

Figure 5
Clustering analysis of the gene expression profiles between sMCs and mMCs. (a) Representation of mRNA expression levels of sMC₁₋₃ and mMC₁₋₃ 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).

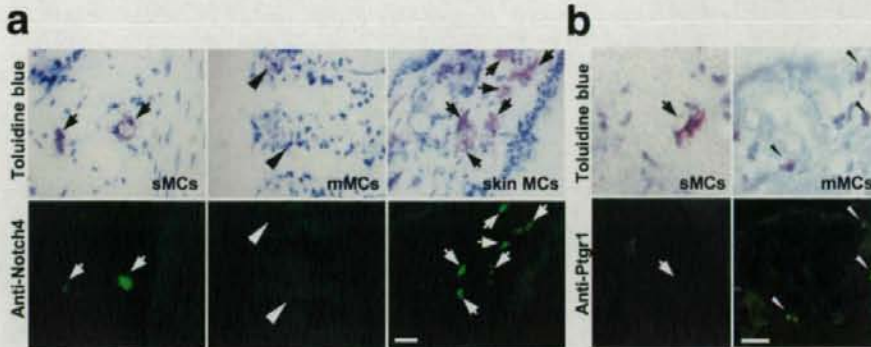


Figure 6
Immunohistochemical analysis of Notch4 and Ptgr1 in sMCs and mMCs in stomach tissue. (a) Stomach submucosa (sMCs; left panels), stomach mucosa (mMCs; middle panels) and skin (skin MCs; right panels) sections were stained with an anti-Notch4 antibody (lower panels) and with toluidine blue (upper 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 μ 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)₂₄ primer [5'-GGCCAGTGAATGTGAATACGACTCACTATAGGGAGGC GG(T)₂₄] 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 μ g, 10 μ g and 2 μ 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)₂₄ 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)₂₄ 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 μ 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, mMCS 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 BMMCs (BMMC-std) 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 mMCS, 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 mMCS were normalized by the signal values of BMMCs. 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; MMC: 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	AATAACGAGTCACGCT
<i>Fcεr1α</i>	GCCCCGTCCTCATTAG	CAATAACCCCGTGCC
<i>Mcpt1</i>	AAACAGTCATAAATGGCAAG	GGGAACAACCCATCATCAC
<i>Mcpt2</i>	TTCATTGCCTAGTTCCTCT	CTTTTCAGCTACTTGCTCT
<i>Mcpt4</i>	CCTTACATGGCCCATCT	CTTCCCAGGCTTGATA
<i>Cma2</i>	GCGGAAATGCAAAGCC	ACAGGGAACAGTCCATC
<i>Anxa10</i>	TACCCACAACCTCGGC	GGCAAGTAGTGTTTCT
<i>Cae</i>	GCAAGCCTATTGGCAG	TGGCATCGTGCAGGA
<i>Fos</i>	TGTGTACTCCCGTGGT	ACGAACAGGTAAGGTCC
<i>Ptgr1</i>	CATCGTGAATCGGTGG	GCTAGGTCAAACGCAT
<i>Cnn1</i>	ACGGCTACGGTACAC	GGTACTCCGGGTTGAG
<i>Ces3</i>	AGTGATTGTCTCGAAG	GTTCCATTCCGAGCA
<i>Cpe</i>	ACCGGAAGAGACTCTCA	CCAGTAATCCCCATCCT
<i>Notch4</i>	CCCTTAAACTCGGTGT	GGTGCTTAATAATAGTTGCC
28S rRNA	CAGTACGAATACAGACCG	GCAACAACACATCATCAC

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 BMHCs.

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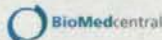
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The list represents 1,272 genes significantly altered between sMCs and mMCs in the order of clustering (Figure 5a). The values represent expression levels normalized to those of sMCs.

Cluster	Accession ID	Gene name	Gene symbol	sMC1 vs sMC2	sMC1 vs mMC1	sMC2 vs mMC1	sMC1 vs sMC2	sMC1 vs mMC2	sMC2 vs mMC2	mMC1 vs mMC2
1	100018_at	matrix metalloproteinase 11	Mmp11	0.511462	0.572251	0.703001	0.281813	0.394193	0.284719	0.250883
1	100018_at	metal response element binding transcription factor 1	Mrf1	0.554119	0.422085	0.465956	0.059218	0.246653	0.250883	0.250883
1	100113_at	keratin-associated protein 3	Krt3p3	0.737326	1.46539	0.271817	-0.737042	0.156232	0.25172	0.25172
1	100120_at	nidogen 1	Nid1	0.280395	0.192659	0.237115	-0.1154	0.053754	0.001118	0.001118
1	100123_f.at	integrin beta 1 (fibronectin receptor beta)	Igfbt1	2.489297	2.305655	2.338496	0.770938	1.855486	0.224388	0.224388
1	100124_f.at	integrin beta 1 (fibronectin receptor beta)	Igfbt1	1.948282	1.486537	1.039819	0.153188	0.769555	-0.090006	-0.090006
1	100231_at	secretory granule neuroendocrine protein 17B2 protein	Spgr1	1.241389	1.090042	1.454221	0.652137	0.491145	0.575043	0.575043
1	100134_at	endoglin	Eng	2.229513	2.106213	2.186617	0.8705	1.081956	0.180156	0.180156
1	100139_at	proprotein convertase subtilisin/kexin type 1 inhibitor	Pcatn1	1.646031	0.683004	1.473005	0.33196	0.147274	0.233457	0.233457
1	100153_at	neural cell adhesion molecule 1	Ncam1	0.320359	0.55204	0.825901	0.185432	0.185496	0.226599	0.226599
1	100281_at	germ cell-less homolog (Drosophila)	Gcl	0.194513	0.187345	0.328264	0.057851	0.025371	0.029123	0.029123
1	100308_at	procollagen type VIII alpha 1	Col8a1	1.400174	0.917507	0.494718	0.065562	0.181995	0.072178	0.072178
1	100379_f.at	actin alpha 1 skeletal muscle	Acta1	1.33833	1.329571	1.344001	0.223555	0.486532	1.127727	1.127727
1	100381_at	actin alpha 1 skeletal muscle	Acta1	0.707827	1.381241	0.223365	0.653387	0.009795	-0.018281	-0.018281
1	100407_at	gelsolin	Gel	0.78247	0.757807	0.807023	0.074844	0.343101	0.428257	0.428257
1	100435_at	endothelial differentiation (lymphoproliferative) alpha G-protein-coupled receptor 2	Edc92	1.036967	0.834081	0.578455	0.020428	0.216379	0.130438	0.130438
1	100449_g.at	activin A receptor type II-like 1	Actr2	1.202149	0.671188	1.044821	0.154846	0.023308	0.438996	0.438996
1	100453_at	calcium/calmodulin-dependent protein kinase II beta	Camk2b	0.439456	0.738175	0.502174	0.270378	0.340726	0.227007	0.227007
1	100465_f.at	Mus musculus clone IMAGE 331572 mRNA	---	1.28721	0.400486	0.421613	-0.181223	0.024888	0.106454	0.106454
1	100462_at	adaptor protein complex AP-2 alpha 2 subunit	Apo2d	0.760059	1.343029	0.820211	0.386651	0.445334	0.868944	0.868944
1	100567_f.at	fatty acid binding protein 4 adipocyte	Fabp4	1.262047	1.322201	1.482786	0.001857	1.055794	0.910417	0.910417
1	100585_at	suppressor of Ty 4 homolog (S. cerevisiae)	Sup4d	0.37086	0.307065	0.319433	-0.119523	0.186159	-0.135242	-0.135242
1	100605_at	tropomyosin 2 beta	Tpm2	1.145678	1.255101	0.924581	0.476418	0.565651	0.490038	0.490038
1	100737_at	size cut domain family member 1	Onecut1	0.484216	0.536007	0.429803	0.147457	0.31616	0.315304	0.315304
1	100768_at	Mus musculus 0 day neonate thymus cDNA RIKEN full-length enriched library clone AA3005422 product unknown EST full insert sequence	---	0.762899	1.005072	0.916639	0.384331	0.894557	0.895896	0.895896
1	100920_at	fibulin 2	Fbln2	0.554824	0.711038	0.977024	0.208293	0.28458	0.174859	0.174859
1	100923_at	chemokine (C-C motif) ligand 27	Ccl27	0.340703	3.785039	3.95925	1.112524	0.534941	0.448881	0.448881
1	100927_f.at	desmin	Des	0.25044	0.209815	0.370481	-0.209745	-0.202197	0.205481	0.205481
1	101029_f.at	actin alpha cardiac	Actc1	3.781266	3.87824	3.566503	0.185032	0.771857	0.771857	0.771857
1	101039_at	procollagen type IV alpha 2	Col4a2	1.4075	1.133502	1.409558	-0.051078	0.017445	0.249588	0.249588
1	101059_at	procollagen type IV alpha 2	Col4a2	1.938408	2.218719	1.911524	0.843595	1.185534	1.764877	1.764877
1	101059_at	procollagen type IV alpha 2	Col4a2	1.851718	3.478218	3.478218	1.704154	2.921187	0.009369	0.009369
1	101089_at	POZ and LIM domain 3	Plim3	3.145507	3.726834	0.623437	-0.048896	0.347108	0.347108	0.347108
1	101090_at	fibronin 1	Fbn1	0.427321	0.794863	0.992248	-0.081316	0.140119	0.081918	0.081918
1	101093_at	procollagen type IV alpha 1	Col4a1	4.113555	2.993704	3.249275	1.215995	2.06443	2.828304	2.828304
1	101097_f.at	cDNA sequence BC028706	BC028706	1.18872	1.504265	1.049754	0.963716	0.374062	-0.300398	-0.300398
1	101136_at	procollagen type I alpha 2	Col1a2	3.342328	3.14027	3.542025	3.381133	2.849679	1.968363	1.968363
1	101174_at	oncosultin	Ocn	0.285991	0.214832	0.202569	-0.00188	0.149508	0.018951	0.018951
1	101210_at	RIKEN cDNA 4732420M22 gene	4732420M22Rk	0.732951	0.414063	0.304227	0.109412	0.256007	0.043257	0.043257
1	101210_at	---	---	0.388598	0.490494	0.305273	0.022511	0.245674	0.164634	0.164634
1	101339_at	---	---	0.530102	0.529242	0.59062	0.342317	0.380027	0.323276	0.323276
1	101356_at	lamin B2	Lamb2	2.90273	2.849178	2.939951	0.157152	0.189448	0.189448	0.189448
1	101450_at	colony stimulating factor 1 (macrophage)	Csf1	0.608843	1.038817	1.097404	0.301527	0.597073	0.582535	0.582535
1	101453_at	melanoma inhibitory activity	Mia	0.32182	0.342938	0.296282	-0.028466	0.099941	0.193332	0.193332
1	101456_at	zinc finger protein 106	Zfp106	0.274388	0.396398	0.36977	-0.043618	0.181655	0.170483	0.170483
1	101532_at	carboxylesterase 3	Ces3	4.642101	1.27441	4.505246	0.545029	0.607796	0.069363	0.069363
1	101539_f.at	carboxylesterase 3	Ces3	8.891501	8.901353	6.889655	0.708279	0.738843	0.024575	0.024575
1	101571_g.at	insulin-like growth factor binding protein 4	Igfbp4	0.715691	0.595936	0.827766	0.158754	0.50356	0.275222	0.275222
1	101574_f.at	serine (or cysteine) proteinase inhibitor clade A member 1a	Serpina1a	0.452789	0.796882	0.876207	-0.014238	0.280359	0.200278	0.200278
1	101582_at	lysine rich protein 2	Lrp2	3.759106	4.168891	3.671871	0.399683	1.426049	0.39727	0.39727
1	101676_at	glutathione peroxidase 3	Gpx3	1.096212	1.204637	0.864813	0.157152	0.406511	-0.195023	-0.195023
1	101693_f.at	---	---	1.195543	0.78057	0.85563	-0.057406	0.27827	0.247085	0.247085
1	101694_f.at	MYST histone acetyltransferase 2	Myst2	0.638852	0.440016	1.210534	-0.160281	0.206531	0.254137	0.254137
1	101726_at	luteinizing hormone beta	Lhb	0.193036	0.197948	0.392077	-0.054212	0.080492	-0.021311	-0.021311
1	101787_f.at	---	---	0.981114	0.427301	0.382956	-0.205789	0.304402	0.344402	0.344402
1	101806_at	galactin receptor 3	Gal3	0.254535	0.218823	0.277413	0.110484	0.064021	0.042939	0.042939
1	101863_at	---	---	1.358129	1.280414	0.848713	0.220427	0.708806	0.823114	0.823114
1	101963_at	cathepsin L	Ctsl	3.194853	3.904917	1.896483	2.143156	0.631088	0.443457	0.443457
1	101966_at	RIKEN cDNA 4833420G17 gene	4833420G17Rk	1.852481	2.044055	1.440025	0.475697	0.38772	0.347337	0.347337
1	102056_at	nicotin 1	Nicot1	2.402004	1.845068	1.449145	0.406531	0.406531	0.542865	0.542865
1	102169_f.at	---	---	1.87377	0.74019	0.962202	0.188516	0.375191	0.542865	0.542865
1	102207_f.at	cDNA sequence BC011488	BC011488	0.781877	0.607464	0.605246	0.367946	0.420472	0.276705	0.276705
1	102215_at	cardinal (deficiency)-associated gene expressed in ventricle 1	Cdca1	0.891342	0.412561	0.499899	0.073951	0.185282	0.117288	0.117288
1	102230_at	hyaluronectase 1	Hyal1	1.437037	0.498337	0.711502	-0.152281	0.200002	0.269949	0.269949
1	102314_at	solute carrier family 2 (facilitated glucose transporter) member 4	Slc2a4	0.302507	1.388491	0.533460	0.161111	0.208182	0.07378	0.07378
1	102327_at	amine oxidase copper containing 3	Aoc3	1.156012	0.84782	0.445843	0.173982	0.46373	0.032556	0.032556
1	102386_f.at	growth associated protein 43	Gap43	0.671487	1.435401	1.252912	0.120272	0.041834	0.03096	0.03096
1	102395_at	peripheral myelin protein	Pmp22	2.30602	2.292389	2.545891	3.46964	0.60398	1.544583	1.544583
1	102399_at	RNA binding protein gene with multiple splicing casequestrin 1	Rbpms	1.010739	0.222562	0.778597	0.001751	0.187113	0.130094	0.130094
1	102425_at	---	---	0.936514	0.215412	0.838816	0.05813	0.078883	0.185298	0.185298
1	102721_at	Unknown (protein for MGC 88300)	MGC88300	0.476836	0.57312	0.481236	0.239717	0.381001	0.341167	0.341167
1	102763_at	plasma membrane associated protein 63-12	SP-12-pending	0.894045	0.895563	1.180099	0.150597	0.128441	0.274224	0.274224
1	102870_at	RIKEN cDNA 5530418K15 gene	5530418K15Rk	1.919447	1.147007	1.099422	0.582348	0.776568	0.803372	0.803372
1	102916_g.at	deletion X	DnaX	0.798737	0.325226	0.407851	-0.021143	0.080626	0.104787	0.104787
1	102924_at	delta 1 homolog (Drosophila)	Delt1	0.428649	0.632652	0.525576	0.005244	0.355733	0.220449	0.220449
1	103016_at	B-cell leukemia/lymphoma 8	Bcl8	0.865414	0.814218	0.832133	0.687501	0.94372	0.543959	0.543959
1	103026_f.at	---	---	0.366488	0.422888	0.478771	0.09927	0.276022	0.173052	0.173052
1	103030_f.at	dyxnanin	Dyxn	1.224849	1.177825	1.688771	0.651428	0.49911	0.203032	0.203032
1	103031_g.at	dyxnanin	Dyxn	2.129489	1.71115	2.840473	1.533128	0.712465	0.791232	0.791232
1	103050_at	transcription factor 21	Tcf21	1.184304	0.302077	0.859118	0.30842	0.840455	0.490079	0.490079
1	103086_at	SAM domain and HD domain 1	Samhd1	0.298026	0.256233	2.367102	0.247354	-0.202326	-0.152069	-0.152069
1	103100_at	Mus musculus clone IMAGE 5372338 mRNA	---	0.772444	0.997249	0				

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

Cluster	AF/matrix	Gene name	Gene symbol	sMC1 vs. sMC2	sMC2 vs. sMC3	sMC1 vs. sMC3	mMC1 vs. mMC2	mMC2 vs. mMC3	mMC1 vs. mMC3
1	103600_at	catenin gamma 3	Cenpf3	0.183363	0.35252	0.442515	0.101506	-0.15231	-0.14594
1	103604_at	insulin-like growth factor binding protein 6	igfbp6	0.566118	0.622154	0.478337	0.021588	0.260596	0.272866
1	103954_at	regenerating islet-derived 3 alpha	Rgs3a	0.296349	0.280351	0.138008	-0.056744	0.061981	0.014715
1	104063_at	cathepsin 5	Ctsh5	1.1859	0.995401	1.088509	0.4746	0.240055	0.047831
1	104091_at	RIKEN cDNA 5430079M16 gene	5430079M16Ra	1.759333	1.300085	0.994483	0.784297	0.474915	0.533583
1	104100_at	RIKEN cDNA 2310075G7 gene	2310075G7Ra	0.803339	0.95952	0.605512	0.095833	0.340216	0.024467
1	104126_at	cytochrome P450 family 4 subfamily 1 polypeptide 13	Cyp4f13	0.720293	0.616794	1.088127	0.241178	0.407471	0.288695
1	104136_at	cDNA sequence BC024558	BC024558	0.580731	1.4762	1.448896	0.826501	0.524727	0.320899
1	104210_at	integrin alpha 3	Irga3	0.632968	0.746033	0.670845	0.426534	0.203822	0.484994
1	104280_at	synuclein gamma	Sngg	1.452453	2.188471	1.861209	-0.155431	0.037797	0.215862
1	104312_at	RIKEN cDNA 1110213B18 gene	1110213B18Ra	0.488855	0.65949	0.689917	0.256157	0.245404	0.271102
1	104348_at	DNA segment Chr 10 ERATO Doi 810 expressed	D10E10810e	0.56361	1.288425	0.894744	0.021053	0.180306	-0.008826
1	104360_at	supervillin	Svl	1.182612	2.01035	1.416411	0.467551	0.562541	0.419187
1	104382_at	mast cell protease 4	Mcp4	1.282229	2.11251	1.230968	0.062271	0.337337	0.342882
1	104407_at	activated leukocyte cell adhesion molecule	Alcam	1.38561	2.818925	2.897701	1.614429	0.454801	0.222104
1	104408_s_at	SRY-like containing gene 18	Scn18	3.98032	4.20983	3.53582	0.257111	0.207949	0.193099
1	104412_at	guanine nucleotide binding protein alpha inhibiting 1	Gnai1	1.002043	0.669771	0.688557	0.400831	0.196202	0.362911
1	104414_at	guanine nucleotide binding protein alpha 0	Gnao0	0.514358	0.586243	0.562499	0.197294	0.389287	0.270866
1	104501_at	vesicle-associated membrane protein associated protein B and C	Vapb	2.210027	2.280308	1.1495	-0.112277	0.334416	0.392933
1	104571_at	chemokine (C-X-C motif) ligand 4	Cxcl4	0.486336	0.427887	0.472085	0.178823	0.286342	0.29627
1	104578_f_at	actin alpha 1	Actn1	0.739925	0.529623	0.935646	0.456628	0.40302	0.807473
1	104587_f_at	laminin alpha 4	Lama4	1.015854	0.801482	0.802068	0.063145	0.283006	0.185104
1	104595_at	stromal antigen 2	Stag2	1.583911	1.703806	1.023366	0.598441	0.546011	0.383708
1	104645_at	kluppel-like factor 7 (ubiquitous)	Klf7	2.710001	1.943818	3.150932	0.848486	0.01194	-0.071099
1	104655_at	T-box 2	Tbx2	1.182671	0.951618	0.89091	0.492949	0.828891	0.544028
1	104685_s_at	glutamate receptor ionotropic NMDA1 (rats 1)	Gria1	0.187448	0.21844	0.269911	0.030515	0.089179	0.081337
1	104716_at	ubiquitin-associated protein 2	Uba2	0.136492	0.710594	0.709969	0.132782	0.021281	0.041618
1	104729_at	retinoic acid binding protein 1 cellular	Rbp1	2.08343	1.708152	0.929779	0.88264	0.690076	0.966491
1	104731_at	gap junction membrane channel protein alpha 4	Gja4	2.258936	2.011996	0.960022	0.330458	0.509719	0.441387
1	104761_f_at	arrestin train receptor 2	Artr2	1.118277	1.546283	1.488881	0.84615	-0.249495	0.245404
1	104763_at	ectonucleotide pyrophosphatase/phosphodiesterase 5	Eppa5	0.685216	0.563145	0.584202	0.248088	0.495892	0.397107
1	104819_at	crystallin alpha C	Cryac	1.406116	1.378156	0.947136	0.296977	0.499905	0.564573
1	104810_at	stathmin like 3	Stmn3	2.577889	1.208706	1.57791	-0.04015	0.141249	0.248143
1	104812_at	GTL1 imprinted maternally expressed untranslated mRNA	Gtlc	0.132785	0.506257	0.35794	-0.089429	-0.090549	-0.094312
1	104835_at	transcript 3	Tsp3	0.548058	0.518556	0.999317	-0.099501	0.338666	0.264328
1	104855_at	RIKEN cDNA 1200013P24 gene	1200013P24Ra	0.902598	1.58016	0.915152	0.859112	-0.192481	0.255218
1	1049251_f_at	large tumor suppressor 2	Ltn2	2.488905	2.872936	2.269251	0.561089	0.231884	0.628509
1	104928_at	caveolin caveolin 2 gene	Cav2	3.151803	3.389821	3.667522	0.254281	0.556004	0.506004
1	104930_at	RIKEN cDNA 2610001E11 gene	2610001E11Ra	1.184261	1.483269	1.739751	0.107525	0.323672	0.213877
1	104936_at	myelin homologue responsive SPOT14 homolog (Rattus)	Thy1	1.134403	1.287734	1.148919	0.104045	0.509009	0.463139
1	104939_at	SPARC like 1 (mouse hevni)	Sparrc1	3.7269	3.414883	3.230289	1.349557	1.304425	0.488692
1	104932_at	platelet derived growth factor receptor alpha polypeptide	Pdgfra	0.598266	0.648619	0.332894	0.078396	0.673435	0.103581
1	104937_at	RIKEN cDNA 1200017C10 gene	1200017C10Ra	0.889649	0.257872	0.650414	0.031389	0.077165	0.184234
1	104973_f_at	serum deprivation response	Sdr	4.011485	3.759669	2.782836	0.282839	0.207182	0.883753
1	104978_f_at	cardiac ankyrinase 3	Cak3	2.305311	2.378804	2.800909	1.208919	0.624441	0.414031
1	104945_at	RIKEN cDNA 2610005H11 gene	2610005H11Ra	0.316782	0.355868	0.510127	0.029515	0.197283	0.188579
1	104945_s_at	DNA segment Chr 10 ERATO Doi 749 expressed	D10E10749e	0.830312	0.165447	0.799218	-0.09584	0.280191	-0.213438
1	104956_at	melanoma cell adhesion molecule	Mcam	1.750156	1.446289	1.207186	0.444821	0.117088	0.378711
1	104963_at	transcription factor 4	Tcf4	1.63387	2.680489	1.894828	0.722889	0.272034	0.228018
1	105011_at	chemokine (C-X-C motif) ligand 12	Cxcl12	1.896618	1.720111	1.829192	1.048228	1.048237	0.549323
1	105019_at	tissue inhibitor of metalloproteinase 3	Timp3	3.328807	0.523622	0.514753	2.350040	2.30753	0.015420
1	105032_at	retinol inducible alpha	Rtn1	3.37897	3.676243	2.606652	1.410874	1.54131	0.902334
1	105061_at	growth differentiation factor 9	Gdf9	0.202576	0.222772	0.112706	0.045415	0.027778	-0.078653
1	105074_f_at	regulator of G-protein signaling 3	Rgs3	0.003687	0.53319	0.907792	0.249971	0.149189	0.31955
1	105076_at	DNA segment Chr 1 University of California at Los Angeles 4	D1Ucla4	0.307282	0.770245	0.547715	0.139673	0.045606	-0.452866
1	1050819_at	N-myc downstream regulated 4	Ndr4	2.110034	2.171961	1.578338	0.475588	0.099195	0.307247
1	105084_f_at	D-site albumin promoter binding protein	Dsp	1.62416	1.554591	2.485228	0.373586	-0.381884	-0.646331
1	1050879_at	Mus musculus proteasome beta-subunit C5 (PainB1) mRNA partial cds	—	0.578747	0.38732	0.904296	0.225614	-0.018731	-0.33819
1	105087_f_at	osteoglycin	Ogn	1.500441	1.512377	1.885185	0.584884	0.587348	0.817599
1	105088_at	RasBP1 associated Eps domain containing protein	Rasbp1	0.580398	0.448103	0.448738	0.282289	0.395622	0.329783
1	105094_at	CCAAT/enhancer binding protein (C/EBP) delta	Cebpd	4.849469	4.953275	4.187117	0.267348	0.161623	0.533091
1	105096_at	Purkinje cell protein 4	Pcp4	3.217344	4.206196	2.929161	0.038089	-0.194409	0.029772
1	105097_f_at	angiotensin converting enzyme	Ace	0.854807	0.69768	0.480632	0.309648	0.303494	0.343607
1	105094_s_at	—	—	0.964306	1.245568	1.514429	0.790333	0.860037	0.48994
1	105092_at	Bcl2-associated atrophin 2	Bap2	0.151385	1.210443	0.513155	-0.123444	0.029001	-0.138081
1	105094_f_at	DNA segment Chr 16 Brigham & Women's Genetics 1494 expressed	D16Bwg1494e	0.221001	0.279649	0.302187	-0.121953	-0.088172	0.172045
1	1051013_f_at	RIKEN cDNA 493042J18 gene	493042J18Ra	1.118043	2.254079	1.308091	0.783869	0.078495	-0.004404
1	1051029_f_at	SRY-like containing gene 18	Scn18	1.829181	2.083436	1.638611	0.398699	0.736446	0.400056
1	1051030_f_at	DNA segment Chr 9 Brigham & Women's Genetics 0860 expressed	D9Bwg0860e	0.610247	1.523375	1.302448	0.461823	0.536871	0.333091
1	1051096_f_at	Mus musculus transcribed sequence	—	1.246080	2.042064	0.514002	0.15574	0.296115	0.300235
1	1051139_f_at	Development and differentiation enhancing	Dclh1	0.309536	0.544053	0.464844	-0.039255	0.016597	-0.129298
1	1051184_f_at	tyrosine kinase receptor 1	Tie1	1.42055	2.818751	0.533963	0.478383	0.377942	0.028756
1	1051256_f_at	Wilms tumor homolog	Wt1	0.675314	0.439812	0.825992	0.307091	0.309697	0.258415
1	1051285_f_at	peleto homolog (Drosophila)	Pelo	0.732575	0.78278	0.898837	0.33513	0.619118	0.471581
1	1051341_f_at	GA repeat binding protein beta 1	Gahyb1	1.080024	0.195195	0.888094	0.657117	0.632474	0.434713
1	1051350_f_at	ectonucleotide pyrophosphatase/phosphodiesterase 2	Eppa2	0.497113	0.528286	0.894141	0.005728	0.151397	0.283215
1	1051367_f_at	Hennary-Futak syndrome 1 homolog (human)	Hfsr1	0.389727	0.296128	0.342627	0.105891	0.207963	0.113568
1	1051376_f_at	lun1 related transcription factor 2	Lunr2	0.338215	0.318914	0.837865	0.052303	0.257737	0.014547
1	1051436_s_at	adenosine deaminase RNA-specific B1	Adain1	4.866021	4.191238	2.549239	0.129137	0.088397	0.085378
1	1051482_f_at	perlecan 1	Prlp1	1.100204	1.820657	1.305611	0.378096	0.733766	0.279332
1	1051497_f_at	integrin alpha 7	Irga7	1.499087	1.060009	1.460572	0.090989	0.233773	0.710692
1	1051504_f_at	DNA segment Chr 10 ERATO Doi 214 expressed	D10E10214e	0.961785	0.924441	0.789845	0.268824	0.657312	0.448007
1	1051509_f_at	matrin metalloproteinase 2	Mmp2	0.318851	0.318851	-0.020943	0.186226	0.060225	-0.060225
1	1051522_f_at	matrin C	Cst3	1.38513	1.33998	1.305116	0.062983	-0.180729	-0.063004
1	1051530_f_at	semaphorin domain immunoglobulin domain (lig) transmembrane domain (TM) and short cytoplasmic domain (semaphorin) 4A	Sema4a	0.798059	0.992336	0.938157	0.492612	0.759059	0.61221
1	1051535_at	Mus musculus transcribed sequence with moderate similarity to pituitary prf2203412a (H sapiens) 2203412a polycystin [homo sapiens]	—	0.585236	0.679441	0.699903	0.362183	0.488185	0.488572
1	1051557_f_at	menage a trois 1	Mnat1	0.492057	0.439342	0.427422	0.057326	0.335228	0.018503
1	1051569_f_at	creatine kinase muscle	Ckm	1.385176	1.583798	1.128106	0.035111	0.821888	0.432635
1	1051596_f_at	A kinase (PKA) anchor protein 8	Akap8						

The list represents 1272 genes significantly altered between iMCs and nMCs in the order of clustering (Figure 3e). The values represent expression levels normalized to those of iMCs.

Cluster	Accession ID	Gene name	Gene symbol	AMC1 vs. BMC1	AMC2 vs. BMC1	AMC3 vs. BMC1	nMC1 vs. BMC1	nMC2 vs. BMC1	nMC3 vs. BMC1
1	161188_f_1	endothelial differentiation sproutlike 3-protein-coupled receptor 1	Edy7	0.905999	0.954412	1.010638	0.816712	0.745192	0.420187
1	161187_f_1	RIKEN cDNA 493042J2.6 gene	493042J2.6R18a	1.343762	3.031968	1.25978	0.964873	0.003785	0.069862
1	161182_f_1	glutamate ammonia ligase (glutamine synthase)	Glu1	0.648999	0.603877	0.694053	0.361046	0.473200	0.457239
1	161180_f_1	sproutin gamma 2	Spr2	1.86345	1.789133	2.515361	1.03786	0.064842	0.216519
1	161170_f_1	ubiquitin specific protease 15	Usp15	0.331039	0.199921	0.324623	-0.121176	0.078735	-0.124137
1	161169_f_1	metaxin 1	Mtx1	0.437056	0.288841	0.258942	-0.100635	0.119659	0.130688
1	161197_s_1	hemaxin KB	Hmb	1.561713	1.537811	1.348727	0.245617	0.454517	0.831602
1	161193_f_1	—	—	0.145894	0.750225	0.808756	0.132438	0.533984	0.216897
1	161191_f_1	lymphocyte specific 1	Lsp1	1.429567	0.637383	0.804422	-0.32276	0.58781	0.643396
1	161193_f_1	stathmin-like 3	Stmn3	0.822955	0.752124	0.966375	0.55096	0.727783	0.528991
1	161194_f_1	procollagen type III alpha 1	Col3a1	3.408255	3.011828	3.497500	1.073484	2.505636	2.522895
1	161168_f_1	low density lipoprotein receptor-related protein associated protein 1	Lrpap7	0.590725	0.320524	0.265031	0.190388	0.019678	-0.042115
1	161196_f_1	N-myc downstream regulated 4	Ndr4	0.915945	0.594347	0.541116	0.44032	0.436882	0.233078
1	162034_f_1	antrax toxin receptor 2	Antr2	0.8314	0.529427	0.707656	0.335426	0.195148	0.256459
1	162089_f_1	tailin	Tln	0.246207	0.142744	0.331380	-0.264291	0.082493	-0.04997
1	162088_f_1	Mus musculus Similar to GDC61 cell division cycle 91-like 1 (S cerevisiae) clone IMAG25574056 mRNA partial cds	—	0.226498	0.424128	0.376189	0.071887	0.212207	0.073882
1	162186_f_1	vesicular membrane protein p24	Vmp	1.340159	1.382054	0.774431	-0.18186	-0.18477	0.011883
1	162192_f_1	chromogranin A	Chga	1.99967	1.780585	2.11369	1.488031	0.917212	1.264237
1	162204_f_1	Notch gene homolog 1 (Drosophila)	Notch1	1.323874	0.895257	0.393657	0.185514	0.433175	0.108305
1	162201_f_1	zeta pellucida glycoprotein 2	Zp2	0.247841	0.311152	0.196565	-0.070456	0.064329	0.010968
1	162308_f_1	tenascin C	Tnc	1.033901	1.051039	1.028926	0.698226	0.693479	0.612216
1	162321_f_1	Barr-like homeobox 1	Bhlh1	2.008126	1.602012	1.711168	0.156868	0.577681	0.372778
1	162320_f_1	—	—	0.785007	0.731521	0.607315	0.22678	0.472232	0.40524
1	162342_f_1	fatty acid binding protein 1 liver	Fabp1	0.814188	0.838445	1.006818	0.720087	0.76273	0.727737
1	162347_f_1	biglycan	Bgn	1.013354	0.819459	1.047377	0.326989	0.886168	0.448501
1	162342_f_1	tenascin R	Tnc	0.932382	0.936033	0.392606	0.117184	0.183894	0.096056
1	162365_f_1	C1q and tumor necrosis factor related protein 1	C1qf1	0.455611	0.402467	0.474837	0.141344	0.380024	0.280024
1	162448_f_1	crystallin alpha C	Cryac	0.505955	0.490141	0.309773	0.12277	-0.014008	0.11154
1	162468_f_1	ras homolog gene family member C	Ras	0.430125	0.367972	0.335919	0.174806	0.356800	0.277609
1	162493_f_1	general transcription factor II 1	Gtf2b	0.581814	0.81730	0.781758	0.376567	0.536958	0.259307
1	162223_g_1	Mus musculus transcribed sequence with strong similarity to protein Q05116 (H sapiens) Z145_HUMAN Zinc finger protein PLZF (Promyelocytic leukemia zinc finger protein) (Zinc finger protein 145)	—	2.078102	3.018708	2.034989	0.283574	0.081803	-0.144734
1	162223_g_1	complement component 1 g subcomponent gamma polypeptide	C11g	1.569287	1.71967	0.958468	0.32836	0.631186	0.843881
1	162224_g_1	tetrahidin (plasmogonium binding protein)	Tpp1	0.695234	0.850556	0.888053	0.444856	0.626465	0.723476
1	162225_f_1	RNA polymerase 1-2	Rpo1-2	1.636302	0.76187	0.761817	0.139684	0.148876	-0.009079
1	162241_f_1	RIKEN cDNA 1500041016 gene	1500041016R1a	0.50543	0.100778	0.704491	0.114345	0.251289	-0.118733
1	162270_f_1	tophin	Top	0.529712	0.682707	0.539787	0.297188	0.548626	0.348626
1	162276_f_1	mann-6-phosphate protein kinase kinase kinase 5	Mpk3k5	0.2501	0.356688	1.207222	0.741729	-0.299523	-0.299523
1	162296_f_1	protein tyrosine phosphatase receptor type B	Ptpb	3.265086	1.270234	1.486022	0.568857	0.716207	0.372778
1	162348_f_1	thyroid hormone receptor alpha	Thra	0.940174	0.779542	1.226701	0.06802	-0.014878	-0.032523
1	162301_f_1	ELAV (embryonic lethal abnormal vision (Drosophila))-like 4 (Hu antigen) D	Elavl4	0.281179	0.450502	0.414747	0.069597	0.17866	0.00858
1	162306_f_1	tenascin R2	Tnc2	2.645899	0.821586	1.529442	0.072151	0.368921	0.347676
1	162307_f_1	centaurin gamma 2	Cent2	0.487252	0.899604	0.684342	0.489138	0.324155	0.283011
1	162407_f_1	myosin 1	Myo1f	0.861400	1.400203	1.689314	0.408484	0.587163	0.116802
1	162498_f_1	vesicle-associated membrane protein 5	Vamp5	1.353541	1.509007	0.734885	0.746252	0.637962	0.406571
1	162514_f_1	Barr-like homeobox 1	Bhlh1	0.783503	0.564072	1.866306	0.25541	0.489145	0.522664
1	162518_f_1	neogenin	Neogen	0.342469	0.327448	0.344847	0.119178	0.218806	0.304409
1	162535_f_1	early B-cell factor 1	Ebf1	0.730339	0.881233	0.537204	0.203464	0.448778	0.259661
1	162509_f_1	vascular cell adhesion molecule 1	Vcam1	2.572895	3.785986	2.320555	0.258956	0.371177	0.133839
1	162560_g_1	vascular cell adhesion molecule 1	Vcam1	0.721964	1.274186	1.112	0.342406	0.857804	0.484914
1	162563_f_1	neurotrophin repeat (in FLN) interacting protein 1	Nflp1	1.145026	1.106152	0.873221	0.178388	0.712288	0.404534
1	162602_f_1	Nutch gene homolog 4 (Drosophila)	Nutch4	0.348227	0.891524	1.317896	0.018186	0.18833	0.62885
1	162702_f_1	astroctadin 1	Astr1	0.516223	0.534719	1.133489	0.077443	0.243567	0.243567
1	162705_f_1	T-box 2	Tbx2	0.376794	0.438878	0.455183	0.233087	0.265339	0.225891
1	162725_f_1	growth arrest specific 6	Gas6	0.245327	0.261274	0.367599	-0.152721	0.011601	-0.131432
1	162742_f_1	growth chemokine (C-C motif) ligand 11	Ccl11	0.751864	0.846838	0.974333	0.11687	0.24567	0.296426
1	162796_f_1	secretin	Scl	0.706106	0.815651	0.879866	0.484283	0.564247	0.410594
1	162820_f_1	ubiquitin specific protease 2	Usp2	0.700829	0.330194	0.499329	0.180081	0.02197	0.102045
1	162821_f_1	ubiquitin specific protease 2	Usp2	1.707029	0.865901	1.381511	0.405664	0.528178	0.822218
1	162836_f_1	cin	Cin	3.205994	1.598448	2.127168	-0.181531	0.539815	0.444173
1	162852_f_1	fibronectin 1	Fnt1	1.92813	0.201945	1.830353	0.294092	0.935667	0.123306
1	162892_f_1	vesicular membrane protein p24	Vmp	1.213315	0.602586	0.178887	0.102558	0.039731	0.132666
1	162927_f_1	ets variant gene 1	Etv1	1.444174	2.378048	2.563501	0.331531	0.20024	0.088644
1	162981_f_1	serotransferrin II	Sct2	1.628026	1.998618	1.384451	0.520605	0.286487	0.329728
1	162987_f_1	solute carrier family 4 (anion exchanger) member 3	Slc4a3	0.538004	1.298103	0.938649	-0.0291	0.250578	0.323725
1	162996_f_1	SRY-box containing gene 17	Sov17	0.491187	1.203035	0.490334	-0.162183	0.170619	-0.180564
1	163040_f_1	FXD domain-containing ion transport regulator 1	Fxyf1	2.456759	2.218308	1.601813	0.254859	0.821203	0.698416
1	163054_f_1	RIKEN cDNA 1110054069 gene	1110054069R1a	0.781986	0.998485	1.373649	0.591442	0.893367	0.556442
1	163051_f_1	migrin alpha 7	Migr7	1.366885	0.931322	1.360543	0.582051	0.147385	0.710368
1	163077_s_1	lymphocyte antigen 6 complex locus C	Ly6c	1.061277	0.767894	0.692096	0.079608	0.098821	0.104512
1	163078_f_1	lymphocyte antigen 6 complex locus A	Ly6a	3.470607	2.289636	3.490013	1.27782	1.760733	1.877025
1	163084_f_1	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator) member 4	Slc25e4	2.269890	2.090947	1.689294	0.354748	-0.058192	0.283992
1	163087_f_1	—	—	0.848011	0.830683	0.79515	0.098505	0.479563	0.309281
1	163094_f_1	cerebellar degeneration-related 2	Cdr2	1.524977	1.951939	0.360288	-0.071769	0.140248	0.028114
1	163100_f_1	actin alpha 2 smooth muscle actin	Acta2	8.816781	5.025255	6.374036	0.97462	0.544313	0.288084
1	163102_f_1	actin gamma 2 smooth muscle actin	Actg2	3.752954	4.194382	3.493477	-0.106227	0.309063	0.268002
1	163109_f_1	senex (or cysteine) protease inhibitor clade A member 1d	Senp1d	0.428814	0.454769	0.737087	0.187937	0.317037	0.164031
1	163125_f_1	creative vision brain 1	Cvb1	2.285789	2.895567	2.915748	1.542978	0.962186	0.285421
1	163130_f_1	RIKEN cDNA 2000050C20 gene	2000050C20R1a	0.01881	0.153441	0.41259	-0.028788	0.018009	-0.14168
1	163153_f_1	adenosine deaminase RNA-specific B1	Adarb1	1.390581	0.662234	0.460891	0.072703	0.269804	0.13402
1	163187_f_1	RIKEN cDNA 2210023P24R1a gene	2210023P24R1a	1.691242	1.938205	1.651923	0.810752	0.981838	0.749788
1	163188_f_1	deklapp homolog 3 (Xenopus laevis)	Dnk3	1.381948	3.259465	2.862543	0.278116	0.638773	0.441887
1	163195_f_1	malignant fibrous histiocytoma amplified sequence 1	Mfas1	0.530026	0.625921	2.130026	0.638264	0.378916	0.281448
1	163224_f_1	zinc finger protein 39 CSH type 1	Zfp39f1	1.430552	1.147438	1.564563	0.759446	-0.047174	0.822364
1	163252_f_1	transglutaminase 2 C polypeptide	Tgm2	0.467151	0.011307	0.555312	-0.008879	0.361204	-0.047402
1	163253_f_1	lumican	Lum	3.949133	2.742546	3.471802	0.435029	-0.01302	0.183148
1	163421_f_1	PPTAIRE protein kinase 1	Ppk1	1.700981	1.833369	0.348939	0.201417	0.349839	0.028844
1	163431_f_1	dystronia myotonia kinase B15	Dmrb15	2.645024	3.038498	2.587772	0.340009	0.572211	0.295421
1	163448_f_1	RIKEN cDNA E330036I10 gene	E330036I10R1a	0.866890	0.517147	0.639677	0.373406	0.373406	0.342157
1	163455_s_1	bone morphogenetic protein 4							

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

Cluster	Admiralty id	Gene name	Gene symbol	aMC1 vs. BMAC	aMC2 vs. BMAC	aMC3 vs. BMAC	mMC1 vs. BMAC	mMC2 vs. BMAC	mMC3 vs. BMAC
1	93692_at	LIM domain binding 2	Ldb2	1.502695	1.026565	1.739929	0.915662	0.239275	0.277283
1	93693_at	RIKEN cDNA F63002C16 gene	F63002C16Rk	1.626176	1.484375	0.463034	0.485308	0.335148	1.125559
1	93696_x_at	neuroin gamma-carboxylglutamate (iga) protein	Magp	4.079321	3.895669	3.897731	0.373086	0.21004	0.207380
1	93697_at	H.2A.B associated transcript 3	Bac3	0.321292	0.48060	0.446335	0.943305	0.164816	0.256839
1	93698_at	cytochrome P450 family 2 subfamily e polypeptide 1	Cyp2d1	1.651056	0.944351	0.883445	0.296371	0.363559	0.323400
1	94006_at	Mus musculus 13 days embryo spinal cord cDNA RIKEN full-length enriched library clone G63002J15 product unclassifiable full insert sequence	Azr2	0.980029	0.619637	0.471954	0.264428	-0.226162	-0.284673
1	94027_at	CD84 antigen	Ct84	2.867607	2.582484	2.852338	1.488718	1.858117	1.174100
1	94028_x_at	fucosyltransferase 7	Fuc7	0.494225	0.606017	0.608887	0.213281	0.41678	0.226617
1	94022_at	muscle-like growth factor binding protein 4	Igf4	0.223316	0.331398	0.317822	-0.031217	0.118372	0.001506
1	94299_x_at	melanoma antigen family D 2	Mage2	0.655562	1.068377	1.002468	0.518075	0.736867	0.438653
1	94307_at	fibulin 1	Fbln1	2.065577	1.712132	1.066542	0.67199	1.063221	0.443806
1	94308_at	fibulin 1	Fbln1	1.378655	1.26742	1.400118	0.178322	0.535559	1.242386
1	94345_at	interleukin 6 signal transducer	Fbln1	1.148000	1.043472	1.276121	0.778874	0.320971	0.079672
1	94354_at	ATP-binding cassette sub-family A (ABC1) member 1	Abca1	3.587308	3.68823	3.07295	0.726537	0.849847	0.231643
1	94377_at	guanine nucleotide binding protein (G protein) gamma 11	Gng11	3.081093	2.906972	2.496963	-0.070715	0.391888	0.602827
1	94384_at	Harvey rat sarcoma oncogene subgroup R	Rras	0.52795	0.545537	0.711468	0.020456	0.375602	0.025535
1	94429_at	erythrocyte translation elongation factor alpha 2	Eef2e2	2.001538	1.675456	2.006772	0.242331	0.843484	0.175332
1	94432_at	sulfatransferase 1 (beta-galactoside alpha-2,6-sulfatransferase)	Enpep2	0.679590	0.616974	1.074941	0.122876	0.299196	0.21381
1	94492_at	desitin	Des1	1.662119	2.867134	1.119738	0.002614	2.269144	0.298114
1	94493_at	desitin	Des1	3.209782	3.260338	2.977867	2.566915	2.100335	3.362878
1	94493_at	desitin	Des1	0.157765	0.24187	0.147618	-0.119413	0.047124	-0.068016
1	94520_at	RIKEN cDNA 261000J.06 gene	C61000J.06Rk	0.518973	0.646066	0.560606	0.193691	0.370265	0.372893
1	94545_at	retinon 1	Rtn1	1.381025	1.951689	1.925563	0.517184	-0.027382	0.964566
1	94712_at	vascular endothelial growth factor C	Vegf3	1.680686	1.948388	0.947431	0.670442	0.988759	1.018473
1	94780_at	zinc finger protein 298	Zfp298	1.396853	2.016672	3.011385	0.482379	0.985507	0.485507
1	94791_x_at	leukocyte tyrosine kinase	Ltk	0.216447	0.11004	0.313088	0.011168	-0.089844	-0.03283
1	94813_at	growth arrest specific 1	Gas1	2.418645	0.81036	1.440617	0.477389	0.481308	0.176049
1	94820_at	superoxide dismutase 3 extracellular	Sod3	0.713948	0.97715	0.629529	0.378233	0.423808	0.420981
1	94906_at	acetylcholinesterase 1 (class I)	Ache1	2.047799	3.237766	1.848103	1.201866	0.811229	1.913448
1	94930_at	thrombospondin 2	Thbs2	0.426238	0.604118	0.487935	0.201871	0.340148	0.298482
1	95027_at	ubiquitin specific protease 21	Usp21	1.100001	1.329583	0.656555	0.487761	0.58867	0.43011
1	95079_at	platelet derived growth factor receptor alpha polypeptide	Pdgfra	3.074300	3.733821	2.041402	1.489937	0.896573	2.160052
1	95104_at	tyrosinase 2	Tyr2	0.423636	0.333785	0.224182	0.333785	0.103469	0.103469
1	95112_at	peptidylprolyl isomerase (cyclophilin)-like 2	Ppi2	0.803500	0.636965	0.651473	0.457148	0.035966	0.406878
1	95125_x_at	ring box 1	Rbx1	0.803912	0.684759	0.628812	0.135133	0.488541	0.207678
1	95184_x_at	---	---	2.0541	2.391203	1.888828	0.811202	1.033199	1.237816
1	95208_at	acetylglucosylase 4	Acgbp	0.389495	0.591585	0.457153	0.01328	0.119788	0.119788
1	95232_at	pleckstrin homology domain Drc7 and coiled-coil domains 1	Pkczt1	0.212568	0.426117	0.192117	0.022812	0.181344	0.140298
1	95332_at	5-hydroxytryptamine (serotonin) receptor 2B	Htr2b	0.550306	0.741144	0.255792	-0.152601	-0.002978	0.034877
1	95557_at	bone morphogenetic protein 1	Bmp1	0.941213	0.496951	0.573073	0.12624	0.410425	0.127159
1	95584_at	developmental pluripotency associated 2	Dppa2	0.179541	0.469118	0.530758	0.041126	0.084400	-0.112019
1	95618_at	DNA segment Ctr 6 ERATD box 32 expressed	D561802N.6	0.631826	0.792406	1.160953	0.686638	2.440762	0.303562
1	95686_g_at	stathmin-like 2	Stmn2	1.85381	1.878308	1.509966	-0.019147	0.488661	0.317701
1	95670_at	stathmin-like 2	Stmn2	4.932282	3.861166	4.411137	0.268090	0.168633	0.385887
1	95723_x_at	RIKEN cDNA 261000E.16 gene	C261000E.16Rk	0.304847	0.196911	0.367096	-0.019737	0.114028	0.065781
1	95696_x_at	chymase 2 mouse cl.	Cma2	2.073095	2.238603	1.430985	-0.074152	0.34912	0.889959
1	95676_at	Dlx zinc and double PHD fingers family 3	Dlx3	0.389524	0.238988	0.403386	0.03914	0.167033	0.119229
1	95049_at	lygcan	Lyg	2.700899	1.924057	1.587376	0.981961	0.177963	0.984432
1	95088_at	N-kip1 downstream regulated 2	Nkd2	2.028898	1.377796	0.884338	0.485378	0.787129	0.536811
1	95109_at	Kruppel-like factor 2 (lung)	Klf2	1.151838	0.95701	0.893695	0.360678	0.179918	0.096607
1	95144_at	inhibitor of DNA binding 4	Id4	0.330965	0.347361	0.457353	0.00872	0.141624	0.141624
1	95146_at	B-cell translocation gene 3	Btg3	2.534541	2.713806	2.01699	1.34291	2.03166	2.001083
1	95204_at	SH3-binding domain glutamic acid-rich protein	Sh3bp	0.621242	0.687859	0.859117	0.385236	0.532266	0.440073
1	95205_at	SH3-binding domain glutamic acid-rich protein	Sh3bp	2.678416	2.052708	3.969654	0.304212	0.738448	0.328186
1	95208_at	RIKEN cDNA 643029G.11 gene	G643029G.11Rk	1.889839	0.871387	1.495213	0.331334	1.389669	-0.106599
1	95244_at	ubiquitin carboxyl-terminal hydrolase L1	Ubr1	0.500407	0.779884	3.456683	-0.117843	2.203379	-0.145017
1	95051_at	C-type (calcium dependent) carbohydrate recognition domain lectin superfamily member 9	Clec9f	0.150406	0.205939	0.170322	-0.05061	-0.035836	0.042828
1	95703_at	melanoma antigen family D 1	Magep1	2.012893	1.467517	1.389709	1.001444	0.123691	0.040028
1	95735_at	RIKEN cDNA 643029K.16 gene	K643029K.16Rk	1.315763	1.905564	1.520101	1.022415	-0.203211	-0.759991
1	95742_at	dermatopontin	Dpr	1.044586	0.978907	0.9594	0.551654	0.598425	0.831554
1	95774_at	pleckstrin homology domain containing family C (with FERM domain) member 1	Ptkchc1	2.592977	2.293884	3.368833	0.244814	0.116846	0.017043
1	95812_at	smoothelin homolog (Drosophila)	Smc	0.784748	0.579354	0.660847	0.422018	0.274547	0.348476
1	95818_at	dellet 2 homolog (Drosophila)	Dcl2	0.728734	0.444006	0.584996	0.111406	0.345758	0.348764
1	95920_at	protease serine 11 (lgf binding)	Psr11	3.951482	3.061029	2.147711	0.167315	0.200035	0.287593
1	95926_at	SPARC related modular calcium binding 2	Smoc2	1.964449	2.096881	0.880029	0.370238	0.140787	0.30992
1	95929_at	myosin light polypeptide 9 regulatory	Myr9	6.960774	6.864482	5.812334	3.395336	1.207484	0.991783
1	95954_at	serine/threonine kinase 24 (STE20 homolog yeast)	Skp24	0.487528	0.486007	0.599739	0.165057	0.302668	0.311111
1	97004_at	---	---	0.369124	0.381025	0.491979	0.14833	0.298236	0.218550
1	97062_at	pink-eyed dilution	P	0.835889	0.220968	0.470042	-0.041286	0.069823	0.058576
1	97101_at	cDNA sequence BC037527	BC037527	0.501542	0.468564	0.613746	0.374545	0.286220	0.301129
1	97112_at	MRV integration site 1	Mv1	2.195141	1.378165	2.194341	-0.334945	-0.159895	-0.236307
1	97222_at	RANK member RANK oncogene family	Rank	0.736578	0.856469	0.807854	0.23632	0.579753	0.423896
1	97297_at	RIKEN cDNA 150003M.F1 gene	F150003M.F1Rk	1.784033	0.892988	2.248529	0.777757	0.488629	0.042121
1	97317_at	ectonucleotide pyrophosphatase/phosphodiesterase 2	Eppa2	3.639979	3.428208	3.574533	0.926317	0.380979	1.130471
1	97326_at	cathepsin F	Ctsef	1.863342	2.169601	1.188331	0.830883	0.414111	0.525514
1	97347_at	latent transforming growth factor beta binding protein 4	Ltbrf4	1.485156	1.738748	2.810336	0.866333	1.54008	1.441478
1	97402_at	histone H5-methyltransferase	Hmt5	1.063524	0.83718	0.324241	-0.033922	0.218942	0.132286
1	97429_at	SNF related kinase	Snk	0.236889	0.939278	1.317532	0.143464	-0.185828	-0.193471
1	97487_at	serine (or cysteine) proteinase inhibitor clade E member 2	Serpine2	1.393578	0.894950	0.684328	0.353571	0.429501	0.3776
1	97496_x_at	RIKEN cDNA 633051M.23 gene	G33051M.23Rk	4.599706	5.041787	4.001069	1.440554	2.983994	0.814441
1	97510_at	monoglyceride lipase	Mglp	0.729283	0.742951	0.490909	0.289574	0.448784	0.48787
1	97521_at	argininosuccinate synthetase 1	Asf1	1.7789	0.624933	1.042401	0.175153	0.512911	0.512911
1	97533_at	Fc receptor IgG alpha chain transporter	Fcgrt	0.274283	0.278411	0.601874	0.098415	0.034907	0.178073
1	97550_at	histone deacetylase 7A	Hdac7a	0.228112	0.466606	0.489335	-0.187678	0.142475	-0.06389
1	97559_x_at	muslin 1	Msl1	4.335502	3.991866	0.508828	0.12806	0.318684	0.245252
1	97775_at	Mus musculus transcribed sequences	C-3031	0.252121	0.642208	0.216437	0.274883	0.168484	0.396176
1	97885_at	RIKEN cDNA 181000M.C1 gene	C181000M.C1Rk	0.524779	3.00325	3.270821	1.621651	0.218531	0.218531
1	97933_at	RIKEN cDNA 230009M.17 gene	M172009M.17Rk	0.642224	0.301222	0.228169	-0.026288	0.006121	0.127007
1	97983_x_at	synatan binding protein 1	Sbp1	0.244206	0.397656	0.28228	-0.11185	0.139402	-0.207188
1	97985_x_at	Mus musculus 0 day neonate myrmus cDNA RIKEN full-length enriched library clone A43004K.06 product hypothetical type 1							

The list represents 1,272 genes significantly altered between aMCs and mMCs in the order of clustering (F-gene list). The values represent expression levels normalized to those of BMSCs.

Cluster	Altitude of	Gene symbol	Gene symbol	mMC vs BMSC	aMC vs BMSC	mMC vs BMSC	aMC vs BMSC	mMC vs BMSC	aMC vs BMSC
1	98359_at	Mus musculus transcribed sequences	—	0.245000	0.387665	0.520318	0.180113	-0.107499	-0.529378
1	10434_at	Rho guanine nucleotide exchange factor (GEF7)	Arhgef7	1.257891	0.523652	1.705718	0.42613	0.224119	-0.681156
1	10454_at	paracrine	Rpm3	1.097196	0.790645	1.267114	0.186123	0.540586	0.217677
1	10465_f_t	interferon activated gene 204	Irg204	1.388213	2.063035	1.367117	0.100272	0.765521	0.621481
1	10475_at	matrin 2	Matn2	1.250154	0.913524	0.808126	0.100742	0.320218	0.130027
1	10496_at	glycogen synthase 1 muscle	Gys1	0.542811	0.7899	0.833384	0.263756	0.363083	0.373193
1	10507_at	nuclear receptor subfamily 1 group D member 1	Nr1u1	1.619945	1.394848	1.955972	0.858218	0.596853	-0.073534
1	10513_at	smoothelin	Smn3	1.673196	1.6962	1.301352	0.196027	0.413389	0.207995
1	10598_at	adipose differentiation related protein	Adip1	1.158411	1.372007	0.931091	0.879983	0.523334	0.454722
1	10599_at	hepatoma derived growth factor related protein 2	Hdgp2	1.155505	0.678072	0.104357	0.282699	-0.124888	-0.396476
1	10613_g_at	insulin-like growth factor 3	Igf2	2.277825	2.582761	3.312313	0.72494	0.915154	0.230401
1	10624_at	ADP-ribosyltransferase 3	Art3	1.437265	3.332592	1.419254	0.435912	1.216574	0.398102
1	10610_at	immunoglobulin superfamily containing leucine-rich repeat	Irbp	2.497552	1.708294	1.269685	0.307722	0.467941	0.302846
1	10603_at	RAS dexamethasone-induced 1	Rasd1	1.237424	1.148503	1.212571	-0.211691	0.586206	0.152238
1	10605_at	intercellular adhesion molecule 2	Icam2	1.351107	1.81037	1.536783	0.130055	0.52811	0.325798
1	10607_at	thymus cell antigen 1 theta	Thy1	1.358159	1.548617	2.22848	0.215748	0.805187	0.424456
1	10609_at	serine (or cysteine) proteinase inhibitor clade G member 1	Shpp1	2.569993	3.613923	3.780809	0.180848	0.896041	0.131718
1	10617_at	DNA segment Chr 10 ERATO Do 749 expressed	D10Ernt749e	1.311864	0.148825	1.316825	0.069625	0.138019	-0.746553
1	101136_at	AXL receptor tyrosine kinase	Axl	0.984148	1.12434	1.280548	0.616345	0.728944	0.702474
1	101184_at	cysteine sulfonic acid decarboxylase	Csd	1.491750	0.702931	1.078862	0.812178	0.49806	0.505427
1	101201_at	acetic preferentially expressed gene 1	Apng1	1.301330	0.542602	1.426284	-0.117547	-0.156327	0.254908
1	101202_at	MAS1 oncogene	Mer1	0.244928	0.411208	0.245497	0.020806	0.142594	0.090959
1	101442_at	regulated endonuclease specific protein 18	Reep18	0.779954	0.91699	0.320578	0.115053	0.374817	0.233727
1	101444_at	receptor (calcatin) activity modifying protein 2	Ramp2	0.985145	1.990005	0.920646	0.085843	0.258031	-0.11021
1	101453_at	phosphodiesterase 1A calcitriol-dependent	Pde1a	0.690707	0.537702	0.461043	0.267391	0.193677	0.147544
1	101475_at	suppressor of cytokine signaling 2	Socs2	1.248330	0.556774	0.67398	0.094379	0.036903	-0.917897
1	101494_at	serine (or cysteine) proteinase inhibitor clade I member 1	Serpint1	0.822428	0.802176	0.72139	0.488979	0.509959	0.55115
1	101517_at	microfilament associated protein 5	Mfab5-pending	0.26897	0.410443	0.411717	0.067614	0.196837	0.130389
1	101518_at	microfilament associated protein 5	Mfab5-pending	2.325941	1.84401	1.265354	0.2992	0.202623	0.074332
1	101524_at	solute carrier family 8 (nondictyosin/exchanger) member 1	Slat1	2.409443	2.248426	0.958831	0.021106	0.505765	0.271344
1	101545_at	ostegonin	Ogn	1.244943	1.32226	2.864023	0.506181	0.420285	0.20684
1	101642_at	carboxypeptidase E	Cpe	0.534032	0.891479	0.897547	0.273087	0.320788	-0.41486
1	101643_at	carboxypeptidase E	Cpe	6.408891	6.073041	5.782408	3.274852	4.885454	0.273381
1	101644_at	zinc finger protein 289	Zfp289	0.715337	0.456263	0.428908	0.068527	-0.082629	-0.046885
1	101685_at	special AT-rich sequence binding protein 1	Satt1	0.442867	2.122483	1.37903	0.359374	0.281796	0.127239
1	101686_at	cat eye syndrome chromosome region candidate 5 homolog	Cew5	0.564974	0.452465	0.678471	0.102148	0.468045	0.004048
1	101687_at	DNA segment Chr 18 ERATO Do 232 expressed	D18Ernt232e	0.837399	0.010689	1.153069	-0.175868	0.475888	0.320553
1	101690_at	Mus musculus cDNA clone IMAGE 6432820 partial cds	—	0.269954	0.417604	0.212412	-0.11807	0.134196	0.107633
1	101692_at	procollagen type XIV alpha 1	Col14a1	0.75821	0.513356	0.744714	0.139939	0.361512	0.433611
1	101694_at	Notch homolog 9 (Drosophila)	Notch9	0.279854	0.589179	0.597547	0.237087	0.320788	-0.41486
1	101696_at	forkhead box F2	Foxf2	1.251075	0.628714	1.16321	0.266689	0.268166	0.094054
1	101697_at	lamun alpha 5	Lam5	0.544776	0.603486	1.04748	0.16395	0.466221	0.55961
1	101698_at	calponin 1	Cpn1	4.238935	3.93245	4.129301	3.303558	1.007419	0.41208
1	101700_at	—	—	0.704111	0.580427	0.370687	-0.293	0.060228	0.401687
1	101701_at	—	—	1.612759	1.658911	1.530261	-0.114744	0.116035	0.942836
1	101702_at	—	—	0.885173	0.848433	0.915092	0.285283	0.367304	0.730259
1	101703_at	—	—	0.183192	0.163991	0.224813	-0.218848	0.078979	-0.097188
1	101704_at	—	—	0.844835	0.735641	1.507362	0.581781	0.5688	0.382486
1	101705_at	development and differentiation enhancing	Ddel1	0.100335	0.467458	0.000578	-0.246917	-0.063274	-0.376516
1	101706_at	phosphoprotein enriched in astrocytes 15	Pew15	0.458431	0.5760	0.267009	0.022451	-0.331017	-0.136748
1	101707_at	inosine 5'-phosphate dehydrogenase 2	Impdh2	0.898338	-0.357727	0.308871	-0.717353	-0.137588	-1.108209
1	101708_at	DNA segment Chr 14 ERATO Do 209 expressed	D14Ernt209e	3.247606	-0.079472	0.188378	-0.273746	-0.083791	-2.284337
1	101709_at	procollagen type VI alpha 3	Col6a3	0.373754	1.561637	0.691871	0.508762	0.261196	0.847951
1	101710_at	germinal center expressed transcript	Gct	0.058687	0.432212	0.18339	0.098873	0.03722	-0.064202
1	101711_at	zinc finger protein interacting with K protein 1	Zfk1	0.08424	0.124271	0.062888	-0.079313	-0.121973	-0.085687
1	101712_at	—	—	0.138403	0.334275	0.311678	0.150086	0.251877	0.034949
1	101713_at	ubiquitin B	Ubib	0.081422	0.188189	0.100322	0.154247	0.048292	0.026292
1	101714_at	HGF-regulated tyrosine kinase substrate	Hgr	0.087518	0.071773	0.192294	-0.359118	-0.007181	-0.061129
1	101715_at	—	—	0.321294	0.217747	0.79004	0.530083	0.268878	-0.278429
1	101716_at	histocompatibility 2 G region locus 10	H2-G10	0.016881	0.208864	0.381712	-0.242748	-0.116935	-0.063074
1	101717_at	RIKEN cDNA 1100203P17 gene	R1100203P17RA	0.43189	0.085447	0.217908	-0.313926	-0.09846	-2.339977
1	101718_at	RIKEN cDNA 1100206G01 gene	R1100206G01RA	-0.828447	0.934901	0.618288	0.657212	-1.344816	1.083322
1	101719_at	cDNA sequence BC013529	BC013529	0.11684	-0.022138	-0.010302	-0.269322	-0.19745	-0.193647
1	101720_at	RIKEN cDNA 2610102M01 gene	R2610102M01RA	1.156331	1.742861	-0.011787	-0.128261	-0.734463	-0.528356
1	101721_at	F-box only protein 21	Fbxo21	0.324917	0.335116	-0.230621	-0.745212	-0.47484	-0.47484
1	101722_at	asparagine linked glycosylation 2 homolog (yeast alpha 1-3-mannosyltransferase)	Alg2	0.130202	0.194219	0.231008	-0.221538	-0.072525	-0.078921
1	101723_at	RIKEN cDNA 1100324O3 gene	R1100324O3RA	0.380278	-0.094213	0.466882	-0.678233	-0.178058	-0.084328
1	101724_at	RIKEN cDNA 2610100E10 gene	2610100E10RA	0.394832	-0.118843	0.436687	-0.48287	-0.096866	-0.243719
1	101725_at	LMI domains containing 1	Lmi1	0.332536	0.022628	-0.031401	-0.872474	0.338336	0.823449
1	101726_at	RIKEN cDNA 110004C08 gene	R110004C08RA	2.340337	0.388978	0.268132	0.720773	-0.548221	-0.015566
1	101727_at	microtubule-associated protein 1 light chain 3	Map1lc3	0.838673	0.674382	-0.173823	-0.178662	-0.309823	-0.309823
1	101728_at	RIKEN cDNA 110006I15 gene	R110006I15RA	-0.06913	0.46604	0.308898	0.308187	-0.01171	-0.278968
1	101729_at	poly(A)-specific ribonuclease (deadenylation nuclease)	Pam	-0.048381	0.233418	0.228919	0.088961	0.258891	-0.088424
1	101730_at	protein tyrosine phosphatase 4a3	Ptp4a3	0.596801	0.436051	0.456671	-0.19138	0.584009	0.696328
1	101731_at	mitogen activated protein kinase 8 interacting protein 3	Mkip3	0.40811	0.363544	0.566337	0.586119	0.123115	-0.134124
1	101732_at	MYB binding protein (P180) 1a	Mybbp1a	0.13759	0.018443	0.183996	-0.144781	-0.012799	-0.213649
1	101733_at	—	—	0.416387	0.424793	0.178536	-0.354561	-0.38804	-0.026247
1	101734_at	—	—	0.40474	-0.130493	0.153149	-0.241978	-0.257133	-0.588888
1	101735_at	neuronal precursor cell expressed developmentally down-regulated gene 4	Nepcd	0.505248	1.32895	0.430483	-0.180024	-0.225723	-0.310395
1	101736_at	—	—	0.041149	0.07487	0.112389	-0.188584	-0.83237	-0.220748
1	101737_at	CHK2 checkpoint homolog (S. pombe)	Chk2	0.353378	0.688941	0.370337	0.282764	0.0665	-0.370329
1	101738_at	irin-1 like 1	Irin1	0.171493	0.028728	0.074208	-0.258806	-0.087391	-0.138394
1	101739_at	hepatocellular carcinoma 2 class II locus D1a	H2-Cd49	1.32425	0.54118	0.188258	-0.187184	-0.34744	-0.13304
1	101740_at	ribosomal protein S24	Rplp24	0.218701	0.243117	0.181433	-0.216481	0.021458	-0.089279
1	101741_at	histidine decarboxylase	Hdc	1.00852	-0.00235	-0.120703	-0.14289	-0.414882	-0.414882
1	101742_at	mast cell protease 8	Mcp8	0.105959	0.900489	0.507458	-1.670573	-0.587374	0.15464
1	101743_at	galactin	Gan	0.815432	1.217017	-0.048328	-1.457837	-1.897278	0.264541
1	101744_at	nicotinyl-Coenzyme A desaturase 1	Ncd1	1.322099	0.97249	0.972441	-0.63584	-0.896743	-0.917842
1	101745_at	steryl-Coenzyme A desaturase 1	Scd1	2.364119	1.549664	0.070297	-0.028251	-1.678211	1.588003
1	101746_at	golg SNAP receptor complex member 2	Gosr2	0.819419	0.157091	-0.344809	-1.189577	-1.449206	-0.614802
1	101								

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 BMSCs.

Cluster	Allylics id	Gene name	Gene symbol	LMC1 vs BMSC	sMC2 vs BMSC	mMC1 vs BMSC	mMC2 vs BMSC	mMC3 vs BMSC	mMC4 vs BMSC
2	95395_at	RIKEN cDNA 6130022A11 gene	R130022A11RA	0.355933	0.434448	-0.3722	-0.261366	-0.505997	-1.088926
2	95698_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 7	Ndufb7	-0.40018	-0.202824	0.184425	0.346571	-0.434448	-0.119328
2	95754_at	membrane-bound transcription factor protease site 1	Mbtq1	0.074017	0.175161	0.485309	-0.290077	0.013652	-0.094278
2	96207_at	RIKEN cDNA 2600014B10 gene	2600014B10RA	-0.300363	0.335548	0.297156	-0.15411	-0.07084	0.753437
2	96218_at	farnesyltransferase CAAAX box beta	Farb	0.225474	0.006262	-0.040712	-0.240783	0.218214	-0.103084
2	96252_at	RIKEN cDNA 240001E08 gene	240001E08RA	0.364191	0.429471	0.209696	-0.13158	-0.273878	0.0064872
2	96695_at	N-terminal Asn amidase	Nam1	0.471749	0.474749	0.384359	0	-0.00702	-0.405826
2	96694_at	T-cell leukemia/lymphoma 1B 1	Tl0101	0.154223	0.109814	0.182037	-0.181703	-0.012051	-0.162238
2	96924_at	RIKEN cDNA 9430077D24 gene	9430077D24RA	0.098518	0.297862	0.300718	-0.191425	-0.562882	0
2	96948_at	quinoid hydroxyindole reductase	Qlpr	0.037344	0.21441	0.563723	-0.073934	-0.695547	-0.736825
2	97197_at	elac1 homolog 2 (E. coli)	Elac2	0.037893	0.247367	0.132457	-0.137618	-0.124203	-0.075041
2	97795_at	UBX domain containing 2	Ubx2c	1.214652	1.124868	0.801402	0.052486	-0.204332	-0.565696
2	97374_at	RIKEN cDNA 2810025M15 gene	2810025M15RA	0.058438	0.194796	0.054904	-0.083781	-0.154726	-0.190238
2	97473_at	---	---	0.451743	0.879858	-0.196245	-1.962451	-1.630149	-0.619934
2	97794_at	sem5 domain immunoglobulin domain (Ig) and GPI membrane anchor (semaphorin) 7A	Sema7a	0.046257	0.060194	0.012361	-0.141006	-0.080941	-0.262581
2	97887_at	Mus musculus mRNA for mRNAA0620 protein	---	0.047336	0.061036	0.006184	-0.302004	-0.170203	-0.330308
2	98063_at	glycosylation dependent cell adhesion molecule 1	Glycam1	0.017393	0.244334	0.306712	-0.138556	-0.06956	-0.08471
2	98405_at	serine (or cysteine) protease inhibitor clade B member 9	Scpirb9	0.449300	0.133873	0.489331	-0.975081	0.124037	-0.451417
2	98503_at	sarcolenin associated protein	Smap	0.579144	0.711444	0.068919	-0.67422	-1.500608	-1.375456
2	98504_at	novel nuclear protein	Nucp1	0.407197	0.608345	0.184487	0.077782	-1.486104	-0.813145
2	98505_at	ATP binding cassette sub-family D (ALD) member 1	Aldc1	0.265801	0.182117	0.097456	-0.25037	0.044102	-0.202419
2	99051_at	S100 calcium binding protein A4	S100a4	0.013689	0.130574	0.111441	0.005745	-0.347487	-0.101788
2	99096_at	cystatin C	Cst3	1.165593	0.780889	0.918469	-0.4088	-0.948133	-1.543234
2	99676_at	anti-ile adaptor	Ila	-0.047611	0.226007	-0.038665	-0.28201	-0.300891	-0.177551
2	99949_at	double C2 alpha	Dc2a	0.332159	0.747294	0.278242	-0.240296	-0.224485	-0.370333
3	100033_at	mus-homolog 2 (E. coli)	Msh2	0.157113	-0.520637	-0.000501	-1.399841	-1.86713	-1.944992
3	100148_at	CCTC-binding factor	Ctcf	0.083006	-0.01939	-1.789787	-1.951677	-2.106437	-1.721837
3	100151_at	transcription factor 1	Tcf1	-1.38446	1.115445	-1.883478	-1.983502	-2.102689	-1.907156
3	100468_g_at	lymphoblastoid leukemia	Lpl1	4.387078	-3.892293	-3.614078	-5.144748	-4.521369	-6.08373
3	100508_at	mannose binding lectin (Drosophila)	Mblg	-0.878217	-0.318637	-0.658332	-1.164551	-0.964116	-0.990335
3	100530_at	RIKEN cDNA 2410041A17 gene	2410041A17RA	-2.779523	-1.985776	-1.844119	-3.422508	-3.308111	-3.420921
3	100566_at	muslin-like growth factor binding protein 5	lglfb5	-0.574568	0.097201	-0.472131	-2.214891	-1.444704	-2.809693
3	100616_at	centrinome autoantigen A	Centpa	-0.490484	-0.305929	-0.461614	-0.708296	-0.595912	-0.888953
3	100685_at	NIMA (never in mitosis gene a)-related expressed kinase 2	Nak2	-1.43239	-1.586229	-1.415381	-1.701874	-1.614487	-1.817133
3	100691_at	oral host factor C1	Hcf1	-0.316513	-0.289906	-0.249293	-0.555202	-0.485322	-0.558966
3	101000_at	histone decarboxylase antisense 2	Oaz2	-0.335306	-0.704808	-0.781486	-1.27479	-0.200005	-1.353176
3	101104_at	RIKEN cDNA 2410026X10 gene	2410026X10RA	-2.848673	-2.782719	-2.573878	-3.681044	-2.802871	-4.059209
3	101247_at	integral membrane protein 28	Imt28	-0.801282	-0.81165	-0.711999	-0.905303	-1.745804	-1.898622
3	101487_f_at	lymphocyte antigen 8 complex locus B	L8b	-0.361926	-3.38451	-0.045481	-3.79799	-4.70304	-4.731715
3	101610_at	proteasome (prosome macroprol) 28 subunit alpha	Psmf1	-2.571799	-1.094795	-2.117036	-3.22809	-2.547001	-3.27061
3	102033_at	testis specific protein kinase 1	Tskp1	-0.337659	-0.449221	-0.422193	-1.094399	-0.585708	-0.81874
3	102279_at	RIKEN cDNA 130004C08 gene	130004C08RA	-0.695248	0.099548	0.071294	-1.137271	-1.142815	-1.131672
3	102304_at	RIKEN cDNA 2610209L14 gene	2610209L14RA	-1.920216	2.510341	-1.807883	-2.545668	-2.471822	-3.864487
3	102407_at	mast cell protease 5	Mup5	-0.234568	-0.107507	-0.994668	-4.560541	-2.298076	-1.625887
3	102408_g_at	mast cell protease 5	Mup5	-2.818439	-2.547011	-3.703756	-5.524831	-4.313645	-6.688329
3	102791_at	proteasome (prosome macroprol) subunit beta type 8 (large multifunctional protease 7)	Psm8	-2.018910	-3.116742	-3.747387	-4.300658	-2.803206	-4.513848
3	102865_at	RIKEN cDNA 621816A06 gene	621816A06RA	-1.485013	-0.303843	0.047788	-1.062804	-0.673696	-0.627804
3	103070_at	protein tyrosine phosphatase non-receptor type substrate 1	Ptprs1	-1.428005	-1.427845	-1.33994	-1.653258	-1.647373	-1.616602
3	103101_at	TAR (HIV) RNA binding protein 2	Tarbp2	-0.190449	0.03412	0.357837	-0.299421	-0.256355	-0.450024
3	103223_at	RIKEN cDNA 5830A09C15 gene	5830A09C15RA	-1.284421	-1.581992	-1.251197	-2.007339	-1.918804	-2.010443
3	103349_at	Yamaguchi sarcoma viral (yeast-1) oncogene homolog	Lyn	-0.012335	-1.455002	-2.024665	-3.263704	-3.299528	-3.248974
3	103510_at	colicin 12	Colc12	-2.070184	-1.803252	-2.00872	-2.401011	-2.242446	-2.314951
3	103567_at	RIKEN cDNA 2010313D22 gene	2010313D22RA	0.060742	0.095809	-0.104347	-0.337873	-0.104347	-0.513607
3	103578_at	target of mytil homolog (chicken)	Tmt1	-0.696148	-0.246073	-0.499706	-0.748575	-0.748303	-1.07841
3	103834_at	serine carrier family 8 (neurotransmitter transporter GABA) member 13	Sclt13	-0.348583	-0.377884	-0.500387	-0.805923	-0.52894	-0.8548
3	103935_at	ATPase Ca++ transporting ubiquitous	Alpca3	-0.431783	-0.395057	-0.493472	-1.044882	-2.11495	-1.404318
3	103971_f_at	purinergic receptor P2X ligand-gated ion channel 1	P2rx1	-0.534370	-0.083641	-0.997245	-1.064314	-1.45876	-1.779019
---	---	---	---	-0.400462	-0.884053	-0.409206	-0.922112	-0.910251	-0.748182
---	---	---	---	0.702347	0.24847	-0.737636	-1.548718	-1.148594	-1.026602
---	---	---	---	-1.003002	-0.491653	-1.447731	-3.345451	-2.18959	-1.627032
---	---	---	---	-0.285818	-0.707491	-0.478061	-1.11098	-0.888999	-2.19414
---	---	---	---	-0.103088	0.121914	-0.344717	-0.631582	0.36832	1.734682
---	---	---	---	0.025714	0.363137	0.03833	-0.57172	-0.48727	-0.404642
---	---	---	---	-0.467845	0.121572	-0.006882	-0.927885	-1.111036	-0.900976
---	---	---	---	-0.591779	-0.424781	-0.824721	-1.236278	-1.098971	-0.940755
---	---	---	---	-1.046023	0.760279	-1.125404	-2.297357	-1.235356	-1.741621
---	---	---	---	-1.173087	-0.878637	-1.178035	-1.386556	-1.24231	-1.49494
---	---	---	---	-0.378215	-0.068586	-0.061132	-0.536100	-0.475018	-0.849727
---	---	---	---	-0.360528	-0.735751	-0.232756	-1.003958	-1.244302	-1.440979
---	---	---	---	-1.70789	-2.202215	-2.011644	-2.660382	-2.474089	-2.96150
---	---	---	---	0.528307	0.502042	0.666816	-1.01788	0.81189	0.957332
---	---	---	---	-0.146015	-0.197631	-0.591384	-0.277857	-0.459606	-0.32322
---	---	---	---	-1.248449	-1.120125	-1.246652	-1.615815	-1.531187	-1.449570
---	---	---	---	-0.283415	0.023438	-0.192229	-0.044244	-0.349796	-0.490300
---	---	---	---	-1.768331	-1.702208	-1.171037	-2.058739	-1.921583	-1.892421
---	---	---	---	-0.367966	-0.528851	-0.500766	-1.277482	-1.186159	-0.807533
---	---	---	---	0.149949	-0.583489	-0.09861	-1.030477	-0.811997	-0.98777
---	---	---	---	-0.079791	-1.294707	-1.296368	-1.425247	-1.191345	-3.262554
---	---	---	---	-0.187995	-0.260762	-0.069959	-0.489715	-0.364578	-0.428911
---	---	---	---	-1.920215	-0.050909	0.236483	-0.600291	-3.18327	-3.864403
---	---	---	---	0.212474	-0.414264	0.444847	-0.655704	-0.670007	-0.895752
---	---	---	---	0.169776	0.018335	-0.067235	-0.38260	-0.26184	-0.202206
---	---	---	---	0.220783	-1.632008	-0.38736	-2.033883	-2.27098	-1.400289
---	---	---	---	-0.180274	-0.301246	-0.839665	-0.853283	-1.230589	-1.34297
---	---	---	---	-0.18844	-0.424	-0.184296	-0.949296	-2.80012	-0.683882
---	---	---	---	-1.348177	-1.35999	-1.819387	-2.338811	-1.619397	-0.929501
---	---	---	---	-0.359120	0.227131	-0.613475	-0.94248	-1.887719	-1.116878
---	---	---	---	0.049133	1.202338	-1.569718	-2.118458	-3.183265	-1.70823
---	---	---	---	-1.918782	-0.450909	-1.299332	-3.285407	-3.43526	-3.437257
---	---	---	---	-0.382246	0.104616	-0.300008	-0.823116	-0.685883	-0.854332
---	---	---	---	-0.247478	0.28271	-0.394296	-0.102196	-0.616683	-0.50481
---	---	---	---	-0.378134	0.344685	-0.404284	-1.353079	-1.033531	-2.891708
---	---	---	---	-0.433718	-0.179138	-0.562207	-0.916887	-1.719916	-1.250907
---	---	---	---	-0.757586	-1.088969	-1.251961	-2.260165	-2.848504	-3.789578
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The table represents 1372 genes significantly altered between sMCs and mMCs in the order of clustering (Figure 5a). The values represent expression levels normalized to those of sMCs.

Cluster	AlphA1a ID	Gene name	Gene symbol	sMC vs. sMC	sMC vs. mMC	mMC vs. mMC	sMC vs. mMC	sMC vs. mMC	sMC vs. mMC	sMC vs. mMC
3	93471_f	solute carrier family 4 sodium bicarbonate cotransporter member 7	Slc4a7	-0.31968	-1.77419	-1.90274	-3.35969	3.38822	-3.49951	
3	93593_f	epithelial membrane protein 3	Emp3	-1.83032	-2.54284	-2.03033	-3.87456	-4.31743	-4.23019	
3	93504_f	immunoglobulin superfamily member 4	Igfb4	-0.12319	-1.75018	-1.82073	-2.82846	-2.34887	-1.94238	
3	93623_f	glycogen muscular dystrophy	Gmd1	-0.81996	0.02286	0.05816	-0.49886	-0.28702	-0.14988	
3	93714_f	histocompatibility 2 Q region locus 7	H2-Q7	-0.30011	-0.19379	0.23718	-0.17181	-1.02713	-0.86676	
3	93762_f	protein phosphatase 2A regulatory subunit B (PP2A)	Ppp2r4	-0.05274	-0.00922	0.05209	-0.18120	-0.78218	-0.48825	
3	93709_f	expressed sequence A1316787	A1316787	-0.878374	-0.89866	-0.43811	-1.23253	-0.16257	-1.21287	
3	93804_f	solute carrier family 2 (facilitated glucose transporter) member 3	Slc2a3	-0.71839	-0.56195	0.70243	-1.23710	-0.74333	-1.32710	
3	93806_f	SH3-binding domain glutamic acid-rich protein like	Sh3bp1	-1.42621	-1.0525	2.35715	-3.87045	-2.84471	-2.78374	
3	93923_f	eukaryotic translation initiation factor 3 subunit 9 (eIF3)	Eif3d	-1.65326	-0.96594	1.23221	-1.87147	-1.88615	-1.83348	
3	94015_f	TH1-like homolog (Drosophila)	Th1	-0.485037	-0.4672	-0.34872	-0.850091	-0.80331	-1.07809	
3	94069_f	ring finger protein 14	Rfx14	-0.24564	-0.08723	0.05649	-0.73421	-0.30262	-0.58871	
3	94209_f	Rab receptor 1 (prenylated)	Rabarp1	-0.07843	-0.70201	-0.37329	-0.17793	-1.88049	-1.34320	
3	94204_f	annexin A3	Anxa3	-0.70781	-1.73403	-1.08656	-2.2006	-2.02318	-1.69225	
3	94500_f	cleavage and polyadenylation specific factor 5	Cpsf5	-0.37021	-0.87208	-0.35188	-1.92108	-1.65284	-1.40575	
3	94535_f	adducin 1 (alpha)	Adst1	-0.73483	-0.96450	-0.96153	-1.38338	-1.02307	-1.16120	
3	94539_f	tubulin beta 2	Tuba2	-2.128572	-1.36019	-2.00875	-3.99987	-3.54874	-2.49722	
3	94578_f	expressed sequence AL022810	AL022810	0.22608	0.018972	-0.31578	0.156405	-0.421223	-0.424421	
3	95035_f	mitogen activated protein kinase kinase 1	Mek2	-0.02334	-0.544865	-1.20044	-1.48132	-1.74878	-1.98126	
3	95049_f	small nuclear ribonucleoprotein D2	Snrdp2	0.40821	-0.21302	-0.31282	-0.03376	-1.36919	-2.88019	
3	95097_f	ARF10 actin-related protein 10 homolog (S. cerevisiae)	Acr10	-0.138759	-1.23716	-1.84275	-1.73531	-2.62444	-3.22145	
3	95129_f	nuclear receptor co-repressor 2	NcoR2	-1.188737	-0.28111	0.78031	-2.12608	-2.12344	-1.88218	
3	95140_f	RIKEN cDNA 523040324 gene	D323040324Rk	-0.489795	0.282732	-0.25471	-0.821705	-0.33082	-1.65884	
3	95143_f	FXYD domain-containing ion transport regulator 6	Fxyd6	-0.37832	-0.89286	-1.88183	-2.59148	-2.96110	-2.86022	
3	95147_f	DNA segment Chr 11 Wayne State University 68 expressed	D11WayState	0.088839	0.000641	0.04023	0.438406	-0.49184	-0.08886	
3	95180_f	RIKEN cDNA 583041710 gene	583041710Rk	-0.923887	-0.821356	-0.628242	-1.028771	-1.07188	-1.314071	
3	95191_f	prostaglandin-endoperoxide synthase 1	Cyc11p	-0.320623	-0.569008	-0.758778	-0.973862	-0.791421	-1.009141	
3	95652_f	rich domain containing 2	Rchd2	-0.025382	0.495234	-0.831555	0.211342	-2.91891	-1.94718	
3	95682_f	damage specific DNA binding protein 1	Dsbp1	-0.003075	-0.553043	-0.268813	-1.201439	-1.486419	-0.71741	
3	95731_f	Mus musculus Sestrin 1 mRNA (cDNA clone MGC:87136)	Sestn1	-1.1487	-0.899576	-2.81046	-2.819743	-3.394539	-3.383363	
3	95733_f	IMAGE 54145211 complete cds	IMAGE54145211	-0.169384	-0.701404	-0.85729	-1.551961	-1.200789	-1.35468	
3	95945_f	RIKEN cDNA 2010221M03 gene	2010221M03Rk	-1.546671	-1.537317	-1.489175	-3.037994	-1.74627	-1.735004	
3	96073_f	D4 zinc and double PHD fingers family 2	Dpf2	-0.483082	-0.320855	-0.301178	-0.576659	-0.52352	-0.58881	
3	96188_f	low-density lipoprotein receptor-related protein 10	Lrp10	-0.458862	0.050349	-0.434262	-0.523675	-0.93581	-1.181006	
3	96215_f	Mus musculus cDNA clone MGC:67258 IMAGE:6413648 complete cds	IMAGE6413648	-0.713073	-0.381105	-0.380627	-1.458787	-2.088701	-2.387202	
3	96218_f	RIKEN cDNA 0610036C21 gene	0610036C21Rk	-0.540306	-0.300849	-0.487348	-1.020005	-1.026907	-1.117688	
3	96378_f	Sjogren's syndrome/keratoconjunctivitis sicca 1 homolog (human)	Ssca1	-0.562255	-0.997078	-0.595744	-0.805113	-0.830706	-1.03480	
3	96734_f	synaptotagmin 2 binding protein	Syngbp2	-0.186579	-0.320054	-0.328889	-0.809992	-0.523889	-0.610791	
3	96744_f	acid phosphatase 8 (lysosomal) gene	Acph8	-0.283297	-0.853548	0.050488	-0.90172	-1.088214	-1.348991	
3	96750_f	RIKEN cDNA 071007A14Rk gene	071007A14Rk	-0.445431	-0.548095	-1.421602	-1.82704	-2.01143	-2.02938	
3	96757_f	membrane bound C2 domain containing protein	Mbc2	-1.847908	-0.155249	-0.871023	-2.205005	-2.06695	-2.20291	
3	96810_f	LIM domain only 2	Lmo2	-0.522117	-0.858336	-0.838884	-1.766557	-1.373337	-1.481181	
3	96852_f	protein kinase cAMP dependent regulatory type I alpha	Pkaria1	0.260287	-0.117072	-0.195352	-1.540101	-1.473093	-0.851883	
3	97175_f	MHC (A/GA)H-2K-f class I antigen	A2M	-0.38918	-0.233781	-0.157221	-0.712338	-0.786471	-0.598791	
3	97190_f	copine 1	Copn1	0.103316	0.418288	0.65783	0.880763	0.848888	0.869448	
3	97205_f	RIKEN cDNA 2700079K059Rk gene	2700079K059Rk	0.708137	-0.11257	-0.355611	-0.364547	-1.23227	-0.943891	
3	97315_f	RIKEN cDNA 2610028L19 gene	2610028L19Rk	0.4158085	-0.190316	-0.045109	-0.647288	-0.894173	-1.115419	
3	97356_f	telomerase	Lpn1	-1.10214	-0.13888	-0.462087	-1.472833	-1.200693	-1.385044	
3	97484_f	RIKEN cDNA 2210402C23 gene	2210402C23Rk	-0.219672	-0.130525	-0.959565	-2.11023	-2.815347	-2.815347	
3	97540_f	histocompatibility 2 D region locus 1	H2-D1	-0.57242	-0.383259	-0.507275	-1.271898	-1.626281	-1.31128	
3	97844_f	regulator of G-protein signaling 2	Rgs2	-1.459644	-0.87048	-1.795834	-3.20146	-2.974997	-4.588002	
3	98010_f	nuclear factor erythroid derived 2	Nfe2l2	-0.571584	-0.380276	-0.884778	-1.562443	-1.488721	-1.83571	
3	98052_f	tailed early in factor-1 homolog (S. cerevisiae)-like	Tef1l	-0.230209	-0.326165	-0.156528	-0.887222	-0.816683	-1.063898	
3	98084_f	ADP-ribosylation factor-2 binding protein	Arb2p	-0.081027	-0.028411	-0.061403	-0.381288	-0.325205	-0.154818	
3	98125_f	RIKEN cDNA 1110025O16 gene	1110025O16Rk	-0.501648	-0.288598	-0.358887	-1.08123	-1.21802	-0.624087	
3	98154_f	RIKEN cDNA 130004C11 gene	130004C11Rk	-1.671739	-0.961711	-0.900018	-2.04174	-2.94901	-3.140132	
3	98155_f	cytokine receptor-like factor 3	Crlf3	-1.318519	-1.31248	-1.289	-1.918881	-1.910911	-1.85544	
3	98156_f	histocompatibility 2 Q region locus 2	H2-Q2	-0.748348	-0.571807	-0.45325	-2.251839	-2.381377	-2.815347	
3	98235_f	erythroid differentiation regulator 1	Erd1	-0.35435	-0.670485	-0.845106	-1.18119	-2.57016	-3.344308	
3	98635_f	DNA segment Chr 11 Kl. Morike 35	D11Morike35	0.204808	0.018299	-0.184444	-0.282372	-0.335702	-0.25211	
3	98894_f	RIKEN cDNA 2810018F04 gene	2810018F04Rk	-0.982881	-0.572918	-0.231593	-1.727575	-1.400834	-1.78702	
3	98953_f	transient receptor potential cation channel subfamily V member 2	Trpv2	0.479326	0.102591	-0.874249	-1.823256	-1.708781	-1.518414	
3	99040_f	solute carrier family 6 (neurotransmitter transporter serotonin) member 4	Scl6a4	0.714386	0.615839	0.030439	-1.797803	-1.941511	-2.02748	
3	99055_f	Max protein	Max	-1.187228	-1.316884	-1.320518	-1.628706	-1.840418	-2.27484	
3	99109_f	immediate early response 2	Ier2	-2.819482	-3.540883	-2.75705	-3.921514	-3.4737	-4.070328	
3	99462_f	topoisomerase (DNA) II beta	Rpb2b	-0.298737	-0.737496	-0.883837	-0.897225	-2.22169	-1.374204	
3	99593_f	spodin	Spn1	-0.040268	0.214531	-0.30561	-0.319105	-0.410181	-0.327511	
3	99596_f	guanine nucleotide binding protein alpha inhibiting 2	Gnai2	-0.279819	-0.738066	-0.587777	-1.832073	-1.322035	-1.07875	
3	99597_f	guanine nucleotide binding protein alpha inhibiting 2	Gnai2	-0.327874	-1.218756	-0.544898	-1.781581	-1.346025	-1.07875	
3	99598_f	guanine nucleotide binding protein alpha inhibiting 2	Gnai2	-0.390026	-0.897737	-0.545066	-1.17828	-0.86006	-1.02882	
3	99633_f	neurochordin	Nchrp	-0.677222	-0.252548	0.47819	-0.82687	-0.62881	-1.271324	
3	99669_f	lectin galactose binding soluble 1	Lgals1	-1.75598	-1.99279	-1.709212	-4.216014	-3.842372	-4.356648	
3	99670_f	ADFX	ADFX							
3	99671_f	Gasp(MuM)	Gasp							
3	10002_f	glyoxaldehyde-3-phosphate dehydrogenase	Gsd	-0.886116	-0.678917	-0.892252	-1.01298	-1.180488	-1.199237	
3	10004_f	Strom	Strom	0.214771	0.174873	0.134524	0.150002	0.164362	0.112838	
3	100034_f	serine (or cysteine) proteinase inhibitor clade B member 5	Serpib5	-0.006385	0.051363	0.142333	0.680802	0.182006	0.4153	
3	100043_f	RIKEN cDNA 2310020A21 gene	2310020A21Rk	0.213783	0.431209	0.473298	0.657725	3.470247	0.988428	
3	100090_f	lysosomal dehydrogenase family 1 subfamily A1	Aldh1a1	0.1374	0.098878	0.1374	0.356651	0.27888	0.283308	
3	100088_f	glycosylated membrane glycoprotein 2	Lamp2	0.70509	1.725841	1.853386	4.73889	2.887189	3.894742	
3	100130_f	lysosomal membrane glycoprotein 1	Lamp1	0.309321	-0.096308	0.280297	1.31124	1.08421	0.388817	
3	100278_f	cyclin-dependent kinase inhibitor 1B (P27)	Cdkn1b	0.231045	0.33825	0.283292	0.948227	0.781142	0.507555	
3	100336_f	bone gamma carboxylglutamate protein 1	Bglap1	0.50744	0.475118	0.705653	0.842208	0.70073	1.233004	
3	100426_f	lamin gamma 2	Lamc2	0.704904	0.468423	0.750755	1.291347	1.418277	1.537861	
3	100501_f	ATPase H(+)-K(+) transporting beta polypeptide gastric specific	Atpa4b	1.465458	0.945758	2.088517	4.818454	3.857889	2.928297	
3	100571_f	lysosomal-associated protein transmembrane 4B	Lamp4b	1.388745	1.045103	0.868394	1.980578	2.190527	1.860319	
3	100600_f	CD24 antigen	Cd24a	2.479525	3.38354	2.478128	4.513485	3.994413	4.401381	
3	10072									

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

Cluster	Affinity	Gene name	Gene symbol	aMC1 vs BMC	aMC2 vs BMC	aMC3 vs BMC	mMC1 vs BMC	mMC2 vs BMC	mMC3 vs BMC
4	152042_f	Mus musculus cDNA clone MGC 31332 IMAGE 4224574 complete cds	—	0.425922	0.233473	0.389991	1.134753	0.847742	0.501332
4	152114_f	ubiquitin specific protease 46	Usp48	0.251264	0.434442	0.283863	0.817048	0.768528	0.925208
4	152274_f	liver-specific bHLH-Zip transcription factor	Lach3-pending	0.473831	0.519738	0.436496	0.872643	1.107102	1.030763
4	152331_f	alkyllye dehydrogenase family 3 subfamily A1	Alch3a1	0.025102	0.079459	0.134643	0.783518	0.967086	1.130742
4	152348_f	Clq and tumor necrosis factor related protein 1	C1qrf1	0.385227	0.206356	0.351836	1.288023	1.62103	1.107798
4	152374_f	Mus musculus cDNA clone IMAGE 5687890 partial cds	—	-0.044495	-0.03974	0.07012	0.467284	0.455453	0.382633
4	152404_f	annexin A10	Anxa10	0.640479	1.332669	1.242244	0.557735	1.21874	0.273348
4	152550_f	keratin complex 1 acidic gene 19	Krt19	2.481556	1.004707	1.931461	6.528964	5.745304	7.399216
4	152553_f	esterase 10	Esr10	-0.192618	0.879999	-0.607466	1.579138	1.677823	1.934173
4	152642_f	carbonic anhydrase 2	Ca2	1.534991	2.499131	1.614724	0.949887	5.938709	6.421921
4	152658_f	forkhead box Q1	Foxq1	0.410391	1.023212	0.385587	2.016281	1.675174	2.813244
4	152697_f	forkhead box A1	Foxa1	1.743791	1.430374	1.622756	3.354813	4.126479	2.789112
4	152759_f	lamin beta 3	Lamb3	1.385631	0.30362	0.436811	1.882296	1.866691	2.387041
4	152770_f	S100 calcium binding protein A6 (calyculin)	S100a6	0.778265	0.022366	0.796183	1.62883	2.039487	3.371468
4	152802_f	keratin complex 1 acidic gene 17	Krt17	1.018959	0.207475	0.929299	0.51109	0.48556	0.629236
4	152866_f	histocompatibility 3 class 1 antigen A alpha	H2-As	1.022740	-0.257909	0.178353	0.927777	1.747362	2.201594
4	152920_f	paired-like homeodomain transcription factor 1	Plex1	0.817018	1.121867	0.575562	2.484498	1.391186	1.653289
4	153045_f	ATP-binding cassette sub-family D (ALD) member 3	Abcd3	1.733071	2.159259	1.189903	4.129138	3.026226	3.586054
4	153102_f	open reading frame 9	ORF9	-0.042395	0.080999	0.383253	0.882966	3.003613	4.961817
4	153162_f	NK6 transcription factor related locus 2 (Drosophila)	Nkxv-2	0.56997	0.319296	0.895981	0.845452	2.016478	1.887058
4	153352_f	tubulifactor 2 (nematostyle protein 1)	Tf2	2.913699	0.812447	0.513358	3.240271	6.688938	7.144543
4	153475_f	RIKEN cDNA A031426K16 gene	A031426K16Rk	0.485191	0.674465	0.453085	1.761506	1.110698	2.848821
4	153479_f	RIKEN cDNA A930031D01 gene	A930031D07Rk	0.983811	1.064883	0.3885	1.462203	0.209788	1.278714
4	153500_f	systeme and glycine-rich protein 2	Cap2	0.221963	0.291441	0.436743	1.120434	0.468796	0.781717
4	153747_f	bcl2-like-induced transcript 1	Blcl2-1-pending	0.882911	0.814851	0.333766	1.90244	1.239878	2.385110
4	153815_f	RIKEN cDNA 061004 L09 gene	061004L09Rk	-0.314448	0.380265	-0.296113	0.943137	0.827873	0.181705
4	153848_f	thiamin pyrophosphokinase	Tpk1	0.097929	-0.028367	0.042813	0.312525	0.21521	0.270414
4	153889_f	forkhead box A2	Foxa2	0.33937	0.176456	0.522341	1.063808	0.845293	0.503182
4	153950_f	phosphatidylinositol 3-kinase C2 domain containing gamma polypeptide	Pi3k2g	0.347049	0.588997	0.517128	0.719328	0.897086	1.243807
4	154108_f	ATPase H+K+ transporting alpha polypeptide	PIA3r2	0.128897	0.247048	0.255792	0.605079	0.603813	0.355204
4	154183_f	RIKEN cDNA 572045J04 gene	Atp4a	0.630945	1.119881	1.509980	4.750172	2.324792	3.262225
4	154247_f	RIKEN cDNA 1810024J12 gene	1810024J12Rk	0.075901	0.377536	-0.003412	4.190506	3.91813	5.258745
4	154260_f	RIKEN cDNA 1810024J12 gene	1810024J12Rk	-0.244341	0.093384	0.188828	2.388615	0.586795	0.496512
4	154270_f	keratin complex 1 acidic gene 18	Krt18	1.09912	0.190258	0.501956	3.248191	2.40927	4.84289
4	154285_f	histocompatibility 2 class 1 antigen E beta	H2-Eb1	0.149187	0.02868	0.040335	0.825262	1.016384	0.744524
4	154324_f	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	0.383001	1.133959	0.410462	1.473541	1.629428	1.876113
4	154350_f	16kDa dehydrogenase cytochrome 1	Nppl1	0.371475	0.04216	0.148226	0.355459	0.919172	1.273394
4	154370_f	oncospin induced transcript 1	Oit1	0.717096	0.090331	1.726748	4.770077	0.481911	4.411174
4	154458_f	casease 6	Case6	0.62915	0.439919	1.090594	3.366531	1.427214	2.124689
4	154473_f	RIKEN cDNA 1810010L20 gene	1810010L20Rk	0.378555	-0.101784	-0.385398	1.721429	1.81264	2.289633
4	154501_f	serpin/thrombin-1-phosphate phosphatase 1	Stpp1	0.489336	0.518642	0.418902	1.254208	0.874031	1.498349
4	154531_f	RIKEN cDNA 1650001M02 gene	1500001M02Rk	0.168223	-0.208204	0.077456	2.562881	0.534453	0.205647
4	154728_f	mast cell protease 1	Mcp1	0.788374	0.817718	0.695644	1.092272	1.900768	1.991503
4	154729_f	mast cell protease 1	Mcp1	0.389397	0.382135	0.274317	1.183788	1.430294	2.889972
4	154752_s	Ski-like	Ski1	0.181948	0.095796	0.148026	0.351783	0.389808	0.297970
4	154765_f	retinol dehydrogenase 13 (all trans and 9-cis)	Rdh13	0.519568	0.370442	0.359112	0.196441	0.438222	0.520945
4	154770_f	DNA segment Chr X immunex 46 expressed	Dx1mxf6e	0.152042	0.265161	0.251052	0.807889	1.048191	1.292886
4	154831_f	cathespin B	Ctzb	1.564976	1.375283	1.527796	2.339045	1.870522	2.795952
4	154907_f	RIKEN cDNA 1110001J03 gene	1110001J03Rk	0.254216	-0.320245	0.125402	0.200951	1.076629	0.796829
4	154916_f	cytochrome P450 51	Cyp51	0.079108	0.167063	0.187417	0.302892	0.535357	0.625861
4	154951_f	RIKEN cDNA 1810030A06 gene	1810030A06Rk	0.643747	0.24467	0.261317	1.676401	0.763227	0.962508
4	155064_f	Acas2	Acas2	2.274529	2.724733	2.120853	3.68899	4.065491	4.0414
4	155088_f	DnaJ (Hsp40) homolog subfamily A member 2	Dnaj2	0.175418	0.302037	0.387795	1.573915	0.955137	1.961788
4	155206_f	chaperin	Chp1	1.484857	1.786446	1.895632	3.989597	1.911477	3.388871
4	155259_f	endoplasmic reticulum (ER) to nucleus signaling 2	Ensc2	0.284436	0.381988	0.498922	1.684464	1.96719	1.68149
4	155440_f	RIKEN cDNA 281043Z1 J2Rk gene	281043Z1J2Rk	0.441311	0.860037	0.218063	1.742045	1.381526	1.907404
4	155472_f	ubiquitin-cytochrome c reductase binding protein	Ucbrp	0.408838	0.581712	-0.85181	1.027795	1.210713	1.164089
4	155520_f	RIKEN cDNA 2310061B02 gene	2310061B02Rk	0.615199	0.242369	0.097438	1.280413	0.108887	1.738848
4	155554_f	cDNA sequence BC018601	BC018601	0.17068	0.1261	0.183708	0.872828	0.382248	0.689988
4	155603_f	glycine decarboxylase	Gdc1	0.132516	0.21828	0.098889	0.410327	0.650536	0.795920
4	155621_f	RIKEN cDNA 9030623C06 gene	9030623C06Rk	-0.075632	-0.433568	0.073952	1.836185	2.832716	3.398708
4	155660_f	RIKEN cDNA 0610025L15 gene	0610025L15Rk	1.882787	2.493241	1.509777	2.963559	3.808345	3.605421
4	155722_f	glutaredoxin 1 (thioltransferase)	Glx1	0.311553	1.000015	0.62871	2.839794	1.111274	1.961911
4	155794_f	small proline-rich protein 2	Sprr2	0.318031	0.350155	0.350442	0.502504	0.44258	0.558707
4	155805_f	glutathione S-transferase alpha 4	Gsta4	1.136513	1.429637	1.861648	5.612005	4.648717	5.519313
4	156110_f	carboxyl reductase 1	Cbr1	-0.201206	0.070049	0.331658	0.901187	2.97101	3.813892
4	156198_f	protein kinase C zeta	Pkczt	0.119485	0.024458	0.14787	0.463026	0.758428	0.781891
4	156217_f	polymerase (DNA directed) beta	Pola	0.260434	0.168252	0.423303	0.874073	0.589917	0.541388
4	156222_f	cDNA sequence BC020393	BC020393	0.241055	0.353112	0.05572	0.82273	0.481471	0.488184
4	156258_f	microsomal glutathione S-transferase 3	Mgst3	1.162482	1.200481	2.227192	3.647198	4.60371	5.289974
4	156322_f	endothelial differentiation-related factor 1	Edrf1	-0.170884	0.129284	0.15718	0.89147	0.283536	0.385801
4	156565_f	Mus musculus transcribed sequence with moderate similarity to protein p9 THYKZF (H.sapiens) THYKZF fibroblast growth factor receptor lig-2 precursor - human	—	0.118166	0.122519	0.387918	0.422784	0.703942	0.888896
4	156577_f	—	—	-0.075006	0.333105	1.819429	3.861423	2.05291	2.717588
4	156608_f	phytanoyl-CoA hydroxylase	Phyh	0.877440	0.521648	1.881717	2.146265	2.443916	2.524868
4	156670_f	glutathione S-transferase kappa 1	Gstk1	0.582327	0.483347	1.882777	2.813888	2.724839	1.735951
4	156725_f	START domain containing 10	Start10	0.035417	0.244966	0.422545	2.558444	2.020223	2.179294
4	156747_f	ras homolog gene family member U	Arhu	0.087159	0.099552	0.442447	1.590558	1.6429	1.50007
4	156748_f	RIKEN cDNA 9130018I11 gene	9130018I11Rk	0.584495	0.477324	0.504673	2.210579	0.987247	1.427307
4	156749_f	RIKEN cDNA 9130018I11 gene	9130018I11Rk	0.029525	-0.001078	-0.007711	1.189922	1.307452	2.148559
4	156790_f	RIKEN cDNA A530027M15 gene	A530027M15Rk	0.888215	0.481456	0.317208	1.073846	0.865424	1.024083
4	156790_f	RIKEN cDNA A530027M15 gene	A530027M15Rk	1.905264	0.372757	0.787326	2.881781	2.186147	0.508104
4	156791_f	RIKEN cDNA 1500050K14 gene	1500050K14Rk	0.47346	0.287677	2.072954	5.200621	6.788144	5.711258
4	156829_f	DNA segment Chr 19 Wayne State University 162 expressed	D19Wsu162e	1.509238	1.84894	1.068775	1.965105	1.600947	4.838282
4	156900_f	RIKEN cDNA 1820401E04 gene	1820401E04Rk	1.632029	1.783039	1.514448	2.234115	1.803247	2.739568
4	156957_f	calcium and integrin binding 1 (calstabin)	Cbl1	0.019297	-0.096912	0.089965	0.007891	0.868897	0.617241
4	157135_f	Mus musculus	—	0.0848	0.121028	0.121028	0.198116	0.456484	0.364248
4	157236_f	serine protease inhibitor Kunitz type 1	Spink1	-0.015674	0.193794	0.129838	1.584898	1.447949	1.501133

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

Cluster	Alphabetic id	Gene name	Gene symbol	LMC1 vs sMCs	sMC2 vs sMCs	LMC1 vs mMCs	sMC2 vs mMCs	LMC1 vs sMCs	sMC2 vs sMCs	LMC1 vs mMCs	sMC2 vs mMCs
4	47941_at	capain B	Capn6	0.202131	0.172497	0.176795	0.348622	0.444205	0.366929	0.444205	0.366929
4	47972_at	ring finger protein 103	Rfp103	0.166553	0.176528	0.478479	2.160077	1.974176	0.52918	1.974176	0.52918
4	48009_x_at	RIKEN cDNA 2400031A09 gene	2400031A09RA	-0.141337	0.003742	0.087131	0.274599	1.383395	1.020046	1.383395	1.020046
4	480092_at	placenta-specific 8	Plac8	0.277824	0.170767	0.35519	2.137161	0.757936	1.789058	0.757936	1.789058
4	481222_at	LIM domain only 4	Lmo4	0.096274	-0.351322	0.58875	1.487807	1.425306	1.8551	1.425306	1.8551
4	481229_at	thymosin beta 10	Tmsb10	0.088175	-0.039942	-0.03022	0.344313	0.832029	0.521961	0.832029	0.521961
4	481332_at	cytochrome c sarcoplasmic	CytC	-0.022884	0.001945	0.073871	0.501188	0.209559	0.290549	0.209559	0.290549
4	481442_at	leucine aminopeptidase 12-hydroxydehydrogenase	Lap-12h	0.890447	3.607132	1.503886	6.676472	6.287733	7.204121	6.287733	7.204121
4	484845_at	RIKEN cDNA C23005212 gene	C23005212RA	0.39879	-0.00058	0.580987	2.866557	0.702675	2.187658	0.702675	2.187658
4	48543_at	cathepsin B	Ctsb	1.501826	1.693228	0.430551	2.465607	2.92824	1.77186	2.92824	1.77186
4	486973_at	RIKEN cDNA 281031809B gene	281031809BRA	-0.003505	0.091845	0.07383	0.501188	0.209559	0.290549	0.209559	0.290549
4	486995_at	E2F transcription factor 5	E2f5	-0.268353	-0.005323	0.080168	0.340338	0.266662	0.374894	0.266662	0.374894
4	490034_at	inositol related homeobox 3 (Drosophila)	Inr3	0.131053	0.16783	0.208113	0.701361	0.683719	0.88476	0.683719	0.88476
4	490059_at	ET4-like factor 3	Elf3	0.468831	0.811378	0.38024	1.139748	1.149711	1.849711	1.149711	1.849711
4	490099_at	nuclear and lymphocyte protein T-cell differentiation protein	Ntp	0.188142	0.357025	0.335991	1.177784	0.800208	1.864263	0.800208	1.864263
4	49440_at	myosin factor 1B	Myf6	1.007136	0.735007	0.983395	1.817603	1.471357	1.286115	1.471357	1.286115
4	494452_at	liver specific H4-H2p transcription factor	Lact7-binding	0.831566	0.471108	0.549029	1.618446	1.451381	2.430239	1.451381	2.430239
4	495132_at	transducer of ERB-2 1	Tbr1	0.489795	0.858744	0.900215	2.802619	2.411302	1.225313	2.411302	1.225313
4	49580_x_at	UDP glycosyltransferase 1 family polypeptide A8	Ugt1a8	0.098007	0.200248	0.637768	3.838027	2.794668	3.067427	2.794668	3.067427
4	495809_at	protamine 1	Pm1	0.151017	0.200233	0.342006	0.436077	1.05499	0.879122	1.05499	0.879122
4	495922_at	Kruppel-like factor 4 (gpl)	Klf4	3.137422	3.713659	3.080303	5.04019	4.67344	6.021266	4.67344	6.021266
4	495932_at	mitochondrial ribosomal protein L54	Myl54	0.070452	0.196046	0.025643	0.35414	0.244398	0.458333	0.244398	0.458333
4	495938_at	ubiquitin C-terminal hydrolase related polypeptide	Ubr3p	-0.025260	0.242277	-0.216356	0.543728	0.510436	0.444113	0.510436	0.444113
4	495949_at	glutamate-cysteine ligase catalytic subunit	Gclt1	0.609693	0.485646	0.628385	1.055385	0.73928	1.494171	0.73928	1.494171
4	495960_x_at	cytochrome c oxidase subunit VIIc	Cox7c	0.347884	0.072328	0.444851	0.530173	0.727852	0.968047	0.727852	0.968047
4	496101_at	myosin rich protein 2B	Myr2b	0.824864	0.783871	0.981227	1.020626	2.391739	2.430239	2.391739	2.430239
4	496810_at	glutathione peroxidase 2	Gpx2	0.406851	0.301736	0.543061	1.430008	0.831751	0.741885	0.831751	0.741885
4	496833_at	capain B (mCL 4)	Capn6	0.200327	0.240743	0.396787	2.115427	1.640831	2.863298	1.640831	2.863298
4	496915_at	angrepurin	Angp	-0.077643	0.104504	0.104504	0.278228	0.292479	0.292479	0.292479	0.292479
4	496968_at	mat cell protease 2	Mcp2	0.30847	0.388621	0.399229	4.989802	6.576148	7.247786	6.576148	7.247786
4	499173_x_at	potassium inwardly-rectifying channel subfamily J member 19	Kir19	0.078557	0.235471	0.402831	3.853621	1.901728	2.448607	1.901728	2.448607
4	500174_at	potassium inwardly-rectifying channel subfamily J member 19	Kir19	-0.045768	0.081846	0.275635	0.502348	5.601171	4.552888	5.601171	4.552888
5	510004_at	villin 2	Vil2	-1.56247	-0.005389	0.298024	1.938797	1.878596	2.06972	1.878596	2.06972
5	510010_at	Jun oncogene	Jun	-0.078024	-0.151002	-0.080604	0.315408	0.251886	0.474322	0.251886	0.474322
5	510022_at	immunoglobulin heavy chain 4 (serum IgD1)	Igh4	-0.047293	0.778373	-0.062696	0.107319	2.581028	2.448607	2.581028	2.448607
5	510018_at	invariant motif protein 25	Im25	1.188334	0.086714	1.480489	0.652071	0.492086	3.05664	0.492086	3.05664
5	510051_at	choline kinase	Chk	0.100449	-0.033309	0.000692	0.037819	0.300390	0.291121	0.300390	0.291121
5	5100617_at	mitochondrial carrier family 25 (mitochondrial carrier, adenine nucleotide translocator) member 6	Slc25a5	-0.191291	-0.166674	-0.094926	0.17236	0.115481	0.54433	0.115481	0.54433
5	5101074_at	bag3	Bag3	-0.048164	-0.208113	-0.493114	0.559994	0.014747	0.944136	0.014747	0.944136
5	5101431_at	serine/threonine kinase 2	Sk2	-0.464352	-0.544571	-0.381314	0.50671	0.805466	0.30001	0.805466	0.30001
5	5101877_at	solute carrier family 31 member 1	Slc31a1	-0.308795	0.622414	-0.636422	2.727803	3.150815	2.813808	3.150815	2.813808
5	510214_f.at	cytochrome c oxidase subunit IV isoform 1	Cox4i1	-0.133719	-0.279676	-0.098886	0.106597	0.281965	0.33596	0.281965	0.33596
5	5102232_at	RIKEN cDNA 4833420E20 gene	4833420E20RA	-0.334212	-0.610625	-0.025577	0.548489	0.018121	0.148665	0.018121	0.148665
5	5102232_at	UDP-glucose 4-epimerase	Ugp1	-0.070452	0.025427	-0.030362	2.444887	1.729167	3.279952	1.729167	3.279952
5	5102306_at	RIKEN cDNA 2810208E05 gene	2810208E05RA	-0.430689	-0.357739	-0.355881	0.081001	0.647456	1.007448	0.647456	1.007448
5	5102370_at	retinal short-chain dehydrogenase/reductase 2	Retld2-pending	0.128226	0.758887	-1.04936	0.822006	1.340873	1.818775	1.340873	1.818775
5	5102796_at	chondral channel 3	Chn3	0.099904	-1.140385	-0.841756	0.821175	0.521961	1.120699	0.521961	1.120699
5	5103009_at	progesterone cell death 4	Pcd4	-0.238172	-0.12066	-0.802844	0.616746	0.295616	1.237878	0.295616	1.237878
5	5103332_at	RIKEN cDNA 3830613C22 gene	3830613C22RA	-0.214361	-0.211969	-0.113756	0.268881	-0.031134	0.236306	-0.031134	0.236306
5	5103514_at	lumin receptor family class C member 21	Lumbr21	-0.315776	-0.06407	-0.083672	1.705857	1.006693	1.639951	1.006693	1.639951
5	5103601_at	RIKEN cDNA 2210013M04 gene	2210013M04RA	-0.087589	-0.094755	-0.033397	0.54887	0.200465	0.322289	0.200465	0.322289
5	5103925_at	myxoid lymphoid or mixed lineage leukemia translocation to 3 homolog (Drosophila)	Mlx3	-1.177851	-1.790094	-0.208113	0.867462	1.582894	3.234818	1.582894	3.234818
5	5104033_at	nervegrowth expressed antigen 6 (coiled-coil protein-rich)	Nrg6	-0.238342	-0.638003	-0.279732	1.798249	0.020806	2.591097	0.020806	2.591097
5	5104305_at	arginyl-tRNA synthetase-like	Rars	-0.147823	0.854889	-0.180962	1.242361	0.809323	2.415003	0.809323	2.415003
5	5104378_at	paroxonase 2	Pon2	-0.128208	-1.129178	-0.557317	1.952762	0.898971	2.071993	0.898971	2.071993
5	5104385_x_at	Mus musculus cDNA clone IMAGE:6331951 partial cds	1110004F14RA	-0.047462	-0.121823	0.391395	2.348817	0.117913	0.248617	0.117913	0.248617
5	5104713_at	RIKEN cDNA 2410002M02 gene	2410002M02RA	-0.377226	0.102334	-0.153391	1.039897	0.330351	0.380186	0.330351	0.380186
5	5105000_at	RIKEN cDNA 3230401D17 gene	3230401D17RA	-0.182716	0.071195	-0.153294	0.544481	0.41024	0.143258	0.41024	0.143258
5	5105020_at	ring finger protein 44	Rfp44	-0.481891	-0.910986	-0.482769	0.214918	-0.086193	0.720395	-0.086193	0.720395
5	5105248_at	lamin protein D2	Lamd2	-0.065292	-0.309814	-0.420136	0.306881	-0.130343	1.030961	-0.130343	1.030961
5	5105429_at	NF2-related export protein 1	Nxf1	-0.221535	-0.154648	-0.276254	0.558581	0.474899	0.407920	0.474899	0.407920
5	5106095_x_at	RIKEN cDNA 4833420C05 gene	4833420C05RA	-0.071082	0.073249	-0.002833	0.202482	0.141099	0.18898	0.141099	0.18898
5	5106233_at	RNA and export factor binding protein 1	Rebp1	-0.200736	-0.319885	-0.09466	0.070946	0.870898	0.574121	0.870898	0.574121
5	511239_f.at	chaperonin subunit 3 (gamma)	Cpn3	-0.045692	0.191168	-0.102625	0.380079	0.274168	0.568561	0.274168	0.568561
5	5116401_f.at	alkylglyoxal dehydrogenase family 3 subfamily A2	Ald3a2	0.183307	-0.010126	-0.081126	0.663101	0.648175	0.900022	0.648175	0.900022
5	5116452_f.at	upregulated during skeletal muscle growth 5	Umy8	0.087268	0.016602	-0.18053	0.168519	0.362511	0.400947	0.362511	0.400947
5	5116498_f.at	---	---	-0.198412	-0.033379	-0.236307	0.181171	0.097913	0.308837	0.097913	0.308837
5	5116736_f.at	FVB (bacterial acetylactate synthase)-like	Rfb1	-0.591768	-0.261978	-0.59937	0.870078	-0.113902	0.200929	-0.113902	0.200929
5	5120336_f.at	flavory carrier membrane protein 2	Fcm2	-0.025620	-0.264815	-0.150684	0.06263	0.110784	0.225064	0.06263	0.225064
5	512144_f.at	electron transferring flavoprotein beta polypeptide	Etfb	-0.00914	-0.194095	-0.099931	0.002777	0.17172	0.102119	0.17172	0.102119
5	512149_f.at	Hsp41 tiny fragments locus B	Hsp41	-0.170594	-0.190986	0.0	-0.001939	0.157844	0.206902	0.157844	0.206902
5	5123113_f.at	UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetylglucosaminyltransferase 3	Galt3	-0.001858	-0.290119	0.026262	0.400938	0.708521	1.229204	0.400938	1.229204
5	512415_f.at	Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase	Shcy-pending	0.013667	-0.304688	0.041197	0.095333	0.298743	0.519199	0.298743	0.519199

The file represents 1272 genes significantly altered between sMCs and hMCs in the order of clustering (Figure 1a). The values represent expression levels normalized to those of BMMC's.

Cluster	Allylthia ID	Gene name	Gene symbol	sMC1 vs. hMC1	sMC2 vs. hMC2	sMC1 vs. hMC1	sMC2 vs. hMC2	sMC1 vs. hMC1	sMC2 vs. hMC2
5	97935_1	CD151 antigen	CD151	-0.160791	0.273400	0.607911	0.363553	0.328555	0
5	97947_1	a disintegrin and metalloprotease domain 10	Adam10	-0.214849	-0.2816	-0.377756	0.051998	0.674211	1.508609
5	98555_1	coproporphyrinogen oxidase	Cpe	-0.028927	0.419924	-0.420556	0.538975	0.592957	0.831657
5	99070_1	conserved helix-loop-helix ubiquitous kinase	Chuk	-0.673811	0.182171	-0.85782	0.137766	0.71824	0.40441
5	99548_1	aldohyde dehydrogenase family 3 subfamily A2	Aldh3a2	-0.812113	-0.584807	-0.447588	0.256427	0.381451	1.690720
5	99550_1	aldohyde dehydrogenase family 3 subfamily A2	Aldh3a2	-0.332538	0.180617	-0.45727	1.365551	0.385123	0.852647
5	99563_1	glutathione S-transferase pi 2	Gstp2	-0.602102	-0.01813	-1.152785	1.223447	0.820025	2.082302
5	99631_1	cytochrome c oxidase subunit VI a polypeptide 1	Cox6a1	-0.482232	-0.311819	-0.598431	0.322233	0.719427	0.48189
6	100041_1	RIKEN cDNA 3010027G13 gene	C010027G13Rik	-0.642749	-0.059251	-1.433482	0.029285	0.222783	0.142457
6	100081_1	UOP-galactose transferase 2	Ugat2	-0.675409	-1.665088	-1.150082	0.118736	-0.453031	-0.244216
6	100057_2	RIKEN cDNA Z110048H11 gene	Z110048H11Rik	-0.325512	-0.380817	-0.354881	0.229669	-0.11261	0.39803
6	100081_1	cystatin B	Cstb	-1.317105	-1.051365	-1.623321	0.615506	0.50954	1.193613
6	100994_1	arabinosyl A4	Ara4a	-0.448474	-1.888513	-0.843044	1.173109	0.10069	0.885328
6	100753_1	ATP synthase H+ transporting mitochondrial F1 complex alpha subunit isoform 1	Atp5a1	-1.454204	-1.040165	-1.345442	-0.075129	-0.445014	0.14898
6	100993_1	serine palmitoyltransferase long chain base subunit 2	Spst2	-0.608264	-0.773658	-0.672085	0.62071	0.035261	-0.028347
6	101918_1	RIKEN cDNA 1610099H4 gene	1610099H4Rik	-0.171388	-1.901139	-1.378887	-0.045981	-0.499579	-0.097316
6	101982_1	cytochrome c oxidase subunit VIII	Cox7b	-0.186206	-0.136284	-1.045279	0.21988	0.19827	0.343755
6	101581_1	X-prolyl aminopeptidase (aminopeptidase F) 1 soluble	Xpmp1	-0.335390	-0.183732	-0.351435	0.060244	0.389793	-0.026094
6	101939_1	ring finger protein 141	Rnf141	-0.069896	-0.049225	-0.462628	0.168828	-0.087433	0.117811
6	102090_1	golgii autoarrestin golgin subfamily a 4	Golgaf4	-0.980042	-0.404935	-1.066941	-0.100985	-0.485383	0.190699
6	102099_1	RIKEN cDNA 2410038A03 gene	2410038A03Rik	-0.87131	-0.813328	-1.188498	0.582827	0.015246	-0.029838
6	102198_1	solute carrier family 10 (sulfonate acid cotransporter family) member 3	Slc10a3	-0.470783	-0.445890	-0.241248	0.260708	0.199158	-0.272159
6	102868_1	ELOVL family member 6 elongation of long chain fatty acids (yeast)	Elovl6	-1.691789	-1.903328	-1.423426	0.869919	-1.44626	-0.07910
6	103896_1	RIKEN cDNA 1300011P16 gene	1300011P16Rik	-0.452116	-0.574105	-0.839965	-0.28131	-0.146396	0.064576
6	104015_1	methionyl aminopeptidase 1	Metap1	-0.276234	-1.376657	-0.868656	0.431871	0.078022	0.599918
6	104279_1	RIKEN cDNA 1810060C16Rik	1810060C16Rik	-0.071127	-1.858734	-0.912871	-0.07498	0.302307	0.080197
6	104288_1	cutin 4A	Cufa	-2.395049	-1.688805	-2.300422	-0.655457	0.13537	-0.062623
6	104502_1	RIKEN cDNA 2900018D05 gene	2900018D05Rik	-0.253964	-0.305104	-0.20782	0.048704	0.175509	0.127649
6	104696_1	calpain E	Capn5	-0.593923	-0.889773	-2.54528	0.078699	0.773188	1.890227
6	105112_1	RIKEN cDNA 1150009E07 gene	1150009E07Rik	-0.167344	-0.319727	-0.399967	0.14481	-0.270578	0.387328
6	180182_1	transglut 2	Tglu2	-1.011194	-1.407541	-1.847081	-0.086952	-0.061135	-0.055522
6	180230_1	Mus musculus cDNA clone MGC 58837 IMAGE 6773043 complete cds		-0.805214	-0.460085	-1.178852	0.408708	-0.373282	0.627453
6	180236_1	oxidative deficiency-associated gene expressed in ventricle 3	Odv3	-2.72244	-2.653195	-2.054933	-0.355106	-1.74009	0.378988
6	180381_1	RIKEN cDNA 0610011D08Rik	0610011D08Rik	-2.580765	-2.78902	-1.678166	0.353618	-0.93618	-0.685068
6	180428_1	mitochondrial ribosomal protein L50	Mpl50	-0.63304	-1.03516	-0.764426	-0.128255	-0.472087	0.29144
6	180428_1	succinate Coenzyme A ligase GDP-forming beta subunit	Succ2	-0.836133	-1.006974	-1.071919	-0.299993	-0.322394	-1.339959
6	180522_1	voltage-dependent anion channel 2	Vdac2	-1.161125	-0.247074	-1.028324	-0.366203	0.249042	0.573388
6	180543_1	hydroxymethylglutaryl-CoA lyase 2	Hmgcl2	-1.04778	-0.656887	-0.865887	0.231471	-0.658003	0.280197
6	180555_1	carboxypeptidase D	Cpef	-1.038455	-1.056464	-0.66783	0.23866	0.50502	-0.021779
6	180688_1	golgi phosphoprotein 3	Golp3	-1.485156	-1.169308	-0.8335	1.362095	0.537078	0.666099
6	180789_1	RIKEN cDNA 953000G24Rik	953000G24Rik	-0.379808	-0.237796	-0.208025	0.234765	0.243351	0.074562
6	180797_1	FBJ myeloid sarcoma oncogene	Fos	-1.752298	-0.483991	-4.375074	0.836003	-0.75182	-0.087810
6	180930_1	SAC1 (suppressor of actin mutations 1 homology)-like (5 cerevisiae)	Sac1l1	-0.048839	-1.229165	-1.654944	0.69129	1.129294	0.584596
6	181272_1	SH3 domain GRB2-like B1 (endorphin)	Sh3b1	-0.667729	-0.559747	-0.191149	0.062245	-0.191148	-0.070910
6	181301_1	actin galactose binding subunit 3	Galg3	-0.661605	-0.965818	-0.754798	-0.293831	-0.055222	0.352078
6	181342_1	RIKEN cDNA Z310048H11 gene	Z310048H11Rik	-1.473807	-0.679321	-1.25691	0.178942	-0.165771	0.562238
6	181400_1	casein kinase 1 delta	Csk1b	-0.588028	-1.546754	-1.783392	-0.110333	-0.391904	-0.052946
6	181551_1	RIO kinase 3 (yeast)	Rio3	-0.769914	-1.43335	-0.478929	-0.24878	-0.165636	0.280668
6	181648_1	complement receptor related protein	Crry	-0.528881	-2.720017	-0.948111	0.853222	-0.025368	0.589008
6	181774_1	lysophospholipase 1	Lyp1l1	-0.171883	-0.556402	-1.182488	0.414802	-0.245164	0.52438
6	181811_1	eukaryotic translation initiation factor 4E like 3	Eif4e3	-0.428991	-0.323903	-0.13814	0.205222	0.263979	0.121988
6	182091_1	asparagine-linked glycosylase 3 homolog (yeast alpha-1,3-mannosyltransferase)	Cark1d	-0.363505	-0.620843	-0.340417	-0.068704	0.05241	0.229997
6	182237_1	RIKEN cDNA D330001F17 gene	D330001F17Rik	-0.217943	-0.338853	-0.221486	0.260741	-0.164836	0.128601
6	182350_1	solute carrier family 25 (mitochondrial carrier: citrate transporter) member 1	Slc25a1	-0.345443	-0.713124	-0.230345	-0.004711	-0.143709	-0.028039
6	182398_1	thioredoxin 1	Txn1p	-1.752947	-0.380897	-0.556808	0.023548	-0.033504	0.390348
6	182807_1	thioredoxin 1	Txn1p	-2.240664	-0.530184	-1.227212	1.038783	-0.330268	0.575002
6	182954_1	RAB11a member RAS oncogene family	Rab11a	-2.365748	-0.719233	-0.854324	0.405966	0.240376	-0.331619
6	183058_1	eukaryotic translation initiation factor 1A	Eif1a	-1.46903	-0.295959	-1.201035	-0.595969	0.107012	-0.113020
6	183277_1	Heck shock protein 1 (chaperonin)	Hsp90	-0.83277	-0.602728	-0.612779	0.565007	0.315125	-0.846958
6	183337_1	vascular protein sorting 4b (yeast)	Vps4b	-2.386528	-2.388541	-4.238828	0.794363	-0.25782	0.828232
6	183573_1	metallothionein 1	Mt1	-2.232024	-0.694775	-0.557211	0.665297	-0.126985	0.182688
6	183600_1	leptin receptor gene-related protein	Lrgp1	-0.618099	-1.620381	-1.350775	-0.141701	-0.1936	0.314488
6	183787_1	mitochondrial ribosomal protein L18	Mpl18	-1.485426	-0.602977	-2.400827	0.048332	-0.448442	-0.042935
6	183793_1	LIM and SH3 protein 1	Limg1	-0.702059	-1.302307	-1.093653	-0.186407	-0.569291	0.614091
6	183835_1	fucosylase alpha-L 1 tissue	Fuca	-0.504230	-1.150507	-1.095041	0.108514	-0.83904	0.185210
6	183980_1	cDNA sequence BC018943	BC018943	-0.889862	-1.122463	-1.081964	-0.281743	-0.547732	0.504925
6	183984_1	ATPase inhibitor	Atp6i	-0.711426	-0.878203	-0.902724	1.136487	-0.207498	-0.081937
6	184042_1	guanine nucleotide binding protein (G protein) gamma 5 subunit	Gng5	-0.421158	-0.672359	-0.869991	-0.009776	0.131928	0.899227
6	184048_1	cell division cycle 34 homolog (S. cerevisiae)	Cdc34	-1.587428	-0.707463	-0.634182	0.378867	0.143562	-0.349246
6	184369_1	glucosamine-phosphate N-acetyltransferase 1	Gnpat1	-0.789993	-1.154851	-1.017956	0.018194	0.359055	0.629606
6	184428_1	uvrB (bacterial acetoactin synthase) like	UvrB	-2.808715	-3.061629	-3.156213	0.586174	-2.734807	0.379579
6	184464_1	chloride channel 3	Clcn3	-3.488348	-3.520335	-3.424907	-0.657189	-0.4818	0.870833
6	184465_2	chloride channel 3	Clcn3	-1.254785	-1.270559	-1.312858	0.742551	1.160732	-0.44614
6	184514_1	archan 1	Arcn1	-0.228233	-0.877439	-0.815027	-0.024816	-0.134204	0.347700
6	184607_1	solute carrier family 25 (mitochondrial carrier: citrate transporter) member 1	Slc25a1	-0.85787	-0.424896	-0.822434	0.118328	0.243025	0.338478
6	184640_1	methylcrotonyl Coenzyme A carboxylase 1 (alpha)	Mcc1	-1.205491	-0.891814	-0.791585	0.07091	-0.892711	0.573976
6	184656_1	glucose 6-phosphate dehydrogenase K-like	G6pd	-1.194132	-0.738423	-0.427501	0.425714	0.184091	0.95731
6	184667_1	DNA segment Chr 19 Wayne State University 12 expressed	D19Wsu12e	-2.760353	-2.93015	-2.121865	0.837947	-0.100207	-0.591669
6	185002_1	DNA segment Chr 17 Wayne State University 92 expressed	D17Wsu92e	-0.358715	-1.900586	-1.7306	0.358635	-0.432455	1.144185
6	185042_1	RIKEN cDNA C03002N13 gene	C03002N13Rik	-0.277634	-0.524238	-0.533675	0.482087	0.001597	0.15296
6	185102_1	actin gene	Acta1	-1.526533	-1.748845	-1.307443	0.148805	0.028914	-0.031198
6	185135_1	RIKEN cDNA 3110038B17Rik	3110038B17Rik	-0.48178	-1.257038	-1.864529	0.40718	0.315125	-0.846958
6	185141_1	RIKEN cDNA 1110004F10 gene	1110004F10Rik	-2.381772	-1.790841	-1.118299	-0.222455	0.450156	0.142178
6	185441_1	translocase of inner mitochondrial membrane 23 homolog (yeast)	Timm23	-1.480479	-1.224821	-1.291325	0.295389	-0.11827	0.748024
6	185444_1	RIKEN cDNA 4920579A11 gene	4920579A11Rik	-3.258095	-1.857478	-1.841785	0.396385	-0.789971	-0.336297
6	185452_1	actin gene	Acta1	-0.287629	-1.688709	-1.337689	0.216612	-0.276441	-0.388673
6	185452_1	actin gene	Acta1	-0.48178	-1.257038	-1.864529	0.40718	0.315125	-0.846958
6	185455_1	RIKEN cDNA 1110004F10 gene	1110004F10Rik	-2.381772	-1.790841	-1.118299	-0.222455	0.450156	0.142178
6	185455_1	translocase of inner mitochondrial membrane 23 homolog (yeast)	Timm23	-1.480479	-1.224821	-1.291325	0.295389	-0.11827	0.748024
6	185444_1	RIKEN cDNA 4920579A11 gene	4920579A11Rik	-3.258095	-1.857478	-1.841785	0.396385	-0.789971	-0.336297
6	185452_1	actin gene	Acta1	-0.287629	-1.688709	-1.337689	0.216612	-0.276441	-0.388673
6	185452_1	actin gene	Acta1	-0.48178	-1.257038	-1.864529	0.40718	0.315125	-0.846958
6	185455_1	RIKEN cDNA 1110004F10 gene	1110004F10Rik	-2.381772	-1.790841	-1.118299	-0.222455	0.450156	0.142178
6	185455_1	translocase of inner mitochondrial membrane 23 homolog (yeast)	Timm23	-1.480479	-1.224821	-1.291325	0.295389	-0.11827	0.748024
6	185444_1	RIKEN cDNA 4920579A11 gene	4920579A11Rik	-3.258095	-1.85747				

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

Cluster	Affinity	Gene name	Gene symbol	aMC1 vs. BMC	aMC2 vs. BMC	mMC1 vs. BMC	aMC1 vs. mMC1	aMC2 vs. mMC2	aMC1 vs. BMC	aMC2 vs. BMC	mMC1 vs. BMC	aMC1 vs. BMC
6	97758_at	proteasom 1	Psct1	-1.148455	-0.888930	-1.488997	-0.218101	0.190473	0.588038	0.160236	0.153103	0.588038
6	97924_at	ADP3 acetyl-related protein 3 homolog (yeast)	Adp3	-1.182182	-1.100779	-2.238652	-0.680514	-0.193284	-1.352898	0.092030	0.092030	0.092030
6	97908_at	RKEN cDNA 1110007A06 gene	1110007A06RA	-2.136109	-1.303088	-2.617456	-0.805520	-0.476602	-1.448266	0.144876	0.144876	0.144876
6	97974_at	zinc finger protein multiple type 1	Zfpn1	-0.710811	-0.786612	-0.476602	-0.213337	0.144876	0.144876	0.144876	0.144876	0.144876
6	98013_at	cDNA sequence BC033809	BC033809	-0.801431	-1.265470	-1.707428	-0.464655	-0.689191	0.291688	0.291688	0.291688	0.291688
6	98538_at	RKEN cDNA 2810507B11 gene	2810507B11RA	-0.678987	-0.313606	-0.480832	0.147847	-0.260572	0.199906	0.199906	0.199906	0.199906
6	98577_at	DNAJ1 (Hsp40) homolog subfamily B member 11	Dnajp11	-2.617760	-1.349526	-1.874538	-0.040375	-0.674383	0.840916	0.840916	0.840916	0.840916
6	98584_f.at	glycyl phosphate dehydrogenase 2 mitochondrial	Gpd2	-0.958289	-2.192709	-1.725951	0.430099	0.474906	0.868323	0.868323	0.868323	0.868323
6	98128_at	ATP synthase H+ transporting mitochondrial F1 complex O subunit	Atp5o	-0.711187	-0.360534	-0.64359	0.162337	-0.392761	-0.048953	0.162337	0.162337	0.162337
6	98140_at	mitochondrial ribosomal protein L18	Mpl18	-0.613741	-0.698436	-0.502067	-0.340733	0.147146	0.160569	0.160569	0.160569	0.160569
6	98949_at	AFX	---	-0.558922	-0.659261	-1.051971	0.497501	-0.249853	0.575313	0.575313	0.575313	0.575313
6	108192_3.at	PyrCarbMud	---	---	---	---	---	---	---	---	---	---
7	100750_at	pyruvate carboxylase	Pcc	0.688554	0.899944	0.308096	0.433178	-0.131320	0.678495	0.678495	0.678495	0.678495
7	100756_at	platelet-activating factor acetylhydrolase isoform 1b (alpha) subunit	Plaf1b1b3	-1.600203	-0.772368	-2.215861	-0.889486	-0.535514	-0.323944	0.323944	0.323944	0.323944
7	100759_at	activating transcription factor 4	Atf4	-0.805298	-0.915791	-1.174899	-0.400604	-0.632899	-0.291356	0.291356	0.291356	0.291356
7	100761_at	ribonucleasase/lysozyme inhibitor 1	Rlyi1	-1.919066	-1.847053	-0.963778	-0.823513	-0.963778	-0.399191	0.399191	0.399191	0.399191
7	100718_at	prothymosin alpha	Ptma	-1.387527	1.321	-2.388877	-0.718303	-0.901431	-0.224191	0.224191	0.224191	0.224191
7	101095_at	proliferating cell nuclear antigen	Pcna	-3.577729	-2.568995	-2.965659	-2.22862	-1.070873	0.107087	0.107087	0.107087	0.107087
7	101213_at	cytosolic ribosomal phosphoprotein P0	Arpp	-1.830078	-1.884497	-2.712503	-0.841964	-1.521003	-0.626852	0.626852	0.626852	0.626852
7	101254_at	RAN member RAS oncogene family	Ran	-3.082007	-1.586825	-2.8195	-0.972904	-1.276524	-1.792561	1.792561	1.792561	1.792561
7	101390_at	yeast RNA binding protein 2	Ryb2	-2.81189	-2.628995	-2.818182	-1.121723	-1.440286	0.144029	0.144029	0.144029	0.144029
7	101409_at	ligatin	Lgatn	-1.558694	-1.164919	-1.284125	-0.747111	-1.160718	-0.277158	0.277158	0.277158	0.277158
7	101523_at	RKEN cDNA 2610510D13 gene	2610510D13RA	-0.920894	-1.01881	-1.545301	-0.650181	-0.709424	-0.382140	0.382140	0.382140	0.382140
7	101621_at	phosphatidylserine synthase 1	Pls1	-3.201294	-3.143533	-3.361403	-1.189181	-1.585032	-0.291652	0.291652	0.291652	0.291652
7	101958_f.at	transcription factor Dp. 1	Dp1	-2.354472	-2.447789	-2.446857	-1.624711	-1.917684	-2.278471	2.278471	2.278471	2.278471
7	101964_at	transketolase	Tkt	-1.565115	-1.810536	-1.831783	-0.320324	-1.307748	-0.430829	0.430829	0.430829	0.430829
7	102290_at	proton kinase C alpha	Pkca	-1.571552	-1.566873	-1.473796	-1.278605	-0.915412	-0.276661	0.276661	0.276661	0.276661
7	102708_1.at	sterol-C-Desaturase (fungal ERG3 delta-5-desaturase) homolog (S. cerevisiae)	Scd5l	-0.786557	-0.972383	-0.918112	-0.554548	-0.637033	-0.446037	0.446037	0.446037	0.446037
7	102850_at	lysine kinase non-receptor 2	Ltk2	-1.424488	-1.268171	-1.950885	-0.631109	-0.544727	-0.618181	0.618181	0.618181	0.618181
7	102872_f.at	zinc finger protein 51	Zfp51	-0.798487	-0.810007	-0.860708	-0.43799	-0.476887	-0.127353	0.127353	0.127353	0.127353
7	103018_at	vesicle docking protein	Vdp-pending	-1.089125	-1.24548	-1.228795	-0.493886	-0.849395	-0.60849	0.60849	0.60849	0.60849
7	103207_at	calcium stimulating factor 2 receptor beta 2 low-affinity (granulocyte macrophage)	CaStb2	-5.908931	-5.488853	-6.327886	-4.681018	-4.22726	-2.650944	2.650944	2.650944	2.650944
7	103334_at	calcitonin gene-related peptide-receptor component protein	Cgrp	-1.337032	-1.453022	-1.584332	-0.11767	-1.104779	-0.694417	0.694417	0.694417	0.694417
7	103335_at	leucin galactose binding soluble 9	Lgal9	-2.768991	-2.454032	-2.359666	-1.223785	-1.855339	-0.90733	0.90733	0.90733	0.90733
7	103367_at	UDP-N-acetyl-alpha-D-glucosamine (N-acetylhexosamine)-galactose 4-epimerase beta-1,4-N	Galgt1	-1.11336	-2.027165	-1.184335	0.352758	-0.404995	-1.048523	1.048523	1.048523	1.048523
7	103435_at	RKEN cDNA 943008K19 gene	943008K19RA	-1.831822	-1.868668	-1.6661	-1.310209	-1.423382	-1.532772	1.532772	1.532772	1.532772
7	103917_at	decay accelerating factor 1	Daf1	-5.09847	-5.200728	-5.260526	-4.811438	-4.638487	-4.626383	4.626383	4.626383	4.626383
7	103967_at	Mus musculus transcribed sequence with weak similarity to protein ref NP_079266.1 (H saevens) hypothetical protein FLJ12547	---	-1.228283	-1.889931	-1.742386	-0.46051	-0.431982	-0.705435	0.705435	0.705435	0.705435
7	103972_at	RKEN cDNA 241014M05 gene	241014M05RA	-1.386509	-1.489973	-1.205915	-0.88172	-0.871096	-1.19887	1.19887	1.19887	1.19887
7	103985_at	Mus musculus transcribed sequences	---	-2.75859	-2.52443	-2.889165	-3.212165	-3.191258	-2.869231	2.869231	2.869231	2.869231
7	103990_at	myofibrillin related protein 9	Mirr9	-1.854411	-1.583734	-1.681445	-0.867854	-1.052895	-1.155473	1.155473	1.155473	1.155473
7	103991_at	U2 small nuclear ribonucleoprotein auxiliary factor (UZAF) 1 related sequence 2	---	-2.028545	-2.912662	-2.049286	-1.451872	-1.915436	-0.785338	0.785338	0.785338	0.785338
7	103988_at	adrenic receptor kinase beta 1	Adra1	-1.749137	-1.613328	-1.792002	-1.032355	-0.887245	-0.613431	0.613431	0.613431	0.613431
7	104030_at	secretory carrier membrane protein 2	Scamp2	-3.020639	-2.823772	-2.854888	-2.109366	-2.781341	-2.087028	2.087028	2.087028	2.087028
7	104380_at	solute carrier family 35 (CAMP-staic acid transporter) member 1	Slc35a1	-2.14282	-2.079598	-2.165789	-0.282877	-0.475875	-1.629956	1.629956	1.629956	1.629956
7	104410_at	midrin	Midn	-0.860526	-1.178881	-1.000000	-0.846460	-0.904613	-0.412389	0.412389	0.412389	0.412389
7	104416_at	Mus musculus transcribed sequences	---	-0.860576	-3.72084	-4.10259	-1.600659	-2.714787	-1.317335	1.317335	1.317335	1.317335
7	104616_3.at	galactose-1-phosphate uridylyl transferase	Gal1t1	-1.810918	-1.734179	-1.891932	-1.195848	-1.320207	-1.80777	1.80777	1.80777	1.80777
7	104623_at	DNA-stimulated enhancer of split 3 homolog of Drosophila (Esplit)	Ths3	-0.963566	-1.263227	-1.118796	-0.809560	-0.543352	-0.991161	0.991161	0.991161	0.991161
7	104717_at	RAN segment Chr 5 ERATO DO 689 expressed	O689se	-2.818152	-2.781779	-2.662323	-1.06692	-0.811152	-2.37898	2.37898	2.37898	2.37898
7	104759_at	TFNAP3 interacting protein 1	Tfnp1	-1.005137	-0.9378	-0.730091	-0.642671	-0.105556	-0.418818	0.418818	0.418818	0.418818
7	105204_at	ornithine decarboxylase structural	Odc	-2.23524	-2.380064	-2.444808	-0.924666	-1.650023	-0.889149	0.889149	0.889149	0.889149
7	105270_at	cyclin G1	Cng1	-2.232444	-1.798621	-1.854220	-1.482151	-1.532848	1.532848	1.532848	1.532848	1.532848
7	105156_at	RKEN cDNA 081000A06 gene	081000A06RA	-1.20200	-1.00824	-1.487087	-1.118787	-1.055819	-1.151152	1.151152	1.151152	1.151152
7	105252_at	clathrin heavy polypeptide (Hc)	Cla	-1.015648	-1.523803	-1.689996	-1.089031	-1.144095	-0.291845	0.291845	0.291845	0.291845
7	105301_at	RIO kinase 3 (yeast)	Rio3	-1.458993	-2.041303	-1.525871	-1.302302	-0.80885	-0.694739	0.694739	0.694739	0.694739
7	105377_at	TAR DNA binding protein	Tarbp	-1.561877	-1.816226	-2.045282	-0.553626	-0.70849	-1.243809	1.243809	1.243809	1.243809
7	105385_at	RKEN cDNA 8720591C18 gene	8720591C18RA	-1.814962	-0.842038	-1.506268	-0.230813	-0.484248	-0.729491	0.729491	0.729491	0.729491
7	105388_at	sterol-C4-methyl oxidase-like	Sc4mo	-3.918855	-3.454247	-3.571321	-1.782186	-2.82678	-2.609102	2.609102	2.609102	2.609102
7	105479_at	cathepsin	Cat	-2.153307	-2.838801	-2.520522	-1.86635	-2.063073	-1.321328	1.321328	1.321328	1.321328
7	105483_at	C9orf3 antigen	C9orf3	-1.784585	-1.66912	-1.873442	-1.131747	-1.258381	-0.889149	0.889149	0.889149	0.889149
7	105495_at	aryl hydrocarbon receptor	Ahr	-3.262078	-3.203806	-3.11481	-2.877328	-2.745892	-2.688278	2.688278	2.688278	2.688278
7	105540_at	BC2-associated athanogene 1	Bat1	-1.860178	-1.955900	-1.317915	-0.766691	-1.05343	-0.258401	0.258401	0.258401	0.258401
7	105569_at	RKEN cDNA 231008M10 gene	231008M10RA	-3.849621	-3.030895	-3.69602	-0.473267	-0.205212	-1.118273	1.118273	1.118273	1.118273
7	105598_at	zinc finger protein 131	Zfp131	-1.336024	-1.341245	-1.427127	-0.749649	-1.288475	-0.608331	0.608331	0.608331	0.608331
7	105696_at	RKEN cDNA 573005F13 gene	573005F13RA	-1.827941	-1.398821	-1.358787	-0.677815	-0.588956	-1.181898	1.181898	1.181898	1.181898
7	105721_at	E74-like factor 1	E74l1	-2.030161	-2.264599	-2.236736	-1.713891	-2.04761	-1.78856	1.78856	1.78856	1.78856
7	105734_at	actuator-related protein complex 3 sigma 1 subunit	Act3t1	-1.957716	-2.585474	-2.157818	-0.978385	-1.361551	-0.888695	0.888695	0.888695	0.888695

The list represents 1272 genes significantly altered between sMCs and mMCs in the order of clustering (Figure 5a). The values represent expression levels normalized to those of sMCs.

Cluster	Accession ID	Gene name	Gene symbol	sMC1 vs. sMC2	sMC1 vs. mMC1	sMC2 vs. mMC1	sMC1 vs. mMC2	sMC2 vs. mMC2	sMC1 vs. mMC1	sMC2 vs. mMC1	sMC1 vs. mMC2	sMC2 vs. mMC2
7	92788_s_at	transcriptional regulator SIN3B (yeast)	Sin3b	-1.91193	-2.06272	-1.87104	-1.11959	-1.44127	-1.11959	-1.44127	-1.11959	-1.44127
7	93053_at	proteasome (prosome macrosome) 26 subunit 3	Psom3	-0.537962	-0.674922	-0.597978	-0.461162	-0.428991	-0.597978	-0.461162	-0.428991	-0.428991
7	93816_at	RIKEN cDNA 1110032D12 gene	TT10032D12Hk	-0.851262	-1.872316	-1.754933	-0.50896	-0.652662	-1.754933	-0.50896	-0.652662	-0.652662
7	93829_at	ROD1 regulator of differentiation 1 (S. pombe)	Rod1	-0.733003	-1.779325	-1.737808	-0.878373	-0.344465	-1.737808	-0.878373	-0.344465	-0.344465
7	93940_at	peroxanase 3	Pnc3	-1.846907	-2.102888	-2.036737	-1.581572	-1.777934	-2.036737	-1.581572	-1.777934	-1.777934
7	93976_at	calcium binding protein 39	Calb39	-1.243481	-0.995138	-1.022839	-0.487478	-0.487581	-1.022839	-0.487478	-0.487581	-0.487581
7	93983_at	RIKEN cDNA 1110021N07 gene	TT10021N07Hk	-1.062265	-1.472191	-1.031155	-0.82671	-0.874038	-1.031155	-0.82671	-0.874038	-0.874038
7	93993_at	leucin mannosyl-binding 2	Lman2	-2.744614	-2.583076	-2.064508	-1.2422	-1.417405	-2.064508	-1.2422	-1.417405	-1.417405
7	93994_at	synaptosomal complex protein 3	Sycp3	-1.156334	-1.471387	-1.672481	-0.118119	-0.680258	-1.672481	-0.118119	-0.680258	-0.680258
7	93999_at	small nuclear ribonucleoprotein polypeptide G	Snrgp	-1.442187	-1.52588	-1.884588	-0.769914	-1.101595	-1.884588	-0.769914	-1.101595	-1.101595
7	94064_at	zinc finger protein 91	Zfp91	-2.367905	-2.125876	-3.637456	-3.201512	-1.27722	-3.637456	-3.201512	-1.27722	-0.414779
7	94086_at	succinate dehydrogenase complex subunit A flavoprotein (Fp)	Sdhf	-1.703152	-1.801183	-1.815863	-1.010901	-0.234218	-1.815863	-1.010901	-0.234218	0.519953
7	94237_at	ribophan 1	Rph1	-2.435725	-3.746561	-3.758646	-1.612307	-2.06655	-3.746561	-3.758646	-1.612307	-2.06655
7	94268_t_at	---	---	-2.000734	-1.710943	-2.991266	-0.16741	-1.532859	-2.991266	-0.16741	-1.532859	-0.343316
7	94326_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	-2.152005	-2.819511	-2.749972	-0.330817	-0.968453	-2.749972	-0.330817	-0.968453	-0.564952
7	94449_at	phenylalanine-ribNA synthetase-like	Fanal	-1.382829	-1.402592	-1.350595	-0.701799	-1.004059	-1.402592	-1.350595	-0.701799	-1.004059
7	94502_at	DNA segment Chr 13 Wayne State University 50 expressed	D13Wau50e	-0.895862	-0.793108	-0.873205	-0.848995	-0.198691	-0.793108	-0.848995	-0.198691	-0.234218
7	94768_at	RAD21 homolog (S. pombe)	Rad21	-1.274783	-1.484391	-1.840396	-0.821747	-0.734279	-1.484391	-1.840396	-0.821747	-0.680258
7	94805_t_at	---	---	-3.215994	-2.844875	-4.637947	-1.559435	-1.772731	-4.637947	-1.559435	-1.772731	-1.00032
7	94823_at	Mus musculus clone IMAGE 358830 mRNA partial cts	---	-0.826035	-1.336646	-1.310405	-0.47399	-0.959572	-1.310405	-0.47399	-0.959572	-0.495414
7	94843_at	polymerase (DNA directed) delta 4	Pold4	-1.337111	-1.312652	-1.450625	-1.114102	-1.220719	-1.312652	-1.450625	-1.114102	-1.019047
7	94881_t_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	-3.153401	-3.031583	-2.831085	-1.812815	-2.084488	-3.031583	-2.831085	-1.812815	-0.849698
7	94947_s_at	myogenin activated protein kinase kinase kinase 3	Map3k3	-2.378793	-2.26672	-2.244911	-1.660231	-1.639701	-2.26672	-2.244911	-1.660231	-1.639701
7	95015_at	aldo-keto reductase family 1 member C13	Akr1c13	-3.402291	-3.917439	-3.902154	-2.00723	-2.03038	-3.917439	-3.902154	-2.00723	-2.03038
7	95044_at	endothelial-derived gene	Eg1-pending	-0.912787	-1.014431	-0.871013	-0.85621	-0.551237	-1.014431	-0.871013	-0.85621	-0.551237
7	95068_at	transactin	Tan101	-2.769984	-2.782721	-3.942988	-1.674148	-2.303174	-3.942988	-1.674148	-2.303174	-1.631005
7	95086_at	structure specific recognition protein 1	Ssrp1	-1.531401	-0.747487	-1.701398	-0.960676	-0.382698	-0.747487	-1.701398	-0.960676	-0.382698
7	95118_t_at	kinesin family member 22	Kif22	-1.188787	-1.398883	-1.248518	-0.968071	-0.587533	-1.398883	-1.248518	-0.968071	-0.587533
7	95477_at	RIKEN cDNA 1110001M20 gene	TT10001M20Hk	-1.005948	-1.21514	-1.760493	-0.38003	-0.987819	-1.760493	-0.38003	-0.987819	-0.498596
7	95488_at	cDNA sequence BC010304	BC010304	-1.378709	-1.652188	-2.145489	-0.798107	-1.322516	-2.145489	-0.798107	-1.322516	-0.283833
7	95523_at	debrin-like	Debrl	-0.82677	-0.100095	-1.042056	-0.389209	-0.732055	-1.042056	-0.389209	-0.732055	-0.520906
7	95541_at	DNA segment Chr 6 Wayne State University 176 expressed	D16Wsu176e	-3.551991	-3.508282	-3.412001	-1.191321	-2.321769	-3.508282	-3.412001	-1.191321	-0.91612
7	95544_at	filamin beta	Flnb	-2.442893	-2.557838	-2.738368	-1.26715	-2.000521	-2.557838	-2.738368	-1.26715	-2.282296
7	95547_t_at	RIKEN cDNA 402240H07b gene	402240H07bHk	-1.638045	-1.913064	-1.812583	-1.737426	-0.796681	-1.913064	-1.812583	-1.737426	-1.185608
7	95554_at	chondro intracellular chondroitin 4	Clct1	-3.483509	-3.478942	-3.159455	-2.749869	-2.718978	-3.478942	-3.159455	-2.749869	-1.881225
7	95557_t_at	DNA segment Chr 13 Wayne State University 177 expressed	D13Wsu177e	-2.831689	-3.155311	-3.18025	-1.651238	-0.536491	-3.155311	-3.18025	-1.651238	-0.536491
7	95594_at	topoisomerase (DNA I)	Top1	-1.098452	-1.420465	-0.738689	-0.448531	-0.340996	-1.420465	-0.738689	-0.448531	-0.789523
7	95702_at	RIKEN cDNA 1300009C19 gene	1300009C19Hk	-1.133617	-1.272024	-1.608781	-0.47824	-1.133617	-1.272024	-1.608781	-0.47824	-0.865964
7	95706_at	lectin galactose binding soluble 3	Lgals3	-2.888702	-2.947273	-2.516021	-1.707028	-1.614276	-2.947273	-2.516021	-1.707028	-1.784462
7	95781_s_at	---	---	-1.306079	-1.387401	-1.288184	-0.442785	-0.571474	-1.387401	-1.288184	-0.442785	-0.751474
7	96032_at	open reading frame 11	ORF11	-1.531111	-0.747487	-1.169597	-0.876761	-0.756631	-0.747487	-1.169597	-0.876761	-0.756631
7	96268_at	aspartenyl-diphosphate dehydratase	Asp1	-3.615888	-4.226996	-3.840913	-0.85931	-3.288846	-4.226996	-3.840913	-0.85931	-1.815811
7	96275_t_at	RIKEN cDNA 181007J023 gene	TT181007J023Hk	-1.341917	-1.715589	-1.823293	-0.904803	-0.789373	-1.715589	-1.823293	-0.904803	-0.789373
7	96278_at	RIKEN cDNA 1110020C13 gene	TT10020C13Hk	-2.209101	-2.020598	-2.476647	-1.496325	-1.704002	-2.020598	-2.476647	-1.496325	-1.242287
7	96286_at	ubiquitin-associated protein 1	Uba1p	-0.327856	-0.071623	-0.763586	-0.473949	-0.448571	-0.071623	-0.763586	-0.473949	-0.448571
7	96540_at	melenaphilin	Mfn	-1.032673	-0.578196	-0.712787	-0.255666	-0.513654	-0.578196	-0.712787	-0.255666	-0.513654
7	96564_at	heat shock protein 8	Hsp8	-1.727816	-1.137776	-1.760225	-0.860149	-0.868359	-1.137776	-1.760225	-0.860149	-0.868359
7	96613_at	RIKEN cDNA 573053A07 gene	573053A07Hk	-1.024842	-1.460862	-0.938729	-0.388217	-0.642445	-1.460862	-0.938729	-0.388217	-0.642445
7	96658_at	RIKEN cDNA 290015J23 gene	290015J23Hk	-0.455489	-0.460861	-0.388749	-0.199473	-0.24806	-0.460861	-0.388749	-0.199473	-0.19980
7	96708_at	RIKEN cDNA 1200002G139A gene	1200002G139AHk	-1.506887	-2.049338	-1.72268	-0.537811	-0.859113	-2.049338	-1.72268	-0.537811	-1.891426
7	96713_at	RAP1 GTP-GDP dissociation stimulator 1	Rap1gds1	-4.724005	-3.716825	-4.673941	-2.603727	-3.294893	-3.716825	-4.673941	-2.603727	-3.294893
7	96843_at	eukaryotic translation initiation factor 4E like 3	Eif4e3	-0.624716	-0.524048	-0.704827	-0.180033	-0.172737	-0.524048	-0.704827	-0.180033	-0.341008
7	96855_at	RIKEN cDNA 573040B15 gene	573040B15Hk	-1.562224	-1.474295	-1.118186	-0.522089	-0.695901	-1.474295	-1.118186	-0.522089	-0.695901
7	96875_t_at	DNA segment Chr 8 ERATO Doi 772 expressed	D8Erat772e	-0.168095	-0.551415	-0.849165	-0.443807	-0.073206	-0.551415	-0.849165	-0.443807	-0.207119
7	96891_at	acidic nuclear phosphoprotein 32 family member B	Ans2b	-1.850199	-3.825016	-2.93289	-1.481478	-0.180210	-3.825016	-2.93289	-1.481478	-0.180210
7	97273_at	arsenate resistance protein 2	Asr2-pending	-1.212186	-2.523562	-2.14481	-0.914227	-1.041712	-2.523562	-2.14481	-0.914227	-1.041712
7	97320_at	RIKEN cDNA 160022H18 gene	160022H18Hk	-2.307928	-2.233361	-2.31625	-1.863792	-1.600017	-2.233361	-2.31625	-1.863792	-1.600017
7	97426_at	ribosomal protein S6 kinase polypeptide 1	Rps6k1	-2.127708	-2.20212	-2.25467	-1.174205	-1.363329	-2.20212	-2.25467	-1.174205	-1.363329
7	97456_at	fatty acid Coenzyme A ligase long chain 5	Fac5	-2.500778	-1.697552	-1.869565	-0.801034	-1.1981	-1.697552	-1.869565	-0.801034	-0.902878
7	97505_at	ADP-ribosylation factor-like 1	Arf1	-1.263516	-2.407286	-1.755017	-0.407774	-1.003684	-2.407286	-1.755017	-0.407774	-1.003684
7	97515_at	hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	-0.688725	-1.550474	-3.225006	-0.817072	-1.054181	-1.550474	-3.225006	-0.817072	-1.054181
7	97518_at	farnesyl diphosphate farnesyl transferase 1	Fftr1	-0.869592	-0.9568	-0.721331	-0.566669	-0.586014	-0.9568	-0.721331	-0.566669	-0.586014
7	97525_at	glycerol kinase	Gya	-1.612026	-1.430648	-1.453087	-0.289451	-1.11281	-1.430648	-1.453087	-0.289451	-1.11281
7	97527_at	CDC28 protein kinase regulatory subunit 2	Cks2	-0.425163	-0.124317	-0.511746	-0.258423	-0.369695	-0.124317	-0.511746	-0.258423	-0.369695
7	97750_at	lamin receptor 1 (ribosomal protein SA)	Lamr1	-1.289616	-1.099339	-1.462477	-0.367236	-0.834268	-1.099339	-1.462477	-0.367236	-0.834268
7	97824_at	DNA segment Chr 11 ERATO Doi 175 expressed	D11Erat175e	-3.04173	-3.212021	-3.042389	-1.244135	-1.144018	-3.212021	-3.042389	-1.244135	-1.144018
7	97871_at	ERO1-like (S. cerevisiae)	Ero1l	-4.841442	-4.893373	-4.269571	-2.508746	-3.13424	-4.893373	-4.269571	-2.508746	-3.13424
7	97922_at	NADPH cytochrome B5 oxidoreductase	Nce3p	-1.626727	-0.967893							

Involvement of CD44 in mast cell proliferation during terminal differentiation

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By using the recently established culture system that reproduces the terminal differentiation process of connective tissue-type mast cells, we found significant transcriptional induction of CD44. As CD44 is a primary receptor for hyaluronan (HA), which is one of the major extracellular matrix components, we investigated the role of CD44 in cutaneous mast cells. When co-cultured with fibroblasts, mouse bone marrow-derived cultured mast cells (BMDCs) were found to form clusters in an HA-dependent manner. As compared with BMDCs derived from the wild-type mice, those from the CD44^{-/-} mice exhibited impaired growth during the co-cultured period. Furthermore, in the peritoneal cavities and ear tissues, mature mast cells were fewer in number in the CD44^{-/-} mice than in the wild-type mice. We investigated roles of CD44 in mast cell proliferation by reconstituting BMDCs into the tissues of mast cell-deficient, *Kit^W/Kit^{W^{ex}}* mice, and found that the number of metachromatic cells upon acidic toluidine blue staining in the tissues transplanted with CD44^{-/-} BMDCs was not significantly changed for 10 weeks, whereas that in the tissues transplanted with the CD44^{+/+} BMDCs was significantly increased. These results suggest that CD44 plays a crucial role in the regulation of the cutaneous mast cell number.

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KEYWORDS: CD44; fibroblast; hyaluronan; mast cell; proliferation

Mast cells have the potential to produce diverse arrays of mediators, and release them in the context of the responses, in which local mast cells are involved.^{1,2} Mast cells originate from hematopoietic progenitor cells and undergo terminal differentiation in tissues where they are ultimately resident.³ As heterogeneity of tissue mast cells arise as a result of differences in the microenvironment that affects the process of the terminal differentiation, extensive investigation of the maturation process is required for precise understanding of the roles of tissue mast cells. Although several mast cell lines and IL-3-dependent bone marrow-derived cultured mast cells (BMDCs) have been used as models to investigate the process of mast cell activation and subsequent production of proinflammatory mediators, these models have limitations in analyzing functions specific to mature mast cells. Hence,

recent studies have often employed the mast cell knock-in models using the mast cell-deficient mice, such as WBB6F1-*Kit^W/Kit^{W^{ex}}* (*Kit^W/Kit^{W^{ex}}*) and C57BL/6-*Kit^{W^{sh}}/Kit^{W^{sh}}* (*Kit^{W^{sh}}/Kit^{W^{sh}}*), to investigate the roles of mature mast cells *in vivo*.¹

By modifying the co-culturing method of BMDCs together with fibroblasts in the presence of stem cell factor (SCF), we have recently established a culture system for development of mature mast cells, which exhibit properties characteristic of connective tissue-type mast cells (CTMCs), such as degranulation induced by cationic secretagogues, Safranin-positive granules, and high levels of mast cell protease expression.⁴ We then investigated the gene expression profile during the culture period and identified a cluster of candidate genes, which have potentials to modulate mast cell

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maturation. Among these genes, whose expression levels are upregulated, we focused on *CD44* in the current study.

An array of studies has revealed that CD44 is involved in various cellular responses, such as adhesion to the extracellular matrix, migration, cytokine synthesis, and proliferation.³⁻⁷ As CD44 is a surface receptor for hyaluronan (HA), which is one of the major components of the extracellular matrix in the cutaneous tissues,⁸ we speculated that CD44 plays some roles in the terminal differentiation of mast cells in the cutaneous tissues. Cutaneous mast cells have recently received much attention as one of the essential immune modulators. For example, TNF- α derived from the cutaneous mast cells was found to be involved in lymph node hypertrophy upon bacterial infection and in the migration of Langerhans cells to the draining lymph nodes in response to bacterial peptidoglycan.^{9,10} Cutaneous mast cells are also crucial for appropriate peripheral tolerance to skin allografts.¹¹

In this study, we investigated the roles of CD44, during the terminal differentiation of mast cells. We used two approaches to determine the function of CD44 in mast cells: one is the SCF-dependent co-culture system of BMMCs with fibroblasts and the other is a reconstitution system of mast cells into the *Ki^W/Ki^W* mice. We show here that CD44 is involved in the proliferation of mast cells during their terminal differentiation in cutaneous tissues.

MATERIALS AND METHODS

Mice

Specific-pathogen-free, 8-week-old female Balb/c mice and 6- to 8-week-old male WBB6F1-*Ki^W/Ki^W* mice were obtained from Japan SLC (Hamamatsu, Japan), and all mice were kept in a specific pathogen-free animal facility at Kyoto University. The *CD44^{+/-}* mice¹² backcrossed for 6-10 generations to C57BL/6 were bred to generate the *CD44^{+/+}* and *CD44^{-/-}* mice. All animal experiments were performed according to the Guidelines for Animal Experiments of Kyoto University and were approved by the Committee for Animal Experiments.

Materials

The following materials were purchased from the sources indicated: hyaluronidase from bovine testis, and an anti-dinitrophenyl (DNP) IgE (clone SPE-7) from Sigma-Aldrich (St Louis, MO, USA); an anti-CD44 antibody (clone KM81) from Cedarlane (Burlington, ON, Canada); an anti-CD44 antibody (clone KM201) from Southern Biotech (Birmingham, AL, USA); a rat IgG_{2b} antibody from BioLegend (San Diego, CA, USA); a horseradish peroxidase-conjugated anti-mouse IgG and anti-rat IgG antibodies from DAKO (Glostrup, Denmark); an anti-CD16/32 (24G2), an FITC-conjugated anti-mouse IgE, and a phycoerythrin-conjugated anti-c-kit antibody from BD Biosciences (San Diego, CA, USA); an anti-actin and an FITC-conjugated anti-CD44 antibody (clone KM201) from Chemicon (Temecula, CA,

USA); an RNeasy mini kit from Qiagen (Valencia, CA, USA); M-MLV reverse transcriptase, an Alexa546-conjugated anti-rat IgG antibody, and 293FT cells from Invitrogen (Carlsbad, CA, USA); LightCycler-Fast Start DNA Master SYBR Green I from Roche Diagnostics (Mannheim, Germany); an ECL kit from GE Healthcare (Uppsala, Sweden); biotinylated HA-binding protein (bHABP); an HA determination kit from Seikagaku Corp. (Tokyo, Japan); FITC-labeled avidin from Vector Laboratories (Burlingame, UK); and [³H]thymidine (20 Ci/mmol) from PerkinElmer (Boston, MA, USA). All other chemicals were commercial products of the reagent grade.

Preparation of BMMCs and Co-Culture with Swiss 3T3 Cells

Preparation of BMMCs was performed as described elsewhere using 10 ng/ml IL-3 instead of the WEHI-conditioned medium.¹³ The method for development of the CTMC-like cultured mast cells was reported earlier.⁴ Briefly, BMMCs were co-cultured with mitomycin C-treated Swiss 3T3 cells in the presence of the recombinant mouse SCF (100 ng/ml). The subculture was performed every 4 days. Overall > 80% of the viable mast cells were confirmed to be mature mast cells, as assessed by staining with Safranin-O at day 16.

Quantitative RT-PCR Analysis

Total RNAs were isolated from the cultured mast cells using an RNeasy Mini Kit, according to the manufacturer's instruction. Total RNAs were reverse-transcribed using the M-MLV reverse transcriptase and amplified by PCR using a primer offset for GAPDH or CD44 as follows: GAPDH, 5'-TGAACGGGAAGCTCACTGG-3' (forward) and 5'-TCCAC CACCCTGTGCTGTA-3' (reverse); and CD44, 5'-TTGG GGACTTTGCCTC-3' (forward) and 5'-CAGATAGCGTTG GGATG-3' (reverse).

Immunoblot Analysis

Immunoblot analysis was performed as described earlier.¹³ An antibody against actin (1:1000) or CD44 (1:200, clone KM201) was used as the primary antibody.

Flow Cytometry

Mast cells in the ear tissues were enriched as described earlier.¹⁴ The flow cytometric analysis was performed as described earlier with FACSCalibur (Becton Dickinson, Franklin Lakes, NJ, USA) equipped with the CELLQUEST software.¹⁵ The dead cell population was gated out by propidium iodide staining.

Immunofluorescence Staining

The cultured cells were gently rinsed with PBS, fixed with 2% paraformaldehyde, and incubated with the biotinylated HA-binding protein (5 μ g/ml, bHABP) and an anti-CD44 antibody (KM81, 1:500) in the presence of 1% bovine serum albumin overnight at 4 °C. The slides were washed and in-