**Supplementary Materials and Methods**

1. Cell culture and RNA isolation

NT2 cell line was purchased from STRATAGENE (CA, USA) [9] and was cultured according to the recommendations of the supplier. The stock solution (10 mM) of RA (SIGMA, MO, USA) was prepared in dimethyl sulfoxide. On day 0, the culture medium was replaced with fresh medium containing 10 uM RA. After 24h, 48h, 7day, 14day and 35day incubation with RA, we collected the cells for RNA isolation and designated them as 1-day, 2-day, 7-day, 14-day and 35-day samples, respectively. Medium containing 10 uM RA was replaced every 2-3 days. The 0-day sample (cells immediately before the addition of RA) was used as the control. Total RNAs were extracted from these cells using the ISOGEN Reagent (Nippongene, Tokyo, Japan). Subsequently, polyA(+) RNAs were isolated from each total RNA sample using a MicroPoly(A) Purist Kit (Life Technologies, CA, USA).

2. Microarray analysis

Synthetic polynucleotides (80-mers), representing 31,917 human transcripts, (MicroDiagnostic, Tokyo, Japan) were arrayed by using a custom arrayer. Microarray analyses were performed as previously described [8, M1]. All the data in accordance with the MIAME guideline were deposited at DDBJ via CIBEX database (http://cibex.nig.ac.jp/index.jsp) in Accession Numbers CBX132. 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 ($P < 0.01$). Among the extracted 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.

3. Analysis of splicing patterns of cDNAs

The splicing patterns of genes were analyzed by using the information available in the FLJ Human cDNA Database ver. 3.0, http://flj.lifesciencedb.jp, as described previously [10]. 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 transcripts, and ignored a lot of non-coding RNAs and mRNAs in which AS occurred only in the untranslated region [M2].

4. Quantitative real-time PCR analysis

Synthesis of template cDNA, performance of real-time PCR and design of primers were

performed as previously described [8, 10]. The expression values of individual genes were calculated by comparing their Ct values to that of the control using the RQ software (Life Technologies). And the expression levels of genes were normalized with respect to that of the human glyceraldehyde-3phosphate dehydrogenase (GAPDH) and were represented in log2 base. Samples were run in triplicates and the data shown are average of three experiments.

**Supplementary References**

[M1] Miura, A. et al. (2006). Differential responses of normal human coronary artery endothelial cells against multiple cytokines comparatively assessed by gene expression profiles. *FEBS Lett., 580,* 6871-6879.

[M2] Tollervey, D. (2006). Molecular biology: RNA lost in translation. *Nature, 440,* 425-426.

[S1] Mahnke-Zizelman, D.K. & Sabina, R.L. (2002). N-terminal sequence and distal histidine residues are responsible for pH-regulated cytoplasmic membrane binding of human AMP deaminase isoform E. *J. Biol. Chem., 277,* 42654-42662.

[S2] Barnes, K.C. et al. (2006). Polymorphisms in the novel gene acyloxyacyl hydroxylase (AOAH) are associated with asthma and associated phenotypes. *J. Allergy Clin. Immunol., 118,* 70-77.

[S3] Chen, Y. & Tang, B.L. (2006). The amyloid precursor protein and postnatal neurogenesis/neuroregeneration. *Biochem. Biophys. Res. Commun., 341,* 1-5.

[S4] Maloney, B. et al. (2004). Presence of a "CAGA box" in the APP gene unique to amyloid plaque-forming species and absent in all APLP-1/2 genes: implications in Alzheimer's disease. *FASEB J., 18,* 1288-1290.

[S5] Mowrer, K.R. & Wolfe, M.S. (2008). Promotion of BACE1 mRNA alternative splicing reduces amyloid beta-peptide production. *J. Biol. Chem., 283,* 18694-18701.

[S6] Tanahashi, H. & Tabira, T. (2007). A novel beta-site amyloid precursor protein cleaving enzyme (BACE) isoform regulated by nonsense-mediated mRNA decay and proteasome-dependent degradation. *Neurosci. Lett., 428,* 103-108.

[S7] Bros, M. et al. (2011). Differential gene expression analysis identifies murine Cacnb3 as strongly upregulated in distinct dendritic cell populations upon stimulation. *Gene, 472,* 18-27.

[S8] Vendel, A.C. et al. (2006). Alternative splicing of the voltage-gated Ca2+ channel beta4 subunit creates a uniquely folded N-terminal protein binding domain with cell-specific expression in the cerebellar cortex. *J. Neurosci., 26,* 2635-2644.

[S9] Philibert, R.A. et al. (2009). Examination of the nicotine dependence (NICSNP) consortium findings in the Iowa adoption studies population. *Nicotine Tob. Res., 11,* 286-292.

[S10] Hood, F.E. & Royle, S.J. (2009). Functional equivalence of the clathrin heavy chains CHC17 and CHC22 in endocytosis and mitosis. *J. Cell. Sci., 122,* 2185-2190.

[S11] Maeda, Y. et al. (2008). CUL2 is required for the activity of hypoxia-inducible factor and vasculogenesis. *J. Biol. Chem., 283,* 16084-16092.

[S12] Sartori da Silva, M.A. et al. (2010). Essential role for the d-Asb11 cul5 Box domain for proper notch signaling and neural cell fate decisions in vivo. *PLoS One, 5,* e14023.

[S13] Manneville, J.B. et al. (2010). Dlg1 binds GKAP to control dynein association with microtubules, centrosome positioning, and cell polarity. *J. Cell Biol., 191,* 585-598.

[S14] Eichenmuller, B. et al. (2002). The human EMAP-like protein-70 (ELP70) is a microtubule destabilizer that localizes to the mitotic apparatus. *J. Biol. Chem., 277,* 1301-1309.

[S15] Laramie, J.M. et al. (2008). Polymorphisms near EXOC4 and LRGUK on chromosome 7q32 are associated with Type 2 Diabetes and fasting glucose; the NHLBI Family Heart Study. *BMC Med. Genet., 9,* 46.

[S16] Greene, J.M. et al. (1998). Identification and characterization of a novel member of the fibroblast growth factor family. *Eur. J. Neurosci., 10,* 1911-1925.

[S17] Wang, C. et al. (2011). Identification of novel interaction sites that determine specificity between fibroblast growth factor homologous factors and voltage gated sodium channels. *J. Biol. Chem.,* .

[S18] Reinke, S.O. et al. (2009). Biochemical characterization of human and murine isoforms of UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase (GNE). *Glycoconj. J., 26,* 415-422.

[S19] Zhang, C.L. et al. (2002). Association of class II histone deacetylases with heterochromatin protein 1: potential role for histone methylation in control of muscle differentiation. *Mol. Cell. Biol., 22,* 7302-7312.

[S20] Chen, B. & Cepko, C.L. (2009). HDAC4 regulates neuronal survival in normal and diseased retinas. *Science, 323,* 256-259.

[S21] Kresse, S.H. et al. (2009). LSAMP, a novel candidate tumor suppressor gene in human osteosarcomas, identified by array comparative genomic hybridization. *Genes Chromosomes Cancer, 48,* 679-693.

[S22] Yen, C.C. et al. (2009). Identification of chromosomal aberrations associated with disease progression and a novel 3q13.31 deletion involving LSAMP gene in osteosarcoma. *Int. J. Oncol., 35,* 775-788.

[S23] Huang, X. et al. (2010). Mutational analysis of NHAoc/NHA2 in Saccharomyces cerevisiae. *Biochim. Biophys. Acta, 1800,* 1241-1247.

[S24] Ha, J.S. et al. (2010). Nox4-dependent H2O2 production contributes to chronic glutamate toxicity in primary cortical neurons. *Exp. Cell Res., 316,* 1651-1661.

[S25] Hou, S.W. et al. (2010). PTPH1 dephosphorylates and cooperates with p38gamma MAPK to increase ras oncogenesis through PDZ-mediated interaction. *Cancer Res., 70,* 2901-2910.

[S26] Menigatti, M. et al. (2009). The protein tyrosine phosphatase receptor type R gene is an early and frequent target of silencing in human colorectal tumorigenesis. *Mol. Cancer., 8,* 124.

[S27] Hendriks, W.J. et al. (2009). PTPRR protein tyrosine phosphatase isoforms and locomotion of vesicles and mice. *Cerebellum, 8,* 80-88.

[S28] Dupe, V. & Pellerin, I. (2009). Retinoic acid receptors exhibit cell-autonomous functions in cranial neural crest cells. *Dev. Dyn., 238,* 2701-2711.

[S29] Tran, P.X. et al. (2011). Association of retinoic acid receptor genes with meningomyelocele. *Birth Defects Res. A. Clin. Mol. Teratol., 91,* 39-43.

[S30] Sun, L. et al. (2003). Rim, a component of the presynaptic active zone and modulator of exocytosis, binds 14-3-3 through its N terminus. *J. Biol. Chem., 278,* 38301-38309.

[S31] Dossena, S. et al. (2005). The expression of wild-type pendrin (SLC26A4) in human embryonic kidney (HEK 293 Phoenix) cells leads to the activation of cationic currents. *Eur. J. Endocrinol., 153,* 693-699.

[S32] Bodoy, S. et al. (2005). Identification of LAT4, a novel amino acid transporter with system L activity. *J. Biol. Chem., 280,* 12002-12011.

[S33] Banerjee, S.K. et al. (2009). SGLT1 is a novel cardiac glucose transporter that is perturbed in disease states. *Cardiovasc. Res., 84,* 111-118.

[S34] Briski, K.P. & Marshall, E.S. (2001). Induction of ependymal, glial, and neuronal transactivation by intraventricular administration of the SGLT1 Na+-D-glucose cotransporter inhibitor phlorizin. *Neurochem. Res., 26,* 783-792.

Supplementary Table 2. Quantitative analysis of expression of 58 RA-responsive genes by real-time PCR.

Relative expression to 0-day sample (Log2RQ)

| Gene symbol | cDNA name | 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. | 14-day Log2RQ mean ± S.D. | 35-day Log2RQ mean ± S.D. |
|---|---|---|---|---|---|---|---|---|
| DCLK1 | FLJ50539 | 018_01 | 0.0 ± 1.0 | -0.2 ± 0.4 | -1.0 ± 0.6 | -5.2 ± 0.3 | -6.0 ± 0.1 | -3.5 ± 0.5 |
| DCLK1 | NM_004734.2 | 018_02 | 0.0 ± 0.5 | -0.3 ± 0.0 | 0.0 ± 0.0 | 2.5 ± 0.1 | 3.3 ± 0.0 | 6.2 ± 0.4 |
| ETV1 | NM_004956.3 | NT-PS_01_01 | 0.0 ± 0.3 | -0.1 ± 0.4 | -1.1 ± 0.4 | -0.5 ± 0.3 | 1.7 ± 0.8 | 2.7 ± 0.6 |
| ETV1 | FLJ50494 | NT-PS_01_02 | 0.0 ± 0.1 | 0.3 ± 0.1 | -0.7 ± 0.6 | -1.4 ± 0.2 | 3.0 ± 0.8 | 4.0 ± 0.4 |
| ETV4 | NM_001986.1 | NT-PS_02_01 | 0.0 ± 0.2 | -0.4 ± 0.1 | -1.0 ± 0.4 | -5.8 ± 0.2 | -5.9 ± 0.5 | -4.0 ± 0.6 |
| ETV4 | BC007242.1 | NT-PS_02_03 | 0.0 ± 0.0 | -1.0 ± 0.4 | -2.6 ± 0.4 | -4.6 ± 0.2 | -2.0 ± 0.8 | -0.9 ± 0.5 |
| ETV5 | NM_004454.1 | NT-PS_03_01 | 0.0 ± 0.5 | -2.4 ± 0.6 | -3.9 ± 1.2 | -3.2 ± 1.0 | -2.0 ± 0.8 | -0.6 ± 0.5 |
| ETV5 | FLJ56169 | NT-PS_03_02 | 0.0 ± 0.1 | -0.2 ± 0.2 | -1.4 ± 0.7 | -1.5 ± 0.3 | -0.2 ± 0.5 | 1.8 ± 0.7 |
| GPRC5B | NM_016235.1 | BT_0078_01 | 0.0 ± 0.0 | 0.6 ± 0.1 | -0.3 ± 0.4 | 0.0 ± 0.1 | -1.6 ± 0.2 | 0.8 ± 0.4 |
| GPRC5B | FLJ55176 | BT_0078_02 | 0.0 ± 0.1 | -0.6 ± 0.3 | -1.6 ± 0.5 | -0.8 ± 0.4 | -2.1 ± 0.2 | 0.9 ± 0.2 |
| HOXA3 | NM_030661.3 | N-A2_020_01 | 0.0 ± 0.3 | 7.7 ± 0.4 | 10.9 ± 0.4 | 15.6 ± 0.2 | 16.7 ± 0.3 | 17.7 ± 0.0 |
| 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 | 6.5 ± 0.5 | 7.6 ± 0.6 |
| MEIS2 | NM_020149.2 | N-A3_016_01 | 0.0 ± 0.7 | 3.4 ± 0.7 | 3.8 ± 0.3 | 6.1 ± 0.1 | 4.3 ± 0.2 | 6.3 ± 0.5 |
| MEIS2 | NM_002399.2 | N-A3_016_02 | 0.0 ± 0.4 | 2.2 ± 0.4 | 2.1 ± 0.1 | 4.0 ± 0.1 | 2.6 ± 0.3 | 4.4 ± 0.3 |
| MEIS2 | NM_172316.1 | N-A3_016_03 | 0.0 ± 1.1 | 2.6 ± 0.6 | 2.6 ± 0.3 | 4.8 ± 0.1 | 3.6 ± 0.4 | 5.6 ± 0.2 |
| NEFM | FLJ58361 | E7 | 0.0 ± 0.1 | -0.3 ± 0.4 | 0.2 ± 0.2 | 2.8 ± 0.3 | 1.0 ± 0.3 | 3.9 ± 1.4 |
| NEFM | NM_005382.1 | E10 | 0.0 ± 0.0 | 1.0 ± 0.3 | 1.0 ± 0.1 | 5.1 ± 0.3 | 3.3 ± 0.1 | 4.3 ± 1.5 |
| PAX6 | NM_000280.2 | NT-PS_05_01 | 0.0 ± 1.5 | 1.7 ± 1.8 | 4.9 ± 0.4 | 8.2 ± 0.2 | 7.6 ± 1.2 | 7.5 ± 1.0 |
| PAX6 | FLJ36930 | NT-PS_05_03 | 0.0 ± 1.4 | 1.7 ± 1.5 | 5.0 ± 0.6 | 8.4 ± 0.3 | 8.7 ± 0.5 | 8.6 ± 0.3 |
| PDZRN3 | FLJ55043 | 023_01 | 0.0 ± 0.0 | 2.2 ± 1.7 | 7.4 ± 0.8 | 11.7 ± 0.2 | 9.0 ± 0.7 | 10.2 ± 0.7 |
| PDZRN3 | FLJ54746 | 023_02 | 0.0 ± 0.3 | 0.9 ± 0.8 | 4.0 ± 0.2 | 6.3 ± 0.1 | 5.6 ± 0.5 | 4.9 ± 0.1 |
| PDZRN3 | FLJ54738 | 023_03 | 0.0 ± 0.7 | -0.1 ± 0.2 | 1.3 ± 0.7 | 7.0 ± 0.0 | 6.0 ± 0.1 | 4.1 ± 1.0 |
| PDZRN3 | FLJ97766 | 023_04 | 0.0 ± 0.0 | 0.4 ± 0.6 | 1.9 ± 0.7 | 4.7 ± 0.0 | 3.9 ± 0.0 | 3.0 ± 0.7 |
| PDZRN3 | NM_015009.1 | 023_05 | 0.0 ± 0.1 | -0.3 ± 0.7 | 1.3 ± 0.3 | 3.7 ± 0.2 | 2.7 ± 0.1 | 1.7 ± 0.2 |
| 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 | -6.5 ± 0.1 | -5.8 ± 0.0 |
| POU5F1 | NM_203289.3 | NT-PS_04_02 | 0.0 ± 0.3 | -0.8 ± 0.7 | -4.8 ± 0.3 | -5.2 ± 0.2 | -5.1 ± 0.1 | -5.2 ± 0.1 |
| RARB | NM_000965.2 | TC13_01 | 0.0 ± 0.5 | 6.1 ± 0.2 | 8.0 ± 0.0 | 7.6 ± 0.2 | 7.5 ± 0.3 | 8.9 ± 0.0 |
| RARB | FLJ56241 | TC13_02 | 0.0 ± 0.1 | 1.7 ± 0.3 | 3.2 ± 0.3 | 3.4 ± 0.5 | 3.7 ± 0.2 | 5.9 ± 0.0 |
| SEMA3C | FLJ55486 | C8 | 0.0 ± 1.4 | -0.8 ± 1.7 | 0.3 ± 0.4 | 4.6 ± 0.5 | 2.6 ± 0.1 | 5.2 ± 0.6 |
| SEMA3C | NM_006379.2 | C9 | 0.0 ± 0.6 | 1.6 ± 0.5 | 2.2 ± 0.4 | 7.3 ± 0.5 | 4.8 ± 0.6 | 7.3 ± 0.2 |
| SKAP2 | FLJ50630 | N-A3_026_01/067_01 | 0.0 ± 0.2 | 9.1 ± 0.1 | 11.4 ± 0.3 | 11.1 ± 0.0 | 14.4 ± 0.2 | 15.3 ± 0.6 |
| SKAP2 | FLJ51950 | N-A3_026_02/067_02 | 0.0 ± 0.3 | 9.0 ± 0.0 | 10.3 ± 0.6 | 12.2 ± 0.3 | 8.2 ± 1.0 | 11.8 ± 1.2 |
| SKAP2 | NM_003930.3 | N-A3_026_03/067_03 | 0.0 ± 1.0 | 6.7 ± 0.4 | 7.6 ± 0.4 | 10.2 ± 0.5 | 12.4 ± 0.2 | 13.9 ± 0.8 |
| TGIF1 | NM_003244.2 | N-A3_014_01 | 0.0 ± 0.4 | -1.3 ± 0.1 | -1.9 ± 0.2 | -0.5 ± 0.0 | -2.2 ± 0.8 | -1.9 ± 0.4 |
| TGIF1 | NM_173207.1 | N-A3_014_02 | 0.0 ± 0.2 | -0.5 ± 0.4 | -0.1 ± 0.2 | 1.6 ± 0.1 | -0.7 ± 0.1 | -1.1 ± 0.8 |
| TGIF1 | NM_170695.2 | N-A3_014_03 | 0.0 ± 0.0 | -1.3 ± 0.1 | -0.9 ± 0.1 | -0.2 ± 0.2 | -1.9 ± 1.1 | -2.2 ± 0.4 |
| TXNIP | NM_006472.1 | A1 | 0.0 ± 0.2 | 0.8 ± 0.3 | 2.7 ± 0.6 | 7.2 ± 0.0 | 4.1 ± 0.5 | 5.6 ± 0.4 |
| TXNIP | FLJ59613 | A2 | 0.0 ± 0.0 | 0.8 ± 0.5 | 3.2 ± 0.7 | 5.9 ± 0.1 | 3.5 ± 0.8 | 5.2 ± 0.3 |
| ASRGL1 | NM_025080.2 | N-A3_006_01 | 0.0 ± 0.2 | 0.5 ± 0.2 | 1.4 ± 0.5 | 3.2 ± 0.2 | -0.5 ± 0.1 | -0.3 ± 0.4 |
| ASRGL1 | BC064963.1 | N-A3_006_02 | 0.0 ± 0.1 | 0.9 ± 0.2 | 1.8 ± 0.7 | 3.5 ± 0.4 | 0.3 ± 0.0 | 0.4 ± 0.4 |
| CYP2S1 | NM_030622.6 | N-A2_010_01 | 0.0 ± 0.3 | 1.2 ± 0.0 | 0.2 ± 0.0 | -2.9 ± 0.3 | -5.8 ± 1.1 | -4.9 ± 1.1 |
| CYP2S1 | FLJ52866 | N-A2_010_02 | 0.0 ± 0.2 | 1.0 ± 0.2 | -0.1 ± 0.1 | -3.1 ± 0.5 | -5.7 ± 0.7 | -5.2 ± 0.7 |
| CYP26B1 | NM_019885.2 | N-A2_017_01 | 0.0 ± 1.0 | -0.5 ± 0.8 | 0.9 ± 0.5 | 7.5 ± 0.2 | 5.7 ± 0.8 | 9.5 ± 0.5 |
| CYP26B1 | FLJ51622 | N-A2_017_02 | 0.0 ± 1.3 | -0.5 ± 1.4 | 0.6 ± 0.5 | 7.0 ± 0.8 | 4.9 ± 0.0 | 8.7 ± 0.3 |
| DNMT3B | NM_006892.3 | B2 | 0.0 ± 0.7 | 0.3 ± 0.1 | -1.4 ± 0.2 | -6.8 ± 0.2 | -11.4 ± 1.6 | -10.5 ± 0.2 |
| DNMT3B | NM_175849.1 | B4 | 0.0 ± 0.7 | 1.0 ± 0.4 | -0.4 ± 0.3 | -3.2 ± 0.2 | -4.9 ± 0.1 | -3.5 ± 0.7 |
| GSTO2 | NM_183239.1 | N-A3_017_01 | 0.0 ± 0.0 | -2.0 ± 0.2 | -1.1 ± 0.3 | -0.7 ± 0.2 | -2.0 ± 1.2 | -0.9 ± 0.4 |
| GSTO2 | FLJ52232 | N-A3_017_02 | 0.0 ± 0.0 | -1.9 ± 0.1 | -1.2 ± 0.2 | -1.5 ± 0.2 | -2.9 ± 1.4 | -2.3 ± 1.1 |
| HOXA1 | NM_005522.3 | N-A2-3_003_04 | 0.0 ± 0.9 | 15.0 ± 0.1 | 14.3 ± 0.3 | 14.5 ± 1.1 | 11.1 ± 0.1 | 12.7 ± 0.8 |
| HOXA1 | NM_153620.1 | N-A2-3_003_02 | 0.0 ± 1.9 | 13.8 ± 0.1 | 14.1 ± 0.2 | 13.5 ± 0.7 | 9.8 ± 0.3 | 10.5 ± 0.1 |
| ISYNA1 | NM_016368.3 | N-A3_024_01 | 0.0 ± 0.0 | 1.0 ± 0.6 | 1.4 ± 0.2 | 2.9 ± 0.0 | 1.8 ± 0.4 | 2.2 ± 0.3 |
| ISYNA1 | FLJ34860 | N-A3_024_05 | 0.0 ± 0.0 | 1.2 ± 0.7 | 1.5 ± 0.2 | 3.2 ± 0.1 | 2.0 ± 0.3 | 2.5 ± 0.6 |
| ISYNA1 | FLJ36142 | N-A3_024_03 | 0.0 ± 1.2 | 0.4 ± 0.7 | 0.3 ± 0.1 | 1.8 ± 0.2 | 0.2 ± 0.3 | -0.2 ± 1.0 |
| NMU | NM_006681.1 | N-A3_025_01 | 0.0 ± 0.1 | 1.7 ± 0.2 | 2.3 ± 0.3 | 2.7 ± 0.3 | 2.3 ± 0.4 | 1.3 ± 0.0 |
| NMU | ENST00000381315 | N-A3_025_02 | 0.0 ± 0.1 | 2.7 ± 0.3 | 3.5 ± 0.0 | 3.2 ± 0.3 | 2.9 ± 0.2 | 1.6 ± 0.3 |
| PKNOX2 | NM_022062.1 | N-A3_020_04 | 0.0 ± 0.2 | 1.0 ± 0.1 | 1.9 ± 0.2 | 2.8 ± 0.1 | 2.4 ± 0.1 | 2.1 ± 0.7 |
| PKNOX2 | FLJ58605 | N-A3_020_05 | 0.0 ± 0.2 | 1.1 ± 0.0 | 1.9 ± 0.2 | 2.8 ± 0.1 | 2.0 ± 0.2 | 1.9 ± 0.9 |
| RFX2 | NM_000635.2 | NT-PS_07_01 | 0.0 ± 0.5 | -0.2 ± 0.4 | 1.2 ± 0.1 | 3.4 ± 0.3 | 7.2 ± 0.7 | 8.4 ± 0.8 |
| RFX2 | FLJ53376 | NT-PS_07_02 | 0.0 ± 0.5 | -0.4 ± 0.5 | 1.3 ± 0.1 | 3.7 ± 0.1 | 7.0 ± 0.8 | 8.2 ± 0.8 |
| RNF207 | NM_173795.2 | N-A3_018_01 | 0.0 ± 2.5 | 1.4 ± 0.3 | 0.8 ± 0.4 | 2.9 ± 0.1 | 2.0 ± 0.4 | 1.3 ± 0.7 |
| RNF207 | FLJ54599 | N-A3_018_02 | 0.0 ± 0.0 | 2.1 ± 0.0 | 2.1 ± 0.0 | 4.6 ± 0.1 | 3.6 ± 0.9 | 4.1 ± 0.5 |
| SPP1 | FLJ54682 | D5 | 0.0 ± 0.1 | 0.4 ± 0.0 | -0.5 ± 0.5 | -0.5 ± 0.5 | -4.3 ± 1.3 | -4.3 ± 0.1 |
| SPP1 | FLJ52507 | D6 | 0.0 ± 0.1 | 0.3 ± 0.0 | 0.0 ± 0.6 | -0.1 ± 0.5 | -3.5 ± 1.9 | -4.3 ± 0.0 |
| SPP1 | FLJ78337 | D7 | 0.0 ± 0.5 | 0.4 ± 0.3 | -0.3 ± 0.6 | -0.4 ± 0.5 | -4.2 ± 1.5 | -4.7 ± 0.2 |
| SPP1 | NM_000582.2 | D8 | 0.0 ± 1.2 | -0.3 ± 0.0 | -0.5 ± 0.6 | -1.0 ± 1.1 | -4.1 ± 1.0 | -5.3 ± 0.3 |
| ATG9B | NM_173681.3 | CE-07_01 | 0.0 ± 0.5 | 1.1 ± 0.3 | 3.2 ± 0.3 | 0.6 ± 0.9 | 0.4 ± 0.0 | -0.6 ± 0.1 |
| ATG9B | FLJ39415 | CE-07_02 | 0.0 ± 0.7 | 0.6 ± 0.4 | 2.2 ± 0.2 | -0.2 ± 0.3 | 0.1 ± 0.0 | -0.7 ± 0.2 |
| CDH6 | NM_004932.2 | CE-14_01 | 0.0 ± 0.4 | 0.5 ± 0.4 | -1.5 ± 0.3 | 3.6 ± 0.0 | 3.3 ± 0.0 | 2.9 ± 0.0 |
| CDH6 | BC000019.2 | CE-14_02 | 0.0 ± 0.2 | 0.1 ± 0.3 | -0.2 ± 0.2 | 2.5 ± 0.1 | 2.0 ± 0.1 | 0.9 ± 0.1 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| CKMT1B | NM_020990.3 | CE-17_01 | 0.0 ± 0.3 | -0.6 ± 0.2 | -0.6 ± 0.3 | -2.9 ± 0.1 | -1.8 ± 0.0 | -0.6 ± 0.0 |
| CKMT1B | FLJ52224 | CE-17_02 | 0.0 ± 1.1 | -0.6 ± 0.2 | -0.3 ± 0.4 | -2.6 ± 0.1 | -0.9 ± 0.0 | 1.0 ± 0.0 |
| CKMT1B | FLJ52454 | CE-17_03 | 0.0 ± 0.9 | -0.8 ± 0.2 | -0.6 ± 0.3 | -2.8 ± 0.0 | -1.1 ± 0.1 | 1.1 ± 0.1 |
| CLIP4 | NM_024692.3 | CE-16_01 | 0.0 ± 0.6 | -0.4 ± 0.6 | 0.8 ± 0.4 | 2.9 ± 0.1 | 4.6 ± 0.0 | 5.6 ± 0.1 |
| CLIP4 | FLJ55798 | CE-16_02 | 0.0 ± 0.4 | -0.3 ± 0.5 | 1.5 ± 0.4 | 2.3 ± 0.2 | 3.6 ± 0.2 | 4.1 ± 0.0 |
| CTHRC1 | NM_138455.2 | N-A3_013_01 | 0.0 ± 0.3 | 3.1 ± 0.3 | 5.0 ± 0.2 | 5.1 ± 0.6 | 2.8 ± 0.0 | 1.3 ± 0.2 |
| CTHRC1 | FLJ57590 | N-A3_013_02 | 0.0 ± 0.7 | 0.5 ± 0.1 | 1.7 ± 0.2 | 1.9 ± 0.2 | 3.5 ± 0.1 | 3.4 ± 0.4 |
| DENND5B | NM_144973.2 | CE-21_01 | 0.0 ± 0.2 | -0.2 ± 0.3 | 0.4 ± 0.1 | 2.1 ± 0.1 | 2.3 ± 0.0 | 3.4 ± 0.0 |
| DENND5B | BC020855.1 | CE-21_02 | 0.0 ± 0.2 | -0.2 ± 0.2 | 0.3 ± 0.1 | 1.4 ± 0.1 | 1.0 ± 0.0 | 1.6 ± 0.0 |
| DMKN | NM_033317.2 | CE-19_01 | 0.0 ± 0.3 | -0.3 ± 0.2 | -1.1 ± 0.3 | -0.8 ± 0.0 | -2.1 ± 0.0 | -2.9 ± 0.1 |
| DMKN | FLJ57785 | CE-19_04 | 0.0 ± 1.0 | -0.2 ± 0.2 | 0.5 ± 0.3 | -1.0 ± 0.1 | -1.8 ± 0.0 | -1.7 ± 0.0 |
| EPB41L5 | NM_020909.2 | CE-27_01 | 0.0 ± 0.2 | -0.2 ± 0.1 | -0.1 ± 0.1 | 1.8 ± 0.1 | 0.7 ± 0.0 | 0.6 ± 0.0 |
| EPB41L5 | BC032822.2 | CE-27_02 | 0.0 ± 0.7 | -0.5 ± 0.3 | -0.2 ± 0.3 | 0.5 ± 0.1 | -0.3 ± 0.0 | -0.1 ± 0.0 |
| EVL | NM_016337.2 | CE-29_01 | 0.0 ± 0.3 | -0.1 ± 0.2 | 0.2 ± 0.3 | 1.1 ± 0.2 | 1.7 ± 0.1 | 1.9 ± 0.1 |
| EVL | FLJ58489 | CE-29_02 | 0.0 ± 0.1 | 0.6 ± 0.2 | 0.7 ± 0.2 | 2.2 ± 0.2 | 2.5 ± 0.0 | 3.3 ± 0.1 |
| FEZ1 | NM_005103.3 | CE-10_01 | 0.0 ± 0.1 | -0.6 ± 0.2 | -0.7 ± 0.3 | -2.0 ± 0.1 | -1.1 ± 0.1 | 0.4 ± 0.0 |
| FEZ1 | NM_022549.2 | CE-10_02 | 0.0 ± 0.7 | 0.0 ± 0.4 | -0.8 ± 0.3 | -1.2 ± 0.1 | -2.5 ± 0.0 | -1.4 ± 0.0 |
| FNDC5 | NM_153756.1 | N-A3_023_01 | 0.0 ± 0.4 | 3.1 ± 0.1 | 4.0 ± 0.3 | 4.0 ± 0.3 | 5.5 ± 0.0 | 6.2 ± 0.1 |
| FNDC5 | BC062297.1 | N-A3_023_04 | 0.0 ± 0.3 | 3.0 ± 0.1 | 4.1 ± 0.5 | 3.7 ± 0.3 | 5.4 ± 0.0 | 5.5 ± 0.0 |
| FST | NM_013409.1 | CE-26_01 | 0.0 ± 0.4 | -0.7 ± 0.1 | -2.3 ± 0.4 | -2.8 ± 0.7 | -4.0 ± 0.1 | -5.0 ± 0.1 |
| FST | NM_006350.2 | CE-26_02 | 0.0 ± 0.4 | -0.1 ± 0.2 | -2.6 ± 0.4 | -2.7 ± 0.6 | -4.7 ± 0.1 | -6.1 ± 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 | 8.7 ± 3.1 | 8.0 ± 2.3 |
| 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 | 10.8 ± 1.8 | 10.2 ± 1.1 |
| HOXA2 | NM_006735.3 | N-A2_011_01 | 0.0 ± 0.7 | 12.8 ± 0.5 | 14.1 ± 0.1 | 17.3 ± 0.2 | 16.4 ± 0.1 | 17.9 ± 0.2 |
| HOXA2 | FLJ39423 | TC10_N-A2_011_05 | 0.0 ± 0.3 | 8.1 ± 0.2 | 9.2 ± 0.4 | 11.6 ± 0.2 | 11.9 ± 0.3 | 13.6 ± 0.2 |
| 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 | 5.5 ± 0.0 | 4.8 ± 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 | 4.7 ± 0.1 | 3.9 ± 0.0 |
| LMCD1 | NM_014583.2 | N-A2_015_04 | 0.0 ± 0.5 | -2.0 ± 0.4 | -2.7 ± 0.1 | -0.5 ± 0.1 | 0.1 ± 0.1 | -2.3 ± 0.1 |
| LMCD1 | FLJ55005 | N-A2_015_02 | 0.0 ± 0.4 | -0.9 ± 0.1 | -1.3 ± 0.4 | 0.0 ± 0.1 | 0.0 ± 0.0 | -1.4 ± 0.1 |
| MAPKAPK2 | NM_004759.3 | CE-30_01 | 0.0 ± 0.3 | 2.0 ± 0.1 | 3.1 ± 0.3 | 0.5 ± 0.1 | 0.3 ± 0.0 | -1.3 ± 0.0 |
| MAPKAPK2 | NM_032960.2 | CE-30_02 | 0.0 ± 0.4 | 1.4 ± 0.1 | 1.6 ± 0.3 | 1.0 ± 0.0 | 0.8 ± 0.0 | -0.2 ± 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 | -0.2 ± 0.0 | -1.0 ± 0.1 |
| MRPS15 | FLJ56752 | CE-24_02 | 0.0 ± 0.1 | 0.3 ± 0.2 | 0.1 ± 0.1 | 0.7 ± 0.1 | 0.5 ± 0.0 | 0.4 ± 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 | 1.1 ± 0.2 | 4.2 ± 0.1 |
| MS4A6A | NM_022349.2 | CE-22_02 | 0.0 ± 0.7 | -0.6 ± 0.7 | -1.0 ± 0.2 | -1.7 ± 0.7 | 0.5 ± 1.3 | 4.8 ± 0.1 |
| MTA3 | NM_020744.2 | CE-28_01 | 0.0 ± 0.1 | -0.2 ± 0.1 | -0.1 ± 0.2 | -0.6 ± 0.1 | -1.0 ± 0.0 | -2.4 ± 0.0 |
| MTA3 | FLJ45312 | CE-28_04 | 0.0 ± 0.2 | -0.4 ± 0.3 | -1.0 ± 0.4 | -1.2 ± 0.3 | -0.5 ± 0.0 | 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 | 3.3 ± 0.0 | 2.8 ± 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 | 0.9 ± 0.0 | -0.5 ± 0.1 |
| NRP2 | NM_003872.2 | N-A3_007_01 | 0.0 ± 0.2 | 1.0 ± 0.3 | 2.9 ± 0.3 | 3.3 ± 0.5 | 0.9 ± 0.0 | 1.6 ± 0.0 |
| NRP2 | NM_018534.3 | N-A3_007_02 | 0.0 ± 0.6 | 2.1 ± 0.3 | 3.7 ± 0.2 | 4.2 ± 0.3 | 1.3 ± 0.1 | 2.2 ± 0.0 |
| NRP2 | NM_201264.1 | N-A3_007_03 | 0.0 ± 0.3 | 0.6 ± 0.1 | 1.7 ± 0.2 | 1.5 ± 0.4 | -1.5 ± 0.1 | -1.3 ± 0.0 |
| PEG3 | NM_006210.1 | NT-PS_06_03 | 0.0 ± 0.5 | 1.0 ± 0.8 | 1.0 ± 0.3 | 3.0 ± 0.3 | 5.4 ± 0.8 | 6.5 ± 0.8 |
| PEG3 | NM_015363.3 | NT-PS_06_04 | 0.0 ± 0.2 | 0.2 ± 0.0 | 0.2 ± 0.2 | 0.7 ± 0.1 | 4.3 ± 1.0 | 4.0 ± 0.8 |
| 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 | 4.9 ± 0.0 | 5.1 ± 0.0 |
| RBP1 | FLJ50903 | N-A2-3_004_02 | 0.0 ± 0.3 | 2.4 ± 0.3 | 2.5 ± 0.4 | 5.2 ± 0.1 | 5.8 ± 0.1 | 6.5 ± 0.0 |
| SLC44A5 | NM_152697.2 | CE-11_01 | 0.0 ± 0.5 | 0.1 ± 0.1 | 0.7 ± 0.1 | 3.1 ± 0.3 | 4.5 ± 0.1 | 5.9 ± 0.0 |
| SLC44A5 | FLJ35851 | CE-11_02 | 0.0 ± 0.4 | 0.3 ± 0.1 | 0.5 ± 0.1 | 2.8 ± 0.3 | 4.3 ± 0.0 | 5.1 ± 0.1 |
| ST3GAL5 | NM_003896.2 | CE-08_01 | 0.0 ± 0.3 | 0.4 ± 0.3 | 0.7 ± 0.1 | 2.5 ± 0.1 | 2.4 ± 0.0 | 4.2 ± 0.0 |
| ST3GAL5 | FLJ55056 | CE-08_02 | 0.0 ± 0.2 | 0.8 ± 0.3 | 1.1 ± 0.2 | 2.6 ± 0.1 | 2.0 ± 0.0 | 3.6 ± 0.0 |
| TES | NM_015641.2 | CE-12_01 | 0.0 ± 0.2 | -0.5 ± 0.3 | 0.0 ± 0.2 | 2.1 ± 0.0 | 2.9 ± 0.0 | 2.5 ± 0.0 |
| TES | FLJ59160 | CE-12_02 | 0.0 ± 0.7 | -1.2 ± 0.3 | -0.5 ± 0.3 | 1.7 ± 0.1 | 3.7 ± 0.0 | 4.3 ± 0.0 |
| WDR74 | NM_018093.1 | CE-23_01 | 0.0 ± 0.2 | 0.2 ± 0.2 | -0.5 ± 0.2 | -0.4 ± 0.1 | -2.2 ± 0.0 | -2.2 ± 0.0 |
| WDR74 | FLJ57690 | CE-23_02 | 0.0 ± 0.1 | 0.0 ± 0.1 | -0.2 ± 0.1 | 0.1 ± 0.1 | -0.4 ± 0.0 | 0.2 ± 0.0 |
| YPEL3 | NM_031477.3 | CE-20_01 | 0.0 ± 0.1 | 0.2 ± 0.3 | 1.3 ± 0.2 | 2.3 ± 0.1 | 2.9 ± 0.0 | 3.7 ± 0.1 |
| YPEL3 | FLJ12347 | CE-20_02 | 0.0 ± 0.8 | 0.9 ± 0.2 | 2.2 ± 0.3 | 2.5 ± 0.0 | 3.0 ± 0.0 | 3.6 ± 0.0 |
| ZNF483 | NM_133464.1 | TC12_02 | 0.0 ± 0.4 | 0.0 ± 0.2 | -1.1 ± 0.4 | -1.6 ± 0.3 | -3.4 ± 0.2 | -2.3 ± 0.1 |
| ZNF483 | FLJ35492 | TC12_01 | 0.0 ± 1.4 | -0.9 ± 0.5 | 0.8 ± 0.5 | -1.2 ± 0.2 | -5.8 ± 0.6 | -4.6 ± 1.1 |

Supplementary Table 3. Quantitative analysis of genes containing multiple TSSs by real-time PCR

Relative expression to 0-day sample (Log2RQ)

| Gene symbol | cDNA name | 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. | 14-day Log2RQ mean ± S.D. | 35-day Log2RQ mean ± S.D. |
|---|---|---|---|---|---|---|---|---|
| AGPS | FLJ51873 | 027_01 | 0.0 ± 0.2 | 0.6 ± 0.5 | -2.5 ± 1.2 | 4.5 ± 0.3 | 2.8 ± 0.7 | 3.4 ± 0.5 |
| AGPS | NM_003659.1 | 027_02 | 0.0 ± 0.1 | -0.1 ± 0.2 | 0.1 ± 0.0 | 1.1 ± 0.2 | -1.5 ± 0.4 | -1.1 ± 0.2 |
| AKT1 | FLJ53606 | 019_01 | 0.0 ± 0.1 | 0.5 ± 0.0 | -0.6 ± 0.5 | 4.1 ± 0.1 | 7.4 ± 0.8 | 8.7 ± 1.1 |
| AKT1 | NM_005163.2 | 019_02 | 0.0 ± 0.2 | -0.6 ± 0.4 | 0.1 ± 0.1 | 1.0 ± 0.1 | 0.4 ± 0.2 | 1.2 ± 0.7 |
| ARHGEF3 | FLJ55856 | 032_01 | 0.0 ± 0.1 | -1.1 ± 0.2 | -0.2 ± 0.2 | -0.8 ± 0.1 | -3.5 ± 1.2 | -1.3 ± 0.1 |
| ARHGEF3 | FLJ55591 | 032_02 | 0.0 ± 1.0 | 1.9 ± 0.3 | 2.7 ± 0.7 | 3.1 ± 0.7 | 0.5 ± 0.1 | 2.9 ± 0.2 |
| ARHGEF3 | NM_019555.1 | 032_03 | 0.0 ± 0.5 | 0.5 ± 0.7 | 1.4 ± 0.5 | 2.5 ± 0.6 | 0.8 ± 1.8 | 4.0 ± 0.7 |
| CRISPLD1 | FLJ57290 | 034_01 | 0.0 ± 0.4 | 0.2 ± 0.2 | 0.9 ± 0.7 | 2.7 ± 0.5 | 2.9 ± 0.6 | 4.3 ± 0.9 |
| CRISPLD1 | NM_031461.3 | 034_02 | 0.0 ± 0.3 | -0.8 ± 0.5 | -0.4 ± 0.6 | 1.7 ± 0.1 | 0.3 ± 0.2 | 1.0 ± 0.5 |
| DYSF | FLJ55344 | 008_01 | 0.0 ± 1.3 | -3.2 ± 2.7 | -2.3 ± 1.0 | 1.5 ± 4.0 | -0.8 ± 2.4 | 1.4 ± 0.8 |
| DYSF | NM_003494.2 | 008_02 | 0.0 ± 0.0 | -0.1 ± 0.1 | 0.3 ± 0.0 | 1.1 ± 0.5 | -3.7 ± 0.8 | -8.2 ± 1.8 |
| FAM65B | FLJ56137 | 026_02 | 0.0 ± 1.2 | 1.3 ± 0.5 | 2.3 ± 0.1 | 3.9 ± 0.6 | 1.5 ± 0.5 | 0.6 ± 0.6 |
| FAM65B | AB002384.1 | 026_03 | 0.0 ± 0.7 | 0.7 ± 0.5 | 1.5 ± 0.1 | 3.3 ± 0.0 | 2.1 ± 0.8 | 4.0 ± 0.3 |
| FAM65B | NM_015864.2 | 026_04 | 0.0 ± 0.9 | -1.8 ± 1.1 | 0.2 ± 0.5 | -2.0 ± 0.6 | -3.6 ± 0.9 | -2.0 ± 0.7 |
| FGD4 | FLJ56188 | 040_01 | 0.0 ± 1.4 | 0.8 ± 1.3 | 2.5 ± 1.0 | 5.0 ± 0.7 | 2.6 ± 2.4 | 5.7 ± 0.5 |
| FGD4 | FLJ55905 | 040_02 | 0.0 ± 0.2 | -1.5 ± 0.9 | -1.3 ± 0.1 | -1.5 ± 0.9 | -3.3 ± 0.2 | -2.9 ± 0.3 |
| FGD4 | NM_139241.1 | 040_03 | 0.0 ± 0.2 | 0.2 ± 0.4 | 0.9 ± 0.1 | 2.5 ± 0.6 | 0.2 ± 0.2 | 1.5 ± 0.3 |
| HDAC9 | FLJ55607 | 065_01 | 0.0 ± 0.8 | -2.2 ± 0.8 | -2.1 ± 0.4 | -0.3 ± 0.1 | -2.0 ± 0.6 | 0.4 ± 1.0 |
| HDAC9 | FLJ54577 | 065_02 | 0.0 ± 1.7 | -1.1 ± 0.1 | -0.5 ± 0.1 | 0.1 ± 0.5 | -3.0 ± 0.1 | -0.6 ± 1.0 |
| HDAC9 | NM_178423.1 | 065_03 | 0.0 ± 0.6 | -1.8 ± 0.1 | -0.7 ± 0.2 | -0.8 ± 0.5 | -3.9 ± 0.5 | -1.5 ± 0.4 |
| MAGI2 | FLJ99053 | 060_01 | 0.0 ± 2.2 | 1.5 ± 0.0 | 1.1 ± 0.4 | 1.4 ± 0.4 | 0.4 ± 0.3 | 4.1 ± 0.0 |
| MAGI2 | FLJ50810 | 060_02 | 0.0 ± 0.6 | 0.5 ± 0.1 | 1.3 ± 0.1 | 0.9 ± 0.2 | 0.5 ± 0.6 | 3.2 ± 1.2 |
| MAGI2 | NM_012301.3 | 060_03 | 0.0 ± 0.8 | -0.6 ± 0.9 | 0.3 ± 0.7 | 3.7 ± 0.2 | 2.7 ± 0.2 | 3.6 ± 0.9 |
| MAP7 | FLJ56145 | 066_01 | 0.0 ± 1.4 | 0.6 ± 2.4 | 2.3 ± 1.9 | 10.4 ± 0.4 | 8.0 ± 0.6 | 7.8 ± 0.4 |
| MAP7 | FLJ50558 | 066_02 | 0.0 ± 0.6 | 0.4 ± 1.2 | 3.1 ± 0.9 | 3.4 ± 1.0 | -0.2 ± 1.8 | 5.2 ± 0.1 |
| MAP7 | FLJ50557 | 066_03 | 0.0 ± 0.2 | 0.4 ± 0.7 | 2.7 ± 0.7 | 3.0 ± 0.7 | 1.5 ± 1.2 | 4.4 ± 0.7 |
| MAP7 | FLJ78961 | 066_04 | 0.0 ± 1.2 | 0.7 ± 0.7 | 2.9 ± 0.1 | 3.7 ± 1.4 | -0.2 ± 1.4 | 4.6 ± 0.1 |
| MAP7 | NM_003980.3 | 066_05 | 0.0 ± 0.1 | -0.9 ± 0.2 | 0.3 ± 0.5 | 2.4 ± 0.2 | 0.6 ± 0.5 | 2.1 ± 0.6 |
| MCF2 | FLJ51685 | 084_01 | 0.0 ± 0.2 | -1.3 ± 0.3 | -1.1 ± 0.7 | 1.1 ± 0.2 | 0.0 ± 0.2 | -1.2 ± 0.4 |
| MCF2 | NM_005369.2 | 084_02 | 0.0 ± 0.1 | -2.3 ± 0.0 | -3.5 ± 0.6 | 0.6 ± 0.1 | -1.5 ± 0.3 | -0.8 ± 1.9 |
| NCAM2 | FLJ54289 | 073_01 | 0.0 ± 0.5 | -0.5 ± 0.2 | 0.3 ± 0.0 | 2.1 ± 0.2 | 1.3 ± 0.1 | 3.5 ± 0.3 |
| NCAM2 | FLJ53114 | 073_02 | 0.0 ± 0.8 | -0.6 ± 1.6 | 1.0 ± 0.9 | 2.3 ± 0.2 | 1.0 ± 0.5 | 3.5 ± 1.2 |
| NCAM2 | NM_004540.2 | 073_03 | 0.0 ± 0.9 | -0.3 ± 0.1 | 0.2 ± 0.1 | 2.4 ± 0.0 | 0.3 ± 1.5 | 2.0 ± 0.7 |
| NEDD4L | FLJ53199 | 006_01 | 0.0 ± 0.9 | 0.9 ± 0.3 | 1.4 ± 0.5 | 3.5 ± 0.3 | -0.8 ± 0.7 | -3.5 ± 1.8 |
| NEDD4L | FLJ61249 | 006_02 | 0.0 ± 0.8 | 0.0 ± 0.9 | 0.3 ± 0.1 | 1.2 ± 0.1 | -0.1 ± 0.4 | 1.7 ± 1.1 |
| NEDD4L | NM_015277.2 | 006_03 | 0.0 ± 0.1 | -0.5 ± 0.2 | 0.4 ± 0.1 | 1.2 ± 0.1 | -1.2 ± 0.3 | 0.6 ± 0.4 |
| OXR1 | FLJ42450 | 090_01 | 0.0 ± 0.1 | 0.0 ± 0.8 | 0.7 ± 0.7 | 4.7 ± 0.2 | 1.1 ± 1.0 | 2.4 ± 0.1 |
| OXR1 | NM_181354.3 | 090_04 | 0.0 ± 0.7 | -0.4 ± 0.2 | 0.7 ± 0.1 | 1.2 ± 0.3 | -1.6 ± 0.5 | -2.2 ± 0.7 |
| OXR1 | FLJ55036 | 090_05 | 0.0 ± 0.2 | -0.9 ± 0.6 | 0.0 ± 0.0 | 2.3 ± 0.3 | 0.3 ± 0.2 | 2.0 ± 0.6 |
| PEX5L | FLJ50526 | 077_01 | 0.0 ± 0.5 | -0.9 ± 0.5 | 0.1 ± 0.7 | 0.0 ± 0.1 | -1.5 ± 0.9 | 0.1 ± 0.3 |
| PEX5L | FLJ53911 | 077_02 | 0.0 ± 0.7 | -2.6 ± 0.5 | -3.5 ± 1.9 | -3.0 ± 0.3 | -4.2 ± 1.1 | -0.7 ± 1.7 |
| PEX5L | FLJ50489 | 077_03 | 0.0 ± 2.0 | -1.9 ± 0.5 | -3.4 ± 1.0 | -2.7 ± 1.1 | -5.3 ± 1.3 | -3.1 ± 3.3 |
| PEX5L | NM_016559.1 | 077_04 | 0.0 ± 0.8 | -2.9 ± 0.1 | -4.5 ± 0.3 | -3.7 ± 0.5 | -5.1 ± 0.5 | -2.2 ± 1.1 |
| PPP2R2C | FLJ58008 | 033_01 | 0.0 ± 1.1 | -3.0 ± 0.1 | -1.7 ± 0.7 | -3.0 ± 0.4 | -4.3 ± 0.9 | -1.4 ± 1.6 |
| PPP2R2C | NM_020416.2 | 033_02 | 0.0 ± 0.1 | -0.4 ± 0.3 | -0.6 ± 0.0 | -2.4 ± 0.1 | -1.9 ± 1.1 | 1.9 ± 1.4 |
| RAPGEF4 | FLJ50956 | 010_02 | 0.0 ± 0.6 | 0.5 ± 0.6 | 0.4 ± 1.1 | 2.8 ± 0.0 | 2.3 ± 0.4 | 2.5 ± 0.9 |
| RAPGEF4 | FLJ58368 | 010_04 | 0.0 ± 1.0 | 1.9 ± 0.8 | 3.6 ± 1.3 | 9.8 ± 0.1 | 7.2 ± 0.3 | 10.0 ± 0.8 |
| RAPGEF4 | FLJ51189 | 010_05 | 0.0 ± 1.3 | 4.2 ± 0.1 | 4.6 ± 0.3 | 8.4 ± 0.1 | 5.2 ± 0.2 | 4.5 ± 0.4 |
| RAPGEF4 | NM_007023.1 | 010_07 | 0.0 ± 0.0 | -1.2 ± 0.0 | -1.5 ± 0.3 | 0.8 ± 0.1 | 0.1 ± 0.8 | 0.8 ± 0.2 |
| SEMA5B | FLJ55460 | 039_01 | 0.0 ± 0.7 | -0.3 ± 0.2 | -0.4 ± 0.1 | -1.6 ± 0.5 | 0.7 ± 1.5 | 1.7 ± 0.4 |
| SEMA5B | FLJ34162 | 039_02 | 0.0 ± 0.0 | 0.3 ± 0.3 | 0.6 ± 0.3 | 2.0 ± 0.2 | 4.1 ± 1.3 | 5.5 ± 0.4 |
| SEMA5B | AB040878.1 | 039_03 | 0.0 ± 0.7 | -0.2 ± 0.0 | -0.1 ± 0.2 | -1.3 ± 0.4 | 0.3 ± 0.8 | 1.4 ± 0.4 |
| SEMA5B | NM_018987.1 | 039_04 | 0.0 ± 0.9 | 0.0 ± 0.4 | -0.8 ± 0.3 | -2.0 ± 1.3 | -1.8 ± 0.0 | 1.8 ± 0.2 |
| SH3KBP1 | FLJ54612 | 025_01 | 0.0 ± 0.9 | 0.6 ± 0.4 | 0.4 ± 0.4 | 0.3 ± 0.9 | -4.5 ± 0.3 | -5.5 ± 1.9 |
| SH3KBP1 | FLJ54623 | 025_02 | 0.0 ± 0.4 | 1.0 ± 1.4 | -1.5 ± 2.2 | 2.6 ± 0.9 | 1.1 ± 2.0 | 4.4 ± 0.1 |
| SH3KBP1 | NM_031892.1 | 025_03 | 0.0 ± 0.0 | -0.9 ± 0.4 | 0.0 ± 0.1 | 0.7 ± 0.0 | -1.6 ± 0.4 | -1.1 ± 0.7 |
| SPRED2 | FLJ52731 | 031_01 | 0.0 ± 1.7 | 0.1 ± 0.4 | 0.0 ± 0.5 | 1.8 ± 0.4 | 1.2 ± 1.1 | 6.5 ± 1.2 |
| SPRED2 | NM_181784.1 | 031_02 | 0.0 ± 0.9 | 1.1 ± 0.2 | 1.3 ± 0.6 | 0.4 ± 0.2 | -1.4 ± 0.4 | -0.4 ± 1.0 |
| TFEC | FLJ55256 | 047_01 | 0.0 ± 0.8 | 2.2 ± 1.5 | 4.3 ± 0.4 | 10.8 ± 0.2 | 9.4 ± 0.1 | 6.0 ± 0.3 |
| TFEC | NM_012252.2 | 047_02 | 0.0 ± 2.6 | -0.3 ± 0.5 | -1.4 ± 0.9 | 2.6 ± 0.3 | 5.0 ± 8.2 | -5.6 ± 1.4 |
| TMC5 | FLJ54454 | 042_01 | 0.0 ± 0.2 | -1.4 ± 0.3 | -1.2 ± 0.4 | -0.8 ± 0.4 | -2.6 ± 0.2 | 0.5 ± 0.4 |
| TMC5 | FLJ54906 | 042_02 | 0.0 ± 0.4 | -2.5 ± 0.6 | -1.0 ± 0.9 | -3.8 ± 0.0 | -6.7 ± 2.7 | -7.3 ± 0.8 |
| TMC5 | NM_024780.3 | 042_03 | 0.0 ± 0.1 | -1.2 ± 0.4 | -1.4 ± 0.5 | -1.9 ± 0.6 | -2.1 ± 1.1 | 0.5 ± 0.7 |
| AMPD3 | FLJ51124 | 064_01 | 0.0 ± 0.5 | -1.1 ± 0.4 | -0.7 ± 0.1 | 0.5 ± 0.1 | -0.1 ± 0.7 | -0.3 ± 0.2 |
| AMPD3 | NM_000480.2 | 064_02 | 0.0 ± 1.4 | -0.5 ± 0.1 | -0.1 ± 0.3 | 1.6 ± 0.5 | 0.0 ± 0.1 | 1.3 ± 0.5 |
| AOAH | NM_001637.1 | 002_02 | 0.0 ± 0.8 | -1.1 ± 0.0 | 0.1 ± 0.7 | -1.6 ± 0.9 | -1.9 ± 0.9 | 2.4 ± 1.2 |
| AOAH | FLJ51934 | 002_03 | 0.0 ± 0.3 | -0.9 ± 0.4 | -0.9 ± 0.5 | 0.4 ± 0.7 | -2.1 ± 1.3 | 1.8 ± 1.1 |
| APLP1 | FLJ56046 | 007_01 | 0.0 ± 2.1 | -1.3 ± 0.3 | -0.1 ± 0.1 | 0.6 ± 0.4 | 1.7 ± 0.3 | 2.9 ± 0.4 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| APLP1 | NM_005166.3 | 007_03 | 0.0 ± 1.5 | -1.0 ± 1.2 | 0.2 ± 0.9 | 1.6 ± 0.8 | 1.7 ± 0.6 | 3.3 ± 1.4 |
| BACE1 | FLJ54690 | 054_01 | 0.0 ± 0.8 | -0.6 ± 0.3 | 1.0 ± 0.4 | 1.2 ± 0.3 | -0.1 ± 0.7 | 1.3 ± 1.0 |
| BACE1 | NM_012104.3 | 054_02 | 0.0 ± 1.7 | -0.5 ± 0.5 | 1.2 ± 0.1 | 1.6 ± 0.5 | -0.5 ± 0.9 | 0.8 ± 0.4 |
| CACNB3 | FLJ58411 | 041_01 | 0.0 ± 0.3 | -0.7 ± 0.4 | -0.6 ± 0.0 | -1.5 ± 0.0 | -3.3 ± 0.3 | -2.1 ± 0.4 |
| CACNB3 | FLJ57401 | 041_02 | 0.0 ± 0.6 | -0.1 ± 0.2 | -1.8 ± 0.1 | 1.1 ± 0.0 | 0.3 ± 0.4 | 1.5 ± 0.8 |
| CACNB3 | NM_000725.2 | 041_03 | 0.0 ± 0.3 | -0.9 ± 0.5 | 0.2 ± 0.4 | 1.0 ± 0.1 | -0.2 ± 0.2 | 1.2 ± 0.5 |
| CHRNB1 | FLJ52354 | 005_01 | 0.0 ± 0.1 | -1.5 ± 0.4 | 0.5 ± 0.2 | 0.0 ± 0.3 | -1.4 ± 0.4 | -2.7 ± 0.1 |
| CHRNB1 | NM_000747.2 | 005_02 | 0.0 ± 0.8 | -0.9 ± 0.2 | 0.1 ± 0.1 | 0.7 ± 0.2 | 0.3 ± 0.6 | 1.3 ± 0.8 |
| CLTCL1 | FLJ56961 | 021_01 | 0.0 ± 1.5 | -0.5 ± 0.0 | -0.2 ± 0.4 | -0.8 ± 0.2 | -2.0 ± 0.2 | -0.7 ± 1.8 |
| CLTCL1 | NM_001835.1 | 021_02 | 0.0 ± 1.6 | -0.3 ± 0.1 | 0.3 ± 0.2 | 0.4 ± 0.0 | -1.2 ± 0.5 | -0.3 ± 1.2 |
| CUL2 | NM_003591.2 | 036_02 | 0.0 ± 1.8 | -0.4 ± 1.0 | 0.4 ± 1.2 | 1.8 ± 1.7 | -0.6 ± 0.6 | 0.6 ± 0.2 |
| CUL2 | FLJ37898 | 036_03 | 0.0 ± 0.1 | -0.3 ± 0.0 | -0.6 ± 0.5 | 0.4 ± 0.4 | -2.0 ± 0.2 | -2.0 ± 1.0 |
| DLGAP1 | FLJ56525 | 043_01 | 0.0 ± 0.5 | -0.4 ± 0.4 | 0.2 ± 0.1 | -0.6 ± 0.2 | -1.1 ± 0.3 | -1.1 ± 1.0 |
| DLGAP1 | NM_004746.2 | 043_02 | 0.0 ± 0.5 | -0.7 ± 0.2 | 0.6 ± 0.1 | -0.2 ± 0.2 | -1.1 ± 0.6 | -1.0 ± 1.0 |
| DLGAP1 | FLJ54734 | 043_04 | 0.0 ± 1.6 | -1.5 ± 0.9 | -1.1 ± 0.3 | 1.0 ± 1.4 | 1.3 ± 3.4 | 1.0 ± 0.3 |
| DLGAP1 | NM_001003809.1 | 043_05 | 0.0 ± 0.4 | -0.5 ± 0.1 | 0.4 ± 0.2 | 1.1 ± 0.7 | -0.4 ± 1.1 | -0.1 ± 0.8 |
| EML2 | FLJ56452 | 030_01 | 0.0 ± 0.7 | -1.0 ± 1.1 | 0.1 ± 0.3 | 0.8 ± 1.1 | -0.2 ± 1.0 | 1.5 ± 1.5 |
| EML2 | NM_012155.1 | 030_02 | 0.0 ± 0.2 | -2.0 ± 0.5 | 0.6 ± 0.3 | -1.3 ± 0.1 | -2.5 ± 0.9 | -1.1 ± 0.7 |
| EXOC4 | FLJ54541 | 014_01 | 0.0 ± 0.6 | 0.1 ± 0.0 | 0.6 ± 0.3 | 1.3 ± 0.1 | 0.6 ± 0.0 | 1.9 ± 0.3 |
| EXOC4 | FLJ38176 | 014_02 | 0.0 ± 0.5 | 0.1 ± 0.0 | 0.6 ± 0.4 | 1.4 ± 0.3 | 0.5 ± 0.1 | 1.9 ± 0.3 |
| EXOC4 | FLJ53330 | 014_03 | 0.0 ± 0.0 | -0.5 ± 0.3 | -0.1 ± 0.5 | 0.4 ± 0.2 | -1.7 ± 0.5 | -0.9 ± 0.6 |
| EXOC4 | NM_021807.2 | 014_04 | 0.0 ± 0.0 | -0.9 ± 0.3 | 0.0 ± 0.0 | 1.0 ± 0.2 | -1.4 ± 0.6 | -0.3 ± 0.2 |
| FGF13 | FLJ57884 | 003_01 | 0.0 ± 0.4 | 1.5 ± 0.3 | 0.7 ± 0.3 | 1.3 ± 0.2 | -0.1 ± 0.5 | 0.4 ± 1.6 |
| FGF13 | FLJ57068 | 003_02 | 0.0 ± 0.6 | 0.2 ± 0.3 | 0.5 ± 0.2 | 1.0 ± 0.4 | -1.2 ± 0.6 | -0.2 ± 1.3 |
| FGF13 | NM_033642.1 | 003_03 | 0.0 ± 0.5 | 0.8 ± 0.9 | 0.2 ± 0.5 | 0.9 ± 0.4 | -1.3 ± 0.2 | -0.8 ± 1.2 |
| FGF13 | NM_004114.2 | 003_04 | 0.0 ± 0.3 | 0.9 ± 0.8 | 0.3 ± 0.5 | 0.9 ± 0.3 | -1.2 ± 0.0 | -0.8 ± 0.9 |
| GNE | NM_005476.3 | 062_03 | 0.0 ± 0.2 | -1.1 ± 0.4 | 0.2 ± 0.0 | 0.1 ± 0.2 | -0.9 ± 0.2 | -1.4 ± 0.5 |
| GNE | FLJ51479 | 062_04 | 0.0 ± 0.1 | -2.2 ± 0.0 | -0.4 ± 0.2 | -0.7 ± 0.6 | -1.6 ± 0.7 | -2.5 ± 1.0 |
| HDAC4 | FLJ51177 | 044_02 | 0.0 ± 0.4 | -0.4 ± 0.1 | 0.1 ± 0.3 | 0.3 ± 0.1 | 0.6 ± 0.5 | 1.7 ± 0.7 |
| HDAC4 | FLJ51174 | 044_03 | 0.0 ± 0.5 | -0.5 ± 0.0 | 0.4 ± 0.9 | 0.0 ± 0.4 | 0.0 ± 0.2 | 1.0 ± 0.3 |
| HDAC4 | NM_006037.2 | 044_04 | 0.0 ± 0.4 | -0.4 ± 0.0 | 0.1 ± 0.0 | 0.8 ± 0.0 | 0.3 ± 0.4 | 1.1 ± 0.7 |
| LSAMP | FLJ54658 | 022_01 | 0.0 ± 1.1 | -1.1 ± 1.2 | 0.7 ± 0.9 | 1.1 ± 0.3 | -0.3 ± 0.4 | 2.5 ± 0.2 |
| LSAMP | NM_002338.2 | 022_02 | 0.0 ± 0.8 | -1.1 ± 0.5 | -0.3 ± 0.2 | -1.0 ± 1.0 | -1.1 ± 0.8 | -0.4 ± 0.8 |
| NHEDC2 | FLJ54331 | 069_01 | 0.0 ± 0.5 | 0.0 ± 0.4 | -0.1 ± 0.4 | 1.4 ± 0.4 | 1.1 ± 0.4 | 2.0 ± 0.0 |
| NHEDC2 | NM_178833.3 | 069_02 | 0.0 ± 0.1 | -0.9 ± 0.4 | -0.3 ± 0.4 | 0.1 ± 0.0 | -1.4 ± 0.2 | -0.2 ± 1.0 |
| NOX4 | FLJ51027 | 055_01 | 0.0 ± 1.2 | 0.1 ± 0.1 | -2.4 ± 0.0 | 0.5 ± 0.2 | 0.1 ± 0.7 | 1.1 ± 1.8 |
| NOX4 | FLJ51025 | 055_02 | 0.0 ± 0.0 | 1.3 ± 0.1 | -0.7 ± 1.6 | 2.5 ± 0.5 | 2.0 ± 0.8 | 0.9 ± 1.2 |
| NOX4 | NM_016931.2 | 055_03 | 0.0 ± 1.9 | -0.3 ± 0.3 | 0.1 ± 0.5 | 0.3 ± 0.2 | -2.5 ± 0.9 | 0.0 ± 1.6 |
| PLD5 | FLJ57051 | 035_01 | 0.0 ± 0.4 | -0.7 ± 0.9 | -0.3 ± 0.6 | 2.5 ± 0.9 | 0.6 ± 2.0 | 1.9 ± 0.4 |
| PLD5 | NM_152666.1 | 035_02 | 0.0 ± 0.2 | -0.7 ± 0.0 | -0.5 ± 0.1 | 0.2 ± 0.1 | 0.1 ± 3.0 | -0.9 ± 0.3 |
| PTPN3 | NM_002829.2 | 061_03 | 0.0 ± 0.4 | -2.4 ± 0.1 | -1.0 ± 0.2 | 0.2 ± 0.5 | -1.3 ± 0.2 | -1.4 ± 0.1 |
| PTPN3 | FLJ50545 | 061_04 | 0.0 ± 0.4 | -2.2 ± 0.2 | 0.2 ± 0.4 | -0.9 ± 0.3 | -1.7 ± 0.9 | -2.3 ± 0.2 |
| PTPRR | FLJ55167 | 016_02 | 0.0 ± 1.0 | -1.3 ± 1.1 | -0.5 ± 2.0 | 1.8 ± 0.2 | 1.0 ± 0.8 | 3.3 ± 1.8 |
| PTPRR | NM_002849.2 | 016_03 | 0.0 ± 0.1 | -1.4 ± 0.5 | -0.9 ± 0.5 | 1.2 ± 0.2 | -0.3 ± 0.0 | 2.6 ± 0.9 |
| RARG | FLJ54463 | 087_01 | 0.0 ± 0.3 | 1.3 ± 0.3 | 2.0 ± 0.3 | -0.6 ± 0.4 | -1.9 ± 0.8 | -1.0 ± 0.4 |
| RARG | FLJ54482 | 087_02 | 0.0 ± 0.4 | 1.0 ± 0.0 | 1.6 ± 0.2 | -1.1 ± 0.5 | -1.7 ± 0.5 | -1.0 ± 0.2 |
| RARG | NM_000966.3 | 087_03 | 0.0 ± 0.3 | -0.9 ± 0.3 | 0.4 ± 0.3 | -2.4 ± 0.4 | -3.1 ± 0.8 | -1.8 ± 1.6 |
| RIMS1 | FLJ52438 | 028_01 | 0.0 ± 0.3 | -0.6 ± 0.5 | -1.0 ± 0.4 | 0.8 ± 0.3 | -0.4 ± 0.2 | 2.9 ± 1.3 |
| RIMS1 | FLJ53578 | 028_02 | 0.0 ± 0.4 | -1.0 ± 0.0 | -1.4 ± 1.1 | 0.3 ± 0.2 | 0.0 ± 0.3 | 2.1 ± 1.2 |
| RIMS1 | NM_014989.2 | 028_03 | 0.0 ± 1.4 | -2.0 ± 0.1 | -1.1 ± 0.7 | 0.9 ± 0.2 | -0.9 ± 0.0 | 2.0 ± 0.7 |
| SLC26A4 | FLJ50484 | 013_01 | 0.0 ± 1.6 | -0.6 ± 0.2 | 0.4 ± 0.6 | 0.7 ± 0.8 | -0.6 ± 0.6 | -0.1 ± 0.0 |
| SLC26A4 | FLJ50684 | 013_02 | 0.0 ± 0.7 | -1.0 ± 0.3 | -1.6 ± 1.9 | -1.7 ± 1.5 | -3.1 ± 2.5 | -1.5 ± 3.1 |
| SLC26A4 | NM_000441.1 | 013_04 | 0.0 ± 0.8 | -1.0 ± 0.0 | -0.7 ± 0.4 | -0.1 ± 0.2 | -1.4 ± 0.7 | -0.4 ± 0.1 |
| SLC43A2 | FLJ55865 | 037_01 | 0.0 ± 0.9 | -1.2 ± 0.5 | -0.7 ± 1.0 | 2.0 ± 0.3 | 0.6 ± 1.2 | 0.3 ± 0.4 |
| SLC43A2 | NM_152346.1 | 037_02 | 0.0 ± 0.7 | -0.7 ± 0.2 | -0.4 ± 0.1 | 0.2 ± 0.2 | 0.0 ± 0.4 | 1.2 ± 1.2 |
| SLC5A1 | FLJ55281 | 011_01 | 0.0 ± 0.1 | -1.6 ± 0.2 | -0.6 ± 0.6 | 0.7 ± 0.5 | -1.6 ± 2.5 | 2.4 ± 1.6 |
| SLC5A1 | NM_000343.1 | 011_02 | 0.0 ± 0.4 | -0.2 ± 0.3 | 0.2 ± 0.0 | 1.1 ± 0.4 | 0.7 ± 0.0 | 0.8 ± 0.6 |

Supplementary Table 4. Quantitative evaluation of 25 genes including multiple TSSs by real-time PCR.

| Gene symbol | cDNA name | Expression pattern | Gene description | References |
|---|---|---|---|---|
| AMPD3 | FLJ51124<br>NM_000480.2 | Same | adenosine monophosphate deaminase (isoform E) | [S1] |
| AOAH | NM_001637.1<br>FLJ51934 | Same | acyloxyacyl hydrolase (neutrophil) | [S2] |
| APLP1 | FLJ56046<br>NM_005166.3 | Same | amyloid beta (A4) precursor-like protein 1 | [S3, S4] |
| BACE1 | FLJ54690<br>NM_012104.3 | Same | beta-site APP-cleaving enzyme 1 | [10, S5, S6] |
| CACNB3 | FLJ58411<br>FLJ57401<br>NM_000725.2 | Same | calcium channel, voltage-dependent, beta 3 subunit | [10, S7, S8] |
| CHRNB1 | FLJ52354<br>NM_000747.2 | Same | cholinergic receptor, nicotinic, beta 1 (muscle) | [S9] |
| CLTCL1 | FLJ56961<br>NM_001835.1 | Same | clathrin, heavy polypeptide-like 1 | [S10] |
| CUL2 | NM_003591.2<br>FLJ37898 | Same | cullin 2 | [S11, S12] |
| DLGAP1 | FLJ56525<br>NM_004746.2<br>FLJ54734<br>NM_001003809.1 | Same | discs, large (Drosophila) homolog-associated protein 1 | [S13] |
| EML2 | FLJ56452<br>NM_012155.1 | Same | echinoderm microtubule associated protein like 2 | [S14] |
| EXOC4 | FLJ54541<br>FLJ38176<br>FLJ53330<br>NM_021807.2 | Same | exocyst complex component 4 | [S15] |
| FGF13 | FLJ57884<br>FLJ57068<br>NM_033642.1<br>NM_004114.2 | Same | fibroblast growth factor 13 | [10, S16, S17] |
| GNE | NM_005476.3<br>FLJ51479 | Same | glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase | [S18] |
| HDAC4 | FLJ51177<br>FLJ51174<br>NM_006037.2 | Same | histone deacetylase 4 | [S19, S20] |
| LSAMP | FLJ54658<br>NM_002338.2 | Same | limbic system-associated membrane protein | [S21, S22] |
| NHEDC2 | FLJ54331<br>NM_178833.3 | Same | Na+/H+ exchanger domain containing 2 | [S23] |
| NOX4 | FLJ51027<br>FLJ51025<br>NM_016931.2 | Same | NADPH oxidase 4 | [S24] |
| PLD5 | FLJ57051<br>NM_152666.1 | Same | phospholipase D family, member 5 | [10] |
| PTPN3 | NM_002829.2<br>FLJ50545 | Same | protein tyrosine phosphatase, non-receptor type 3 | [S25] |
| PTPRR | FLJ55167<br>NM_002849.2 | Same | protein tyrosine phosphatase, receptor type, R | [S26, S27] |
| RARG | FLJ54463<br>FLJ54482<br>NM_000966.3 | Same | retinoic acid receptor, gamma | [S28, S29] |
| RIMS1 | FLJ52438<br>FLJ53578<br>NM_014989.2 | Same | regulating synaptic membrane exocytosis 1 | [S30] |
| SLC26A4 | FLJ50484<br>FLJ50684<br>NM_000441.1 | Same | solute carrier family 26, member 4 | [S31] |
| SLC43A2 | FLJ55865<br>NM_152346.1 | Same | solute carrier family 43, member 2 | [S32] |
| SLC5A1 | FLJ55281<br>NM_000343.1 | Same | solute carrier family 5 (sodium/glucose cotransporter), member 1 | [S33, S34] |

* 25 genes were selected as tissue specific expression and multiple protein coding.
But these genes were not RA responsive gene.

Supplementary Table 5.. GO functional classification of selected 156 genes containing multiple TSSs by real-time PCR.

| Functional category (GO : Molecular function) | | Number of matched genes | | | |
|---|---|---|---|---|---|
| | | Selected genes (156 genes) | % | RefSeq (24,210 cDNAs) | % |
| Binding | Nucleic acid binding | 10 | ( 9.3 ) | 706 | ( 8.9 ) |
| | Nucleotide binding | 12 | ( 11.2 ) | 1,047 | ( 13.2 ) |
| | Ion binding | 4 | ( 3.7 ) | 245 | ( 3.1 ) |
| | Protein binding | 9 | ( 8.4 ) | 450 | ( 5.7 ) |
| | Other bindings | 2 | ( 1.9 ) | 304 | ( 3.8 ) |
| Catalytic activity | Transferase activity | 8 | ( 7.5 ) | 808 | ( 10.2 ) |
| | Hydrolase activity | 8 | ( 7.5 ) | 902 | ( 11.3 ) |
| | Ligase activity | 4 | ( 3.7 ) | 107 | ( 1.3 ) |
| | Other catalytic activity | 9 | ( 8.4 ) | 653 | ( 8.2 ) |
| Transcription regulator | | 5 | ( 4.7 ) | 364 | ( 4.6 ) |
| Signal transducer activity | | 11 | ( 10.3 ) | 879 | ( 11.0 ) |
| Transporter activity | | 11 | ( 10.3 ) | 997 | ( 12.5 ) |
| Structural molecule activity | | 1 | ( 0.9 ) | 163 | ( 2.0 ) |
| Enzyme regulator activity | | 10 | ( 9.3 ) | 142 | ( 1.8 ) |
| Others | | 3 | ( 2.8 ) | 193 | ( 2.4 ) |
| Total | | 107 | | 7,960 | |

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 selected 156 genes.
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.