< Supplementary Information >

Alternative splicing of genes during neuronal differentiation of NT2 pluripotential human embryonal carcinoma cells

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Supplementary methods

Supplementary method 1. Microarray analysis

A set of synthetic polynucleotides (80-mers) representing 31,917 human transcripts, including most of the RefSeq clones deposited in the NCBI database (MicroDiagnostic, Tokyo, Japan) was arrayed on aminosilane-coated glass slides (Type I; Matsunami, Kishiwada, Japan) using a custom-made arrayer. Two micrograms of each polyA(+) RNA sample was labeled with Cyanine 5-dUTP or Cyanine 3-dUTP (PerkinElmer, MA, USA). Human common reference RNA was prepared by mixing equal amounts of polyA(+) RNA extracted from 22 human cancer cell lines to reduce the cell type-specific expression bias [13]. Hybridization was performed using the reagents provided in a Labeling and Hybridization Kit (MicroDiagnostic). Signals were measured with a GenePix 4000A scanner (Axon Instruments Inc., CA, USA) and then processed into primary expression ratios (ratio of the Cyanine-5 intensity of each cell line to the Cyanine-3 intensity of the human common reference RNA) [13]. Each ratio was normalized by multiplication with the normalization factor using the Gene Pix Pro 3.0 software (Axon Instruments Inc.). The primary expression ratios were converted into log2 values (designated as log ratios). In accordance with the Minimum Information about a Microarray experiment (MIAME) guideline, all the data were deposited (accession number CBX132) at the DNA Data Bank of Japan (DDBJ) via the Center for Information Biology gene EXpression (CIBEX) database (http://cibex.nig.ac.jp/index.jsp). Data processing was performed using a MDI gene expression analysis software package (MicroDiagnostic). To identify genes demonstrating significant changes in expression, t-test was performed between the 0-day sample (negative control) and each RA time point sample ($p < 0.01$) [S1-S3]. Among the identified genes, we further selected those genes that exhibited differences greater than 1.0 between the mean averages of log ratios for the two sample groups.

A total of 31,917 probes were made for detecting 31,210 human transcripts, which covered 20,107 of 31,309 loci that we identified in our previous study [11]. Based on the classification data shown in our previous study [11], these transcripts covered 17,129 of 23,241 protein-coding genes.

Supplementary method 2. Analysis of splicing patterns and functional classification of cDNAs by GO

Sequences of proteins encoded by the transcripts produced from each one of the 358 genes selected in this paper were analyzed for motifs using Pfam 19.0 program (November 2005) (http://pfam.sanger.ac.uk/). From this analysis, we obtained information on motifs showing

E-values of e-30 or more, and based on these results we then categorized each cDNA and the corresponding gene according to its GeneOntology (GO) (http://www.geneontology.org/) classification by using InterPro (http://www.ebi.ac.uk/interpro/). We also categorized 24,210 human RefSeq (NCBI Reference Sequences; http://www.ncbi.nlm.nih.gov/RefSeq/) listed in the FLJ Human cDNA Database ver. 3.0 by GO. We then extracted functional categories of the selected genes in which the ratio of category was over 2.0 fold as compared to the RefSeq result. The splicing patterns of the selected genes were analyzed for AS by using the information available in the FLJ Human cDNA Database ver. 3.0 (http://flj.lifesciencedb.jp) as described previously [11]. For analyzing the N-terminus splicing patterns, we only used our FLJ ESTs constructed by an optimized oligo-capping method, 90% or more of which contained the transcription start site (TSS) [10,11]. In our analysis, we only focused on the protein-coding mRNA transcripts, and ignored a lot of noncoding RNAs and mRNAs in which AS only occurred in the untranslated region (UTR) [14].

Supplementary method 3. Quantitative real-time PCR analysis

First-strand cDNAs were synthesized from each polyA(+) RNA sample using random primers and the Superscript III reverse transcriptase (Life Technologies) following the instructions provided with the transcriptase. Real-time PCR was performed using the FastStart Universal SYBR Green Master (Roche Diagnostics, Basel, Switzerland) on an ABI Fast7500 System (Life Technologies) according to the instructions provided by the manufacturer of the PCR machine. Approximately 10 ng of the first-strand cDNA was used as a template in each reaction. Primers were designed using the Primer Express3.0 (Life Technologies) software (Supplemental Table 4). The expression levels of genes were normalized with respect to that of the human GAPDH, and the expression values of individual genes were calculated by comparing their Ct values to that of the control using the RQ software (Life Technologies). The expression levels of genes were represented in log2 base. Samples were run in triplicates and the data shown are average of three experiments.

Supplementary analysis results : ***Analysis of expression patterns of selected genes***

1. Analysis of expression patterns of selected transcription factors

Because transcription factors regulate various genes and transcription factor genes producing multiple transcripts are known to work mutually as regulating factors in transcription [26, S4], it is necessary to examine the expression profile and function of each alternatively spliced protein-coding transcripts produced from a transcription factor gene. We analyzed the mRNA diversity of the transcription factor genes and the results are summarized in Table 1 and Supplemental Fig 3.

(1) PEG3

In Fig 2A, we compared the expression profiles of two transcripts originated from one genome locus, namely the NM_006210.1 transcript that encodes for PEG3 [27, S5], a member of the Kruppel C2H2-type zinc finger protein family, and the NM_015363.3 transcript that encodes for ZIM2, a zinc finger protein. They share multiple 5' exons and a common promoter, but their C-terminus regions are unique. Although in the 7-day sample the expression level of NM_006210.1 increased to 8-fold, the expression level of NM_015363.3 increased to < 1.6-fold of the 0-day sample. These results have been discussed in the section 3.3 of the text.

(2) HOXA2

In Fig 2B, we compared the expression profiles of HOXA2 (NM_006735.3) and FLJ39423, which were identified as the splicing variants resulting from Alt. C-term utilization. HOXA2 is part of the homeotic genes and encodes a protein that might be involved in the placement of hindbrain segments in the proper location along the anterior-posterior axis during development [S6, S7], whereas FLJ39423 was predicted to lack the homeobox domain (Supplemental Fig 7I). Although RA induction increased the expression of both transcripts very significantly (7.2×10^3-fold and 1.6×10^5-fold for NM_006735.3, and 2.8×10^2-fold and 3.1×10^3-fold for FLJ39423 in 1-day and 7-day samples, respectively), their ratios of up-regulation were greatly different. These results have been discussed in the section 3.3 of the text.

(3) HNF1B

In Fig 2C, we compared the expressions of two transcripts, NM_000458.1 and NM_006481.1, produced from the HNF1B gene by utilizing Alt. C-terms. RA-induced increase in the expression levels of both HNF1B generated transcripts were very similar. HNF1B, also known as TCF2, is a member of the homeodomain-containing superfamily of transcription factors [S8].

As reported previously [S9], both transcripts of HNF1B had transactivation potential, even though their C-terminus regions were unique. These results have been discussed in the section 3.3 of the text.

(4) POU5F1 (OCT4)

POU5F1, also known as OCT4, which contains POU homeodomain and is one of transcription factors, is known to convert human fetal neural stem cells into induced pluripotent stem (iPS) cells [S10, S11]. Down-regulation of the POU5F1 expression level required for the neuronal differentiation. We compared the expression profiles of two different transcripts of the POU5F1 gene, resulting from the Alt. N-term utilization - NM_002701.3 known as OCT4A and NM_203289.3 known as OCT4B [29, S12]; both transcripts shared the POU DNA-binding and C-terminal transactivation domains, but their N-terminus regions including the TSS are unique. The expression level of NM_002701.3 (OCT4A) decreased to one tenth of the 0-day value between 2- and 7-day, whereas the expression level of NM_203289.3 (OCT4B) decreased rapidly to one tenth of the 0-day value between 1-day and 2-day (Fig 2D). These results have been discussed in the section 3.3 of the text.

(5) HOXA3 and ETV5

Finally, we report on two other genes, HOXA3 and ETV5, of unknown functions.

i) HOXA3

HOXA3 is part of the homeotic genes and encodes a DNA-binding transcription factor [S13, S14]. HOXA3 produced two transcripts, NM_030661.3 and NM_153632.1, which differed in their N-terminal regions, but shared the homeobox domain (Supplemental Fig 7D). The expression level of NM_030661.3 increased on 1-day and 7-day samples to $2.1\text{x}10^2$-fold and $5.1\text{x}10^4$-fold, respectively, of the 0-day value (Fig 2E). On the other hand, the expression level of NM_153632.1 increased to less than 4-fold and 70-fold of the 0-day value on day 2 and day 7, respectively. These results have been discussed in the section 3.3 of the text.

ii) ETV5

ETV5, also known as ERM, belongs to the PEA3 group of ETS transcription factors, and is involved in a number of developmental processes and required for the transcriptional control of the spermatogonial stem cell niche [S15, S16]. We examined expression of ETV5 (NM_004454.1) and FLJ56169. The expression level of NM_004454.1 decreased rapidly to one fifth and one tenth of its 0-day value in 1-day and 2-day samples, respectively (Fig 2F). On the other hand, the expression level of FLJ56169 decreased to one half of the 0-day in 2-day sample. Interestingly, the expression level of NM_004454.1 increased back to the control (0-day) level upon 35-day incubation with RA (Supplemental Table 8) whereas the expression level of

FLJ56169 increased back to the control (0-day) level after 14-day and then increased by 4-fold after 35-day incubation with RA. These results have been discussed in the section 3.3 of the text.

2. Analysis of expression patterns of selected genes producing multiple protein-coding transcripts using alternate C-terminus

Out of the 358 RA-responsive genes in NT2 cells, we analyzed the mRNA diversity of 59 genes producing multiple protein-coding transcripts using Alt. C-term. We performed quantitative real-time PCR analysis to examine the expression profiles of the protein-coding transcripts produced by each one of the 30 genes for which we succeeded in making specific primers. The results obtained for 4 genes in the "transcription regulator activity" category are described in section 3.3 of the text and the results obtained for another 26 genes are summarized in the Supplemental Table 6. Results obtained for 3 of these genes are described below in detail.

(1) NRP2

In Supplemental Fig 5A, we compared the expression profiles of three different transcripts resulting from the NRP2 gene by utilizing Alt. C-term - NM_003872.2 known as NRP2a, NM_018534.3 known as NRP2b and NM_201264.1 known as s9NRP2 [18]. Two transcripts, NRP2a (NM_003872.2) and NRP2b (NM_018534.3), encoded for proteins that shared a transmembrane domain (TM), and are described as membrane-form encoding transcripts. But, the protein encoded by the transcript s9NRP2 (NM_201264.1) lacked the TM domain, and is described as a soluble-form encoding transcript [18]. The expression levels of the membrane-form encoding transcripts NRP2a (NM_003872.2) and NRP2b (NM_018534.3) increased to 10-fold and 18-fold, respectively, whereas the expression level of the soluble-form encoding transcript s9NRP2 (NM_201264.1) increased to only 3-fold in 7-day sample.

NRPs are receptors for the class-3 semaphorin (SEMA) family of axon guidance molecules and also for the vascular endothelial growth factor (VEGF) family of angiogenic factors [30]. DNA microarray results described in this study showed that the expression level of NRP1 did not change by RA induction (Supplemental Fig 8). We compared expressions of five SEMA3 family genes (SEMA3A, SEMA3B, SEMA3C, SEMA3D, and SEMA3F), and we found that the expression levels of SEMA3C and SEMA3D increased in 7-day sample (Supplemental Fig 8). VEGF-NRP interactions have been suggested to be involved in mediating tumor progression [30]. NRPs are also thought to be valuable targets for developing new anti-cancer therapies. In addition, there are studies suggesting that the NRP soluble isoforms might act as VEGF antagonists and prevent the tumorigenic and angiogenic effects mediated by the other types of

NRPs [30].

We found that RA-induced increase in the expression levels of NRP2 gene transcripts were different in NT2 cells –the expression levels of the membrane-form encoding transcripts, NRP2a and NRP2b, were preferentially up-regulated as compared to that of the soluble-form encoding transcript, s9NRP2.

(2) EPB41L5

We compared the expression profiles of the transcripts NM_020909.2 and BC032822.2 generated from the EPB41L5 gene as a result of Alt. C-term utilization. The expression level of NM_020909.2 increased by 4-fold, whereas the expression level of BC032822.2 did not change in 7-day sample (Supplemental Fig 5B).

EPB41L5 gene belongs to the band 4.1 superfamily, members of which are known to maintain epithelial integrity and to act as tumor suppressors. EPB41L5 gene coded protein binds p120 catenin through its N-terminal FERM domain, thereby inhibiting the p120ctn–E-cadherin binding, and also binds to paxillin through its C-terminus, enhancing the integrin/paxillin association [23]. It might be possible that by combining these two processes EPB41L5 could play a role in cancer invasion. It has been reported that EPB41L5 transcript lacking the C-terminus binding site could not associate with paxillin [23].

The BC032822.2 transcript, which was analyzed in this study and was formed as a result of AS of EBP41L5 gene, lacked the C-terminus binding site for paxillin. We found that in the NT2 cells, RA preferentially induced the expression of the transcript NM_020909.2, which possessed the binding sites for both p120 catenin and paxillin, but did not induce the expression of the BC032822.2 transcript.

(3) CTHRC1

We examined expressions of two transcripts produced by the CTHRC1 gene – transcript NM_138455.2, which encodes for the CTHRC1 protein, and transcript FLJ57590, a spliced variant that differed from the former in the C-terminus, and was identified in our previous study [11]. The expression level of NM_138455.2 increased by 32-fold in the 7-day sample, and then decreased by 2-fold in the 35-day sample (Supplemental Fig 5C, Supplemental Fig 6A). In contrast, the expression level of FLJ57590 increased by 4-fold in the 7-day sample, and by 11-fold in the 35-day sample.

CTHRC1, a secreted glycoprotein, is involved in the selective activation of the planar cell polarity (PCP) pathway mediated by Wnt proteins [24]. It has been suggested that CTHRC1 interacted with the components of Wnt/PCP signaling pathway, and CTHRC1 binds to these components of Wnt/PCP signaling pathway through its C-terminal region [24]. Therefore, any

CTHRC1 construct lacking the C-terminus binding site could not associate with these components of Wnt/PCP signaling pathway. In HEK293T cells, Cthrc1 activated the PCP pathway but suppressed the canonical pathway [S17]. In neural precursor cells (NPCs), Wnt signaling of canonical pathway induces neuronal differentiation [S18], and Wnt signaling does so in the late stage (neurogenic phase) of NPCs but not in the early stage (expansion phase) of NPCs. These stage-dependent responses of NPCs might play a central role in determining the timing of differentiation.

The FLJ57590 transcript, which resulted from the CTHRC1 gene by AS, lacked the C-terminus binding site for these factors of Wnt/PCP signaling pathway. In NT2 cells, we found that the expression of the CTHRC1 protein-coding transcript, NM_138455.2, was preferentially up-regulated by RA until day 7. Interestingly, after day 7, and as expected at the later-stage of neuronal differentiation, the expression level of the FLJ57590 transcript, lacking the C-terminus that was needed for the Wnt/PCP pathway, was up-regulated by RA.

<u>**Supplementary references**</u>

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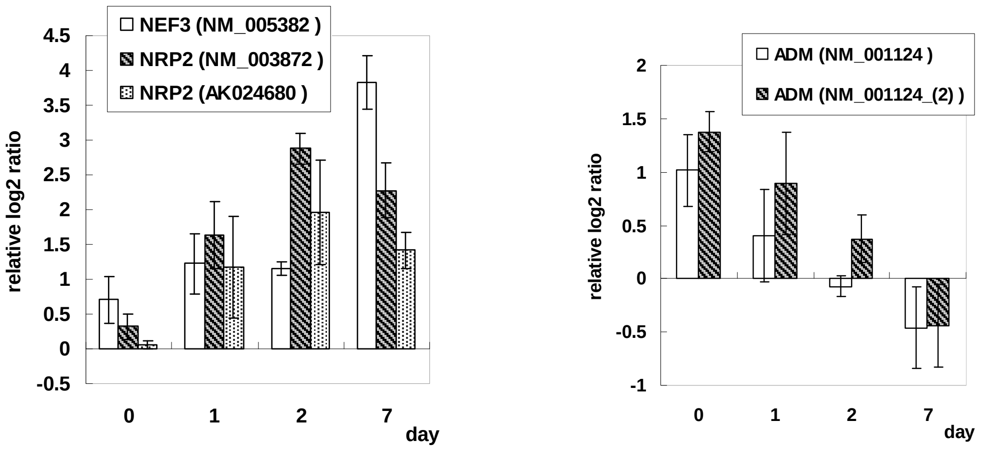
Probe ID	Gene symbol	0-day mean ±S.D.	1-day mean ±S.D.	2-day mean ±S.D.	7-day mean ±S.D.
NM_005382	NEF3	0.71 ± 0.34	1.22 ± 0.43	1.16 ± 0.10	3.82 ± 0.38
NM_003872	NRP2	0.32 ± 0.19	1.63 ± 0.48	2.88 ± 0.22	2.28 ± 0.39
AK024680	NRP2	0.06 ± 0.06	1.18 ± 0.73	1.96 ± 0.75	1.42 ± 0.26
NM_001124	ADM	1.02 ± 0.31	0.41 ± 0.34	-0.07 ± 0.35	-0.46 ± 0.14
NM_001124_(2)	ADM	1.38 ± 0.30	0.89 ± 0.55	0.37 ± 0.44	-0.44 ± 0.14

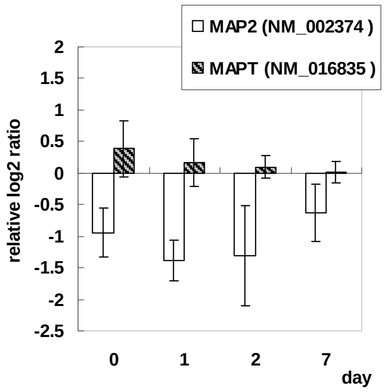


Supplementary Fig. 1. **Expression profiles of neurodifferentiation marker genes by DNA microarray.**

Log2 values for each sample were averaged and S.D. values were calculated.
0-day, Negative control; cells were collected after 1-day (24 h), 2-day (48 h) and 7-day (168 h) induction with RA.

A.

Probe ID	Gene symbol	0-day mean ±S.D.	1-day mean ±S.D.	2-day mean ±S.D.	7-day mean ±S.D.
NM_002374	MAP2	-0.94 ± 0.39	-1.39 ± 0.32	-1.32 ± 0.80	-0.63 ± 0.46
NM_016835	MAPT	0.38 ± 0.44	0.17 ± 0.38	0.10 ± 0.18	0.02 ± 0.16



B.

Gene symbol	0-day Log2RQ mean ± S.D.	14-day Log2RQ mean ± S.D.	35-day Log2RQ mean ± S.D.
MAP2	0.0 ± 0.2	1.6 ± 0.1	3.8 ± 0.1
MAPT	0.0 ± 0.2	1.6 ± 0.2	6.9 ± 0.0

Supplementary Fig. 2. **Expression profiles of later-stage nerve differentiation marker genes.**

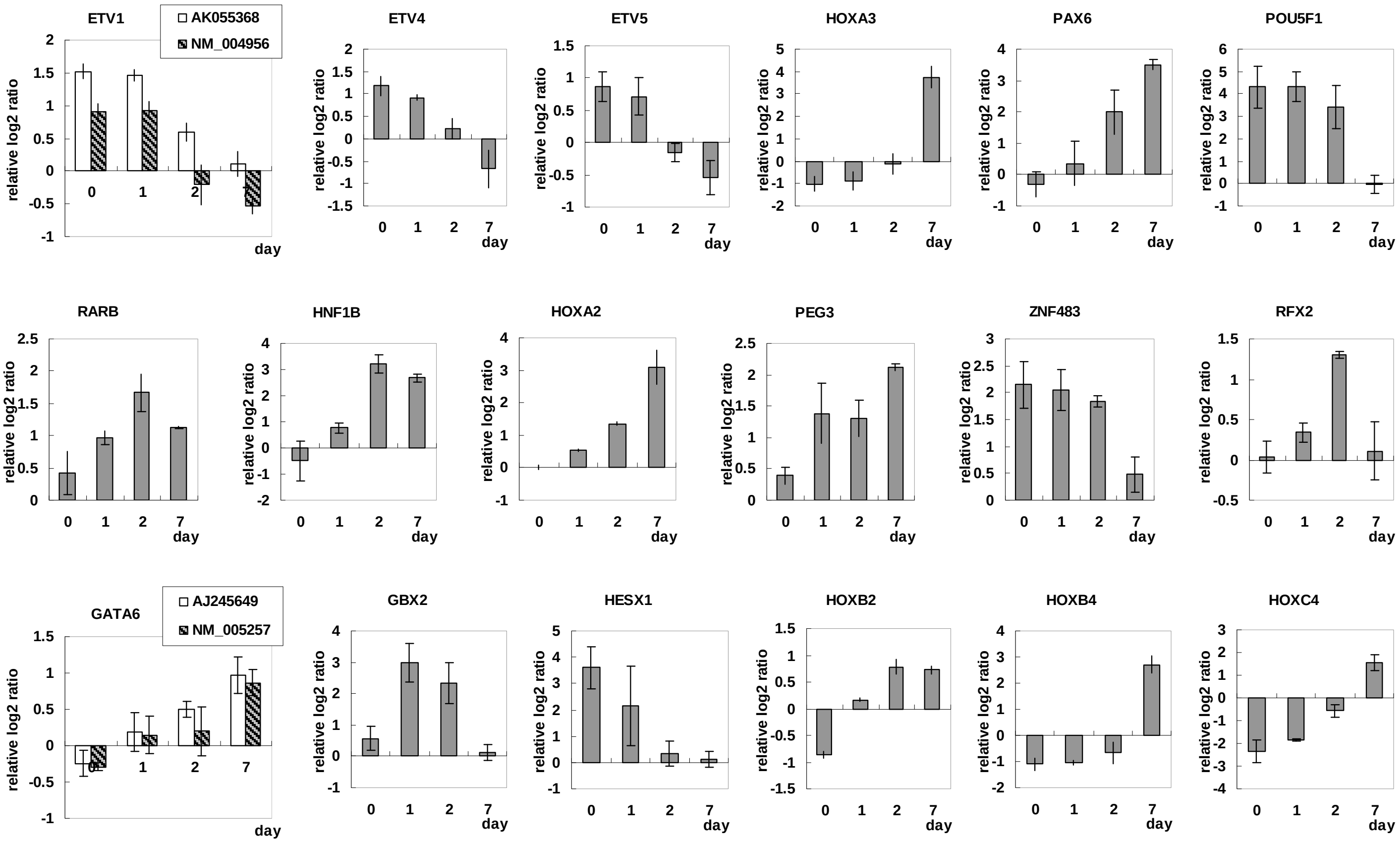
(A) Expression profiles of later-stage nerve differentiation marker genes by DNA microarray. Log2 values for each sample were taken an average and calculated S.D.

0 day, Negative control; 1 day, Cells were collected after 24 hours by RA induction; 2 days, after 48 hours by RA induction; 7 days, after 7 days by RA induction

(B) Real-time PCR analysis of cells after long-term induction with RA.

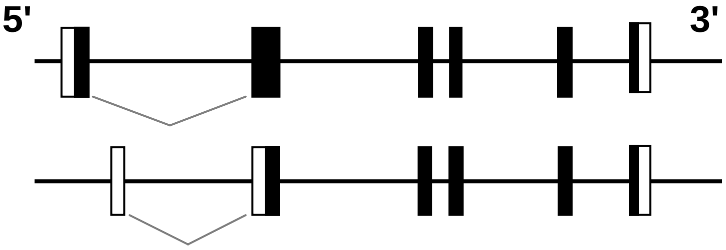
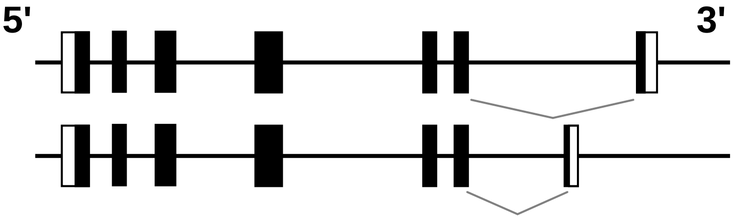
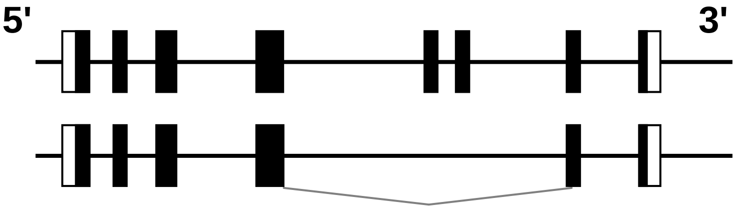
RNA was prepared from cells: 14-day, after 14 days of treatment and 35-day, after 35 days of treatment with RA.

Probe ID	Gene symbol	Gene full name	0-day mean ±S.D.	1-day mean ±S.D.	2-day mean ±S.D.	7-day mean ±S.D.
AK055368	ETV1	ets variant 1	1.52 ± 0.12	1.46 ± 0.09	0.59 ± 0.13	0.11 ± 0.19
NM_004956	ETV1	ets variant 1	0.90 ± 0.13	0.93 ± 0.13	-0.20 ± 0.30	-0.53 ± 0.13
NM_001986	ETV4	ets variant 4	1.18 ± 0.22	0.91 ± 0.06	0.22 ± 0.23	-0.67 ± 0.42
NM_004454	ETV5	ets variant 5	0.86 ± 0.23	0.72 ± 0.29	-0.15 ± 0.15	-0.54 ± 0.26
NM_030661	HOXA3	homeobox A3	-1.03 ± 0.33	-0.88 ± 0.39	-0.12 ± 0.45	3.75 ± 0.48
NM_000280	PAX6	paired box 6	-0.31 ± 0.39	0.36 ± 0.71	2.00 ± 0.71	3.50 ± 0.17
NM_002701	POU5F1	POU class 5 homeobox 1	4.32 ± 0.94	4.32 ± 0.66	3.43 ± 0.96	-0.04 ± 0.42
NM_000965	RARB	retinoic acid receptor, beta	0.42 ± 0.33	0.98 ± 0.10	1.66 ± 0.29	1.13 ± 0.02
NM_000458	HNF1B	HNF1 homeobox B	-0.48 ± 0.76	0.77 ± 0.19	3.23 ± 0.35	2.69 ± 0.16
NM_006735	HOXA2	homeobox A2	0.03 ± 0.08	0.53 ± 0.03	1.36 ± 0.04	3.09 ± 0.54
NM_006210	PEG3	paternally expressed 3	0.40 ± 0.14	1.38 ± 0.48	1.31 ± 0.29	2.12 ± 0.06
AK092811	ZNF483	zinc finger protein 483	2.15 ± 0.43	2.05 ± 0.38	1.83 ± 0.10	0.48 ± 0.33
NM_000635	RFX2	regulatory factor X, 2 (influences HLA class II expression)	0.04 ± 0.20	0.34 ± 0.12	1.31 ± 0.05	0.11 ± 0.36
AJ245649	GATA6	GATA binding protein 6	-0.24 ± 0.18	0.19 ± 0.26	0.50 ± 0.11	0.97 ± 0.25
NM_005257	GATA6	GATA binding protein 6	-0.29 ± 0.06	0.15 ± 0.26	0.20 ± 0.33	0.86 ± 0.18
NM_001485	GBX2	gastrulation brain homeobox 2	0.56 ± 0.38	2.99 ± 0.60	2.34 ± 0.64	0.13 ± 0.25
NM_003865	HESX1	HESX homeobox 1	3.60 ± 0.81	2.16 ± 1.51	0.33 ± 0.47	0.12 ± 0.29
NM_002145	HOXB2	homeobox B2	-0.86 ± 0.06	0.16 ± 0.03	0.79 ± 0.13	0.73 ± 0.07
NM_024015	HOXB4	homeobox B4	-1.10 ± 0.23	-1.06 ± 0.09	-0.67 ± 0.42	2.70 ± 0.33
NM_014620_(2)	HOXC4	homeobox B4	-2.37 ± 0.50	-1.84 ± 0.06	-0.57 ± 0.27	1.56 ± 0.34



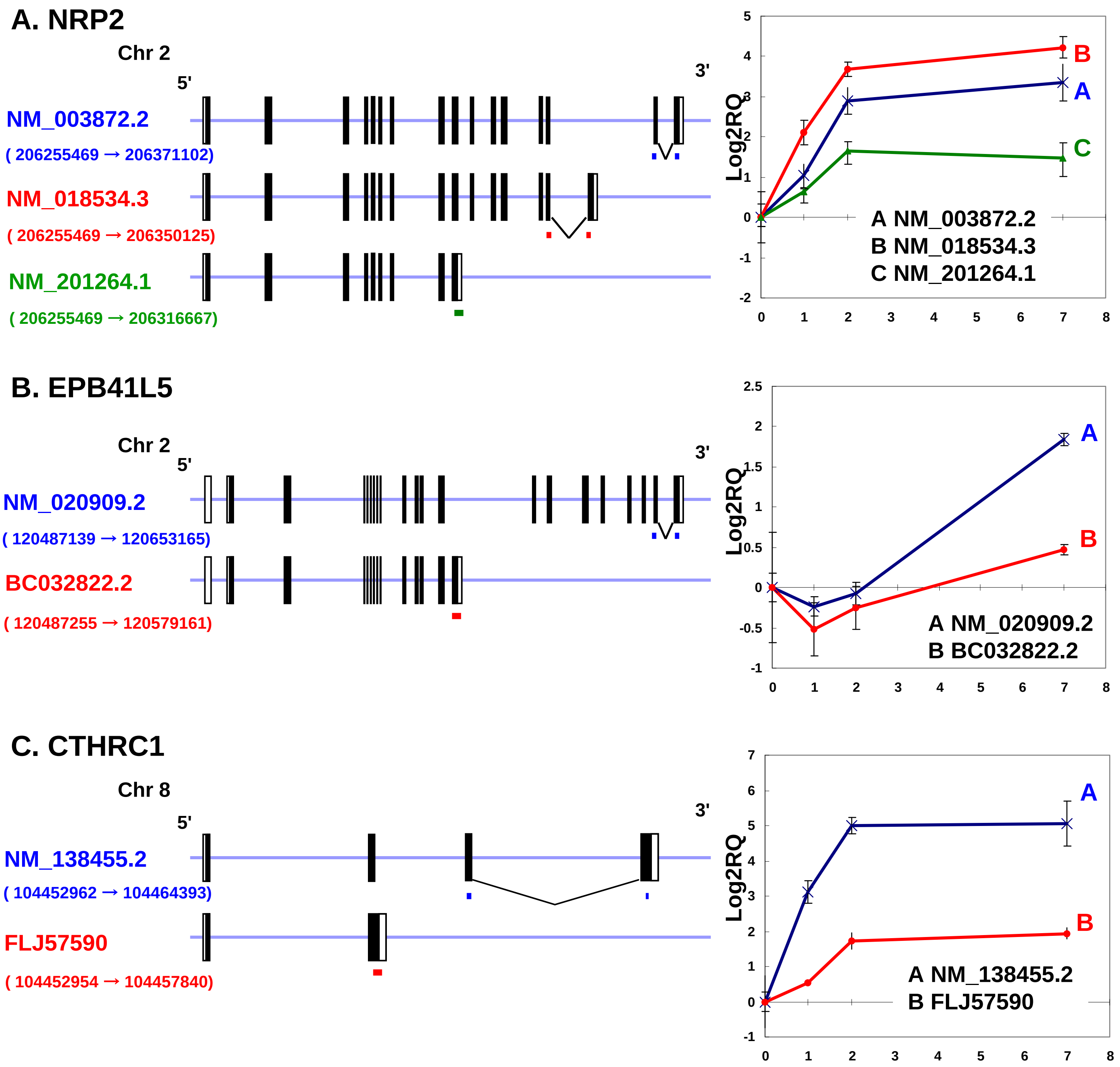
Supplementary Fig. 3. **Expression profiles of transcription factors by DNA microarray.**

Log2 values for each sample were taken an average and calculated S.D.
0 day, Negative control; 1 day, Cells were collected after 24 hours by RA induction;
2 days, after 48 hours by RA induction; 7 days, after 7 days by RA induction

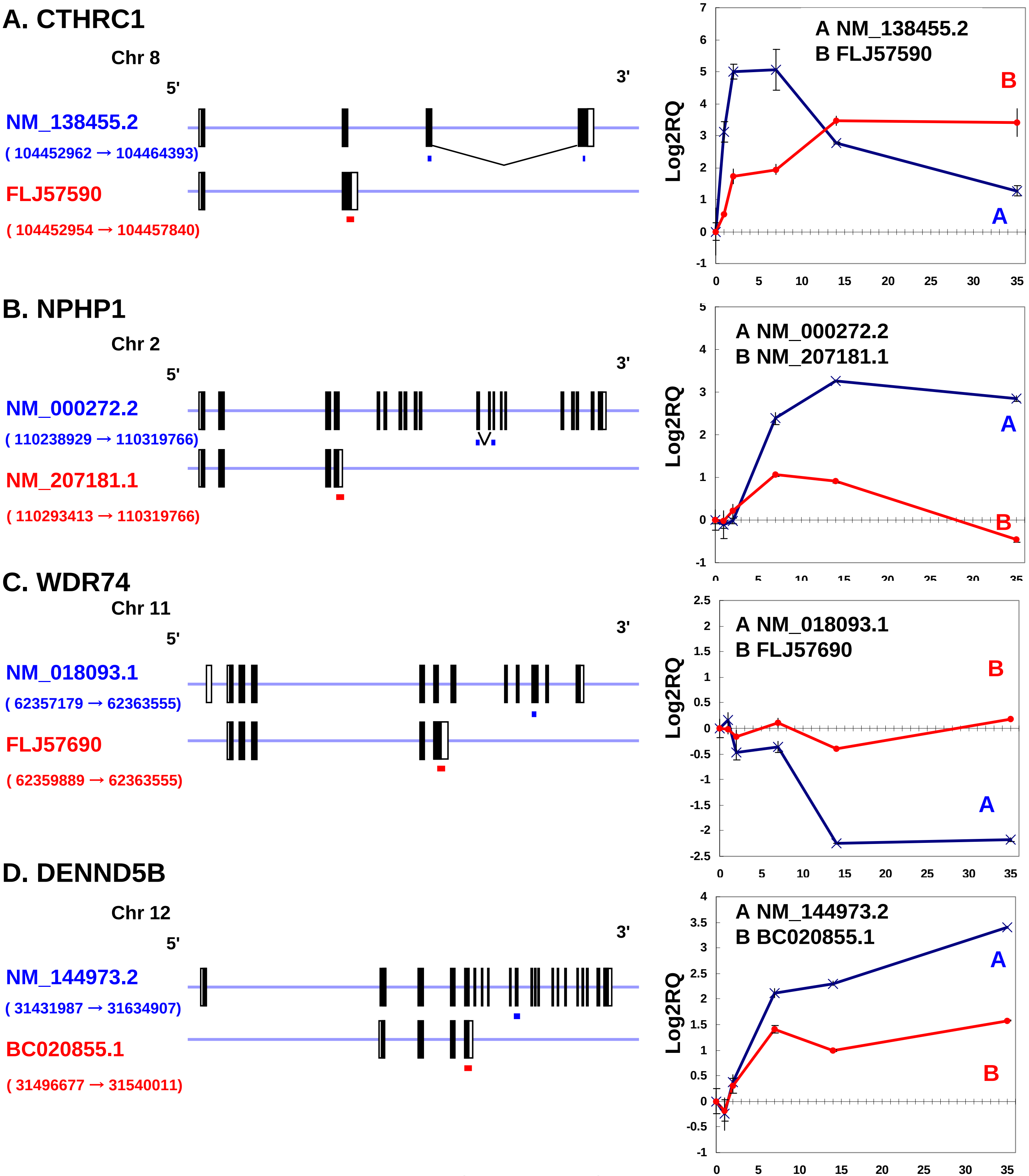
Type of protein-coding transcripts	Splicing patterns
Multiple: 274 genes (76.5 %)	**Alternative N-terminus: 136 genes*** 
	Alternative C-terminus: 59 genes* 
	Other types (ex. alternative cassette-exon): 105 genes 
Single : 84 genes (23.5 %)	**The following types are included.** **mRNAs where AS only occurred in the UTR.** **mRNAs which we could not predict ORF regions.**

Supplementary Fig. 4. **Classifications of selected 358 genes based on splicing patterns.**

Selected 358 genes were classified according to their mRNA diversity as a result of AS.
Multiple: gene producing multiple protein-coding transcripts by AS.
Single: gene producing a single protein-coding transcript.
Alternative N-terminus: gene producing multiple protein-coding transcripts as a result of alternative splicing of N-terminus.
Alternative C-terminus: gene producing multiple protein-coding transcripts as a result of alternative splicing of C-terminus.
Other types: gene producing multiple protein-coding transcripts with other splicing patterns.
*: 26 genes produced multiple protein-coding transcripts with alternatively spliced N- and C-terminuses.
Boxes, exons; gray lines, introns; black boxes, coding regions; white boxes, untranslated regions



Supplementary Fig. 5. **Quantitative analysis of expression of 3 selected genes that showed AS in their C-terminus by real-time PCR until 7-day.**
Expression levels of two transcripts produced by AS from each gene were analyzed by real-time PCR, and were represented in log2 base. The data were normalized with respect to that of the human GAPDH.
Name of the genes: (A) NRP2, (B) EPB41L5, (C) CTHRC1
Schematic views of selected genes: Boxes, exons; purple lines, introns; black boxes, coding regions; white boxes, untranslated regions; red, blue or green bars, amplified regions of real-time PCR; and numbers given in parentheses, genomic alignment positions.



***Supplementary Fig. 6.* Quantitative analysis of expression of 4 selected genes that showed AS in their C-terminus by real-time PCR.**

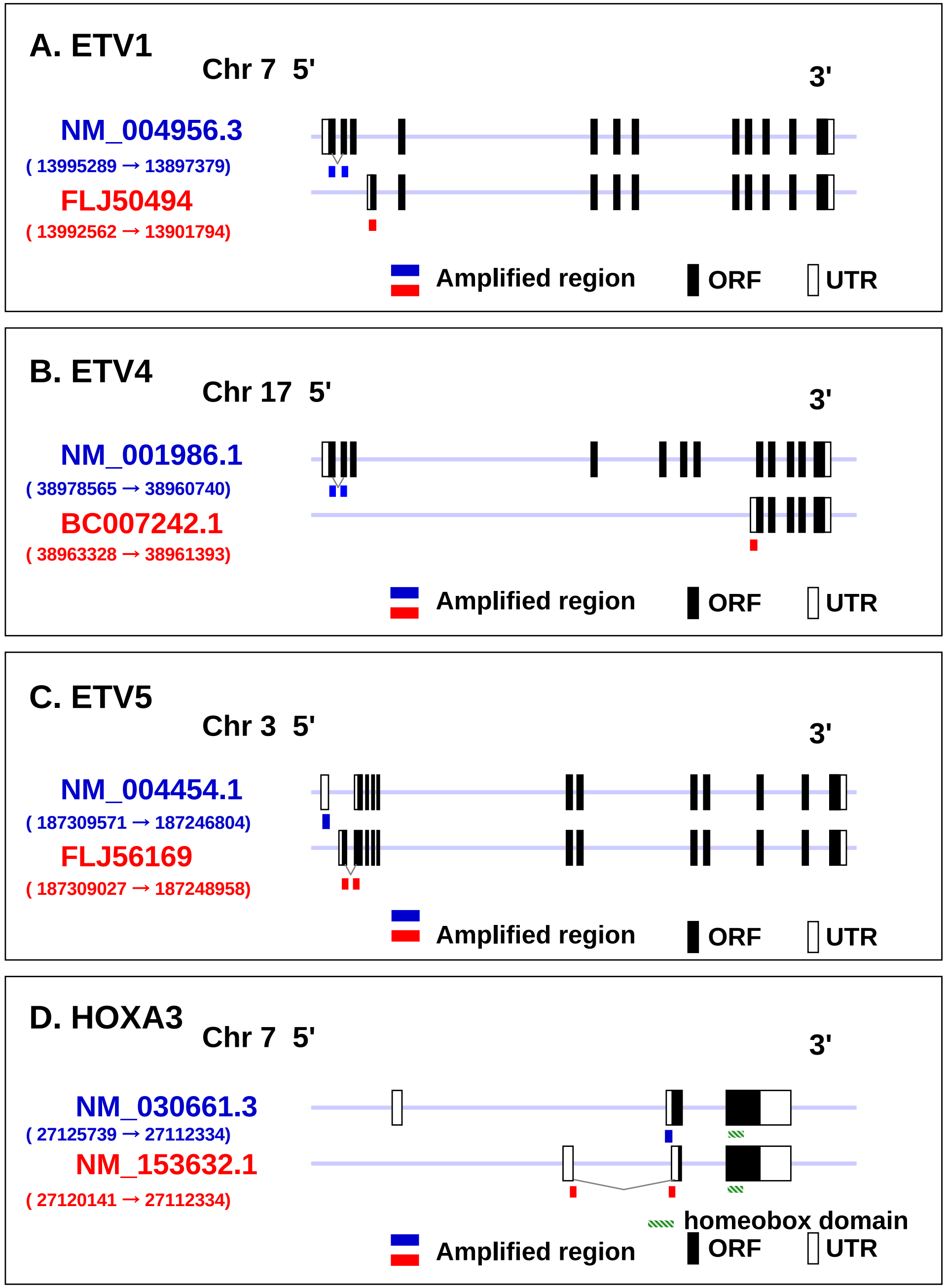
Expression levels of two transcripts produced by AS from each gene were analyzed by real-time PCR, and were represented in log2 base. The data were normalized with respect to that of the human GAPDH.

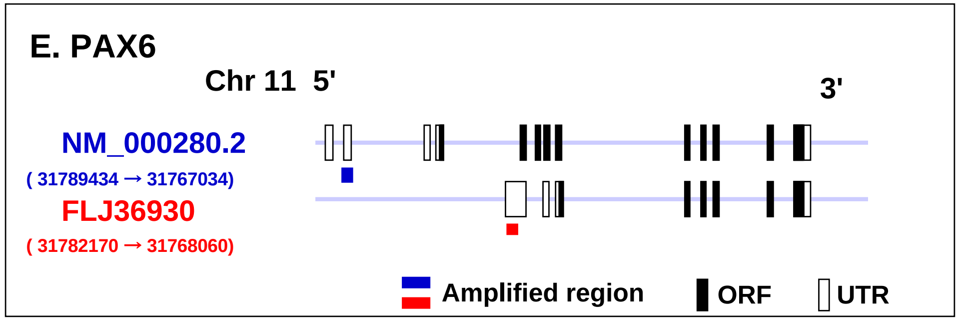
Name of the genes: (A) CTHRC1, (B) NPHP1, (C) WDR74, (D) DENND5B

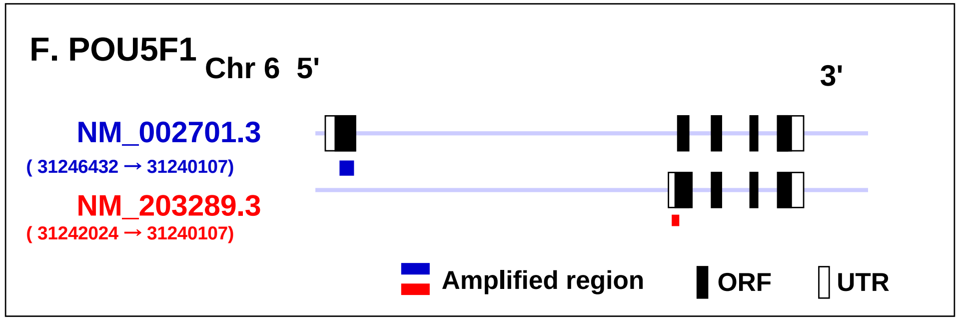
Schematic views of selected genes: Boxes, exons; purple lines, introns; black boxes, coding regions; white boxes, untranslated regions; red or blue bars, amplified regions of real-time PCR; and numbers given in parentheses, genomic alignment positions.

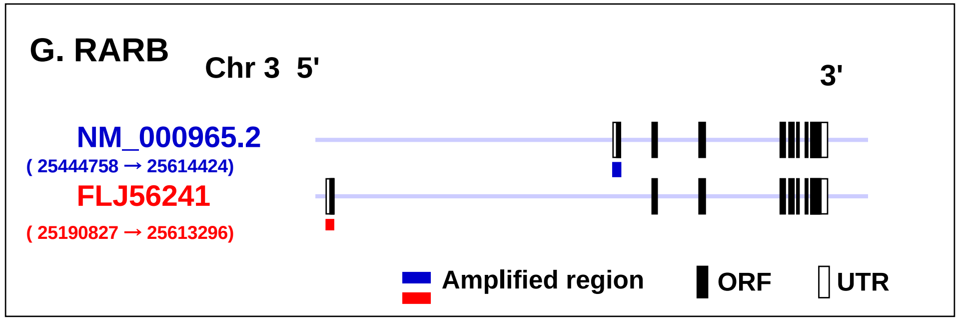
Supplementary Fig. 7. **Schematic views of selected 12 transcription factors.**

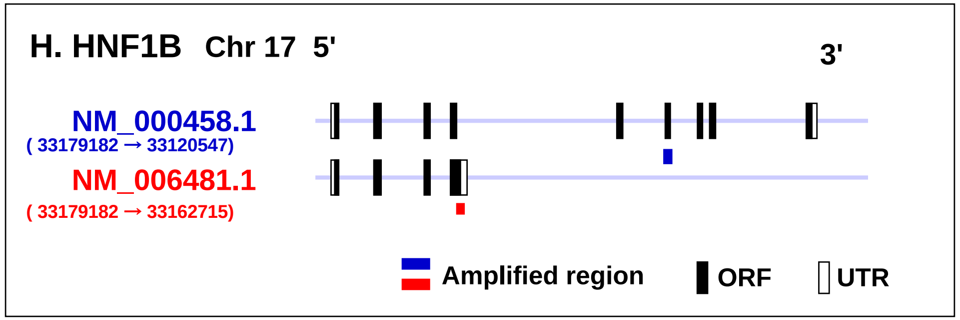
Boxes, exons; purple lines, introns; black boxes, coding regions; white boxes, untranslated regions; pink or blue bars, amplified regions of real-time PCR; and numbers given in parentheses, genomic alignment positions.

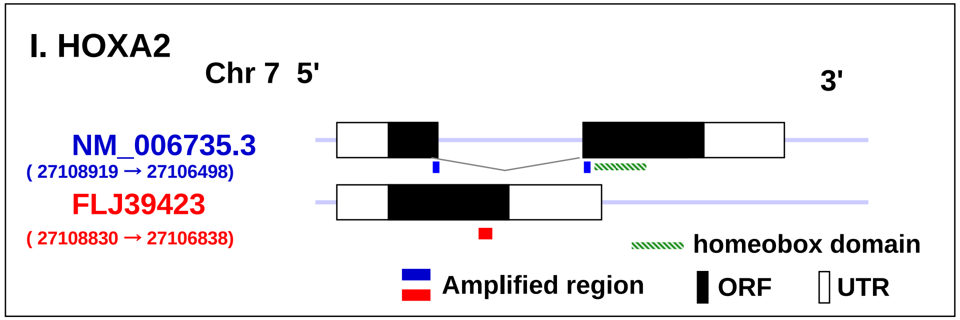


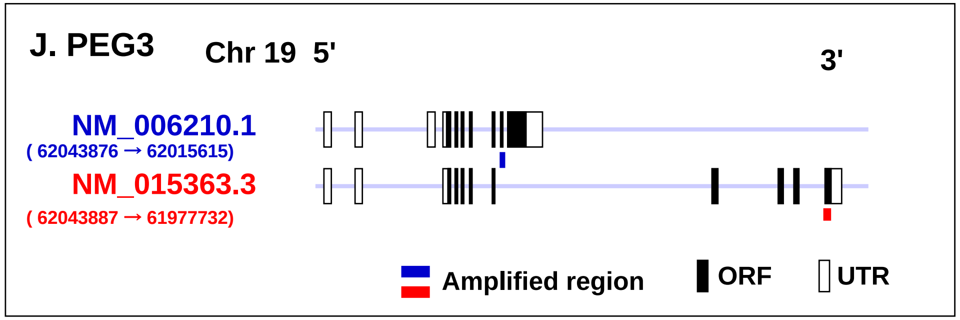

E. PAX6
Chr 11 5'
3'
NM_000280.2
(31789434 → 31767034)
FLJ36930
(31782170 → 31768060)
Amplified region
ORF
UTR

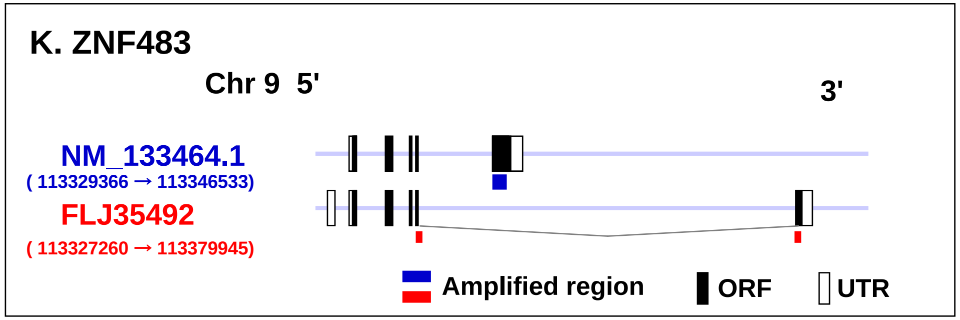

F. POU5F1
Chr 6 5'
3'
NM_002701.3
(31246432 → 31240107)
NM_203289.3
(31242024 → 31240107)
Amplified region
ORF
UTR

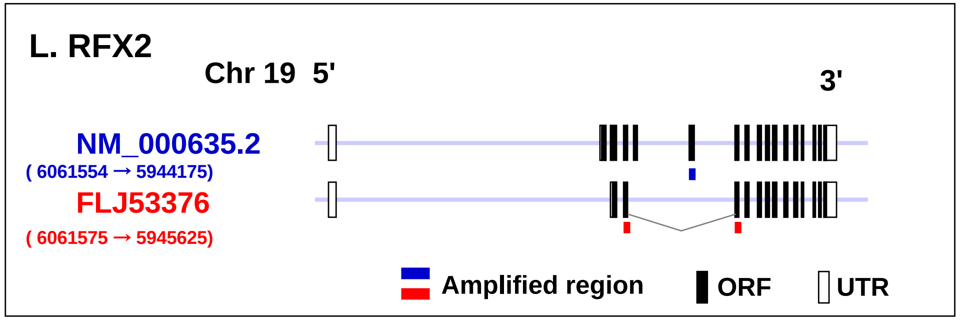

G. RARB
Chr 3 5'
3'
NM_000965.2
(25444758 → 25614424)
FLJ56241
(25190827 → 25613296)
Amplified region
ORF
UTR


H. HNF1B
Chr 17 5'
3'
NM_000458.1
(33179182 → 33120547)
NM_006481.1
(33179182 → 33162715)
Amplified region
ORF
UTR

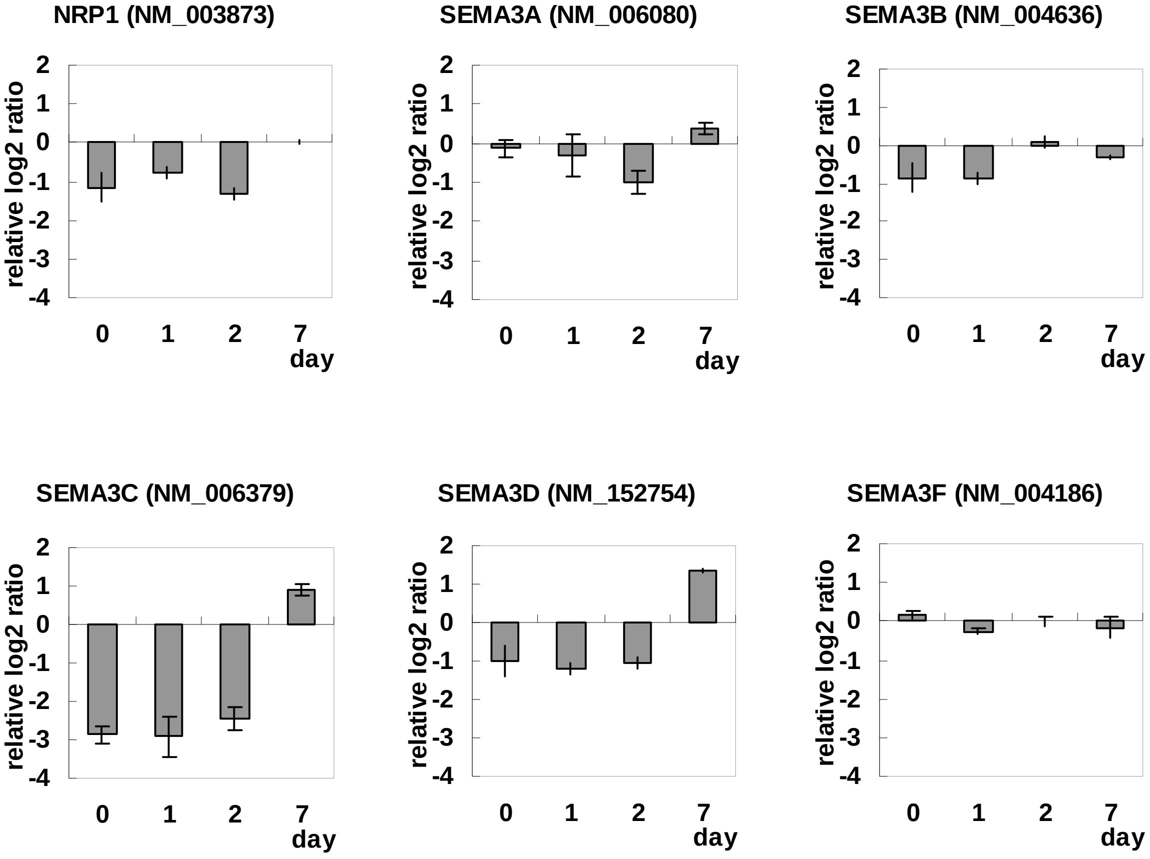

I. HOXA2
Chr 7 5'
3'
NM_006735.3
(27108919 → 27106498)
FLJ39423
(27108830 → 27106838)
homeobox domain
Amplified region
ORF
UTR


J. PEG3
Chr 19 5'
3'
NM_006210.1
(62043876 → 62015615)
NM_015363.3
(62043887 → 61977732)
Amplified region
ORF
UTR


K. ZNF483
Chr 9 5'
3'
NM_133464.1
(113329366 → 113346533)
FLJ35492
(113327260 → 113379945)
Amplified region
ORF
UTR


L. RFX2
Chr 19 5'
3'
NM_000635.2
(6061554 → 5944175)
FLJ53376
(6061575 → 5945625)
Amplified region
ORF
UTR

Probe ID	Gene symbol	0-day mean ±S.D.	1-day mean ±S.D.	2-day mean ±S.D.	7-day mean ±S.D.
NM_003873	NRP1	-1.15 ± 0.59	-0.79 ± 0.13	-1.34 ± 0.49	0.01 ± 0.12
NM_006080	SEMA3A	-0.14 ± 0.12	-0.32 ± 0.13	-0.98 ± 0.34	0.39 ± 0.15
NM_004636	SEMA3B	-0.86 ± 0.39	-0.87 ± 0.15	0.06 ± 0.15	-0.31 ± 0.06
NM_006379	SEMA3C	-2.86 ± 0.22	-2.92 ± 0.54	-2.45 ± 0.30	0.90 ± 0.15
NM_152754	SEMA3D	-0.99 ± 0.27	-1.19 ± 0.38	-1.05 ± 0.13	1.36 ± 0.08
NM_004186	SEMA3F	0.17 ± 0.11	-0.27 ± 0.08	0.01 ± 0.13	-0.16 ± 0.25



Supplementary Fig. 8. **Expression profiles of genes related NRP2 by DNA microarray.**

Log2 values for each sample were averaged and S.D. values were calculated.

0-day, Negative control; cells were collected after 1-day (24 h), 2-day (48 h) and 7-day (168 h) induction with RA.

***Supplementary Table 1.* List of genes whose expressions were altered in RA-induced NT2 cells as determined by DNA microarray analysis.**

1. 40 probes, 1-day sample (from Fig 1A).

Row No.	Probe Name	Probe ID	Probe sequence	0-day (mean ±S.D.)	1-day (mean ±S.D.)	2-day (mean ±S.D.)	7-day (mean ±S.D.)
1	hypothetical protein MGC48332 (MGC48332), mRNA.	NM_178450	GCACTCTTCACTATTTACCTCTTTTGGACACTAGTGTCATTTAGGTACCACTGTCGATTGTACAACGAGTGGCGTCGGAC	-0.16 ± 0.25	1.17 ± 0.33	0.74 ± 0.20	0.13 ± 0.16
2	chimerin (chimaerin) 2 (CHN2), mRNA.	NM_004067	ATCTCAAGAGGATCAAGAAAGTGTACTGTTGTGACCTCACAACACTTGTGAAGGCTCACAACACTCAGAGACCCATGGTG	-0.24 ± 0.05	0.94 ± 0.15	0.81 ± 0.46	0.07 ± 0.09
3	fibronectin type III domain containing 5 (FNDC5), mRNA.	NM_153756	CATCAAGGACAATGAACCCAATAACAACAAGGAAAAAACCAAGAGTGCATCAGAAACCAGCACACCAGAGCACCAGGGCG	-0.53 ± 0.23	0.73 ± 0.07	0.75 ± 0.15	0.61 ± 0.28
4	single Ig IL-1R-related molecule (SIGIRR), mRNA.	NM_021805	ACCAGTGGGGTCTCGCTGGGAGAGAGCCGGAGCAGCGAAGTGGACGTCTCGGATCTCGGCTCGCGAAACTACAGTGCCCG	-0.46 ± 0.14	0.73 ± 0.09	0.80 ± 0.02	0.06 ± 0.11
5	acyl-CoA synthetase long-chain family member 3 (ACSL3), transcript variant 1, mRNA.	NM_004457	ACAGATGCCTTCAAGCTGAAACGCAAAGAGCTTAAAACACATTACCAGGCGGACATTGAGCGAATGTATGGAAGAAAATA	-0.36 ± 0.27	1.11 ± 0.05	1.28 ± 0.18	-0.21 ± 0.05
6	cDNA FLJ35135 fis, clone PLACE6009237.	AK092454	TGGGCTGCTAGACTACCCCTCTTCATCAGCCTGCTGGAAAGAGCAGACAGCGTAACAGCAGCCTATGCCAAACAGCACTA	0.05 ± 0.31	1.40 ± 0.27	0.98 ± 0.18	0.98 ± 0.26
7	cDNA FLJ39354 fis, clone PEBLM2002455.	AK096673	TTCTCCCAAGCCTTTCTCCCTCCACAGGAAACAGATTTTTCAGGGCCTTCCATGCCTGCCACTTTGTCCGTCTCTTTTTT	0.05 ± 0.14	1.09 ± 0.24	0.88 ± 0.27	0.66 ± 0.21
8	retinoic acid induced 17 (RAI17), mRNA.	XM_166091	GTGGATCAGTACATGTGGGGAATCCTGAATGCCATCCAACACTCCGAGTTTGAAGAGGTCACCATCGATCCCACGTGCAG	-0.54 ± 0.20	1.15 ± 0.11	0.96 ± 0.08	0.73 ± 0.17
9	carboxypeptidase E (CPE), mRNA.	NM_001873	ACCTTGAGCAGATACACCGAGGAGTTAAAGGATTTGTCCGAGACCTTCAAGGTAACCCAATTGCGAATGCCACCATCTCC	-0.73 ± 0.17	1.47 ± 0.11	1.60 ± 0.41	0.69 ± 0.45
10	sialoadhesin (SN), mRNA.	NM_023068	GGTGGAGATGGCTTTTCAGAAAGAGACCACGCAGCTCATTGATCCTGATGCAGCCACATGTGAGACCTCAACCTGTGCCC	0.39 ± 0.12	1.48 ± 0.07	1.04 ± 0.40	0.00 ± 0.42
11	transcription factor 7 (T-cell specific, HMG-box) (TCF7), transcript variant 1, mRNA.	NM_003202	CCCCTCAATGCCTTCATGCTGTACATGAAGGAGATGAGAGCCAAGGTCATTGCAGAGTGCACACTTAAGGAGAGCGCTGC	-0.51 ± 0.23	1.07 ± 0.23	0.31 ± 0.41	-0.56 ± 0.14
12	cocaine- and amphetamine-regulated transcript (CART), mRNA.	NM_004291	CGCTGCAAGAAGTCTTGAAGAAGCTCAAGAGTAAACGTGTTCCCATCTATGAGAAGAAGTATGGCCAAGTCCCCATGTGT	0.33 ± 0.29	1.89 ± 0.07	0.26 ± 0.14	0.10 ± 0.37
13	LOC148646 (LOC148646), mRNA.	XM_086262	CAGGAGATTTGGGAGGAAGCCTATCAGCGAGTGGCTAATGAGCAGGAGATTTATGAAGGTTCCAGACAGTTGGCTGCCGA	-1.14 ± 0.24	0.10 ± 0.16	-0.06 ± 0.18	0.20 ± 0.39
14	homeo box B2 (HOXB2), mRNA.	NM_002145	GAGCCTCTCCCACCCTCAGTCGCATAGACTTATGTGTTTTGCTAAAATTCAGGTATTACTGAATTAGCGTTTAATCCACT	-0.86 ± 0.06	0.16 ± 0.03	0.79 ± 0.13	0.73 ± 0.07
15	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9 (SERPINB9), mRNA.	NM_004155_(2)	AGGCTCTTTGGAGAGAAAACTTGTCAGTTCCTCTCAACGTTTAAGGAATCCTGTCTTCAATTCTACCATGCTGAGCTGAA	0.39 ± 0.36	2.10 ± 0.33	2.29 ± 0.29	-0.67 ± 0.21
16	myc target 1 (MYCT1), mRNA.	NM_025107	GGAAACTGAGAGTCAGCTGGTGACTCTCCCTTCTTCCAATATCTCTCCCACCATCAGCACTTCCCACAGTCTGAGCCGTC	0.34 ± 0.15	1.56 ± 0.29	1.97 ± 0.61	0.24 ± 0.27
17	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcript variant 2, mRNA.	NM_175851	AACCATGGACATCGGAGGATCTTAAAGTGAAATTGCTGCCTCAAAGGACCATCATCTTGTGGGAACTAATGAAAAACATA	1.23 ± 0.22	0.14 ± 0.09	1.26 ± 0.44	0.94 ± 0.00
18	interferon, gamma-inducible protein 16 (IFI16), mRNA.	NM_005531	TGAACACAATCAACTGTGAGGAAGGAGATAAACTGAAACTCACCAGCTTTGAATTGGCACCGAAAAGTGGGAATACCGGG	-1.67 ± 0.34	0.06 ± 0.26	0.74 ± 0.23	-1.39 ± 0.08
19	filamin B, beta (actin binding protein 278) (FLNB), mRNA.	NM_001457	ACGGCCTGGGATTTAAGCCTTTTGACCTGGTCATTCCGTTTGCTGTCAGGAAAGGAGAAATCACTGGAGAGGTCCACATG	-1.03 ± 0.11	0.05 ± 0.07	0.28 ± 0.23	-0.90 ± 0.12
20	multimerin 2 (MMRN2), mRNA.	NM_024756	CCTGCAGACAGTGAAGTTCAACACCACATACATCAACATTGGCAGCAGCTACTTCCCTGAACATGGCTACTTCCGAGCCC	0.08 ± 0.07	1.91 ± 0.16	1.77 ± 0.25	1.40 ± 0.23
21	claudin 2 (CLDN2), mRNA.	NM_020384	CTCATCCCAGAGAAATCGCTCCAACTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTG	0.03 ± 0.20	1.17 ± 0.24	1.52 ± 0.54	1.97 ± 0.29
22	REC8-like 1 (yeast) (REC8L1), mRNA.	NM_005132	CCTGCTCCTGGTGCTCTCAGCGCAACAGATTCTTCACGTGAAACAAGAAAAGCCATATGGTCGCCTCCTGATCCAGCCGG	-0.67 ± 0.19	1.16 ± 0.16	1.98 ± 0.18	1.88 ± 0.11
23	inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA.	NM_030569	GTCCCAGTGGTCTGGAAGCAAAGGAAGATTTACAACGGGGAAGAGCAGATAGACTGCTGGTTTGCCAGGAACAATGCCGC	-0.07 ± 0.23	1.60 ± 0.40	2.53 ± 0.16	2.43 ± 0.12
24	src family associated phosphoprotein 2 (SCAP2), mRNA.	NM_003930	GAAGAAGAAGAGGACAGTGCTCCAGTGAAAGTGGAAGAACAAAGGAAGATGAGTCAGGATAGTGTCCATCACACCTCAGG	-1.82 ± 0.38	1.32 ± 0.03	2.30 ± 0.20	1.79 ± 0.37
25	hypothetical protein FLJ14299 (FLJ14299), mRNA.	NM_025069	TCGCTGTCCTTGCGGAATCCACACACTTTGGGCCTAAGCCGGTACCACCCCTATGGCAAGAGCCACTTATCCACAGCGGG	-0.81 ± 0.49	1.81 ± 0.40	3.59 ± 0.05	2.58 ± 0.36
26	cDNA FLJ10561 fis, clone NT2RP2002672.	AK001423	TCACATAGCTGTTTTGCAACAGCCTTTATTGCCAACACCCTTGGAAGAACATCTCCTGTAGAAGTACAAGTTTTGCAATA	-1.08 ± 0.16	0.28 ± 0.29	0.72 ± 0.25	2.03 ± 0.19
27	dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), mRNA.	NM_016651	CAAGCAGTCTGTGGTCTGCTTCCCATCCTTCATCCAGCAAGAAAATGGATGGCTACATTCTGAGCCTGGTCCAGAAAAAA	0.58 ± 0.39	3.05 ± 0.58	2.35 ± 0.50	1.13 ± 0.40
28	gastrulation brain homeo box 2 (GBX2), mRNA.	NM_001485	CTTCTCGCTGGAGAGCGATGTGGACTACAGCTCGGATGACAATCTGACTGGCCAGGCAGCTCACAAGGAGGAAGACCCGG	0.56 ± 0.38	2.99 ± 0.60	2.34 ± 0.64	0.13 ± 0.25
29	endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfamily) (EBAF), mRNA.	NM_003240	TGGATTCTGGTTCTGACAGGGCCACAAGCTAGGATCTCTAACAAACGCAGAAGGCTTTGGCTCGTCATTTCCTCTTAAAA	0.93 ± 0.43	3.53 ± 0.70	1.65 ± 0.22	1.28 ± 0.32
30	tetraspanin similiar to uroplakin 1 (LOC90139), mRNA.	NM_130783	GGGAAGGAGCCTATTCCTAAACAAGCAGGGCTGTTACACGGTGATCCTCAACACCTTCGAGACCTACGTCTACTTGGCCG	2.05 ± 0.10	3.38 ± 0.01	2.83 ± 0.08	2.49 ± 0.20
31	LIM and cysteine-rich domains 1 (LMCD1), mRNA.	NM_014583	AGGAACCGGATGATCATGACCAACCCTATTGCTACTGGGAAAGATCCCACTTTTGACACCATCACCTACGAGTGGGCTCC	-0.08 ± 0.20	-1.25 ± 0.11	-1.96 ± 0.26	-0.67 ± 0.07
32	LIM and cysteine-rich domains 1 (LMCD1), mRNA.	NM_014583_(2)	GGAACCGGATGATCATGACCAACCCTATTGCTACTGGGAAAGATCCCACTTTTGACACCATCACCTACGAGTGGGCTCCC	-0.15 ± 0.24	-1.18 ± 0.18	-1.55 ± 0.31	-0.57 ± 0.17
33	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) (RELA), mRNA.	NM_021975	GGCCTCCTTTCAGGAGATGAAGACTTCTCCTCCATTGCGGACATGGACTTCTCAGCCCTGCTGAGTCAGATCAGCTCCTA	1.01 ± 0.03	-1.22 ± 0.20	-1.43 ± 0.13	-0.95 ± 0.09
34	cDNA FLJ33783 fis, clone BRSSN2007504.	AK091102	GTTCGACCTCTTCCAAGAAGACGTCAGGAATGTCCTTCTGAATGCCTTTCCTAGTTCTCATGAGAACACAGCAGTTTTTA	1.10 ± 0.18	0.09 ± 0.11	-0.79 ± 0.34	-0.92 ± 0.41
35	hypothetical protein FLJ23469 (FLJ23469), mRNA.	NM_024710	CTGTCCTGTTCCTGTGTGACATGCAGGAGAAGTTCCGCCACAACATCGCCTACTTCCCACAGATCGTCTCAGTGGCTGCC	-1.19 ± 0.16	-2.22 ± 0.15	-1.75 ± 0.30	-1.84 ± 0.26
36	epithelial membrane protein 1 (EMP1), mRNA.	NM_001423	TTAGCACCATTGCCAATGTCTGGTTGGTTTCCAATACGGTAGATGCATCAGTAGGTCTTTGGAAAAACTGTACCAACATT	-3.11 ± 0.18	-1.97 ± 0.28	-3.25 ± 0.47	-1.67 ± 0.61

37	homeo box A1 (HOXA1), transcript variant 1, mRNA.	NM_005522	AGACTTTTGACTGGATGAAAGTCAAAAGAAACCCTCCCAAAACAGGGAAAGTTGGAGAGTACGGCTACCTGGGTCAACCC	-0.58 ± 0.78	5.20 ± 0.11	5.72 ± 0.21	3.80 ± 0.54
38	cDNA FLJ12777 fis, clone NT2RP2001720.	AK022839	TCTCTCCTGGCCTCTTTTCTGGGGCATCCTGGGTGGAGTGTTTTTCTTGGGATCACGAGCTTGCACTCGCACACAGGCCC	-0.38 ± 0.03	3.69 ± 0.38	5.16 ± 0.59	3.06 ± 0.44
39	cellular retinoic acid binding protein 2 (CRABP2), mRNA.	NM_001878	AGGTTGGGGAGGAGTTTGAGGAGCAGACTGTGGATGGGAGGCCCTGTAAGAGCCTGGTGAAATGGGAGAGTGAGAATAAA	1.49 ± 0.38	4.31 ± 0.27	5.19 ± 0.11	3.38 ± 0.28
40	retinol binding protein 1, cellular (RBP1), mRNA.	NM_002899	ACTTCCAAGTTGGGAAGGAGTTTGAGGAGGATCTGACAGGCATAGATGACCGCAAGTGCATGACAACAGTGAGCTGGGAC	1.15 ± 0.31	3.30 ± 0.56	4.15 ± 0.42	5.66 ± 0.12

2. 106 probes, 2-day sample (from Fig 1B).

Row No.	Probe Name	Probe ID	Probe sequence	0-day (mean ±S.D.)	1-day (mean ±S.D.)	2-day (mean ±S.D.)	7-day (mean ±S.D.)
1	methyltransferase-like 1 (METTL1), transcript variant 3, mRNA.	NM_023033	GGGGCTGGTGTATACCATAACCGATGTGCTGGAGCTACACGACTGGATGTGCACTCATTTCGAAGAGCACCCACTGTTTG	0.82 ± 0.19	0.56 ± 0.10	-0.36 ± 0.14	-0.24 ± 0.30
2	solute carrier family 6 (neurotransmitter transporter, creatine), member 8 (SLC6A8), mRNA.	NM_005629	GCATGGGCATCTTCATCTTCAACGTTGTGTACTACGAGCCGCTGGTCTACAACAACACCTACGTGTACCCGTGGTGGGGT	0.69 ± 0.15	0.54 ± 0.14	-0.34 ± 0.18	-0.22 ± 0.14
3	sprouty homolog 4 (Drosophila) (SPRY4), mRNA.	NM_030964	ACCCACTCACCATCCTACCCATTGACCAGGTGAAGACCAGCCATGTGGAGAATGACTACATAGACAACCCTAGCCTGGCC	0.69 ± 0.07	0.52 ± 0.18	-0.62 ± 0.13	-0.76 ± 0.24
4	pim-2 oncogene (PIM2), mRNA.	NM_006875	TGGTGTGTGGGGACATTCCCTTTGAGAGGGACCAGGAGATTCTGGAAGCTGAGCTCCACTTCCCAGCCCATGTCTCCCCA	0.92 ± 0.27	0.62 ± 0.32	-0.14 ± 0.18	-0.94 ± 0.43
5	ets variant gene 5 (ets-related molecule) (ETV5), mRNA.	NM_004454	CGATTCAGAAGTGCCTAACTGCCAGTCATCCTACATGAGAGGGGGTTATTTCTCCAGCAGCCATGAAGGTTTTTCATATG	0.86 ± 0.23	0.72 ± 0.29	-0.15 ± 0.15	-0.54 ± 0.26
6	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase) (ACAT2), mRNA.	NM_005891	TGTTGCTCTTATGAAGAAGTCAGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGG	0.77 ± 0.11	0.58 ± 0.11	-0.60 ± 0.21	-0.58 ± 0.48
7	Homo sapiens cDNA FLJ52649 complete cds.	AK303891	ACAGGCTGTAAAGGAAGGCAGTGACCTCTGCATGTTTCTGTCTCTCTCACTAACCCTTTGCCTCTGTTTCTCTTTCTTCT	0.46 ± 0.22	0.18 ± 0.22	-0.63 ± 0.15	-0.20 ± 0.53
8	TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 4, mRNA.	NM_003244_(2)	AGCATCTGGCAGTGAGACTGAGGATGAGGACAGCATGGACATTCCCTTGGACCTTTCTTCATCCGCTGGCTCAGGCAAGA	1.16 ± 0.22	0.31 ± 0.16	-0.16 ± 0.11	0.01 ± 0.14
9	synaptotagmin-like 2 (SYTL2), transcript variant b, mRNA.	NM_032379	AAGATGGTAAACTCCCCCAATACTTGGATTGAAGCAACACTGCCTCTCAGAATGCTTTTGATTGCCAAGATTTCCAAATG	0.94 ± 0.23	0.24 ± 0.32	-0.36 ± 0.19	0.41 ± 0.03
10	suppressor of cytokine signaling 2 (SOCS2), mRNA.	NM_003877	CCGCTCTACACGTCAGCACCATCTCTGCAGCATCTCTGTAGGCTCACCATTAACAAATGTACCGGTGCCATCTGGGGACT	1.47 ± 0.52	0.42 ± 0.16	-0.76 ± 0.34	-0.51 ± 0.04
11	cDNA FLJ33783 fis, clone BRSSN2007504.	AK091102	GTTCGACCTCTTCCAAGAAGACGTCAGGAATGTCCTTCTGAATGCCTTTCCTAGTTCTCATGAGAACACAGCAGTTTTTA	1.10 ± 0.18	0.09 ± 0.11	-0.79 ± 0.34	-0.92 ± 0.41
12	tumor-associated calcium signal transducer 1 (TACSTD1), mRNA.	NM_002354	CAAGAGAAAAACCTTATGATAGTAAAAGTTTGCGGACTGCACTTCAGAAGGAGATCACAACGCGTTATCAACTGGATCCA	1.22 ± 0.00	0.56 ± 0.08	0.00 ± 0.12	-0.92 ± 0.45
13	tumor-associated calcium signal transducer 1 (TACSTD1), mRNA.	NM_002354_(2)	CGACGGCGACTTTTGCCGCAGCTCAGGAAGAATGTGTCTGTGAAAACTACAAGCTGGCCGTAAACTGCTTTGTGAATAAT	1.47 ± 0.28	0.85 ± 0.03	0.31 ± 0.19	-0.64 ± 0.43
14	sodium channel, nonvoltage-gated 1 alpha (SCNN1A), mRNA.	NM_001038	CTTCCAGATGCTATCGCGACAGAACAATTACACCGTCAACAACAAGAGAAATGGAGTGGCCAAAGTCAACATCTTCTTCA	1.27 ± 0.28	0.67 ± 0.15	-0.09 ± 0.37	-1.54 ± 0.49
15	follistatin (FST), transcript variant FST317, mRNA.	NM_006350_(2)	GCAAGATGTAAAGAGCAGCCAGAACTGGAAGTCCAGTACCAAGGCAGATGTAAAAAGACTTGTCGGGATGTTTTCTGTCC	1.76 ± 0.62	0.93 ± 0.30	-0.49 ± 0.51	-1.46 ± 0.78
16	TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 4, mRNA.	NM_003244	GTTTTGGCTCGTCCATCAGTGATCTGCCATACCACTGTGACTGCATTGAAAGATGTCCCTTTCTCTCTCTGCCAGTCGGT	1.51 ± 0.26	0.97 ± 0.30	0.12 ± 0.34	0.38 ± 0.04
17	leucine-rich repeat-containing 8 (LRRC8), mRNA.	XM_026998	GATCCTGGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTATACACTGTGGTGGATGCTACGGC	1.39 ± 0.28	1.26 ± 0.15	0.30 ± 0.17	0.65 ± 0.18
18	cDNA FLJ30432 fis, clone BRACE2008999.	AK054994	GGCAGCACAGACTATTTCTTGAGCAGTGGTGACAAGATTCGATTCTTCTTTGAGAAAGGCGTTTTTGATGAGAAAGGAAA	2.15 ± 0.33	1.26 ± 0.23	0.74 ± 0.21	0.43 ± 0.23
19	ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA.	NM_003633	GCTCTGCTTATAAATTCAACAGTGAGACTTACCAGTGGACCAAAGTGGGAGATGTGACAGCAAAGCGCATGAGCTGCCAT	0.54 ± 0.15	0.11 ± 0.22	-0.87 ± 0.21	1.22 ± 0.08
20	CD9 antigen (p24) (CD9), mRNA.	NM_001769	ACAAGGATGAGGTGATTAAGGAAGTCCAGGAGTTTTACAAGGACACCTACAACAAGCTGAAAACCAAGGATGAGCCCCAG	0.92 ± 0.14	0.27 ± 0.40	-0.88 ± 0.23	-2.33 ± 0.32
21	cDNA FLJ23705 fis, clone HEP11066.	AK074285	GTTAAGTGGTACAGCCATGGCTATCGTCAGGCCTGTTGCCTGGAGATCTCTAAGTTAAGGCAACAAGACTTAAAGAATTT	0.04 ± 0.29	0.53 ± 0.21	1.35 ± 0.14	1.05 ± 0.18
22	brain specific protein (CGI-38), mRNA.	NM_015964	CGGCAGGACATCCTGGACGACAGTGGCTACGTGAGCGCCTACAAGAATGCAGGCACCTACGATGCCAAGGTGAAGAAGTG	-0.06 ± 0.31	0.33 ± 0.34	1.17 ± 0.30	1.05 ± 0.26
23	asparaginase like 1 (ASRGL1), mRNA.	NM_025080	TATATGAAGTCAAGGGTTAAAGGTTTAGGTGGCCTCATCGTGGTTAGCAAAACAGGAGACTGGGTGGCAAAGTGGACCTC	0.07 ± 0.14	0.77 ± 0.13	1.15 ± 0.16	1.51 ± 0.39
24	retinoic acid induced 17 (RAI17), mRNA.	XM_166091	GTGGATCAGTACATGTGGGGAATCCTGAATGCCATCCAACACTCCGAGTTTGAAGAGGTCACCATCGATCCCACGTGCAG	-0.54 ± 0.20	1.15 ± 0.11	0.96 ± 0.08	0.73 ± 0.17
25	cDNA: FLJ22539 fis, clone HRC13227.	AK026192	ACAGGGCACATGCACAGAGCTTTGAAGAACATACACAAACCTGTTGAATCAAGTTACTTTCCTCATCCTCAGAGACTTTG	-0.01 ± 0.30	0.92 ± 0.13	1.42 ± 0.20	0.90 ± 0.35
26	carboxypeptidase E (CPE), mRNA.	NM_001873	ACCTTGAGCAGATACACCGAGGAGTTAAAGGATTTGTCCGAGACCTTCAAGGTAACCCAATTGCGAATGCCACCATCTCC	-0.73 ± 0.17	1.47 ± 0.11	1.60 ± 0.41	0.69 ± 0.45
27	cDNA FLJ31907 fis, clone NT2RP7004396, highly similar to Mus musculus mRNA for Fish protein.	AK056469	TGGAGGTTCTGGAGAGGAACCCTAATGGCTGGTGGTACTGCCAGATCCTGGATGGTGTGAAGCCCTTCAAAGGCTGGGTG	0.00 ± 0.32	0.19 ± 0.22	1.56 ± 0.12	0.00 ± 0.12
28	regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 1, mRNA.	NM_000635	AGTTCAACGATCTCGCCTCTCTGTCGCTGACGCTGCTCGACAAAGATGACATGGGCGATGAGCAGCGTGGCAGCGAGGCG	0.04 ± 0.20	0.34 ± 0.12	1.31 ± 0.05	0.11 ± 0.36
29	DnaJ (Hsp40) homolog, subfamily B, member 5 (DNAJB5), mRNA.	NM_012266	ATTGTTGAGTTCAAAGTTCGCTTCCCAGACAGATTAACACCACAGACAAGACAGATCCTTAAGCAGCACCTACCCTGTTC	0.40 ± 0.22	0.60 ± 0.24	1.41 ± 0.13	0.30 ± 0.15
30	CDW52 antigen (CAMPATH-1 antigen) (CDW52), mRNA.	NM_001803	CTCACCATCAGCCTCCTGGTTATGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCC	-0.16 ± 0.10	0.87 ± 0.39	1.44 ± 0.17	0.15 ± 0.10
31	START domain containing 8 (STARD8), mRNA.	NM_014725_(2)	GTTCATTTTCAAAGCAAGCAGAATGAAGACTCAGAAGAGGAAGAGCAGTGTACCATCAGTAGCCACTGGGCCTTCCAGCA	-0.19 ± 0.18	0.71 ± 0.49	1.08 ± 0.12	0.14 ± 0.15
32	thyroid hormone receptor interactor 10 (TRIP10), mRNA.	NM_004240	CCAGCGAGGGCACTATCTCTATGGCCGAGGGTGAAGACCTCAGTCTTATGGAAGAAGACAAAGGGGACGGCTGGACCCGG	0.24 ± 0.19	0.51 ± 0.06	1.44 ± 0.10	-0.54 ± 0.33
33	acyl-CoA synthetase long-chain family member 3 (ACSL3), transcript variant 1, mRNA.	NM_004457	ACAGATGCCTTCAAGCTGAAACGCAAAGAGCTTAAAACACATTACCAGGCGGACATTGAGCGAATGTATGGAAGAAAATA	-0.36 ± 0.27	1.11 ± 0.05	1.28 ± 0.18	-0.21 ± 0.05

34	fibronectin type III domain containing 5 (FNDC5), mRNA.	NM_153756	CATCAAGGACAATGAACCCAATAACAACAAGGAAAAAACCAAGAGTGCATCAGAAACCAGCACACCAGAGCACCAGGGCG	-0.53 ± 0.23	0.73 ± 0.07	0.75 ± 0.15	0.61 ± 0.28
35	cDNA FLJ34110 fis, clone FCBBF3008689.	AK091429	TTCCAGATAGCTTATTCTCTTACCTTTCTTGTCTCTGCTCAGACATCTGCTTAGTGAAGGCTTTTCTGCCCATCTATTTA	-0.25 ± 0.17	0.60 ± 0.03	0.90 ± 0.27	0.47 ± 0.05
36	single Ig IL-1R-related molecule (SIGIRR), mRNA.	NM_021805	ACCAGTGGGGTCTCGCTGGGAGAGAGCCGGAGCAGCGAAGTGGACGTCTCGGATCTCGGCTCGCGAAACTACAGTGCCCG	-0.46 ± 0.14	0.73 ± 0.09	0.80 ± 0.02	0.06 ± 0.11
37	inositol hexaphosphate kinase 3 (IHPK3), mRNA.	NM_054111	CCGAGTACCCAGAGAACAAGCGGCATCGGTTCTTGTTGCTGGAAAATGTAGTGTCACAGTACACGCATCCCTGTGTCCTG	-0.15 ± 0.23	0.28 ± 0.28	0.97 ± 0.24	0.46 ± 0.40
38	KIAA1404 protein (KIAA1404), mRNA.	NM_021035	AAACATGTAAGTTCACCCAAGAGGATGAACAACTTGTGCAGGAAAAGATGGAAGCTCTGAAAGCCACCCTTCCCTGCTCT	-0.29 ± 0.21	0.33 ± 0.07	0.75 ± 0.15	0.61 ± 0.15
39	zinc finger protein 503 (ZNF503), mRNA.	NM_032772	CCAACCGCCTGCCAATCAAGGTGCTGAAGATGCTGACGGCACGAACTGGCCACATTTTGCACCCCGAGTACCTGCAGCCC	-0.28 ± 0.12	0.66 ± 0.14	1.06 ± 0.19	0.75 ± 0.14
40	retinoic acid induced 17 (RAI17), mRNA.	NM_020338	TGAAACCCACTCTGTCGCACAGTGATGGGTCGTTCCCCTATGACTCTGTCCCTTGGCAGCAGAACACCAACCAGCCTCCC	-0.44 ± 0.08	0.59 ± 0.30	0.73 ± 0.23	0.50 ± 0.38
41	protein O-fucosyltransferase 2 (POFUT2), transcript variant 1, mRNA.	NM_015227	TGTCCCAAGTACTCGGTGTCAGAGCAGATGGTCGCCTGTGTTCACAGTGGTCATTTCCATACTGTTTGCCTCCTCGTCTG	-0.01 ± 0.30	0.62 ± 0.26	1.14 ± 0.19	0.30 ± 0.21
42	homeo box B2 (HOXB2), mRNA.	NM_002145	GAGCCTCTCCCACCCTCAGTCGCATAGACTTATGTGTTTTGCTAAAATTCAGGTATTACTGAATTAGCGTTTAATCCACT	-0.86 ± 0.06	0.16 ± 0.03	0.79 ± 0.13	0.73 ± 0.07
43	zinc finger homeobox 1b (ZFHX1B), mRNA.	NM_014795	TCCATGGACGATAGTTCGGAGGATGGGAAAATGGAAACCAAATCAGACCACGAGGAAGACAATATGGAAGATGGCATGTA	-0.53 ± 0.24	0.14 ± 0.38	0.76 ± 0.27	0.38 ± 0.16
44	cDNA FLJ39415 fis, clone PLACE6016160.	AK096734	CTGGTCCAACTGCTTCGCTCAGTCTGCAACCTCTTCAGCTACTGGGACATCCAGGTGTTTTACAGGGAGGCCCTGCACAT	-0.28 ± 0.17	-0.28 ± 0.29	0.79 ± 0.25	-0.06 ± 0.34
45	tetratricopeptide repeat domain 16 (TTC16), mRNA.	NM_144965	GCTCCGAAGTTCCACCAAGACTGAGGCTTTCTATGACTCAAACTGGAGCCTCAGCAAAACTGAGTATGCCCAAGGCCAGG	-0.20 ± 0.16	0.21 ± 0.41	0.81 ± 0.20	0.18 ± 0.19
46	very low density lipoprotein receptor (VLDLR), mRNA.	NM_003383	GTGGACTTGAATGGCCAAGATCGTAGGATAGTACTAAAGTCTCTGGAGTTCCTAGCTCATCCTCTTGCACTAACAATATT	0.84 ± 0.09	1.33 ± 0.45	2.02 ± 0.26	1.25 ± 0.33
47	cDNA FLJ32863 fis, clone TESTI2003615.	AK057425	TCCTTTTGGCAATGCAAGTTTCCATTCATTTTCTGCATTACTGGTCTCCTCTCTTCTCCCCTACTACTAGATCTTACAAT	0.92 ± 0.23	1.19 ± 0.22	2.04 ± 0.19	1.22 ± 0.08
48	retinoic acid receptor, beta (RARB), transcript variant 1, mRNA.	NM_000965	AACACAGCAGAGCACAGTCCTAGCATCTCACCCAGCTCAGTGGAAAACAGTGGGGTCAGTCAGTCACCACTCGTGCAATA	0.42 ± 0.33	0.98 ± 0.10	1.66 ± 0.29	1.13 ± 0.02
49	LOC121633 (LOC121633), mRNA.	XM_062724	AACATTGGGAAAAGATCCCAGTTCATCCTTTCGGAGCTGAGCACTAGTCAGTGCCCTGTCTCTGAGCATCTCAGGCAGGG	0.67 ± 0.22	1.24 ± 0.15	1.73 ± 0.22	1.16 ± 0.05
50	cDNA FLJ34090 fis, clone FCBBF3006399.	AK091409	GAACGGGTGCTGCCAGCTGACAGATGCAGCTGTTGCGACAACCAGGCGTCATAGCTGGAGTCCACCGTGCGCACCTTCGC	0.31 ± 0.09	1.29 ± 0.33	1.67 ± 0.19	0.88 ± 0.06
51	multimerin 2 (MMRN2), mRNA.	NM_024756	CCTGCAGACAGTGAAGTTCAACACCACATACATCAACATTGGCAGCAGCTACTTCCCTGAACATGGCTACTTCCGAGCCC	0.08 ± 0.07	1.91 ± 0.16	1.77 ± 0.25	1.40 ± 0.23
52	PRO1318 mRNA, complete cds.	AF116633	GTTCACGCTCTGCTGTTGCTGTCTTCGAATTCCTAGTGATGTTTGAACAAAGGCCCTATGTTTGCATTTTGCACTGGGCC	0.45 ± 0.25	0.77 ± 0.15	1.84 ± 0.03	0.30 ± 0.25
53	cDNA FLJ14885 fis, clone PLACE1003711.	AK027791	TTTTGGGCTGAAACCACCATTACTTTGGCTGTTTCATCTCTAAGAGAGTGTAGAATGCTTTCACAGAGACCCTGCACAGC	0.30 ± 0.32	0.99 ± 0.51	1.59 ± 0.21	0.48 ± 0.43
54	LOC166490 (LOC166490), mRNA.	XM_093899	CCCAAAGTCTAAATTCCAGGGGTCAGCAGAGTTGATTGCCTCTGAAATTTGTGAGGGAGAACCTGTTGCTGCGTCTCTCC	0.62 ± 0.39	1.08 ± 0.26	2.11 ± 0.36	0.42 ± 0.12
55	mitogen-activated protein kinase-activated protein kinase 2 (MAPKAPK2), transcript variant 1, mRNA.	NM_004759	GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCGACCAGGCCACTTGGCTGACCAGGTTGTG	-0.06 ± 0.33	1.20 ± 0.04	1.66 ± 0.28	0.31 ± 0.19
56	cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA.	NM_016952	TGCTGTCAGGACATTGTAAATGACGTCAGCTCTGATGGCTCAGAAGATCCAGCAGAGTTCAGCAGAGGAGACAGCTGTGC	-0.44 ± 0.34	-0.04 ± 0.34	1.04 ± 0.39	1.62 ± 0.29
57	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant e, mRNA.	NM_020149	GGCTCCTCCACAAATCTCGCTGACCATAACCCTTCTTCTTGGCGAGACCACGATGATGCAACCTCAACCCACTCAGCAGG	-0.67 ± 0.29	0.36 ± 0.28	0.75 ± 0.15	1.34 ± 0.04
58	cDNA FLJ10561 fis, clone NT2RP2002672.	AK001423	TCACATAGCTGTTTTGCAACAGCCTTTATTGCCAACACCCTTGGAAGAACATCTCCTGTAGAAGTACAAGTTTTGCAATA	-1.08 ± 0.16	0.28 ± 0.29	0.72 ± 0.25	2.03 ± 0.19
59	REC8-like 1 (yeast) (REC8L1), mRNA.	NM_005132	CCTGCTCCTGGTGCTCTCAGCGCAACAGATTCTTCACGTGAAACAAGAAAAGCCATATGGTCGCCTCCTGATCCAGCCGG	-0.67 ± 0.19	1.16 ± 0.16	1.98 ± 0.18	1.88 ± 0.11
60	matrix metalloproteinase 11 (stromelysin 3) (MMP11), mRNA.	NM_005940	TCTTCCCCAAGACTCACCGAGAAGGGGATGTCCACTTCGACTATGATGAGACCTGGACTATCGGGGATGACCAGGGCACA	-0.13 ± 0.16	0.68 ± 0.58	1.94 ± 0.27	1.75 ± 0.36
61	homeo box A2 (HOXA2), mRNA.	NM_006735	CCCGTAGATATTTCAGCTGACAGCTTAGACTTTTTACAGACACACTCACCACAATCGACTTGCAGCATCTGAATTACTA	0.03 ± 0.08	0.53 ± 0.03	1.36 ± 0.04	3.09 ± 0.54
62	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9 (SERPINB9), mRNA.	NM_004155_(2)	AGGCTCTTTGGAGAGAAAACTTGTCAGTTCCTCTCAACGTTTAAGGAATCCTGTCTTCAATTCTACCATGCTGAGCTGAA	0.39 ± 0.36	2.10 ± 0.33	2.29 ± 0.29	-0.67 ± 0.21
63	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9 (SERPINB9), mRNA.	NM_004155	TCTTTGGAGAGAAAACTTGTCAGTTCCTCTCAACGTTTAAGGAATCCTGTCTTCAATTCTACCATGCTGAGCTGAAGGAG	0.03 ± 0.47	1.72 ± 0.42	1.85 ± 0.48	-0.46 ± 0.22
64	src family associated phosphoprotein 2 (SCAP2), mRNA.	NM_003930	GAAGAAGAAGAGGACAGTGCTCCAGTGAAAGTGGAAGAACAAAGGAAGATGAGTCAGGATAGTGTCCATCACACCTCAGG	-1.82 ± 0.38	1.32 ± 0.03	2.30 ± 0.20	1.79 ± 0.37
65	LIM and cysteine-rich domains 1 (LMCD1), mRNA.	NM_014583	AGGAACCGGATGATCATGACCAACCCTATTGCTACTGGGAAAGATCCCACTTTTGACACCATCACCTACGAGTGGGCTCC	-0.08 ± 0.20	-1.25 ± 0.11	-1.96 ± 0.26	-0.67 ± 0.07
66	LIM and cysteine-rich domains 1 (LMCD1), mRNA.	NM_014583_(2)	GGAACCGGATGATCATGACCAACCCTATTGCTACTGGGAAAGATCCCACTTTTGACACCATCACCTACGAGTGGGCTCCC	-0.15 ± 0.24	-1.18 ± 0.18	-1.55 ± 0.31	-0.57 ± 0.17
67	glutathione S-transferase omega 2 (GSTO2), mRNA.	NM_183239	GGAATTCAGCAACCTGGAAGAGATTCTTGAGTATCAGAACACCACCTTCTTTGGTGGAACCTGTATATCCATGATTGATT	-0.16 ± 0.16	-1.64 ± 0.39	-1.30 ± 0.27	-1.02 ± 0.25
68	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) (RELA), mRNA.	NM_021975	GGCCTCCTTTCAGGAGATGAAGACTTCTCCTCCATTGCGGACATGGACTTCTCAGCCCTGCTGAGTCAGATCAGCTCCTA	1.01 ± 0.03	-1.22 ± 0.20	-1.43 ± 0.13	-0.95 ± 0.09
69	family with sequence similarity 20, member C (FAM20C), mRNA.	NM_020223	AAGTTTGGGAATGAAACGTTCATCATCCACTTAGACAATGGAAGAGGGTTTGGGAAGTATTCGCACGACGAGCTCTCCAT	-0.14 ± 0.13	-0.41 ± 0.50	-1.22 ± 0.08	-0.02 ± 0.09
70	KIAA0746 protein (KIAA0746), mRNA.	XM_045277	CTTTCTGGGAACCTTTCTGCTATCCATATTGATCGCCTGGACTGTGCAGTATTTCCAGTCTGTCTCAGCAAGCGATCCCC	0.44 ± 0.16	-0.19 ± 0.15	-0.65 ± 0.01	-1.33 ± 0.05
71	hypothetical protein FLJ13352 (FLJ13352), mRNA.	NM_024592	GGAGACTGGTTTGAATATGTTTCTTCCCCTAACTACTTAGCAGAGCTGATGATCTACGTTTCCATGGCCGTCACCTTTGG	0.15 ± 0.09	-0.72 ± 0.11	-0.87 ± 0.18	-0.98 ± 0.15
72	similar to endo-alpha-mannosidase (LOC255715), mRNA.	XM_172030	CTGGTCCCTTCCTGGTATACACCTGGCATGGCTGATGGTCAGGATGACATCACTGTACATGACAACATCAAGTATATCAT	-0.52 ± 0.34	-1.22 ± 0.04	-2.27 ± 0.15	-1.72 ± 0.29

73	SAM domain and HD domain 1 (SAMHD1), mRNA.	NM_015474	AATCAGGATTACTAAAAACCAGGTTTCACAACTTCTGCCAGAGAAATTTGCAGAGCAGCTGATTCGAGTATATTGTAAGA	-0.51 ± 0.15	-1.06 ± 0.14	-1.74 ± 0.27	-1.79 ± 0.75
74	similar to KIAA1501 protein (LOC162279), mRNA.	XM_091459	CCTACTCTCAGGTCATAGCTCTGATCCAGAATAGTGATGACACTCTGGAGCTGTCTATCATGCCCAAGGACGAGGACATC	-1.11 ± 0.15	-1.61 ± 0.40	-2.31 ± 0.28	-2.09 ± 0.23
75	SIPL protein (SIPL), mRNA.	NM_018269	ACGAGGAGCATTTGCACTTGGACGATGAGATCCGCTACATCCTGGATGGCAGTGGGTACTTCGACGTGAGGGACAAGGAG	-1.13 ± 0.28	-1.13 ± 0.08	-2.36 ± 0.13	-1.09 ± 0.20
76	similar to Phorbolin 3 (APOBEC1-like) (LOC200316), mRNA.	XM_114205	GATGAGCCATTCAAGCCTTGGAAGGGACTACAAACCAACTTTCGACTTCTGAAAAGAAGGCTACGGGAGATTCTCCAGTG	-1.93 ± 0.30	-1.72 ± 0.42	-0.74 ± 0.24	-1.37 ± 0.25
77	PDZ and LIM domain 1 (elfin) (PDLIM1), mRNA.	NM_020992	TTGGAAATGCTCAGAAGTTGCCTATGTGTGACAAATGTGGCACTGGGATTGTTGGTGTGTTTGTGAAGCTGCGGGACCGT	-1.96 ± 0.15	-1.50 ± 0.15	-0.91 ± 0.10	-1.19 ± 0.53
78	similar to agCP13869 (LOC153222), mRNA.	XM_087631	TGTTTGTAATCAACTCCATCAAGCAAGAGATTGTAAACCGGGTACAGAATCCAAGAGATGAGAGAGGACCCAACATGGGG	-1.26 ± 0.25	-1.49 ± 0.47	-0.09 ± 0.23	-0.20 ± 0.31
79	filamin B, beta (actin binding protein 278) (FLNB), mRNA.	NM_001457	ACGGCCTGGGATTTAAGCCTTTTGACCTGGTCATTCCGTTTGCTGTCAGGAAAGGAGAAATCACTGGAGAGGTCCACATG	-1.03 ± 0.11	0.05 ± 0.07	0.28 ± 0.23	-0.90 ± 0.12
80	damage-specific DNA binding protein 2, 48kDa (DDB2), mRNA.	NM_000107	CGTGTTCGATGGAAACTCAGGGAAGATGATGTGTCAGCTCTATGACCCAGAATCTTCTGGCATCAGTTCGCTTAATGAAT	-0.80 ± 0.20	-0.70 ± 0.31	0.21 ± 0.15	-1.03 ± 0.16
81	hypothetical protein MGC15668 (MGC15668), mRNA.	NM_032756	GCAAGTTTCTGCTTCAGGTCTTCACCAAGTCCCTTTTTACTGAGGACACTTTCTTCCTGGAGCTGATTCAGAGGCAGGGG	-1.49 ± 0.63	-0.75 ± 0.09	1.06 ± 0.29	-1.87 ± 0.60
82	interferon, gamma-inducible protein 16 (IFI16), mRNA.	NM_005531	TGAACACAATCAACTGTGAGGAAGGAGATAAACTGAAACTCACCAGCTTTGAATTGGCACCGAAAAGTGGGAATACCGGG	-1.67 ± 0.34	0.06 ± 0.26	0.74 ± 0.23	-1.39 ± 0.08
83	collagen triple helix repeat containing 1 (CTHRC1), mRNA.	NM_138455_(2)	GAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAA	-1.23 ± 0.29	-0.24 ± 0.22	0.67 ± 0.22	0.24 ± 0.51
84	LOC148646 (LOC148646), mRNA.	XM_086262	CAGGAGATTTGGGAGGAAGCCTATCAGCGAGTGGCTAATGAGCAGGAGATTTATGAAGGTTCCAGACAGTTGGCTGCCGA	-1.14 ± 0.24	0.10 ± 0.16	-0.06 ± 0.18	0.20 ± 0.39
85	neuromedin U (NMU), mRNA.	NM_006681	CTGCATGAGAGAAGAATGAAGAGATTCAGAGTGGACGAAGAATTCCAAAGTCCCTTTGCAAGTCAAAGTCGAGGATATTT	-1.98 ± 0.49	-0.16 ± 0.12	0.19 ± 0.37	-0.37 ± 0.05
86	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G (APOBEC3G), mRNA.	NM_021822	GACGAATTTCAGCACTGTTGGAGCAAGTTCGTGTACAGCCAAAGAGAGCTATTTGAGCCTTGGAATAATCTGCCTAAATA	-2.77 ± 0.49	-0.91 ± 0.87	0.36 ± 0.47	0.68 ± 0.66
87	similar to RIKEN cDNA 1110014B07 gene (LOC115908), mRNA.	XM_057014	GCTATCTGGGTTGGTACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCTTTCTCGCATCATTATTG	-2.15 ± 0.34	-0.62 ± 0.61	0.84 ± 0.24	0.52 ± 0.49
88	inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA.	NM_030569	GTCCCAGTGGTCTGGAAGCAAAGGAAGATTTACAACGGGGAAGAGCAGATAGACTGCTGGTTTGCCAGGAACAATGCCGC	-0.07 ± 0.23	1.60 ± 0.40	2.53 ± 0.16	2.43 ± 0.12
89	neuropilin 2 (NRP2), transcript variant 2, mRNA.	NM_003872	CAGGGAAACACAGAATGGCTACTACGTCAAATCCTACAAGCTGGAAGTCAGCACTAATGGAGAGGACTGGATGGTGTACC	0.32 ± 0.19	1.63 ± 0.48	2.88 ± 0.22	2.28 ± 0.39
90	cDNA FLJ36189 fis, clone TESTI2027238.	AK093508	AGATCATCTCTCAAAAAGCTCCCATCAGAGCAACCATTCTGGGACTTTGAGCAGAATGCTTAAGGCAGTGGTTCTAAAAT	0.73 ± 0.10	1.68 ± 0.19	2.51 ± 0.33	1.86 ± 0.22
91	PBX/knotted 1 homeobox 2 (PKNOX2), mRNA.	NM_022062	CCATGACAACCGTCAACTCACAAGTTGTGTCAGGTGGAGCCTTATACCAACCGGTTACCATGGTAACCTCCCAGGGTCAG	1.05 ± 0.25	1.94 ± 0.24	2.21 ± 0.20	2.35 ± 0.11
92	gene rich cluster, A gene (GRCA), transcript variant A-2, mRNA.	NM_019858	GGAGTCTGCCAAGACATCCCTGCAGGTCACCAACTTGGTCAGCGCCATCGTCTTTCTCTATGACTCACTCACAGGGGTGC	0.85 ± 0.21	1.28 ± 0.35	1.97 ± 0.22	2.23 ± 0.57
93	hypothetical protein FLJ14299 (FLJ14299), mRNA.	NM_025069	TCGCTGTCCTTGCGGAATCCACACACTTTGGGCCTAAGCCGGTACCACCCCTATGGCAAGAGCCACTTATCCACAGCGGG	-0.81 ± 0.49	1.81 ± 0.40	3.59 ± 0.05	2.58 ± 0.36
94	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), transcript variant a, mRNA.	NM_000458	ATGGTGGTCACAGATACCAGCAGCATCAGTACACTCACCAACATGTCTTCAAGTAAACAGTGTCCTCTACAAGCCTGGTG	-0.48 ± 0.76	0.77 ± 0.19	3.23 ± 0.35	2.69 ± 0.16
95	plakophilin 2 (PKP2), mRNA.	NM_004572	AAGGATGTATCTGTCCTTGATCGCCAAAAGTGTCCGCAACTACACACAAGAAGCATCCTTAGGAGCTCTGCAGAACCTCA	1.13 ± 0.35	2.33 ± 0.59	2.88 ± 0.14	3.09 ± 0.07
96	LOC145844 (LOC145844), mRNA.	XM_085255	TTCCTTCTGCTTTTTGTTTTTCTGCCCAGAAAAACCTGACTTCGATACCAAAAAAGATGAAACCACAGAAACTCAAATTT	1.97 ± 0.24	2.86 ± 0.17	3.27 ± 0.22	3.09 ± 0.50
97	dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), mRNA.	NM_016651	CAAGCAGTCTGTGGTCTGCTTCCCATCCTTCATCCAGCAAGAAAATGGATGGCTACATTCTGAGCCTGGTCCAGAAAAAA	0.58 ± 0.39	3.05 ± 0.58	2.35 ± 0.50	1.13 ± 0.40
98	inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 2, mRNA	NM_032817_(2)	TCAATAGAGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTAAAGACCTTCCT	0.35 ± 0.75	2.91 ± 1.01	3.53 ± 0.58	3.54 ± 0.97
99	homeo box A1 (HOXA1), transcript variant 1, mRNA.	NM_005522	AGACTTTTGACTGGATGAAAGTCAAAAGAAACCCTCCCAAAACAGGGAAAGTTGGAGAGTACGGCTACCTGGGTCAACCC	-0.58 ± 0.78	5.20 ± 0.11	5.72 ± 0.21	3.80 ± 0.54
100	cDNA FLJ12777 fis, clone NT2RP2001720.	AK022839	TCTCTCCTGGCCTCTTTTCTGGGGCATCCTGGGTGGAGTGTTTTTCTTGGGATCACGAGCTTGCACTCGCACACAGGCCC	-0.38 ± 0.03	3.69 ± 0.38	5.16 ± 0.59	3.06 ± 0.44
101	cellular retinoic acid binding protein 2 (CRABP2), mRNA.	NM_001878	AGGTTGGGGAGGAGTTTGAGGAGCAGACTGTGGATGGGAGGCCCTGTAAGAGCCTGGTGAAATGGGAGAGTGAGAATAAA	1.49 ± 0.38	4.31 ± 0.27	5.19 ± 0.11	3.38 ± 0.28
102	retinol binding protein 1, cellular (RBP1), mRNA.	NM_002899	ACTTCCAAGTTGGGAAGGAGTTTGAGGAGGATCTGACAGGCATAGATGACCGCAAGTGCATGACAACAGTGAGCTGGGAC	1.15 ± 0.31	3.30 ± 0.56	4.15 ± 0.42	5.66 ± 0.12
103	chromosome 10 open reading frame 13 (C10orf13), mRNA.	NM_152429	AACGCGGAGCTCACGGAGACCTACTGCGCTGAGAAGTGGCACTCCCTCTGCAACTTCTTTGTCAATTTCTGGAACGGCTG	3.22 ± 0.46	1.51 ± 0.20	0.93 ± 0.16	1.10 ± 0.35
104	protein tyrosine phosphatase, receptor-type, Z polypeptide 1 (PTPRZ1), mRNA.	NM_002851	GAGGATGATATGGGACCATAATGCCCAACTGGTGGTTATGATTCCTGATGGCCAAAACATGGCAGAAGATGAATTTGTTT	3.70 ± 0.41	3.19 ± 0.16	1.56 ± 0.18	0.00 ± 0.00
105	secreted frizzled-related protein 2 (SFRP2), mRNA.	XM_050625	AAGGGACCTGAAGAAATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACGCGC	4.27 ± 0.56	3.20 ± 0.46	1.74 ± 0.67	4.33 ± 0.27
106	laminin, gamma 2 (LAMC2), transcript variant 1, mRNA.	NM_005562	ACCTCCATTTGCTGGAGACAAGCATAGATGGGATTCTGGCTGATGTGAAGAACTTGGAGAACATTAGGGACAACCTGCCC	-2.69 ± 0.15	-3.52 ± 0.04	-3.77 ± 0.13	-3.15 ± 0.34

3. 340 probes, 7-day sample (from Fig 1C).

Row No.	Probe Name	Probe ID	Probe sequence	0-day (mean ±S.D.)	1-day (mean ±S.D.)	2-day (mean ±S.D.)	7-day (mean ±S.D.)
1	immunoglobulin superfamily, member 4 (IGSF4), mRNA.	NM_014333	AATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGG	0.02 ± 0.18	0.21 ± 0.15	-0.08 ± 0.12	1.38 ± 0.25
2	roundabout, axon guidance receptor, homolog 2 (Drosophila) (ROBO2), mRNA.	XM_031246	TGGATCCAGCATGGACAATCTAGACAGCTCTGTGACAGGAAAAGCCTTTACCTCCTCTCAAAGACCTCGACCTACCAGCC	0.07 ± 0.26	0.21 ± 0.22	0.09 ± 0.19	1.25 ± 0.21
3	mRNA for FLJ00141 protein.	AK074070	CTGGACATGGGGAAGATCGAGGAGATGGAGAAGATGCTGAAAGAGGCTCATGCAGAGAAGAACCGGCTCATGGAGTCGAG	0.14 ± 0.18	0.24 ± 0.21	-0.11 ± 0.16	1.42 ± 0.06

4	desmocollin 2 (DSC2), transcript variant Dsc2b, mRNA.	NM_004949_(2)	ACTTGTTGGTAGAGTTAACCTGAAAGAGTGCTTTACAGCTGCAAATCTAATTCATTCAAGTGATCCTGACTTCCAAATTT	-0.07 ± 0.09	0.37 ± 0.21	0.12 ± 0.22	1.61 ± 0.25
5	phosphatidylinositol glycan, class M (PIGM), mRNA.	NM_145167	CTCTGCTTACTGCCTCTTGTGATGCCACTAGTCAGAATGCCTTGGAAAAGAGCTGTAGTTCTCCTAATGTTATGGTTTAT	-0.02 ± 0.24	0.39 ± 0.14	-0.02 ± 0.15	1.72 ± 0.10
6	KIAA1500 protein (KIAA1500), mRNA.	XM_034353	TGGAGAGCCACAAGCTCTTATAACAGGAAGGACTACTCAGGAGAGTACACCATCTACCTGATCCCTTGCACAGTGCAGCC	0.24 ± 0.25	0.44 ± 0.24	-0.05 ± 0.05	1.63 ± 0.27
7	nephronophthisis 1 (juvenile) (NPHP1), transcript variant 1, mRNA.	NM_000272	CCAGACGGAGTTCATGAACCTTTTGACCTTTCAGAGCAGACCTATGACTTCTTGGGTGAAATGAGAAAGAATGCAGTGTG	-0.07 ± 0.08	-0.01 ± 0.00	0.28 ± 0.30	1.83 ± 0.16
8	KIAA1384 protein (KIAA1384), mRNA.	XM_035405	AGTCATCTACAATATGCTATTGTCCAGAGAAAGGAACCTGGACAGAACTCGAAGGAGATGTAGCAGAACCGTTGGCAGGC	0.08 ± 0.37	0.04 ± 0.29	-0.03 ± 0.04	1.74 ± 0.19
9	collagen, type IV, alpha 1 (COL4A1), mRNA.	NM_001845	GGACCTGCAATTACTACGCAAACGCTTACAGCTTTTGGCTCGCCACCATAGAGAGGAGCGAGATGTTCAAGAAGCCTACG	0.44 ± 0.25	0.09 ± 0.30	0.28 ± 0.13	1.72 ± 0.19
10	collagen, type IV, alpha 1 (COL4A1), mRNA.	NM_001845_(2)	CCCTCCAGGTGAAAAGGGACAAATGGGCTTAAGTTTTCAAGGACCAAAAGGTGACAAGGGTGACCAAGGGGTCAGTGGGC	0.48 ± 0.23	0.23 ± 0.30	0.33 ± 0.09	1.52 ± 0.25
11	hypothetical protein MGC34032 (MGC34032), mRNA.	NM_152697	GAAAAACCCTACTTCGTAACCCCTAACCTGCATGGAATTCTGATCAAGAAGCAACTAGTTCCCCAGAAGCAGAAAGAGTA	0.35 ± 0.16	0.12 ± 0.09	0.48 ± 0.09	1.89 ± 0.15
12	LOC123323 (LOC123323), mRNA.	XM_063591	AGATCAGATCCAGCTGCTTCCCTCCAATCGAGATGAAGATAAATGCGGAAGCCACAGAAGTCACTCTCAGGGCAGCTCAC	0.23 ± 0.15	0.25 ± 0.12	0.64 ± 0.24	1.78 ± 0.36
13	signal peptide, CUB domain, EGF-like 3 (SCUBE3), mRNA.	NM_152753	AAACACAAGGAGATGCTGCCAAAATCCTTCATCAAGCTGCTCCGCTCCAAAGTTTCCAGCTTCCTGAGGCCCTACAAATA	0.47 ± 0.32	0.44 ± 0.21	0.10 ± 0.23	1.91 ± 0.29
14	cDNA FLJ30374 fis, clone BRACE2007888.	AK054936	TATGCTGCATCCCCTGGCAGGTTGAGTTGTTGCAGAATGAGTCAGCAGTACCTGAGCTCAGATAGGATTGAGAGAATTTA	0.14 ± 0.15	0.07 ± 0.37	0.31 ± 0.24	1.21 ± 0.01
15	Homo sapiens cDNA FLJ58489 complete cds, highly similar to Ena/VASP-like protein.	AK295919	CAGCCTGGAGCCTAAGCATACACTGCATTAATCAGACTTGCTGGAATGATCACATGGTTTTCTAGCTGCCTCCCCTGTTA	0.18 ± 0.16	0.19 ± 0.10	0.37 ± 0.20	1.19 ± 0.13
16	SERTA domain containing 1 (SERTAD1), mRNA.	NM_013376	CAGGGGGAGCCTGGAATTACCCCCTAGTGATGGAATGACAGGGTCTGGTGGGGACTGAATTCCCTGGCCCTGGGGTCATA	0.13 ± 0.24	0.05 ± 0.33	0.15 ± 0.36	1.19 ± 0.27
17	Homo sapiens cDNA FLJ58712 complete cds, highly similar to Mus musculus myosin, heavy polypeptide 9, non-muscle (Myh9), transcript variant 1, mRNA.	AK302705	CGAGGGCCAGGTGCTAGGGCTAGAAAGGAGGCAGGGCTGGCGCTCTAGGGACTCCTGGAGCTCTCCTCCTGTGAGCCTGG	0.16 ± 0.07	0.17 ± 0.06	0.45 ± 0.13	1.51 ± 0.17
18	LOC167341 (LOC167341), mRNA.	XM_094423	GTCCTCGTCGGATTCACCTTCCTCTCTGGTTTGTGAAGCTGATTGCAGATTGCAAGGACATGCTGACTCCACTGTCCCAG	0.38 ± 0.24	0.27 ± 0.17	0.52 ± 0.33	1.45 ± 0.10
19	mRNA for KIAA0980 protein, partial cds.	AB023197	GAGGGGGAGACCAAAATAGCGCTGGAGAGAGAGAAGGATGACATGGAAACCAAACTTCTACATCTGGAAGACGTCGTCCG	0.21 ± 0.19	0.24 ± 0.15	0.58 ± 0.19	1.25 ± 0.12
20	F-box and leucine-rich repeat protein 7 (FBXL7), mRNA.	NM_012304	GTGTGGAGTACCTCGCCAAGAACTGCACCAAACTCAAATCCCTGGATATCGGCAAATGCCCTTTGGTATCCGACACGGGC	0.26 ± 0.24	0.15 ± 0.33	0.35 ± 0.15	1.38 ± 0.20
21	cDNA FLJ39423 fis, clone PROST1000322, highly similar to HOMEOBOX PROTEIN HOX-A2.	AK096742_(2)	ATCAATCAAGACCTCGACGCTTTCACACTCGACACTGATTCCTCCTCCTTTTGAGCAGACCATTCCCAGCCTGAACCCCG	0.02 ± 0.23	0.29 ± 0.09	0.50 ± 0.18	1.43 ± 0.35
22	cDNA FLJ42197 fis, clone THYMU2034314.	AK124191	GCCTACAACAGTGACTCTGGATCCCCCAAGCAAAGCATTTGGCTGGCTATTGCAAGGCTGGTTAATGGGATCTTTTATCT	-0.07 ± 0.13	0.37 ± 0.07	0.55 ± 0.12	1.32 ± 0.17
23	cDNA FLJ35039 fis, clone OCBBF2017035, highly similar to Mus musculus mRNA for GATS protein.	AK092358	AAGTTCTTCAGTCTGACTGAGACACCAGAGGATTACACTATCATTGTCGATGAGGAAGGATTCCTAGAGCTGCCCTCCTC	-0.21 ± 0.06	0.49 ± 0.06	0.78 ± 0.02	1.44 ± 0.07
24	Homo sapiens cDNA FLJ50903 complete cds, moderately similar to Retinol-binding protein I, cellular.	AK301684	CAGGGGCAGCTCATGGACTTTTTAGCCAGAGAGAACTGGGTTCAAGTTACGGCTCAAGCCCTAACCCCTTGGTGATGGGC	0.12 ± 0.32	0.30 ± 0.30	0.35 ± 0.21	1.44 ± 0.25
25	LOC139545 (LOC139545), mRNA.	XM_066755	GGCAGGAGGAAGCTCACATTTGGCATGAGGTTAAAGCCTGGCCTTTGAAGCTGGAGTGGAGCCATTCAGCAATCATTAAA	-0.15 ± 0.16	-0.07 ± 0.10	0.32 ± 0.11	1.51 ± 0.28
26	BMP-binding endothelial regulator precursor protein (BMPER), mRNA.	NM_133468	GACCTGCCACTCGACTGTGGACTACGCCACTTTCTACCGGTCCTGTGTGACAGACATGTGTGAATGTCCAGTCCATAAAA	-0.13 ± 0.12	0.10 ± 0.16	0.14 ± 0.16	1.05 ± 0.26
27	cDNA FLJ38610 fis, clone HEART2005581.	AK095929	GGCTGGAGGTTGACACAGGAGTGCTCAGGGGAGCAGCATCACAAGAGGGCAGATCGAAAGCATCGTCCTTGCTGAAAAAA	-0.06 ± 0.12	-0.02 ± 0.13	0.14 ± 0.12	1.01 ± 0.15
28	GATA binding protein 6 (GATA6), mRNA.	NM_005257	GAGAGAGCACCAATCCCGAGAACAGCGAGCTCAAGTATTCGGGTCAAGATGGGCTCTACATAGGCGTCAGTCTCGCCTCG	-0.29 ± 0.06	0.15 ± 0.26	0.20 ± 0.33	0.86 ± 0.18
29	partial GATA-6 gene and promoter regions (exon 1a).	AJ245649	GCGAGCGCTGTTTGTTTAGGGCTCGGTGAGTCCAATCAGGAGCCCAGGCTGCAGTTTTCCGGCAGAGCAGTAAGAGGCGC	-0.24 ± 0.18	0.19 ± 0.26	0.50 ± 0.11	0.97 ± 0.25
30	hypothetical protein FLJ20130 (FLJ20130), mRNA.	NM_017681	AAGTACTTTCTTCTCCAGGCCACTCAGGTCAATGCTTGGGACCATACATTGATTGAGAATGGTGAGATGATTCGTATTTT	-0.10 ± 0.24	0.36 ± 0.27	0.48 ± 0.10	1.03 ± 0.18
31	KIAA1799 protein (KIAA1799), mRNA.	XM_059109	TTGCAGTAGAAGTGGGACCCAAATCTACAATGGTTTGTCAACATGTAATGCCTTTGAATGAACGACAAGAATGGATATAT	-0.11 ± 0.31	0.35 ± 0.35	0.22 ± 0.13	1.12 ± 0.24
32	WAS protein family, member 1 (WASF1), mRNA.	NM_003931	CTTGCCATTTAGTCAGATGAGTGAGCTTCTGACTAGAGCTGAGGAAAGGGTATTAGTCAGACCACATGAACCACCTCCAC	-0.02 ± 0.12	0.30 ± 0.16	0.28 ± 0.17	1.04 ± 0.14
33	socius (SOC), mRNA.	NM_145345	TGCTGCGCATCAAGTCTGAGAATGGGGAACAGGCCTTCCTACTGATGATGCAGCCTGACAACACCATTGGGGACGTGCGA	-0.13 ± 0.20	0.20 ± 0.17	-0.19 ± 0.25	1.18 ± 0.12
34	ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA.	NM_001682	TTCAGAGCCTCATATCCCCCTTATTGATGACACTGATGCCGAAGATGATGCTCCTACAAAACGTAACTCCAGTCCTCCAC	-0.13 ± 0.22	0.14 ± 0.25	-0.29 ± 0.27	1.12 ± 0.22
35	lipoma HMGIC fusion partner-like 2 (LHFPL2), mRNA.	NM_005779	GCACAAGCAGAAATTGCAACCTCTAGTGACAAAGTACAGGAAGAAATTGAAGAGGGGAAAAATCTGATCTGCCTCCTTTA	-0.15 ± 0.27	0.10 ± 0.19	-0.18 ± 0.09	1.25 ± 0.06
36	EPS8-like 1 (EPS8L1), transcript variant 1, mRNA.	NM_133180	AGCAGAGGAAGCGTTACTCCACAGTTGTTATGGCTGATGTATCCCAGTACCCAGTCAATCACCTGGTGACGTTCTGCCTG	-0.20 ± 0.18	-0.06 ± 0.04	-0.14 ± 0.09	0.95 ± 0.10
37	tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 1, mRNA.	NM_018647	ACACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTGTCATC	-0.19 ± 0.17	-0.09 ± 0.55	-0.29 ± 0.07	1.06 ± 0.19
38	cDNA FLJ16125 fis, clone BRACE2027018.	AK122677	CACCTAGTTCCTCAGCATGGTGTCTGCAACCACAAGTTTTACGGAAAACAATGCTGCAAGTCATGCACAAGGAAGATCTG	-0.25 ± 0.15	-0.25 ± 0.29	-0.28 ± 0.30	0.91 ± 0.27
39	cDNA FLJ30723 fis, clone FCBBF4000282, highly similar to ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT.	AK055285	AGTAGGGATGATCAAGTCAGATGTCCCTGGTACCCAGGAATGGCTGGATGAGAGAAGGAGACAGGGTGACCTGCCCCTGC	-0.15 ± 0.11	-0.30 ± 0.11	-0.40 ± 0.52	0.91 ± 0.19
40	Homo sapiens cDNA, FLJ17813.	AK310771	GGGCTGCAGACGGGAAAGGAATGTCCTCAGCGTCTGCCAGCACTTTTGTCTTGGTCCCAACGGCTGATAGGAAAATGAGA	-0.23 ± 0.21	-0.25 ± 0.22	-0.24 ± 0.30	1.10 ± 0.24
41	hypothetical protein LOC163782 (LOC163782), mRNA.	NM_181712	GCCGCACAGCTTTGTCCATCGCTCTGAAGTCACCCACCCATATGGAAATTGCTGGGCTTCTGAGAGCCCACGCGGAGCAG	-0.26 ± 0.24	-0.08 ± 0.27	-0.03 ± 0.43	1.37 ± 0.30
42	mitogen-activated protein kinase kinase kinase 1 (MAP3K1), mRNA.	XM_042066	CGTTGTTTAGAACTTCAACCTCAGGACAGACCTCCATCAAGAGAGCTACTGAAGCATCCAGTCTTTCGTACTACATGGTA	-0.14 ± 0.36	-0.18 ± 0.24	-0.16 ± 0.14	1.25 ± 0.27

43	cDNA FLJ31668 fis, clone NT2RI2004916.	AK056230	GGTGTCTTTCTACCATTCAAGGGGTGTCCTCCTGAAGGCGTCTGAGAGGGCCTCTGGCGGTTCCAAGGCTGTGCAGCCGG	-0.24 ± 0.23	-0.20 ± 0.40	-0.05 ± 0.15	1.36 ± 0.27
44	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (SEMA4G), mRNA.	XM_170638	CCACCCACACTCCCTGAGAACTGAGGAGACACCAATGCATTGGCTCAATGATGCGGAGTTTGTGTTCTCCGTCCTCGTGC	-0.39 ± 0.26	-0.41 ± 0.21	0.43 ± 0.15	0.89 ± 0.25
45	tripartite motif-containing 42 (TRIM42), mRNA.	NM_152616	AATGATAATGGTCCTGGGCAATGGAGTGATATCTGCAAGGTGGTAACACCAGATGGACATGGGAAGAACCGAGCTAAGTG	-0.27 ± 0.26	-0.10 ± 0.01	0.37 ± 0.24	0.94 ± 0.25
46	synuclein, gamma (breast cancer-specific protein 1) (SNCG), mRNA.	NM_003087	GCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAGACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGG	-0.48 ± 0.18	-0.09 ± 0.15	0.43 ± 0.22	0.62 ± 0.22
47	GR AF-1 specific protein phosphatase mRNA, partial cds.	AF174498	ACCTGCAGGAAGCGGATATCCTCACCTACAATTACGTCAAGAAGTTTGAGAGCATCAATGATGAGACCGAGCTGGAGGCC	-0.41 ± 0.24	-0.05 ± 0.15	0.31 ± 0.34	0.67 ± 0.27
48	H1 histone family, member 0 (H1F0), mRNA.	NM_005318	AAGCCAAGCCGGTCAAGGCATCCAAGCCCAAAAAGGCCAAACCAGTGAAACCCAAAGCAAAGTCCAGTGCCAAGAGGGCC	-0.50 ± 0.24	-0.30 ± 0.46	0.46 ± 0.19	0.51 ± 0.28
49	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA.	NM_002398	ACACGTCACACAGTGGGGACAACAGCAGTGAGCAAGGTGATGGCTTGGACAACAGTGTAGCTTCCCCCAGCACAGGTGAC	-0.79 ± 0.31	-0.20 ± 0.31	-0.14 ± 0.28	1.29 ± 0.22
50	cDNA FLJ31546 fis, clone NT2RI2000974.	AK056108	CCTCCCAGAGACAATGCAGGGGTGGTTTTCAGCAGAATGTGCCACCTGCACTTCTGATTGTTCTGAGACCCAGCCCAGAG	-0.83 ± 0.29	-0.14 ± 0.08	0.07 ± 0.07	1.07 ± 0.11
51	dual specificity phosphatase 6 (DUSP6), transcript variant 1, mRNA.	NM_001946	CCAACATATCCCCTAACTTCAACTTCATGGGTCAGCTGCTGGACTTCGAGAGGACGCTGGGACTCAGCAGCCCATGTGAC	-0.68 ± 0.34	0.08 ± 0.42	0.15 ± 0.16	1.02 ± 0.32
52	Homo sapiens cDNA FLJ78749 complete cds, clone TESTI2028720, highly similar to Homo sapiens WD repeat domain 74 (WDR74), mRNA.	AK292330	AATGGATTTTTGGAAATAGGAGATGGAATAGAAGCTTGCTCCGTCCACTCCACGCATCGACCTGGTATTGCAGTACTTCC	-0.59 ± 0.41	-0.62 ± 0.10	0.08 ± 0.22	1.10 ± 0.38
53	hypothetical protein FLJ31842 (FLJ31842), mRNA.	NM_152487	GATTGCCTCAATGCTTCCTCATTATGGCTTCATGTATTCCGTGTATGGAACAGAACCCTACATAAGGCTTGGAGTTTTAA	-0.61 ± 0.34	-0.40 ± 0.20	-0.03 ± 0.14	0.67 ± 0.31
54	cDNA FLJ41890 fis, clone OCBBF2024850.	AK123884	ACCACAAGGACTAAATCCTTGTCCCCTAAGCAAAGAATTGGGTCTGAATGCTGTGAGGGATTGCCTTTTTGTGGTAATTT	0.00 ± 0.17	0.56 ± 0.20	0.83 ± 0.24	1.09 ± 0.17
55	NIMA (never in mitosis gene a)-related kinase 3 (NEK3), transcript variant 2, mRNA.	NM_152720	GTCTGAAGAAACAGAAGCATCGGACAGTGTTGATGGAGGTCACGATTCTGTCATTTTGGATCCAGAGCGACTTGAGCCTG	0.27 ± 0.17	0.51 ± 0.32	0.96 ± 0.04	1.27 ± 0.11
56	brain specific protein (CGI-38), mRNA.	NM_015964	CGGCAGGACATCCTGGACGACAGTGGCTACGTGAGCGCCTACAAGAATGCAGGCACCTACGATGCCAAGGTGAAGAAGTG	-0.06 ± 0.31	0.33 ± 0.34	1.17 ± 0.30	1.05 ± 0.26
57	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant e, mRNA.	NM_020149	GGCTCCTCCACAAATCTCGCTGACCATAACCCTTCTTCTTGGCGAGACCACGATGATGCAACCTCAACCCACTCAGCAGG	-0.67 ± 0.29	0.36 ± 0.28	0.75 ± 0.15	1.34 ± 0.04
58	cDNA: FLJ22516 fis, clone HRC12162.	AK026169	TCCCATTTTCTTTTGTCCAGACCCATGTTGGCAATCATGTATGAACTGTGTTATACTTCTCAGTGCTTTCTTTTTTCTTT	-0.48 ± 0.20	0.59 ± 0.48	0.58 ± 0.35	1.02 ± 0.08
59	homeo box B2 (HOXB2), mRNA.	NM_002145	GAGCCTCTCCCACCCTCAGTCGCATAGACTTATGTGTTTTGCTAAAATTCAGGTATTACTGAATTAGCGTTTAATCCACT	-0.86 ± 0.06	0.16 ± 0.03	0.79 ± 0.13	0.73 ± 0.07
60	fibronectin type III domain containing 5 (FNDC5), mRNA.	NM_153756	CATCAAGGACAATGAACCCAATAACAACAAGGAAAAAACCAAGAGTGCATCAGAAACCAGCACACCAGAGCACCAGGGCG	-0.53 ± 0.23	0.73 ± 0.07	0.75 ± 0.15	0.61 ± 0.28
61	zinc finger protein 503 (ZNF503), mRNA.	NM_032772	CCAACCGCCTGCCAATCAAGGTGCTGAAGATGCTGACGGCACGAACTGGCCACATTTTGCACCCCGAGTACCTGCAGCCC	-0.28 ± 0.12	0.66 ± 0.14	1.06 ± 0.19	0.75 ± 0.14
62	retinoic acid induced 17 (RAI17), mRNA.	XM_166091	GTGGATCAGTACATGTGGGGAATCCTGAATGCCATCCAACACTCCGAGTTTGAAGAGGTCACCATCGATCCCACGTGCAG	-0.54 ± 0.20	1.15 ± 0.11	0.96 ± 0.08	0.73 ± 0.17
63	cDNA FLJ34929 fis, clone NT2RP7004728.	AK092248	CACATGGGTCGTTGGTGGTGACACCTCACTGTTTCCTAGGTTTGGATAGAGAGATGTATACAAGACCTTTCCTGTTAAAT	-0.77 ± 0.55	0.78 ± 0.34	0.34 ± 0.16	1.29 ± 0.43
64	chemokine orphan receptor 1 (CMKOR1), mRNA.	NM_020311	TACAGCTTCATCAATCGCAACTACAGGTACGAGCTGATGAAGGCCTTCATCTTCAAGTACTCGGCCAAAACAGGGCTCAC	-0.21 ± 0.47	1.00 ± 0.38	0.74 ± 0.10	1.48 ± 0.36
65	LOC350016 (LOC350016), mRNA.	XM_303730	TGTGAGGTCTTCAGTAGTGAAAGCTGCAGCAGCTCCTCAGTTACTGTAAGAGCTGTTGAAGTTCTCAGCAAAGGCTTCTG	0.13 ± 0.01	0.80 ± 0.19	0.26 ± 0.10	1.76 ± 0.02
66	insulin-like growth factor binding protein 5 (IGFBP5), mRNA.	NM_000599	TACGGGATGAAGCTGCCAGGCATGGAGTACGTTGACGGGGACTTTCAGTGCCACACCTTCGACAGCAGCAACGTTGAGTG	-0.45 ± 0.42	-0.15 ± 0.76	1.41 ± 0.79	2.08 ± 0.11
67	LOC151361 (LOC151361), mRNA.	XM_098048	TCCCATTCTCCAATGACTTCCTCAACCAATGGGTGGCCTTGTGACTGTTCTTTAAGGCTGAAGATATCCAGGAAAGGGGG	-0.39 ± 0.41	-0.20 ± 0.58	1.18 ± 0.64	1.72 ± 0.30
68	cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA.	NM_016952	TGCTGTCAGGACATTGTAAATGACGTCAGCTCTGATGGCTCAGAAGATCCAGCAGAGTTCAGCAGAGGAGACAGCTGTGC	-0.44 ± 0.34	-0.04 ± 0.34	1.04 ± 0.39	1.62 ± 0.29
69	cDNA FLJ10561 fis, clone NT2RP2002672.	AK001423	TCACATAGCTGTTTTGCAACAGCCTTTATTGCCAACACCCTTGGAAGAACATCTCCTGTAGAAGTACAAGTTTTGCAATA	-1.08 ± 0.16	0.28 ± 0.29	0.72 ± 0.25	2.03 ± 0.19
70	AT-binding transcription factor 1 (ATBF1), mRNA.	NM_006885	CTTTGACCAAACTAAGCTGGACAACGATGACTGTTCCTCTGTCAACACAGCAATCACAGATACCACAACTGGAGACGAGG	-0.91 ± 0.47	0.17 ± 0.51	0.42 ± 0.60	1.72 ± 0.43
71	homeo box C12 (HOXC12), mRNA.	NM_173860	CAGGTCAAGATCTGGTTTCAGAACCGGAGAATGAAAAAGAAAAGACTTCTGTTGAGGGAGCAAGCTCTCTCCTTCTTTTA	-1.47 ± 0.69	-0.34 ± 0.28	0.71 ± 0.01	1.64 ± 0.60
72	hypothetical protein FLJ14153 (FLJ14153), mRNA.	NM_022736	TATGGCTTCATGCAGTCCATTCAGAATCTTGGGTTGGCCATCATTTCCATCATTGCTGGTATGATACTGGATTCTCGGGG	-1.54 ± 0.13	-1.28 ± 0.38	-1.43 ± 0.22	-0.18 ± 0.03
73	dynactin 3 (p22) (DCTN3), transcript variant 1, mRNA.	NM_007234	ACCGCATTGCCATACCTGATGCCTCTAAGCTGCAATTCATCCTAGCAGAGGAGCAGTTTATCCTTTCCCAGGTTGCACTC	-1.38 ± 0.23	-1.26 ± 0.18	-1.09 ± 0.16	-0.17 ± 0.26
74	Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA.	NM_002227	GACTTGGCAGCAAGAAATGTCCTTGTTGAGAGTGAACACCAAGTGAAAATTGGAGACTTCGGTTTAACCAAAGCAATTGA	-1.60 ± 0.28	-1.56 ± 0.26	-1.42 ± 0.27	-0.44 ± 0.12
75	solute carrier family 23 (nucleobase transporters), member 2 (SLC23A2), transcript variant 1, mRNA.	NM_005116	TGGAAATGTAACACCACAGATGTTTCAGTTGCCAATGGAACAGCAGAGCTGTTGCACACAGAACACATCTGGTATCCCCG	-1.48 ± 0.14	-1.19 ± 0.28	-1.54 ± 0.19	-0.40 ± 0.24
76	protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA.	NM_000308	AGATGTAGACATGGCCTGCAATTTCATGGGGGATGAGTGGTTTGTGGATTCCCTCAACCAGAAGATGGAGGTGCAGCGCC	-1.79 ± 0.13	-1.14 ± 0.32	-1.71 ± 0.35	0.01 ± 0.03
77	testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA.	NM_015641	AAATGCCTCATTGGGCAGAAGTTCATGCCAGTAGAAGGGATGGTTTTCTGTTCAGTGGAATGTAAGAAGAGGATGTCTTA	-1.44 ± 0.17	-1.91 ± 0.39	-1.40 ± 0.38	0.10 ± 0.30
78	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), mRNA.	NM_003896	TGGCTGCTATGAACTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAAAGAGGGAGTG	-1.65 ± 0.12	-1.59 ± 0.33	-1.05 ± 0.21	-0.31 ± 0.26
79	START domain containing 10 (STARD10), mRNA.	NM_006645	GACACTCTACGACGTCCTACACGACATTGAGTACCGCAAGAAATGGGACAGCAACGTCATTGAGACTTTTGACATCGCCC	-1.59 ± 0.27	-1.55 ± 0.20	-0.58 ± 0.13	-0.25 ± 0.20
80	hypothetical protein MGC46719 (MGC46719), mRNA.	NM_153713	ATGACAGTTTTTCAACTGCTACACTGGAATGGCAGCCTTAAGGCCATGAGGGAACGACAATGCTCTCGGCAGGAGGTGTT	-1.95 ± 0.27	-1.67 ± 0.09	-0.88 ± 0.11	-0.75 ± 0.10
81	KIAA1102 protein (KIAA1102), mRNA.	XM_044461	AGGAACGTTTGCTCCAGGAGAGATACCAGAAGGAGCAGGACAAGCTGAAAGAAGAGTGGGAAAAGGCCCAAAAGGAGGTG	-1.46 ± 0.34	-1.24 ± 0.27	-0.87 ± 0.26	0.32 ± 0.08

82	hypothetical protein MGC5576 (MGC5576), mRNA.	NM_024056	TGAGATCCTGGTGCACAACATAGTGATCTTCATGCGAACTTCAGTGAAGATTTCATACATTGGCCTCATGACCCAGAGCT	-1.30 ± 0.07	-0.95 ± 0.40	-1.09 ± 0.04	0.28 ± 0.16
83	glutathione S-transferase M3 (brain) (GSTM3), mRNA.	NM_000849	AGGCTTTGGAGAAAATCGCTGCCTACTTACAGTCTGATCAGTTCTGCAAGATGCCCATCAACAACAAGATGGCCCAGTGG	-1.27 ± 0.43	-1.24 ± 0.28	-0.99 ± 0.48	0.61 ± 0.28
84	hypothetical protein MGC10500 (MGC10500), mRNA.	NM_031477	TTTGAGAGCAGCCAGAAGTACAAAGAGGGGAAGTACATCATTGAACTCAACCACATGATCAAAGACAACGGCTGGGACTG	-1.49 ± 0.28	-1.30 ± 0.43	-0.46 ± 0.49	0.08 ± 0.27
85	collagen, type I, alpha 1 (COL1A1), mRNA.	NM_000088	AGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCC	-1.12 ± 0.29	-1.06 ± 0.41	-0.58 ± 0.63	0.30 ± 0.31
86	cDNA: FLJ23578 fis, clone LNG12709.	AK027231	GAGCGCAGGCGACAGGAAAAATGGTATCAGGAACAGGAACGTTTGCTCCAGGAGAGATACCAGAAGAGCAGGACAAGCTG	-1.75 ± 0.32	-1.46 ± 0.14	-0.95 ± 0.32	0.18 ± 0.05
87	selenoprotein P, plasma, 1 (SEPP1), mRNA.	NM_005410	CTAAACTCCAATGGTTCAGTGACTGTGGTTGCTCTTCTTCAAGCCAGCTGATACCTGTGCATCATCGAGGCATCTAAATT	-1.15 ± 0.34	-1.32 ± 0.12	-0.70 ± 0.18	0.13 ± 0.23
88	hypothetical protein DKFZp434L142 (DKFZp434L142), mRNA.	NM_016613	CCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTACGGCAGAAACTTCTTCAGTCTCTGTTTCTTGATAAAGTGTA	-1.46 ± 0.32	-1.20 ± 0.30	-1.27 ± 0.83	0.46 ± 0.38
89	chromosome 11 open reading frame 8 (C11orf8), mRNA.	NM_001584	GTTTGGTGGAATCCATGAAGGTTATGGCATCATGACCGACGGTTACACAACGTACATCAATGCCTCGACGTGTACAGTCA	-0.67 ± 0.00	-0.40 ± 0.67	-0.34 ± 0.26	1.84 ± 0.26
90	hypothetical protein FLJ20489 (FLJ20489), mRNA.	NM_017842	CCTGGATCTGTTTTCTTAGCACGCAGTGAGGAATCTTTGTACTTAAGGCCAGGGCAACAAAGTCAAGAGGTCAAGGTGTA	-0.71 ± 0.14	-0.66 ± 0.63	-0.46 ± 0.23	1.70 ± 0.17
91	zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2), mRNA.	NM_175907	TTTGTGAGGTGGACCTTGGAGATCTGTCTCCAGAGGGCAGGTTTACTGGCCTGGAGTCCATATTCCGTGCTGTCAATTAT	-1.24 ± 0.43	-0.94 ± 0.41	-0.35 ± 0.16	1.42 ± 0.07
92	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), mRNA.	NM_152754	CACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCACAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTA	-0.99 ± 0.32	-1.17 ± 0.46	-1.05 ± 0.15	1.36 ± 0.09
93	calcium/calmodulin-dependent protein kinase II, mRNA (cDNA clone MGC:22256 IMAGE:4703846), complete cds	BC020630	CTCTTAAGGCACACCAGCTGCCTGTTTTGCATGGTATTTGCAAAAATGCCTCTTGCGTGAGGAAATCTTTTACCATTTTT	-1.20 ± 0.41	-1.27 ± 0.35	-0.39 ± 0.38	0.95 ± 0.12
94	polyhomeotic-like 2 (Drosophila) (PHC2), transcript variant 2, mRNA.	NM_004427	GTGGACTTTGCCTATAAGTTCAAGCGTTCCAAGCGCTTCTGTTCCATGGCTTGTGCAAAGAGGTACAACGTGGGATGCAC	-0.92 ± 0.21	-0.75 ± 0.59	-0.78 ± 0.57	1.01 ± 0.07
95	transmembrane 4 superfamily member 4 (TM4SF4), mRNA.	NM_004617	TACTCGTTTATCATCTCAGCCATTTCAATCAACAAGGGTCCTAAATGCCTCATGGCCAATAGTACATGGGGCTACCCCTT	-0.70 ± 0.10	-1.25 ± 0.36	-0.91 ± 0.04	1.02 ± 0.18
96	WD and tetratricopeptide repeats 1 (WDTC1), mRNA.	NM_015023	CAGTGAAGCTTCCTGACTACAACAACCGTTTGAGAGTGCTGGTTGCCACCTATGTGACCTTCAGCCCCAATGGCACAGAG	-0.59 ± 0.18	-1.01 ± 0.47	-0.30 ± 0.14	0.56 ± 0.12
97	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) (PCBD), transcript variant 1, mRNA.	NM_000281	GAGAAACTGGACCACCATCCTGAATGGTTTAACGTGTACAACAAGGTCCACATCACGCTGAGCACCCATGAGTGTGCCGG	-0.71 ± 0.07	-0.85 ± 0.18	-0.21 ± 0.05	0.42 ± 0.21
98	ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant 1, mRNA.	NM_001677	GATGAAGTATAACCCAAATGTCCTTCCCGTTCAGTGCACTGGCAAGCGAGATGAAGATAAGGATAAAGTTGGAAATGTGG	-0.77 ± 0.22	-0.95 ± 0.11	-0.39 ± 0.15	0.85 ± 0.21
99	secreted protein of unknown function (SPUF), mRNA.	NM_013349	ATTCTCAATGAGGATGGCAGCCCTAACCTGGACTTCAAGCCTGAAGACCAGCCCCATTTTGACATCAAGGATGAGTTCTG	-0.44 ± 0.13	-0.71 ± 0.27	-0.60 ± 0.24	0.65 ± 0.05
100	5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), mRNA.	NM_000254	TGAGGATTATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGGACCCATTTTGGGATATGATACAG	-0.71 ± 0.05	-0.62 ± 0.38	-0.48 ± 0.56	0.50 ± 0.23
101	HMG-box transcription factor 1 (HBP1), mRNA.	NM_012257	ATATACTCAGATGTATCCAGGGAAAGATAACAGAGCCATAAGTGTGATCCTTGGTGACAGGTGGAAGAAAATGAAGAATG	-0.83 ± 0.10	-0.63 ± 0.39	-0.07 ± 0.35	0.31 ± 0.07
102	G protein-coupled receptor 126 (GPR126), mRNA.	NM_020455	TATGAGCATTCCTTCAACAAAAGTGGATCACTCAGACAGTGCTTCCATGGACAAGTCCTTGTCAAAACTGGCCCATGCTG	-0.80 ± 0.20	-0.60 ± 0.31	-0.69 ± 0.57	0.33 ± 0.27
103	5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), mRNA.	NM_000254_(2)	CCCTGCGGGATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGCTGGATGGAGGGATGGGGACCATGATCCAGCGG	-0.87 ± 0.04	-0.64 ± 0.31	-0.66 ± 0.16	0.26 ± 0.16
104	dachshund homolog 1 (Drosophila) (DACH1), transcript variant 3, mRNA.	NM_004392	AGCAGAACAGACGCTAAAACAGGCAGCTTCAACAGATAGTCTCAGGGTCTTAAATGACTCTCTGACCCCAGAGATAGAGG	-1.10 ± 0.29	-0.89 ± 0.36	-0.71 ± 0.14	-0.01 ± 0.19
105	cDNA FLJ20750 fis, clone HEP05174.	AK000757	GATGACTTGCTGTTCTTTATGACAGGGATCAGTGGCATTTGTTTCCTAGCAGTATTTAGCACCTTTTTGCCACCTTGGTG	-1.38 ± 0.22	-0.68 ± 0.15	-0.58 ± 0.11	0.35 ± 0.16
106	cDNA FLJ23720 fis, clone HEP13757.	AK074300	TATGTGAGGTGCTTTAAGGTCCCTGTCCTCAGGAAGCGCAGTCTGGTGGAAGAGATGAGCGCTGAACAAATCACTAAATA	-0.74 ± 0.28	-0.92 ± 0.05	-1.17 ± 0.39	0.41 ± 0.17
107	cDNA FLJ32362 fis, clone PUAEN1000057.	AK056924	AGGCATAGTTACACCAAAAGTGATCTATGAGGAAGCAACTGACCTAGACAAATTCATCACCAATACAGAAACTCCTTTAA	-0.76 ± 0.22	-0.34 ± 0.34	-0.88 ± 0.58	0.33 ± 0.22
108	paraoxonase 2 (PON2), mRNA.	NM_000305	TACAGTTTATGCCAACAATGGGTCTGTTCTCCAAGGAAGTTCTGTAGCCTCAGTGTATGATGGGAAGCTGCTCATAGGCA	-0.50 ± 0.26	-0.59 ± 0.18	-0.98 ± 0.15	0.92 ± 0.08
109	hypothetical protein (LOC387882), mRNA.	NM_207376	AATGTGCACAGACATTTCCAAGGAAATTCTAAACAGTCACCCTTCCCTTTTGCATTCCCCCAAATCTTAAGTGTATACAT	-0.41 ± 0.10	-0.83 ± 0.26	-0.78 ± 0.25	1.01 ± 0.20
110	pleckstrin homology domain containing, family G (with RhoGef domain) member 1 (PLEKHG1), mRNA.	XM_027307	TCTGACTCAAAGTTTGTGGATGCTGACTTTTCTGATAATGTCTGCAGCGGCAACACATTGCATTCTTTGAATAGTCCGCG	-0.56 ± 0.28	-0.78 ± 0.14	-1.10 ± 0.20	0.81 ± 0.24
111	sphingosine-1-phosphate phosphotase 2 (SGPP2), mRNA.	NM_152386	AAGTTTGTTACCTACACATCTGTTGGCATCTGCGCTACAACCTTTGTGCCGATGCTTCACAGGTTTCTGGGATTACCCTG	-0.40 ± 0.32	-0.46 ± 0.15	-0.67 ± 0.16	1.38 ± 0.42
112	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) (SATB1), mRNA.	NM_002971	TGATGAGATTCAGCAGGAAATGAAGCGTGCTAAAGTGTCTCAAGCACTGTTTGCAAAGGTTGCAGCAACCAAAAGCCAGG	-1.20 ± 0.05	-0.09 ± 0.00	-0.40 ± 0.17	0.03 ± 0.18
113	hypothetical protein FLJ34154 (FLJ34154), mRNA.	NM_173813	GGATCAGACTGCCTCCAGGAATCATGATAAAGCTCAGGGAAATTTCTGGGCGTGCTAGACCTCAATTTAGACCAAGTATA	-0.88 ± 0.28	-0.26 ± 0.20	0.03 ± 0.29	0.17 ± 0.19
114	hypothetical protein FLJ21069 (FLJ21069), mRNA.	NM_024692	CCATTCTTATCCTGGTTTTAGGAGAAGTTTTAGCACAACTTCTGCTTCTTCCCAAAAGGAGATTAACAGAAGAAATGCTT	-1.93 ± 0.09	-1.91 ± 1.02	-1.38 ± 0.49	-0.78 ± 0.13
115	homeo box B4 (HOXB4), mRNA.	NM_024015	CCCGTCCCACTCCGCGTGCAAAGAGCCCGTCGTCTACCCCTGGATGCGCAAAGTTCACGTGAGCACGGTAAACCCCAATT	-1.10 ± 0.23	-1.06 ± 0.09	-0.67 ± 0.42	2.70 ± 0.33
116	cytochrome P450, family 26, subfamily B, polypeptide 1 (CYP26B1), mRNA.	NM_019885	GTGCTGCAGACCTTCGAGCTTGATGGTTTCCAGATCCCCAAAGGCTGGAGTGTCATGTATAGCATCCGGGACACCCATGA	-0.61 ± 0.35	-0.59 ± 0.34	-0.43 ± 0.46	2.27 ± 0.73
117	homeo box A3 (HOXA3), transcript variant 1, mRNA.	NM_030661	CACAGTGGCCAAACAAATCTTCCCCTGGATGAAAGAGTCTCGACAAAACACAAAGCAGAAAACCAGCAGCTCCAGCTCAG	-1.03 ± 0.33	-0.88 ± 0.39	-0.12 ± 0.45	3.75 ± 0.48
118	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G (APOBEC3G), mRNA.	NM_021822	GACGAATTTCAGCACTGTTGGAGCAAGTTCGTGTACAGCCAAAGAGAGCTATTTGAGCCTTGGAATAATCTGCCTAAATA	-2.77 ± 0.49	-0.91 ± 0.87	0.36 ± 0.47	0.68 ± 0.66
119	KIAA1039 protein (KIAA1039), mRNA.	XM_085748	CAAGAGGAAAACACGCCGTTTGTCCCAGACATGATAGCCTCCAATTTCTTACATGCCTACATCGTCGTGCAGGTCGAGAC	0.43 ± 0.22	0.68 ± 0.13	0.28 ± 0.27	-0.64 ± 0.12
120	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS), mRNA.	NM_006452	ATGGAGCAAACTGCGAGCAAGCATTTTGAACACATGGATTTCCTTGAAGCAGGCTGACAAGAAAATCAGAGAATGTAATT	0.40 ± 0.22	0.57 ± 0.14	0.31 ± 0.05	-0.61 ± 0.27

121	hypothetical protein FLJ25416 (FLJ25416), mRNA.	NM_145018	TGTTGCCTTCCATTTTCAGAAAAAGGCCCACCTTCAGTGTGTGAAACTCGAAGTGCTTGGTCACCTGAATTGTTTTCATA	0.50 ± 0.22	0.76 ± 0.12	0.20 ± 0.22	-0.51 ± 0.16
122	phosphoserine phosphatase (PSPH), mRNA.	NM_004577	TAATATCTGGTGGCTTTAGGAGTATTGTAGAGCATGTTGCTTCAAAGCTCAATATCCCAGCAACCAATGTATTTGCCAAT	0.82 ± 0.04	0.55 ± 0.14	0.21 ± 0.02	-0.47 ± 0.21
123	mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction (Magmas), nuclear gene encoding mitochondrial protein, mRNA.	NM_016069	CGCGCAAAGGAGCGCCTGGATGAGGAACTCAAAATCCAGGCCCAGGAGGACAGAGAAAAATGGCAGATGCCCCATACGTG	0.55 ± 0.19	0.29 ± 0.10	0.21 ± 0.12	-0.59 ± 0.30
124	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa (EIF2S2), mRNA.	NM_003908	GTCATTCTAGATGTTCTGTTGCCAGTATCAAAACCGGCTTCCAGGCTGTCACGGGCAAGCGAGCACAGCTCCGTGCCAAA	0.77 ± 0.05	0.47 ± 0.14	0.58 ± 0.14	-0.46 ± 0.14
125	sine oculis homeobox homolog 3 (Drosophila) (SIX3), mRNA.	NM_005413	TAGACCTCTATTCCTCCCACTTCTTGTTGCCAAACTTCGCCGATTCTCACCACCGCTCCATACTTCTGGCGAGTAGCGGC	0.94 ± 0.25	0.60 ± 0.10	0.56 ± 0.20	-0.28 ± 0.19
126	hypothetical protein FLJ21901 (FLJ21901), mRNA.	NM_024622	CAGATTTCCCAGTTTGAATGGAACTCTATGGCACTGTCAACAAAGGATGCTCGGATGGACTACCTGAGAGAATGTATATT	0.61 ± 0.27	0.43 ± 0.19	0.61 ± 0.18	-0.48 ± 0.26
127	farnesyl-diphosphate farnesyltransferase 1 (FDFT1), mRNA.	NM_004462	GCCTTTCCCGTCTTTTCTCAGCCTCAGAGTTTGAAGACCCCTTAGTTGGTGAAGATACAGAACGTGCCAACTCTATGGGC	0.77 ± 0.17	0.43 ± 0.14	0.38 ± 0.11	-0.24 ± 0.21
128	phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA.	NM_021154	AGGCTGGAAACAGCTCCTTGTACAACACGCCTCCATGTTTCAGCATCTACGTCATGGGCTTGGTTCTGGAGTGGATTAAA	0.86 ± 0.16	0.44 ± 0.19	0.58 ± 0.47	-0.54 ± 0.30
129	hypothetical protein FLJ22635 (FLJ22635), mRNA.	NM_025092	AAGGTACCCTTTGACGTGGAGCAGAACTTCCACCCGAAGTTCCAGCTCCGAGTTCCCTGGGAGGACTTTTTCAGATGTTA	0.59 ± 0.32	0.31 ± 0.19	0.49 ± 0.39	-0.58 ± 0.23
130	phosphoribosyl pyrophosphate synthetase 1 (PRPS1), mRNA.	NM_002764	CTTTGAGGCAGTAGTAGTCACCAATACCATACCTCAGGAGGACAAGATGAAGCATTGCTCCAAAATACAGGTGATTGACA	0.81 ± 0.16	0.93 ± 0.10	0.68 ± 0.18	-0.46 ± 0.17
131	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa (POLR3K), mRNA.	NM_016310	AGAATGTTGACTCTACTGCAGAGTCGTGTCCCAAATGCGAACATCCTCGTGCTTACTTCATGCAGCTTCAGACCCGCTCT	0.83 ± 0.28	0.97 ± 0.02	0.65 ± 0.05	-0.17 ± 0.23
132	chromosome 14 open reading frame 156 (C14orf156), mRNA.	NM_031210	GGCTTTCACAGAGGTTTGGGTTGGGTTCAGTTTTCTTCAGAAGAAGGACTTCGGAATGCACTACAACAGGAAAATCATAT	0.90 ± 0.28	0.85 ± 0.08	0.22 ± 0.16	-0.46 ± 0.17
133	kinesin family member 5A (KIF5A), mRNA.	NM_004984	CCACAACCTTCGCAAGCTGTTCGTTCAAGACGTCACGACTCGAGTCAAGAAAAGTGCAGAAATGGAGCCCGAAGACAGTG	0.91 ± 0.24	0.84 ± 0.02	0.28 ± 0.33	-0.16 ± 0.27
134	copine VII (CPNE7), transcript variant 2, mRNA.	NM_014427	ACGACTCTCGAGGAAAGCACGACTTCATCGGAGAATTCTCTACCACCTTCGAGGAGATGCAGAAGGCCTTTGAGGAGGGG	0.99 ± 0.36	0.80 ± 0.11	0.69 ± 0.10	-0.77 ± 0.36
135	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast) (PAK1), mRNA.	NM_002576	GCTGTCTCGATATGGATGTGGAGAAGAGAGGTTCAGCTAAAGAGCTGCTACAGCATCAATTCCTGAAGATTGCCAAGCCC	0.81 ± 0.34	1.20 ± 0.15	0.62 ± 0.28	-0.58 ± 0.31
136	PREDICTED: paraneoplastic antigen MA2 (PNMA2), mRNA.	XM_376764	TATCAGGAGGAAGGAGAGAAGGTCTCAGCCTATGTGTTACGGCTAGAAACCCTGCTCCGGAGAGCGGTGGAGAAACGCGC	1.02 ± 0.19	0.06 ± 0.30	0.39 ± 0.12	-0.46 ± 0.23
137	mitogen-activated protein kinase 8 interacting protein 1 (MAPK8IP1), mRNA.	NM_005456	AGTTTGAGGATGAAGACCTCTCGGAGATCACTGATGAGTGTGGCATCAGCTTACAGTGCAAAGACACCCTGTCCTTACGG	1.04 ± 0.10	0.10 ± 0.29	0.56 ± 0.29	-0.44 ± 0.25
138	matrix metalloproteinase 15 (membrane-inserted) (MMP15), mRNA.	NM_002428	CTACGAGCGCCAAGACGGTCGTTTTGTCTTTTTCAAAGGTGACCGCTACTGGCTCTTTCGAGAAGCGAACCTGGAGCCCG	1.10 ± 0.34	0.30 ± 0.20	0.29 ± 0.22	-0.46 ± 0.26
139	ARF protein (LOC51326), mRNA.	NM_016632	CGGCACAAATGATGAGGCATCTCCTGGAAAGCTTAACTTCTTATCCATCCCATCTCTTGGACAGATGATGCCAGTTAATT	1.08 ± 0.16	0.29 ± 0.54	0.41 ± 0.11	-0.11 ± 0.30
140	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), mRNA.	NM_013264	AAGATTCGTGTGTTTGTCCTGGATGAAGCAGATGTGATGATTGACACTCAAGGATTCTCAGATCATAGTATCCGTATTCA	1.15 ± 0.36	0.55 ± 0.38	0.60 ± 0.22	-0.49 ± 0.27
141	tumor-associated calcium signal transducer 1 (TACSTD1), mRNA.	NM_002354_(2)	CGACGGCGACTTTTGCCGCAGCTCAGGAAGAATGTGTCTGTGAAAACTACAAGCTGGCCGTAAACTGCTTTGTGAATAAT	1.47 ± 0.28	0.85 ± 0.03	0.31 ± 0.19	-0.64 ± 0.43
142	ets variant gene 4 (E1A enhancer binding protein, E1AF) (ETV4), mRNA.	NM_001986	AACCTCTGCGACCATTCCCAGATGATGTCTGCGTTGTCCCTGAGAAATTTGAAGGAGACATCAAGCAGGAAGGGGTCGGT	1.18 ± 0.22	0.91 ± 0.06	0.22 ± 0.23	-0.67 ± 0.42
143	nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA.	NM_004289_(2)	CAGCATGAGGAAAATGAAGAAAGGGTGTCAGCCCAGAAGGAGAACTCACTTCAGCAGAATGATGATGATGAAAACAAAAT	1.07 ± 0.17	0.96 ± 0.37	0.29 ± 0.18	-1.02 ± 0.21
144	hemopoietic cell kinase (HCK), mRNA.	NM_002110	GCCATCAACTTTGGCTCCTTCACCATCAAGTCAGACGTCTGGTCCTTTGGTATCCTGCTGATGGAGATCGTCACCTACGG	0.56 ± 0.26	0.76 ± 0.19	0.29 ± 0.20	-1.00 ± 0.36
145	ets variant gene 1 (ETV1), mRNA.	NM_004956	CAGAAGCTCAGGTACCTGACAATGATGAGCAGTTTGTACCAGACTATCAGGCTGAAAGTTTGGCTTTTCATGGCCTGCCA	0.90 ± 0.13	0.93 ± 0.13	-0.20 ± 0.30	-0.53 ± 0.13
146	ets variant gene 5 (ets-related molecule) (ETV5), mRNA.	NM_004454	CGATTCAGAAGTGCCTAACTGCCAGTCATCCTACATGAGAGGGGGTTATTTCTCCAGCAGCCATGAAGGTTTTTCATATG	0.86 ± 0.23	0.72 ± 0.29	-0.15 ± 0.15	-0.54 ± 0.26
147	family with sequence similarity 20, member A (FAM20A), mRNA.	NM_017565	GGACCGGCACCATTATGAGATGTTCACCAAGTTCGGGGATGATGGGTTCCTTATTCACCTTGACAACGCCAGAGGGTTCG	0.90 ± 0.30	0.77 ± 0.24	0.12 ± 0.14	-0.37 ± 0.23
148	pim-2 oncogene (PIM2), mRNA.	NM_006875	TGGTGTGTGGGGACATTCCCTTTGAGAGGGACCAGGAGATTCTGGAAGCTGAGCTCCACTTCCCAGCCCATGTCTCCCCA	0.92 ± 0.27	0.62 ± 0.32	-0.14 ± 0.18	-0.94 ± 0.43
149	adrenomedullin (ADM), mRNA.	NM_001124	CGGAGTTTCGAAAGAAGTGGAATAAGTGGGCTCTGAGTCGTGGGAAGAGGGAACTGCGGATGTCCAGCAGCTACCCCACC	1.02 ± 0.31	0.41 ± 0.34	-0.07 ± 0.35	-0.46 ± 0.14
150	pleckstrin homology domain containing, family C (with FERM domain) member 1 (PLEKHC1), mRNA.	NM_006832	GTCTAATTGAAGCCAAGATGAGATTTATTCAAGCTTGGCAGTCACTACCTGAATTTGGCATCACTCACTTCATTGCAAGG	0.79 ± 0.22	0.44 ± 0.16	-0.02 ± 0.57	-0.28 ± 0.19
151	likely ortholog of mouse limb-bud and heart gene (LBH), mRNA.	NM_030915	AAGGATGGCCTTTCCTACCAGATCTTCCCAGACCCGTCAGATTTTGACCGCCGCTGCAAACTGAAGGACCGTCTGCCCTC	0.54 ± 0.19	0.37 ± 0.09	-0.06 ± 0.47	-0.52 ± 0.23
152	solute carrier family 39 (zinc transporter), member 14 (SLC39A14), mRNA.	NM_015359	TCTGGCTGATATGTTCCCTGAGATGAATGAGGTCTGTCAAGAGGATGAAAGGAAGGGCAGCATCTTGATTCCATTTATCA	0.40 ± 0.24	0.43 ± 0.28	-0.26 ± 0.16	-0.85 ± 0.34
153	hypothetical protein LOC92558 (LOC92558), mRNA.	XM_045787	AGTGCAGGATGGATATGATGTCTCTGAACAGCCAGTTGCTGGATGCCATTCAGCAGAAACTGAACCTCTCGCAGCAGCTG	0.52 ± 0.29	0.11 ± 0.40	-0.19 ± 0.26	-0.52 ± 0.20
154	sprouty homolog 4 (Drosophila) (SPRY4), mRNA.	NM_030964	ACCCACTCACCATCCTACCCATTGACCAGGTGAAGACCAGCCATGTGGAGAATGACTACATAGACAACCCTAGCCTGGCC	0.69 ± 0.07	0.52 ± 0.18	-0.62 ± 0.13	-0.76 ± 0.24
155	adrenomedullin (ADM), mRNA.	NM_001124_(2)	AAGCTGGTTTCCGTCGCCCTGATGTACCTGGGTTCGCTCGCCTTCCTAGGCGCTGACACCGCTCGGTTGGATGTCGCGTC	1.38 ± 0.30	0.89 ± 0.55	0.37 ± 0.44	-0.44 ± 0.14
156	synapsin III (SYN3), transcript variant IIIa, mRNA.	NM_003490	TCGATGATGCCCATACAGACTGGTCGAAGTATTTCCATGGGAAGAAGGTGAATGGAGAGATTGAGATCCGAGTGGAGCAG	1.17 ± 0.20	0.78 ± 0.64	0.68 ± 0.44	-0.06 ± 0.21
157	TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 4, mRNA.	NM_003244_(2)	AGCATCTGGCAGTGAGACTGAGGATGAGGACAGCATGGACATTCCCTTGGACCTTTCTTCATCCGCTGGCTCAGGCAAGA	1.16 ± 0.22	0.31 ± 0.16	-0.16 ± 0.11	0.01 ± 0.14
158	ischemia/reperfusion inducible protein (FLJ23476), mRNA.	NM_024640	GAATGTCGAGGAGTTCCAGGATCTCTGGCCTCAGTTGTCCTTGGTTATTGATGGGGGACAAATTGGGGATGGCCAGAGCC	1.19 ± 0.26	0.65 ± 0.19	0.18 ± 0.49	0.18 ± 0.15
159	phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA.	NM_021127	GAAGAAAGACTGCATTGTAATTGAGAGGAATGTGAAGGTGCATTCATGGGTGCCCTTGGAAACGGAAGATGGAATACATC	1.23 ± 0.24	0.42 ± 0.54	-0.01 ± 0.55	-1.18 ± 0.08

160	F11 receptor (F11R), transcript variant 1, mRNA.	NM_016946	TGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCC	0.39 ± 0.05	0.22 ± 0.32	0.66 ± 0.22	-0.87 ± 0.22
161	HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), mRNA.	NM_006410	TGACCGTGGTTAGAGCAATGCTGAACAATGTGGTGAGACCAAGAGACAAGCAGATGGAACTGCTGGAGAACAAGGCCATC	0.22 ± 0.17	0.09 ± 0.05	0.46 ± 0.21	-0.90 ± 0.14
162	methionine-tRNA synthetase (MARS), mRNA.	NM_004990	AGGATAACTATACCTTGGTCAGCCACCTCATTGCTACAGAGTACCTGAACTATGAGGATGGGAAATTCTCTAAGAGCCGC	0.63 ± 0.24	0.23 ± 0.08	0.25 ± 0.13	-0.77 ± 0.18
163	seizure related 6 homolog (mouse)-like 2 (SEZ6L2), mRNA.	NM_012410	GTCATTGTCCTCGGCAGTGGCGTTTACATCTACTACACCAAGCTTCAGGGAAAGTCCCTTTTCGGCTTCTCGGGCTCCCA	0.33 ± 0.27	0.15 ± 0.20	0.44 ± 0.17	-0.68 ± 0.15
164	alanyl-tRNA synthetase (AARS), mRNA.	NM_001605	CTTGTGTTCATCCAGTATAACAGGGAAGCTGATGGCATTCTGAAACCTCTTCCCAAGAAAAGCATTGACACAGGGATGGG	0.52 ± 0.22	-0.12 ± 0.15	0.49 ± 0.12	-1.06 ± 0.21
165	polymerase (DNA directed), epsilon 2 (p59 subunit) (POLE2), mRNA.	NM_002692	TAAAGCTCAGTTCCATAGTGGTTTATACACAGAGGCATGCTTTGTCTTAGCAGAAGGTTGGTTTGAAGATCAAGTGTTTC	0.19 ± 0.10	0.12 ± 0.28	0.07 ± 0.34	-0.85 ± 0.23
166	hypothetical protein DKFZp434I2117 (DKFZP434I2117), mRNA.	NM_031478	CTGTGCCCTACTTCATCTACGACATCTACGCCATGTTCCTCTGTCACTGGCACAAGCACCAGGTCAAAGGGCATGGAGGG	0.39 ± 0.38	0.33 ± 0.43	0.54 ± 0.53	-1.00 ± 0.33
167	activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), transcript variant 1, mRNA.	NM_001675	CCCAAACCTTACGATCCTCCTGGAGAGAAGATGGTAGCAGCAAAAGTAAAGGGTGAGAAACTGGATAAGAAGCTGAAAAA	0.05 ± 0.27	-0.17 ± 0.16	0.01 ± 0.05	-1.45 ± 0.25
168	eukaryotic translation initiation factor 4E binding protein 1 (EIF4EBP1), mRNA.	NM_004095	TATGACCGGAAATTCCTGATGGAGTGTCGGAACTCACCTGTGACCAAAACACCCCCAAGGGATCTGCCCACCATTCCGGG	0.19 ± 0.17	-0.11 ± 0.03	0.12 ± 0.12	-1.26 ± 0.35
169	phosphatidic acid phosphatase type 2C (PPAP2C), transcript variant 1, mRNA.	NM_003712	TCTTCCTTTGGGATGTACTGCATGGTGTTCTTGGCGCTGTATGTGCAGGCACGACTCTGTTGGAAGTGGGCACGGCTGCT	0.07 ± 0.18	0.18 ± 0.37	0.08 ± 0.30	-1.53 ± 0.39
170	hypothetical protein FLJ21918 (FLJ21918), mRNA.	NM_024939	TTATCCTCCATCTACTCAAAGAGCCCAGCAGTCAATTGTTTTCGAAGCCCGAGGTGATAAAGCAGAAATACGAGACGGGG	0.52 ± 0.38	0.14 ± 0.19	-0.13 ± 0.12	-1.07 ± 0.25
171	dudulin 2 (TSAP6), mRNA.	NM_018234	GTGACCTCACTGCCGTCCATTGCAAACTCGCTCAACTGGAGGGAGTTCAGCTTCGTTCAGTCCTCACTGGGCTTTGTGGC	0.15 ± 0.22	0.14 ± 0.28	-0.37 ± 0.23	-1.10 ± 0.31
172	follistatin (FST), transcript variant FST317, mRNA.	NM_006350_(2)	GCAAGATGTAAAGAGCAGCCAGAACTGGAAGTCCAGTACCAAGGCAGATGTAAAAAGACTTGTCGGGATGTTTTCTGTCC	1.76 ± 0.62	0.93 ± 0.30	-0.49 ± 0.51	-1.46 ± 0.78
173	sodium channel, nonvoltage-gated 1 alpha (SCNN1A), mRNA.	NM_001038	CTTCCAGATGCTATCGCGACAGAACAATTACACCGTCAACAACAAGAGAAATGGAGTGGCCAAAGTCAACATCTTCTTCA	1.27 ± 0.28	0.67 ± 0.15	-0.09 ± 0.37	-1.54 ± 0.49
174	cDNA FLJ33783 fis, clone BRSSN2007504.	AK091102	GTTCGACCTCTTCCAAGAAGACGTCAGGAATGTCCTTCTGAATGCCTTTCCTAGTTCTCATGAGAACACAGCAGTTTTTA	1.10 ± 0.18	0.09 ± 0.11	-0.79 ± 0.34	-0.92 ± 0.41
175	CD9 antigen (p24) (CD9), mRNA.	NM_001769	ACAAGGATGAGGTGATTAAGGAAGTCCAGGAGTTTTACAAGGACACCTACAACAAGCTGAAAACCAAGGATGAGCCCCAG	0.92 ± 0.14	0.27 ± 0.40	-0.88 ± 0.23	-2.33 ± 0.32
176	carbonic anhydrase XI (CA11), mRNA.	NM_001217	TCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGCCG	0.15 ± 0.14	-0.61 ± 0.25	-0.82 ± 0.14	-1.09 ± 0.03
177	hypothetical protein FLJ13352 (FLJ13352), mRNA.	NM_024592	GGAGACTGGTTTGAATATGTTTCTTCCCCTAACTACTTAGCAGAGCTGATGATCTACGTTTCCATGGCCGTCACCTTTGG	0.15 ± 0.09	-0.72 ± 0.11	-0.87 ± 0.18	-0.98 ± 0.15
178	propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), mRNA.	NM_000532	CACAATTGTCCCTTTGGAATCAACCAAAGCCTACAACATGGTGGACATCATACACTCTGTTGTTGATGAGCGTGAATTTT	-0.12 ± 0.19	-0.78 ± 0.22	-0.63 ± 0.17	-1.20 ± 0.17
179	protein phosphatase 1, regulatory (inhibitor) subunit 16B (PPP1R16B), mRNA.	NM_015568	CTGCTGCTGGAGCTAAAACACAAGCATGATGTGATCATGAAGTCACAGCTGAGGCACAAGTCATCCTTGAGCCGGAGGAC	-0.16 ± 0.32	-0.64 ± 0.50	-0.77 ± 0.17	-1.47 ± 0.25
180	TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA.	NM_004619	AATGCCAAGAACGCCTACATTAAAGATGACACTCTGTTCTTGAAAGTGGCCGTGGACTTAACTGACCTGGAGGATCTCTA	0.18 ± 0.34	-0.37 ± 0.25	-0.40 ± 0.20	-1.04 ± 0.26
181	GTP binding protein 4 (GTPBP4), mRNA.	NM_012341	TTAGGGATGTCAAGATGGTGAAGAAAGCCAAGACTATGAAGAATGCTCAGAAGAAGATGAATCGGTTGGGGAAGAAAGGG	0.01 ± 0.28	-0.20 ± 0.13	-0.41 ± 0.24	-1.05 ± 0.28
182	cDNA FLJ32027 fis, clone NTONG1000246, weakly similar to CYCLIN-DEPENDENT KINASE INHIBITOR 1C.	AK056589	CCTCAGGGAGTAAACCCCTAAGGGGCTCACTTAAGGAGGAGGTAGCCCTGGATTTGAGTGTGAGGAAGCCCACAGCAGAG	0.06 ± 0.03	0.05 ± 0.30	-0.48 ± 0.22	-0.97 ± 0.17
183	KIAA0746 protein (KIAA0746), mRNA.	XM_045277	CTTTCTGGGAACCTTTCTGCTATCCATATTGATCGCCTGGACTGTGCAGTATTTCCAGTCTGTCTCAGCAAGCGATCCCC	0.44 ± 0.16	-0.19 ± 0.15	-0.65 ± 0.01	-1.33 ± 0.05
184	creatine kinase, mitochondrial 1 (ubiquitous) (CKMT1), nuclear gene encoding mitochondrial protein, mRNA.	NM_020990	AAGCAAAGATAGCCGCTTCCCAAAGATCCTGGAGAACCTAAGACTCCAAAAACGTGGTACTGGAGGAGTGGACACTGCTG	0.30 ± 0.38	-0.27 ± 0.08	-0.36 ± 0.29	-1.70 ± 0.14
185	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA.	NM_003045	TCAACCAGCCTTATAGCTGTTCTCATCATCACCTTCTGCATTGTGACCGTGCTTGGAAGGGAGGCTCTCACCAAAGGGGC	0.16 ± 0.29	-0.30 ± 0.11	-0.27 ± 0.29	-1.76 ± 0.04
186	coronin, actin binding protein, 2A (CORO2A), transcript variant 1, mRNA.	NM_003389	TCTGTCATCACAAGCCCCATGAGTACGATTAGCTGTCACCAAGATGTGATCCTCTCCATGTCCTTCAACACCAACGGGAG	0.13 ± 0.41	-0.31 ± 0.15	-0.17 ± 0.10	-1.73 ± 0.41
187	solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA.	NM_005628	TCGAAGCAGTCAACCTCCCGGTCGACCATATCTCCTTGATCCTGGCTGTGGACTGGCTAGTCGACCGGTCCTGTACCGTC	-0.34 ± 0.11	-0.32 ± 0.18	-0.26 ± 0.08	-1.51 ± 0.19
188	cytokine receptor-like factor 3 (CRLF3), mRNA.	NM_015986	TGGTTACTTGATCAGTCTTGTGGTTCTCTTTACTTTGGATGCTCATTTTTCTATCCTGGATGGAAAGTGTTAGTGTTTTA	-0.37 ± 0.17	-0.36 ± 0.23	-0.23 ± 0.14	-1.49 ± 0.22
189	nucleoside phosphorylase (NP), mRNA.	NM_000270	ACTGTGGACTTCGAGTCTTTGGCTTCTCACTCATCACTAACAAGGTCATCATGGATTATGAAAGCCTGGAGAAGGCCAAC	-0.19 ± 0.05	-0.39 ± 0.18	-0.64 ± 0.37	-1.56 ± 0.19
190	regulator of G-protein signalling 2, 24kDa (RGS2), mRNA.	NM_002923	ATACAGCTTGATGGAGAACAACTCTTATCCTCGTTTCTTGGAGTCAGAATTCTACCAGGACTTGTGTAAAAAGCCACAAA	-0.11 ± 0.12	-0.21 ± 0.15	-0.63 ± 0.22	-1.76 ± 0.30
191	threonyl-tRNA synthetase mRNA, complete cds.	M63180	CCCAAAACGTACGACAACAATTCCACGATGCCAAATTCATGGCAGACATTGATCTGGATCCAGGCTGTACATTGAATAAA	-0.05 ± 0.18	-0.36 ± 0.17	-0.61 ± 0.09	-1.46 ± 0.30
192	complement component 1, q subcomponent binding protein (C1QBP), nuclear gene encoding mitochondrial protein, mRNA.	NM_001212	GAGGATGAGGTTGGACAAGAAGACGAGGCTGAGAGTGACATCTTCTCTATCAGGGAAGTTAGCTTTCAGTCCACTGGCGA	-0.02 ± 0.11	0.05 ± 0.08	-0.43 ± 0.10	-1.44 ± 0.27
193	isoleucine-tRNA synthetase (IARS), transcript variant short, mRNA.	NM_002161	CAGGAAGCTAAAGCTGTTTCTGAATGAGACCCAAACGCAGGAAATTACAGAAGACATCCCCGTGAAGACTTTGAATATGA	-0.20 ± 0.09	-0.73 ± 0.33	-0.54 ± 0.25	-1.81 ± 0.30
194	serine protease inhibitor, Kunitz type 1 (SPINT1), transcript variant 2, mRNA.	NM_003710_(2)	CAGGTGGAACTGTGGGGACTCAAGGAAGGCACCTACCTGTTCCAGCTGACAGTGACTAGCTCAGACCACCCAGAGGACAC	-0.30 ± 0.14	-0.89 ± 0.22	-0.24 ± 0.15	-1.32 ± 0.21
195	cysteinyl-tRNA synthetase (CARS), transcript variant 2, mRNA.	NM_001751	AAGCTGAAGAAGCTCTTCGAGGCTCAGGAGAAGCTCTACAAGGAATATCTGCAGATGGCCCAGAATGGAAGCTTCCAGTG	0.48 ± 0.52	-0.40 ± 0.22	0.09 ± 0.10	-1.51 ± 0.32
196	tyrosyl-tRNA synthetase (YARS), mRNA.	NM_003680	TTGCTGCTGAGGTTGTACATCCTGGAGACCTGAAGAATTCTGTTGAAGTCGCACTGAACAAGTTGCTGGATCCAATCCGG	0.00 ± 0.28	-0.41 ± 0.22	0.05 ± 0.29	-1.83 ± 0.31
197	formyltetrahydrofolate synthetase domain containing 1 (FTHFSDC1), mRNA.	NM_015440	GACCCACCTTTCTCTATCTCACCAACCTGACAAAAAAGGTGTGCCAAGGGACTTCATCTTACCTATCAGTGACGTCCGGG	-0.71 ± 0.13	-1.08 ± 0.04	-1.28 ± 0.08	-1.99 ± 0.04
198	amino-terminal enhancer of split (AES), mRNA.	NM_001130_(2)	TACGGCTTGAACATCGAGATGCACAAACAGGCTGAGATCGTCAAAAGGCTGAACGGGATTTGTGCCCAGGTCCTGCCCTA	-0.70 ± 0.23	-1.08 ± 0.19	-1.30 ± 0.15	-1.81 ± 0.18

199	CD20-like precusor mRNA, complete cds.	AF142409	CAGTCTGGCTGGATCTCTCTCTCTGATGCTGATTTGCACTCTGCTGGAATTCTGCCTAGCTGTGCTCACTGCTGTGCTGC	-0.66 ± 0.15	-0.66 ± 0.36	-1.44 ± 0.18	-1.79 ± 0.01
200	tumor necrosis factor receptor superfamily, member 21, mRNA (cDNA clone IMAGE:3684533), complete cds.	BC005192	GAACTTCACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTTGGAAAGTCAAAATCAAGTGCCAGTGGCGC	-0.50 ± 0.29	-0.58 ± 0.19	-1.11 ± 0.32	-1.93 ± 0.39
201	PHD finger protein 15 (PHF15), mRNA.	NM_015288	CAGCCTGCATTTTGACACTGAGACTGATGGCTACTTCTCTGATGGGGAGATGAGCGACTCAGATGTAGAGGCCGAGGACG	-0.34 ± 0.09	-0.77 ± 0.17	-1.42 ± 0.42	-1.59 ± 0.07
202	hypothetical protein MGC13096 (MGC13096), mRNA.	NM_032346	TGAGGGACTATCAGCAGAGAGAAGGCATTGCCATGGATCAGTTGCTTTCCCAAAGCCTTCCTAATGATGGTGATGAAAAA	-0.56 ± 0.05	-0.72 ± 0.16	-0.90 ± 0.28	-1.64 ± 0.15
203	CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA.	NM_006561	AAGGCGTAACGAGTTCATCTTTCTTTCACCATAGGGGTTATAGTTGGCTTGTGCTACTCTGGAATCATTTTACTGTTTGT	-0.95 ± 0.24	-1.32 ± 0.43	-1.55 ± 0.17	-2.24 ± 0.31
204	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA.	NM_006636	CCAAACCCAAGTTGGTTGGAGATGTGGATTTTGAAGGAGTCAGACAAAAAGCTGGGTATATCACTCCAGTTCCTGGAGGT	-0.01 ± 0.36	-0.70 ± 0.15	-0.17 ± 0.27	-2.62 ± 0.19
205	cDNA FLJ12937 fis, clone NT2RP2005020.	AK022999	GTGATAGATGCATTTTCCCCAGGCTGTCTCAGAAAGGTCGCTAAATGTATACTGTTGTCAGAATTGCTGAGATCTCCCCC	-0.05 ± 0.40	-0.66 ± 0.12	-0.50 ± 0.07	-2.42 ± 0.10
206	L-type amino acid transporter subunit LAT1 mRNA, complete cds	AF104032	TGTCCAATCTAGATCCCAACTTCTCATTTGAAGGCACCAAACTGGATGTGGGGAACATTGTGCTGGCATTATACAGCGGC	-0.46 ± 0.34	-0.76 ± 0.11	-1.05 ± 0.10	-2.58 ± 0.40
207	galanin (GAL), mRNA.	NM_015973	CTTTGACAGGTCCATACCTGAAAACAATATCATGCGCACAATCATTGAGTTTCTGTCTTTCTTGCATCTCAAAGAGGCCG	-0.14 ± 0.34	0.20 ± 0.15	-0.73 ± 0.16	-3.02 ± 0.23
208	high mobility group AT-hook 1 (HMGA1), transcript variant 2, mRNA.	NM_002131	CCAAGACCCGGAAAACCACCACAACTCCAGGAAGGAAACCAAGGGGCAGACCCAAAAAACTGGAGAAGGAGGAAGAGGAG	1.74 ± 0.24	1.76 ± 0.02	1.49 ± 0.02	0.53 ± 0.21
209	ubiquinol-cytochrome c reductase hinge protein (UQCRH), mRNA.	NM_006004	AGAGGAAGAGGAGGAATTAGTGGATCCCCTAACAACAGTGAGAGAGCAATGCGAGCAGTTGGAGAAATGTGTAAAGGCCC	1.75 ± 0.10	1.68 ± 0.04	1.58 ± 0.10	0.72 ± 0.20
210	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA.	NM_000582	AAGCCAATGATGAGAGCAATGAGCATTCCGATGTGATTGATAGTCAGGAACTTTCCAAAGTCAGCCGTGAATTCCACAGC	1.62 ± 0.22	1.99 ± 0.11	1.57 ± 0.12	0.46 ± 0.14
211	cDNA FLJ37383 fis, clone BRAMY2026168.	AK094702	CACACTCGTGCAGTGGGGGAGTTCTGGCTCCCCAACCTAACCCCTAGCCGTCATCTCCACACTCACCAGGCCCACCAGGG	1.80 ± 0.22	1.97 ± 0.24	1.43 ± 0.06	0.80 ± 0.08
212	cDNA FLJ14398 fis, clone HEMBA1003569, moderately similar to METASTASIS-ASSOCIATED PROTEIN MTA1.	AK027304	ACCTACAGCAAACCAAATCCCAACCAAATATCCACTAGTAATGGGAAGCCTGGTGCTGTGAATGGAGCTGTGGGGACCAC	1.94 ± 0.13	1.76 ± 0.05	1.60 ± 0.25	0.90 ± 0.12
213	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA.	NM_000582_(2)	GGCTGATTCTGGAAGTTCTGAGGAAAAGCAGCTTTACAACAAATACCCAGATGCTGTGGCCACATGGCTAAACCCTGACC	1.86 ± 0.29	2.17 ± 0.16	1.76 ± 0.21	0.71 ± 0.31
214	cathepsin L2 (CTSL2), mRNA.	NM_001333_(2)	TGGGTTGCTTTCGAAACCAGAAATTCAGGAAGGGGAAAGTGTTCCGTGAGCCTCTGTTTCTTGATCTTCCCAAATCTGTG	1.91 ± 0.21	1.83 ± 0.11	1.58 ± 0.20	0.90 ± 0.27
215	similar to Synaptotagmin II (SytII) (LOC127833), mRNA.	XM_060678	TGAAGAAGAAGACCCTGAACCCATACTTCAACGAGTCCTTCAGCTTTGAGATCCCCTTCGAGCAGATTCAGGAGGGCTGG	1.87 ± 0.16	1.64 ± 0.41	1.33 ± 0.45	0.59 ± 0.25
216	G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA.	NM_016235	GCAGCTTGGGGAAAAGACCCAGCGCTCCGTTTAGAAGCAACGTGTATCAGCCAACTGAGATGGCCGTCGTGCTCAACGGT	1.57 ± 0.24	1.41 ± 0.31	1.23 ± 0.31	0.50 ± 0.17
217	cDNA FLJ35568 fis, clone SPLEN2005727.	AK092887	TGCAAGTCCTCAGACTGCAGGAGGAGGAACTCCCGTCCTTCGGTAGTGTCACTACTTAGAGGCAACTGTGAGGAGCTGTG	1.64 ± 0.18	1.54 ± 0.26	1.47 ± 0.29	0.39 ± 0.06
218	gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA.	NM_000165	TTGCCGCAATTACAACAAGCAAGCAAGTGAGCAAAACTGGGCTAATTACAGTGCAGAACAAAATCGAATGGGGCAGGCGG	2.17 ± 0.23	2.14 ± 0.22	1.22 ± 0.21	0.51 ± 0.30
219	LOC137038 (LOC137038), mRNA.	XM_070191	AGCCCGTTTCTTCACTCACAGGCCATGTCTGAGTGGATCAAGAAGAACAGAGTGCCCTTTTATGAGATTTTGTCTGCGTA	1.34 ± 0.13	1.72 ± 0.14	2.02 ± 0.19	0.17 ± 0.06
220	F-box and leucine-rich repeat protein 10 (FBXL10), mRNA.	NM_032590	CGAGAAAAGGATGGACTGGGAATTAAGATGCCTGACCCTGATTTCACAGTCCGAGACGTCAAACTCCTAGTGGGGAGCCG	2.45 ± 0.08	2.16 ± 0.12	2.04 ± 0.15	0.83 ± 0.20
221	AT rich interactive domain 3B (BRIGHT- like) (ARID3B), mRNA.	NM_006465	AGCTGTATGAACTGGACGGTGATCCTGAAAGGAAAGAGTTCCTGGATGACCTCTTCGTCTTTATGCAGAAGAGGGGGACC	2.25 ± 0.25	2.47 ± 0.14	1.58 ± 0.10	0.92 ± 0.16
222	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (SEMA6B), transcript variant SEMA6B.1, mRNA.	NM_020241	CCTCTTCTCTGACGGGATGCTCTTCACAGCTACTGTTACCGACTTCCTAGCCATTGATGCTGTCATCTACCGCAGCCTCG	2.15 ± 0.13	2.01 ± 0.29	2.02 ± 0.37	1.12 ± 0.22
223	cDNA FLJ35492 fis, clone SMINT2008672, moderately similar to ZINC FINGER PROTEIN 191.	AK092811	GCTAAAGTGGGTTGAATTGCCATGGCTGCTGGAAGAAGTCTCAAAAAGCTCCCGACTAGACATACATGGAGCAGTAAAAA	2.15 ± 0.43	2.05 ± 0.38	1.83 ± 0.10	0.48 ± 0.33
224	fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA.	NM_005103	TGCAGATGCTGACAAACATTCTCTTTGCCATGAAGGAGGATAATGAGAAGGTGCCTACTTTGCTAACGGACTACATTTTA	2.43 ± 0.24	1.64 ± 0.19	1.74 ± 0.03	0.79 ± 0.29
225	platelet-derived growth factor alpha polypeptide (PDGFA), transcript variant 1, mRNA.	NM_002607	TTAATGTGACATCAAAGCAAGTATTGTAGCACTCGGTGAAGCAGTAAGAAGCTTCCTTGTCAAAAAGAGAGAGAGAGAGA	2.54 ± 0.55	1.99 ± 0.31	2.18 ± 0.35	0.23 ± 0.28
226	calcium channel, voltage-dependent, gamma subunit 7 (CACNG7), mRNA.	NM_031896	CAACGACGAGGTCATGAACAGGCCCAGCAGCTCTGAGCAGTATTTTCATTATCGCTACGGGTGGTCTTTTGCCTTCGCCG	2.58 ± 0.55	1.79 ± 0.14	2.02 ± 0.09	0.30 ± 0.36
227	cDNA FLJ45163 fis, clone BRAWH3044122, highly similar to Rattus norvegicus Munc13-1 (Unc13h1).	AK127106	AGAGGGAACCTCTTGAGAAAACATGGCAAGGGATTAGAAAAGGGCAGGGTGAAATTGCCAAGCCACTCAGACGGAACCCA	2.59 ± 0.17	2.42 ± 0.13	1.87 ± 0.10	-0.06 ± 0.07
228	cDNA FLJ16606 fis, clone TESTI4010095, highly similar to Retrovirus-related POL polyprotein.	AK122924	CTCCAACAGGCATCATTGTTCAAAACACAGATCTTGTGGAGTGGTCCTTCCTTCCTCACAGTACGATTAAGACTTTTACA	2.10 ± 0.15	2.81 ± 0.39	1.93 ± 0.08	0.35 ± 0.04
229	transforming protein (FGF4) gene, complete cds; and unknown gene.	J02986	CTCTGTTTTTAGATCTGCCAAGACTGACCTTTGAACTTTCCTGTAGTCAATCTTCCTCGATCTACCAGATGGGAGAGACC	2.38 ± 0.28	2.80 ± 0.59	2.10 ± 0.93	0.26 ± 0.29
230	olfactomedin-like 3 (OLFML3), mRNA.	NM_020190	ATGTCCCAGAGAGAATGCTGAGGCTGCCTTTGTCATCTGTGGGACCCTCTATGTCGTCTATAACACCCGTCCTGCCAGTC	2.42 ± 0.25	2.13 ± 0.37	2.73 ± 0.38	0.79 ± 0.16
231	LOC347113 (LOC347113), mRNA.	XM_300022	ATCAATAGAATTAGCACAAGAAGAGCTTTGGCCGAACTCTTTAAAGCCAGAGAAAGGCAAAACGACGCTGACTGCCCCAA	2.47 ± 0.12	2.56 ± 0.12	2.64 ± 0.18	1.35 ± 0.14
232	cDNA FLJ12965 fis, clone NT2RP2005741.	AK023027	TCTCTCTGCCTCTTTGGTCTGAAGGACATTTTCCCATACTGTCAGCCATGGTTTTGGGTGCATGTTTTAAGATTGTCCAT	1.82 ± 0.19	2.10 ± 0.80	2.70 ± 0.76	0.24 ± 0.18
233	peroxiredoxin 4 (PRDX4), mRNA.	NM_006406	TCCTGTGGGTAGATCAGTGGATGAGACACTACGTTTGGTTCAAGCATTCCAGTACACTGACAAACACGGAGAAGTCTGCC	1.14 ± 0.12	1.31 ± 0.05	0.77 ± 0.07	0.11 ± 0.15
234	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), mRNA.	NM_005077	CCAGCCACTATGACAGTGATGGTGACAAAAGCGATGACAACTTAGTTGTGGATGTGTCTAATGAGGACCCTTCTTCTCCG	1.29 ± 0.21	1.35 ± 0.15	0.66 ± 0.17	0.26 ± 0.08
235	cDNA FLJ30806 fis, clone FEBRA2001334.	AK055368	ACACAGATCACAGCTCATTTCTCTAAGTGGAGCAGTTATCAAGAAACCCAAACACCAAAATTGCTACTCTTCACATTTAA	1.52 ± 0.12	1.46 ± 0.09	0.59 ± 0.13	0.11 ± 0.19
236	SERTA domain containing 3 (SERTAD3), transcript variant 1, mRNA.	NM_013368	CCTCACAACCTCTTCTGTGCCCCAGGTTCTTGGGAGTGGAATGAACTGGATCACATCATGGAAATCATTCTGGGGTCCTA	1.65 ± 0.28	1.48 ± 0.42	0.78 ± 0.10	0.16 ± 0.06
237	dermokine (ZD52F10), mRNA.	NM_033317	CAAGAACTACAATTACAACCAGCATGCGTATCCCACTGCCTATGGTGGGAAGTACTCAGTCAAGACCCCTGCAAAGGGGG	1.76 ± 0.23	1.51 ± 0.08	0.87 ± 0.15	0.40 ± 0.26

238	RING1 and YY1 binding protein (RYBP), mRNA.	NM_012234	ATCCTCCTAGTGAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAGCGAAACAAATCACACCTCAAGGCCC	1.26 ± 0.24	1.42 ± 0.26	1.03 ± 0.10	0.12 ± 0.23
239	WAP four-disulfide core domain 2 (WFDC2), transcript variant 1, mRNA.	NM_006103	TCGGGACTCTGTATTCCCTCTTGGGGTGACCACAGCTTCTCCCTTTCCCAACCAATAAAGTAACCACTTTCAGCAAAAAA	1.24 ± 0.06	1.37 ± 0.18	1.23 ± 0.27	0.12 ± 0.20
240	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA.	NM_005003	TTTATGAAAGACCTGGGCTTAGACAGTTTGGACCAAGTGGAGATTATCATGGCCATGGAAGACGAATTTGGGTTTGAAAT	1.53 ± 0.20	1.31 ± 0.25	1.16 ± 0.30	0.29 ± 0.24
241	unkempt-like (Drosophila) (UNKL), mRNA.	NM_024023	TGACTCTTGCCCGAGAGCCGCAGCTTCTGGTCGTTGGTGGTTGCCCCACACGGAACTGCTCAGGCCCAGCTGCAAGCCCC	1.33 ± 0.13	1.43 ± 0.15	1.21 ± 0.28	0.30 ± 0.23
242	LOC200074 (LOC200074), mRNA.	XM_117759	TCCAAGAGGCTCCAGGTTTCTCTGTGTGACATCTTAGATGACAGTTGCCCCAGGAAACTTTGTAGCAGGTCTGCTGGCCT	1.42 ± 0.28	1.17 ± 0.12	1.28 ± 0.25	0.21 ± 0.11
243	glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA.	NM_005110	AGGCTTATACCAGTCAGTTCATCTCTCTGGTGATGTTTGGTTTGATGATGTCTGAAGACCGAATTTCACTACAAAACAGG	1.79 ± 0.36	1.39 ± 0.14	1.50 ± 0.28	-0.12 ± 0.18
244	calcium channel, voltage-dependent, alpha 2/delta subunit 2 (CACNA2D2), mRNA.	NM_006030	ACACGTTTTCATTGCTCCCAGAGAGTACTGCAAGGACCTGAATGCCTCAGACAACAACACCGAGTTCCTGAAAAACTTTA	1.83 ± 0.18	1.62 ± 0.48	1.33 ± 0.17	-0.02 ± 0.26
245	serine/threonine kinase 6 (STK6), transcript variant 2, mRNA.	NM_003600	AGCATAATCCCAGCCAGAGGCCAATGCTCAGAGAAGTACTTGAACACCCCTGGATCACAGCAAATTCATCAAAACCATCA	0.89 ± 0.07	0.91 ± 0.17	0.88 ± 0.12	-0.37 ± 0.22
246	transketolase (Wernicke-Korsakoff syndrome) (TKT), mRNA.	NM_001064	TAACAACAATGAGGACTTCCAGGTCGGACAAGCCAAGGTGGTCCTGAAGAGCAAGGATGACCAGGTGACCGTTATCGGGG	0.88 ± 0.02	0.97 ± 0.03	1.15 ± 0.02	-0.29 ± 0.12
247	polycythemia rubra vera 1 (PRV1), mRNA.	NM_020406	GACCACCATTATGACACACGGAAACTTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGG	0.98 ± 0.24	0.78 ± 0.28	0.92 ± 0.18	-0.14 ± 0.26
248	cDNA FLJ14786 fis, clone NT2RP4000737, moderately similar to Mus musculus F-box protein FBL10 mRNA.	AK027692	TGTGAGCAGTTCATAGCCGAGATGTCTGTGAGTGTCCAGTTTGGGCAAGTAGAAGAAAAACTCCTGCAAAAACTGAGTTA	1.07 ± 0.17	0.92 ± 0.28	0.75 ± 0.14	-0.03 ± 0.27
249	glycine cleavage system protein H (aminomethyl carrier) (GCSH), mRNA.	NM_004483	TGGCTGATCAAGATGACACTGAGTAACCCTTCAGAACTAGATGAACTTATGAGTGAAGAAGCATATGAGAAATACATAAA	0.92 ± 0.23	0.83 ± 0.21	0.60 ± 0.14	-0.13 ± 0.29
250	mitochondrial ribosomal protein S15 (MRPS15), nuclear gene encoding mitochondrial protein, mRNA.	NM_031280	AGGCTCTGTGCATTCGGGTTTTCCAGGAGACTCAAAAGCTGAAGAAGCGAAGAAGAGCCTTAAAGGCTGCAGCAGCAGCC	1.09 ± 0.16	0.68 ± 0.17	0.59 ± 0.13	0.07 ± 0.23
251	cDNA FLJ90238 fis, clone NT2RM2000632, weakly similar to EXCISION REPAIR PROTEIN ERCC-6.	AK074719	TAAAGCGTGGAAAAGAACTAAAAGAGTGTGGAAAAATCCAGGAGGCCCTAAACTGCTTAGTTAAAGCGCTTGACATAAAA	1.10 ± 0.18	1.03 ± 0.33	0.73 ± 0.05	0.07 ± 0.28
252	protein phosphatase 1, regulatory (inhibitor) subunit 1A (PPP1R1A), mRNA.	NM_006741	AGAGGCAGTAAGGAACCCAGCACAAAAGAACCCTCAACCCATATACCACCACTGGATTCCAAGGGAGCCAACTCGGTCTG	1.22 ± 0.17	0.55 ± 0.09	1.02 ± 0.14	0.10 ± 0.14
253	MAD2 mitotic arrest deficient-like 2 (yeast) (MAD2L2), mRNA.	NM_006341	CAACATGGAGAAGATCCAGGTCATCAAGGATTTCCCCTGGATCCTGGCGGATGAGCAGGATGTCCACATGCATGACCCCC	0.94 ± 0.01	1.44 ± 0.14	1.15 ± 0.33	-0.34 ± 0.21
254	testis expressed sequence 15 (TEX15), mRNA.	NM_031271	CTTCCTAATCGATTTGTGCCTCCAGAAGTTCCTTGGGTTTATGCTCCATGGCACCAAGAATCCTTTCATCCAGGACACTG	0.99 ± 0.20	1.38 ± 0.09	0.76 ± 0.11	-0.18 ± 0.19
255	cystathionine-beta-synthase (CBS), mRNA.	NM_000071	TCCTGAGCGACAGGTGGATGCTGCAGAAGGGCTTTCTGAAGGAGGAGGACCTCACGGAGAAGAAGCCCTGGTGGTGGCAC	1.21 ± 0.13	0.97 ± 0.34	1.29 ± 0.43	-0.09 ± 0.05
256	vesicle docking protein p115 (VDP), mRNA.	NM_003715	CAGTAGCTGCCAGAAGGCTATGTTCCAGTGTGGGTTATTGCAGCAGCTTTGTACTATCCTAATGGCTACTGGGGTTCCTG	0.95 ± 0.10	1.17 ± 0.12	1.64 ± 0.41	-0.10 ± 0.05
257	potassium channel, subfamily K, member 12 (KCNK12), mRNA.	NM_022055	GTGTGCTGCATTTACTCGCTCTTCAACGTCATCTCCATCCTCATCAAGCAGGTGCTCAACTGGATGCTGCGCAAGCTGAG	1.44 ± 0.14	1.08 ± 0.23	1.17 ± 0.11	-0.42 ± 0.23
258	Homo sapiens cDNA, FLJ79037 complete cds, highly similar to Myosin-10.	AK316138	CAAAGAGTGCTGTTCTTGTTCTCTGGGTGGATTTTCCAAGATCACAACTAAACTGCTTGATTTTGTCCTGGGACTTTTTT	1.20 ± 0.26	1.33 ± 0.93	1.08 ± 0.54	-0.07 ± 0.11
259	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7 (EDG7), mRNA.	NM_012152	ATCTACTCCTACAAGGACGAGGACATGTATGGCACCATGAAGAAGATGATCTGCTGCTTCTCTCAGGAGAACCCAGAGAG	1.24 ± 0.24	1.67 ± 0.42	1.53 ± 0.10	-0.47 ± 0.08
260	LOC126921 (LOC126921), mRNA.	XM_059094	TGTTCCATGTAGTTCCTGTCTTCTTTCCTGCAACAACAGACACTTCTGGATGTTTCACAGCCAGGCAGTTTATGATATTA	0.97 ± 0.35	0.86 ± 0.46	1.85 ± 0.06	-0.47 ± 0.24
261	contactin associated protein-like 2 (CNTNAP2), mRNA.	NM_014141	TAAGAAATGGAGTCAACAGAAACTCGGCTATCATTGGAGGCGTCATTGCTGTGGTGATTTTCACCATCCTGTGCACCCTG	2.30 ± 0.44	1.78 ± 0.21	0.77 ± 0.21	-0.14 ± 0.17
262	hypothetical protein FLJ25801 (FLJ25801), mRNA.	NM_173553	ATCCCAAATGGAGACACAAGTCCAGACTCCCTCACCATCTTACAACATGGTCCTTCTTGTGATGCTACTGTTAGCCCTTA	2.28 ± 0.47	1.57 ± 0.51	0.74 ± 0.14	-0.10 ± 0.12
263	cDNA FLJ30432 fis, clone BRACE2008999.	AK054994	GGCAGCACAGACTATTTCTTGAGCAGTGGTGACAAGATTCGATTCTTCTTTGAGAAAGGCGTTTTTGATGAGAAAGGAAA	2.15 ± 0.33	1.26 ± 0.23	0.74 ± 0.21	0.43 ± 0.23
264	nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA.	NM_004289	TGAAGGTGCTATAGGTTATTGCACTGACCATGAATCTAGTTCCCATCATGACTTAGAAGGTGCTGTAGGTGGCTACTACC	2.14 ± 0.28	1.95 ± 0.55	1.39 ± 0.44	-0.58 ± 0.08
265	doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA.	NM_004734	GGGTCTTTGGACTACTACCAGCAACCAGGAATGTATTGGATAAGACCACCGCTCTTGATAAGGAGAGGCAGGTTTTCCGA	2.08 ± 0.30	2.09 ± 0.32	1.36 ± 0.99	-0.61 ± 0.07
266	cytochrome P450, family 2, subfamily S, polypeptide 1 (CYP2S1), mRNA.	NM_030622_(2)	TCCTGCTGAAGATGGCACAGGAGGAACAAAACCCAGGCACAGAATTCACCAACAAGAACATGCTGATGACAGTCATTTAT	1.51 ± 0.41	2.15 ± 0.31	1.46 ± 0.35	-0.76 ± 0.17
267	gamma-aminobutyric acid (GABA) A receptor, beta 3 (GABRB3), transcript variant 1, mRNA.	NM_000814	GGCCCTCAAAGGCAGAAGAAGCTTGCAGAAAAGACAGCCAAGGCAAAGAATGACCGTTCAAAGAGCGAAAGCAACCGGGT	1.46 ± 0.46	1.86 ± 0.13	1.02 ± 0.57	-0.52 ± 0.34
268	fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene) (FGF4), mRNA.	NM_002007	CCTTCTTCACCGATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACGAGTCCTACAAGTACCCC	1.85 ± 0.37	2.10 ± 1.08	1.08 ± 0.38	-0.13 ± 0.30
269	cytochrome P450, family 2, subfamily S, polypeptide 1 (CYP2S1), mRNA.	NM_030622	TTCAAGCACCCAGAAGAGTTCAACCCAGACCGTTTCCTGGATGCAGATGGACGGTTCAGGAAGCATGAGGCGTTCCTGCC	1.97 ± 0.22	2.49 ± 0.15	2.01 ± 0.11	-0.87 ± 0.22
270	homeo box (expressed in ES cells) 1 (HESX1), mRNA.	NM_003865	GAATCCAGATTTGGTTTCAAAATCGGCGTGCAAAACTGAAAAGGTCCCATAGAGAATCACAGTTTCTAATGGCGAAAAAA	3.60 ± 0.81	2.16 ± 1.51	0.33 ± 0.47	0.12 ± 0.29
271	chromosome 10 open reading frame 13 (C10orf13), mRNA.	NM_152429	AACGCGGAGCTCACGGAGACCTACTGCGCTGAGAAGTGGCACTCCCTCTGCAACTTCTTTGTCAATTTCTGGAACGGCTG	3.22 ± 0.46	1.51 ± 0.20	0.93 ± 0.16	1.10 ± 0.35
272	cDNA FLJ32721 fis, clone TESTI2000850.	AK057283	CGTGGAAATCTATCCTCAAGGAAATAACTTCTCAGTGTTCCATCTGCTATTCTACTGCTCCTCAGGGATTATTCAGGCCC	1.63 ± 0.88	2.04 ± 0.19	1.44 ± 0.22	-2.73 ± 0.30
273	paternally expressed 3 (PEG3), mRNA.	NM_006210	CACAGCATTCAGTGAACACCTGAAAACTCATGCCAGCATGATCATATTTGAGCCTGCAAATGCCTTTGGGGAGTGCTCAG	0.40 ± 0.14	1.38 ± 0.48	1.31 ± 0.29	2.12 ± 0.06
274	myo-inositol 1-phosphate synthase A1 (ISYNA1), mRNA.	NM_016368	TGCAGTTCCGCTCTAAGGAGGTGTCCAAGAGCAACGTGGTGGACGACATGGTGCAGAGCAACCCAGTGCTCTATACGCCC	0.60 ± 0.27	1.40 ± 0.41	1.73 ± 0.36	2.12 ± 0.28
275	cDNA FLJ30617 fis, clone CTONG2001366, weakly similar to GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3).	AK055179	GAAGTTTCAGAGCCTCACTCATACAGGTAAAGGTCACCATCTTTCATTCTCACCGCAGAGTCAAAATGGCCGAGCACCCC	0.74 ± 0.16	1.08 ± 0.11	1.33 ± 0.13	2.37 ± 0.37
276	mRNA for KIAA1548 protein, partial cds.	AB046768	ATTGTTCCGAGTGGTGCCATGTCTAATGGACTTGCGGGATGTGAAATGCTTTTGACAGGGAAGGAGGGACATGGTAATAA	0.67 ± 0.27	0.65 ± 0.35	1.20 ± 0.33	2.14 ± 0.17

277	similar to dopamine-beta-hydroxylase (LOC254733), mRNA.	XM_172636	TGTGTAGGACGGAGAAGTTTGAGGAGATGAATGGAGCTCCTATGCCTGACATACAGGTGTATGGCTACCTGCTGCACACC	0.73 ± 0.15	1.14 ± 0.27	1.52 ± 0.31	1.73 ± 0.21
278	cDNA FLJ45187 fis, clone BRAWH3048548.	AK127130	AATTTGAAATCAGCTAGAAGCCCTCGTCCTACAGGTAAAACTGAGACAAATGAAGGAACACTGGATGATTTTACAGTTAT	0.33 ± 0.12	1.05 ± 0.43	1.71 ± 0.49	2.03 ± 0.09
279	cutaneous T-cell lymphoma-associated tumor antigen se20-4 (SE20-4), mRNA.	NM_022117	AAGTGAAGATGTCTGGGAAGAAGGGGAAGATTCGGACGACTCTGACCTAGAGGATGTGCTTCAGGTCCCAAACGGTTGGG	0.40 ± 0.04	1.58 ± 0.37	1.95 ± 0.36	1.82 ± 0.18
280	multimerin 2 (MMRN2), mRNA.	NM_024756	CCTGCAGACAGTGAAGTTCAACACCACATACATCAACATTGGCAGCAGCTACTTCCCTGAACATGGCTACTTCCGAGCCC	0.08 ± 0.07	1.91 ± 0.16	1.77 ± 0.25	1.40 ± 0.23
281	claudin 2 (CLDN2), mRNA.	NM_020384	CTCATCCCAGAGAAATCGCTCCAACTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTG	0.03 ± 0.20	1.17 ± 0.24	1.52 ± 0.54	1.97 ± 0.29
282	cDNA FLJ10720 fis, clone NT2RP3001116.	AK001582	CTAGGCAAGTTCCTGTCTCCATCTCTTGATTCTGAATTCAGCCATAATACTTGCTCTCCCCAATGTTGTTTTAGCAGATT	-0.05 ± 0.25	0.70 ± 0.66	2.43 ± 0.66	1.86 ± 0.33
283	matrix metalloproteinase 11 (stromelysin 3) (MMP11), mRNA.	NM_005940	TCTTCCCCAAGACTCACCGAGAAGGGGATGTCCACTTCGACTATGATGAGACCTGGACTATCGGGGATGACCAGGGCACA	-0.13 ± 0.16	0.68 ± 0.58	1.94 ± 0.27	1.75 ± 0.36
284	cDNA: FLJ21027 fis, clone CAE07110	AK024680	GTTCGTTTCATCCTCCCGAAAGAACGGTGCTCTCCCACTCTTACTCTATTTCAAAGAGCTACTCTGTCTCAACCACAGCA	0.06 ± 0.06	1.18 ± 0.73	1.96 ± 0.75	1.42 ± 0.26
285	REC8-like 1 (yeast) (REC8L1), mRNA.	NM_005132	CCTGCTCCTGGTGCTCTCAGCGCAACAGATTCTTCACGTGAAACAAGAAAAGCCATATGGTCGCCTCCTGATCCAGCCGG	-0.67 ± 0.19	1.16 ± 0.16	1.98 ± 0.18	1.88 ± 0.11
286	inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA.	NM_030569	GTCCCAGTGGTCTGGAAGCAAAGGAAGATTTACAACGGGGAAGAGCAGATAGACTGCTGGTTTGCCAGGAACAATGCCGC	-0.07 ± 0.23	1.60 ± 0.40	2.53 ± 0.16	2.43 ± 0.12
287	neuropilin 2 (NRP2), transcript variant 2, mRNA.	NM_003872	CAGGGAAACACAGAATGGCTACTACGTCAAATCCTACAAGCTGGAAGTCAGCACTAATGGAGAGGACTGGATGGTGTACC	0.32 ± 0.19	1.63 ± 0.48	2.88 ± 0.22	2.28 ± 0.39
288	PBX/knotted 1 homeobox 2 (PKNOX2), mRNA.	NM_022062	CCATGACAACCGTCAACTCACAAGTTGTGTCAGGTGGAGCCTTATACCAACCGGTTACCATGGTAACCTCCCAGGGTCAG	1.05 ± 0.25	1.94 ± 0.24	2.21 ± 0.20	2.35 ± 0.11
289	cDNA FLJ36189 fis, clone TESTI2027238.	AK093508	AGATCATCTCTCAAAAAGCTCCCATCAGAGCAACCATTCTGGGACTTTGAGCAGAATGCTTAAGGCAGTGGTTCTAAAAT	0.73 ± 0.10	1.68 ± 0.19	2.51 ± 0.33	1.86 ± 0.22
290	hypothetical protein MGC24039 (MGC24039), mRNA.	NM_144973	CAGATTCTAGATAATGAAGATGATGTCCTTATTCAGAAATCATCCTGCAAAACCTTCTGCCACTACGTAAATGCTATTAA	0.62 ± 0.41	0.63 ± 0.53	0.93 ± 0.52	2.40 ± 0.42
291	carboxypeptidase, vitellogenic-like (CPVL), transcript variant 1, mRNA.	NM_031311	TACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTAT	0.51 ± 0.23	0.74 ± 0.50	0.70 ± 0.36	1.90 ± 0.32
292	similar to sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) C; ST6GalNAc III (LOC253929), mRNA.	XM_171293	CTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGCTGGTTTGGATACCATTCGCCTACACATACAGGCGTCCCCTTCGAACT	0.82 ± 0.13	0.66 ± 0.12	0.57 ± 0.28	1.96 ± 0.15
293	cDNA FLJ38831 fis, clone MESAN1000126, weakly similar to Drosophila melanogaster Crossveinless 2 (CV-2) mRNA.	AK096150	GATACCTGTGGTCCGGGATGTATCAAGACCTGTGACAACTGGAATGAAATTGGTCCATGCAACAAGCCGTGCGTTGCTGG	0.20 ± 0.19	0.58 ± 0.39	0.23 ± 0.45	2.12 ± 0.17
294	hydroxyacylglutathione hydrolase-like (HAGHL), transcript variant 2, mRNA.	NM_032304	AGGATGACGTGCCCACTGTGCCGTCGACTCTGGGCGAGGAGCGCCTCTACAACCCCTTCCTGCGGGTGGCAGAGGAGCCG	0.07 ± 0.13	-0.11 ± 0.05	0.60 ± 0.16	2.48 ± 0.36
295	cDNA FLJ14024 fis, clone HEMBA1003646, highly similar to Homo sapiens mRNA for KIAA1013 protein.	AK024086	AACCAGCTGGAAGACAACCTGGAGAGTAGTGAGCAGAGACTCTTTTGGCATGAAGATTCAAAGCCTGGAACATTAGTCTG	0.18 ± 0.17	0.49 ± 0.25	1.09 ± 0.60	2.23 ± 0.29
296	likely ortholog of mouse semaF cytoplasmic domain associated protein 3 (SEMACAP3), mRNA.	XM_041363	CCATAGTGGTGCAGGTGTTGAGAAGAACACCAAGGACCAAAATGTTCACGCCTCCATCAGAGTCTCAGCTGGTGGACACG	0.59 ± 0.03	0.55 ± 0.20	1.19 ± 0.64	3.07 ± 0.31
297	cDNA FLJ38279 fis, clone FCBBF3005444.	AK095598	TCCCTTATCCGAATTCTGCAGACCATTCAGGACTTCACCATAGTCCTAGAAGGATCACTCATCAAAGGAGTGGATGTGTA	0.83 ± 0.22	1.04 ± 0.32	1.18 ± 0.33	2.81 ± 0.14
298	cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA.	NM_004932	GTGAAAAAGCAAAGGCAGATCAGTTGATTCAGACCCTGCATGCTGTTGACAAGGATGACCCTTATAGTGGACACCAATTT	0.95 ± 0.38	1.30 ± 0.68	0.43 ± 0.20	2.98 ± 0.09
299	hypothetical protein LOC349136 (LOC349136), mRNA.	NM_198285	TTGCCAACAACCAGCTCTTCAGCAGCTCCTATGACCGGACAGCTCGGGTCTGGAGTGTGGACAAGGGGCAGATGTCCCGG	0.51 ± 0.20	1.15 ± 0.26	1.04 ± 1.63	2.80 ± 0.32
300	similar to hypothetical protein PRO2605 (LOC257481), mRNA.	XM_028192	GCTCACACTCACGCACACTCGTACTGAGACTCAAGGCCGTCTCCACAACTCCAACCAGTGCAAATGACTTAGTGCAAATT	-0.06 ± 0.02	-0.04 ± 0.14	1.26 ± 0.67	4.27 ± 0.45
301	cDNA FLJ31749 fis, clone NT2RI2007386.	AK056311	AGAGACCCAGATATGGAGTGAAACTGAAGGCAAGCTGGGGATGCCGAGAAAGGCCAGAGCTGAGGCTGGAAAGGAGGGGC	0.29 ± 0.18	0.54 ± 0.07	1.73 ± 0.62	4.00 ± 0.60
302	paired box gene 6 (aniridia, keratitis) (PAX6), mRNA.	NM_000280	AGCAACACACCTAGTCATATTCCTATCAGCAGTAGTTTCAGCACCAGTGTCTACCAACCAATTCCACAACCCACCACACC	-0.31 ± 0.39	0.36 ± 0.71	2.00 ± 0.71	3.50 ± 0.17
303	hypothetical protein FLJ30634 (FLJ30634), mRNA.	NM_153014	CAAAGTCTATCCAGCTTCGCTTCGTTTCATTGATCTGCACAAGAGACAATGCTCTGGAAAAGGAAGAGGACCCCAGAAGG	0.06 ± 0.19	0.61 ± 0.38	0.72 ± 0.48	3.56 ± 0.47
304	homeo box A2 (HOXA2), mRNA.	NM_006735	CCCGTAGATATTTCAGCTGACAGCTTAGACTTTTTTACAGACACACTCACCACAATCGACTTGCAGCATCTGAATTACTA	0.03 ± 0.08	0.53 ± 0.03	1.36 ± 0.04	3.09 ± 0.54
305	cDNA FLJ36498 fis, clone THYMU2019054.	AK093817	CTTCGACCAGAGGAAGAGGAGCAGAGAAAACAGGGAAGGAGAATTCAGGGAAGTGGGGAAAATCGAGGGAGCAGCAGCGT	-0.15 ± 0.31	0.17 ± 0.06	1.20 ± 0.61	3.39 ± 0.27
306	LOC347397 (LOC347397), mRNA.	XM_298005	GGATACTCAAGTGCTTTATGAACTATGGGGATGCCAGAACCAACTGAGGATTTCTGAGAAGAATGAACAAGAAAAGGAAA	0.03 ± 0.13	-0.17 ± 0.38	0.59 ± 0.58	3.43 ± 0.28
307	neurofilament 3 (150kDa medium) (NEF3), mRNA.	NM_005382	AAATCACCAGTGGAAGAGAAAGCCAAATCTCCTGTGCCAAAATCACCAGTGGAAGAGGCAAAGTCAAAAGCAGAAGTGGG	0.71 ± 0.34	1.22 ± 0.43	1.16 ± 0.10	3.82 ± 0.38
308	cDNA FLJ31855 fis, clone NT2RP7000926.	AK056417	TCTCTTCAATGGCTAAGTAAAAAGAAGACGGGTGAAATGGCGACACCAATCTTCCAGGGTTCCTTCTCTCCAAGCGCCAG	0.45 ± 0.11	0.80 ± 0.15	1.93 ± 0.54	3.45 ± 0.40
309	cDNA FLJ32062 fis, clone OCBBF1000042.	AK056624	ATTTGGGCCAGTTCCTTTAGGAAAACAGCAAAGTCCCATCCCAAGTTAGGGACTGAGATTTCACAGCCTCTCAGTCTGCG	0.56 ± 0.15	2.19 ± 0.20	1.62 ± 0.27	3.33 ± 0.26
310	protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA.	NM_002839	TAGAAACTTGTATGCCTACATTCAGAAGCTGACACAAATAGAAACGGGAGAGAATGTCACAGGAATGGAGCTCGAATTTA	1.28 ± 0.11	1.82 ± 0.52	1.98 ± 0.57	3.40 ± 0.11
311	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary) (SERPING1), mRNA.	NM_000062	CCTGCTGGTCTTTGAAGTGCAGCAGCCCTTCCTCTTCGTGCTCTGGGACCAGCAGCACAAGTTCCCTGTCTTCATGGGGC	1.83 ± 0.23	1.86 ± 0.15	2.15 ± 0.27	3.39 ± 0.13
312	plakophilin 2 (PKP2), mRNA.	NM_004572	AAGGATGTATCTGTCCTTGATCGCCAAAAGTGTCCGCAACTACACACAAGAAGCATCCTTAGGAGCTCTGCAGAACCTCA	1.13 ± 0.35	2.33 ± 0.59	2.88 ± 0.14	3.09 ± 0.07
313	erythrocyte membrane protein band 4.1 like 5 (EPB41L5), mRNA.	NM_020909	GCCGACAGTGGTTCTGTTCTAAAGGAAGCTACAGATGAATTGGATGCCTTGCTTGCATCTCTAACTGAGAATCTAATTGA	1.60 ± 0.20	0.96 ± 0.27	1.52 ± 0.09	2.68 ± 0.27
314	src family associated phosphoprotein 2 (SCAP2), mRNA.	NM_003930	GAAGAAGAAGAGGACAGTGCTCCAGTGAAAGTGGAAGAACAAAGGAAGATGAGTCAGGATAGTGTCCATCACACCTCAGG	-1.82 ± 0.38	1.32 ± 0.03	2.30 ± 0.20	1.79 ± 0.37
315	hypothetical protein FLJ14299 (FLJ14299), mRNA.	NM_025069	TCGCTGTCCTTGCGGAATCCACACACTTTGGGCCTAAGCCGGTACCACCCCTATGGCAAGAGCCACTTATCCACAGCGGG	-0.81 ± 0.49	1.81 ± 0.40	3.59 ± 0.05	2.58 ± 0.36

316	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA.	NM_006379_(2)	TAACATTTGATGAACTTCGAGAAACCAAGACCTCTGAATACTTCAGCCTTTCCCACCATCCTTTAGACTACAGGATTTTA	-2.34 ± 0.66	-2.64 ± 0.28	-1.97 ± 0.12	1.49 ± 0.14
317	annexin A4 (ANXA4), mRNA.	NM_001153	TCTCTGTACTCGTTCATCAAGGGTGACACATCTGGAGACTACAGGAAAGTACTGCTTGTTCTCTGTGGAGGAGATGATTA	-2.16 ± 0.16	-2.55 ± 0.13	-2.10 ± 0.14	1.47 ± 0.30
318	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA.	NM_006379	AAGTCTCCGCAGGCATCTATCAAGTGGCTGTTACAGAAAGACAAAGACAGGAGGAAAGAGGTTAAGCTGAATGAACGAAT	-2.86 ± 0.27	-2.92 ± 0.66	-2.45 ± 0.36	0.89 ± 0.18
319	homeo box C4 (HOXC4), transcript variant 1, mRNA.	NM_014620_(2)	TCCTGGAATTAGAGAAAGAGTTTCATTACAACCGCTACCTGACCCGAAGGAGAAGGATCGAGATCGCCCACTCGCTGTGC	-2.37 ± 0.50	-1.84 ± 0.06	-0.57 ± 0.27	1.56 ± 0.34
320	thioredoxin interacting protein (TXNIP), mRNA.	NM_006472	CAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCATGCCACCACCGACTTATACTGAGGTGGATCCCTGCAT	-2.63 ± 0.29	-2.45 ± 0.05	-1.11 ± 0.50	0.71 ± 0.38
321	oligodendrocyte transcription factor 3 (OLIG3), mRNA.	NM_175747	CTGCTCGCCAGAAACTACATCCTCATGCTCACCAGCTCCCTGGAGGAGATGAAGAGGCTGGTTGGCGAGATCTATGGGGG	-1.93 ± 0.04	-1.75 ± 0.10	-2.02 ± 0.08	0.25 ± 0.17
322	polo-like kinase 2 (Drosophila) (PLK2), mRNA.	NM_006622	CACTCCGGACAGACTGTCTTCTAGCTGTTGTCATACAGTTCCAGATTTCCACTTATCAAGCCCAGCTAAGAATTTCTTTA	-2.12 ± 0.21	-1.75 ± 0.34	-1.79 ± 0.12	-0.58 ± 0.26
323	muscleblind-like 2 (Drosophila) (MBNL2), transcript variant 3, mRNA.	NM_207304	GGCTCAACTGCAACTCAGAAACTTCTCAGGACTGACAAACTGGAGGTATGCAGGGAGTTCCAGCGAGGAAACTGTGCCCG	-2.64 ± 0.09	-2.41 ± 0.34	-2.14 ± 0.24	-0.84 ± 0.28
324	integrin, alpha 1 (ITGA1), mRNA.	NM_181501_(2)	GTCTATAAGTGTCCAGTTGGGAGAGGTGAATCATTACCTTGTGTAAAGTTGGATCTACCAGTTAATACATCAATTCCCAA	-2.28 ± 0.10	-2.08 ± 0.29	-2.06 ± 0.23	-1.05 ± 0.27
325	FXYD domain containing ion transport regulator 5 (FXYD5), transcript variant 2, mRNA.	NM_014164	CACAAGAGCACCAAAGCAGCTCATCCCACTGATGACACCACGACGCTCTCTGAGAGACCATCCCCAAGCACAGACGTCCA	-1.31 ± 0.13	-1.79 ± 0.08	-1.47 ± 0.03	-3.15 ± 0.19
326	muscleblind-like (Drosophila) (MBNL1), transcript variant 1, mRNA.	NM_021038	GTATTTTCCAATACCAACAGGCTCTAGCCAACATGCAGTTACAACAGCATACAGCATTTCTCCCACCAGTTCCCATGGTG	-3.30 ± 0.23	-3.03 ± 0.11	-3.36 ± 0.25	-1.90 ± 0.21
327	hypothetical protein FLJ10652 (FLJ10652), mRNA.	NM_018169	GTTAATTCAAGACTCTCGAAGAGAAGCTTCAGTGCAGATGGATTTGAGATGCTACAAAACCCAGTAAAAGATTCAAAAGA	2.39 ± 0.35	2.74 ± 0.09	3.66 ± 0.15	4.07 ± 0.21
328	midkine (neurite growth-promoting factor 2) (MDK), mRNA.	NM_002391	AGATGTGACCCACCAGTGCCTTCTGTCTGCTCGTTAGCTTTAATCAATCATGCCCTGCCTTGTCCCTCTCACTCCCCAGC	2.43 ± 0.24	2.92 ± 0.32	3.59 ± 0.40	3.67 ± 0.24
329	retinol binding protein 1, cellular (RBP1), mRNA.	NM_002899	ACTTCCAAGTTGGGAAGGAGTTTGAGGAGGATCTGACAGGCATAGATGACCGCAAGTGCATGACAACAGTGAGCTGGGAC	1.15 ± 0.31	3.30 ± 0.56	4.15 ± 0.42	5.66 ± 0.12
330	homeo box A1 (HOXA1), transcript variant 1, mRNA.	NM_005522	AGACTTTTGACTGGATGAAAGTCAAAAGAAACCCTCCCAAAACAGGGAAAGTTGGAGAGTACGGCTACCTGGGTCAACCC	-0.58 ± 0.78	5.20 ± 0.11	5.72 ± 0.21	3.80 ± 0.54
331	cDNA FLJ12777 fis, clone NT2RP2001720.	AK022839	TCTCTCCTGGCCTCTTTTCTGGGGCATCCTGGGTGGAGTGTTTTTCTTGGGATCACGAGCTTGCACTCGCACACAGGCCC	-0.38 ± 0.03	3.69 ± 0.38	5.16 ± 0.59	3.06 ± 0.44
332	cellular retinoic acid binding protein 2 (CRABP2), mRNA.	NM_001878	AGGTTGGGGAGGAGTTTGAGGAGCAGACTGTGGATGGGAGGCCCTGTAAGAGCCTGGTGAAATGGGAGAGTGAGAATAAA	1.49 ± 0.38	4.31 ± 0.27	5.19 ± 0.11	3.38 ± 0.28
333	cDNA FLJ30295 fis, clone BRACE2003097.	AK054857	TGGGCCACTCTATCCATGTCTTTGATTTTTCCTGCTTTCTTGAAGATTTCTTCAACTTTATCTTCCAGCTCTACTATTAA	3.52 ± 0.54	3.34 ± 0.47	2.53 ± 0.36	1.17 ± 0.21
334	LOC347342 (LOC347342), mRNA.	XM_297978	GCTTTGAGGATGATAGGACTGCAATGCAACAGAGGCGAGTTTCCAGACCTGAGCCACTTTCAGACCCAGAGCGCATTAAT	3.18 ± 0.23	3.25 ± 0.27	2.72 ± 0.13	1.10 ± 0.29
335	Homo sapiens cDNA FLJ56390 complete cds, highly similar to Metastasis suppressor protein 1.	AK302036	TGAGAAGGCAAGTCATGAAGAGTTGCCCCAGGACATTTTCCTTGTCAGGAATAAGCCAGGCTAAATGTGCCCTTTGGGCA	3.48 ± 0.03	3.34 ± 0.56	3.27 ± 0.15	1.11 ± 0.35
336	POU domain, class 5, transcription factor 1 (POU5F1), transcript variant 1, mRNA.	NM_002701	TCCAGTCCCAGGACATCAAAGCTCTGCAGAAAGAACTCGAGCAATTTGCCAAGCTCCTGAAGCAGAAGAGGATCACCCTG	4.32 ± 0.94	4.32 ± 0.66	3.43 ± 0.96	-0.04 ± 0.42
337	podocalyxin-like (PODXL), mRNA.	NM_005397	TGGAGAATGGTTACCATGACAACCCAACACTGGAAGTGATGGAGACCTCTTCTGAGATGCAGGAGAAGAAGGTGGTCAGC	4.26 ± 0.45	4.65 ± 0.13	4.33 ± 0.17	1.58 ± 0.16
338	unnamed HERV-H protein mRNA, complete cds.	U92817	TCCCCTGTGATTTGAAGGTATATGCCCAGGTGGCCTGAAGTAACCGAAGAATCGCAAAAGAAGTGAAAATGCGCTGCCCC	2.90 ± 0.66	3.16 ± 0.19	2.60 ± 0.32	-1.19 ± 0.13
339	DNA (cytosine-5-)-methyltransferase 3 beta (DNMT3B), transcript variant 1, mRNA.	NM_006892	AATAACCACCAAGTCGAACTCGATCAAACAGGGGAAAAACCAACTTTTCCCTGTTGTCATGAATGGCAAAGAAGATGTTT	3.23 ± 0.46	3.25 ± 0.69	2.37 ± 0.43	-0.61 ± 0.17
340	cDNA FLJ41566 fis, clone CTONG2001513.	AK123560	AAACCCTCTAGCTTGGAAATGAATATGCTGCACTTTACAACCACTGCACTACCTGACTCAGGAATCGGCTCTGGAAGGTG	-4.26 ± 0.22	-1.44 ± 1.30	2.65 ± 1.33	5.87 ± 0.27

Supplementary Table 2. **Functional analysis of selected 358 genes identified in this study.**

Genome locus position: used data are taken from the FLJ Human cDNA Database ver. 3.0 (http://flj.lifesciencedb.jp) [11].
Multiple: gene producing multiple protein-coding transcripts by AS.
Single: gene producing a single protein-coding transcript.
Alt. N-term: gene producing multiple protein-coding transcripts as a result of alternative splicing of N-terminus.
Alt. C-term: gene producing multiple protein-coding transcripts as a result of alternative splicing of C-terminus.

Information of probe by DNA microarray	Information of cDNA	Information of genome locus			
Probe ID	cDNA which used to identify genome locus	Genome locus position	Gene symbol	Type of protein-coding transcript	Variation type by AS
XM_086262	NM_173795.2	chr1+347		Multiple	
NM_001803	NM_001803.2	chr1+1627	CD52	Single	
NM_015023	NM_015023.2	chr1+1696	WDTC1	Multiple	Alt. N-term
NM_032756	NM_032756.2	chr1+2800	GLOXD1	Single	
NM_006004	NM_006004.1	chr1+2857	UQCRH	Multiple	
XM_059109	NM_032437.1	chr1+3638	EFCAB7	Multiple	
NM_152487	NM_152487.1	chr1+4869	TMEM56	Single	
NM_020190	NM_020190.2	chr1+5543	OLFML3	Multiple	
NM_006472	NM_006472.1	chr1+6069	TXNIP	Multiple	Alt. N-term
NM_153713	NM_153713.1	chr1+6072	LIX1L	Multiple	Alt. N-term
NM_005531	NM_005531.1	chr1+7034	IFI16	Multiple	
XM_085255	BX647313.1	chr1+7332	PBX1	Multiple	
AK093508	FLJ36189/AK093508/C-TESTI2027238				
NM_001677	NM_001677.3	chr1+7606	ATP1B1	Multiple	Alt. N-term
NM_005562	NM_005562.1	chr1+7726	LAMC2	Multiple	
NM_002923	NM_002923.1	chr1+8540	RGS2	Single	
NM_004759	NM_004759.3	chr1+9230	MAPKAPK2	Multiple	Alt. C-term
NM_004619	NM_004619.3	chr1+9419	TRAF5	Multiple	
NM_013349	NM_013349.3	chr1+9484	NENF	Single	
NM_000254	NM_000254.1	chr1+10555	MTR	Multiple	
NM_000254_(2)					
NM_012341	NM_012341.2	chr10+50	GTPBP4	Multiple	Alt. N-term
NM_006561	NM_006561.2	chr10+380	CUGBP2	Multiple	Alt. N-term, Alt. C-term
AK055179	FLJ30617/AK055179/C-CTONG2001366	chr10+1039	KIAA1217	Multiple	
NM_020338	NM_020338.2	chr10+3132	RAI17	Multiple	Alt. N-term
XM_166091					
NM_003087	NM_003087.1	chr10+3455	SNCG	Multiple	
XM_170638	NM_017893.2	chr10+4212	SEMA4G	Multiple	
NM_183239	NM_183239.1	chr10+4479	GSTO2	Multiple	Alt. N-term, Alt. C-term
NM_025092	NM_025092.1	chr11+20	ATHL1	Multiple	Alt. N-term
NM_001124	NM_001124.1	chr11+594	ADM	Single	
NM_001124_(2)					
NM_006410	NM_006410.3	chr11+1062	HTATIP2	Single	
NM_130783	NM_130783.2	chr11+1732	TSPAN18	Multiple	
NM_005456	NM_005456.2	chr11+1792	MAPK8IP1	Multiple	Alt. N-term
NM_002391	NM_002391.3	chr11+1822	MDK	Single	
NM_000107	NM_000107.1	chr11+1904	DDB2	Multiple	Alt. N-term
NM_000062	NM_000062.2	chr11+2093	SERPING1	Multiple	
NM_015973	NM_015973.2	chr11+2351	GAL	Single	
NM_025080	NM_025080.2	chr11+2353	ASRGL1	Multiple	Alt. C-term
AK091429	FLJ34110/AK091429/C-FCBBF3008689	chr11+3323	SPCS2	Multiple	
NM_145018	NM_145018.2	chr11+3613	C11orf82	Multiple	Alt. N-term
AK074070	AK074070.1	chr11+4824	PHLDB1	Multiple	Alt. N-term, Alt. C-term
NM_022062	NM_022062.1	chr11+5199	PKNOX2	Multiple	
NM_013264	NM_013264.2	chr11+5238	DDX25	Multiple	Alt. C-term
NM_001769	NM_001769.2	chr12+409	CD9	Multiple	Alt. C-term
NM_019858	NM_019858.1	chr12+478	GPR162	Multiple	
NM_001423	NM_001423.1	chr12+927	EMP1	Multiple	
NM_018169	NM_018169.2	chr12+1677	C12orf35	Multiple	Alt. N-term
NM_017842	NM_017842.1	chr12+2101	SLC48A1	Multiple	
NM_024056	NM_024056.2	chr12+2121	TMEM106C	Multiple	
NM_173860	NM_173860.1	chr12+2548	HOXC12	Single	
NM_014620_(2)	NM_014620.2	chr12+2551	HOXC4	Single	
AK056417	FLJ31855/AK056417/C-NT2RP7000926				
NM_004990	NM_004990.2	chr12+2810	MARS	Multiple	
NM_004984	NM_004984.2	chr12+2816	KIF5A	Multiple	
NM_003877	NM_003877.3	chr12+3995	SOCS2	Multiple	
NM_207376	NM_207376.1	chr12+4553	C12orf75	Single	
AK056924	FLJ32362/AK056924/C-PUAEN1000057	chr12+5525	TCTN2	Multiple	Alt. N-term
NM_018647	NM_018647.2	chr13+187	TNFRSF19	Multiple	Alt. C-term
NM_207304	NM_207304.1	chr13+2300	MBNL2	Multiple	

NM_000270	NM_000270.1	chr14+93	NP	Multiple	
NM_005132	NM_005132.1	chr14+313	REC8L1	Single	
U92817	FLJ46607/AK128464/C-TKIDN2000319	chr14+1053	C14orf29	Multiple	Alt. C-term
NM_016651	NM_016651.4	chr14+1487	DACT1	Multiple	Alt. N-term
NM_031210	NM_031210.3	chr14+2718	C14orf156	Single	
AK295919	FLJ58489/AK295919/D-BRSSN2003639.1	chr14+3517	EVL	Multiple	Alt. N-term, Alt. C-term
AK122924	FLJ16606/AK122924/C-TESTI4010095	chr14+3952		Single	
NM_003710_(2)	NM_003710.3	chr15+849	SPINT1	Multiple	
NM_020990	NM_020990.3	chr15+1090	CKMT1B	Multiple	Alt. N-term, Alt. C-term
NM_006465	NM_006465.1	chr15+2805	ARID3B	Multiple	Alt. C-term
AK056589	FLJ32027/AK056589/C-NTONG1000246	chr15+2866	C15orf39	Multiple	Alt. N-term
NM_032304	NM_032304.2	chr16+118	HAGHL	Multiple	
AK310771	FLJ17813/AK310771/Z-TKIDN2018397-02	chr16+689	ABAT	Multiple	Alt. N-term
NM_002428	NM_002428.2	chr16+2773	MMP15	Multiple	Alt. N-term
NM_014427	NM_014427.3	chr16+4285	CPNE7	Multiple	
XM_085748	NM_015085.3	chr17+226	GARNL4	Multiple	
AK095929	FLJ38610/AK095929/C-HEART2005581	chr17+1915	UNC45B	Multiple	
XM_091459	XM_290799.5	chr17+2129	LOC162279	Multiple	
NM_003244	NM_003244.2	chr18+121	TGIF	Multiple	Alt. N-term
NM_003244_(2)					
AJ245649	NM_005257.3	chr18+771	GATA6	Single	
NM_005257					
NM_021127	NM_021127.1	chr18+1964	PMAIP1	Multiple	
NM_004240	NM_004240.2	chr19+554	TRIP10	Multiple	
AK094702	FLJ37383/AK094702/C-BRAMY2026168	chr19+1039		Single	
NM_032346	NM_032346.1	chr19+1945	PDCD2L	Single	
NM_014164	NM_014164.4	chr19+2013	FXYD5	Multiple	
NM_030622	NM_030622.6	chr19+2536	CYP2S1	Multiple	
NM_030622_(2)					
NM_020406	NM_020406.1	chr19+2680	CD177	Single	
NM_031896	NM_031896.3	chr19+3517	CACNG7	Multiple	Alt. C-term
NM_133180	NM_133180.1	chr19+3581	EPS8L1	Multiple	Alt. N-term
XM_059094	NM_207418.2	chr1_random+72	FAM72A	Single	
NM_024692	NM_024692.3	chr2+1074	RSNL2	Multiple	Alt. N-term, Alt. C-term
NM_030915	NM_030915.1	chr2+1106	LBH	Multiple	Alt. N-term
AK027304	FLJ14398/AK027304/C-HEMBA1003569	chr2+1656	MTA3	Multiple	Alt. C-term
NM_005413	NM_005413.1	chr2+1830	SIX3	Single	
NM_002354	NM_002354.1	chr2+2021	TACSTD1	Single	
NM_002354_(2)					
NM_002398	NM_002398.2	chr2+2756	MEIS1	Multiple	Alt. N-term, Alt. C-term
NM_001153	NM_001153.2	chr2+2923	ANXA4	Multiple	
NM_006636	NM_006636.2	chr2+3216	MTHFD2	Multiple	
NM_018234	NM_018234.2	chr2+4787	STEAP3	Multiple	Alt. N-term
NM_020909	NM_020909.2	chr2+4844	EPB41L5	Multiple	Alt. N-term, Alt. C-term
AB046768	AB046768.1				
NM_003872	NM_003872.2	chr2+7861	NRP2	Multiple	Alt. C-term
AK024680	FLJ21027/AK024680/C-CAE07110				
NM_152386	NM_152386.2	chr2+8552	SGPP2	Multiple	Alt. N-term
NM_004457	NM_004457.3	chr2+8571	ACSL3	Multiple	
NM_020311	NM_020311.1	chr2+9147	CMKOR1	Single	
NM_002110	NM_002110.2	chr20+1214	HCK	Multiple	
NM_006892	NM_006892.3	chr20+1291	DNMT3B	Multiple	Alt. N-term, Alt. C-term
NM_015568	NM_015568.2	chr20+1730	PPP1R16B	Multiple	
NM_006103	NM_006103.3	chr20+1992	WFDC2	Multiple	Alt. N-term, Alt. C-term
NM_000308	NM_000308.1	chr20+2019	PPGB	Multiple	
NM_005940	NM_005940.3	chr22+561	MMP11	Multiple	
NM_005318	NM_005318.2	chr22+1360	H1F0	Multiple	
XM_114205	NM_014508.2	chr22+1459	APOBEC3G	Multiple	
NM_021822	NM_021822.1				
NM_001675	NM_001675.2	chr22+1496	ATF4	Multiple	
NM_014583	NM_014583.2	chr3+213	LMCD1	Multiple	Alt. N-term, Alt. C-term
NM_014583_(2)					
NM_000965	NM_000965.2	chr3+1071	RARB	Multiple	Alt. N-term
NM_001457	NM_001457.1	chr3+2737	FLNB	Multiple	Alt. N-term
XM_031246	NM_002942.1	chr3+3406	ROBO2	Multiple	Alt. N-term
NM_000532	NM_000532.2	chr3+5364	PCCB	Multiple	Alt. N-term, Alt. C-term
NM_152616	NM_152616.3	chr3+5545	TRIM42	Single	
NM_004617	NM_004617.2	chr3+5836	TM4SF4	Single	
NM_021038	NM_021038.3	chr3+5982	MBNL1	Multiple	Alt. N-term
NM_022736	NM_022736.1	chr3+6221	MFSD1	Multiple	
XM_044461	NM_014988.1	chr4+1485	LIMCH1	Multiple	
AK027231	FLJ23578/AK027231/C-LNG12709				
NM_024592	NM_024592.1	chr4+1838	SRD5A2L	Single	
NM_006452	NM_006452.2	chr4+1909	PAICS	Multiple	Alt. N-term
NM_003715	NM_003715.1	chr4+2345	VDP	Multiple	Alt. N-term
XM_034353	AB040933.2	chr4+2480	FRAS1	Multiple	

NM_000582	NM_000582.2	chr4+2904	SPP1	Multiple	
NM_000582_(2)					
NM_001873	NM_001873.1	chr4+5132	CPE	Multiple	
NM_012304	NM_012304.3	chr5+492	FBXL7	Multiple	
NM_004932	NM_004932.2	chr5+729	CDH6	Multiple	Alt. C-term
M63180	NM_152295.3	chr5+831	TARS	Multiple	
NM_181501_(2)	NM_181501.1	chr5+1387	ITGA1	Multiple	
NM_006350_(2)	NM_006350.2	chr5+1428	FST	Multiple	Alt. C-term
XM_042066	XM_042066.9	chr5+1554		Single	
NM_004291	NM_004291.2	chr5+2296	CART	Single	
NM_003202	NM_003202.2	chr5+4291	TCF7	Multiple	Alt. N-term
NM_015288	NM_015288.4	chr5+4327	PHF15	Multiple	Alt. N-term
XM_087631	NM_153607.1	chr5+5946	C5orf41	Multiple	Alt. N-term
NM_002131	NM_002131.2	chr6+1712	HMGA1	Multiple	
NM_152753	NM_152753.2	chr6+1783	SCUBE3	Multiple	Alt. N-term
NM_000165	NM_000165.2	chr6+4505	GJA1	Multiple	
NM_020455	NM_020455.4	chr6+5194	GPR126	Multiple	Alt. N-term
XM_027307	NM_001029884.1	chr6+5636	PLEKHG1	Multiple	Alt. N-term
NM_015440	NM_015440.3	chr6+5674	MTHFD1L	Multiple	Alt. N-term
NM_025107	NM_025107.1	chr6+5788	MYCT1	Multiple	Alt. N-term
NM_005891	NM_005891.1	chr6+6187	ACAT2	Multiple	Alt. N-term
NM_020223	NM_020223.1	chr7+13	FAM20C	Single	
NM_004289	NM_004289.5	chr7+981	NFE2L3	Multiple	Alt. N-term
NM_004289_(2)					
AK022839	FLJ12777/AK022839/C-NT2RP2001720	chr7+1034		Single	
AK056230	FLJ31668/AK056230/C-NT2RI2004916	chr7+1037		Single	
NM_004067	NM_004067.1	chr7+1152	CHN2	Multiple	Alt. N-term
NM_133468	NM_133468.2	chr7+1417	CV-2	Single	
AK096150	FLJ38831/AK096150/C-MESAN1000126				
NM_012257	NM_012257.3	chr7+4516	HBP1	Multiple	Alt. N-term, Alt. C-term
NM_015641	NM_015641.2	chr7+4756	TES	Multiple	Alt. N-term, Alt. C-term
NM_002851	NM_002851.1	chr7+4948	PTPRZ1	Multiple	Alt. N-term
NM_014141	NM_014141.3	chr7+6071	CNTNAP2	Multiple	Alt. N-term
NM_004462	NM_004462.3	chr8+519	FDFT1	Multiple	Alt. N-term
NM_015359	NM_015359.1	chr8+903	SLC39A14	Multiple	Alt. C-term
NM_005382	NM_005382.1	chr8+1036	NEF3	Multiple	Alt. N-term
NM_025069	NM_025069.1	chr8+1493	ZNF703	Multiple	
NM_004095	NM_004095.2	chr8+1515	EIF4EBP1	Single	
NM_138455_(2)	NM_138455.2	chr8+3637	CTHRC1	Multiple	Alt. C-term
XM_057014					
NM_003383	NM_003383.3	chr9+147	VLDLR	Multiple	Alt. N-term
NM_012266	NM_012266.3	chr9+1120	DNAJB5	Multiple	Alt. N-term
NM_021154	NM_021154.3	chr9+2427	PSAT1	Multiple	
AK092811	FLJ35492/AK092811/C-SMINT2008672	chr9+3719	ZNF483	Multiple	Alt. C-term
NM_144965	NM_144965.1	chr9+4505	TTC16	Multiple	Alt. N-term, Alt. C-term
XM_026998	NM_019594.2	chr9+4615	LRRC8A	Multiple	
AK054994	FLJ30432/AK054994/C-BRACE2008999				
NM_006406	NM_006406.1	chrX+626	PRDX4	Multiple	
NM_022117	NM_022117.1	chrX+1311	TSPYL2	Multiple	
NM_014725_(2)	NM_014725.2	chrX+1507	STARD8	Single	
NM_020384	NM_020384.2	chrX+2197	CLDN2	Single	
NM_002764	NM_002764.2	chrX+2209	PRPS1	Multiple	
NM_005629	NM_005629.1	chrX+3156	SLC6A8	Multiple	Alt. N-term
NM_003240	NM_003240.2	chr1-1092	LEFTY2	Multiple	
AK092887	FLJ35568/AK092887/C-SPLEN2005727	chr1-1581		Single	
AK096673	FLJ39354/AK096673/C-PEBLM2002455	chr1-2028	PLEKHA6	Multiple	
AK092454	FLJ35135/AK092454/C-PLACE6009237				
XM_060678	NM_177402.3	chr1-2160	SYT2	Single	
NM_016946	NM_016946.3	chr1-3636	F11R	Multiple	Alt. N-term
NM_145167	NM_145167.1	chr1-3710	PIGM	Single	
NM_001878	NM_001878.2	chr1-3866	CRABP2	Single	
NM_000849	NM_000849.3	chr1-5470	GSTM3	Multiple	
AK000757	FLJ20750/AK000757/C-HEP05174	chr1-5508	SORT1	Multiple	Alt. N-term
NM_012152	NM_012152.1	chr1-6471	EDG7	Single	
NM_152697	NM_152697.2	chr1-6705	SLC44A5	Multiple	Alt. N-term, Alt. C-term
NM_002227	NM_002227.1	chr1-6996	JAK1	Multiple	
NM_181712	NM_181712.2	chr1-7103	ANKRD38	Multiple	
NM_024640	NM_024640.3	chr1-8365	YRDC	Multiple	Alt. N-term
NM_031280	NM_031280.2	chr1-8409	MRPS15	Multiple	Alt. N-term, Alt. C-term
NM_004427	NM_004427.2	chr1-8579	PHC2	Multiple	Alt. N-term
NM_003680	NM_003680.2	chr1-8621	YARS	Multiple	
NM_153756	NM_153756.1	chr1-8634	FNDC5	Multiple	Alt. C-term
XM_117759	NM_144569.3	chr1-8717	SPOCD1	Multiple	Alt. N-term
NM_145345	NM_145345.1	chr1-9045	UBXD5	Multiple	Alt. C-term
BC020630	BC020630.1	chr1-9447	CAMK2N1	Single	
NM_006341	NM_006341.2	chr1-9923	MAD2L2	Multiple	

AK302705	FLJ58712/AK302705/D-TESTI4023180.1	chr10-751	KIAA1598	Multiple	Alt. N-term
AK056469	FLJ31907/AK056469/C-NT2RP7004396	chr10-1113	SH3MD1	Multiple	Alt. N-term
NM_020992	NM_020992.2	chr10-1727	PDLIM1	Single	
NM_152429	NM_152429.2	chr10-1917	FGFBP3	Single	
NM_024756	NM_024756.1	chr10-2152	MMRN2	Multiple	
NM_032772	NM_032772.3	chr10-2555	ZNF503	Multiple	Alt. N-term
NM_000281	NM_000281.2	chr10-2857	PCBD1	Multiple	
AK303891	FLJ52649/AK303891/D-TRACH2007939.1	chr10-3574		Multiple	Alt. N-term, Alt. C-term
AK127130	FLJ45187/AK127130/C-BRAWH3048548	chr10-4690	C10orf140	Multiple	
NM_032817_(2)	NM_032817.2	chr10-5299	ITIH5	Multiple	Alt. N-term, Alt. C-term
NM_030569	NM_030569.3				
NM_016952	NM_016952.3	chr11-346	CDON	Multiple	
NM_005103	NM_005103.3	chr11-377	FEZ1	Multiple	Alt. C-term
NM_014333	NM_014333.2	chr11-923	IGSF4	Multiple	
NM_032379	NM_032379.3	chr11-1980	SYTL2	Multiple	Alt. N-term
NM_002576	NM_002576.3	chr11-2338	PAK1	Multiple	Alt. N-term
NM_006645	NM_006645.1	chr11-2653	STARD10	Multiple	Alt. N-term
NM_002007	NM_002007.1	chr11-2816	FGF4	Single	
NM_021975	NM_021975.2	chr11-3140	RELA	Multiple	Alt. C-term
AK292330	FLJ78749/AK292330/D-TESTI2028720.1	chr11-3386	WDR74	Multiple	Alt. N-term, Alt. C-term
AF142409	AF142409.1	chr11-3559	MS4A6A	Multiple	Alt. C-term
NM_000280	NM_000280.2	chr11-4397	PAX6	Multiple	
NM_001584	NM_001584.1	chr11-4449	MPPED2	Single	
NM_001751	NM_001751.4	chr11-5521	CARS	Multiple	Alt. N-term
NM_021805	NM_021805.1	chr11-5727	SIGIRR	Single	
NM_032590	NM_032590.3	chr12-598	FBXL10	Multiple	Alt. N-term
AK027692	FLJ14786/AK027692/C-NT2RP4000737				
NM_173813	NM_173813.2	chr12-1102	FLJ34154	Single	
AF174498	BC006270.2	chr12-1107	C12orf51	Multiple	
NM_001682	NM_001682.2	chr12-2191	ATP2B1	Multiple	Alt. N-term
NM_001946	NM_001946.2	chr12-2224	DUSP6	Multiple	
NM_023033	NM_023033.1	chr12-3078	METTL1	Multiple	
NM_006741	NM_006741.2	chr12-3315	PPP1R1A	Multiple	Alt. C-term
NM_175851	NM_175851.1	chr12-4000	ADAMTS20	Multiple	Alt. C-term
NM_004572	NM_004572.2	chr12-4171	PKP2	Multiple	Alt. N-term
NM_144973	NM_144973.2	chr12-4254	DENND5B	Multiple	Alt. N-term, Alt. C-term
AK095598	FLJ38279/AK095598/C-FCBBF3005444				
NM_001038	NM_001038.4	chr12-5512	SCNN1A	Multiple	Alt. N-term
NM_001845	NM_001845.3	chr13-260	COL4A1	Multiple	
NM_001845_(2)					
NM_004392	NM_004392.4	chr13-1136	DACH1	Multiple	Alt. N-term
NM_152720	NM_152720.1	chr13-1421	NEK3	Multiple	
NM_004734	NM_004734.2	chr13-2235	DCAMKL1	Multiple	Alt. N-term
NM_003045	NM_003045.3	chr13-2476	SLC7A1	Single	
AK022999	FLJ12937/AK022999/C-NT2RP2005020				
NM_006832	NM_006832.1	chr14-2423	PLEKHC1	Multiple	Alt. N-term
NM_002692	NM_002692.2	chr14-2679	POLE2	Multiple	
NM_020149	NM_020149.2	chr15-3549	MEIS2	Multiple	Alt. N-term
NM_000814	NM_000814.3	chr15-4088	GABRB3	Multiple	Alt. N-term
AF104032	NM_003486.5	chr16-199	SLC7A5	Single	
NM_004483	NM_004483.3	chr16-550	GCSH	Single	
AK122677	FLJ16125/AK122677/C-BRACE2027018	chr16-667	ADAMTS18	Multiple	Alt. N-term, Alt. C-term
NM_006885	NM_006885.2	chr16-857	ATBF1	Multiple	Alt. N-term
NM_001605	NM_001605.1	chr16-1031	AARS	Multiple	
NM_024939	NM_024939.2	chr16-1234	RBM35B	Multiple	Alt. N-term
NM_015964	NM_015964.2	chr16-1316	CGI-38	Multiple	
NM_031477	NM_031477.3	chr16-2281	YPEL3	Multiple	Alt. N-term, Alt. C-term
NM_031478	NM_031478.3	chr16-2285	FAM57B	Single	
NM_012410	NM_012410.1	chr16-2303	SEZ6L2	Multiple	Alt. N-term
NM_005003	NM_005003.2	chr16-2611	NDUFAB1	Single	
NM_016235	NM_016235.1	chr16-2868	GPRC5B	Multiple	Alt. N-term
NM_016069	NM_016069.8	chr16-3595	TIMM16	Single	
NM_024023	NM_024023.1	chr16-3938	UNKL	Multiple	
NM_016310	NM_016310.2	chr16-4093	POLR3K	Single	
AK127106	FLJ45163/AK127106/C-BRAWH3044122	chr17-554	WBP2	Multiple	Alt. C-term
NM_017565	NM_017565.2	chr17-894	FAM20A	Multiple	Alt. N-term
NM_000088	NM_000088.2	chr17-1836	COL1A1	Multiple	Alt. N-term
NM_024015	NM_024015.3	chr17-1985	HOXB4	Single	
NM_002145	NM_002145.2	chr17-1994	HOXB2	Single	
NM_016632	NM_016632.1	chr17-2137	LOC51326	Multiple	Alt. C-term
NM_001986	NM_001986.1	chr17-2515	ETV4	Multiple	Alt. N-term
NM_000458	NM_000458.1	chr17-3015	HNF1B	Multiple	Alt. C-term
NM_015986	NM_015986.2	chr17-3449	CRLF3	Multiple	
NM_001212	NM_001212.3	chr17-4708	C1QBP	Single	
NM_175907	NM_175907.3	chr18-207	ZADH2	Multiple	Alt. N-term
XM_035405	NM_020805.1	chr18-1351	KLHL14	Multiple	Alt. N-term

NM_004949_(2)	NM_004949.2	chr18-1440	DSC2	Multiple	
NM_006210	NM_006210.1	chr19-189	PEG3	Multiple	Alt. C-term
NM_024710	NM_024710.1	chr19-296	ISOC2	Single	
AK055285	FLJ30723/AK055285/C-FCBBF4000282	chr19-574	ETFB	Multiple	Alt. N-term
NM_001217	NM_001217.3	chr19-821	CA11	Single	
NM_005628	NM_005628.1	chr19-950	SLC1A5	Multiple	Alt. N-term
NM_013368	NM_013368.2	chr19-1430	SERTAD3	Single	
NM_013376	NM_013376.1	chr19-1431	SERTAD1	Single	
NM_033317	NM_033317.2	chr19-1821	ZD52F10	Multiple	Alt. N-term, Alt. C-term
NM_016368	NM_016368.3	chr19-2413	ISYNA1	Multiple	Alt. N-term
NM_000635	NM_000635.2	chr19-3309	RFX2	Multiple	
NM_020241	NM_020241.2	chr19-3423	SEMA6B	Multiple	
NM_001130_(2)	NM_001130.5	chr19-3547	AES	Multiple	Alt. N-term
NM_003712	NM_003712.2	chr19-3798	PPAP2C	Multiple	Alt. N-term
NM_001485	NM_001485.2	chr2-335	GBX2	Single	
NM_000599	NM_000599.2	chr2-1080	IGFBP5	Single	
XM_098048					
NM_024622	NM_024622.2	chr2-2990	FASTKD1	Multiple	Alt. N-term
NM_014795	NM_014795.2	chr2-3784	ZFHX1B	Multiple	
NM_000272	NM_000272.2	chr2-4903	NPHP1	Multiple	Alt. C-term
NM_003896	NM_003896.2	chr2-5927	ST3GAL5	Multiple	Alt. N-term, Alt. C-term
NM_019885	NM_019885.2	chr2-6324	CYP26B1	Multiple	Alt. N-term
NM_022055	NM_022055.1	chr2-7353	KCNK12	Single	
NM_018269	NM_018269.1	chr2-9188	MTCBP-1	Multiple	Alt. N-term
NM_003600	NM_003600.2	chr20-422	STK6	Multiple	
NM_021035	NM_021035.1	chr20-665	ZNFX1	Multiple	Alt. N-term
NM_015474	NM_015474.2	chr20-1254	SAMHD1	Multiple	Alt. C-term
NM_003908	NM_003908.3	chr20-1502	EIF2S2	Single	
AB023197	AB023197.1	chr20-1734	NINL	Multiple	Alt. N-term
NM_005116	NM_005116.5	chr20-2421	SLC23A2	Multiple	Alt. C-term
NM_023068	NM_023068.2	chr20-2500	SN	Multiple	Alt. N-term
NM_015227	NM_015227.3	chr21-98	POFUT2	Multiple	Alt. C-term
NM_000071	NM_000071.1	chr21-263	CBS	Multiple	Alt. N-term
NM_003490	NM_003490.2	chr22-1156	SYN3	Multiple	Alt. N-term
NM_004454	NM_004454.1	chr3-661	ETV5	Multiple	Alt. N-term
NM_002899	NM_002899.2	chr3-2376	RBP1	Multiple	Alt. C-term
AK301684	FLJ50903/AK301684/D-TESOP2006848.1				
XM_041363	NM_015009.1	chr3-4516	PDZRN3	Multiple	Alt. N-term
NM_012234	NM_012234.3	chr3-4589	RYBP	Single	
AK024086	FLJ14024/AK024086/C-HEMBA1003646	chr3-4774	FRMD4B	Multiple	Alt. N-term
NM_003865	NM_003865.1	chr3-5435	HESX1	Single	
NM_001064	NM_001064.1	chr3-5568	TKT	Multiple	Alt. N-term
NM_006030	NM_006030.2	chr3-5746	CACNA2D2	Multiple	Alt. N-term
NM_002971	NM_002971.2	chr3-7046	SATB1	Multiple	
NM_173553	NM_173553.1	chr4-41	TRIML2	Multiple	Alt. N-term
NM_016613	NM_016613.4	chr4-789	DKFZp434L142	Multiple	
XM_050625	NM_003013.2	chr4-884	SFRP2	Multiple	
NM_006681	NM_006681.1	chr4-3832	NMU	Multiple	
XM_045277	NM_015187.1	chr4-4622	SEL1L3	Multiple	Alt. N-term
AK056311	FLJ31749/AK056311/C-NT2RI2007386	chr4-5392		Single	
XM_070191	XM_497955.1	chr4-5425		Single	
NM_005110	NM_005110.1	chr5-60	GFPT2	Multiple	Alt. N-term
NM_030964	NM_030964.2	chr5-1516	SPRY4	Single	
AK091409	FLJ34090/AK091409/C-FCBBF3006399	chr5-1630		Single	
AK124191	FLJ42197/AK124191/C-THYMU2034314	chr5-1835		Multiple	
NM_178450	NM_178450.2	chr5-2339	MARCH3	Single	
NM_005779	NM_005779.1	chr5-3611	LHFPL2	Single	
NM_003633	NM_003633.1	chr5-4018	ENC1	Multiple	
NM_006622	NM_006622.1	chr5-4868	PLK2	Multiple	Alt. N-term
NM_005410	NM_005410.2	chr5-5289	SEPP1	Single	
AK316138	FLJ79037/AK316138/D-CTONG3001518.1	chr5-5986	MYO10	Multiple	Alt. N-term
NM_175747	NM_175747.2	chr6-1308	OLIG3	Single	
NM_003931	NM_003931.2	chr6-2392	WASF1	Multiple	
BC005192	BC005192.1	chr6-3959	TNFRSF21	Multiple	Alt. N-term
NM_002701	NM_002701.3	chr6-4792	POU5F1	Multiple	Alt. N-term
NM_054111	NM_054111.2	chr6-4838	IHPK3	Single	
NM_004155	NM_004155.3	chr6-6375	SERPINB9	Multiple	Alt. N-term
NM_004155_(2)					
NM_198285	NM_198285.1	chr7-411	WDR86	Multiple	Alt. N-term
AK056624	FLJ32062/AK056624/C-OCBBF1000042				
AK096734	FLJ39415/AK096734/C-PLACE6016160	chr7-463	ATG9B	Multiple	Alt. C-term
AK027791	FLJ14885/AK027791/C-PLACE1003711				
NM_005397	NM_005397.2	chr7-1301	PODXL	Multiple	
AK092358	FLJ35039/AK092358/C-OCBBF2017035	chr7-2751	GATS	Single	
NM_000305	NM_000305.2	chr7-3025	PON2	Multiple	
NM_152754	NM_152754.2	chr7-3410	SEMA3D	Multiple	Alt. N-term

NM_006379	NM_006379.2	chr7-3524	SEMA3C	Multiple	Alt. N-term, Alt. C-term
NM_006379_(2)					
NM_004577	NM_004577.3	chr7-4542	PSPH	Single	
NM_031311	NM_031311.2	chr7-5532	CPVL	Single	
NM_030661	NM_030661.3	chr7-5636	HOXA3	Multiple	Alt. N-term
NM_006735	NM_006735.3	chr7-5647	HOXA2	Multiple	Alt. C-term
AK096742_(2)	FLJ39423/AK096742/C-PROST1000322				
NM_005522	NM_005522.3	chr7-5652	HOXA1	Multiple	
NM_003930	NM_003930.3	chr7-5653	SCAP2	Multiple	Alt. N-term
NM_004956	NM_004956.3	chr7-6093	ETV1	Multiple	Alt. N-term
AK055368	FLJ30806/AK055368/C-FEBRA2001334				
NM_002607	NM_002607.4	chr7-6633	PDGFA	Multiple	Alt. N-term
AK074285	FLJ23705/AK074285/C-HEP11066	chr8-794	FAM84B	Single	
AK302036	FLJ56390/AK302036/D-TESTI2023534.1	chr8-853	MTSS1	Multiple	Alt. N-term
NM_031271	NM_031271.2	chr8-3869	TEX15	Single	
XM_376764	NM_007257.4	chr8-4119	PNMA2	Single	
NM_003389	NM_003389.2	chr9-2062	CORO2A	Multiple	Alt. N-term
NM_001333_(2)	NM_001333.2	chr9-2128	CTSL2	Single	
NM_002161	NM_002161.2	chr9-2428	IARS	Multiple	
NM_005077	NM_005077.3	chr9-2813	TLE1	Multiple	
NM_007234	NM_007234.3	chr9-4176	DCTN3	Multiple	
NM_002839	NM_002839.1	chr9-4855	PTPRD	Multiple	Alt. N-term
NM_017681	NM_017681.1	chrX-1051	NUP62CL	Multiple	
AK054936	FLJ30374/AK054936/C-BRACE2007888	chrX-1578		Multiple	
AK074719	FLJ90238/AK074719/C-NT2RM2000632	chrX-1599	ERCC6L	Multiple	
NM_006875	NM_006875.2	chrX-2059	PIM2	Single	

Supplementary Table 3. **List of genes with altered expression levels and their GO molecular function categories.**

Functional categorization (GO : Molecular function)	RA time point sample at which expression level of gene was altered	Probe ID	Gene symbol	Gene full name
Catalytic activity, Ligase activity	7-day	NM_001605	AARS	alanyl-tRNA synthetase
	7-day	NM_001751	CARS	cysteinyl-tRNA synthetase
	7-day	NM_002161	IARS	isoleucyl-tRNA synthetase
	7-day	M63180	TARS	threonyl-tRNA synthetase
	7-day	NM_003680	YARS	tyrosyl-tRNA synthetase
	7-day	NM_015440	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
	7-day	NM_006452	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
	7-day	NM_000532	PCCB	propionyl CoA carboxylase, beta polypeptide
	7-day	AF174498	C12orf51	chromosome 12 open reading frame 51

Functional categorization		Probe ID	Gene symbol	Gene full name
Binding, Ion binding	7-day	NM_001153	ANXA4	annexin A4
	2-day, 7-day	NM_021822, XM_114205	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G
	7-day	NM_004932	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)
	7-day	NM_001217	CA11	carbonic anhydrase XI
	7-day	NM_030622, NM_030622_(2)	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1
	7-day	NM_019885	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1
	7-day	NM_005257	GATA6	GATA binding protein 6
	7-day	NM_015641	TES	testis derived transcript (3 LIM domains)
	7-day	NM_175907	ZADH2	zinc binding alcohol dehydrogenase domain containing 2
	1-day, 2-day, 7-day	XM_166091, NM_020338	RAI17	retinoic acid induced 17
	1-day, 2-day	NM_014583, NM_014583_(2)	LMCD1	LIM and cysteine-rich domains 1
	2-day	NM_002851	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1

18 genes in the GO molecular function category "transcription regulator activity" were described in Supplementary Fig. 3.

***Supplementary Table 4* . Sequences of primers used in the real-time PCR.**

1) List of primers detected alternative region

Gene	Target transcript	Primer set Name	Forward primer Name	Forward primer sequence	Reverse primer Name	Reverse primer sequence
ATG9B	NM_173681.3	CE-07_01	CE-07_01F	ATCGACTTTTTTCATCACTTCACTGT	CE-07_01R	CCTCCGCACGCTGAGA
ATG9B	FLJ39415/AK096734/C-PLACE6016160	CE-07_02	CE-07_02F	GAAGGGAAGACACTGGGATGT	CE-07_02R	TCCCAGTCCAGGTTAGTCAAGT
CDH6	NM_004932.2	CE-14_01	CE-14_01F	CCCGAAGCCCTTTTCCTA	CE-14_01R	AAATCTCTGACATCGGTGTTGTC
CDH6	BC000019.2	CE-14_02	CE-14_02F	GGGCTCACACTGTTACTGTGACA	CE-14_02R	CGACTCACCTAGATCAGGCTGTA
CTHRC1	NM_138455.2	N-A3_013_01	N-A3_013_01F	GCATGCTGTCAGCGTTGGTA	N-A3_013_01R	TCAATGGGAAGAGGTCCTGAA
CTHRC1	FLJ57590/AK300273/D-PLACE7001513.1	N-A3_013_02	N-A3_013_02F	GGAAAATTGCGGTAAGTTTGAA	N-A3_013_02R	GCTACCTACTTCTCTAAGTCTTTTAGTTAAAA
EPB41L5	NM_020909.2	CE-27_01	CE-27_01F	CAGGATGCTGCCACAAACA	CE-27_01R	TTCATCTGTAGCTTCCTTTAGAACAG
EPB41L5	BC032822.2	CE-27_02	CE-27_02F	CACAATGTGAAGAATGCAGGAA	CE-27_02R	AAGAGGCTCAACACTCATATCTCAGT
LMCD1	NM_014583.2	N-A2_015_04	N-A2_015_04F	CTGCTTTGTGTGTGCCAAGTG	N-A2_015_04R	GGTGCACCATCCTTCCAGAA
LMCD1	FLJ55005/AK300803/D-SKNSH2002481.1	N-A2_015_02	N-A2_015_02F	GCCAGTCCCACTCGTGTGAT	N-A2_015_02R	AGGGCTCAGGTCCTCAGGAA
MS4A6A	NM_152852.1	CE-22_01	CE-22_01F	TGTGCTGCGGTGGAAAC	CE-22_01R	TGCCAGAATTACCAATGTAACTGT
MS4A6A	NM_022349.2	CE-22_02	CE-22_02F	GGCCGGCTTCACTTAACCTT	CE-22_02R	TCTCGTGATTGGCTGGTTGT
MTA3	NM_020744.2	CE-28_01	CE-28_01F	CGGCCGTTTGTTGCTATTA	CE-28_01R	CAGAAGCACAACATATAAGGTTAAGAA
MTA3	FLJ45312/AK127245/C-BRHIP3005037	CE-28_04	CE-28_04F	CCTGCAAAGAAACCTAATGTAATTC	CE-28_04R	CCAGACCATTGTGATGACTGTAGT
NRP2	NM_003872.2	N-A3_007_01	N-A3_007_01F	CTTCTGCAACCTCAGGGTCTG	N-A3_007_01R	GGTGTACAGCCAGCTCTTTTCT
NRP2	NM_018534.3	N-A3_007_02	N-A3_007_02F	TACCACCGGTTCCGCTATG	N-A3_007_02R	GGCCCCGTTGGTGTAGTG
NRP2	NM_201264.1	N-A3_007_03	N-A3_007_03F	TCTTGGAGGCCTCTGTAACGTT	N-A3_007_03R	GACATCATCAGTCTCAACTCCCTGTA
RSNL2	NM_024692.3	CE-16_01	CE-16_01F	CCTGCTCACGAGCTCCAAT	CE-16_01R	GCGCTTCGGAGCTCAAGTC
RSNL2	FLJ55798/AK302325/D-TESTI2048649.1	CE-16_02	CE-16_02F	GAAAAACACCTTTCAAGATGAACA	CE-16_02R	AAGCAATGCAAAAGATACAGCA
ST3GAL5	NM_003896.2	CE-08_01	CE-08_01F	TCCCCACAATCGGTGTCATT	CE-08_01R	CAAAACCCGCCAAACTGACT
ST3GAL5	FLJ55056/AK295252/D-BRCAN2011189.1	CE-08_02	CE-08_02F	TCAGCCGCTTCTTCATCGT	CE-08_02R	GAGGGCCCTGCTTCCTTTAA
TES	NM_015641.2	CE-12_01	CE-12_01F	CATTGGCCAGGCAGTACATG	CE-12_01R	CCCCCTCTGAGCCTGCTA
TES	FLJ59160/AK299104/D-NT2RI3007951.1	CE-12_02	CE-12_02F	TGAAGTTCCTGGAGTATTTATTTGG	CE-12_02R	GAACCCCGGAAGAATAACAGA
ZD52F10	NM_033317.2	CE-19_01	CE-19_01F	TCAGTCAAGACCCCTGCAAAG	CE-19_01R	CAAGAAATTGCCTACCAAAACTTCA
ZD52F10	FLJ57785/AK304668/D-UTERU2034249.1	CE-19_04	CE-19_04F	AGGTGAGTCTCTGTCCTCAAGTTAC	CE-19_04R	GGAGTGAAAGAGAATTTCAGATTGC
ITIH5	NM_030569.3	N-A2-3_001_01	N-A2-3_001_01F	CACTCACCCTCTGCTCCTTCA	N-A2-3_001_01R	CTTCCAGACCACTGGGACTTG
ITIH5	NM_001001851.1	N-A2-3_001_02	N-A2-3_001_02F	GAAGTCTTGATTGTTGCCTTTCTG	N-A2-3_001_02R	GCGGACTCTATATCCACAGCTCAT
CKMT1B	NM_020990.3	CE-17_01	CE-17_01F	CGTGGCTGGGAGTTCATGT	CE-17_01R	GTGCACTCCTGCCCGAAGT
CKMT1B	FLJ52224/AK294063/D-BRALZ1000056.1	CE-17_02	CE-17_02F	TTGGTCCACAGTAAGTGCTTAATAA	CE-17_02R	CAGAAGGAACCATGCCATAGG
CKMT1B	FLJ52454/AK293939/D-BRACE3032708.1	CE-17_03	CE-17_03F	AGGCCTCAAAGAGGTTAGAGAAG	CE-17_03R	TGGGTTGGTTGGTAAATTACATAA
DENND5B	NM_144973.2	CE-21_01	CE-21_01F	TGGCAACAGGACCAACCAGTA	CE-21_01R	TCGTTGTCCAGCCCAACA
DENND5B	BC020855.1	CE-21_02	CE-21_02F	ACTGCCCAGGACATGGAAT	CE-21_02R	CTTTTTACTTTGTCAAAGTTCTGCAT
EVL	NM_016337.2	CE-29_01	CE-29_01F	CGCAGCCTCACTCTAGGATGA	CE-29_01R	CTCTCTCACCACCTCCTCTAGGAT
EVL	FLJ58489/AK295919/D-BRSSN2003639.1	CE-29_02	CE-29_02F	CCTTCAGTCGCAGCCTCACT	CE-29_02R	GACAGAGGAGCCCCAAACC
FEZ1	NM_005103.3	CE-10_01	CE-10_01F	CAAGCGCTTCAGCATGGA	CE-10_01R	CAGTTCCTGAGGAGCCAAAGG
FEZ1	NM_022549.2	CE-10_02	CE-10_02F	CACATAAGAAAGCATCTAAACTGAACTGA	CE-10_02R	CCACATCACCTAGTTTCCACCTT
FNDC5	NM_153756.1	N-A3_023_01	N-A3_023_01F	TTGCCCTCAGCAGCTAAGAAG	N-A3_023_01R	TCATCATCAGAACCATGAGATCCT
FNDC5	BC062297.1	N-A3_023_04	N-A3_023_04F	AGCAAGGTGAGGGCAAGAC	N-A3_023_04R	AGTCCAGGGATTACCAGAGCAT
FST	NM_013409.1	CE-26_01	CE-26_01F	GTAAGTCGGATGAGCCTGTCTGT	CE-26_01R	CCGAAATGGAGTTGCAAGATC
FST	NM_006350.2	CE-26_02	CE-26_02F	AAGCACTCCGGATCTTGCAA	CE-26_02R	ATGAAGTCAAAAACTGCAGAAAGTTC
MAPKAPK2	NM_004759.3	CE-30_01	CE-30_01F	CCCTTGGATCATGCAATCA	CE-30_01R	CTCACAACCTGGTCAGCCAAGT
MAPKAPK2	NM_032960.2	CE-30_02	CE-30_02F	GGAGGATGTCAAGGAGGAGATG	CE-30_02R	TTTATCTTGATCTGCTCGTAGTCAA
MRPS15	NM_031280.2	CE-24_01	CE-24_01F	ACCTTCCCCCCTCTGTATTACC	CE-24_01R	CGAATGCACAGAGCCTTCTTG
MRPS15	FLJ56752/AK302633/D-TESTI4017571.1	CE-24_02	CE-24_02F	CCTGCTAGTTGGGACCTGATCT	CE-24_02R	ATTGCCCTAGGTCCTTCATGTC
NPHP1	NM_000272.2	CE-09_04	CE-09_04F	CAGCAGACATGTACGCCTCTGT	CE-09_04R	CAAACATGGTAAGATGCGAGTAACC
NPHP1	NM_207181.1	CE-09_02	CE-09_02F	ATGACACTAACAATAGAATCAGTCAACATT	CE-09_02R	GGGCAGAGACTATGACTTACACTTC
RBP1	NM_002899.2	N-A2-3_004_01	N-A2-3_004_01F	CAGTGGATCGAGGGTGATGA	N-A2-3_004_01R	CTTGCTTGCAGACCACACCTT
RBP1	FLJ50903/AK301684/D-TESOP2006848.1	N-A2-3_004_02	N-A2-3_004_02F	TTTCCTCTTGAATGTGCTGACTTT	N-A2-3_004_02R	CTGAGGCCAGGCTGATGAGT
SLC44A5	NM_152697.2	CE-11_01	CE-11_01F	CTGTGAAGATCTGGAAAGAAATGA	CE-11_01R	GAACTAGTTGCTTCTTGATCAGAATTC
SLC44A5	FLJ35851/AK093170/C-TESTI2007040	CE-11_02	CE-11_02F	CCACAAACTAGGAAGCAGTAGAAGA	CE-11_02R	GTTGCTAAACACAAAGCACTTATGA
WDR74	NM_018093.1	CE-23_01	CE-23_01F	CAGTGTGCGTGGGTTGCA	CE-23_01R	CCCGTGTATCCTCAAGACTCTGT
WDR74	FLJ57690/AK303186/D-THYMU2025050.1	CE-23_02	CE-23_02F	TGAAGGAGCTGTTCCTGAAGTC	CE-23_02R	CCTAAGTCCATCTAGTCTCTAATGCA
YPEL3	NM_031477.3	CE-20_01	CE-20_01F	TTGGGCTGGAAATATGAACAG	CE-20_01R	GATCATGTGGTTGAGTTCAATGA
YPEL3	FLJ12347/AK022409/C-MAMMA1002298	CE-20_02	CE-20_02F	TTTGGGCTGGAAATATGTGAGT	CE-20_02R	GGCCTATGCAATCTGAAAGG
ETV1	NM_004956.3	NT-PS_01_01	NT-PS_01_01F	GCAGCATGGATGGATTTTATG	NT-PS_01_01R	CAATTTCTCCCACGCTGACT
ETV1	FLJ50494/AK294572/D-BRAMY4002358.1	NT-PS_01_02	NT-PS_01_02F	CCGGCTGGCTTGCTGT	NT-PS_01_02R	TCAGAAAAGTCCTCCACCAGA
ETV4	NM_001986.1	NT-PS_02_01	NT-PS_02_01F	GATGAAAGCCGGATACTTGGA	NT-PS_02_01R	CATTTCCGGGCGATTTG
ETV4	BC007242.1	NT-PS_02_03	NT-PS_02_03F	TTTCCCTGGGATTTTGTGGTT	NT-PS_02_03R	TCCTTCCAGCCTGCTTCCT
ETV5	NM_004454.1	NT-PS_03_01	NT-PS_03_01F	GGAGCGGTTCACCGTCTT	NT-PS_03_01R	GGCGCCTGGGCGAAA
ETV5	FLJ56169/AK301878/D-TESTI2012536.1	NT-PS_03_02	NT-PS_03_02F	GGAAGCAGTTTGAGGGGAAT	NT-PS_03_02R	GGATCCTCCTGTGTCATTTACC
PAX6	NM_000280.2	NT-PS_05_01	NT-PS_05_01F	CAACTCCTTTAAAACACCGTCATTT	NT-PS_05_01R	GGTTGTCACAGCTTCTGTCAAGA
PAX6	FLJ36930/AK094249/C-BRACE2005251	NT-PS_05_03	NT-PS_05_03F	CCAACACTGCAGAGACCTTGAA	NT-PS_05_03R	CGGCTCTATAAATCCCCCAAA
POU5F1	NM_002701.3	TC04_NT-PS_04_06	TC04_NT-PS_04_06F	AGTCGGGGTGGAGAGCAACT	TC04_NT-PS_04_06R	TTTTGCTCCAGCTTCTCCTTCT
POU5F1	NM_203289.3	NT-PS_04_02	NT-PS_04_02F	GGCAGAGGCACTTCTACAGACTA	NT-PS_04_02R	GTAAGAACATAAACACACCAGTTATCAA
RARB	NM_000965.2	TC13_01	TC13_01F	AGTGAGTCCTGGGCAAATCCT	TC13_01R	TTCGGTTTGGGTCAATCCA
RARB	FLJ56241/AK299756/D-OCBBF2037981.1	TC13_02	TC13_02F	CAGCAGTGAACGGACACATGA	TC13_02R	TCCGATGACAGGTGGAAAGAG
HOXA3	NM_030661.3	N-A2_020_01	N-A2_020_01F	AGGCAGCCAACGGGTTC	N-A2_020_01R	GCGGACGCCGGGTAC
HOXA3	NM_153632.1	TC11_N-A2_020_06	TC11_N-A2_020_06F	CTGCTGCCCTCCCTCTTCT	TC11_N-A2_020_06R	TTGGCCGCGTTGGC
RFX2	NM_000635.2	NT-PS_07_01	NT-PS_07_01F	CCAGTGGCTGTTGGATAATTATG	NT-PS_07_01R	GGATCAGTTTCCCGAAGGA
RFX2	FLJ53376/AK303321/D-THYMU3005661.1	NT-PS_07_02	NT-PS_07_02F	CGGTGCAGCACGTGTATCC	NT-PS_07_02R	CTTCGAGTTGTAGGTGTAGGCTGTT
HNF1B	NM_000458.1	N-A2-3_002_01	N-A2-3_002_01F	CCAGTCAGCACCTTGACGAA	N-A2-3_002_01R	GGGTGTCATGATGAGGTTTTGA
HNF1B	NM_006481.1	N-A2-3_002_02	N-A2-3_002_02F	TGGTTCTTGCCACGGATCT	N-A2-3_002_02R	AGGATCATCTCAAAAGCGTTTG
HOXA2	NM_006735.3	N-A2_011_01	N-A2_011_01F	CACAAAGAATCCCTGGAAATCG	N-A2_011_01R	CTTTTTCCAGCTCTAGAAGCTGTGT
HOXA2	FLJ39423/AK096742/C-PROST1000322	TC10_N-A2_011_05	TC10_N-A2_011_05F	CCACAAAGGTCAGTCCAAAGA	TC10_N-A2_011_05R	CAGCCCGGAGAAGGAAGAG
PEG3	NM_006210.1	NT-PS_06_03	NT-PS_06_03F	GATGGCCACTCCCACATG	NT-PS_06_03R	TGCTTGGGTAGGCACTTCTC
PEG3	NM_015363.3	NT-PS_06_04	NT-PS_06_04F	AAGGCACTGCTCCTGGAATATG	NT-PS_06_04R	TGCAAAATTCACATCTGTTGTGTT
ZNF483	NM_133464.1	TC12_02	TC12_02F	GTGCCTCAGGGATGATGATC	TC12_02R	TTTGTGCGACTCTTCCTTTTG
ZNF483	FLJ35492/AK092811/C-SMINT2008672	TC12_01	TC12_01F	GCTCCCGACTAGACATACATGGA	TC12_01R	TCATCTCTGTGTAACAGTTGAAACAA

2) List of primers detected common region

Gene	Target transcript	Primer set Name	Forward primer Name	Forward primer sequence	Reverse primer Name	Reverse primer sequence
ATG9B	NM_173681.3, FLJ39415	CE-07_03	CE-07_03F	TGCCAACCAACCAAGTAACCA	CE-07_03R	AGGGTAGGATGGCATCTGACA
CDH6	NM_004932.2, BC000019.2	CE-14_03	CE-14_03F	TTTACATCCTTCGAGCTCAAGCT	CE-14_03R	TGGTGAATATTGGTTCATTGTCATT
CTHRC1	NM_138455.2, FLJ57590	N-A3_013_03	N-A3_013_03F	CAATGGCATTCCGGGTACA	N-A3_013_03R	CCTCAAAGCTTTCCCTCAGACA
EPB41L5	NM_020909.2, BC032822.2	CE-27_03	CE-27_03F	GGTCTATGCGTAAACATGCAGAGA	CE-27_03R	GGGACACCCGACACGTGAT
LMCD1	NM_014583.2, FLJ55005	N-A2_015_03	N-A2_015_03F	CCACTGCCTAACATCTGACCTAGA	N-A2_015_03R	AGGGTGGAATACTTGGAGTCCAT
MS4A6A	NM_152852.1, NM_022349.2	CE-22_03	CE-22_03F	CAGCCTGGTTGGAAGCATTC	CE-22_03R	GGTGGCCTGTTTGACAGACA
MTA3	NM_020744.2, FLJ45312	CE-28_03	CE-28_03F	CTCTTTTTGTCACGCCAGTATGA	CE-28_03R	CAGAAGGGCAACACTGCACTT
NRP2	NM_003872.2, NM_018534.3, NM_201264.1	N-A3_007_04	N-A3_007_04F	CGGCCATCGCAACACA	N-A3_007_04R	CATGCCGGTACACCATCCA
RSNL2	NM_024692.3, FLJ55798	CE-16_03	CE-16_03F	GACCCAGTAGATATGCCGTTAGAGA	CE-16_03R	GGCACCGCATCTAGAAGCA
ST3GAL5	NM_003896.2, FLJ55056	CE-08_03	CE-08_03F	GGCCCAGCTTGTTATTAAAAGA	CE-08_03R	GGTCCACATAATGCATTTTTTTC
TES	NM_015641.2, FLJ59160	CE-12_03	CE-12_03F	CGCAATGTTATGATATTGACGAA	CE-12_03R	GCCCACTCATAGGTAACTGTATTGA
ZD52F10	NM_033317.2, FLJ57785	CE-19_05	CE-19_05F	AACTGGGATGCCATAAACAAGAAC	CE-19_05R	TTCTGTTTGAAATCCTCCCAGAGT
ITIH5	NM_030569.3, NM_001001851.1	N-A2-3_001_03	N-A2-3_001_03F	AACTCCGGCAGACCAAGGA	N-A2-3_001_03R	TGATCCGGTTGGAAAATCCA
CKMT1B	NM_020990.3, FLJ52224, FLJ52454	CE-17_04	CE-17_04F	GACCTGGCTGGACGTTACTATAGG	CE-17_04R	CACGAGCATCTGGCCAGTCT
DENND5B	NM_144973.2, BC020855.1	CE-21_03	CE-21_03F	AGATGCAAATCCTTCTCTACTCACAA	CE-21_03R	GTAGAATGGGCACATAAACATGTTG
EVL	NM_016337.2, FLJ58489	CE-29_03	CE-29_03F	GGTCTACGGCTTAAACTTTGCAA	CE-29_03R	GATGTTCAGGGCAAACAGCAT
FEZ1	NM_005103.3, NM_022549.2	CE-10_03	CE-10_03F	GGTTCATCTCCCCACCATCTC	CE-10_03R	TGAAGCTGATTATTTCGGAAGAAA
FNDC5	NM_153756.1, BC062297.1	N-A3_023_03	N-A3_023_03F	CAGGCGAGGTGCTGATCAT	N-A3_023_03R	GTCATACTGGCGGCAGAAGAG
FST	NM_013409.1, NM_006350.2	CE-26_03	CE-26_03F	GTGAATGACAACACACTCTTCAAGTG	CE-26_03R	CCACGTTCTCACACGTTTCTTTAC
MAPKAPK2	NM_004759.3, NM_032960.2	CE-30_03	CE-30_03F	GGCCATCCAGTATCTGCATT	CE-30_03R	GTGGTTTCCTTGGCAAAGC
MRPS15	NM_031280.2, FLJ56752	CE-24_03	CE-24_03F	CGGATATGTCGTCCGGAAAC	CE-24_03R	CAGGGACATTCTGGTAGTCTTTGA
NPHP1	NM_000272.2, NM_207181.1	CE-09_03	CE-09_03F	ACAGGTTGATAGTTTGCTTTCTGA	CE-09_03R	TGCCTGCTTTAACTGGATACATC
RBP1	NM_002899.2, FLJ50903	N-A2-3_004_03	N-A2-3_004_03F	GTGGCCTTGCGCAAAATC	N-A2-3_004_03R	CGTCCTGCACGATCTCTTTGT
SLC44A5	NM_152697.2, FLJ35851	CE-11_03	CE-11_03F	TTTGAACTGCAACAAACATGGTT	CE-11_03R	AATGGCTTTGCTTCCTTCCTT
WDR74	NM_018093.1, FLJ57690	CE-23_04	CE-23_04F	ACGGCACCCTCATCACATGT	CE-23_04R	GGTCTTGGCGCATCCTACAC
YPEL3	NM_031477.3, FLJ12347	CE-20_03	CE-20_03F	TGATTGTCACCGGAGGTATAGCT	CE-20_03R	GGAGATGAGGTCGTCGTGGTT
ETV1	NM_004956.3, FLJ50494	NT-PS_01_03	NT-PS_01_03F	GCTTTCTGAACCCTGTAACTCCTT	NT-PS_01_03R	GGTCGTGGTACTCCTGCTTAAA
ETV4	NM_001986.1, BC007242.1	NT-PS_02_04	NT-PS_02_04F	CGAGGCCCTCTTCTCTTTGG	NT-PS_02_04R	CCGGTCAAACTCAGCCTTGA
ETV5	NM_004454.1, FLJ56169	NT-PS_03_03	NT-PS_03_03F	GTTTGTCCCAGATTTTCAGTCTGAT	NT-PS_03_03R	AGCCTGCTCATGGCTACAAGA
PAX6	NM_000280.2, FLJ36930	NT-PS_05_04	NT-PS_05_04F	CCATGTTGGGCCGAACAG	NT-PS_05_04R	TGGTGAAGCTGGGCATAGG
POU5F1	NM_002701.3, NM_203289.3	TC04_NT-PS_04_05	TC04_NT-PS_04_05F	GAACCGAGTGAGAGGCAACCT	TC04_NT-PS_04_05R	TGGGCGATGTGGCTGAT
RARB	NM_000965.2, FLJ56241	TC13_03	TC13_03F	AGATCGTGGAGTTTGCTAAACGT	TC13_03R	GGGTATACCTGGTGCAAATTCTAAG
HOXA3	NM_030661.3, NM_153632.1	N-A2_020_03	N-A2_020_03F	AGCTATGGGACCCCACACATAC	N-A2_020_03R	TTGCTCATGGGCTCCACAT
RFX2	NM_000635.2, FLJ53376	NT-PS_07_03	NT-PS_07_03F	CTGCCCAAGGACAAGCTTATCT	NT-PS_07_03R	TGTGGTCGCAGCTCCTCAT
HNF1B	NM_000458.1, NM_006481.1	N-A2-3_002_03	N-A2-3_002_03F	AGAAGCGTGCCGCTCTGT	N-A2-3_002_03R	TGGTTGAATTGTCGGAGGATCT
HOXA2	NM_006735.3, FLJ39423	N-A2_011_03	N-A2_011_03F	GCAGCCGCCCGAGTA	N-A2_011_03R	GCAGAAGTGCGGTTTTCTTG
PEG3	NM_006210.1, NM_015363.3	NT-PS_06_05	NT-PS_06_05F	ACCTCACTCAGTCCATTCTTTCAG	NT-PS_06_05R	CCGCGGAGGCATCCT
ZNF483	NM_133464.1, FLJ35492	TC12_03	TC12_03F	ACAGAGGTTTAGGTGGTTTTGTTACTC	TC12_03R	GAACTGCTCAAACACCAGAAGCT
GAPDH	GAPDH	GAPDH	GAPD_01F	CCAGGTGGTCTCCTCTGACTTC	GAPD_01R	GTGGTCGTTGAGGGCAATG

***Supplementary Table 5.* Quantitative analysis of expression of 26 selected genes that showed AS in their C-terminus by real-time PCR.**

Relative expression to 0-day sample (Log2RQ)

1) Data of alternative region

Gene symbol	Target transcript	Primer set Name	0-day Log2RQ mean ± S.D.	1-day Log2RQ mean ± S.D.	2-day Log2RQ mean ± S.D.	7-day Log2RQ mean ± S.D.
ATG9B	NM_173681.3	CE-07_01	0.0 ± 0.5	1.1 ± 0.3	3.2 ± 0.3	0.6 ± 0.9
ATG9B	FLJ39415/AK096734/C-PLACE6016160	CE-07_02	0.0 ± 0.7	0.6 ± 0.4	2.2 ± 0.2	-0.2 ± 0.3
CDH6	NM_004932.2	CE-14_01	0.0 ± 0.4	0.5 ± 0.4	-1.5 ± 0.3	3.6 ± 0.0
CDH6	BC000019.2	CE-14_02	0.0 ± 0.2	0.1 ± 0.3	-0.2 ± 0.2	2.5 ± 0.1
CTHRC1	NM_138455.2	N-A3_013_01	0.0 ± 0.3	3.1 ± 0.3	5.0 ± 0.2	5.1 ± 0.6
CTHRC1	FLJ57590/AK300273/D-PLACE7001513.1	N-A3_013_02	0.0 ± 0.7	0.5 ± 0.1	1.7 ± 0.2	1.9 ± 0.2
EPB41L5	NM_020909.2	CE-27_01	0.0 ± 0.2	-0.2 ± 0.1	-0.1 ± 0.1	1.8 ± 0.1
EPB41L5	BC032822.2	CE-27_02	0.0 ± 0.7	-0.5 ± 0.3	-0.2 ± 0.3	0.5 ± 0.1
LMCD1	NM_014583.2	N-A2_015_04	0.0 ± 0.5	-2.0 ± 0.4	-2.7 ± 0.1	-0.5 ± 0.1
LMCD1	FLJ55005/AK300803/D-SKNSH2002481.1	N-A2_015_02	0.0 ± 0.4	-0.9 ± 0.1	-1.3 ± 0.4	0.0 ± 0.1
MS4A6A	NM_152852.1	CE-22_01	0.0 ± 0.1	-0.4 ± 1.0	-2.7 ± 1.9	-2.0 ± 1.5
MS4A6A	NM_022349.2	CE-22_02	0.0 ± 0.7	-0.6 ± 0.7	-1.0 ± 0.2	-1.7 ± 0.7
MTA3	NM_020744.2	CE-28_01	0.0 ± 0.1	-0.2 ± 0.1	-0.1 ± 0.2	-0.6 ± 0.1
MTA3	FLJ45312/AK127245/C-BRHIP3005037	CE-28_04	0.0 ± 0.2	-0.4 ± 0.3	-1.0 ± 0.4	-1.2 ± 0.3
NRP2	NM_003872.2	N-A3_007_01	0.0 ± 0.2	1.0 ± 0.3	2.9 ± 0.3	3.3 ± 0.5
NRP2	NM_018534.3	N-A3_007_02	0.0 ± 0.6	2.1 ± 0.3	3.7 ± 0.2	4.2 ± 0.3
NRP2	NM_201264.1	N-A3_007_03	0.0 ± 0.3	0.6 ± 0.1	1.7 ± 0.2	1.5 ± 0.4
RSNL2	NM_024692.3	CE-16_01	0.0 ± 0.6	-0.4 ± 0.6	0.8 ± 0.4	2.9 ± 0.1
RSNL2	FLJ55798/AK302325/D-TESTI2048649.1	CE-16_02	0.0 ± 0.4	-0.3 ± 0.5	1.5 ± 0.4	2.3 ± 0.2
ST3GAL5	NM_003896.2	CE-08_01	0.0 ± 0.3	0.4 ± 0.3	0.7 ± 0.1	2.5 ± 0.1
ST3GAL5	FLJ55056/AK295252/D-BRCAN2011189.1	CE-08_02	0.0 ± 0.2	0.8 ± 0.3	1.1 ± 0.2	2.6 ± 0.1
TES	NM_015641.2	CE-12_01	0.0 ± 0.2	-0.5 ± 0.3	0.0 ± 0.2	2.1 ± 0.0
TES	FLJ59160/AK299104/D-NT2RI3007951.1	CE-12_02	0.0 ± 0.7	-1.2 ± 0.3	-0.5 ± 0.3	1.7 ± 0.1
ZD52F10	NM_033317.2	CE-19_01	0.0 ± 0.3	-0.3 ± 0.2	-1.1 ± 0.3	-0.8 ± 0.0
ZD52F10	FLJ57785/AK304668/D-UTERU2034249.1	CE-19_04	0.0 ± 1.0	-0.2 ± 0.2	0.5 ± 0.3	-1.0 ± 0.1
ITIH5	NM_030569.3	N-A2-3_001_01	0.0 ± 0.1	3.4 ± 0.1	4.3 ± 0.2	4.7 ± 0.1
ITIH5	NM_001001851.1	N-A2-3_001_02	0.0 ± 0.3	3.5 ± 0.2	5.1 ± 0.2	4.1 ± 0.2
CKMT1B	NM_020990.3	CE-17_01	0.0 ± 0.3	-0.6 ± 0.2	-0.6 ± 0.3	-2.9 ± 0.1
CKMT1B	FLJ52224/AK294063/D-BRALZ1000056.1	CE-17_02	0.0 ± 1.1	-0.6 ± 0.2	-0.3 ± 0.4	-2.6 ± 0.1
CKMT1B	FLJ52454/AK293939/D-BRACE3032708.1	CE-17_03	0.0 ± 0.9	-0.8 ± 0.2	-0.6 ± 0.3	-2.8 ± 0.0
DENND5B	NM_144973.2	CE-21_01	0.0 ± 0.2	-0.2 ± 0.3	0.4 ± 0.1	2.1 ± 0.1
DENND5B	BC020855.1	CE-21_02	0.0 ± 0.2	-0.2 ± 0.2	0.3 ± 0.1	1.4 ± 0.1
EVL	NM_016337.2	CE-29_01	0.0 ± 0.3	-0.1 ± 0.2	0.2 ± 0.3	1.1 ± 0.2
EVL	FLJ58489/AK295919/D-BRSSN2003639.1	CE-29_02	0.0 ± 0.1	0.6 ± 0.2	0.7 ± 0.2	2.2 ± 0.2
FEZ1	NM_005103.3	CE-10_01	0.0 ± 0.1	-0.6 ± 0.2	-0.7 ± 0.3	-2.0 ± 0.1
FEZ1	NM_022549.2	CE-10_02	0.0 ± 0.7	0.0 ± 0.4	-0.8 ± 0.3	-1.2 ± 0.1
FNDC5	NM_153756.1	N-A3_023_01	0.0 ± 0.4	3.1 ± 0.1	4.0 ± 0.3	4.0 ± 0.3
FNDC5	BC062297.1	N-A3_023_04	0.0 ± 0.3	3.0 ± 0.1	4.1 ± 0.5	3.7 ± 0.3
FST	NM_013409.1	CE-26_01	0.0 ± 0.4	-0.7 ± 0.1	-2.3 ± 0.4	-2.8 ± 0.7
FST	NM_006350.2	CE-26_02	0.0 ± 0.4	-0.1 ± 0.2	-2.6 ± 0.4	-2.7 ± 0.6
MAPKAPK2	NM_004759.3	CE-30_01	0.0 ± 0.3	2.0 ± 0.1	3.1 ± 0.3	0.5 ± 0.1
MAPKAPK2	NM_032960.2	CE-30_02	0.0 ± 0.4	1.4 ± 0.1	1.6 ± 0.3	1.0 ± 0.0
MRPS15	NM_031280.2	CE-24_01	0.0 ± 0.1	-0.1 ± 0.0	-0.1 ± 0.2	-0.1 ± 0.1
MRPS15	FLJ56752/AK302633/D-TESTI4017571.1	CE-24_02	0.0 ± 0.1	0.3 ± 0.2	0.1 ± 0.1	0.7 ± 0.1
NPHP1	NM_000272.2	CE-09_04	0.0 ± 0.2	-0.1 ± 0.3	0.0 ± 0.1	2.4 ± 0.1
NPHP1	NM_207181.1	CE-09_02	0.0 ± 0.1	0.0 ± 0.2	0.2 ± 0.2	1.1 ± 0.0
RBP1	NM_002899.2	N-A2-3_004_01	0.0 ± 0.1	2.0 ± 0.3	2.9 ± 0.2	4.0 ± 0.0
RBP1	FLJ50903/AK301684/D-TESOP2006848.1	N-A2-3_004_02	0.0 ± 0.3	2.4 ± 0.3	2.5 ± 0.4	5.2 ± 0.1
SLC44A5	NM_152697.2	CE-11_01	0.0 ± 0.5	0.1 ± 0.1	0.7 ± 0.1	3.1 ± 0.3
SLC44A5	FLJ35851/AK093170/C-TESTI2007040	CE-11_02	0.0 ± 0.4	0.3 ± 0.1	0.5 ± 0.1	2.8 ± 0.3
WDR74	NM_018093.1	CE-23_01	0.0 ± 0.2	0.2 ± 0.2	-0.5 ± 0.2	-0.4 ± 0.1
WDR74	FLJ57690/AK303186/D-THYMU2025050.1	CE-23_02	0.0 ± 0.1	0.0 ± 0.1	-0.2 ± 0.1	0.1 ± 0.1
YPEL3	NM_031477.3	CE-20_01	0.0 ± 0.1	0.2 ± 0.3	1.3 ± 0.2	2.3 ± 0.1
YPEL3	FLJ12347/AK022409/C-MAMMA1002298	CE-20_02	0.0 ± 0.8	0.9 ± 0.2	2.2 ± 0.3	2.5 ± 0.0

2) Data of primers detected common region

Gene symbol	Target transcript	Primer set Name	0-day Log2RQ mean ± S.D.	1-day Log2RQ mean ± S.D.	2-day Log2RQ mean ± S.D.	7-day Log2RQ mean ± S.D.
ATG9B	NM_173681.3, FLJ39415	CE-07_03	0.0 ± 0.7	1.6 ± 0.5	4.1 ± 0.3	1.7 ± 1.1
CDH6	NM_004932.2, BC000019.2	CE-14_03	0.0 ± 0.2	0.4 ± 0.3	-0.9 ± 0.2	3.4 ± 0.1
CTHRC1	NM_138455.2, FLJ57590	N-A3_013_03	0.0 ± 0.3	3.1 ± 0.8	4.7 ± 0.2	5.2 ± 0.3
EPB41L5	NM_020909.2, BC032822.2	CE-27_03	0.0 ± 0.4	-0.1 ± 0.3	0.3 ± 0.2	2.1 ± 0.4
LMCD1	NM_014583.2, FLJ55005	N-A2_015_03	0.0 ± 0.3	-1.7 ± 0.3	-2.3 ± 0.1	-0.4 ± 0.1
MS4A6A	NM_152852.1, NM_022349.2	CE-22_03	0.0 ± 0.1	-0.5 ± 1.0	-1.6 ± 0.3	-2.1 ± 1.0
MTA3	NM_020744.2, FLJ45312	CE-28_03	0.0 ± 0.0	-0.4 ± 0.1	-0.3 ± 0.2	-0.9 ± 0.0
NRP2	NM_003872.2, NM_018534.3, NM_201264.1	N-A3_007_04	0.0 ± 0.3	1.3 ± 0.4	3.0 ± 0.2	3.3 ± 0.5
RSNL2	NM_024692.3, FLJ55798	CE-16_03	0.0 ± 0.6	-0.5 ± 0.6	0.9 ± 0.2	2.9 ± 0.2
ST3GAL5	NM_003896.2, FLJ55056	CE-08_03	0.0 ± 0.2	0.3 ± 0.4	0.6 ± 0.1	2.3 ± 0.0
TES	NM_015641.2, FLJ59160	CE-12_03	0.0 ± 0.2	-0.6 ± 0.2	0.1 ± 0.2	2.2 ± 0.1
ZD52F10	NM_033317.2, FLJ57785	CE-19_05	0.0 ± 0.1	-0.4 ± 0.2	-0.8 ± 0.3	-1.1 ± 0.1
ITIH5	NM_030569.3, NM_001001851.1	N-A2-3_001_03	0.0 ± 0.1	3.3 ± 0.2	4.1 ± 0.1	4.5 ± 0.1
CKMT1B	NM_020990.3, FLJ52224, FLJ52454	CE-17_04	0.0 ± 0.3	-0.5 ± 0.1	-0.6 ± 0.3	-3.0 ± 0.1
DENND5B	NM_144973.2, BC020855.1	CE-21_03	0.0 ± 0.3	-0.3 ± 0.2	0.2 ± 0.2	1.5 ± 0.1
EVL	NM_016337.2, FLJ58489	CE-29_03	0.0 ± 0.2	0.1 ± 0.2	0.3 ± 0.2	1.2 ± 0.2
FEZ1	NM_005103.3, NM_022549.2	CE-10_03	0.0 ± 0.2	-0.4 ± 0.3	-1.5 ± 1.6	-1.3 ± 0.1
FNDC5	NM_153756.1, BC062297.1	N-A3_023_03	0.0 ± 0.7	2.8 ± 0.2	3.4 ± 0.4	3.8 ± 0.4
FST	NM_013409.1, NM_006350.2	CE-26_03	0.0 ± 0.4	-0.7 ± 0.2	-2.4 ± 0.4	-3.0 ± 0.7
MAPKAPK2	NM_004759.3, NM_032960.2	CE-30_03	0.0 ± 0.3	1.0 ± 0.0	1.3 ± 0.1	0.8 ± 0.0
MRPS15	NM_031280.2, FLJ56752	CE-24_03	0.0 ± 0.0	-0.1 ± 0.1	-0.2 ± 0.1	-0.1 ± 0.1
NPHP1	NM_000272.2, NM_207181.1	CE-09_03	0.0 ± 0.1	0.0 ± 0.3	0.3 ± 0.2	1.8 ± 0.1
RBP1	NM_002899.2, FLJ50903	N-A2-3_004_03	0.0 ± 0.2	2.1 ± 0.3	2.9 ± 0.2	4.2 ± 0.1
SLC44A5	NM_152697.2, FLJ35851	CE-11_03	0.0 ± 0.4	0.1 ± 0.2	0.2 ± 0.2	2.7 ± 0.2
WDR74	NM_018093.1, FLJ57690	CE-23_04	0.0 ± 0.1	0.0 ± 0.1	-0.6 ± 0.1	-0.5 ± 0.0
YPEL3	NM_031477.3, FLJ12347	CE-20_03	0.0 ± 0.1	0.2 ± 0.2	1.6 ± 0.2	2.5 ± 0.1

3) Data of alternative region from result of long-term induction by RA

14-day: Cells were collected for RNA isolation after 14 days by RA induction

35-day: Cells were collected for RNA isolation after 35 days by RA induction

Gene symbol	Target transcript	Primer set Name	0-day Log2RQ mean ± S.D.	14-day Log2RQ mean ± S.D.	35-day Log2RQ mean ± S.D.
ATG9B	NM_173681.3	CE-07_01	0.0 ± 0.0	0.4 ± 0.0	-0.6 ± 0.1
ATG9B	FLJ39415/AK096734/C-PLACE6016160	CE-07_02	0.0 ± 0.0	0.1 ± 0.0	-0.7 ± 0.2
CDH6	NM_004932.2	CE-14_01	0.0 ± 0.0	3.3 ± 0.0	2.9 ± 0.0
CDH6	BC000019.2	CE-14_02	0.0 ± 0.0	2.0 ± 0.1	0.9 ± 0.1
CTHRC1	NM_138455.2	N-A3_013_01	0.0 ± 0.0	2.8 ± 0.0	1.3 ± 0.2
CTHRC1	FLJ57590/AK300273/D-PLACE7001513.1	N-A3_013_02	0.0 ± 0.4	3.5 ± 0.1	3.4 ± 0.4
EPB41L5	NM_020909.2	CE-27_01	0.0 ± 0.1	0.7 ± 0.0	0.6 ± 0.0
EPB41L5	BC032822.2	CE-27_02	0.0 ± 0.0	-0.3 ± 0.0	-0.1 ± 0.0
LMCD1	NM_014583.2	N-A2_015_04	0.0 ± 0.1	0.1 ± 0.1	-2.3 ± 0.1
LMCD1	FLJ55005/AK300803/D-SKNSH2002481.1	N-A2_015_02	0.0 ± 0.0	0.0 ± 0.0	-1.4 ± 0.1
MS4A6A	NM_152852.1	CE-22_01	0.0 ± 0.1	1.1 ± 0.2	4.2 ± 0.1
MS4A6A	NM_022349.2	CE-22_02	0.0 ± 0.1	0.5 ± 1.3	4.8 ± 0.1
MTA3	NM_020744.2	CE-28_01	0.0 ± 0.0	-1.0 ± 0.0	-2.4 ± 0.0
MTA3	FLJ45312/AK127245/C-BRHIP3005037	CE-28_04	0.0 ± 0.0	-0.5 ± 0.0	0.7 ± 0.1
NRP2	NM_003872.2	N-A3_007_01	0.0 ± 0.1	0.9 ± 0.0	1.6 ± 0.0
NRP2	NM_018534.3	N-A3_007_02	0.0 ± 0.1	1.3 ± 0.1	2.2 ± 0.0
NRP2	NM_201264.1	N-A3_007_03	0.0 ± 0.0	-1.5 ± 0.1	-1.3 ± 0.0
RSNL2	NM_024692.3	CE-16_01	0.0 ± 0.0	4.6 ± 0.0	5.6 ± 0.1
RSNL2	FLJ55798/AK302325/D-TESTI2048649.1	CE-16_02	0.0 ± 0.2	3.6 ± 0.2	4.1 ± 0.0
ST3GAL5	NM_003896.2	CE-08_01	0.0 ± 0.0	2.4 ± 0.0	4.2 ± 0.0
ST3GAL5	FLJ55056/AK295252/D-BRCAN2011189.1	CE-08_02	0.0 ± 0.0	2.0 ± 0.0	3.6 ± 0.0
TES	NM_015641.2	CE-12_01	0.0 ± 0.0	2.9 ± 0.0	2.5 ± 0.0
TES	FLJ59160/AK299104/D-NT2RI3007951.1	CE-12_02	0.0 ± 0.2	3.7 ± 0.0	4.3 ± 0.0
ZD52F10	NM_033317.2	CE-19_01	0.0 ± 0.1	-2.1 ± 0.0	-2.9 ± 0.1
ZD52F10	FLJ57785/AK304668/D-UTERU2034249.1	CE-19_04	0.0 ± 0.0	-1.8 ± 0.0	-1.7 ± 0.0
ITIH5	NM_030569.3	N-A2-3_001_01	0.0 ± 0.0	5.5 ± 0.0	4.8 ± 0.1
ITIH5	NM_001001851.1	N-A2-3_001_02	0.0 ± 0.0	4.7 ± 0.1	3.9 ± 0.0
CKMT1B	NM_020990.3	CE-17_01	0.0 ± 0.0	-1.8 ± 0.0	-0.6 ± 0.0
CKMT1B	FLJ52224/AK294063/D-BRALZ1000056.1	CE-17_02	0.0 ± 0.0	-0.9 ± 0.0	1.0 ± 0.0
CKMT1B	FLJ52454/AK293939/D-BRACE3032708.1	CE-17_03	0.0 ± 0.1	-1.1 ± 0.1	1.1 ± 0.1
DENND5B	NM_144973.2	CE-21_01	0.0 ± 0.0	2.3 ± 0.0	3.4 ± 0.0
DENND5B	BC020855.1	CE-21_02	0.0 ± 0.0	1.0 ± 0.0	1.6 ± 0.0
EVL	NM_016337.2	CE-29_01	0.0 ± 0.1	1.7 ± 0.1	1.9 ± 0.1
EVL	FLJ58489/AK295919/D-BRSSN2003639.1	CE-29_02	0.0 ± 0.1	2.5 ± 0.0	3.3 ± 0.1
FEZ1	NM_005103.3	CE-10_01	0.0 ± 0.0	-1.1 ± 0.1	0.4 ± 0.0
FEZ1	NM_022549.2	CE-10_02	0.0 ± 0.2	-2.5 ± 0.0	-1.4 ± 0.0
FNDC5	NM_153756.1	N-A3_023_01	0.0 ± 0.0	5.5 ± 0.0	6.2 ± 0.1
FNDC5	BC062297.1	N-A3_023_04	0.0 ± 0.1	5.4 ± 0.0	5.5 ± 0.0
FST	NM_013409.1	CE-26_01	0.0 ± 0.0	-4.0 ± 0.1	-5.0 ± 0.1
FST	NM_006350.2	CE-26_02	0.0 ± 0.0	-4.7 ± 0.1	-6.1 ± 0.1
MAPKAPK2	NM_004759.3	CE-30_01	0.0 ± 0.0	0.3 ± 0.0	-1.3 ± 0.0
MAPKAPK2	NM_032960.2	CE-30_02	0.0 ± 0.0	0.8 ± 0.0	-0.2 ± 0.0
MRPS15	NM_031280.2	CE-24_01	0.0 ± 0.0	-0.2 ± 0.0	-1.0 ± 0.1
MRPS15	FLJ56752/AK302633/D-TESTI4017571.1	CE-24_02	0.0 ± 0.1	0.5 ± 0.0	0.4 ± 0.1
NPHP1	NM_000272.2	CE-09_04	0.0 ± 0.0	3.3 ± 0.0	2.8 ± 0.1
NPHP1	NM_207181.1	CE-09_02	0.0 ± 0.0	0.9 ± 0.0	-0.5 ± 0.1
RBP1	NM_002899.2	N-A2-3_004_01	0.0 ± 0.0	4.9 ± 0.0	5.1 ± 0.0
RBP1	FLJ50903/AK301684/D-TESOP2006848.1	N-A2-3_004_02	0.0 ± 0.0	5.8 ± 0.1	6.5 ± 0.0
SLC44A5	NM_152697.2	CE-11_01	0.0 ± 0.0	4.5 ± 0.1	5.9 ± 0.0
SLC44A5	FLJ35851/AK093170/C-TESTI2007040	CE-11_02	0.0 ± 0.1	4.3 ± 0.0	5.1 ± 0.1
WDR74	NM_018093.1	CE-23_01	0.0 ± 0.0	-2.2 ± 0.0	-2.2 ± 0.0
WDR74	FLJ57690/AK303186/D-THYMU2025050.1	CE-23_02	0.0 ± 0.0	-0.4 ± 0.0	0.2 ± 0.0
YPEL3	NM_031477.3	CE-20_01	0.0 ± 0.0	2.9 ± 0.0	3.7 ± 0.1
YPEL3	FLJ12347/AK022409/C-MAMMA1002298	CE-20_02	0.0 ± 0.1	3.0 ± 0.0	3.6 ± 0.0

Supplementary Table 6. Quantitative evaluation of expression of 26 selected genes that showed AS in their C-terminus by real-time PCR.

1) Expression pattern of 26 selected genes that compared induction samples (1-day, 2-day and 7-day) by RA with the 0-day sample

			Change in expression level compared to the 0-day sample			
Gene symbol		cDNA name	1-day	2- day	7- day	Expression pattern
ATG9B	ATG9 autophagy related 9 homolog B (S. cerevisiae)	NM_173681.3	↑	↑	±	differ
		FLJ39415	±	↑	±	
CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	NM_004932.2	±	↓	↑	differ
		BC000019.2	±	±	↑	
CTHRC1	collagen triple helix repeat containing 1	NM_138455.2	↑	↑	↑	differ
		FLJ57590	±	↑	↑	
EPB41L5	erythrocyte membrane protein band 4.1 like 5	NM_020909.2	±	±	↑	differ
		BC032822.2	±	±	±	
LMCD1	LIM and cysteine-rich domains 1	NM_014583.2	↓	↓	±	differ
		FLJ55005	±	↓	±	
MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	NM_152852.1	±	↓	↓	differ
		NM_022349.2	±	±	↓	
MTA3	metastasis associated 1 family, member 3	NM_020744.2	±	±	±	differ
		FLJ45312	±	↓	↓	
NRP2	neuropilin 2	NM_003872.2	↑	↑	↑	differ
		NM_018534.3	↑	↑	↑	
		NM_201264.1	±	↑	↑	
RSNL2	CAP-GLY domain containing linker protein family, member 4	NM_024692.3	±	±	↑	differ
		FLJ55798	±	↑	↑	
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_003896.2	±	±	↑	differ
		FLJ55056	±	↑	↑	
TES	testis derived transcript (3 LIM domains)	NM_015641.2	±	±	↑	differ
		FLJ59160	↓	±	↑	
ZD52F10	dermokine	NM_033317.2	±	↓	±	differ
		FLJ57785	±	±	↓	
ITIH5	inter-alpha (globulin) inhibitor H5	NM_030569.3	↑	↑	↑	same
		NM_001001851.1	↑	↑	↑	
CKMT1B	creatine kinase, mitochondrial 1B	NM_020990.3	±	±	↓	same
		FLJ52224	±	±	↓	
		FLJ52454	±	±	↓	
DENND5B	DENN/MADD domain containing 5B	NM_144973.2	±	±	↑	same
		BC020855.1	±	±	↑	
EVL	Enah/Vasp-like	NM_016337.2	±	±	↑	same
		FLJ58489	±	±	↑	
FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	NM_005103.3	±	±	↓	same
		NM_022549.2	±	±	↓	
FNDC5	fibronectin type III domain containing 5	NM_153756.1	↑	↑	↑	same
		BC062297.1	↑	↑	↑	
FST	follistatin	NM_013409.1	±	↓	↓	same
		NM_006350.2	±	↓	↓	
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	NM_004759.3	↑	↑	±	same
		NM_032960.2	↑	↑	±	
MRPS15	mitochondrial ribosomal protein S15	NM_031280.2	±	±	±	same
		FLJ56752	±	±	±	
NPHP1	nephronophthisis 1 (juvenile)	NM_000272.2	±	±	↑	same
		NM_207181.1	±	±	↑	
RBP1	retinol binding protein 1, cellular	NM_002899.2	↑	↑	↑	same
		FLJ50903	↑	↑	↑	
SLC44A5	solute carrier family 44, member 5	NM_152697.2	±	±	↑	same
		FLJ35851	±	±	↑	
WDR74	WD repeat domain 74	NM_018093.1	±	±	±	same
		FLJ57690	±	±	±	
YPEL3	yippee-like 3 (Drosophila)	NM_031477.3	±	↑	↑	same
		FLJ12347	±	↑	↑	

Symbols used to indicate differences of mean averages of log2 ratios between the control (0-day) and experimental samples (1-day, 2-day and 7-day)
: "±", 1/2 but <twofold; " ↓ ", > 1/100 but ≤ 1/2; " ↑ ", ≥ twofold but < 100-fold; " ↑ ↑ ", ≥ 100-fold but < 1000-fold; and " ↑ ↑ ↑ ", ≥ 1000-fold

2) Expression pattern of 26 selected genes that compared long-term induction samples (14-day, 35-day) by RA with the 0-day sample

			Change in expression level compared to the 0-day sample		
Gene symbol		cDNA name	14-day	35- day	Expression pattern
ATG9B	ATG9 autophagy related 9 homolog B (S. cerevisiae)	NM_173681.3	±	±	same
		FLJ39415	±	±	
CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	NM_004932.2	↑	↑	differ
		BC000019.2	↑	±	
CTHRC1	collagen triple helix repeat containing 1	NM_138455.2	↑	↑	same
		FLJ57590	↑	↑	
EPB41L5	erythrocyte membrane protein band 4.1 like 5	NM_020909.2	±	±	same
		BC032822.2	±	±	
LMCD1	LIM and cysteine-rich domains 1	NM_014583.2	±	↓	same
		FLJ55005	±	↓	
MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	NM_152852.1	↑	↑	differ
		NM_022349.2	±	↑	
MTA3	metastasis associated 1 family, member 3	NM_020744.2	±	↓	differ
		FLJ45312	±	±	
NRP2	neuropilin 2	NM_003872.2	±	↑	differ
		NM_018534.3	↑	↑	
		NM_201264.1	↓	↓	
RSNL2	CAP-GLY domain containing linker protein family, member 4	NM_024692.3	↑	↑	same
		FLJ55798	↑	↑	
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_003896.2	↑	↑	same
		FLJ55056	↑	↑	
TES	testis derived transcript (3 LIM domains)	NM_015641.2	↑	↑	same
		FLJ59160	↑	↑	
ZD52F10	dermokine	NM_033317.2	↓	↓	same
		FLJ57785	↓	↓	
ITIH5	inter-alpha (globulin) inhibitor H5	NM_030569.3	↑	↑	same
		NM_001001851.1	↑	↑	
CKMT1B	creatine kinase, mitochondrial 1B	NM_020990.3	↓	±	differ
		FLJ52224	±	±	
		FLJ52454	↓	↑	
DENND5B	DENN/MADD domain containing 5B	NM_144973.2	↑	↑	differ
		BC020855.1	±	↑	
EVL	Enah/Vasp-like	NM_016337.2	↑	↑	same
		FLJ58489	↑	↑	
FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	NM_005103.3	↓	±	differ
		NM_022549.2	↓	↓	
FNDC5	fibronectin type III domain containing 5	NM_153756.1	↑	↑	same
		BC062297.1	↑	↑	
FST	follistatin	NM_013409.1	↓	↓	same
		NM_006350.2	↓	↓	
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	NM_004759.3	±	↓	differ
		NM_032960.2	±	±	
MRPS15	mitochondrial ribosomal protein S15	NM_031280.2	±	↓	differ
		FLJ56752	±	±	
NPHP1	nephronophthisis 1 (juvenile)	NM_000272.2	↑	↑	differ
		NM_207181.1	±	±	
RBP1	retinol binding protein 1, cellular	NM_002899.2	↑	↑	same
		FLJ50903	↑	↑	
SLC44A5	solute carrier family 44, member 5	NM_152697.2	↑	↑	same
		FLJ35851	↑	↑	
WDR74	WD repeat domain 74	NM_018093.1	↓	↓	differ
		FLJ57690	±	±	
YPEL3	yippee-like 3 (Drosophila)	NM_031477.3	↑	↑	same
		FLJ12347	↑	↑	

Symbols used to indicate differences of mean averages of log2 ratios between the control (0-day) and experimental samples (14-day and 35-day) : "±", 1/2 but <twofold; " ↓ ", > 1/100 but ≤ 1/2; " ↑ ", ≥ twofold but < 100-fold; " ↑ ↑ ", ≥ 100-fold but < 1000-fold; and " ↑ ↑ ↑ ", ≥ 1000-fold

Supplementary Table 7. Functional classification and type of protein-coding transcripts from selected 358 genes

Functional categorization (GO : Molecular function)		Number of matched genes	Type of protein-coding transcript				Variation type by AS	
		selected 365 genes	Multiple	%	Single	%	Alt. N-term	Alt. C-term
Binding	Nucleic acid binding	25	18	(72.0)	7	(28.0)	6	6
	Nucleotide binding	20	19	(95.0)	1	(5.0)	8	2
	Ion binding	12	10	(83.3)	2	(16.7)	6(2)	3(2)
	Protein binding	9	4	(44.4)	5	(55.6)	3	0
	Other bindings	3	1	(33.3)	2	(66.7)	1	0
Catalytic activity	Transferase activity	19	17	(89.5)	2	(10.5)	8(2)	3(2)
	Hydrolase activity	15	13	(86.7)	2	(13.3)	5	2
	Ligase activity	9	9	(100.0)	0	(0.0)	4(1)	1(1)
	Other catalytic activity	11	9	(81.8)	2	(18.2)	4	1
Transcription regulator activity		18	12	(66.7)	6	(33.3)	6	4
Signal transducer activity		12	5	(41.7)	7	(58.3)	4	1
Transporter activity		11	11	(100.0)	0	(0.0)	7	2
Structural molecule activity		4	4	(100.0)	0	(0.0)	2	0
Enzyme regulator activity		3	3	(100.0)	0	(0.0)	1	1
Others		3	1	(33.3)	2	(66.7)	0	0
Total		174						

Total refers to the number of cDNAs used for the classification of molecular function.
We categorized each cDNA used for identifying the genomic regions of extracted 423 probes.
Results obtained using the cDNAs transcribed from the same genomic region were merged.
We categorized 24,210 human RefSeq and identified 20,072 protein-coding genes.
Results obtained using the human RefSeq transcribed from the same genomic region were also merged.
If an encoded protein was predicted to belong to two or more categories, it was counted every time.

Multiple protein-coding transcripts produced from each gene by AS were classified according to their AS type.
Alt. N-term: gene producing multiple protein-coding transcripts as a result of alternative splicing of N-terminus.
Alt. C-term: gene producing multiple protein-coding transcripts as a result of alternative splicing of C-terminus.
(): gene poducing multiple protein-coding transcripts as a result of alternative splicing of both N- and C-terminuses.

Supplementary Table 8. **Quantitative analysis of expression of 12 selected transcription factor genes by real-time PCR.**

Relative expression to 0-day sample (Log2RQ)

1) Data of alternative region

Gene symbol	Target transcripts	Primer set Name	0-day Log2RQ mean ± S.D.	1-day Log2RQ mean ± S.D.	2-day Log2RQ mean ± S.D.	7-day Log2RQ mean ± S.D.
ETV1	NM_004956.3	NT-PS_01_01	0.0 ± 0.3	-0.1 ± 0.4	-1.1 ± 0.4	-0.5 ± 0.3
ETV1	FLJ50494/AK294572/D-BRAMY4002358.1	NT-PS_01_02	0.0 ± 0.1	0.3 ± 0.1	-0.7 ± 0.6	-1.4 ± 0.2
ETV4	NM_001986.1	NT-PS_02_01	0.0 ± 0.2	-0.4 ± 0.1	-1.0 ± 0.4	-5.8 ± 0.2
ETV4	BC007242.1	NT-PS_02_03	0.0 ± 0.0	-1.0 ± 0.4	-2.6 ± 0.4	-4.6 ± 0.2
ETV5	NM_004454.1	NT-PS_03_01	0.0 ± 0.5	-2.4 ± 0.6	-3.9 ± 1.2	-3.2 ± 1.0
ETV5	FLJ56169/AK301878/D-TESTI2012536.1	NT-PS_03_02	0.0 ± 0.1	-0.2 ± 0.2	-1.4 ± 0.7	-1.5 ± 0.3
PAX6	NM_000280.2	NT-PS_05_01	0.0 ± 1.5	1.7 ± 1.8	4.9 ± 0.4	8.2 ± 0.2
PAX6	FLJ36930/AK094249/C-BRACE2005251	NT-PS_05_03	0.0 ± 1.4	1.7 ± 1.5	5.0 ± 0.6	8.4 ± 0.3
POU5F1	NM_002701.3	TC04_NT-PS_04_06	0.0 ± 0.3	0.1 ± 0.2	-0.5 ± 0.3	-6.2 ± 0.1
POU5F1	NM_203289.3	NT-PS_04_02	0.0 ± 0.3	-0.8 ± 0.7	-4.8 ± 0.3	-5.2 ± 0.2
RARB	NM_000965.2	TC13_01	0.0 ± 0.5	6.1 ± 0.2	8.0 ± 0.0	7.6 ± 0.2
RARB	FLJ56241/AK299756/D-OCBBF2037981.1	TC13_02	0.0 ± 0.1	1.7 ± 0.3	3.2 ± 0.3	3.4 ± 0.5
HOXA3	NM_030661.3	N-A2_020_01	0.0 ± 0.3	7.7 ± 0.4	10.9 ± 0.4	15.6 ± 0.2
HOXA3	NM_153632.1	TC11_N-A2_020_06	0.0 ± 0.1	-0.1 ± 0.5	1.8 ± 0.4	6.1 ± 0.3
RFX2	NM_000635.2	NT-PS_07_01	0.0 ± 0.5	-0.2 ± 0.4	1.2 ± 0.1	3.4 ± 0.3
RFX2	FLJ53376/AK303321/D-THYMU3005661.1	NT-PS_07_02	0.0 ± 0.5	-0.4 ± 0.5	1.3 ± 0.1	3.7 ± 0.1
HNF1B	NM_000458.1	N-A2-3_002_01	0.0 ± 1.0	6.0 ± 0.2	9.4 ± 0.4	9.2 ± 0.3
HNF1B	NM_006481.1	N-A2-3_002_02	0.0 ± 2.1	6.3 ± 0.3	9.5 ± 0.3	8.8 ± 0.4
HOXA2	NM_006735.3	N-A2_011_01	0.0 ± 0.7	12.8 ± 0.5	14.1 ± 0.1	17.3 ± 0.2
HOXA2	FLJ39423/AK096742/C-PROST1000322	TC10_N-A2_011_05	0.0 ± 0.3	8.1 ± 0.2	9.2 ± 0.4	11.6 ± 0.2
PEG3	NM_006210.1	NT-PS_06_03	0.0 ± 0.5	1.0 ± 0.8	1.0 ± 0.3	3.0 ± 0.3
PEG3	NM_015363.3	NT-PS_06_04	0.0 ± 0.2	0.2 ± 0.0	0.2 ± 0.2	0.7 ± 0.1
ZNF483	NM_133464.1	TC12_02	0.0 ± 0.4	0.0 ± 0.2	-1.1 ± 0.4	-1.6 ± 0.3
ZNF483	FLJ35492/AK092811/C-SMINT2008672	TC12_01	0.0 ± 1.4	-0.9 ± 0.5	0.8 ± 0.5	-1.2 ± 0.2

2) Data of primers detected common region

Gene symbol	Target transcripts	Primer set Name	0-day Log2RQ mean ± S.D.	1-day Log2RQ mean ± S.D.	2-day Log2RQ mean ± S.D.	7-day Log2RQ mean ± S.D.
ETV1	NM_004956.3, FLJ50494	NT-PS_01_03	0.0 ± 0.1	0.0 ± 0.2	-1.2 ± 0.7	-0.3 ± 0.3
ETV4	NM_001986.1, BC007242.1	NT-PS_02_04	0.0 ± 0.3	-0.7 ± 0.1	-1.7 ± 0.4	-5.8 ± 0.3
ETV5	NM_004454.1, FLJ56169	NT-PS_03_03	0.0 ± 0.3	0.1 ± 0.2	-1.8 ± 0.7	-1.8 ± 0.0
PAX6	NM_000280.2, FLJ36930	NT-PS_05_04	0.0 ± 1.6	1.8 ± 1.9	4.9 ± 0.6	7.9 ± 0.3
POU5F1	NM_002701.3, NM_203289.3	TC04_NT-PS_04_05	0.0 ± 0.4	0.1 ± 0.3	-0.5 ± 0.3	-6.4 ± 0.1
RARB	NM_000965.2, FLJ56241	TC13_03	0.0 ± 0.8	5.3 ± 0.1	7.3 ± 0.0	7.0 ± 0.1
HOXA3	NM_030661.3, NM_153632.1	N-A2_020_03	0.0 ± 0.6	7.1 ± 0.5	10.2 ± 0.4	15.3 ± 0.2
RFX2	NM_000635.2, FLJ53376	NT-PS_07_03	0.0 ± 0.5	-0.2 ± 0.5	1.1 ± 0.2	3.7 ± 0.4
HNF1B	NM_000458.1, NM_006481.1	N-A2-3_002_03	0.0 ± 0.7	7.5 ± 0.2	11.1 ± 0.2	11.0 ± 0.3
HOXA2	NM_006735.3, FLJ39423	N-A2_011_03	0.0 ± 0.3	6.4 ± 0.2	7.8 ± 0.1	10.6 ± 0.2
PEG3	NM_006210.1, NM_015363.3	NT-PS_06_05	0.0 ± 0.1	1.0 ± 0.4	1.1 ± 0.2	3.0 ± 0.1
ZNF483	NM_133464.1, FLJ35492	TC12_03	0.0 ± 0.5	-0.1 ± 0.3	-1.0 ± 0.4	-1.8 ± 0.3

3) Data of alternative region from result of long-term induction by RA

14-day: Cells were collected for RNA isolation after 14 days by RA induction

35-day: Cells were collected for RNA isolation after 35 days by RA induction

Gene symbol	Target transcripts	Primer set Name	0-day Log2RQ mean ± S.D.	14-day Log2RQ mean ± S.D.	35-day Log2RQ mean ± S.D.
ETV1	NM_004956.3	NT-PS_01_01	0.0 ± 0.3	1.7 ± 0.8	2.7 ± 0.6
ETV1	FLJ50494/AK294572/D-BRAMY4002358.1	NT-PS_01_02	0.0 ± 0.1	3.0 ± 0.8	4.0 ± 0.4
ETV4	NM_001986.1	NT-PS_02_01	0.0 ± 0.2	-5.9 ± 0.5	-4.0 ± 0.6
ETV4	BC007242.1	NT-PS_02_03	0.0 ± 0.0	-2.0 ± 0.8	-0.9 ± 0.5
ETV5	NM_004454.1	NT-PS_03_01	0.0 ± 0.5	-2.0 ± 0.8	-0.6 ± 0.5
ETV5	FLJ56169/AK301878/D-TESTI2012536.1	NT-PS_03_02	0.0 ± 0.1	-0.2 ± 0.5	1.8 ± 0.7
PAX6	NM_000280.2	NT-PS_05_01	0.0 ± 1.5	7.6 ± 1.2	7.5 ± 1.0
PAX6	FLJ36930/AK094249/C-BRACE2005251	NT-PS_05_03	0.0 ± 1.4	8.7 ± 0.5	8.6 ± 0.3
POU5F1	NM_002701.3	TC04_NT-PS_04_06	0.0 ± 0.3	-6.5 ± 0.1	-5.8 ± 0.0
POU5F1	NM_203289.3	NT-PS_04_02	0.0 ± 0.3	-5.1 ± 0.1	-5.2 ± 0.1
RARB	NM_000965.2	TC13_01	0.0 ± 0.5	7.5 ± 0.3	8.9 ± 0.0
RARB	FLJ56241/AK299756/D-OCBBF2037981.1	TC13_02	0.0 ± 0.1	3.7 ± 0.2	5.9 ± 0.0
HOXA3	NM_030661.3	N-A2_020_01	0.0 ± 0.3	16.7 ± 0.3	17.7 ± 0.0
HOXA3	NM_153632.1	TC11_N-A2_020_06	0.0 ± 0.1	6.5 ± 0.5	7.6 ± 0.6
RFX2	NM_000635.2	NT-PS_07_01	0.0 ± 0.5	7.2 ± 0.7	8.4 ± 0.8
RFX2	FLJ53376/AK303321/D-THYMU3005661.1	NT-PS_07_02	0.0 ± 0.5	7.0 ± 0.8	8.2 ± 0.8
HNF1B	NM_000458.1	N-A2-3_002_01	0.0 ± 1.0	8.7 ± 3.1	8.0 ± 2.3
HNF1B	NM_006481.1	N-A2-3_002_02	0.0 ± 2.1	10.8 ± 1.8	10.2 ± 1.1
HOXA2	NM_006735.3	N-A2_011_01	0.0 ± 0.7	16.4 ± 0.1	17.9 ± 0.2
HOXA2	FLJ39423/AK096742/C-PROST1000322	TC10_N-A2_011_05	0.0 ± 0.3	11.9 ± 0.3	13.6 ± 0.2
PEG3	NM_006210.1	NT-PS_06_03	0.0 ± 0.5	5.4 ± 0.8	6.5 ± 0.8
PEG3	NM_015363.3	NT-PS_06_04	0.0 ± 0.2	4.3 ± 1.0	4.0 ± 0.8
ZNF483	NM_133464.1	TC12_02	0.0 ± 0.4	-3.4 ± 0.2	-2.3 ± 0.1
ZNF483	FLJ35492/AK092811/C-SMINT2008672	TC12_01	0.0 ± 1.4	-5.8 ± 0.6	-4.6 ± 1.1