IQGAP3	MCM6	PDGFRA	PYCARD	SPRY2	U2AF1		
		ASPM	CENPF	E2F8	FNDC3B	IRS1	MDM2	PEA15	RAC2	SPRY4	UBE2C		
		ATF3	CENPW	EDN1	FNTB	IRS2	MITF	PGF	RAD51	ST6GALNAC1	UBE2D3		
		AURKA	CEP55	EFNA5	FST	KAL1	MKI67	PHC2	RANBP2	STC1	UCHL1		
		AZGP1	CFLAR	EGFR	FTH1	KIAA0101	MME	PHF17	RASGRP1	STIL	UHRF1		
		BAX	CHEK1	EGR2	FTL	KIF11	MMP9	PHLDA1	RASSF1	STS	VAV3		
		BCL11A	CLEC7A	EIF3B	FUS	KIF14	MUC15	PLAC1	RBM14	SUZ12	VSNL1		
		BID	CLIC4	EIF3C	GFPT1	KIF4A	MX1	PLAG1	RBP1	TDG	WWC1		
		BIRC5	CNTN1	EIF4A1	GLRX	KLHL24	MYH10	PLAUR	RHOB	TFPI2	ZAK		
		BMP2	CRABP2	EIF5A2	GNB2L1	KNG1	NDC80	PLD1	RHOC	TGFBI	ZBTB10		
		BRAF	CTGF	EML1	GPX1	KRAS	NDRG4	PLK4	RORA	THBD			
		BUB1	CXCL14	EMP1	GSTA4	KRT18	NMU	PLXDC2	RRM2	TIMM44			
		CAND1	CYB5A	ENAH	HELLS	KRT9	NOD2	POU2F3	SAV1	TK1			
		CCL22	CYR61	ENO1	HMGA2	LASS2	NOV	PPIA	SDCBP	TKT			
		CCNA2	DAAM1	EPB41L3	HMMR	LATS2	NPNT	PPP1R15A	SEMA4A	TMEFF1			
		CCNB1	DCBLD2	EPHA4	HPGD	LEF1	NQO1	PPP2R2A	SERPINA12	TMPO			
		apoptosis	234	ACTA2	CCNA2	CYB5A	FANCD2	IFNGR1	MAP1B	PBK	PTGS2	SLC2A3	TNFAIP3
				ADM	CCNB1	CYP1A1	FAS	IGF2R	MAP4K4	PCBP2	PTTG1	SLC35B2	TNFRSF10D
				AIFM2	CCNB2	CYR61	FDFT1	IKBIP	MCM10	PCSK9	PTX3	SLC39A6	TNFSF10
AKR1C1	CD274			CYTH3	FHL1	IL6ST	MCM5	PDGFRA	PYCARD	SLC6A6	TOP2A		
ANPEP	CD44			DDIT3	FLG	ING3	MDM2	PEA15	RAC2	SLC7A11	TPX2		
APITD1	CD86			DEFB1	FST	IRS1	MGLL	PGF	RAD51	SLURP1	TRAF4		
APOD	CD99			DENND2D	FTH1	IRS2	MITF	PHC2	RANBP2	SMG1	TREX2		
ARG1	CDC20			DKK1	FTL	ITSN1	MKI67	PHF17	RASGRP1	SOD2	TTK		
ASPM	CDC42BPB			DSG1	GCLM	KAL1	MME	PHLDA1	RASSF1	SP110	TWIST1		
ATF3	CDC6			DUSP4	GFPT1	KIF14	MMP9	PLAG1	RBM25	SP3	TXNIP		
AURKA	CDCA7			DUT	GLRX	KIF23	MX1	PLAUR	RBP1	SPRR3	TXNRD1		
BAX	CDK1			E2F8	GNB2L1	KIF4A	MYH10	PLD1	RDH12	SPRY2	U2AF1		

BCL11A	CDKN2B	EDN1	GPD2	KNG1	NDC80	PLK4	REV3L	SPRY4	UBE2C
BFAR	CDKN3	EFNA5	GPX1	KRAS	NDRG4	PLTP	RHOB	SQSTM1	UCHL1
BID	CELF2	EGFR	GSR	KRT18	NOD2	POU2F3	RHOC	STC1	UHRF1
BIRC5	CENPA	EGR2	GSTA4	LASS2	NOV	PPIA	RORA	STS	VAV3
BMP2	CENPF	ELOVL6	GULP1	LASS5	NQO1	PPP1R15A	RRM2	SUPV3L1	WWC1
BRAF	CENPW	ENO1	HMGA2	LATS2	NR2F2	PRDX3	SAV1	SUZ12	ZAK
BUB1	CFLAR	EPB41L3	HMMR	LEF1	NRG1	PRKRA	SERPINA12	TFPI2	
BUB1B	CHEK1	EPHA4	HPGD	LGALS7	NT5E	PRMT1	SERPINB4	TGFBI	
CAMK1D	CLEC7A	EPHB6	HSP90B1	LY75	NUF2	PROM2	SERPINB6	THBD	
CAND1	CLIC4	ETNK1	HSPA4	LYNX1	NUSAP1	PTEN	SERPINE1	TIMM44	
CASP14	CRABP2	ETS1	IDE	MAF	P2RY2	PTGER3	SFRP1	TK1	
CCL22	CTGF	EWSR1	IER3	MALAT1	PARVA	PTGER4	SFTPD	TMEFF1	

cell differentiation

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ABHD5	BRAF	CLEC7A	EDN1	FST	IRS2	NOD2	PPIA	RORA	SUZ12
ACTA2	BUB1B	CLIC4	EGFR	FTH1	KAL1	NOV	PPP1R15A	SEMA4A	TCHH
ADAM8	CASP14	CNTN1	EGR2	FUS	KNG1	NPNT	PRDX3	SERPINB6	TDG
ADAMTS1	CCDC64	CRABP2	EID1	GLRX	KRAS	NQO1	PRMT1	SERPINE1	TFPI2
ADM	CCL22	CTGF	EIF4A1	GNB2L1	KRT18	NR2F2	PRPF19	SETBP1	TGFBI
AFF4	CCNA2	CXCL14	EMB	GPD2	LEF1	NRG1	PTEN	SFRP1	THBD
AKR1C1	CCNB1	CYR61	EMP1	GPX1	LGALS7	NT5E	PTGER3	SLC15A1	TMPO
ANPEP	CCNB2	DAAM1	ENO1	HMG20B	LPIN1	NUCB1	PTGER4	SLC2A3	TNFSF10
APITD1	CD274	DDIT3	EPHA4	HMGA2	LRPPRC	P2RY2	PTGS2	SLC35B2	TRAF4
APOD	CD44	DDR2	ETS1	HMMR	LY75	PBK	PTPRG	SLC7A11	TSPAN1
ARHGEF7	CD86	DEFB1	EWSR1	HPGD	LYNX1	PCBP2	PTTG1	SLURP1	TWIST1
ASAP1	CD99	DGAT2	FAM3C	HSP90B1	MACF1	PCSK6	PTX3	SOD2	TXNIP
ASPM	CDC20	DKK1	FAS	HSPA4	MAF	PCSK9	PYCARD	SP110	TXNRD1
ATF3	CDC6	DLX2	FEZ1	IDE	MAP1B	PDGFRA	RAB7B	SP3	TYRP1
AURKA	CDK1	DLX5	FGD2	IER3	MDM2	PGF	RAC2	SPEN	UCHL1
AZGP1	CDKN2B	DNASE1L2	FHL1	IFNGR1	MGLL	PHF17	RASGRP1	SPRR3	UHRF1
BAX	CELF2	DSC1	FLG	IFNK	MITF	PLAC1	RASSF1	SPRY2	VSNL1
BCL11A	CENPF	DSG1	FLRT3	IGF2R	MME	PLAUR	RBM14	SPRY4	ZNF281
BID	CFLAR	DTL	FNDC3B	IL1RL1	MMP9	PLD1	RBP1	SSH1	ZNF451
BIRC5	CHD9	DUSP4	FOXD1	IL6ST	NDRG4	PLTP	RHOB	STC1	
BMP2	CHEK1	E2F8	FRAS1	IRS1	NHS	POU2F3	RHOC	STXBP1	

cell growth

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ACTA2	BMP2	CLIC4	EIF4A1	GNB2L1	LASS2	NQO1	PTEN	SFRP1	TWIST1
ADH1B	BRAF	CRABP2	EIF5A2	GPX1	LATS2	NRG1	PTGER3	SFTPD	TXNIP
ADM	BUB1	CTGF	EMP1	GSR	LGALS7	NT5E	PTGER4	SOD2	TXNRD1
AKR1B1	CAND1	CXCL14	ENO1	HELLS	LY75	NUCB1	PTGS2	SPRY2	UBE2C
AKR1C1	CASP14	CYP1A1	EPB41L3	HMGA2	MAF	PBK	PTPRG	SPRY4	UBE2D3
ANLN	CCNA2	CYR61	EPHA4	HMMR	MALAT1	PDGFRA	PTTG1	SQLE	UBE2T
ANPEP	CCNB1	DAAM1	EPHB6	HPGD	MAP1B	PEA15	PXMP4	STC1	UCHL1
APITD1	CD274	DCBLD2	ETS1	IDE	MCM10	PGF	PYCARD	TAF9B	UHRF1
APOD	CD44	DDIT3	EXOC6	IER3	MCM4	PHF17	RAC2	TFPI2	USP47
ARG1	CD99	DEFB1	F12	IGF2R	MDM2	PHLDA1	RAD51	TGFBI	VAV3
ARHGEF7	CDC20	DKK1	FAS	IL1RL1	MGLL	PLAUR	RASGRP1	THBD	
ASPH	CDC6	DLGAP5	FEZ1	IL6ST	MITF	PLD1	RASSF1	TIMM44	
ASPM	CDK1	DTL	FHL1	ING3	MKI67	PLK4	RBM14	TK1	

		ATF3	CDKN2B	DUSP4	FST	IRS1	MME	POU2F3	RHOB	TMEM173	
		AURKA	CELF2	E2F8	FTH1	IRS2	MMP9	PPIA	RHOC	TNFRSF10D	
		AZGP1	CENPA	EDN1	FTL	ITSN1	MUC15	PPP1R15A	RORA	TNFSF10	
		BAX	CENPF	EFNA5	FUS	KIAA0101	NDC80	PRDX3	RRM2	TPX2	
		BCL11A	CFLAR	EGFR	GINS2	KNG1	NMU	PRKRA	SERPINE1	TRIM8	
		BIRC5	CHEK1	EGR2	GLRX	KRAS	NOV	PSMG4	SETBP1	TTK	
Cell Cycle	168	ACTA2	BUB1B	CENPA	DUT	FST	KIF4A	MME	PLAUR	RBM14	TMEFF1
		ADM	CCL22	CENPF	E2F8	FTH1	KNG1	MMP9	PLD1	REV3L	TMPO
		ANKHD1	CCNA2	CFLAR	EDN1	GINS2	KRAS	NDC80	PLK4	RHOB	TNFSF10
		ANLN	CCNB1	CHEK1	EGFR	GNB2L1	KRT18	NDRG4	POLQ	RORA	TOP2A
		ANPEP	CCNB1IP1	CLIC4	EGR2	GPX1	LATS2	NQO1	PPIA	RRM2	TPX2
		APOD	CCNB2	CRABP2	EIF3B	HELLS	LEF1	NR2F2	PPP1R15A	SERPINE1	TTK
		ARG1	CD274	CTGF	EIF4A1	HMGA2	LGALS7	NRG1	PPP2R2A	SFRP1	TWIST1
		ASPM	CD44	CYP1A1	EMP1	HMMR	LPIN1	NT5E	PRDX3	SFTPD	TXNIP
		ATF3	CD86	CYR61	ENO1	HSP90B1	MAF	NUF2	PRMT1	SMG1	TXNRD1
		AURKA	CD99	DCBLD2	EPB41L3	IER3	MALAT1	NUSAP1	PTEN	SOD2	UBE2C
		BAX	CDC20	DDIT3	EPHA4	IFNGR1	MCM10	P2RY2	PTGER4	SP3	UCHL1
		BCL11A	CDC6	DDR2	ETS1	IL6ST	MCM4	PBK	PTGS2	SPC25	UHRF1
		BID	CDCA3	DEPDC1	FANCD2	ING3	MCM5	PCBP2	PTPRG	SPRY2	VAV3
		BIRC5	CDK1	DHRS2	FAS	IRS1	MCM6	PEA15	PTTG1	SPRY4	ZAK
		BMP2	CDKN2B	DKK1	FDFT1	KIAA0101	MDM2	PHF17	RAD51	SSH1	ZBTB10
		BRAF	CDKN3	DLGAP5	FEZ1	KIF14	MITF	PHLDA1	RASSF1	TDG	
		BUB1	CELF2	DTL	FLG	KIF23	MKI67	PLAG1	RASSF10	TK1	
cell death	162	ADM	CCNB2	CYR61	ETS1	IL6ST	MME	PLAUR	RASGRP1	SQSTM1	TWIST1
		AIFM2	CD274	DDIT3	FANCD2	IRS1	MMP9	PLD1	RASSF1	STC1	TXNIP
		APITD1	CD44	DEFB1	FAS	ITSN1	MX1	PPIA	RDH12	STXBP1	TXNRD1
		ATF3	CD86	DKK1	FDFT1	KIAA0101	NCAPH	PPP1R15A	RHOB	SUPV3L1	TXNRD1
		AURKA	CD99	DSG1	FTH1	KNG1	NDC80	PRDX3	RHOC	TAF9B	TYRP1
		AURKA	CDC20	DUSP4	FTL	KRAS	NOD2	PRKRA	RRM2	TDG	UBE2C
		BAX	CDC6	DUT	GCLM	KRT18	NOV	PROM2	SERPINB4	TGFBI	UCHL1
		BFAR	CDK1	EDN1	GLRX	LASS5	NQO1	PRPF19	SERPINE1	THBD	UHRF1
		BID	CDKN3	EFNA5	GNB2L1	LATS2	NRG1	PTEN	SFRP1	TK1	VSNL1
		BIRC5	CELF2	EGFR	GPX1	LEF1	NUF2	PTGER4	SFTPD	TMEM173	
		BMP2	CENPF	EGR2	GSR	LGALS7	PCBP2	PTGS2	SLC39A6	TNFAIP3	
		BRAF	CFLAR	EIF5A2	GSTA4	MAP1B	PCSK9	PTTG1	SLC7A11	TNFRSF10D	
		BUB1	CFLAR	EMP1	GTF3A	MCM10	PDGFRA	PTX3	SLURP1	TNFSF10	
		BUB1B	CHEK1	ENAH	HMGA2	MDM2	PEA15	PYCARD	SOD2	TOP2A	
		CCL22	CLIC4	ENDOU	HSP90B1	MDM2	PGF	RAC2	SP3	TPX2	
		CCNA2	CTGF	ENO1	IDE	MITF	PHC2	RAD51	SPATS2L	TRAF4	
		CCNB1	CYP1A1	EPHA4	IER3	MKI67	PHLDA1	RANBP2	SPPL3	TTK	
cell migration	112	ABL2	BMP2	CDKN2B	EMB	HMMR	MAP4K4	PCDH18	RAC2	SPRY2	UCHL1
		ACTA2	BRAF	CEP55	ENAH	HPGD	MDM2	PDGFRA	RASGRP1	SPRY4	VAV3
		ADAM8	C5orf13	COL8A2	ENO1	IGF2R	MME	PEA15	RASSF1	SSH1	VSNL1
		ADAMTS1	CAMK1D	CRABP2	EPHA4	IL1R2	MMP9	PGF	RHOB	STC1	WWC1
		ADM	CCL22	CTGF	ETS1	IL6ST	MYH10	PLAUR	RHOC	TFPI2	
		ANPEP	CCNB1	CXCL14	FAM84A	IRS1	NOV	PLD1	SDCBP	TGFBI	

		APOD	CCNB1IP1	CYR61	FAS	IRS2	NPNT	PPIA	SEMA4A	THBD	
		ARHGEF7	CD44	DAAM1	FHL1	KAL1	NR2F2	PTEN	SERPINB4	TK1	
		ASAP1	CD86	DDR2	FST	KNG1	NRG1	PTGER3	SERPINE1	TNFSF10	
		ATF3	CD99	DKK1	FTH1	KRAS	NT5E	PTGER4	SFRP1	TRAF4	
		ATP7A	CDC42BPB	EDN1	GNB2L1	KRT18	P2RY2	PTGS2	SLURP1	TWIST1	
		AURKA	CDK1	EGFR	GPX1	LGALS7	PARVA	PTTG1	SOD2	TXNIP	
cell survival	103	ADM	CD44	E2F8	GLRX	KIF4A	NDC80	PGF	PTGS2	SERPINE1	TWIST1
		ATF3	CD86	EDN1	GNB2L1	KNG1	NOD2	PHLDA1	PTTG1	SFRP1	TXNIP
		AURKA	CDC20	EGFR	GPD2	KRAS	NOV	PLAUR	PYCARD	SMG1	UCHL1
		BAX	CDK1	EGR2	HMGA2	KRT18	NQO1	PPIA	RAC2	SOD2	USP47
		BID	CFLAR	EIF4A1	IER3	LATS2	NRG1	PPP1R15A	RAD51	SPRY2	
		BIRC5	CHEK1	EIF5A2	IGF2R	LEF1	NT5E	PRKRA	RAPGEF4	SQSTM1	
		BMP2	CTGF	EPB41L3	IL6ST	MAF	PARVA	PRMT1	RASSF1	STIL	
		BRAF	CYR61	ETS1	IRS1	MDM2	PBK	PRPF19	RBP1	TICAM2	
		BUB1B	DDIT3	FAS	IRS2	MITF	PCBP2	PTEN	RHOB	TNFRSF10D	
		CCNA2	DKK1	FST	ITSN1	MME	PDGFRA	PTGER3	RHOC	TNFSF10	
		CCNB1	DLGAP5	GFPT1	KIF11	MMP9	PEA15	PTGER4	RORA	TPX2	
mitosis	100	ADM	BUB1	CDKN2B	EDN1	HELLS	KIF4A	MKI67	PGF	RANBP2	TK1
		ANLN	BUB1B	CELF2	EGFR	HJURP	KRAS	MX1	PLD1	RASSF1	TMPO
		APITD1	CCNA2	CENPA	EGR2	HMMR	LATS2	MYH10	PLK4	RHOB	TNFSF10
		ARHGEF7	CCNB1	CENPF	EWSR1	IRS1	MAP1B	MYO5B	POLE2	SAV1	TOP2A
		ASPM	CCNB1IP1	CEP55	FANCD2	IRS2	MCM10	NCAPH	PRKRA	SPC25	TPX2
		AURKA	CCNB2	CHEK1	FAS	KIAA0101	MCM4	NDC80	PTEN	SPEN	TTK
		BID	CD44	CLIC4	FDFT1	KIF11	MCM5	NRG1	PTGS2	SPRY2	U2AF1
		BIRC5	CDC20	CTGF	FEZ1	KIF14	MCM6	NUF2	PTTG1	SSH1	UBE2C
		BMP2	CDC6	DCLRE1B	GINS2	KIF20A	MDM2	NUSAP1	RAD51	STIL	UCHL1
		BRAF	CDK1	DLGAP5	GNB2L1	KIF23	MITF	PBK	RAD54B	TGFBI	VAV3

Supplementary Table 5 A, B, C, D, E:

Cell processes from Supplementary Table 5 presented at least 7 genes from List A that connected. Tables containing the gene list with Medline citations and Medline references justifying the connection.

A. Relation of genes with cell proliferation.

Relation to cell proliferation	Fold Change of the gene in relation with cell process	Medline citation	Number of References	MedLine References					
STC1 --->	23.3541	STC1 inhibits longitudinal bone growth by suppressing growth plate chondrocyte proliferation.	2	17909264	16377640				
MME ---	20.2766	Overexpression of NEP (MME) in hormone-refractory CaP cells significantly inhibits their growth, while loss of NEP activity stimulates CaP cell proliferation and migration.	25	8631021 8943850 23381789 10951272 14500390	1660144 10385588 1469102 9337153 17459884	9227412 14704146 9427606 15840561 16728568	12056552 7962523 20957047 12220742 9861296	19234135 16054017 11350908 15637592 18708424	
PDGFRA -->	15.0401	When activated by ligand binding, both PDGF-R alpha and PDGF-R beta stimulate proliferation.	48	7923614 17079230 15342968 12808148 20924364 17604334 18339881 8548759 11557737 15814780	15811134 1325456 12761844 15837572 12651897 19383909 19126548 11481486 16508943 16331269	17470632 19366796 19366798 10764412 15677564 18502897 18474118 16030188 15781583 11953315	18366137 17440089 16538672 17314398 19553600 20817666 19939260 16818613 9488729	19654211 17632543 15757958 16258521 12436445 15331661 23383310 23041331 16418325	
ATF3 -->	13.4129	The c-Jun/ATF-2 target gene atf3 can regulate cell proliferation both positively and negatively and its expression is strongly induced by both growth factors and stresses. ATF3 can alters proliferation in fibroblasts.	17	11314051 12832543 16516039 11375399	15990869 16469745 16079289 19233874	17764562 17456735 12034827	16278400 21129190 12833146	18511933 16263788 17095753	
IL1RL1 -->	12.6018	TOPK, IL1RL1, and NME1 that are overexpressed in BCR/ABL+ cells are thought to play a role in cell proliferation and differentiation.	7	11207266 14991091	20014349 12589034	11714798	18762778	11441076	
CELF2 --->	10.4316	CUGBP2 overexpression inhibits proliferation of HCT-116 cells.	3	18258790	18292181	18325984			
MAP1B --->	10.1488	Overexpression of HA-Mtap1b-LC1 inhibits proliferation of NIH-3T3 cells.	1	17308336					

FLG -->	-11.5147	Filaggrin associated with 12-O-tetradecanoylphorbol 13-acetate-induced proliferation and differentiation.	1	16537558					
PTGER3 --->	-11.8960	EP3 receptor stimulation decreases proliferation at low prostaglandin E2 concentrations, whereas 10- to 100-fold higher concentrations of prostaglandin E2 stimulate proliferation by activation of the EP2 receptor.	7	11095474	18321859	19099561	16977324	16051640	
SERPINA12 -->	-22.0370	The application of recombinant vaspin and Vaspin-Ad promoted the proliferation and inhibited the apoptosis of human aortic endothelial cells.	1	23307819					
ARG1 --->	-80.3099	Blockade of arginase I induction by IFN-gamma, H-89, or genistein also blocked the increase in cell proliferation.	17	10898736	16773651	19508396	12923240	19890055	
				11470919	11742824	12813022	19703164	15465793	
				20407034	15342423	18323470	19234205	20711410	
				12874210	12787129				

B. Relation of genes with apoptosis.

Relation to apoptosis	Fold Change of the gene in relation with apoptosis	Medline citation	Number of References	MedLine References					
STC1 --->	23.3541	Overexpression of STC1 prevented Abeta-induced apoptosis of human brain microvascular endothelial cells; STC-1 was both necessary and sufficient to reduce apoptosis of the ischemic lung cells; STC-1 mediates the antiapoptotic effects of Multipotent stromal cells.	9	18652825	18786506	19656913	19347030	16377640	
MME --->	20.2766	NEP (MME) expression induces apoptosis and cell cycle G1 arrest; neprilysin (MME) could prevent possible rescue of keratocytes from apoptosis; enzyme neprilysin (MME) reduces β -cell apoptosis.	18	19267325	19509170	19096036	18199603		
PDGFRA --->	15.0401	PDGFRalpha signaling has a protective role in preventing apoptosis in early development.	6	15756002	11118039	11307776	10803579	12748254	
				12363040	11350908	17083125	10385588	10666035	
				12764385	15637592	11186280	11309283	12697667	
				14734478	11901191	15205682			
				15919820	16168125	16818613	17342771	17643098	
				15811134					
ATF3 -->	13.4129	We show that ATF3 promotes apoptosis and cell cycle arrest; ATF3 is involved in the regulation of cell growth, apoptosis, and stress response, depending on the cell type.	60	16469745	18178318	17360647	14718536	15897233	
				18755691	18644986	12909328	21152039	18487508	
				18057093	18194435	16109718	16291753	20565867	
				21205742	20600850	18719024	16079289	9755171	
				11473362	15674352	17178897	20167600	18922905	
				21280179	16613840	12386811	21034493	18728164	
				17764926	20002170	12161427	20137089	16631627	
				19647793	17952119	15199129	15684420	17898295	

				16489044	12832543	20571063	21129190	21396734
				20140008	15713895	15231818	16044158	20140008
				20581861	18511933	15308587	17785797	18178318
				12392999	19074148	17575148	18235102	22033410
CELF2 -->	10.4316	CUGBP2 (CELF2) overexpression induces apoptosis.	8	18325984	18292181	18258790	15226369	17855367
				15033780	16095752	15358864		
MAP1B -->	10.1488	Full-length but not N-terminal truncated form of MAP1B induced apoptosis in cortical neurons; overexpression of N-terminal fragments of MAP1B has been shown to promote neuronal apoptosis.	3	16234245	12376528	18195017		
FLG -->	-11.5147	Because filaggrin is expressed at a level of the epidermis where keratinocytes are in transition between the nucleated granular and the anucleate cornified layers, we hypothesize that filaggrin aids in the terminal differentiation process by facilitating apoptotic machinery.	4	10822280	15175023	15737187	11159940	
PTGER3 -->	-11.8960	The mechanisms by which EP3 receptors/Rho kinase affects inflammation and neuronal apoptosis remain to be identified.	1	20590584				
SERPINA12 ---	-22.0370	The application of recombinant vaspin and Vaspin-Ad promoted the proliferation and inhibited the apoptosis of human aortic endothelial cells.	3	23284999	23135225	23307819		
ARG1 -->	-80.3099	The downstream effects of Arginase can inhibit CD8+ T cell proliferation and activation or trigger T cell apoptosis (v).	4	21029397	17016554	17255300	22926702	

C. Relation of genes with cell growth.

Relation to cell growth	Fold Change of the gene in relation with cell growth	Medline citation	Number of References	MedLine References
STC1 -->	23.3541	Stanniocalcin 1 and IRS-1 contribute to progesterone receptor mediated breast cancer cell growth in the absence of progestins.	1	19706513
MME ---	20.2766	Expression of NEP in androgen-independent prostate cancer cells inhibits cell migration, inhibits cell growth and tumorigenicity in the prostate , and induces apoptosis and cell cycle arrest .	8	9427606 1533518 14704146 10803579 11309283 11350908 16940054 7635530

PDGFRA -->	15.0401	Inhibition of PDGFR-A by RNA interference, small molecule inhibitor or neutralizing antibody, had a dramatic effect on tumor cell growth both in vitro and in vivo, although resistance evolved in one-third of tumors; platelet-derived growth factor receptor (PDGFRA) is a potent activator of cell growth, survival and migration.	5	18679424	19553600	17079230	16354679	17485528
ATF3 ---	13.4129	Over-expression of ATF3 protein moderately suppresses cell growth; the transcription factor ATF-3 stimulates cell growth and protein synthesis; ATF3 is involved in the regulation of cell growth, apoptosis, and stress response, depending on the cell type.	10	12386811	11481491	18511933	15308587	18497336
IL1RL1 --->	12.6018	ST2 (IL1RL1) gene plays a role in cell growth regulation; IL1RL1 promoted cell growth and served as inflammatory cell chemoattractants and inducers of stress response.	2	10491084	17982090			
CELF2 --->	10.4316	Cells overexpressing CUGBP2 had a lower growth rate, eventually underwent apoptosis.	1	18292181				
MAP1B ---	10.1488	These data strongly suggest that MAP1B cooperates with DAPK-1 to reduce cell growth and that this requires functional DAPK-1 kinase activity.	1	18195017				
PTGER3 --->	-11.8960	prostaglandin E2 signals through EP2 promote cell growth; A specific antagonist against EP3 abrogated the cell growth.	6	15331179	15247185	18230618	19180509	16024629
ARG1 --->	-80.3099	induced arginase I in macrophages can enhance tumor cell growth.	1	15465793				

D. Relation of genes with cell differentiation.

Relation to cell differentiation	Fold Change of the gene in relation with cell differentiation	Medline citation	Number of References	MedLine Reference				
STC1 -->	23.3541	STC1 is expressed in chondrocytic and osteoblastic cells during murine development and can enhance differentiation of calvarial cells in culture.	5	11927399	20174869	11737588	11146507	15367391
MME --->	20.2766	CD10(MME) plays a specific role in the control of growth and differentiation of many cell types by cleaving growth factors that are able to promote cellular proliferation.	12	12649673	16405511	7656459	15756002	15751084
PDGFRA --->	15.0401	Pdgfra is expressed in the	11	20506111	10385588	8624907	7890699	19426500
				15870909	11340378			
				15811134	17440089	19939260	16418325	19654211

		mesenchyme of multiple organs during embryonic development and Pdgfralpha is involved in cell proliferation, differentiation, migration, and apoptosis in many tissues.		12761844	15941858	17620431		
				12651897	16467141	19147501		
ATF3 -->	13.4129	ATF3 induction appears to facilitate cell cycle exit and terminal differentiation of chondrocytes.	8	20304822	21372517	16428460	18922905	18808719
				16984628	17102133	19549813		
IL1RL1 --->	12.6018	ST2 (IL1RL1) from fetal liver promotes growth and differentiation of early B lineage cells.	8	2891538	12589034	19841166	19196821	18802081
				1585838	10510079	19196812		
CELF2 -->	10.4316	The neuronal-specific ELAV RNA-binding proteins (CELF2) are necessary and sufficient to induce neuronal differentiation in mammalian cells.	1	16554442				
MAP1B --->	10.1488	MAP1B plays an important role in neuronal differentiation.	4	11121433	7769400	9813091	15528209	
				18795935	9822682	19554025	7688400	20208004
				18717683	6174530	18007582	12230510	12663686
FLG --->	-11.5147	Filaggrin is involved in the terminal differentiation of epidermis but the relative importance of the different functions of filaggrin remains unclear; Only some differentiation proteins (i.e., K10, loricrin, filaggrin) were found to be altered in in vitro reconstructed xeroderma pigmentosum epidermis.	19	7829877	8417356	10822280	17439945	19209157
				16702271	16537558	17079689	11438733	
PTGER3 --->	-11.8960	Prostaglandin E2 receptors of the EP2 and EP4 subtypes regulate activation and differentiation of mouse B lymphocytes to IgE-secreting cells.	4	8855294	15283844	15140225	18666211	

E. Relation of genes with wound healing.

Relation to wound healing	Fold Change of the gene in relation with wound healing	Medline citation	Number of References	MedLine Reference
STC1 --->	23.3541	STC1 protein is considered to have roles in many physiological processes, including bone development, reproduction, wound healing, angiogenesis, and modulation of inflammatory response.	1	16287871
MME ---	20.2766	NEP (MME), represent important control factors for the inflammatory response in skin disorders such as psoriasis or allergic inflammation, but may also be capable of affecting pigmentation, cell survival, wound healing and tissue regeneration.	2	12485446 15507108

ATF3 --->	13.4129	ATF3 is involved in homeostasis, wound healing, metastasis and the signaling pathways mediating cellular response to genotoxic stress	1	12386811
IL1RL1 --->	12.6018	Epidermal-derived proinflammatory cytokines interleukin-1alpha (IL-1alpha) and tumor necrosis factor-alpha (TNF-alpha) were found to mediate synergistically the secretion of these wound-healing mediators (with the exception of sST2) from fibroblasts in dermal substitutes.	1	17971017
PTGER3 --->	-11.8960	EP3 receptor the subtype involved in wound healing and angiogenesis.	1	18042549
CALML5 --->	-12.4239	Clsp/Scarf (CALML5) plays an important role in late epidermal wound healing, perhaps participating in the change from activated to differentiating keratinocyte phenotype.	1	17470426
ARG1 --->	-80.3099	Macrophage-specific expression of Arginase-1 is commonly believed to promote inflammation, fibrosis, and wound healing by enhancing L-proline, polyamine, and Th2 cytokine production.	2	19360123 16556895