

**Figure 1**

**Comparisons of three round-amplified products starting with very small quantities of RNA.** (a-c) Amplification biases in the products starting from a small quantity of RNA. Scatter plots of signal intensity obtained from 5  $\mu$ g of BMMC RNA prepared by the standard protocol and from 30 pg (a), 10 pg (b) and 2 pg (c) of BMMC RNA prepared by three rounds of amplification are shown. (d, e) Reproducibility of the three-round amplification of a small quantity of RNA. Scatter plots of signal intensity between two independent products from 30 pg of BMMC RNA (BMMC 30 pg-1 and BMMC 30 pg-2) (d) or from 2 pg of BMMC RNA (BMMC 2 pg-1 and BMMC 2 pg-2) (e), are shown. Red dots show probe sets judged as "Presence", and yellow dots represent probe sets judged as "Absence" in both arrays. Blue dots show probe sets judged as "Presence" only in either array. The correlation coefficients ( $r$ ) are presented. The same, four-fold induction and suppression thresholds are indicated as diagonal lines. Genes judged as "Presence" are placed in groups corresponding to pairwise overlaps shown in the accompanying Venn diagrams.

samples, while only 57% of 'Presence' genes in the 2 pg-1 and 55% of 'Presence' genes in the 2 pg-2 sample were judged as 'Presence' in both 2 pg RNA samples. These results suggested that the amplified products from the RNA from a single MC (about 2 pg) by the current method may include considerable amplification artifacts causing

problems in accuracy and reproducibility. On the other hand, because of the higher reproducibility (>74%), we concluded that amplification from 30 pg RNA collected from 15 MCs would be suitable for the practical analysis of tissue MCs. Based on these results, we set our goal in this study to acquire gene expression profiles of MCs

pooled from different regions. To minimize the influence of cell-to-cell variations within the same class and potential amplification artifacts, we prepared three sets of 15 MCs for each region and compared genes with significantly different expression between MCs from the different regions (Figure 2b). We chose stomach as the source organ, since we can isolate two kinds of MCs from the mucosa (mMC) and the submucosa (sMC) regions of the same sections, and mMCs and sMCs have been suspected to be different in several MC properties such as protease expression profile and sensitivity to safranin staining [1,11].

#### Gene expression profiles of submucosal and mucosal MCs from the stomach

To visualize two kinds of MCs in the stomach without causing RNA degradation, the sections were fixed with carnoy's fixative and metachromatically stained with toluidine blue for a few seconds. sMCs and mMCs were microdissected using a patch pipette (Figure 2a and 2b). We prepared three sets of 15 MCs for each region, extracted their RNA and individually amplified them (sMC<sub>1</sub>, sMC<sub>2</sub>, sMC<sub>3</sub>, and mMC<sub>1</sub>, mMC<sub>2</sub>, mMC<sub>3</sub>). To improve the recovery of the extraction of as little as 30 pg of RNA, we used 'poly C' as a carrier, which does not interfere with the following RNA amplification or hybridization of the amplified product to the array (data not shown). To examine the effects of nonspecifically amplified artifact products, we performed the RNA extraction/amplification procedure without adding microdissected cells ("no cell") as a negative control (described in "Materials and methods"). The amplified RNAs of sMCs, mMCs and the "no cell" control were separately hybridized to a murine microarray. The signal values in the "no cell" sample were low in general and similar to the background levels (Figure 2c). The scatter plots of the samples independently prepared within the same group (e.g. sMC<sub>1</sub> vs sMC<sub>2</sub>) showed a similar expression pattern; the average correlation coefficient for all probe-sets was  $0.945 \pm 0.004$  and  $0.893 \pm 0.019$  in sMCs and mMCs, respectively ( $n = 3$ ). In contrast, the average correlation coefficient between sMCs and mMCs was  $0.752 \pm 0.034$  ( $n = 3$ ), which was much lower than those within the same group, suggesting that their gene expression patterns are different.

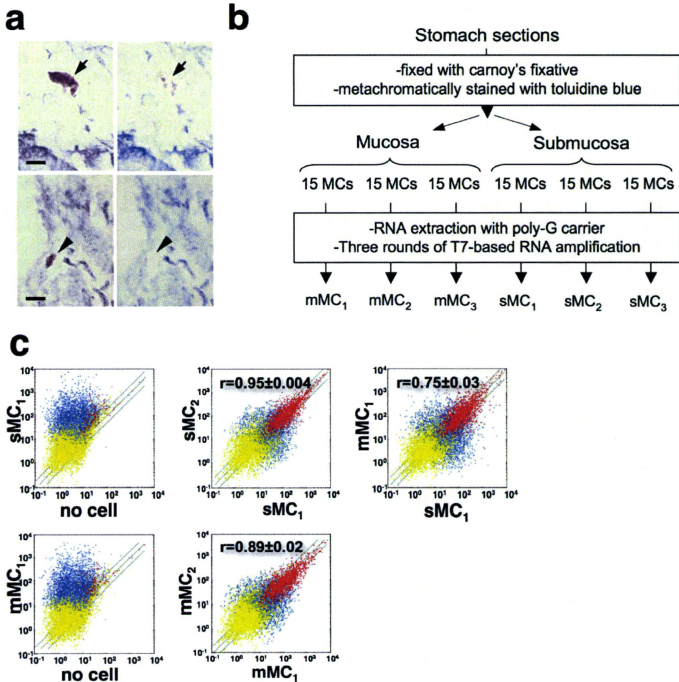
We further evaluated the accuracy and reproducibility of our method by other comprehensive analyses (hierarchical clustering analysis and principal component analysis [PCA]) using all probe sets. Microarray data obtained from sMCs, mMCs, skin-derived MCs, peritoneal MCs, BMMCs and non-MCs (macrophages and fibroblasts) were applied to these analyses. We first checked whether the amplification process in our method affects the global expression profile due to non-linear amplification. The results from the BMMC samples using RNA prepared by

the standard protocol (BMMC-std) or the amplification method (BMMC-amp) were subjected to these analyses. Both hierarchical clustering analysis and PCA revealed that microarray data from BMMC-std and BMMC-amp were clustered in the same group (Figure 3a and 3b), suggesting that the global similarity in gene expression profiles is maintained during the amplification process. We next examined the similarity of expression patterns in three independent sMC or mMC samples. Upon clustering analysis and PCA, sMC<sub>1-3</sub> and mMC<sub>1-3</sub> were clustered in the same group, respectively. PCA also showed that the expression profiles of sMCs, mMCs and BMMCs are mutually different (Figure 3b).

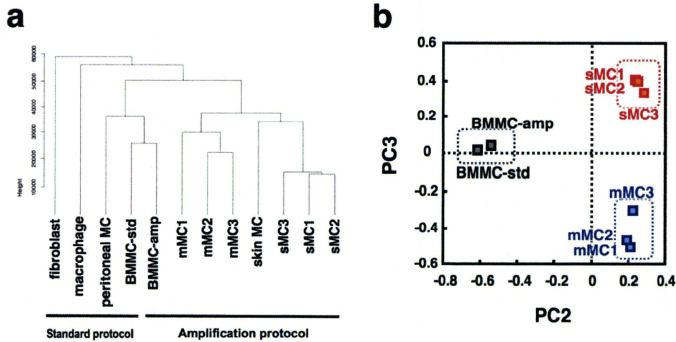
We then compared the stomach-derived MCs (sMCs and mMCs) with skin-derived MCs, peritoneal MCs, BMMCs and non-MCs (macrophages and fibroblasts) by clustering analysis. The tissue-derived MCs (stomach MCs and skin MCs) were clustered separately from peritoneal MCs and BMMCs. These results may reflect different properties between tissue-derived MCs with firm adhesion to the neighboring cells and floating MCs without a tight contact. As to the similarity of MCs with fibroblasts and macrophages, it is reasonable that fibroblasts are most distant from MCs and macrophages are closer to MCs as a leukocyte family.

#### Validation of microarray results by real time RT-PCR analysis

We next investigated whether the hybridization signals of known marker genes specific for sMCs and mMCs showed the expected expression trends [12,14]. The mMC-specific genes, mast cell protease 1 (*Mcp1*) and 2 (*Mcp2*) showed higher values in mMCs, while the sMC-specific marker genes, mast cell protease 4 (*Mcp4*) and chymase 2 (*Cma2*), showed higher signal values in sMCs (Table 1 and Figure 4a) [15-29]. On the other hand, MC-common markers such as kit oncogene (*Kit*) and Fcε receptor (*Fcer1a*) showed significant signal values with no bias between mMCs and sMCs. To further evaluate the results, we measured the expression levels of these marker genes by real-time RT-PCR using RNA from the independently isolated MCs (Figure 4b). Moreover, we randomly selected three genes showing 'mMC-biased' expression and another three genes showing 'sMC-biased' expression; expression of these genes in MCs has not been reported previously (Figure 4a). There were no significant differences in the expression levels of *Kit* and *Fcer1a* between mMCs and sMCs. In contrast, the mMC-specific markers *Mcp1* and *Mcp2* and the 'mMC-biased' genes, *Anxa10*, *Ctsa*, and *Fos* showed higher expression in mMCs, and the sMC-specific markers *Mcp4* and *Cma2* and the 'sMC-biased' genes, *Cnn1*, *Ces3*, and *Cpe* showed higher expression in sMCs. These results indicate that the microarray



**Figure 2**  
**Gene expression profiles of sMCs and mMCs from stomach tissue.** (a) Isolation of toluidine blue-stained MCs in the submucosa (sMC; upper panels) and the mucosa (mMC; lower panels) of stomach sections. A sMC (arrow) and mMC (arrowhead) that was metachromatically stained with toluidine blue before microdissection (left panels) disappeared after microdissection with a patch pipette (right panels). Bars, 10  $\mu$ m. (b) Outline of the experimental strategy. (c) Labeled and fragmented antisense RNAs of three individual sMC samples, three individual mMC samples and the 'no cell' samples were hybridized to a Murine Array. Scatter plots for 'no cell' (x axis) and sMC<sub>1</sub> (y axis) (upper left), 'no cell' (x axis) and mMC<sub>1</sub> (y axis) (lower left), sMC<sub>1</sub> (x axis) and sMC<sub>2</sub> (y axis) (upper center), mMC<sub>1</sub> (x axis) and mMC<sub>2</sub> (y axis) (lower center), sMC<sub>1</sub> (x axis) and mMC<sub>1</sub> (y axis) (upper right) are shown. The correlation coefficients (r) for comparison within sMC<sub>1-3</sub>, within mMC<sub>1-3</sub> and between sMCs and mMCs are presented as means  $\pm$  S.D. Red dots show probe sets judged as "Presence", and yellow dots represent probe sets judged as "Absence" in both arrays. Blue dots show probe sets judged as "Presence" only in either array. The same, two-fold induction and suppression thresholds are indicated as diagonal lines.

**Figure 3**

**Global gene expression analysis of sMC<sub>1-3</sub> and mMC<sub>1-3</sub>.** (a) Hierarchical clustering of global gene expression of various preparations of MCs and non-MCs. Three-round amplified products of sMC<sub>1-3</sub>, mMCI<sub>1-3</sub>, skin MCs and BMMCs, and the standard products of BMMCs, peritoneal MCs, macrophages and fibroblasts were analyzed. (b) The principal component analysis (PCA) reveals different gene expression profiles of sMC<sub>1-3</sub>, mMCI<sub>1-3</sub>, and two preparations of BMMCs. The blue dotted square indicates mMCs, the red dotted square indicates sMCs, and the black dotted square indicates BMMCs.

results are reliable and reflect the gene expression profiles of intact sMCs and mMCs in the stomach.

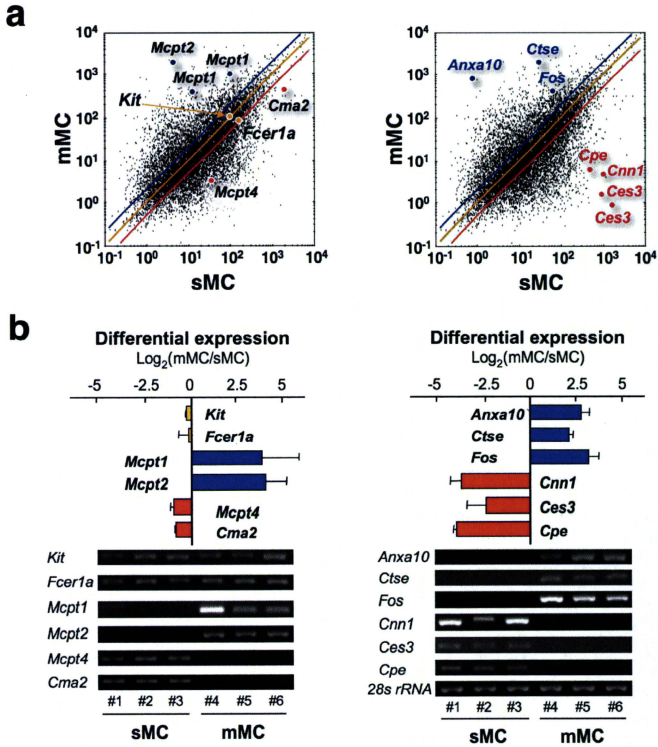
#### Clustering analysis of the gene expression profiles and functional categorization between sMCs and mMCs

Of the ~12,000 genes represented on the oligonucleotide array, we selected 1,272 genes whose expression levels between sMC<sub>1-3</sub> and mMCI<sub>1-3</sub> were significantly different ( $p < 0.05$ , Limma's  $t$  test). The expression level of each gene was normalized by its level in BMMCs, which are cultured MCs with so-called 'immature' properties, and the selected genes were classified into seven clusters using the  $k$ -means clustering algorithm [CL1-7; Figure 5a and Additional file 1]. We also classified the genes into functional categories, and the representative genes are listed (Figure 5b). Among them, 666 genes (52.4%) showed sMC-biased expression (CL1-3); in 78% (519 genes) of sMC-rich genes, the expression levels were relatively low in BMMCs and augmented in sMC (CL1&2). For example, the expression level of *Mcpt4* was relatively low in BMMCs, and if the expression profile of BMMCs reflects the immature properties of MC progenitors, *Mcpt4* can be concluded to be induced during the final maturation into sMCs. Interestingly, the sMC marker genes *Mcpt5* and

*Mcpt6* were classified into CL2/3, suggesting that these genes were expressed to some extent in 'immature' BMMCs, but their expression was suppressed during maturation into mMCs. On the other hand, 606 genes (47.6%) showed mMC-biased expression (CL4-7); in 51% (334 genes) of mMC-rich genes, their expression levels in BMMCs were low but were augmented in mMCs (CL4&5). For example, expression of *Mcpt1* was low in 'immature' BMMCs but was drastically induced during maturation into mMCs.

#### Protein expression of Notch4 in sMCs and Ptgfr1 in mMCs in stomach tissue

Among the genes showing differential expression (Figure 5b), we further focused on the expression of *Notch4* in sMCs and *Ptgfr1* in mMCs, both of which have never been previously characterized in MCs. The *Notch4* gene product is a member of the Notch family, consisting of transmembrane receptors which are activated by cell surface ligands on adjacent cells. Recent studies have suggested that Notch signaling is involved in lymphocyte and mast cell differentiation [30,31]. We first confirmed that *Notch4* expression is significantly higher in the separately pooled sMCs than mMCs by real-time RT-PCR (data not shown).



**Figure 4**  
**Validation of the differentially expressed genes between sMCs and mMCs.** (a) sMC-specific (*Cma2*, *Mcpt4*), mMC-specific (*Mcpt1*, *Mcpt2*) and MC-common markers (*Fcer1a* and *Kit*) (left panel) and six randomly selected genes (*Ces3*, *Cnn1*, *Cpe*, *Anxa10*, *Ctse* and *Fos*) (right panel) are indicated in the representative scatter correlation graphs between sMC, and mMC<sub>i</sub>. The same, two-fold induction and suppression thresholds are indicated as a yellow, blue and red line, respectively. (b) The expression levels of the genes in (a) were verified by real-time RT-PCR. The values represent the ratio of relative expression levels of mMCs to sMCs, and are shown as mean  $\pm$  S.D. (n = 3). The specificity of the PCR product was confirmed by gel electrophoresis and analysis of the melting temperature. The expression level of each gene was normalized to 28S ribosomal RNA.

**Table 1: Summary of genes examined by real-time PCR analysis.**

Gene Symbol	Gene Name	RefSeq Transcript ID	Reference
<i>Kit</i>	kit oncogene	NM_021099	15
<i>Fcgr1a</i>	Fc fragment of IgG, high affinity I, receptor for alpha polypeptide	NM_010184	16
<i>Mcp1</i>	mast cell protease 1	NM_008570	17, 18
<i>Mcp2</i>	mast cell protease 2	NM_008571	19
<i>Mcp4</i>	mast cell protease 4	NM_010779	2, 20
<i>Cma2</i>	chymase 2, mast cell (mast cell protease 10)	NM_001024714	14*
<i>Anxa10</i>	annexin A10	NM_011922	21
<i>C5e</i>	cathepsin E	NM_007799	22
<i>Fos</i>	FBJ osteosarcoma oncogene	NM_010234	23
<i>Ptgr1</i>	Prostaglandin reductase 1 (leukotriene B <sub>4</sub> 12-hydroxydehydrogenase)	NM_025968	24 (porcine)
<i>Cnn1</i>	calponin 1	NM_009922	25
<i>Ces3</i>	carboxylesterase 3	NM_053200	26
<i>Cpe</i>	carboxypeptidase E	NM_013494	27 (bovine)
<i>Notch4</i>	Notch gene homolog 4	NM_010929	28
28S rRNA	28S ribosomal RNA	NR_003279	29

\*. The coding sequence presented in this paper is the N-terminus truncated-form of *Cma2*, while the RefSeq "NM\_001024714" is the complete sequence of *Cma2*.

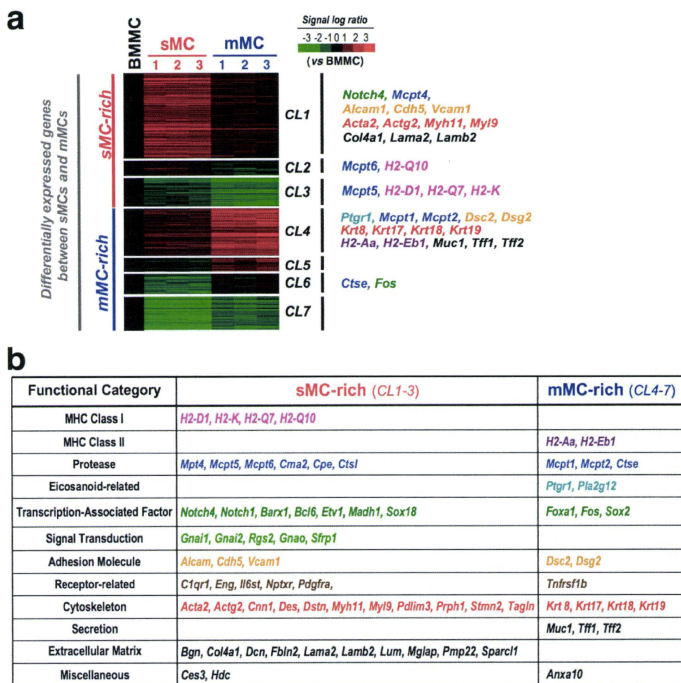
We next investigated whether the Notch4 protein is exclusively present in sMCs by immunostaining of stomach tissue (Figure 6a). Notch4 signals were detected in the nucleus-like structures of sMCs but not in those of mMCs. Furthermore, Notch4 signals were also found in the skin MCs, which were adjacently clustered with sMCs (Figure 3a). These results show that Notch4 is present in sMCs but not in mMCs, and suggest that Notch4 participates in sMC-specific transcription of Notch-target genes, which may be required for some SMC functions. In hematopoietic cells, it has been reported that constitutively active Notch4 promotes the expansion of progenitor cells and inhibits myeloid differentiation [32]. Since Notch ligands have been shown to exist in connective tissues such as skin dermis [33], it will be interesting to explore whether Notch4 plays a role in the differentiation of sMCs and the maintenance of SMC functions.

The *Ptgr1* product, 15-oxo-prostaglandin 13-reductase/leukotriene (LT) B<sub>4</sub> 12-hydroxydehydrogenase is an essential enzyme for inactivation of eicosanoids such as prostaglandin E<sub>2</sub> (PGE<sub>2</sub>) and LTB<sub>4</sub> [34]. Although it has been reported that the pathways of eicosanoid synthesis differ among the different MC subclasses [1,4], our results suggest that the inactivation system of eicosanoids also varies among the MC subclasses. *Ptgr1* expression was found to be significantly higher in the separately pooled mMCs by real-time RT-PCR (data not shown). We also examined *Ptgr1* expression in stomach sections by immunostaining. Signals for the *Ptgr1* protein were found in granule-like structures of mMCs in the stomach mucosa but not in sMCs (Figure 6b), suggesting that the *Ptgr1* enzyme may be released from mMCs upon degranulation. Since PGE<sub>2</sub> plays critical roles in the maintenance of gut homeostasis through mucosal protection and inhibition of acid secre-

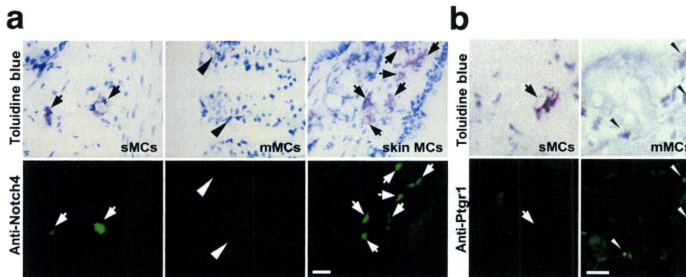
tion, it is possible that when activated, mMCs negatively regulate the cytoprotective actions of PGE<sub>2</sub> through rapid inactivation by *Ptgr1*.

#### Gene expression pattern of extracellular matrix components, adhesion molecules, and cytoskeletal proteins in sMCs and mMCs

MC phenotypes have been shown to depend on their interactions with the surrounding extracellular matrices (ECMs) and neighboring cells [1]. One of the most remarkable findings in this study is the difference in gene expression of ECM protein components, adhesion molecules, and cytoskeletal proteins, which may reflect functional adaptation of each type of MC to the mucosal or submucosal environment in the stomach (Figure 5b). mMCs express genes for mucosa-specific ECM proteins such as *Muc1* (Mucin) and *Tff1* (Trefol factor), while sMCs express genes for conventional ECM proteins such as *Col4a* (procollagen) and *Lama2* (laminin). Moreover, sMCs express genes for adhesion molecules such as *Alcam* and *Vcam1*, and genes for ordinary cytoskeletal proteins such as *Acta2* (actin), while mMCs express desmosome-component genes such as *Dsc2* (desmocollin) and *Dsg2* (desmoglein), and genes for keratin intermediate filaments such as *Krt8* and *Krt19*. Desmosomes were reported to be present in the stomach epithelia [35], and it was found that desmosome-like structures are detected in a particular type of MC [36]. It is thus possible that mMCs interact with adjacent epithelia through desmosomal adhesion in the stomach. In contrast, sMCs appear to interact with neighboring cells via adhesion molecules such as VCAM-1, ALCAM and VE-cadherin (*Vcam1*, *Alcam1* and *Cdh5*). Since these adhesion molecules have been shown to be involved in dynamic regulation of the actin cytoskeleton [37,38], such molecule-mediated inter-



**Figure 5**  
**Clustering analysis of the gene expression profiles between sMCs and mMCs.** (a) Representation of mRNA expression levels of sMC<sub>1-3</sub> and mMC<sub>1-3</sub> compared with BMMCs. The color of the bars represents the ratio of signal intensity between independent samples and BMMCs, according to the scale shown on the top right. Genes with significantly different expression between sMCs and mMCs ( $p < 0.05$ , Limma's t test) were selected (1,272 genes) and classified into 7 clusters using the k-means algorithm (CL1-7). (b) Functional categorization of representative genes from (a).



**Figure 6**  
**Immunohistochemical analysis of Notch4 and Ptgr1 in sMCs and mMCS in stomach tissue.** (a) Stomach submucosa (sMCs; left panels), stomach mucosa (mMCs; middle panels) and skin (skin MCs; right panels) sections were stained with an anti-Notch4 antibody (lower panels) and with toluidine blue (upper panels). sMCs stained with the anti-Notch4 antibody in the gastric submucosa and skin dermis are indicated by arrows. No staining was observed in mMCs (arrowheads) localized in the gastric mucosa. sMCs and mMCs were metachromatically stained with toluidine blue. (b) Stomach submucosa (sMCs; left panels) and stomach mucosa (mMCs; right panels) sections were stained with an anti-Ptgr1 antibody (lower panels) and with toluidine blue (upper panels). No staining with the anti-Ptgr1 antibody was found in the sMCs (arrow). Small signals were observed in the mMCs (arrowheads). sMCs and mMCs were metachromatically stained with toluidine blue. Bars, 25  $\mu$ m (a, b).

actions with submucosal cells may be critical to maintain the functional and morphological properties of sMCs. Indeed, it should be noted that most sMCs are variable in shape, and are often stretched and winding as compared with mMCS [1].

### Conclusion

We established a method of RNA amplification from pooled intact MCs isolated from frozen tissue sections, which enables us to conveniently obtain the global gene expression pattern of MCs from various tissues, organs, and species including humans. By using this method, we demonstrated for the first time the distinct gene expression profiles of submucosal and mucosal MCs in the mouse stomach. Our findings offer insight into possible unidentified properties specific for each MC subclass.

### Methods

#### Materials

The following materials were obtained from the sources indicated: HPLC purified T7-(dT)<sub>24</sub> primer [5'-GGCCAGTGAATTGTAATACGACTCACTATAGGGAGCCGG(1)<sub>24</sub>] from GE Healthcare UK Ltd. (Buckinghamshire, England), RNase-free water, dNTP, SuperScript II, *Escherichia coli* (*E. coli*) RNase H, *E. coli* DNA polymerase I, *E. coli* DNA ligase, T4 DNA polymerase and random hexamers from Invitrogen (San Diego, CA), RNase inhib-

itor, glycogen, and MEGAscript T7 kit from Ambion (Austin, TX). Balb/c mice were obtained from JapanClea (Hamamatsu, Japan). This study was approved by the Committee on Animal Research of Kyoto University Graduate School of Pharmaceutical Sciences.

#### RNA amplification and oligonucleotide microarray

Mouse interleukin-3-dependent BMMCs were prepared as described previously [39]. Total RNA of BMMCs was extracted using RNeasy mini kit (Qiagen, Valencia, CA). Five micrograms of total RNA from BMMCs were labeled and prepared for hybridization according to the manufacturer's instructions (standard protocol). On the other hand, 30  $\mu$ g, 10  $\mu$ g and 2  $\mu$ g of BMMC total RNA were amplified and labeled by our original three-round amplification method, which is described below.

#### First round

Total RNA was incubated with T7-(dT)<sub>24</sub> primer and first-strand cDNA was then synthesized by SuperScript II (Invitrogen). Second-strand synthesis was carried out by adding RNase H, DNA polymerase I and DNA ligase. The antisense RNA was synthesized using MEGAscript T7 kit.

#### Second round

The antisense RNA product was annealed with random hexamers, and cDNA was again synthesized by Super-



Script II. Then, the RNA-cDNA hybrid was digested with RNase H and annealed with the T7-(dT)<sub>24</sub> primer, and then second-strand synthesis was carried out by adding DNA polymerase I. The antisense RNA was again synthesized using MEGAscript T7 kit. Quality and size distribution of the antisense RNA product were confirmed by an RNA 6000 Nano LabChip on the Agilent Bioanalyzer (Palo Alto, CA).

#### Third round

As in the case of the second round, the double-stranded cDNA with a T7-promoter sequence was prepared from the second-round RNA product. Biotin-labeled antisense RNA was synthesized by RNA Transcript Labeling Kit (Enzo, Farmingdale, NY).

These labeled RNAs were hybridized to GeneChip Murine Expression oligonucleotide arrays (Affymetrix, Santa Clara, CA). We used microarray suite 5.0 of Affymetrix GeneChip Operating Software for quantification of the GeneChip data and decision of "Presence" or "Absence" of expression of each probe set using the values of 11 paired (perfect-matched and mismatched) probes.

#### Microdissection of MCs from tissue sections, RNA extraction, and microarray data analysis

Tissue sections 7  $\mu$ m in thickness were prepared using a Jung Frigocut 3000E cryostat (Leica, Nussloch, Germany), and thaw-mounted onto poly-L-lysine-coated glass slides. To visualize MCs, the sections were fixed with carnoy's fixative, and immersed in toluidine blue using the following protocol: carnoy's fixative for 1 min, RNase-free water for 10 sec, toluidine blue (0.5% in 0.12N hydrochloric acid) for 5 sec, RNase-free water for 10 sec, 70% ethanol for 15 sec, and 100% ethanol for 15 sec three times; the sections were then vacuumed for 10 min to dry. Each single MC was microdissected from the sections using a patch pipette, and 15 cells were collected with an LCM Cap using the PixCell IIe Laser Capture Microdissection System (Arcturus, Mountain View, CA). As a negative control, LCM Caps just put on tissue sections without MCs were subjected to the same protocols (no cell). Fifteen microdissected MCs were homogenized in denaturing buffer of RNeasy mini kits. Twenty nanograms of poly G (Sigma, Saint Louis, MO) was added to the lysate as a nucleic acid carrier, and total RNA was extracted. Fifty picograms of BMMC total RNA (BMMC-amp) and total RNAs extracted from sMCs in the stomach submucosa, mMCCs in the stomach mucosa and skin MCs in the ear dermis were amplified and labeled using the three-round amplification method, and were hybridized to U74Av2 Murine Genome Array (Affymetrix). On the other hand, total RNA of BMCCs (BMCC-stud) and peritoneal MC, which were collected from mouse peritoneal cavities and purified by density gradient centrifugation using metrizamide, were

labeled and hybridized by the standard protocol. Raw microarray data of macrophages (E-MEXP-38/298290452) and fibroblasts (E-GEOD-6697/1629511747) using the standard protocol were obtained from ArrayExpress, a public repository for transcriptomics data. We used either microarray suite 5.0 of Affymetrix GeneChip Operating Software or the robust multi-array average (RMA) expression measure for log transformation ( $\log_2$ ) and normalization of the GeneChip data [40,41]. To determine the similarity in the data, hierarchical clustering analysis and PCA using the R statistical environment <http://www.r-project.org> were performed as a visualization technique. For comparison of the expression profiles of sMCs with that of mMCCs, we selected 1,272 genes identified as having significantly different expression levels by the Limma's *t*-test ( $p < 0.05$ ,  $n = 3$ ). Signal values of sMCs and mMCCs were normalized by the signal values of BMCCs. Using the *k*-means clustering algorithm, these genes were classified into seven clusters on the basis of similarity of their expression profiles.

#### Real-time reverse-transcription polymerase chain reaction (RT-PCR)

Total RNA extracted from 60 captured MCs was subjected to real-time RT-PCR. Real-time PCR was performed in a LightCycler (Roche, Mannheim, Germany) using Fast Start DNA Master SYBR Green I. The expression level of each gene was quantified using external standardized dilution, and normalized by 28S ribosomal RNA. Primer sequences are shown in Table 2. The specificity of the primers was confirmed by checking the product size and restriction enzyme pattern by gel electrophoresis and the melting temperature (data not shown).

#### Immunostaining

For tissue staining, frozen sections were fixed in 4% formaldehyde and incubated with a rabbit anti-Notch4 antibody (1:20, Santa Cruz Biotechnology, Santa Cruz, CA) or a rabbit anti-Ptgr1 antibody (1:20) which was a kind gift from Prof. Takao Shimizu (University of Tokyo) [42].

#### Abbreviations

BMMC: bone marrow-derived mast cell; CL: cluster; sMC: submucosa mast cell; DEPC: diethylpyrocarbonate; ECM: extracellular matrix; LCM: laser capture microdissection; LT: leukotriene; MC: mast cell; mMCC: mucosa mast cell; PCA: principal component analysis; PG: prostaglandin; *r*: correlation coefficient; RMA: robust multi-array average; rRNA: ribosomal RNA; RT-PCR: reverse transcription-polymerase chain reaction.

#### Authors' contributions

ST designed the research, performed the research and wrote the paper; YT performed the research and wrote the paper; ES-N wrote the paper; YO performed the microar-

**Table 2: List of primers used for real-time PCR analysis.**

Gene Symbol	Forward primer (5' → 3')	Reverse primer (5' → 3')
<i>Kit</i>	ATAGACCCGACGCAAC	AATAACCGAGTCACGCT
<i>Fcεr1α</i>	GCCCCGTCTCCATTAG	CAATAACCCCGGTGTCC
<i>Mcp1</i>	AAACAGCTATAAATGGCAAG	GGGACAAACCATCATCAAC
<i>Mcp2</i>	TTGATTGGCTAGTCTCTCT	CTTTCAGCTACTTGGCTCT
<i>Mcp4</i>	CCTTACATGGCCACTCT	CTTCCCGGGTGTGATA
<i>Cma2</i>	CGGAAATGCAAAAGCC	ACAGGGAACAGTCCATC
<i>Anxa10</i>	TACCACCAACTTCGGC	GGCAAGTAGTGTTTCT
<i>Ctse</i>	GCAAGCCTATTGGCAG	TGGCATCGTGTCCGAGA
<i>Fos</i>	TGTGTACTCCCGTGGT	ACGAAACAGTAAAGGCT
<i>Ptgr1</i>	CATCGTGAATCGGTGG	GCTAGGTAAACCGCAT
<i>Cnn1</i>	ACGGCTACGGTACAC	GGTACTCCGGGTCGAG
<i>Ces3</i>	AGTGATTGTGCTCGAAG	GTCCCATTCGAGACA
<i>Cpe</i>	ACCGGAAGAGACTCTCA	CCAGTAATCCCCTACTCT
<i>Notch4</i>	CCCTTAAACTCGGTTGT	GGTGCTTAATAAATAGTTGCC
28S rRNA	CAGTACGAATACAGACCG	GGCAACAAACATCATCAAC

ray data and statistical analysis; ST performed the research; GT designed the research; ST performed the research; YS designed the research and wrote the paper. Conflict-of-interest: The authors declare no competing financial interests.

#### Additional material

##### Additional file 1

Genes with significantly different expression between sMCs and mMCS. The list represents 1,272 genes significantly altered between sMCs and mMCS in the order of clustering (Figure 5a). The values represent expression levels normalized to those of BMMCS.

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<http://www.biomedcentral.com/content/supplementary/1471-2164-10-35-S1.xls>

#### Acknowledgements

This work was supported by Grants-in-Aid for Scientific Research on Priority Areas "Applied Genomics" from the Ministry of Education, Science, Sports, and Culture of Japan and from the Ministry of Health and Labor of Japan. We thank Dr. K. Nakayama (Kyoto University) for their invaluable advice on this study. We appreciate Drs. T. Shimizu and T. Yokomizo for providing an anti-Ptgr1 antibody and generous instructions. We also thank Dr. HA Popiel and Ms. Y. Nakamimani for careful reading and secretary assistance, respectively.

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The list represents 1,277 genes significantly altered between sMCs and mMCs in the order of clustering (Figure 5a). The values represent expression levels normalized to those of BMACs.

Cluster	Gene name	Gene symbol	mMCs vs sMCs	mMCs vs BMACs	sMCs vs BMACs	mMCs vs BMACs	mMCs vs sMCs	mMCs vs BMACs	mMCs vs sMCs	mMCs vs BMACs
10390_0	catenin 3	Cttnb3	0.321463	0.321463	0.321463	0.321463	0.321463	0.321463	0.321463	0.321463
10390_4	insulin-like growth factor binding protein 3	igfbp6	0.866118	0.622154	0.478337	0.021586	0.250556	0.272869	0.272869	0.272869
10390_4	regenerating islet-derived 3 alpha	Rgs16a	0.226349	0.262301	0.138008	-0.056744	0.061981	0.041716	0.041716	0.041716
10403_1	cathepsin B	Ctbs	0.964041	0.964041	0.964041	0.473206	0.240026	0.240026	0.240026	0.240026
10409_1	RIKEN cDNA R430078M16 gene	R430078M16	1.755933	1.300085	0.904483	0.784007	0.474915	0.033338	0.033338	0.033338
10410_0	cytochrome P450 family 4 subfamily 1 polypeptide 13	Cyp4f13	0.230722	0.230722	0.230722	0.055523	0.055523	0.055523	0.055523	0.055523
10410_0	RIKEN cDNA BC24558 gene	BC24558	0.792003	0.616794	0.058127	0.241176	0.507471	0.208695	0.208695	0.208695
10413_0	integrin alpha 2	Itga2	0.563719	1.4762	1.448686	0.628001	0.524727	0.208695	0.208695	0.208695
10421_0	myosin VI	Myo6	0.632968	0.746033	0.670455	0.426634	0.203862	0.444494	0.444494	0.444494
10428_0	synectin gamma	Sng	1.452453	1.98471	1.991200	-0.155431	0.037797	0.21862	0.21862	0.21862
10431_2	RIKEN cDNA 1110013816 gene	1110013816	0.468955	0.696649	0.959517	0.258157	0.234044	0.271062	0.271062	0.271062
10435_0	DNA segment Chr 10 ERATO D6 E10 expressed	D10E10001	1.593201	1.699255	0.804744	0.021063	0.190320	0.008869	0.008869	0.008869
10436_0	supervillin	Svf	1.162612	2.01035	1.416411	0.687551	0.562541	0.419187	0.419187	0.419187
10436_2	metastatic prostate 4	Mgp4	0.23289	2.1251	1.230698	0.002271	0.331237	0.342865	0.342865	0.342865
10440_7	activated leukocyte cell adhesion molecule	Aicam	1.88261	2.818625	2.697001	1.814409	0.454801	0.222104	0.222104	0.222104
10448_0	SRY-box containing gene 18	Sor18	3.988832	4.30883	3.535262	0.250711	0.267049	0.193096	0.193096	0.193096
10448_12	guanine nucleotide binding protein alpha inhibiting 1	Gnai1	1.002043	0.69077	0.866567	0.400831	1.08202	0.36281	0.36281	0.36281
10441_4	guanine nucleotide binding protein alpha	Gnao	0.514358	0.566243	0.562469	0.197204	0.386287	0.270988	0.270988	0.270988
10450_1	vesicle-associated membrane protein associated protein B and C	Vhpb	2.16027	2.26368	1.1405	-0.12277	0.334418	0.302373	0.302373	0.302373
10451_1	chemokine (C-C motif) ligand 4	Ccl4	0.460336	0.477881	0.412085	0.178223	0.285342	0.256927	0.256927	0.256927
10457_8	actinin alpha 1	Actn1	5.208825	5.208823	5.935598	4.603928	4.40302	4.40141	4.40141	4.40141
10460_7	lamrin alpha 4	Lamn4	1.015854	0.601462	0.802068	0.093145	0.28306	0.185104	0.185104	0.185104
10465_5	stromal antigen 2	Stag2	1.983011	1.20309	1.023396	0.598441	0.549071	0.383708	0.383708	0.383708
10465_5	Kruppel-like factor 7 (ubiquitous)	Klf7	1.56391	1.943818	3.159032	0.864688	0.01194	-0.079199	-0.079199	-0.079199
10465_5	T-box 2	Tbx2	0.261018	0.1618	0.86001	0.406409	0.544028	0.544028	0.544028	0.544028
10468_0	glutamate receptor ionotropic NMDA1 (zeta) 1	Gri1	0.182148	0.21844	0.288911	0.035015	0.089791	-0.085137	-0.085137	-0.085137
10471_5	retinol binding protein 1 cellular	Rbp1	0.28642	0.10594	0.709669	0.132762	0.021285	0.041616	0.041616	0.041616
10472_9	gap junction membrane channel protein alpha 4	Gj4	2.08343	1.788152	0.927778	0.8864	0.600778	0.566441	0.566441	0.566441
10473_1	ectonucleoside diphosphate-phosphatidylesterase 5	Enpp5	2.258939	2.01956	0.950022	0.330458	0.5079	0.441387	0.441387	0.441387
10473_1	crystallin alpha C	Cryac	1.450239	4.68691	0.9461	0.049469	0.244964	0.244964	0.244964	0.244964
10473_1	crystallin alpha C	Cryac	1.42616	1.371916	0.847139	0.986877	0.499898	0.864574	0.864574	0.864574
10473_1	crystallin alpha C	Cryac	1.287078	0.907038	1.871391	0.681486	0.15446	0.24888	0.24888	0.24888
10473_1	crystallin alpha C	Cryac	0.122785	0.509237	0.337894	-0.088428	0.905049	0.904312	0.904312	0.904312
10473_1	crystallin alpha C	Cryac	0.968855	0.521858	0.085137	-0.095651	0.32098	0.07865	0.07865	0.07865
10473_1	crystallin alpha C	Cryac	0.289258	1.56018	0.915152	0.699712	-0.102581	0.25216	0.25216	0.25216
10473_1	crystallin alpha C	Cryac	2.46095	0.672936	2.250251	0.951089	0.203884	0.058404	0.058404	0.058404
10473_1	crystallin alpha C	Cryac	3.194623	3.88921	3.88921	0.362522	0.104881	0.062873	0.062873	0.062873
10473_1	crystallin alpha C	Cryac	0.74804	1.448336	0.738751	0.190759	0.421367	0.399972	0.399972	0.399972
10473_1	crystallin alpha C	Cryac	1.28734	1.465109	0.9461	0.071769	0.168158	0.168158	0.168158	0.168158
10473_1	crystallin alpha C	Cryac	3.7289	3.414883	3.236289	1.346571	1.304425	0.48862	0.48862	0.48862
10473_1	crystallin alpha C	Cryac	0.582926	0.648819	0.332894	0.078396	0.267345	0.102581	0.102581	0.102581
10473_1	crystallin alpha C	Cryac	0.28642	0.850414	0.085137	0.171769	0.168158	0.168158	0.168158	0.168158
10473_1	crystallin alpha C	Cryac	4.601585	3.750995	2.762839	0.207162	0.883573	-0.064338	-0.064338	-0.064338
10473_1	crystallin alpha C	Cryac	2.305131	2.378824	2.800009	1.02819	0.622441	0.414031	0.414031	0.414031
10473_1	crystallin alpha C	Cryac	0.16182	0.359986	0.510217	0.18162	0.046464	0.046464	0.046464	0.046464
10473_1	crystallin alpha C	Cryac	0.830312	1.64547	0.796218	-0.05854	0.280139	-0.134331	-0.134331	-0.134331
10473_1	crystallin alpha C	Cryac	1.750156	1.448286	0.9461	0.444821	0.217168	0.168158	0.168158	0.168158
10473_1	crystallin alpha C	Cryac	1.268497	2.860499	1.854826	0.72889	0.272034	0.126939	0.126939	0.126939
10473_1	crystallin alpha C	Cryac	1.696816	1.703311	1.694182	0.169226	0.146237	0.262327	0.262327	0.262327
10473_1	crystallin alpha C	Cryac	0.289258	0.289252	0.289252	0.141703	0.057497	0.161027	0.161027	0.161027
10473_1	crystallin alpha C	Cryac	3.737087	3.676243	3.206662	0.140874	0.042313	0.092364	0.092364	0.092364
10473_1	crystallin alpha C	Cryac	0.202005	0.202005	0.202005	0.222712	0.117008	-0.07865	-0.07865	-0.07865
10473_1	crystallin alpha C	Cryac	0.803687	0.53319	0.807782	0.420971	0.146189	0.292364	0.292364	0.292364
10473_1	crystallin alpha C	Cryac	0.362522	0.770245	0.547175	0.139673	0.046506	-0.045931	-0.045931	-0.045931
10473_1	crystallin alpha C	Cryac	1.103244	1.271961	1.578338	0.087486	0.182026	0.307249	0.307249	0.307249
10473_1	crystallin alpha C	Cryac	1.67216	1.554551	2.406428	0.373586	0.381884	-0.049363	-0.049363	-0.049363
10473_1	crystallin alpha C	Cryac	0.578747	0.35732	0.804296	0.225614	-0.018731	-0.33819	-0.33819	-0.33819
10473_1	crystallin alpha C	Cryac	1.500441	1.512377	1.856185	0.584884	0.587346	0.617589	0.617589	0.617589
10473_1	crystallin alpha C	Cryac	0.603266	0.481603	0.448736	0.262269	0.209269	0.329763	0.329763	0.329763
10473_1	crystallin alpha C	Cryac	4.964558	4.95322	1.87171	2.387458	1.121441	0.097762	0.097762	0.097762
10473_1	crystallin alpha C	Cryac	3.213444	0.260199	9.209191	0.038008	-0.140469	0.292364	0.292364	0.292364
10473_1	crystallin alpha C	Cryac	0.684807	0.88078	0.480522	0.306848	0.303694	0.345897	0.345897	0.345897
10473_1	crystallin alpha C	Cryac	0.964306	1.245568	1.514429	0.786033	0.680037	0.436991	0.436991	0.436991
10473_1	crystallin alpha C	Cryac	0.151385	1.219463	0.511315	-0.123444	0.029301	-0.100804	-0.100804	-0.100804
10609_2	BC2-associated antigen 2	BAG2	0.221001	0.279649	0.302197	-0.121963	0.088172	0.172045	0.172045	0.172045
10609_4	expressed	D16Bw1494e	1.115043	2.25079	3.00891	0.78389	0.078695	0.004404	0.004404	0.004404
10610_5	RIKEN cDNA 430022118 gene	430022118	1.829181	2.083439	1.638071	0.399599	0.736446	0.400658	0.400658	0.400658
10610_2	SRY-box containing protein 8	Sov18	0.610247	1.50275	1.365448	0.461953	0.536761	0.532981	0.532981	0.532981
10610_9	DNA segment Chr 5 Brnham & Woman's Genetics 0860 expressed	D5Bw0860e	1.246086	2.642084	0.514602	0.1674	0.296115	0.302938	0.302938	0.302938
10611_9	development and differentiation enhancing 3	Deaf1	0.309536	0.544053	0.468484	0.039255	0.016597	-0.230899	-0.230899	-0.230899
10611_9	development and differentiation enhancing 3	Deaf1	1.42055	2.81971	3.633965	0.478863	0.371762	0.029756	0.029756	0.029756
10611_9	development and differentiation enhancing 3	Deaf1	0.675314	0.48812	0.626862	0.307091	0.309519	0.254151	0.254151	0.254151
10611_9	development and differentiation enhancing 3	Deaf1	0.782075	0.18726	0.896857	0.35513	0.081919	0.171491	0.171491	0.171491
10611_9	development and differentiation enhancing 3	Deaf1	1.051965	0.82612	0.837865	0.087486	0.182026	0.434204	0.434204	0.434204
10611_9	development and differentiation enhancing 3	Deaf1	0.487113	0.523636	0.884141	-0.005738	0.151397	0.282125	0.282125	0.282125
10611_9	development and differentiation enhancing 3	Deaf1	1.42055	2.81971	3.633965	-0.008621	0.207963	0.113558	0.113558	0.113558
10611_9	development and differentiation enhancing 3	Deaf1	0.338219	0.319914	0.837865	0.02203	0.07207	0.014541	0.014541	0.014541
10611_9	development and differentiation enhancing 3	Deaf1	4.866021	1.91236	2.556239	0.129137	0.085357	0.095378	0.095378	0.095378
10611_9	development and differentiation enhancing 3	Deaf1	1.092041	1.82857	3.05611	0.780571	0.180571	0.		

The list represents 1277 genes significantly altered between mMCs and mMCs in the order of clustering (Figure S4). The values represent expression levels normalized to those of BMAL1.

Cluster	Accession	Gene name	Gene symbol	mMC1 vs. BMAL1	mMC2 vs. BMAL1	mMC3 vs. BMAL1	mMC4 vs. BMAL1	mMC5 vs. BMAL1	mMC6 vs. BMAL1	mMC7 vs. BMAL1
1161181_L	ENCL	essential differentiation sphingoid 6'-phosphate-coupled receptor 1	ENCL	1.01038	0.84119	0.61619	0.57815	0.28156	0.42070	0.20718
1161187_L	ENCL	RKFN1 CDNA 493042J18 gene	493042J18	1.343762	3.031995	2.92978	0.984973	0.003785	0.69682	0.27823
1161189_L	ENCL	glutamate decarboxylase (glutamine synthase)	GAD67	0.420259	0.92957	0.694653	0.84346	0.29133	0.22569	0.22476
1161189_L	ENCL	synuclein gamma	Sncg	1.88245	1.76733	2.15361	1.103788	0.084462	0.21619	0.16189
1161187_L	ENCL	ubiquitin specific protease 15	Usp15	0.331039	0.19621	0.24623	0.10778	0.07178	0.124137	0.130688
1161189_L	ENCL	metaxin	Mtx	0.437039	0.28841	0.25842	0.10081	0.06662	0.21687	0.16899
1161190_L	ENCL	tensin XB	Tnb2	1.56173	1.53791	1.54872	0.242671	0.454517	0.63102	0.21887
1161193_L	ENCL	lymphocyte specific 1	Lys1	0.145894	0.06223	0.09756	0.06176	0.12438	0.16899	0.16899
1161194_L	ENCL	startin-like 3	Stmn3	0.823395	0.752124	0.99375	0.55096	0.722793	0.520991	0.520991
1161198_L	ENCL	procollagen type III alpha 1	Col3a1	0.420255	0.015138	3.497056	1.073484	2.55638	0.152365	0.152365
1161198_L	ENCL	low density lipoprotein receptor-related protein associated protein 1	Lrpap1	0.504075	0.320254	0.265031	0.100399	0.101978	0.054215	0.054215
1161198_L	ENCL	N-myc downstream regulator 4	Ndr4	0.978945	0.694347	0.846116	0.44623	0.436882	0.25376	0.25376
1162004_L	ENCL	arrestin toxin receptor 2	Attr2	0.145894	0.529427	0.767966	0.338459	0.195148	0.338459	0.338459
1162008_L	ENCL	talin	Tln	0.248207	0.142747	0.331386	0.04281	0.089493	0.04987	0.04987
1162008_L	ENCL	centrievinculin-like IMAGE5374066 mRNA partial cds	—	0.228498	0.424128	0.37196	0.071687	0.212207	0.073882	0.073882
1162100_L	ENCL	vesicular membrane protein p24	Vmp	1.949189	0.36204	0.774531	-0.18198	-0.18472	-0.08186	-0.08186
1162102_L	ENCL	chromogranin A	Cgpa	1.99687	1.79855	1.149801	0.04201	0.917122	1.04637	1.04637
1162204_L	ENCL	Notch gene homolog 1 (Drosophila)	Notch1	1.323874	0.89827	0.93807	0.185514	0.433175	0.108305	0.108305
1162205_L	ENCL	zona pellucida glycoprotein 2	Zgp2	0.247841	0.311152	0.198556	-0.070458	0.094329	0.101988	0.101988
1162300_L	ENCL	crystallin alpha B	Cyab	1.033501	0.51026	1.02826	0.698226	0.693479	0.61216	0.61216
1162301_L	ENCL	BarH-like homeobox 1	Bar1	2.008126	2.560072	1.715106	0.155689	0.527081	0.372778	0.372778
1162326_L	ENCL	—	—	0.185007	0.713151	0.807135	0.22675	0.472232	0.40824	0.40824
1162342_L	ENCL	fatty acid binding protein 1 liver	Fabp1	0.914198	0.638445	1.008516	0.720657	0.788275	0.727373	0.727373
1162345_L	ENCL	biglycan	Bgn	1.103554	0.814546	1.47377	0.326969	0.689168	0.448001	0.448001
1162349_L	ENCL	tensin C	Tnc	0.913292	0.89333	0.302066	0.117164	0.163664	0.086205	0.086205
1162367_L	ENCL	Ctla and tumor necrosis factor related protein 1	Ctla1	0.655611	0.400497	0.049937	0.141344	0.30973	0.280224	0.280224
1162448_L	ENCL	crystallin alpha C	Cycc	0.256565	0.493141	0.309773	0.12277	-0.014008	0.11164	0.11164
1162449_L	ENCL	ras homology gene family member C	Rhc	0.403125	0.56792	0.535919	0.174606	0.358606	0.277869	0.277869
1162449_L	ENCL	general transcription factor II C	GTF2C	0.081614	0.61735	0.761758	0.176557	0.536828	0.292957	0.292957
1162449_L	ENCL	Mus musculus transcribed sequence with strong similarity to protein ap Q05510 (H sapiens) Z145_HUMAN Zinc finger protein PLZF (Proteolytic leukemia zinc finger) (Zinc finger protein 145)	—	2.078102	3.016708	2.034989	0.283574	0.081803	-0.154734	-0.154734
1162202_g	at	—	—	1.59207	1.77967	0.998486	0.93396	0.531186	0.643861	0.643861
1162223_f	at	component 1 of 1 subcomponent gamma polypeptide heterotrimeric (inositol binding) protein	—	1.949189	0.36204	0.774531	-0.18198	-0.18472	-0.08186	-0.08186
1162225_f	at	RNA polymerase 1	Rpo1-2	1.653002	0.7947	1.76617	0.761817	0.196824	1.48876	-0.00976
1162241_f	at	RKFN1 CDNA 1500041O16 gene	1500041O16Rk	0.30543	0.107078	0.704491	0.143445	0.251288	-0.18733	-0.18733
1162275_f	at	troglyrin	Tro	0.662707	0.122	0.973829	0.288857	0.19328	0.19328	0.19328
1162276_f	at	muscle-activated protein kinase kinase kinase 6	Mak3	1.2501	-0.015988	1.22227	-0.141729	-0.175375	-0.296232	-0.296232
1162280_f	at	protein tyrosine phosphatase receptor type B	Ptpn22	2.85898	2.176324	1.488022	0.76328	0.15207	0.44429	0.44429
1162348_f	at	thyroid hormone receptor alpha	Thra	0.940174	0.78542	1.226701	0.09602	-0.014919	-0.032523	-0.032523
1162391_f	at	ELAV (embryonic lethal abnormal vision Drosophila)-like 4 (Hu antigen D)	Elavl4	0.281179	0.450502	0.414747	0.006857	0.17896	0.05858	0.05858
1162396_f	at	lamina alpha 2	Lama2	2.344589	0.823386	1.534462	0.072151	0.369921	0.347676	0.347676
1162397_f	at	centaurin gamma 2	Cenpf2	0.647202	0.898004	0.884342	0.468138	0.324155	0.283011	0.283011
1162401_f	at	myosin IIF	Myo1f	1.400223	0.660114	0.960114	0.28852	0.28852	0.28852	0.28852
1162496_f	at	vesicle-associated membrane protein 5	Vamp5	1.363341	1.506077	1.748865	0.749252	0.637962	0.408571	0.408571
1162511_f	at	BarH-like homeobox 1	Bar1	2.008126	2.560072	1.715106	0.155689	0.527081	0.372778	0.372778
1162512_f	at	isocognin	Neop1	0.34269	0.327448	0.344547	0.131976	0.218986	0.139406	0.139406
1162535_f	at	early B-cell factor 1	Ebf1	0.703399	0.81732	0.537204	0.203464	0.445778	0.289861	0.289861
1162550_f	at	vesicular membrane protein 1	Vamp1	3.578295	1.78955	2.362525	0.28852	0.28852	0.28852	0.28852
1162560_g	at	vascular cell adhesion molecule 1	Vcam1	0.727994	1.274186	1.112	0.342406	0.657804	0.489414	0.489414
1162563_f	at	heparan sulfate proteoglycan interacting protein 1	Hsp1	1.145955	1.106152	0.76328	0.16328	0.16328	0.16328	0.16328
1162565_f	at	Notch gene homolog 4 (Drosophila)	Notch4	0.348227	0.891719	1.187896	0.101816	0.17833	0.162885	0.162885
1162700_f	at	astrotatin 1	Astn1	0.516223	0.534719	1.113489	0.277072	0.077443	0.243897	0.243897
1162705_f	at	Tbr2	Tbr2	0.31754	0.435878	0.455183	0.233087	0.265339	0.258861	0.258861
1162725_f	at	growth arrest specific 8	Gas8	0.425327	0.251274	0.307556	-0.152721	0.011901	-0.131432	-0.131432
1162740_f	at	small chemokine (C-C motif) ligand 11	Ccl11	0.701896	0.96988	0.872432	0.11987	0.24567	0.295426	0.295426
1162761_f	at	securin	Scn	1.891008	0.81981	0.978966	0.464203	0.864247	0.410564	0.410564
1162820_f	at	ubiquitin specific protease 2	Usp2	0.707829	0.330194	0.499329	0.193081	0.02197	-0.120425	-0.120425
1162821_f	at	ubiquitin specific protease 2	Usp2	1.701209	0.862091	1.591511	0.456664	0.548178	0.822216	0.822216
1162836_f	at	elafin	Elafl	3.205994	1.596448	1.271286	-0.181531	0.588447	0.544711	0.544711
1162850_f	at	fibronectin 1	Fln1	1.62813	2.071945	1.93853	0.294052	0.658367	0.123688	0.123688
1162852_f	at	vesicular membrane protein p24	Vamp2	1.949189	0.36204	0.774531	-0.18198	-0.18472	-0.08186	-0.08186
1162927_f	at	ets variant gene 1	Etv1	1.144174	2.374049	2.63501	0.321319	0.2024	0.08844	0.08844
1162981_f	at	secretogranin 1	Socg1	1.632028	1.99818	1.384451	0.520605	0.288487	0.239726	0.239726
1162987_f	at	isoleucine carrier family 4 (anion exchanger) member 3	Slc24a3	0.363643	2.281103	0.938497	0.1091	0.239726	0.363726	0.363726
1162996_f	at	SRY-box containing gene 1	Soc17	0.491167	1.203035	0.400249	-0.162193	0.179819	-0.180964	-0.180964
1163040_f	at	FXYD domain-containing ion transport regulator 1	Fxyd1	2.456789	2.213306	1.651113	0.248896	0.621203	0.686616	0.686616
1163054_f	at	RKFN1 CDNA 1110054N06K gene	1110054N06K	0.671896	0.995846	1.373546	0.591442	0.693997	0.565442	0.565442
1163061_f	at	integrin alpha 7	Ibp7	1.306685	0.951322	1.365643	0.583951	0.747388	0.710368	0.710368
1163073_f	at	lymphocyte antigen 6 complex locus C	Lys6	1.081717	0.787864	0.86206	0.07905	0.098921	0.104512	0.104512
1163078_f	at	lymphocyte antigen 6 complex locus C	Lys6	3.470687	3.288356	3.480013	1.27782	1.769073	1.97705	1.97705
1163084_f	at	isoleucine carrier family 25 (mitochondrial carrier; adenine nucleotide translocator) member 4	Slc25a4	2.296985	2.099477	1.686294	0.394748	-0.059192	0.283992	0.283992
1163084_f	at	Mus musculus transcribed sequence with moderate similarity to protein Q8UBP3 (H sapiens) UBPP_HUMAN Ubiquitin carboxyl-terminal hydrolase 25 (Ubiquitin thiolesterase 25) (Ubiquitin-specific processing protease 25) (Deubiquitinating enzyme 25) (USP on chromosome 21)	—	0.581011	0.83063	0.79515	0.088055	0.47853	0.300281	0.300281
1163094_f	at	ceramide degeneration-related 2	Cdr2	1.524597	1.951939	0.302888	-0.077769	0.142246	0.026114	0.026114
1163105_f	at	actin alpha 2 smooth muscle actin	Acta2	0.502025	0.574836	0.64946	0.246313	0.246313	0.268689	0.268689
1163102_f	at	actin gamma 2 smooth muscle actin	Actg2	3.752064	1.94382	3.493477	-0.10627	0.309693	0.866002	0.866002
1163106_L	at	serine (or cysteine) proteinase inhibitor clade A member 1d	Serpina1d	0.429814	0.454769	0.730877	0.187937	0.310737	0.194031	0.194031
1163126_f	at	crystallin alpha B	Cyab	2.22128	0.51315	1.01748	0.157448	0.112348	0.091786	0.091786
1163130_f	at	RKFN1 CDNA 260005C20 gene	260005C20	0.01981	0.163441	0.41029	-0.028768	-0.019208	-0.14198	-0.14198
1163153_f	at	adenosine deaminase RNA-specific B1	Adarb1	1.390581	0.862234	0.603891	0.072703	0.289804	0.13402	0.13402
1163157_f	at	RKFN1 CDNA 221002R24K gene	221002R24K	1.891008	1.819263	1.938295	0.181023	0.618338	0.749786	0.749786
1163188_f	at	dickkopf homolog 3 (Xenopus laevis)	Dkk3	1.381848	3.295445	2.66243	0.278116	0.639773	0.441867	0.441867
1163195_f	at	myosin heavy chain 11B	Myh11	0.625591	0.951068	0.802662	0.097967	0.102609	0.102609</	

Cluster	Allylmyc15	Gene name	Gene symbol	mMC vs. iMC	mMC vs. BMC	mMC vs. BMC	mMC vs. BMC	mMC vs. BMC	mMC vs. BMC	mMC vs. BMC	mMC vs. BMC
159592_1	LM22	ribosomal binding 2	IR2	1.23296	1.23296						0.271252
159593_1	LM22	RIKEN cDNA F83020C16Rk	F83020C16Rk	1.682876	1.484375	0.463434	0.685308	0.335748	0.335748	0.112556	
159596_s_at		matrix gamma-carboxylglutamate (gla) protein	Nglypo	4.079321	3.896966	3.897731	3.370069	0.112044	0.112044	0.207262	
159597_1		Hu-B-300000 encodes 3	Gact2	0.221663	0.446303	0.043308	0.043308	0.164619	0.164619	0.320792	
159598_s_at		cytochrome P450 family 2 subfamily A polypeptide 1	Cyp2e1	1.611056	0.944351	0.083445	0.293761	0.363539	0.363539	0.324005	
159606_1		B-acylindole induced gene 2	A2i2	0.960029	0.615837	0.417954	0.664428	-0.221627	-0.221627	-0.264615	
159607_1		Mus musculus T3 alpha embryo spinal cord cDNA RIKEN full-length enriched library clone GS300215 product unclassified full insert sequence	---	2.587807	2.592464	2.852338	2.488718	1.858171	1.858171	1.174109	
159620_s_at		CD84 antigen	Co84	0.484425	0.500917	0.600897	0.132561	0.41678	0.41678	0.226817	
159621_s_at		Lycophylliferase 7	Lyc7	1.223116	0.31196	0.317922	-0.031721	0.115372	0.115372	0.015068	
159622_s_at		insulin-like growth factor binding protein 4	Igfbp4	0.825262	1.068377	1.002468	0.917907	0.728857	0.728857	0.438803	
159628_r_at		melanoma antigen family D 2	Maged2	2.095577	1.721372	1.095542	0.87189	1.092221	1.092221	0.479092	
159637_1		fibulin 1	Fbln1	1.37685	1.359742	1.400118	0.178322	0.536465	0.536465	1.242396	
159640_1		fibulin 1	Fbln1	1.144809	1.043472	1.276121	0.778674	0.328071	0.328071	0.07872	
159645_1		interleukin D signal transducer	Iltst	3.987308	3.68623	1.307305	0.792637	0.848847	0.848847	0.231945	
159646_1		ATP-binding cassette sub-family A (ABC1) member 1	Abca1	3.081063	2.929972	2.498883	-0.275115	0.391988	0.391988	1.82057	
159647_1		guanine nucleotide binding protein (G-protein) gamma 11	Gng11	0.52795	0.545537	0.711468	0.502046	0.174562	0.174562	0.025335	
159649_1		Harvey rat sarcoma oncogene subgroup R	Hras	2.001538	1.875456	2.009772	0.242331	0.844044	0.844044	0.175333	
159651_1		eukaryotic translation elongation factor 1 alpha 2	Eef2a2	0.676306	0.418974	1.074941	0.122878	0.299798	0.299798	0.21381	
159652_s_at		isyltransferase 1 (beta-galactosyl alpha-2-sialyltransferase)	Siatf	1.882119	2.862134	1.119738	-0.005914	0.299144	0.299144	0.211191	
159653_1		desmin	Dnm1	3.229762	3.259308	2.877887	2.566615	2.103335	2.103335	2.363978	
159654_1		claudin 3	Cln3	0.167755	0.241487	0.147818	-0.118413	0.047124	0.047124	-0.09216	
159655_1		RIKEN cDNA 261003J06 gene	261003J06Rk	0.519673	0.645066	0.5896	0.168981	0.372605	0.372605	0.173883	
159656_1		retinol 1	Rbt1	1.22105	1.651695	1.925503	0.517184	-0.027382	-0.027382	0.646559	
159657_1		vascular endothelial growth factor C	Vegfc	1.66086	1.848388	0.784731	0.092742	0.088755	0.088755	0.119475	
159670_1		zinc-finger protein 2	Zfp288	1.326565	1.256447	3.011385	0.462379	0.368051	0.368051	0.468597	
159713_s_at		leukocyte tyrosine kinase	Ltk	0.830312	0.11004	0.313088	0.011168	-0.088844	-0.088844	-0.33823	
159813_1		growth arrest specific 1	Gast	2.418645	0.81036	1.440517	0.477395	0.481308	0.481308	0.176049	
159822_1		superoxide dismutase 3 extracellular	Sod3	0.777115	0.920526	0.732635	0.283863	0.423038	0.423038	0.160468	
159840_1		alcohol dehydrogenase 1 (class I)	Ahd1	0.909975	2.527676	1.848103	1.201598	0.611629	0.611629	0.519348	
159840_2		thrombospondin 2	Tbsp2	2.023238	8.041116	4.897638	0.216711	0.540148	0.540148	0.298462	
159851_1		ubiquitin-conjugating enzyme 2	Ubc2	1.106061	1.326883	0.658595	0.487351	0.453071	0.453071	0.453071	
159857_1		platelet derived growth factor receptor alpha polypeptide	Pdgfra	3.074306	3.733821	2.014402	1.488937	0.896073	0.896073	2.160685	
159858_1		synectin 1	Sytn1	0.898813	0.698133	0.635465	0.125457	0.125457	0.125457	0.125457	
159112_1		peptidylprolyl isomerase (cyclophilin) beta 2	Ppi2	0.803399	0.639955	0.851473	0.497149	0.036868	0.036868	0.460778	
159125_1		rng-bp 1	Rngb1	0.830312	0.884758	0.628812	1.135133	0.485851	0.485851	0.207876	
159148_1		adenylyl cyclase 4	Adcy4	0.942123	0.591185	0.457163	0.0138	0.123098	0.123098	0.119977	
159320_1		pleckstrin homology Gec7 and coiled-coil domains 1	Pchd7	0.225988	0.225988	0.501917	0.423282	0.281544	0.281544	0.400605	
159557_1		alpha 2-macroglobulin (serpin) receptor 2B	Fr2b	0.565506	0.741144	0.257153	-0.120681	-0.023970	-0.023970	0.038919	
159558_1		bone morphogenetic protein 2	Bmp2	0.941213	0.498851	0.573073	0.12824	0.414045	0.414045	0.327109	
159561_1		developmental transcription factor associated 2	Dtaf2	0.481118	0.537158	0.537158	0.537158	0.537158	0.537158	0.301216	
159565_1		DNA element Chr 6 ERATO 0232 compressed	D6ER232e	1.311834	0.78429	1.160063	0.860638	0.440762	0.440762	0.121356	
159680_1		starmatin-like 2	Stmr2	1.853591	1.167608	1.909969	-0.019147	0.488861	0.488861	0.317071	
159681_1		starmatin-like 2	Stmr2	1.431137	0.881168	0.658595	0.487351	0.388589	0.388589	0.285891	
159723_s_at		RIKEN cDNA 261000E16Rk gene	261000E16Rk	0.304847	1.099111	0.307609	-0.019377	1.114328	1.114328	0.099111	
159802_1		chymase 2	Cma2	0.278026	0.278026	0.413917	0.413917	0.413917	0.413917	0.413917	
159824_1		Dz4	Dz4	0.386234	2.236889	0.433589	0.03974	0.216703	0.216703	0.53623	
159848_1		Nr5c downstream regulated 2	Nrg2	2.07089	2.07089	0.84587	0.84587	0.84587	0.84587	0.84587	
159849_1		biphenylamine 2	Bpa2	0.206208	1.377795	0.884439	0.486379	0.787129	0.787129	0.538218	
159810_1		Kruppel-like factor 2 (lung)	Klf2	1.151838	0.87071	0.893885	0.260878	1.178516	1.178516	0.096907	
159811_1		inhibitor of DNA methylase 4	Idm4	0.241783	0.547173	0.108317	0.457357	0.281544	0.281544	0.143254	
159814_1		B-cell maturation gene 3	Bmg3	2.534441	2.713806	2.01669	1.34291	2.03165	2.03165	0.21083	
159820_1		SH3-binding domain glutamic acid-rich protein	Sb3br	0.821242	0.687859	0.858117	0.365236	0.532296	0.532296	0.400279	
159825_1		SH3-binding domain glutamic acid-rich protein	Sb3br	2.825738	2.052708	2.052708	0.884445	0.884445	0.884445	0.238166	
159826_1		RIKEN cDNA G43059G11 gene	G43059G11Rk	1.866939	0.971357	1.455213	0.331334	1.306666	1.306666	0.109575	
159827_1		ubiquitin carboxyl terminal hydrolase 1	Uch1	0.300407	0.775844	0.345963	-0.117443	0.203379	0.203379	-0.145817	
159851_1		C-type lectin domain dependent carbohydrate recognition domain lectin	Clec7d	1.054026	2.005839	0.170322	-0.00991	-0.038936	-0.038936	0.042818	
159702_1		melanoma antigen family D 1	Maged1	2.012893	1.467519	1.398769	1.00144	1.023681	1.023681	1.040608	
159736_1		RIKEN cDNA G43020K16Rk gene	G43020K16Rk	1.379503	1.906544	1.526181	1.102475	-0.003217	-0.003217	0.783953	
159742_1		pleckstrin homology domain containing family C (with FERM domain) member 1	Pchd1	1.044588	0.97097	0.9584	0.595184	0.594625	0.594625	0.331965	
159774_1		smoothed homology (Drosophila)	RhoA	0.292747	2.293884	1.368833	0.244814	0.118846	0.118846	0.077043	
159812_1		Smoo	Smoo	0.578478	0.578478	0.666547	0.420218	0.712047	0.712047	0.364765	
159813_1		delta 2 homology (Drosophila)	Dlx2	0.444906	0.444906	0.708499	0.114008	0.345766	0.345766	0.345766	
159820_1		protease serine 11 (dog lung)	Prss11	3.951482	3.951482	2.147711	1.673415	2.009325	2.009325	0.287829	
159821_1		SPARC related nuclear calcium binding 2	Sprr2	0.169449	2.068811	0.800209	0.302335	0.045657	0.045657	0.30865	
159836_1		myosin light polypeptide 5 regulatory	Myf5	5.550774	6.684842	5.123344	3.565535	1.207484	1.207484	0.961763	
159838_1		serine/threonine kinase 24 (STE20 homology yeast)	Ste24	0.447828	0.480007	0.599739	0.105857	0.303588	0.303588	0.311211	
159700_1		prk-eyc dilution	P	0.381024	0.381024	0.481078	0.14603	0.298206	0.298206	0.218236	
159705_1		cDNA sequence BC0337327	BC0337327	0.683289	2.025998	0.470042	-0.041298	0.968283	0.968283	0.059778	
159710_1		RIKEN cDNA G43038F01 gene	G43038F01Rk	0.205142	0.485854	0.613748	0.754565	0.298969	0.298969	-0.301235	
159712_1		MV1 integration site 1	Mv1i1	1.265141	1.378165	1.94341	-0.334445	-0.158986	-0.158986	0.238307	
159722_1		RAB8 member RAS oncogene family	Rab8	0.763578	0.655449	0.807554	0.2382	0.577505	0.577505	0.296909	
159725_1		RIKEN cDNA G43038F01 gene	G43038F01Rk	0.629689	0.629689	0.246928	0.246928	0.246928	0.246928	0.246928	
159731_1		adenocorticoid synthetase/phosphodiesterase 4	Enpp2	3.963979	3.429028	3.575433	0.026317	1.300793	1.300793	0.130471	
159733_1		cathespin F	Csf1	1.985342	2.169251	1.185331	0.830863	0.141111	0.141111	0.252514	
159741_1		leucin to forming growth factor beta binding protein 2	Lfbp4	2.728746	2.728746	0.688335	0.688335	0.688335	0.688335	0.147475	
159742_1		thrombin S-methyltransferase	Tent	1.063324	0.628719	0.324241	-0.033922	0.214942	0.214942	0.332738	
159743_1		serpin (cysteine) proteinase inhibitor domain E member 2	Serp2e2	0.298283	0.298283	0.092978	0.131532	0.131532	0.131532	0.131532	
159746_1		RIKEN cDNA G43035L4M23 gene	G43035L4M23Rk	4.978786	5.047187	4.801099	1.440554	2.893994	2.893994	0.814441	
159751_1		monocyte chemoattractant protein 1	Mcp1	0.729623	0.729623	0.490679	0.286174	0.445044	0.445044		

The list represents 1,272 genes significantly altered between sMCs and mMCs in the order of clustering (Figure 5a). The values represent expression levels normalized to those of BMMC.

Cluster	Allylmito	Gene	Symbol	AMC1	sMC	mMC	BMMC	mMC1	BMMC	mMC2	BMMC	mMC3	BMMC
1	166356_at	Mus musculus transcribed sequence		0.245099	0.387645	0.529318	0.160113	0.107499	-0.029758				
2	166434_at	Rho guanine nucleotide exchange factor (GEFT)	<i>Arhgef7</i>	1.227891	0.532052	1.705718	-0.42613	0.224149	-0.881756				
3	166454_at	parvalbumin	<i>Pvalb</i>	1.207765	0.789545	1.267174	0.199139	0.450369	0.377499				
4	166465_f.at	interferon activated gene 204	<i>Irf204</i>	1.386213	2.083939	1.236717	0.100072	0.705531	0.621657				
5	166475_at	matrin 2	<i>Matn2</i>	1.250154	0.513204	0.800116	0.320740	0.232021	0.181924				
6	166485_at	phosphocyanin 1 muscle	<i>Pcy1</i>	0.843111	0.7899	0.833304	0.253796	0.363263	0.374133				
7	166507_at	nuclear receptor subfamily 1 group D member 1	<i>Nr1d1</i>	1.619345	1.354488	1.655972	0.630818	0.599853	-0.037334				
8	166525_at	smothelin	<i>Smthl</i>	1.277358	1.66021	2.01202	0.19087	0.413369	0.207895				
9	166535_at	adipose differentiation related protein 1	<i>Adip1</i>	1.198411	1.372007	0.631091	0.879953	0.523034	0.454722				
10	166599_at	hepatoma-derived growth factor related protein 2	<i>Hrgfp2</i>	1.155205	0.678072	0.104257	0.028299	-0.124688	-0.396476				
11	166621_s.at	insulin-like growth factor 2	<i>Igf2</i>	2.071625	2.66761	3.312313	0.72494	0.715154	0.290405				
12	166624_at	ADP-ribosyltransferase 3	<i>Art3</i>	1.437385	2.332562	1.418254	0.435912	1.216574	0.296102				
13	166625_at	immunoglobulin superfamily containing leucine-rich repeat	<i>Islr</i>	2.489762	1.700294	1.259865	0.207732	0.467941	0.302448				
14	166632_at	RAS desamethylase-induced 1	<i>Rasd1</i>	1.231742	1.18503	1.212571	-0.119951	0.59921	0.152326				
15	166625_at	thymus cell adhesion molecule 2	<i>Tcam2</i>	1.361107	1.611971	1.538763	0.139055	0.52811	0.327976				
16	166627_at	thymus cell antigen 1 theta	<i>Thy1</i>	1.338159	1.646817	2.226498	0.157488	0.836167	0.424456				
17	166608_at	serine (or cysteine) proteinase inhibitor clade G member 1	<i>Scp1g1</i>	2.599593	3.613223	3.98009	0.165848	0.886641	0.137178				
18	166607_at	DNA segment Chr 18 ERATO Do 232 expressed	<i>Chr18ERATDo232</i>	1.311964	1.069625	1.718265	0.059620	1.398159	-0.748645				
19	166618_at	AXL receptor tyrosine kinase	<i>Axl</i>	0.884148	0.984148	1.14348	0.280548	0.616345	0.728684				
20	166618_at	cysteine sulfinic acid decarboxylase	<i>Cisd</i>	1.491792	0.702393	1.078862	0.621278	0.450906	0.505427				
21	166623_at	acidic proleptin-related gene 1	<i>Alpr1</i>	1.301338	0.543602	1.439234	-0.171567	-0.155327	0.254606				
22	166630_at	MAS1 oncogene	<i>Mas1</i>	0.244508	0.411500	0.245497	0.020806	0.145544	0.089050				
23	166442_at	regulated endonuclease-specific protein 18	<i>Resp18</i>	0.769894	1.010999	0.630676	0.115903	0.374617	0.233727				
24	166442_at	receptor (calotropin) activity modifying protein 2	<i>Ramp2</i>	0.985145	0.990505	0.909406	0.066643	0.259031	-0.11651				
25	166452_at	phosphodiesterase 1A calmodulin-dependent	<i>Pde1a</i>	0.096070	0.537762	0.461343	0.267381	0.318677	0.147544				
26	166452_at	suppressor of cytochrome c signaling 2	<i>Soc2</i>	1.542535	0.556774	0.87308	0.043319	0.039963	-0.917897				
27	166454_at	serine (or cysteine) proteinase inhibitor clade 1 member 1	<i>Scp1s1</i>	0.822428	0.800178	0.71129	0.468975	0.500959	0.5513				
28	166617_at	microfilament associated protein 5	<i>Mfap5</i>	0.26897	0.410443	0.421791	0.067614	0.166935	0.130297				
29	166618_at	microfilament associated protein 5	<i>Mfap5</i>	0.26897	0.410443	0.421791	0.067614	0.166935	0.130297				
30	166524_at	solute carrier family 8 (sodium/calcium exchanger) member 1	<i>Scl8a1</i>	2.204842	2.294228	2.85043	0.021105	0.509765	0.213444				
31	166545_at	ostrogyn	<i>Ostg</i>	1.246443	1.32226	0.960313	0.508161	0.420285	0.20854				
32	166642_at	carboxypeptidase E	<i>Cpe</i>	0.691479	0.423306	0.697847	0.267889	0.414202	0.167897				
33	166642_at	carboxypeptidase E	<i>Cpe</i>	0.620851	0.670041	1.782406	0.5274852	0.485454	0.277381				
34	166642_at	zinc finger protein 289	<i>Zfp289</i>	0.219567	0.426823	0.426823	0.290525	0.469527	0.064554				
35	166665_at	special AT-rich sequence binding protein 1	<i>Sab1</i>	0.442897	0.224652	0.71219	0.068875	0.251796	0.127296				
36	166665_at	rat eye syndrome chromosome region candidate 5 homolog	<i>Chr5ERATDo5</i>	0.564974	0.452546	0.678471	0.108146	0.468045	0.004048				
37	166622_f.at	DNA segment Chr 18 ERATO Do 232 expressed	<i>Chr18ERATDo232</i>	0.637399	0.610989	1.15396	-0.164837	0.475888	0.320955				
38	166622_f.at	Mus musculus transcribed sequence AGE 8432820 partial cds		0.285145	0.417604	0.621306	-0.181468	0.287181	0.302555				
39	166642_at	procollagen type XIX alpha 1	<i>Col19a1</i>	0.75821	0.513355	0.744114	0.139939	0.361512	0.438317				
40	166644_at	frozed homolog (Drosophila)	<i>Fzd9</i>	0.15567	0.424124	0.237189	0.069067	0.041637	0.09293				
41	166645_at	forkhead box protein O3	<i>Foxo3</i>	1.251275	0.628714	0.93231	0.168338	0.329527	0.204897				
42	166693_at	laminin alpha 5	<i>Lama5</i>	0.644776	0.903486	1.04745	0.19395	0.468221	0.55861				
43	166924_s.at	catopson 1	<i>Catp1</i>	0.439935	0.693245	1.129301	0.330559	1.007419	0.41208				
44	166924_s.at			0.704117	0.580427	0.370867	-0.283	0.050228	0.401897				
45	166924_s.at			1.612759	1.658911	1.536281	-0.114744	0.118035	0.642836				
46	166924_s.at			0.885173	0.848433	0.915992	0.285283	0.367304	0.702059				
47	166932_at	ubiquitin 1	<i>Ubi1</i>	0.183192	0.163991	0.248113	-0.218849	0.078975	-0.087186				
48	166932_at	development and differentiation enhancing 10	<i>Def1</i>	0.698355	0.457688	-0.000578	-0.240917	-0.063274	-0.378516				
49	166948_at	phosphoprotein enriched in astrocytes 15	<i>Plea15</i>	0.104831	0.467456	0.207009	0.022461	-0.331017	-0.187646				
50	166958_at	inosine 5'-phosphatase dehydrogenase 2	<i>Ispah2</i>	0.669339	0.357727	0.358871	0.117253	0.133768	-1.09029				
51	166964_at	DNA segment Chr 14 ERATO Do 209 expressed	<i>D14ERATDo209</i>	0.647506	-0.07642	0.188378	-0.27346	-0.083791	-0.238437				
52	166911_at	procollagen type VI alpha 3	<i>Col6a3</i>	0.373754	1.961397	0.979811	-0.066762	0.351186	-0.46781				
53	166911_at	permal cortex expressed transcript	<i>Cort</i>	0.086687	0.432122	0.163396	0.068873	-0.083722	-0.96402				
54	166913_at	zinc finger protein interacting with K protein 1	<i>Zfk1</i>	0.08424	0.124271	0.062888	-0.079313	-0.121973	-0.085897				
55	166920_at	ubiquitin B	<i>Ubb</i>	0.115603	0.334275	0.319176	0.150086	-0.225877	0.394645				
56	166925_at	ubiquitin B	<i>Ubb</i>	0.088122	0.156919	0.105302	-0.146698	-0.112427	-0.068956				
57	166948_at	HGF-regulated tyrosine kinase substrate	<i>Hgs</i>	0.097518	0.071732	0.192294	-0.259118	-0.097551	-0.391235				
58	166925_at	histomaptopin 2 of 2 region locus 10	<i>H2-010</i>	0.018681	0.208684	0.287112	-0.242748	-0.116535	-0.053074				
59	166925_at	RKEN CDNA 573050F17 gene	<i>573050F17</i>	0.41489	0.98547	0.217008	-0.313269	-0.08845	-0.233027				
60	166925_at	RKEN CDNA 2810102G01 gene	<i>2810102G01</i>	0.88447	0.68712	0.94041	-0.118987	-1.344815	-1.093329				
61	166925_at	RKEN CDNA 8C013529	<i>8C013529</i>	0.11884	-0.025138	-0.003292	-0.263922	-0.319745	-0.193847				
62	166925_at	RKEN CDNA 110102M017 gene	<i>110102M017</i>	1.553311	1.742612	0.01197	1.202891	-0.734463	-0.529356				
63	166925_at	F-box only protein 21	<i>Fbxo21</i>	0.324917	0.336116	-0.20021	-0.145212	-0.427262	-0.47404				
64	166925_at	asparagine-linker glycosylation 2 homolog yeast alpha-1.3	<i>Agp2</i>	0.139202	0.194219	0.230091	-0.221538	-0.073283	-0.076921				
65	166925_at	RKEN CDNA 1110032A03 gene	<i>1110032A03</i>	0.360275	-0.064213	0.468882	-0.578233	-0.178058	-0.084348				
66	166925_at	RKEN CDNA 2810102E10P08 gene	<i>2810102E10P08</i>	0.88447	0.68712	0.94041	-0.118987	-1.344815	-1.093329				
67	166925_at	LIM domains containing 1	<i>Limt1</i>	0.332536	0.022628	-0.03401	-0.574274	-0.338336	-0.024349				
68	166925_at	RKEN CDNA 1110004C05 gene	<i>1110004C05</i>	0.246337	0.388675	0.288132	-0.205773	-0.546821	-0.879595				
69	166925_at	microtubule-associated protein 1 light chain 3	<i>Maptlc3</i>	0.89073	0.874382	0.178023	0.177662	-1.398925	-0.706811				
70	166925_at	RKEN CDNA 111000615R gene	<i>111000615R</i>	-0.006913	0.465624	0.398136	-0.370617	-0.01171	-0.278969				
71	166925_at	poly(A)-specific nucleosidase (deadenylation nuclease)	<i>Pam</i>	-0.043831	0.23418	0.228919	-0.069691	-0.258691	-0.066024				
72	166925_at	protein tyrosine phosphatase 4a3	<i>Ptp4a3</i>	0.450621	0.450621	-0.719148	-0.194209	-0.164009	-0.650239				
73	166925_at	mitogen-activated protein kinase 8 interacting protein 3	<i>Mapk8ip3</i>	0.40911	0.365844	0.868877	-0.535616	0.123115	-0.124124				
74	166925_at	MYB binding protein (PB5) 1a	<i>Mbyp1a</i>	0.153996	0.018443	0.183396	-0.076796	-0.027096	-0.14146				
75	166925_at	161384a.1		0.163887	-0.424943	0.175349	-0.364561	-0.36804	-0.028247				
76	166925_at	RKEN CDNA 091010E05 gene	<i>091010</i>										



Cluster	Accession Id	Gene name	Gene symbol	sMCs vs. mMCs	sMCs vs. sMCs	mMCs vs. mMCs	sMCs vs. mMCs	sMCs vs. sMCs	mMCs vs. mMCs	sMCs vs. sMCs
2	25595_at	RIKEN DNA 91302221 gene	91302221/TNKS	0.24445	-0.24445	0.24445	-0.24445	0.24445	-0.24445	0.24445
2	25666_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 7	Nduo7	-0.04016	-0.02824	0.18425	-0.34631	-0.43446	-0.15528	-0.09276
2	25724_at	membrane-bound transcription factor protease site 1	Mdbp1	0.074107	0.175161	0.485309	-0.240077	0.011892	-0.094276	-0.094276
2	26257_at	RIKEN DNA 260054B10 gene	260054B10	-0.200623	0.297156	-0.154111	-0.17949	-0.33346	-0.23346	-0.23346
2	26282_at	fibrinogen-like protein CAXA box beta	Fmb	0.224274	0.006262	-0.240783	-0.261824	-0.218214	-0.103064	-0.103064
2	26625_at	RIKEN DNA 241004A177R gene	241004A177R	-0.420247	-0.420247	-0.420247	-0.420247	-0.420247	-0.420247	-0.420247
2	26666_at	N-terminal Anin amidase	Ntan1	0	0.142426	0.384359	0	-0.00702	-0.00702	-0.00702
2	26694_at	T-cell leukemia/lymphoma 18 1	Tl18a1	0.154223	0.10881	0.182637	-0.181733	-0.012661	-0.012661	-0.012661
2	26694_at	RIKEN DNA 9430071024R gene	9430071024R	0.096615	0.296362	0.300118	0.191425	0.068892	0.068892	0.068892
2	26948_at	quinnoid hydrolytic/oxidoreductase	Qodr	0.007337	0.214441	0.863723	-0.073934	-0.655457	-0.739629	-0.739629
2	27167_s_at	acth homolog 2 (E. coli)	Ela2c	0.033763	0.247387	0.132457	-0.137619	-0.124023	-0.075014	-0.075014
2	27265_s_at	UBX domain-containing 2	Ubx2c2	0.124052	0.124868	0.052489	-0.052489	-0.204332	-0.095696	-0.095696
2	27374_at	RIKEN DNA 2810025M15Rk gene	2810025M15Rk	0.066438	0.194799	0.054904	-0.063781	-0.154726	-0.195028	-0.195028
2	27473_s_at	semaphorin domain immunoglobulin domain (lg) and GPI membrane anchor (semaphorin) 7A	Sema7a	0.048257	0.091194	0.121281	-0.111008	-0.088841	-0.262281	-0.262281
2	27667_at	Mus musculus mRNA for mKIA4920 protein	Gycym7	0.047336	0.061036	0.906194	-0.352004	0.178203	-0.333969	-0.333969
2	28063_at	glycosylation dependent cell adhesion molecule 1	Gyca1f	0.017303	0.244334	0.305712	-0.138566	-0.08566	-0.08566	-0.08566
2	28405_at	serine (or cysteine) proteasome inhibitor class B member 9	Scp9b9f	0.449306	0.133873	0.489321	-0.077081	-0.124037	-0.454147	-0.454147
2	28553_at	sarcolamine associated protein	Slnap	0.579144	0.711144	0.066919	-0.67422	-1.506028	-1.274548	-1.274548
2	28686_at	novel nuclear protein	Nlpp1	0.407187	0.005345	0.194487	-0.077782	-0.48007	-0.131446	-0.131446
2	28690_at	ATP-binding cassette sub-family D (ALD) member 1	Abcd1	0.296601	0.182117	0.097456	-0.25037	0.044102	-0.221026	-0.221026
2	29001_s_at	S100 calcium binding protein A4	S100a4	0.013989	0.136074	0.114441	-0.066745	-0.347487	-0.101788	-0.101788
2	29598_at	tyrosin C	Ctyc	0.155593	0.780689	0.916469	-0.4208	-0.945133	-1.754204	-1.754204
2	29678_at	src-like adaptor	Sla	-0.047611	0.228907	-0.036655	-0.28381	-0.300891	-0.171772	-0.171772
2	29849_at	double cut binding factor 2	Dcb2a	0.333219	0.747394	0.78242	-0.240256	-0.124845	-0.370335	-0.370335
3	100303_at	mu2b homolog 2 (E. coli)	Mu2b	0.157113	0.320337	1.000501	-0.336641	-1.85762	-1.194962	-1.194962
3	101048_at	CCCTC-binding factor	Cbtf	0.063906	-0.01939	-1.769767	-0.951677	-2.106347	-1.721637	-1.721637
3	101051_at	tumor differentially expressed 1	Tdf1	-1.36446	-1.115445	-1.883478	-0.963022	-2.120586	-1.992136	-1.992136
3	101045_at	lymphoblastoid cell line	Lcl	0.157113	0.320337	1.000501	-0.336641	-1.85762	-1.194962	-1.194962
3	101056_at	muscle fringe homolog (Drosophila)	Mfrg	0.878217	-0.313637	-0.685332	-1.164551	-0.964116	-0.964116	-0.964116
3	101059_at	RIKEN DNA 241004A177R gene	241004A177R	-0.799624	-0.985778	-1.844119	-0.225959	-0.949791	-0.420811	-0.420811
3	101066_at	insulin-like growth factor binding protein 5	Igfbb5	0.578466	0.097391	-0.472131	-2.145891	-1.444704	-2.809663	-2.809663
3	101016_at	centromere autoterminator A	Cenpa	0.440464	0.363620	0.481614	-0.702809	-0.895612	-0.895612	-0.895612
3	101085_at	NIMA homolog 2 in mitosis gene 1-related serine/threonine kinase 2	Nimr2	0.282257	0.009285	0.415381	-0.447187	-0.949791	-1.314723	-1.314723
3	101091_at	host cell factor 3	Hcfc1	0.311513	0.285606	0.249253	-0.555022	-0.485322	-0.538896	-0.538896
3	101050_at	ornithine decarboxylase antizyme 2	Odc2	0.278682	0.704808	0.748685	-0.27479	-0.209565	-0.376176	-0.376176
3	101047_at	RIKEN DNA 241002K10Rk gene	241002K10Rk	-2.848673	-2.782719	-2.578276	-3.361044	-2.882011	-2.038926	-2.038926
3	101123_at	integral membrane protein 2B	Iimp2b	0.801262	0.810855	0.731999	-0.906383	-1.74804	-1.989892	-1.989892
3	101145_at	lymphoblastoid cell line	Lcl	0.157113	0.320337	1.000501	-0.336641	-1.85762	-1.194962	-1.194962
3	101150_at	proteasome (prosome macropain) 28 subunit alpha	Psm21	0.257199	-1.084376	-1.170306	-2.328009	-2.547001	-3.27067	-3.27067
3	101203_at	testis specific protein kinase 1	Tspk	0.237605	0.442271	0.422193	-0.043939	-0.580708	-0.818174	-0.818174
3	101219_at	RIKEN DNA 900004C03Rk gene	900004C03Rk	-0.006944	-0.130094	-0.377213	-0.281314	-0.618625	-0.618625	-0.618625
3	101284_at	letrin specific protein 14 gene	Lsp14	0.809216	0.281041	0.807663	-2.545466	-3.471252	-3.684847	-3.684847
3	101247_at	muscle cell process 5	Mcp5	0.224657	-0.264948	0.079468	-0.27479	-0.605689	-0.605689	-0.605689
3	101208_at	muscle cell process 5	Mcp5	0.281439	-2.547011	-3.703755	-3.524831	-4.31945	-3.966309	-3.966309
3	101279_at	proteasome (prosome macropain) subunit beta type 8 (large multifunctional protease 7)	Psm8	-2.018919	-2.116742	-2.747367	-3.400558	-2.802106	-3.543465	-3.543465
3	101285_at	RIKEN DNA 921518A05Rk gene	921518A05Rk	0.485913	0.303483	0.047788	-1.02804	-0.67396	-0.67396	-0.67396
3	101370_at	protein tyrosine phosphatase non-receptor tyrosine substrate 1	Ptprs1	-1.420305	-1.427465	-1.31004	-3.3773	-2.91491	-1.618065	-1.618065
3	101310_at	TAR RNA binding protein 2	Tarbp2	0.190409	0.03412	0.387833	-0.299421	-0.255355	-0.427004	-0.427004
3	101323_at	RIKEN DNA 583046C15Rk gene	583046C15Rk	-1.284421	-1.58139	-1.251197	-2.007339	-1.91804	-2.20443	-2.20443
3	101349_at	Yarnaguchikaric acid (yarn) 1 oncogene homolog	Yarn1	0.310235	-1.455002	-0.209565	-3.267394	-3.296528	-3.018673	-3.018673
3	101350_s_at	muscle (prosome macropain) subunit beta type 8 (large multifunctional protease 7)	Psm8	-2.018919	-2.116742	-2.747367	-3.400558	-2.802106	-3.543465	-3.543465
3	101367_at	member 12	Msb12l	0.207184	-1.803252	-2.0072	-2.401101	-2.24446	-2.314851	-2.314851
3	101367_at	RIKEN DNA 241003J302Z gene	241003J302Z	0.056214	0.056214	0.056214	0.056214	0.056214	0.056214	0.056214
3	101378_at	member of myo1b homolog (chicken)	Tom1	0.069148	-0.326073	0.499776	-0.748575	-0.748303	-1.014875	-1.014875
3	101391_at	muscle (prosome macropain) subunit beta type 8 (large multifunctional protease 7)	Psm8	-2.018919	-2.116742	-2.747367	-3.400558	-2.802106	-3.543465	-3.543465
3	101394_at	13	Sklc13	0.346683	0.377884	0.500387	-0.809523	-0.52094	-0.6549	-0.6549
3	101395_at	ATPase, Ca <sup>2+</sup> transporting ubiquitous	Atp2a3	-0.431783	-0.396657	-0.493472	-1.944862	-2.014495	-1.404316	-1.404316
3	101397_at	permeable receptor CXCR1-gated calcium channel 1	Cxcr1	0.524378	0.683441	0.997243	1.645414	1.45576	1.776016	1.776016
3	101430_at	muscle (prosome macropain) subunit beta type 8 (large multifunctional protease 7)	Psm8	-2.018919	-2.116742	-2.747367	-3.400558	-2.802106	-3.543465	-3.543465
3	101437_at	DNA segment Chr 10 ERATO D0 641 expressed	D10Ernf41e	-0.702347	0.44847	-0.773308	-1.548718	-1.465994	-1.025862	-1.025862
3	101429_at	importin 11	Ipp11	-1.069032	-0.491553	-1.447731	-2.34541	-2.16559	-1.627032	-1.627032
3	101430_at	acidic leucine-rich nuclear phosphoprotein 32 family member A	Alp32	-0.285818	-0.707441	-0.478081	-1.11099	-0.889599	-2.18414	-2.18414
3	101436_at	RIKEN DNA 1110033J03Z gene	1110033J03Z	-1.010088	-1.019194	-1.34477	-0.631562	-0.38832	-0.734382	-0.734382
3	101440_at	glutamate receptor ionotropic kainate 5 (gamma 2)	Grik5	-0.026714	0.381317	0.0283	-0.67172	-0.46727	-0.404942	-0.404942
3	101435_at	RIKEN DNA 281004D19Rk gene	281004D19Rk	-0.494645	-0.121572	-0.069092	-0.627685	-1.110096	-0.706786	-0.706786
3	101448_at	proteasome (prosome macropain) catalytic sorting protein 1	Psmc1	-0.509719	-0.424781	-0.824721	-1.29278	-1.080771	-0.949791	-0.949791
3	101460_at	receptor (calcitonin) complex locus 1	Ramp1f	0.069283	0.782079	1.25464	-2.297357	-2.23526	-1.741627	-1.741627
3	101470_at	ring finger protein 20	Rfr20	-1.713087	-0.87637	-1.170035	-1.388556	-1.254231	-1.449404	-1.449404
3	101607_at	nucleoside 6P	Nud6p	-0.378751	0.065886	0.081132	-0.538105	-0.476109	-0.649727	-0.649727
3	162278_at	RIKEN DNA 281004B15Rk gene	281004B15Rk	0.269208	0.735751	0.130368	-0.242376	-1.244302	-1.440978	-1.440978
3	163038_at	moesin	Msr	-1.78789	-2.252115	-2.01844	-2.68032	-2.474899	-2.86152	-2.86152
3	163096_at	RIKEN DNA 061001317T gene	061001317T	-0.526307	-0.520242	-0.669816	-1.11789	-0.81789	-0.957327	-0.957327
3	163414_at	RIKEN DNA 18100780A0Rk gene	18100780A0Rk	-0.146015	0.197815	0.091364	-0.304347	-0.190347	-0.493292	-0.493292
3	163442_at	DEAD (Asp-Glu-Ala-Gln) box polypeptide 18	Ddx18	-1.254849	-1.120125	-1.29852	-1.615815	-1.531187	-1.449607	-1.449607
3	163512_at	DEAD domain expressed BCL7A63	Bcl7a63	-0.283415	0.023836	-0.018226	-0.646244	-0.340796	-0.486239	-0.486239
3	163546_at	adipose	Adip	-1.89331	1.02226	-1.715317	-2.059739	-2.61632	-1.866624	-1.866624
3	163547_at	threonine interacting protein	Timp	-0.384999	-0.528991	-0.508756	-1.274462	-1.188159	-0.607337	-0.607337
3	163592_at	synaptotagmin-like protein 2 binding protein 1	Sllp2b1	0.069197	0.069197	0.069197	0.069197	0.069197	0.069197	0.069197
3	163648_at	zinc finger and homeobox protein 2	Zfp2	-0.678791	-1.264677	-1.068366	-1.425427	-1.21344	-3.26254	-3.26254
3	163639_at	twist homolog 2 (Drosophila)	Twist2	-0.191865	-0.260762	-0.095699	-0.488715	-0.366871		

The list represents 1,272 genes significantly altered between sMCs and mMCs in the order of clustering (Figure S5). The values represent expression levels normalized to those of BMACs.

Gene	Cluster	Symbol	sMC vs mMC	sMC vs BMAC	mMC vs BMAC	sMC vs BMAC	mMC vs BMAC	
35471_fat	solute carrier family 4 sodium bicarbonate cotransporter member 7	SCLY7	-0.31968	-1.77121	0.69274	-2.35569	3.38522	-3.49051
35959_fat1	epithelial membrane protein 3	Emp3	-1.83032	-0.54364	-2.03933	-3.87456	-4.31745	-4.23219
35959_fat2	intracellular matrix protein 4	IMT4	-1.42027	-1.75017	0.25217	-2.82625	-2.82625	-2.82625
35982_3	dystrophin muscular dystrophy	Dmd	-0.08796	0.02268	0.05169	-0.48893	-0.28702	-0.14688
35974_fat1	histopathology 2 region locus 1	H2C7	-0.30011	-0.19379	-0.23781	-0.74893	-1.02713	-0.85678
35974_fat2	protein kinase, glycerol acyl-cochrol protein PR (R) S3	PKC3	-1.42027	-0.05522	0.05265	-2.82625	-2.82625	-2.82625
35979_fat	expressed sequence 2 AC1316737	AC1316737	-0.67934	-0.65866	-0.43611	-1.25253	-0.91627	-1.21267
35980_fat	solute carrier family 2 (facilitated glucose transporter) member 3	SCL2A3	-0.17899	-0.59168	-0.70248	-1.23718	-0.74313	-1.13701
35980_fat2	BH3-binding protein, acidic, pro-rich protein	Bcl2L1	-0.46637	-0.2925	-0.29166	-2.48045	-0.84471	-0.70474
35987_fat	eukaryotic translation initiation factor 3 subunit 9 (eta)	EIF3A9	-1.65328	-0.99914	-1.23221	-1.87447	-1.868515	-1.83348
354015_fat	TH1-like homing (Diaplasia)	TH1H	-0.46637	-0.4672	-0.34972	-0.65091	-0.83331	-0.70566
354066_fat	ring finger protein 14	Rfrf14	-0.28476	-0.08738	-0.05646	-0.74421	-0.362582	-0.24816
35426_fat	Rab acceptor 1 (prevalence)	Rabac1	-0.07843	-0.70201	-0.37285	-1.01723	-1.89026	-1.13423
35430_fat	arvenex A5	Arav5	-0.77781	-1.74403	-1.08966	-2.2068	-2.02319	-1.89959
35450_fat	cleavage and polyadenylation specific factor 5	Cpsf5	-0.37201	-0.87288	-0.35188	-1.92158	-1.68284	-1.40575
35453_fat	adducin 1 (alpha)	ADD1	-0.73483	-0.56458	-0.56153	-1.36338	-1.02337	-1.41818
35483_fat	tubulin beta 2	Tubb2	-1.26572	-1.39019	-1.20085	-2.99887	-3.84874	-2.46752
35497_fat	expressed sequence AL02210	AL02210	0.23808	0.016972	-0.31578	-0.91605	-0.42123	-0.42421
35503_fat	mitogen activated protein kinase kinase 1	Map3k1	-0.60734	-0.54655	-1.20034	-1.61322	-1.74784	-1.748136
35604_fat	small nuclear ribonucleoprotein D2	Snrpd2	0.40621	-0.23120	-0.31828	-1.00378	-1.36591	-0.82719
35609_fat	ARF1 to actin-related protein 10 homolog (S. cerevisiae)	Arf10	-1.19679	-1.23176	-1.86276	-1.73515	-2.62444	-3.22144
35612_fat	nuclear receptor co-repressor 2	NcoR2	-1.16617	-0.24811	-0.76019	-1.23688	-1.25344	-1.48214
35610_fat	RKEN CDNA 523040024	523040024RAC	-0.48876	0.28273	-0.25471	-0.62105	-0.93055	-1.56584
35647_3_fat	FXYD domain-containing ion transport regulator 6	Fxyd6	-0.27832	-0.86269	-1.88133	-2.26148	-2.57418	-2.86527
35648_fat	DNA segment Chr 11 Wayne State University HS expressed	D11WVU636	0.088839	0.00041	-0.05423	-0.00848	-0.49184	-0.08886
35650_fat	RKEN CDNA S83041710	S83041710RAC	-0.92587	-0.82136	-0.62842	-1.02871	-1.08788	-1.34071
35651_fat	postaglandin-endoperoxide synthase 1	Ptgfr1	-0.23063	-0.60909	-0.78878	-0.67052	-0.79147	-0.91641
35662_fat	ketch domain containing 2	Kchc2	-1.02582	-0.49524	-0.43155	-2.41342	-2.51951	-1.36728
35662_fat2	damage specific DNA binding protein 1	Ddb1	-0.03075	-0.55343	-0.28813	-1.20149	-1.48419	-1.71741
35673_fat	IMAGE 6414521 complete cds	—	-1.1487	-0.69576	-2.91646	-2.81943	-3.36439	-3.33343
35673_fat2	solute carrier family 29 (neutral transporter) member 1	SCL29A1	0.04983	-0.71484	-0.82789	-1.65288	-1.65288	-1.65288
35604_fat	RKEN CDNA 201021M09RAC	201021M09RAC	-1.54652	-1.53731	-1.49175	-2.03794	-1.746627	-1.73504
35607_fat	Dt zinc and double PHD fingers family 2	Dyrf2	-0.45302	-0.32655	-0.30618	-0.97669	-0.62357	-0.88887
356186_fat	low-molecular-weight protein receptor-related protein 2	Lrp2	-0.46862	-0.05649	-0.43022	-0.25675	-0.82691	-1.15106
356215_fat	Max musculus CDNA clone MGC 87258 IMAGE 6413648 complete cds	—	-0.713073	-0.393105	-0.380827	-1.458707	-2.088781	-2.357203
35634_fat	RKEN CDNA 061039C21RAC	061039C21RAC	-0.646306	-0.300949	-0.487348	-1.032005	-1.029607	-1.117998
356716_fat	Spogans syndromic/neuroendocrine autologin 1 homolog (human)	Saoc1	-0.52525	-0.697078	-0.559744	-0.888811	-1.83706	-1.034936
356716_fat2	synaptotagmin 2 androgen protein	Syn2ap	-0.195319	-0.36789	-0.309899	-0.36789	-0.36789	-0.36789
35674_fat	acid phosphatase 6 lysosomal/acidic	Acp6	-0.28327	-0.855489	0.052486	-0.90122	-1.088214	-1.248991
356750_fat	RKEN CDNA D71000A14RAC	D71000A14RAC	-0.455411	-0.546005	-1.42152	-1.820441	-2.03143	-2.08283
356773_fat	member of the protein tyrosine kinase containing protein	PTK27	-0.67723	-0.67723	-0.70329	-1.20528	-1.20528	-1.20528
356810_fat	LIM domain only 2	Lmo2	-0.85217	-0.856336	-0.93884	-1.78967	-1.37337	-1.48111
356883_fat	protein tyrosine kinase dependent regulator type 1 alpha	Prkcd1	-0.11072	-0.08952	-0.10408	-0.16832	-0.20489	-0.20489
357125_fat	MHC (IA/CAH)2K.1 class I antigen	CIIC06628	-0.269116	-0.237811	-0.21521	-0.712356	-0.784841	-0.988781
35719_fat	copine 1	Copin1	0.310136	0.618289	-0.620793	-0.80762	-0.643886	-0.69646
357202_fat	RKEN CDNA 2700079K05	2700079K05	-0.17827	-0.356117	-0.11927	-0.356117	-0.356117	-0.356117
357315_fat	RKEN CDNA 2610028L19	2610028L19RAC	0.415896	-0.190316	-0.045109	-0.647288	-0.694713	-1.15419
357382_fat	laminA	LaminA	-0.18227	-0.11688	-0.18227	-1.47388	-1.47388	-1.47388
357484_fat	RKEN CDNA 2210402G22RAC	2210402G22RAC	-0.119573	-0.132825	-0.71023	-0.42108	-2.281547	-2.861347
357540_fat	histopathology 2 region locus 1	H2C1	-0.57142	-0.38259	-0.50775	-1.27166	-1.626281	-1.31728
35784_fat	regulator of G-protein signaling 2 binding protein	Rgs2	-0.14592	-0.02611	-0.27624	-1.76534	-1.46927	-1.65884
358010_fat	nuclear factor erythroid derived 2	Nfe2l2	-0.51164	-0.380276	-0.89478	-1.95243	-1.485721	-1.63371
358052_fat	blocked area 1 in transition 1 homolog (S. cerevisiae)-like	Batt1	-0.270209	0.329765	-0.419529	-0.829528	-0.816883	-1.08395
35806_fat	ADP-ribosylation factor 4 binding protein	Arbp4	-0.02911	-0.02911	-0.02911	-0.02911	-0.02911	-0.02911
358125_fat	RKEN CDNA 111002509	111002509RAC	-0.501848	-0.288598	-0.836897	-1.08123	-1.218022	-0.924087
358154_fat	RKEN CDNA 130004C11RAC	130004C11RAC	-1.617339	-0.981171	-0.80025	-2.041918	-2.584901	-3.140132
358415_fat	cytosine receptor-like factor 3	Crfl3	-1.16159	-1.12449	-1.2891	-1.91581	-1.910911	-1.65544
358439_fat	histopathology 2 region locus 1	H2C2	-0.748348	-0.577627	-0.448265	-1.251639	-2.58401	-1.75225
358525_fat	erythroid differentiation regulator 1	Erd1	-0.35435	-0.870458	-0.848108	-1.18118	-2.57018	-2.345436
358635_fat	DNA segment Chr 11 kL10k1e 35	D11K10k1e35	0.204808	0.016299	-0.18444	-0.28272	-0.335702	-0.25211
35866_fat	RKEN CDNA 2610016F6RAC	2610016F6RAC	-0.869881	-0.572816	-0.231593	-1.172751	-1.40534	-1.78702
35866_fat2	transient receptor potential cation channel subfamily V member 2	Trpv2	0.479326	-0.102591	-0.87429	-1.83226	-1.708781	-1.516414
359040_fat	solute carrier family 6 (neurotransmitter transporter serotonn) member 4	Scl6a4	0.714386	-0.615639	0.03649	-1.79703	-1.941611	-2.27449
359056_fat	Max protein	Max	-1.187228	-1.318094	-1.326518	-1.628706	-1.840418	-2.27464
359100_fat	immediate early response 2	Irf2	-1.814462	-3.540983	-2.7506	-3.92154	-3.4737	-4.07029
359402_fat	topoisomerase (DNA) II beta	Top2b	-0.289717	-0.737496	-0.69887	-0.88725	-2.21199	-1.37404
359563_fat	sprindin	Sprn	-0.042826	-0.214637	-0.23001	-0.311105	-0.419191	-0.67311
35967_fat	guanine nucleotide binding protein alpha inhibiting 2	Gnas2	-0.275819	-0.75806	-0.59777	-1.82073	-2.31053	-3.22305
35969_fat	guanine nucleotide binding protein alpha inhibiting 2	Gnas2	-0.29274	-1.21856	-0.54466	-1.78156	-1.340263	-1.97875
359696_fat	guanine nucleotide binding protein alpha inhibiting 2	Gnas2	-0.26026	-0.89737	-0.45006	-1.137028	-0.960606	-1.062892
359693_fat	neurotrophin	Ntrp	-0.67722	-0.25526	-0.47819	-0.90807	-0.820991	-1.21334
359699_fat	lectin galactose binding soluble 1	Lgals1	-1.755986	-1.998279	-1.709212	-4.21904	-3.842572	-4.355648
AFPA								
35999_fat	glyeraldehyde 3-phosphate dehydrogenase	Gapd	-0.858116	-0.878917	-0.822252	-1.012969	-1.182498	-1.139237
410002_fat	thrombin	Thrb	-0.214771	-0.214771	-0.174873	-0.34264	-0.844021	-0.112836
410004_fat	serine (or cysteine) proteinase inhibitor class B member 5	Seipn5	-0.003695	-0.05363	-0.24333	-0.698002	-0.162006	-0.4153
410004_fat2	RKEN CDNA 231002A21RAC	231002A21RAC	0.213763	-0.431209	-0.47308	-0.682725	-3.470247	-0.988428
410005_fat			0.13174	-0.298878	-0.13174	-0.298878	-0.298878	-0.298878
410006_fat	aldhyde dehydrogenase family 1 subfamily A1	Aldh1f1	0.7059	1.78411	1.85306	4.73389	2.607199	3.894742
4100136_fat	lysosomal membrane glycoprotein 2	Lmp2	0.20321	-0.09838	0.20287	1.31124	1.09841	0.369917
4100218_fat	cytochrome b5 cytochrome oxidase reductase 1B (P27)	CytoB5	0.17116	0.39252	0.29322	0.948227	0.71642	0.507586
4100336_fat	bone gamma carboxylglutamate protein 1	Bglp1	0.50744	0.475118	0.70985	0.942208	0.770073	1.23306
4100425_fat	laminA	LaminA	-0.18227	-0.11688	-0.18227	-1.47388	-1.47388	-1.47388
4100501_fat	ATPase H+K+ transporting beta polypeptide gastric specific	Atp4b	1.492459	0.848755	2.086517	4.81454	3.357899	2.96297
4100571_fat	lysosomal-associated protein transmembrane 4B	Lamp4b	3.38748	2.45123	0.899394	1.98078	2.190557	2.887335
4100603_fat	CD24	CD24	2.47655	3.98394	2.47655	2.47655	2.47655	2.47655
4100723_fat	small proline-rich protein Z2	Sprz2	0.275273	0.211749	0.315371	0.534936	0.400259	0.442276
4100885_fat	alko-keto reductase family 1 member B8	Akr1b8	0.117315	0.04678	0.30559	2.52004	1.930209	2.688682
4100909_fat	protease serine 6 (protease)	Prss6	0.32785	0.30517	0.30628	0.514293	0.478334	0.56584
4100944_fat	Max musculus transcribed sequences	—	0.171898	0.09965	0.83282	1.864034	1.854346	1.740892
4100988_fat	actin-binding protein 2	Actb2	-0.10816	-0.10816	-0.10816	-0.10816	-0.10816	-0.10816
4101009_fat	keratin component 2 basic gene B	Krtf2	1.380684	0.799517	1.04502	4.22279	4.12151	4.69619
4101024_fat	small proline-rich protein Z1	Sprz1	0.527664	0.588664	0.794975	2.06496	1.624283	3.301309
4101025_fat	small proline-rich protein Z1A	Sprz1a	0.32785	0.681343	0.47211	4.209664	4.912021	5.146857
4101026_fat	anterior gradient 2 (Zenopus laevis)	Agp2	0.692876	0.12909	-0.09085	3.831681	3.842057	5.081306
4101082_fat	male amine oxidase	Maoo	0.98617	0.98617	0.98617	2.83333	2.83333	2.83333
4101343_fat	EWS-FLI1 activated transcript 2	Eat2	0.09828	-0.10771	-0.31878	0.246001	-0.29787	0.160426
4101371_fat	cleavage and polyadenylation specific factor 4	Cpsf4	0.066001	0.844718	0.02405	0.84011	1.98238	1.44005
4101383_fat	arvenex A5	Arav5	-0.77781	-1.74403	-1.08966	-2.2068	-2.02319	-1.89959
4101421_fat	ring finger protein 5	Rfrf5	0.03382	0.49055	-0.06848	0.696364	0.96357	0.485739
4101425_fat	glutathione synthetase	Gst	0.213688	0.23158	0.29718	0.61401	0.686419	0.63911
4101466_fat	phosphoenolpyruvate decarboxylase class F	Pdcf	-0.151433	-0.74264	-0.74264	-1.92096	-1.64473	-1.16014

The list represents 1,277 genes significantly altered between sMCs and mMCs in the order of clustering (Figure 5a). The values represent expression levels normalized to those of BM14Cs.

Cluster	Accession	Gene name	Gene symbol	mMCs vs. BM14Cs	sMCs vs. BM14Cs	mMCs vs. BM14Cs	sMCs vs. BM14Cs	mMCs vs. BM14Cs	sMCs vs. BM14Cs
410156		neighbor of Brca1 gene 1	Nbr1	-0.650811	0.650811	0.650811	0.650811	0.650811	1.177221
410157		acyl-CoA oxidase 1 palmitoyl	Acox1	0.073271	0.921306	7.92723	0.17722	1.56544	1.776733
410158		metallothionein 2	MT2	0.102298	1.299922	0.898262	3.745978	2.683112	2.449997
410160		cytochrome P450 family 2 subfamily 1 polypeptide 9	Cyp2b9	0.402867	0.734051	0.270083	3.401265	1.652068	1.547265
410162		cytochrome P450 family 2 subfamily 1 polypeptide 9	Cyp2b9	0.127248	2.164522	0.276256	0.505299	3.291103	1.430643
410172		glutathione S-transferase alpha 2 (Yc2)	GstA2	0.565229	0.781385	0.166738	0.564289	0.781385	0.447397
410172_1		liver toxic	Fts	0.062855	0.450424	0.077593	1.829622	0.357445	1.733036
410195		sema4 cytoplasmic domain associated protein 2	Semaap2	0.400178	0.598254	0.281908	1.587555	2.794249	1.939299
410197		autophagy 12-like c (retrovirus)	Atg12c	-0.062581	0.331538	0.179017	0.51643	1.027969	1.128125
410200		RIKubulin cytochrome c reductase core protein 2	Ugcn2	-0.285926	0.036738	0.796642	0.862294	1.544908	1.099723
410204_1		Mus musculus nuclear core binding protein subunit 1 B0kDa mRNA (cDNA clone IMAGE 642922)	Nucb1	1.584178	1.207885	1.676795	2.65437	1.98775	1.534738
410211_1		keratin connective 1 acidic gene 19	Krt19-1	0.593445	0.175841	0.526183	2.574445	2.661176	4.419382
410235		potassium channel subfamily K member 1	Kcnk1	0.418339	0.265817	0.35362	0.596821	0.474171	0.796225
410240		carboxin anhydrolase 1	Carb1	0.319114	0.189737	0.28725	0.639822	0.401927	0.549137
410242		interleukin 18	Il18	0.427293	0.329409	0.269982	1.55231	0.831262	1.527126
410281		solute carrier family 22 (organic cation transporter) member 1-like	Slc22a9f1	0.198891	0.265332	0.320963	1.388854	0.76015	1.870396
410296		UDP-Gal 4-epimerase beta 1 4-galactosyltransferase polypeptide 6	Bgalat6	0.471616	1.244989	0.286796	3.832116	0.860001	1.445965
410309		brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	0.059631	0.063007	0.260334	0.679635	0.349637	0.51024
410327		expressed sequence variant AT8959	AT8959	0.141757	0.083913	0.133588	4.286229	3.804666	3.73122
410338		winged-helix domain protein 1	Hmx1	0.414209	0.411004	0.318875	0.624713	0.681033	0.780301
410354		myofibrillin related protein 4	Mirr4	-0.059673	-0.057306	0.081831	0.324855	0.211154	0.21015
410396		peroxisomal acyl-CoA thioesterase 1	Pex1	0.212829	0.146165	0.270584	0.713031	0.593736	0.814347
410443		absent in melanoma 1	Aim1	0.418622	0.308927	0.547488	4.238082	3.220203	0.780215
410434		transmembrane 4 superfamily member 3	Tm4sf3	0.542144	0.773816	0.429209	1.775998	3.460499	2.936345
410504		desmoplakin 2	Dspk2	0.169922	0.169922	0.174291	1.29701	2.202752	1.674133
410635		RIKEN cDNA 261002M23R gene	261002M23R	0.88107	0.270406	0.327293	0.931797	1.275318	0.442311
410699		ATP-binding cassette subfamily C (CFTR/MRP) member 3	Abcc3	0.612499	0.521343	0.86877	1.76242	2.73020	2.395164
410714		RIKEN cDNA 091009A07R gene	091009A07R	0.471616	1.448438	0.309224	3.27843	2.82483	3.136351
410761		Tcfcp2-related transcription repressor 1	Tcrp1	0.321444	0.165122	0.627727	2.37958	2.427107	2.107125
410771		RIKEN cDNA 1110061N2G gene	1110061N2G	0.480222	0.216222	0.402978	0.607978	0.595788	1.257788
410845		solute carrier family 31 member 1	Slc31a1	0.388253	0.545839	0.697827	1.581174	1.39962	0.940788
410873_1		RIKEN cDNA 231001N07R gene	231001N07R	1.062035	-0.111737	2.202525	3.452770	4.05898	4.279297
410952		nodal	Nodal	0.199522	0.336873	0.217885	1.270865	0.52056	0.20586
410974		transmembrane protease serine 2	Tmprs2	0.112958	0.163035	0.185888	0.247513	2.08006	2.044775
410987		erythropoietin receptor	Epor	-0.027973	0.101747	0.46295	0.28474	0.312022	0.184729
410991		junctional protein 4	Jp4	0.898397	0.650047	0.800047	0.671929	0.881033	0.868509
410155		activating transcription factor 3	Atf3	0.232448	0.01985	0.831564	2.24592	1.538864	1.433916
410175		RIKEN cDNA E0300214Rk gene	E0300214Rk	0.296403	0.62313	0.329203	1.82089	1.88855	1.68446
410198		RIKEN cDNA E030027H19R gene	E030027H19R	0.450215	0.368711	0.597836	1.016248	1.856694	0.809004
410222		geranylgeranyl phosphotransferase 1	Ggpi1	0.211175	0.525292	0.521417	0.748237	0.822021	0.804396
410431		RIKEN cDNA 120000014R gene	120000014R	0.296403	0.62313	0.329203	1.82089	1.88855	1.68446
410438		RIKEN cDNA 120000014R gene	120000014R	0.407174	0.16131	0.238995	1.901301	1.601952	0.534536
410435		phospholipase A2 group XII	Pla2g12	0.086173	3.997235	2.74197	4.920878	7.94522	1.095523
410450		desmoplakin 2	Dspk2	0.169922	0.169922	0.174291	1.29701	2.202752	1.674133
410452		intressin (SH3 domain protein 1A)	Itan	0.59887	0.45288	0.211317	0.814872	0.696997	1.330044
410459		suppressor of tumorigenesis 15 member 1	Stt15	0.169922	0.169922	0.174291	1.29701	2.202752	1.674133
410450		cytochrome P450 family 2 subfamily 1 polypeptide 1	Cyp2b1	1.043822	0.303002	0.744021	3.448145	3.263551	0.508816
410454		crumbs homolog 3 (Drosophila)	Crb3	0.552051	0.006203	0.389226	1.11798	1.244053	2.929616
410455		chemokine receptor family 8 member 1	Chrf8	0.154526	0.191129	0.174291	1.29701	2.202752	1.674133
410461		Mus musculus mRNA similar to RIKEN cDNA 930862A2G3 gene (cDNA clone IMAGE 538244)	930862A2G3	-	0.135623	0.013579	-1.420205	0.215582	0.502979
410463		cDNA sequence BC037008	BC037008	0.059635	0.18442	0.234455	2.84142	1.965862	2.358717
410472		microsomal glutathione S-transferase 2	Mgst2	-0.04802	0.348296	0.177709	1.305882	0.71745	1.378204
410609		lectin galactose binding subunit 4	Lgals4	0.481623	0.190882	0.169504	3.102604	2.385094	3.933626
410615		thrombospondin 1	Tsp1	0.521238	0.545084	0.835248	1.033728	1.154062	0.781541
410183		RIKEN cDNA 3930401E15R gene	3930401E15R	0.229611	0.65015	0.623025	0.824969	0.919226	2.129738
410201		lectin galactose-binding subunit 4	Lgals4	0.194531	0.03783	1.829529	1.254052	1.19294	0.841331
410233		adenylyl kinase 3 alpha-like	Ak3	0.738138	-0.147044	1.46678	0.762005	0.658816	1.350536
410277		tefoid factor 1	Tef1	0.062855	-0.025117	0.113933	0.51321	0.164877	0.53114
410300		protein 12	P12	0.444155	0.51342	0.520306	3.824501	2.231227	3.881941
410311		lysatin 2	Lys2	1.11099	0.898358	1.175278	1.53011	2.001339	2.69887
410314		RIKEN cDNA 2010317E03R gene	2010317E03R	0.254454	0.86841	0.895457	1.787458	1.903684	2.368818
410482		acetyl-Coenzyme A acyltransferase 1	Acaa1	0.748545	0.207367	0.828348	0.892299	1.4486	1.151233
410498		prostate stem cell antigen 1	Psc1	1.207215	1.540738	1.205478	4.944823	3.545992	4.530156
410518		RIKEN cDNA 1110060F11Rk gene	1110060F11Rk	0.177981	0.457532	0.844406	1.641513	1.609575	1.542516
410536		hepatite rat sarcoma virus oncogene 1	Hras1	0.62053	-0.042454	0.005873	0.944871	1.273354	0.698392
410537		N-sulfotransferase	Sulf1	0.247603	0.188289	0.346829	1.502736	1.374417	1.812638
410565		Carny rat muscle mitochondrial 1 ubiquitous	Cmif1	0.273013	0.188146	0.410224	3.571058	3.468396	1.671514
410607		glutathione hydrolyase 1 (NADP+ dependent)	Gth1	0.162889	0.011039	0.162889	0.315432	0.459966	0.527288
410646		lactate dehydrogenase 5	Ldh5	0.39186	0.39186	0.390629	1.22023	0.73336	0.788484
410662		catenin beta binding protein 9	Cat9	0.090905	1.94755	-0.108111	0.644409	0.519963	0.423964
410729		RAB27 member 9 B9ts	Rab27b	0.192959	0.27088	0.688268	1.270584	1.29294	1.841331
410731		RAB27 member R43 oncogene family 1	Rab25	0.336861	0.470076	0.836881	0.795048	1.18969	0.914511
410744		chromatophyllin-like	Chr1	-0.081834	1.657115	-0.242201	1.456777	0.4575	0.396813
410752		maternal expression 10-like 1	Meis1	0.204817	0.204817	0.204817	1.274827	0.671929	0.717201
410859		nuclear factor IIB	Nf1b	0.598187	0.820042	0.890085	1.482004	1.301455	0.860227
410920		Bcl-2 like 1	Bcl2l1	-0.20082	0.129308	0.305867	0.747826	0.862678	1.526268
410934		phospholipase A2 group X	Pla2g10	0.25324	0.480465	0.734291	2.932991	1.938296	3.319021
410942		carbonyl reductase 3	Cbr3	0.655001	0.406727	0.360545	3.002327	1.668814	1.868818
410971		RIKEN cDNA 2700038P16R gene	2700038P16R	0.188289	0.188289	0.188289	0.188289	0.188289	0.188289
410991_1		---	---	0.435644	0.435648	0.435648	0.762512	0.438871	0.892132
410998		F-box and leucine-rich repeat protein 12	Fbxl12	0.23792	0.232521	0.35328	0.256979	0.470146	0.517278
410998_1		lamin A	Lama3	0.840274	0.840274	0.840274	0.840274	0.840274	1.850136
410998_2		Mus musculus mRNA similar to ribosomal protein L7 (cDNA clone MGC 58373 IMAGE 6771139) complete cds	L7	-0.067135	-0.023638	0.042035	0.205418	0.190208	0.107428
410998_3		clustering	Clu	1.685109	1.951415	1.960239	2.446511	2.452689	1.192624
410998_4		dehalogenated 12-hs homolog (Drosophila)	Dv12	0.999899	0.96944	1.021414	1.125449	1.282329	1.429649
410998_5		Mus musculus transcript sequence with strong similarity to protein pP48201 (H sapiens) ATP3_HUMAN ATP synthase lipid-binding protein mitochondrial precursor (ATP synthase proteolipid P3)	atp3-vj558	0.342743	0.119338	0.486837	0.48138	0.919198	0.814915
410847		ATPase subunit 9 (ATPase subunit C)	Atp9c1	0.024217	0.162445	0.285254	0.258624	0.800472	0.726113
410928		RNA polymerase II transcriptional coactivator	Rpc1c2	0.024217	0.162445	0.285254	0.258624	0.800472	0.726113
410944		RIKEN cDNA A530057M15Rk gene	A530057M15Rk	0.841885	0.52497	0.77688	1.038985	1.118138	1.25712
410970		DNA segment Chr1 ERATO D0 161 expressed	D16n161e	0.168222	0.504765	0.498699	0.677189	1.315573	1.036008
410945		T-cell leukemia virus group 1	Tclv1	0.024217	0.162445	0.285254	0.258624	0.800472	0.726113
410960		RIKEN cDNA E167043E02Rk gene	E167043E02Rk	0.168222	0.19998	0.051083	0.337899	0.317462	0.373477
410970_1		3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	0.19483	0.497369	0.172794	0.828564	0.643373	1.266209
410971_1		ras homologous family member U	RhfU	0.168222	0.168222	0.168222	0.168222	0.168222	0.168222
410931		RIKEN cDNA A530057M15Rk gene	A530057M15Rk	0.841885	0.52497	0.77688	1.038985	1.118138	1.25712
410938		RIKEN cDNA A530057M15Rk gene	A530057M15Rk	0.841885	0.52497	0.77688	1.038985	1.118138	1.25712

