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No identical "mesenchymal stem cells" at different times and sites: Human committed progenitors of distinct origin and differentiation potential are incorporated as adventitial cells in microvessels

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Corresponding Author:	Paolo Bianco, MD Sapienza University of Rome Rome, ITALY
First Author:	Benedetto Sacchetti, PhD
Order of Authors:	Benedetto Sacchetti, PhD
	Cristina Remoli, PhD
	Alessia Funari, PhD
	Giuseppe Giannicola, MD
	Pamela G. Robey, PhD
	Gesine Kogler, PhD
	Stefanie Liedtke, PhD
	Giulio Cossu, MD
	Marta Serafini, PhD
	Maurilio Sampaolesi, PhD
	Enrico Tagliafico, MD, PhD
	Elena Tenedini, PhD
	Isabella Saggio, PhD
	Mara Riminucci, MD, PhD
	Paolo Bianco, MD
Abstract:	A widely shared view reads that "MSCs" are ubiquitous in human connective tissues, can be defined by a common in vitro phenotype, share a skeletogenic potential as assessed by in vitro differentiation assays, and coincide with the ubiquitous "pericytes." Using stringent in vivo differentiation assays and transcriptome analysis, we show here that human cell populations from different anatomical sources, which would all be regarded as "MSCs" based on these criteria and assumptions, actually differ widely in their transcriptomic signature and in vivo differentiation potential. In contrast, they share the capacity to guide the assembly of functional microvessels in vivo, regardless of their anatomical source, or in situ identity as perivascular or circulating cells. This analysis further reveals that muscle "pericytes," which are not spontaneously osteo-chondrogenic as previously claimed, may indeed coincide with an ectopic perivascular subset of committed myogenic cells similar to satellite cells. Cord blood-derived stromal cells, on the other hand, display the unique capacity to form cartilage in vivo spontaneously, in addition to an assayable osteogenic capacity. These data suggest the need to revise current misconceptions on the origin and function of so-called "MSCs," with important applicative implications. The data also support the view that rather than a uniform class of "MSCs," different mesoderm derivatives include distinct classes of tissue-specific committed progenitors, likely of different developmental origin.



July 8, 2015

Dear Prof. Mummery:

On behalf my co-authors and myself, I would like to submit the manuscript entitled "No identical "mesenchymal stem cells" at different times and sites: Human committed progenitors of distinct origin and differentiation potential are incorporated as adventitial cells in microvessels" by Sacchetti, Funari, Remoli, Giannicola, Robey, Kogler, Liedtke, Cossu, Serafini, Sampaolesi, Tagliafico, Tendini, Saggio, Riminucci and Bianco for consideration for publication in Stem Cell Reports.

In this paper, we provide evidence that "MSCs" derived from different sources (bone marrow, muscle, cord blood) vary widely in their transcriptional profile, and their differentiation capacity as assessed by rigorous in vitro and in vivo transplantation assays. Bone marrow "MSCs" form bone and support hematopoiesis, but are not myogenic; muscle "MSCs" are spontaneously myogenic, but do not form bone; cord blood "MSCs" are inherently chondrogenic, and do form bone, but do not support hematopoiesis. However, in spite of their significant differences, "MSCs" from different sources are capable of forming pericytes when co-transplanted with endothelial cells in vivo, resulting in the development of functional blood vessels.

Based on our data, we have debunked the common notion that human "MSCs" from different tissues are equivalent, but have provided rigorous evidence supporting the existence of tissue-specific committed progenitors. These findings are important not only in understanding the biology of specific tissues, but also from an applicative clinical angle.

We have added suggested reviewers into the website (Irving Weissman, Margaret Buckingham, Elly Tanaka, Moustapha Kassem, Xu Cao, Jozef Dulak), along with reviewers that we respectfully request that you not use due to conflicts of research interests (Arnold Caplan, Bruno Peault, Francesco Dazzi, Willem Fibbe, Darwin Prockop, Camillo Ricordi).

The authors of this paper have declared that they have no conflicts of interest relating to this work.

Please do not hesitate to contact me should you need further information regarding this submission.

With best regards,

A handwritten signature in black ink that reads 'Paolo Bianco'.

Paolo Bianco, M.D.

HIGHLIGHTS

- “MSCs” from different tissues (bone marrow, muscle, cord blood) exhibit different transcriptional profiles
- Stringent in vivo assays show that “MSCs” from different tissues have different differentiation capacities
- In spite of their differences, “MSCs” from different tissues share an ability to organize blood vessel formation and acquire a pericyte fate in vivo

eTOC blurb

Sacchetti and coworkers have provided evidence that “mesenchymal stem cells” derived from different sources (bone marrow, muscle, cord blood) vary widely in their transcriptional profile, and their differentiation capacity as assessed by in vitro assays, and by in vivo transplantation assays. Bone marrow “MSCs” form bone and support hematopoiesis, but are not myogenic; muscle “MSCs” are spontaneously myogenic, but do not form bone; cord blood “MSCs” are inherently chondrogenic, and do form bone, but do not support hematopoiesis. However, in spite of their significant differences, “MSCs” from different sources are capable of forming pericytes when co-transplanted with endothelial cells in vivo, resulting in the development of functional blood vessels. These findings are important not only in understanding the biology of specific tissues, but also from an applicative clinical angle.

No identical “mesenchymal stem cells” at different times and sites: Human committed progenitors of distinct origin and differentiation potential are incorporated as adventitial cells in microvessels

Benedetto Sacchetti,^a Alessia Funari,^a Cristina Remoli,^a Giuseppe Giannicola,^b Pamela G. Robey,^c Gesine Kogler,^d Stefanie Liedtke,^d Giulio Cossu,^e Marta Serafini,^f Maurilio Sampaolesi,^g Enrico Tagliafico,^h Elena Tenedini,^h Isabella Saggio,ⁱ Mara Riminucci,^a Paolo Bianco^{a,#}

^aStem Cell Lab, Department of Molecular Medicine, Sapienza University of Rome, Rome, Italy;

^bDepartment of Anatomical, Histological, Forensic Medicine and Orthopedics Sciences, Sapienza University of Rome, Rome, Italy; ^cCraniofacial and Skeletal Diseases Branch, National Institute of Dental and Craniofacial Research, National Institutes of Health, Department of Health and Human Services, Bethesda, MD 20892, USA; ^dInstitute for Transplant Diagnostics and Cellular Therapeutics, Medical Center Heinrich-Heine University, Duesseldorf, Germany; ^eInstitute of Inflammation and Repair, University of Manchester, Manchester M13 9PL, UK; ^fTettamanti Research Center, Pediatric Department, University of Milano-Bicocca, San Gerardo Hospital, Monza, Italy; ^gTranslational Cardiology Laboratory, Stem Cell Biology and Embryology, Department of Development and Regeneration, KU Leuven, Leuven, Belgium; ^hCenter for Genome Research, University of Modena and Reggio Emilia, Modena, Italy; ⁱDepartment of Biology and Biotechnology “C. Darwin,” Sapienza University, and IBPM CNR, Rome, Italy

[#]Correspondence: paolo.bianco@uniroma1.it

Running Title: Human committed mesodermal progenitors

Key words: Bone marrow stromal cell; mesenchymal stem cell; skeletal progenitors; myogenic progenitors; transplantation; differentiation; in vivo assays; hematopoietic microenvironment

SUMMARY

A widely shared view reads that “MSCs” are ubiquitous in human connective tissues, can be defined by a common *in vitro* phenotype, share a skeletogenic potential as assessed by *in vitro* differentiation assays, and coincide with ubiquitous “pericytes.” Using stringent *in vivo* differentiation assays and transcriptome analysis, we show that human cell populations from different anatomical sources, regarded as “MSCs” based on these criteria and assumptions, actually differ widely in their transcriptomic signature and *in vivo* differentiation potential. In contrast, they share the capacity to guide the assembly of functional microvessels *in vivo*, regardless of their anatomical source, or *in situ* identity as perivascular or circulating cells. This analysis reveals that muscle “pericytes,” which are not spontaneously osteo-chondrogenic as previously claimed, may indeed coincide with an ectopic perivascular subset of committed myogenic cells similar to satellite cells. Cord blood-derived stromal cells, on the other hand, display the unique capacity to form cartilage *in vivo* spontaneously, in addition to an assayable osteogenic capacity. These data suggest the need to revise current misconceptions on the origin and function of so-called “MSCs,” with important applicative implications. The data also support the view that rather than a uniform class of “MSCs,” different mesoderm derivatives include distinct classes of tissue-specific committed progenitors, likely of different developmental origin.

INTRODUCTION

The anatomical identity of “mesenchymal stem cells,” their phenotype, their distribution in different tissues, their lineage, their physiological functions and biological properties represent one of the most controversial and confusing areas in stem cell biology. At this time, two quite distinct descriptions of “MSCs” are found in the literature. One, which emanates from ~50 yrs of widely reproduced experimental work *in vivo*, sees “MSCs” as the same biological object previously known as cultured bone marrow stromal cells (BMSCs); these cells are unique to bone marrow (BM), and include a subset of physically identifiable clonogenic, multipotent, self-renewing progenitor of skeletal tissues, and skeletal tissues only (Bianco et al., 2013). This progenitor is endowed with the unique capacity to organize the hematopoietic microenvironment and the hematopoietic stem cell niche (Bianco, 2011; Friedenstein et al., 1982). The other view sees “MSCs” as progenitors of multiple tissues beyond the range of skeletal tissues, such as skeletal muscle (Caplan, 1991, 2008; Crisan et al., 2008). The demonstration that “MSCs” are perivascular cells in bone marrow (adventitial reticular cells) (Sacchetti et al., 2007) was later extrapolated to claim that in virtually all tissues, pericytes (identified as CD34⁺/CD45⁻/CD146⁺ cells) would represent “MSCs” (Caplan, 2008; Crisan et al., 2008). Hence, these broadly multipotent progenitors, essentially defined by *in vitro* assays (Dominici et al., 2006; Pittenger et al., 1999) that are neither specific nor stringent, would be found in multiple tissues well beyond BM (skeletal muscle, fat, placenta, umbilical cord, etc.) (Caplan, 2008; da Silva Meirelles et al., 2006).

Definition of the origin, anatomy, biological properties and function of so-called “MSCs” has obvious implications, for understanding both their biology and for their use in potential therapies. Notably, assuming that “MSCs” with identical differentiation properties can be isolated from virtually every tissue would imply that multiple tissues are equally suitable cell sources to regenerate multiple tissues.

On the other hand, the assumption that “MSCs” are the *ex vivo* counterpart of “pericytes” would lend support to the view that a number of non-progenitor functions (Bianco et al., 2013) of “MSCs” (anti-inflammatory, immunomodulatory, trophic), claimed to be of major import for therapy of a number of unrelated disorders (Caplan and Correa, 2011), are traceable to an identifiable and ubiquitous *in vivo* cell type. Nonetheless, “pericytes” are only defined by anatomy and do not represent a distinct lineage (Armulik et al., 2011; Diaz-Flores et al., 2009). In addition, their role in tissue injury and repair is pleiotropic, and spans multiple distinct processes including inflammation; furthermore, their participation in the repair of tissues (e.g., through the formation of scar tissue) does not necessarily coincide with a regenerative function.

We previously identified a minimal surface phenotype suited not only to enrich for the archetypal human “MSCs” in uncultured BM cell suspensions, but also to correlate their *ex vivo*-assayed clonogenic capacity with their *in situ* identity and *in vivo* fate following transplantation (Sacchetti et al., 2007). As applied to the study of BMSCs, this led to identification of “MSCs” as subendothelial, perivascular CD146⁺ cells on BM sinusoids, and also provided evidence for their self-renewal *in vivo*, which had long been the missing evidence to support the claim that BMSCs indeed include a subset of *bona fide* stem cells, rather than multipotent progenitors (Bianco et al., 2013; Sacchetti et al., 2007). Using an identical approach to prospectively isolate “MSCs” from a variety of non-BM tissues, Crisan and coworkers later reported that a ubiquitous population of highly myogenic and skeletogenic CD146⁺ cells, coinciding with “MSCs,” is found in association with microvessels of skeletal muscle and other tissues, lending support to the view of pericytes as a uniform, widely distributed population of cells that can be explanted and cultured as “MSCs” (Caplan, 2008; Caplan and Correa, 2011; Crisan et al., 2008). However, striated muscle and skeletal lineages such as bone, cartilage and marrow fat diverge early in development, and no common progenitor of bone and muscle is found in prenatal life past the time of

myotome specification in somites. The notion of a common postnatal progenitor of bone and muscle, therefore, would be at odds with established tenets in developmental biology (Bianco and Robey, 2015).

We show here that MCAM/CD146-expressing stromal cells from different human tissues diverge radically from their BM counterparts in differentiation potency and transcriptional profile, reflective of their different developmental origin. While BM-derived “MSCs”/pericytes are natively skeletogenic but not myogenic, muscle-derived “MSCs”/pericytes are inherently myogenic, but not natively skeletogenic, and appear to represent a subset of cells with functional features of satellite cells, but not the characteristic anatomical location. We further show that prenatal, cord blood-borne “MSCs” in turn exhibit a distinct transcriptional and potency profile, and an inherent cartilage commitment, which diverges markedly from that of postnatal BM-derived “MSCs.” Finally, we show that, irrespective of the postnatal tissue source of these perivascular cells or from fetal blood, these committed progenitors of mesoderm derivatives can associate with nascent blood vessels (BVs) *in vivo* and be recruited to a mural cell fate. These data reveal that a system of committed and self-renewing progenitors with distinct native potency, and not a uniform, equipotent class of “MSCs,” is associated with microvascular walls in postnatal mesoderm-derived tissues. Pericyte recruitment from pre-existing local progenitors is a simple developmental process that explains the very existence of such progenitors in post-natal life and their tissue-specific properties.

RESULTS

The phenotype of “MSCs” *in vitro* does not reflect cell identity and function

Stromal cell strains were established from four different tissue sources: bone marrow (BM), skeletal muscle (MU), periosteum (PE), and perinatal cord blood (CB). For all postnatal tissue sources, clonogenic cells were prospectively isolated based on a minimal surface phenotype as previously described for human BMSCs (CD34⁺/CD45⁻/CD146⁺); colonies of CB stromal cells were established as described (Kluth et al., 2010; Kogler et al., 2004). Of note, CD146 identified a clonogenic subset in MU (presented below) and PE (data not shown), as it does in BM. Multi-clonal strains derived from growth of the originally explanted cells were then expanded under identical culture conditions; all resulting cell strains exhibited the canonical *in vitro* cell surface markers regarded as characteristic of “MSCs” (Figure 1A).

To characterize the specificity and functional significance of the cell surface phenotype of “MSCs” that is widely regarded as a defining feature of “MSCs” across tissues, we performed gene expression profiling using AffimetrixTM technology. Both unsupervised hierarchical clustering (Figure 1Ba) and Principal Component Analysis (PCA) (Figure 1Bb) revealed that gene expression profiles of “MSCs” are clearly separated by an “origin” factor, indicating the lack of specificity and sensitivity of the widely used “minimum” surface phenotype. ANOVA-based supervised analysis selected 1614 class-specific, differentially expressed genes (DEGs) (Supplementary Table 1) showing a fold difference >3 and a False Discovery Rate (FDR) q value <0.05. While perinatal CB cells are characterized by over-representation of genes related to proliferation and cell-cycle regulation (Figure 2A-C), the postnatal MU cells are characterized by over-representation of tissue-specific genes related to their tissue origin (Figure 2D,E). Supplementary Tables 2 and 3 show the first 100 enriched gene sets for CB and MU classes, respectively, while Figure 2A1,B1,C1,D1,E1 show enrichment plots and heatmaps for selected gene sets. The over-represented gene sets coming from Gene Set Enrichment Analysis (GSEA) (Subramanian et al., 2005) support the notion that the prospectively purified CB “MSCs” are highly

proliferative, since the majority of gene sets enriched in this phenotype are related to proliferation, S-phase, RNA and DNA synthesis or DNA repair. On the other hand, prospectively purified MU “MSCs” are clearly characterized by the over-representation of gene sets specifically related to either muscle development or muscle differentiated function (muscle contraction, muscle development and energy metabolism).

“MSCs” from different sources have radically different differentiation properties

BM “MSCs,” prospectively sorted as CD34⁻/CD45⁻/CD146⁺, regularly form bone and establish the hematopoietic microenvironment when transplanted heterotopically using osteoconductive carriers (Sacchetti et al., 2007) (Figure 3Aa). Cells sorted based on the same phenotype from BM and other tissues, including MU, were later reported to be highly myogenic both *in vitro* and *in vivo*, in addition to sharing the ability to differentiate in culture towards skeletal lineages (Crisan et al., 2008), based on widely used, artificial differentiation assays. *In vivo* transplantation of MU “MSCs” of identical surface phenotype as BM “MSCs” revealed no spontaneous *in vivo* osteogenic potential (Figure 3Ab). Likewise, cells established in culture from skin, adipose tissue and amniotic fluid, all sharing the *in vitro* phenotype of “MSCs,” regularly failed to form any histology-proven bone (Supplementary Figure 1), whereas PE “MSCs” did form bone *in vivo*, as previously reported [(Sacchetti et al., 2007) Figure 3Ad]. Using the same *in vivo* assay and carrier, CB “MSCs” did form histology-proven bone of donor origin (Figure 3Ad, human LAMIN A/C positive osteocytes, not shown). Of note, they also generated Safranin O⁺, Alcian blue⁺, COL2⁺ hyaline cartilage intermingled with bone in the same assay (3/3 strains from different donors, and 1/3 single colony-derived strain), but never established a hematopoietic microenvironment (Figure 3Ba-h). This was unique, as BM “MSCs” never form cartilage in the same assay, which is usually interpreted as a need for an hypoxic environment for

chondrogenesis *in vivo*, which is not provided in an open transplantation system permissive for neovascularization.

The *in vitro* myogenic capacity of the same cell strains was tested under stringent conditions [i.e., in the absence of exogenous myoblasts (Sherwood et al., 2004), or of demethylating agents such as 5-azacytidine (Wakitani et al., 1995)]. MU “MSCs” readily and efficiently generated myotubes in culture, using canonical differentiation conditions [2% horse serum on MatrigelTM (Dellavalle et al., 2007)], whereas no myogenesis was observed under identical conditions with non-MU-derived stromal cells (Figure 4A). With these non-MU “MSCs,” myotubes could only be obtained in co-cultures with myoblasts (C2C12 cells). Notably, the vast majority of nuclei incorporated in the newly formed myotubes were murine, indicating that human non-MU “MSCs” did not contribute significantly to myogenesis *in vitro* even in non-stringent differentiation assays (data not shown). In cultures of MU CD146⁺ cells (Figure 4C), highly efficient myogenesis was observed, even in clonal strains established by single CD146⁺ cells (Figure 4B), and occurred spontaneously; i.e., with no recourse but to canonical differentiation conditions (Figure 4D).

Local transplantation of CD146⁺ BM, PE or CB cells into CTX-injured *tibialis anterior* muscle of SCID/beige (Figure 5A) or SCID/mdx mice (not shown) (Dellavalle et al., 2007) failed to contribute to regenerating muscle. In contrast, CD146⁺ MU cells revealed an efficient incorporation of donor nuclei (Figure 5B and Supplementary Tables 4 and 5), and expression of human muscle proteins in regenerating myofibers (Figure 5C (CD56), Figure 5D (Dystrophin 2, Spectrin) and Supplementary Table 6). However, the canonical *in vivo* myogenesis assay relies on fusion between donor cells and host myoblasts, which brings about reprogramming of donor cells by host myogenic factors. A stringent *in vivo* myogenesis assay thus requires the exclusion of such events. To this end, we

suspended equal numbers of MU, BM, or CB cells with identical surface phenotype, grown in culture under identical conditions, in growth factor reduced Matrigel™, and injected the resulting suspension into the epifascial space of the back of SCID/beige mice. Plugs harvested at 3 wks demonstrated that MU cells had generated myotubes, myofibers and a unique spheroidal syncytia expressing a differentiated muscle phenotype (Figure 5E, desmin, MyHC, CD56), indicating that the myogenic capacity of MU cells is independent of fusion with local myoblasts. The myosac phenotype may result from spontaneous contraction of the myotube poorly adhering to the substrate and obviously not constrained by tendons. BM cells, while remaining viable, did not generate bone, cartilage or muscle. CB cells, which formed bone and cartilage upon transplantation with an osteoconductive carrier, generated hyaline cartilage but not bone (Figure 5F).

MU CD146⁺ cells are perivascular, committed myogenic progenitors.

These data revealed a strong, spontaneous myogenic capacity specific for MU CD146⁺ cells, fully consistent with the high expression of myogenic regulatory factors and genes reflecting the differentiated function of muscle (Supplementary Figure 2). Cell sorting, immunolocalization, and colony forming efficiency (CFE) assays identified MU CD146⁺ cells as distinct from CD56⁺/CD146⁻ satellite cells and CD34⁺/CD146⁺ endothelial cells (Supplementary Figure 3, Supplementary Tables 7-9). In cultures established from highly purified CD56⁻/CD146⁺ cells, CD146 expression was turned off over time while expression of CD56, PAX7, alkaline phosphatase (ALP), MyoD, Myogenin, were turned on (Figure 6A and Supplementary Figure 2). Only a small subset of clonogenic, myogenic CD146⁺ cells coexpressed the pericyte marker, ALP [(Dellavalle et al., 2007), Figure 6B and Supplementary Table 10], and myogenic cells were highly enriched in the CD146⁺/ALP⁻ fraction (Figure 6C). In situ, ALP and CD146 were expressed in a mutually exclusive fashion in precapillary arterioles and postcapillary venules, respectively, suggesting that the venous compartment represents

the largest repository of perivascular CD146⁺ perivascular cells that can be assayed as myogenic progenitors (Figure 6D). Immunolocalization studies further revealed the presence of a relatively rare population of adventitial cells expressing muscle regulatory factor proteins (PAX3, PAX7) in post-capillary venules (Figure 6E). A small subset of freshly isolated MU CD146⁺ cells coexpressed PAX7 (Figure 6F).

Generation of perivascular cells from different types of stromal cells *in vivo*

In heterotopic transplants made with osteoconductive carriers (HA/TCP), BM-derived skeletal stem cells can guide and organize the formation of BVs, with which a subset of them ultimately associates (Sacchetti et al., 2007). To test the ability of BM and non-BM derived progenitors to guide and organize nascent BVs under simplified conditions that bar the formation of bone, we co-transplanted BM- and non-BM-derived progenitors in MatrigelTM, along with human umbilical vein endothelial cells (HUVECs). With BM-derived progenitors, this resulted in the formation of an extensive network of capillary-like BVs at 3 wks. Their wall was made by two cell layers – an inner hCD34⁺ endothelial layer, and an outer, discontinuous layer of mural cells made by transplanted, GFP-tagged BM progenitors, expressing CD146 and α SM actin (Figure 7A). In transplants harvested at 8 wks, extensive maturation of the BV wall was observed, as indicated by the formation of thick-walled artery- and vein-like BVs, with a multilayered GFP⁺, α SM actin⁺ smooth muscle coat. The BVs were functional and perfused by host blood (Figure 7A). Experiments made with MU CD146⁺ progenitors also resulted in the formation of a capillary lattice, which was less extensive than with BM CD146⁺ cells, but similarly well organized (Figure 7B). No obvious differentiation of muscle structures were observed in these transplants, at variance with transplants of MU CD146⁺ cells without HUVECs, suggesting that contribution to BV formation and myogenesis could be alternative fates dictated by endothelial cells. With CB CD146⁺ cells, again the formation of functional BVs was observed. Strikingly, these BVs,

lined by a continuous hCD34⁺ endothelial layer, were coated by a thin layer of subendothelial CD146⁺ mural cells, and an outer coat of differentiated chondrocytes (Figure 7C), making these BVs a unique kind of cartilage-armored BVs, not known to occur in natural tissues. Knockdown of CD146 in BM progenitors partially interfered with the organization of BVs, resulting in the formation of BVs of irregular size and shape, often devoid of a lumen, and devoid of a mural cell coat (Supplementary Figure 4).

DISCUSSION

A widely accepted view in the literature holds that “MSCs” can be defined by rather loose and non-specific *in vitro* properties, and exhibit identical functional and differentiation properties regardless of their tissue source. This view, complemented by the notion that “MSCs” would coincide with ubiquitous “pericytes,” was recently reinforced by the claim that MU-derived “pericytes” would be both myogenic and skeletogenic, and exhibit an *in situ* surface phenotype similar to the one characteristic of BMSCs (skeletal stem cells). We have shown here that CD34⁻/CD45⁻/CD146⁺ “MSCs” isolated from different tissues have inherently distinct transcriptomic signatures and differentiation capacities. By gauging their native differentiation potential with a variety of stringent differentiation assays, we demonstrated that human BM CD146⁺ cells are inherently geared to generate bone and BM stroma, including BM adipocytes, but are not myogenic, and are not spontaneously chondrogenic *in vivo*; MU “MSCs” cells with an identical cell surface phenotype are not inherently skeletogenic, and are inherently myogenic; CB “MSCs” are not myogenic, but are chondro-osteoprogenitors, and are the only kind of human “MSCs” ever shown to actually form cartilage consistently in open heterotopic transplants *in vivo*, independent of any *ex vivo* induction to cartilage differentiation as applied in the widely used pellet culture assay. BM- and MU-derived clonogenic progenitors of mesoderm derivatives are associated with BV walls *in situ*, include cells in a position

characteristic of mural cells/pericytes, but also include vascular wall cells that do not necessarily exhibit anatomical features of pericytes proper - for example, adventitial cells in muscular veins. More strikingly, fetal chondro- osteoprogenitors that circulate in cord blood, by definition, are neither associated with BV walls nor represent pericytes. The origin of these cells remains to be elucidated. It is conceivable, however, that skeletal progenitors located at sites of active skeletal growth can accidentally spillover into the bloodstream. Nonetheless, independent of their origin, native differentiation potencies, gene expression profiles, and *in situ* anatomical positioning, perinatal and postnatal mesoderm progenitors of different origins can dynamically associate with, and organize, nascent BVs as shown here using a simple *in vivo* assay.

Our data reveal that *in lieu* of a uniform, broadly multipotent, and equipotent class of ubiquitous “MSCs,” perinatal and postnatal assayable progenitors found in cord blood, skeletal tissues and skeletal muscle comprise a varied system of tissue-specific progenitors. Each member of the system is committed to a specific differentiation range. CB “mesenchymal” progenitors are committed to cartilage and bone formation, reminiscent of the potential of prenatal skeletal progenitors to generate skeletal rudiments made of cartilage and bone. Postnatal BM skeletal progenitors are instead committed to bone and BM stroma formation, but not to cartilage, mirroring an “adult” structure of skeletal segments. Myogenic and skeletogenic potential are mutually exclusive, as dictated by a specific set of master transcriptional regulators.

Even if updated to equate “MSCs” with pericytes (Caplan, 2008; Crisan et al., 2008), the widespread concept of broadly and uniformly multipotent “MSCs” that are invariant in anatomical space and developmental time leaves the developmental origin of such cells unaddressed, and in fact collides with certain fundamental tenets of developmental biology, such as the early segregation of inherent

osteogenic and myogenic potential into different lineages (Bianco and Robey, 2015). Our data now reveal a simple mechanism whereby assayable skeletogenic or myogenic progenitors can be established in different tissues. As previously postulated (Bianco et al., 2013; Bianco et al., 2008), we have now directly shown that committed progenitors of different origin and differentiation potential can physically associate with nascent BV walls in an experimental assay, and be recruited to a mural cell fate. In an earlier study, the most robust contribution of grafted mesoderm progenitor cells in quail-chick chimeras was, in fact, to the adventitia of BVs of any caliber (Minasi et al., 2002). In development, somite-derived cells associate with, and are incorporated into, the wall of the dorsal aorta (Esner et al., 2006). Pericytes originate from the recruitment of non-endothelial, mesenchymal cells to vascular walls (Armulik et al., 2011; Hellstrom et al., 1999; Hirschi and D'Amore, 1996; Jain, 2003; Lindahl et al., 1997). Obviously, the same mechanism may operate in different tissues and at different developmental times. General mechanisms regulating mural cell recruitment have largely been elucidated, and provide the background against which to seek additional determinants operating in the retention of quiescent mesoderm progenitors in a vascular niche. CD146 itself may represent a player in this scenario, consistent with its nature as a cell adhesion molecule (Shih, 1999), and with evidence provided here that its knockdown perturbs the establishment of properly structured BVs *in vivo*.

The direct interaction of committed progenitors with endothelial walls of nascent BV can be related to their arrested proliferation and differentiation, leading to retention, within specific tissue types, of a compartment of progenitors with pre-defined commitment, and a potential for further growth defined by their replicative history prior to incorporation into BV walls. The long-known heterogeneity of clonogenic mesodermal progenitors (CFU-Fs) in proliferative potential *ex vivo* might find in this view a simple explanation.

Our data have additional implications of applicative nature. Prospective isolation of putative “MSCs” from different tissues, based on the use of the minimal effective surface phenotype CD34⁻/CD45⁻/CD146⁺ (Sacchetti et al., 2007) leads to isolation of committed tissue-specific progenitors, not of broadly multipotent, equivalent cells. Hence, design of cell therapy strategies for specific tissues must remain cognizant of the specificity of the isolatable progenitors. In fact, reliance on this specificity leads to highly effective isolation of tissue specific progenitors. This is best illustrated by the case of skeletal muscle, where we have shown that CD146⁺ cells are far more enriched in spontaneously myogenic cells than previously identified populations of putative non-satellite cell classes (Dellavalle et al., 2007). Importantly, we have shown that these cells, which do express the satellite lineage marker, PAX7, and behave like satellite cells in *in vitro* and *in vivo* assays (Montarras et al., 2005), may in fact represent subsets of the same original population, recruited to distinct anatomical niches based on distinct, local cell-cell interactions, randomly directing individual progenitors to either the surface of developing fibers (satellite cells) or the surface of nascent BVs (myogenic “pericytes,” or else, ectopic satellite cells). Consistent with this hypothesis, proximity of one anatomical locale to the other can amount, in fact, to less than 1 cell diameter.

In summary, we have provided a rigorous analysis of mesodermal progenitors isolated from perinatal and postnatal tissues that reveals their inherent differentiation potential. These data underscore the fact that a ubiquitous “MSC” with identical differentiation capacities does not exist, and thus, the “MSC” terminology should be abandoned for the sake of clarity. Furthermore, we have demonstrated that irrespective of their inherent differences, tissue-specific mesodermal progenitors are capable of being recruited to a mural cell fate, providing a plausible mechanism by which pericytes are formed, and how they serve as a source of local stem/progenitor cells.

EXPERIMENTAL PROCEDURES

Cell isolation

Samples were obtained with informed consent per institutionally approved protocols. BMSCs were isolated and cultured as previously described (Sacchetti et al., 2007). PE cells were generated as per established methods (Cicconetti et al., 2007). Human CB cells (≥ 36 weeks of gestation) were isolated and cultured as described previously (Kluth et al., 2010).

Muscle-derived cells. Normal muscle samples ($1\text{--}30 \times 10^2 \text{mg}$) were obtained from 17 human adult patients (aged 25-65 yrs) undergoing orthopedic surgery, from *vastus lateralis* (1), *quadriceps femoris* (5), *triceps brachii* (2), *deltoides* (4), *gluteus maximus* (5). Samples were washed with Hank's balanced salt solution without $\text{Ca}^{2+}/\text{Mg}^{2+}$ (HBSS, Invitrogen Life Technologies Corp) with 30mM HEPES (Sigma), 100U/ml penicillin, 100 $\mu\text{g}/\text{ml}$ streptomycin (Invitrogen) for 10min at room temperature with gentle agitation. Tissue samples were used for explant cultures, or to obtain single cell suspensions. For explant cultures, tissues were manually minced into 1x1mm fragments, and placed into 100mm dishes containing complete medium [αMEM (Invitrogen) with 20% FBS (Invitrogen), 2mM L-glutamine, 100U/ml penicillin, 100 $\mu\text{g}/\text{ml}$ streptomycin]. Explants were monitored daily for outgrowth of adherent cells and fresh medium was added every 3 days. At sub-confluence, adherent cells were detached with trypsin and replated, and tissue fragments were discarded. To obtain single cell suspensions, tissue fragments were digested twice with 100U/ml *Clostridium histolyticum* type II collagenase (Invitrogen) supplemented with 3mM CaCl_2 in $\text{Ca}^{2+}/\text{Mg}^{2+}$ -free PBS (Invitrogen) for 40 min at 37°C with gentle agitation. The samples were centrifuged at 1000 rpm for 5min at 4°C , washed with $\text{Ca}^{2+}/\text{Mg}^{2+}$ -free PBS, resuspended in PBS, passed through 18 gauge needles to break up cell aggregates, and filtered through a 40 μm pore size cell strainer (Becton Dickinson) to obtain a single cell suspension. Nucleated

cells were counted using a haemocytometer. Cell suspensions were used to obtain cultures of unfractionated total cells, or for sorting of CD146⁺ cells, CD146⁺/CD56⁺ cells, CD146⁺/CD34⁺ cells, or CD146⁺/ALP⁺ cells. To obtain non-clonal cultures, cells were seeded at a density of 1.6×10^3 - 1.6×10^5 cells/cm² in 75cm² flasks or in 100mm dishes (Becton Dickinson Labware). For multi-clonal cultures (combining multiple colonies), cells were seeded into 100mm dishes at a density of 1.6 cells/cm², and formation of discrete colonies was scored after 14 days. Non-clonal cultures were passaged when subconfluent; multi-clonal cultures were passaged on day 14.

Cell sorting and flow cytometry

Surface markers were assessed by using a FACSCalibur flow cytometer with CellQuest software (Becton Dickinson Biosciences) as reported previously (Sacchetti et al., 2007) with mouse anti-human monoclonal antibodies (listed in Supplementary Table 11). CD146⁺, CD146⁺/CD56⁺, CD146⁺/CD34⁺ cell subsets and CD146⁺/ALP⁺ cell subsets were separated using a FACS DIVAntageSE flow cytometer (Becton Dickinson Labware). Alternatively, CD146⁺, CD146⁺/CD56⁺, CD146⁺/CD34⁺ and CD146⁺/ALP⁺ fractions were separated using a MiniMACS magnetic column separation unit (Miltenyi Biotec) per the manufacturer's instructions.

Gene expression profiling and data analysis.

Total RNA was isolated from multiclonal cultures of CD146⁺ cell populations using RNeasy RNA isolation kit (Qiagen) per the manufacturer's instructions. Disposable RNA chips (Agilent RNA 6000 Nano LabChip kit) were used to determine the concentration and purity/integrity of RNA samples using an Agilent 2100 bioanalyzer. cDNA synthesis, biotin-labeled target synthesis, HG-U133 plus 2.0 GeneChip (Affymetrix) array hybridization, staining and scanning were performed according to the standard protocol supplied by Affymetrix. Probe level data were normalized and converted to

expression values using Partek Genomics Suite 6.2 (Partek Inc), following the RMA algorithm (Irizarry RA, et al. 2003) or DChip procedure (invariant set) (Li and Hung Wong, 2001; Li and Wong, 2001). Quality control assessment was performed using different Bioconductor packages such as R-AffyQC Report, R-Affy-PLM, R-RNA Degradation Plot and Partek's QC. Low quality samples were removed from analysis. Before significance analysis, Partek's batch correction method, which reduces variation due to random factors, was used to enhance signal. Sample data were then filtered in order to remove probesets having a standard deviation/mean ratio greater the 0.8 and less that 1000. Principal Component Analysis (PCA) as well as the unsupervised hierarchical clustering were performed using Partek GS®. The agglomerative hierarchical clustering was performed using the Euclidean distance and the average linkage method. Differentially expressed genes were selected using a supervised approach using the ANOVA package included in Partek GS® Software. Formally, an unpaired t-test using a contrast fold change of at least 3 and an FDR (q-value) <0.05 was used in order to perform multiple pairwise comparisons between each class and the rest. Raw data of gene expression profiling were submitted to GEO repository (GSE69991).

Gene Set Enrichment Analysis

Gene Set Enrichment Analysis (GSEA) was performed using GSEA software [(<http://www.broadinstitute.org/gsea/index.jsp>; (Subramanian et al., 2005)] on log2 expression data of CD146⁺ cell population purified from BM, CB, MU and PE and classified in the corresponding classes. Gene sets were taken from the Molecular Signatures Database (<http://www.broadinstitute.org/gsea/msigdb/index.jsp>). In particular, we investigated whether each class of CD146⁺ cells was associated with over- or under-represented genes in pairwise comparisons between each class and the rest. Gene sets significantly over- or under-represented were returned by

GSEA as showing an Enrichment Score $ES < 0$ and an FDR $< 25\%$ when using Signal2Noise as metric and 1,000 permutations of phenotype labels.

Colony forming efficiency assays

CFE assays were performed with different cell fractions obtained by cell sorting, and unfractionated total cells. CD146⁺ cells were seeded at 1.6-3.3 cells/cm², CD146⁺/CD34⁺, CD146⁺/CD56⁻ cells were seeded at 1.6-8.3 cells/cm² and CD146⁺/ALP[±] were seeded at 0.083-3.3 cells/cm². CD146⁻ (CD56[±] or CD34[±] or ALP[±]) and unsorted total cells were seeded at an equivalent or higher density (1.6-1.6x10⁵ cells/cm²) and grown under identical conditions. After 14 days, CFE was determined as the mean number $\pm$ SD of colonies (>50 cells)/10²-10⁵ cells initially plated. Alkaline phosphatase cytochemistry was done using naphthol-AS-phosphate as substrate and Fast Blue BB as coupler.

***In vitro* differentiation assays**

Spontaneous myogenic differentiation was assessed by plating cells onto MatrigelTM coated dishes, with DMEM/2% HS, or on plastic with MEM/20% FBS at clonal density. After 7 days, cultures were fixed and labeled for immunofluorescence with a monoclonal antibody against striated myosin heavy chain. Efficiency of myogenic differentiation was estimated as the % of DAPI⁺ nuclei found within myosin positive myotubes. Fluorescence images were obtained using Nikon Eclipse TE2000 Inverted Microscope (Nikon Inc). Data were compared by ANOVA.

***In vivo* transplantation assays**

All animal procedures were approved by the relevant institutional committees.

Heterotopic bone formation: To assess osteogenic potential, constructs of test cells and osteoconductive material (hydroxyapatite/tricalcium phosphate (HA/TCP), Zimmer) were transplanted heterotopically into the subcutaneous tissue of SCID/beige mice (CB17.Cg-*Prkdc*^{scid}*Lyst*^{bg-J}/CrI, Charles River), using an established assay (Krebsbach et al., 1997; Sacchetti et al., 2007).

Orthotopic in vivo myogenesis, CTX model: MU- BM-, CB-derived cell populations (1×10^6) were injected i.m. into the left *tibialis anterior* of 2 month-old female SCID/beige mice injured 1 day earlier by an i.m. injection of cardiotoxin (CTX, Latoxan) (Dellavalle et al 2007). Normal human dermal fibroblasts or STO mouse embryonic fibroblasts [a gift from Dr Ana Cumano, Pasteur Institute, Paris], were cultured in Dulbecco's modified Eagle's medium (DMEM)-high glucose (Invitrogen), supplemented with 2mM glutamine].

Orthotopic in vivo myogenesis, SCID/mdx model: MU and BM derived cell populations were also injected via the femoral artery of 2 month-old female SCID/*mdx* dystrophic mice (C57BL/10ScSn-*mdx*/J; Jackson Laboratory) as described (Dellavalle et al 2007). Two injections of 5×10^5 cells at a 15-day interval were performed, and animals were euthanized 15 days after the last injection. The injected *tibialis anterior* muscles were analyzed for myogenic markers by immunofluorescence, with un-injected contralateral muscles serving as controls.

Heterotopic in vivo differentiation, MatrigelTM: 1×10^6 cells from multiclonal cultures of MU, BM, CB, skin fibroblast cultures and sorted cell cultures, were suspended in 1ml of MatrigelTM Growth factor-reduced (BD Biosciences Labware), either alone or admixed with an equal number of HUVECs (Cambrex Corporation). Aliquots (~0.7ml) were injected in the subcutaneous tissue of the back of SCID/beige mice. Mice were euthanized after 20 days and transplants were immediately fixed for

histology. HUVECs were grown in Clonetics EGM-2 BulletKit (Cambrex Corporation) following the manufacturer's instructions. In some experiments, cells from multiclonal cultures of MU and BM cells were transduced with LV-EF-GFP lentiviral vectors.

Lenti-viral vectors

Lentiviral vectors for eGFP expression, and for CD146 silencing were produced and used as described (Piersanti et al., 2010; Sacchetti et al., 2007). Sorted CD146⁺ cells from BM and MU were transduced with lentiviral vectors at an MOI of 5 and cultured for 2 wks in complete medium before use.

Immunohistochemistry studies

Orthotopic and heterotopic transplants were snap-frozen in OCT embedding medium in liquid nitrogen and cryostat-sectioned serially, or alternatively fixed in 4% formaldehyde (and decalcified in the case of bone- or ceramic-containing transplants) and processed for paraffin embedding. Five- μ m thick paraffin sections were stained with H&E, Safranin O and Light Green, Alcian blue or Sirius red for histology. All primary antibodies used for immunolocalization studies are listed in Supplementary Table 12 and were used as per standard immunoperoxidase (DAB reaction) or immunofluorescence protocols. Secondary antibodies labeled with Alexa Fluor 594 and 488, were from Molecular Probes (Invitrogen). Nuclei were stained by DAPI or Propidium Iodide (Sigma). Fluorescence images-stacks were obtained using confocal microscopy laser scanning (Leica TCS SP5, Leica Microsystems). Brightfield light and polarized light microscopy images were obtained using Zeiss Axiophot microscope (Carl Zeiss).

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REFERENCES

- Armulik, A., Genove, G., and Betsholtz, C. (2011). Pericytes: developmental, physiological, and pathological perspectives, problems, and promises. *Dev Cell* 21, 193-215.
- Bianco, P. (2011). Bone and the hematopoietic niche: a tale of two stem cells. *Blood* 117, 5281-5288.
- Bianco, P., Cao, X., Frenette, P.S., Mao, J.J., Robey, P.G., Simmons, P.J., and Wang, C.Y. (2013). The meaning, the sense and the significance: translating the science of mesenchymal stem cells into medicine. *Nat Med* 19, 35-42.
- Bianco, P., and Robey, P.G. (2015). Skeletal stem cells. *Development* 142, 1023-1027.
- Bianco, P., Robey, P.G., and Simmons, P.J. (2008). Mesenchymal stem cells: revisiting history, concepts, and assays. *Cell Stem Cell* 2, 313-319.
- Caplan, A.I. (1991). Mesenchymal stem cells. *J Orthop Res* 9, 641-650.
- Caplan, A.I. (2008). All MSCs are pericytes? *Cell Stem Cell* 3, 229-230.
- Caplan, A.I., and Correa, D. (2011). The MSC: an injury drugstore. *Cell Stem Cell* 9, 11-15.
- Cicconetti, A., Sacchetti, B., Bartoli, A., Michienzi, S., Corsi, A., Funari, A., Robey, P.G., Bianco, P., and Riminucci, M. (2007). Human maxillary tuberosity and jaw periosteum as sources of osteoprogenitor cells for tissue engineering. *Oral Surg Oral Med Oral Pathol Oral Radiol Endod* 104, 618 e611-612.
- Crisan, M., Yap, S., Casteilla, L., Chen, C.W., Corselli, M., Park, T.S., Andriolo, G., Sun, B., Zheng, B., Zhang, L., *et al.* (2008). A perivascular origin for mesenchymal stem cells in multiple human organs. *Cell Stem Cell* 3, 301-313.
- da Silva Meirelles, L., Chagastelles, P.C., and Nardi, N.B. (2006). Mesenchymal stem cells reside in virtually all post-natal organs and tissues. *J Cell Sci* 119, 2204-2213.
- Dellavalle, A., Sampaioles, M., Tonlorenzi, R., Tagliafico, E., Sacchetti, B., Perani, L., Innocenzi, A., Galvez, B.G., Messina, G., Morosetti, R., *et al.* (2007). Pericytes of human skeletal muscle are myogenic precursors distinct from satellite cells. *Nat Cell Biol* 9, 255-267.
- Diaz-Flores, L., Gutierrez, R., Madrid, J.F., Varela, H., Valladares, F., Acosta, E., Martin-Vasallo, P., and Diaz-Flores, L., Jr. (2009). Pericytes. Morphofunction, interactions and pathology in a quiescent and activated mesenchymal cell niche. *Histol Histopathol* 24, 909-969.
- Dominici, M., Le Blanc, K., Mueller, I., Slaper-Cortenbach, I., Marini, F., Krause, D., Deans, R., Keating, A., Prockop, D., and Horwitz, E. (2006). Minimal criteria for defining multipotent mesenchymal stromal cells. The International Society for Cellular Therapy position statement. *Cytotherapy* 8, 315-317.
- Esner, M., Meilhac, S.M., Relaix, F., Nicolas, J.F., Cossu, G., and Buckingham, M.E. (2006). Smooth muscle of the dorsal aorta shares a common clonal origin with skeletal muscle of the myotome. *Development* 133, 737-749.
- Friedenstein, A.J., Latzinik, N.W., Grosheva, A.G., and Gorskaya, U.F. (1982). Marrow microenvironment transfer by heterotopic transplantation of freshly isolated and cultured cells in porous sponges. *Exp Hematol* 10, 217-227.
- Hellstrom, M., Kalen, M., Lindahl, P., Abramsson, A., and Betsholtz, C. (1999). Role of PDGF-B and PDGFR-beta in recruitment of vascular smooth muscle cells and pericytes during embryonic blood vessel formation in the mouse. *Development* 126, 3047-3055.

Hirschi, K.K., and D'Amore, P.A. (1996). Pericytes in the microvasculature. *Cardiovasc Res* 32, 687-698.

Irizarry, R.A., Hobbs, B., Collin, F., Beazer-Barclay, Y.D., Antonellis, K.J., Scherf, U., Speed, T.P. (2003) Exploration, normalization, and summaries of high density oligonucleotide array probe level data. *Biostatistics* 4, 249-264.

Jain, R.K. (2003). Molecular regulation of vessel maturation. *Nat Med* 9, 685-693.

Kluth, S.M., Buchheiser, A., Houben, A.P., Geyh, S., Krenz, T., Radke, T.F., Wiek, C., Hanenberg, H., Reinecke, P., Wernet, P., *et al.* (2010). DLK-1 as a marker to distinguish unrestricted somatic stem cells and mesenchymal stromal cells in cord blood. *Stem Cells Dev* 19, 1471-1483.

Kogler, G., Sensken, S., Airey, J.A., Trapp, T., Muschen, M., Feldhahn, N., Liedtke, S., Sorg, R.V., Fischer, J., Rosenbaum, C., *et al.* (2004). A new human somatic stem cell from placental cord blood with intrinsic pluripotent differentiation potential. *J Exp Med* 200, 123-135.

Li, C., and Hung Wong, W. (2001). Model-based analysis of oligonucleotide arrays: model validation, design issues and standard error application. *Genome Biol* 2, RESEARCH0032.

Li, C., and Wong, W.H. (2001). Model-based analysis of oligonucleotide arrays: expression index computation and outlier detection. *Proc Natl Acad Sci U S A* 98, 31-36.

Lindahl, P., Johansson, B.R., Leveen, P., and Betsholtz, C. (1997). Pericyte loss and microaneurysm formation in PDGF-B-deficient mice. *Science* 277, 242-245.

Minasi, M.G., Riminucci, M., De Angelis, L., Borello, U., Berarducci, B., Innocenzi, A., Caprioli, A., Sirabella, D., Baiocchi, M., De Maria, R., *et al.* (2002). The meso-angioblast: a multipotent, self-renewing cell that originates from the dorsal aorta and differentiates into most mesodermal tissues. *Development* 129, 2773-2783.

Montarras, D., Morgan, J., Collins, C., Relaix, F., Zaffran, S., Cumano, A., Partridge, T., and Buckingham, M. (2005). Direct isolation of satellite cells for skeletal muscle regeneration. *Science* 309, 2064-2067.

Piersanti, S., Remoli, C., Saggio, I., Funari, A., Michienzi, S., Sacchetti, B., Robey, P.G., Riminucci, M., and Bianco, P. Transfer, analysis, and reversion of the fibrous dysplasia cellular phenotype in human skeletal progenitors. *J Bone Miner Res* 25, 1103-1116.

Pittenger, M.F., Mackay, A.M., Beck, S.C., Jaiswal, R.K., Douglas, R., Mosca, J.D., Moorman, M.A., Simonetti, D.W., Craig, S., and Marshak, D.R. (1999). Multilineage potential of adult human mesenchymal stem cells. *Science* 284, 143-147.

Sacchetti, B., Funari, A., Michienzi, S., Di Cesare, S., Piersanti, S., Saggio, I., Tagliafico, E., Ferrari, S., Robey, P.G., Riminucci, M., *et al.* (2007). Self-renewing osteoprogenitors in bone marrow sinusoids can organize a hematopoietic microenvironment. *Cell* 131, 324-336.

Sherwood, R.I., Christensen, J.L., Conboy, I.M., Conboy, M.J., Rando, T.A., Weissman, I.L., and Wagers, A.J. (2004). Isolation of adult mouse myogenic progenitors: functional heterogeneity of cells within and engrafting skeletal muscle. *Cell* 119, 543-554.

Shih, I.M. (1999). The role of CD146 (Mel-CAM) in biology and pathology. *J Pathol* 189, 4-11.

Subramanian, A., Tamayo, P., Mootha, V.K., Mukherjee, S., Ebert, B.L., Gillette, M.A., Paulovich, A., Pomeroy, S.L., Golub, T.R., Lander, E.S., *et al.* (2005). Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* 102, 15545-15550.

Wakitani, S., Saito, T., and Caplan, A.I. (1995). Myogenic cells derived from rat bone marrow mesenchymal stem cells exposed to 5-azacytidine. *Muscle Nerve* 18, 1417-1426.

FIGURES

Figure 1. A) FACS analysis of multiconal BM, MU, PE and CB cells. All strains express the canonical *in vitro* “phenotype” of “MSCs” and CD146. B) Unsupervised clustering of gene-expression profiling data of CD146⁺ cells purified from BM, CB, MU, and PE. Unsupervised analysis was performed to investigate whether there was evidence for native groupings of samples based on correlations between gene expression profiles. Results of the hierarchical clustering (Ba) and the Principal Component Analysis (PCA) (Bb) revealed that gene expression profiles of CD146⁺ cells are clearly separated by the “origin” factor.

Figure 2. Prenatal CB “MSCs” are characterized by the over-representation of many genes related to proliferation and cell-cycle regulation. Postnatal MU “MSCs” are characterized by the over-representation of tissue-specific genes related to their tissue origin, specifically by genes regulating muscle contraction, muscle development and energy metabolism. The over-represented gene sets from GSEA showed prenatal CB CD146⁺ cells are enriched in gene sets related to proliferation S-phase, RNA and DNA synthesis or DNA repair. For each enriched gene set, the gene expression is also represented as a Blue-Pink O' Gram in panels A1, B1, C1, D1, and E1.

Figure 3. A) *In vivo* osteogenic differentiation of BM (Aa), MU (Ab), PE (Ac) and CB-derived cells (Ad), Sirius red stain; polarized light. When CD146⁺ “MSC” strains were transplanted, using the same *in vivo* assays and HA/TCP as a carrier, osteogenic potential was restricted to BM-, PE- and CB-derived cells. In fact, cells derived in culture from muscle tissue, regularly failed to form any histologically identifiable bone, “MSCs” from periosteum and cord blood did form bone, but never established a hematopoietic microenvironment, whereas CD146⁺ “MSCs” strains from BM did form bone and establish the hematopoietic microenvironment *in vivo* (astericks in Aa, third panel). B) Clonal

strains of cord blood CD146⁺ “MSCs” transplanted using HA/TCP as a carrier, generated abundant bone and hyaline cartilage (a,b,f-h - Safranin O/Light Green; c – H&E; d - Alcian blue, e – anti-COL2).

Figure 4. A) Conventional *in vitro* differentiation assays were conducted using subcultured “MSCs” from BM (a), PE (b), CB (c), MU (d). With MU CD146⁺ “MSCs,” extensive formation of myotubes expressing specific myogenic markers were observed. No myogenic differentiation was observed with BM or any non-MU derived cell strain. (MyHC, Myosin Heavy Chain, Bar=120μ). B) Specimens of skeletal muscle tissue were collagenase-digested to generate single cell suspensions. Cultures were established by plating cell suspensions at clonal density (1.6 cells/cm²). Cell density is indicated in the upper left corner of each image. At clonal density, MU CD146⁺ but not MU CD146⁻ cells formed discrete fibroblastic colonies (Giemsa-stain). C) Cell morphology in single colonies generated by CD146⁺ muscle derived clonogenic cells at 6 and 14 days in culture, in 20% serum, on plastic. D) Single colony of CD146⁺ muscle-derived cells, 28 days of primary culture. Multinucleated myotubes are obvious after Giemsa staining (*arrows*).

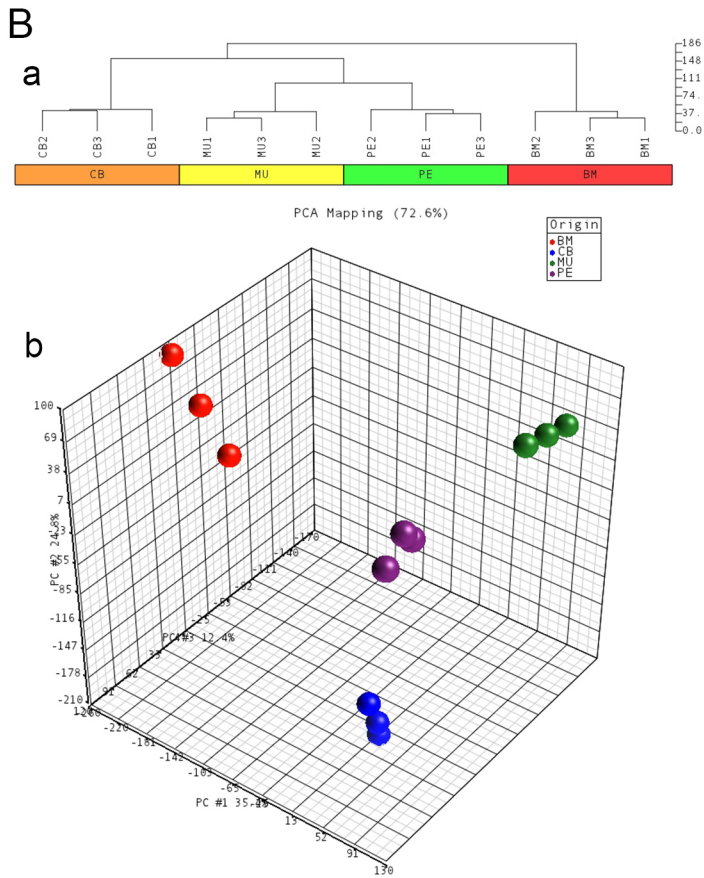
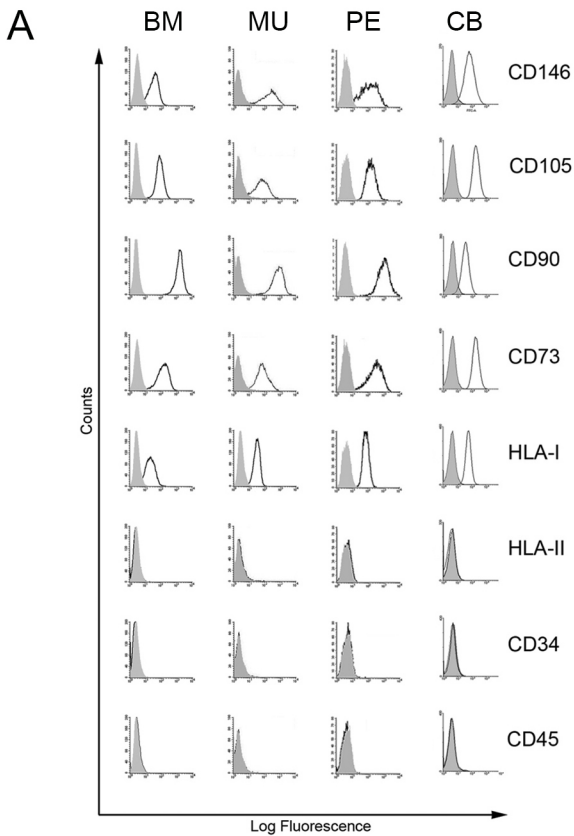
Figure 5. A) Human BM, PE and CB-derived cells, in orthotopic transplantation into cardiotoxin-injured muscle in SCID/beige mice, failed to contribute to generation of muscle cells or regenerating myofibers as would be detected by anti-human Lamin A/C. B) Human CD34⁻/CD56⁻/CD146⁺ muscle-derived cells were injected i.m. into the left *tibialis anterior* of 2 month-old female SCID/beige mice, injured 1 day earlier by an i.m. injection of cardiotoxin. Transplanted human MU cells, identified by expression of human Lamin A/C, were distributed to the interstitium (*arrow*), but also to the surface of myofibers (MF) in a satellite cell-like position (*arrowhead*). C) Cells in a characteristic satellite cell-like position express human CD56. D) Clusters of myofibers expressing human Dystrophin 2 and Spectrin were generated by MU cells by *in vivo* transplantation into SCID beige/ctx and SCID/mdx mice

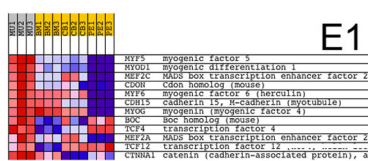
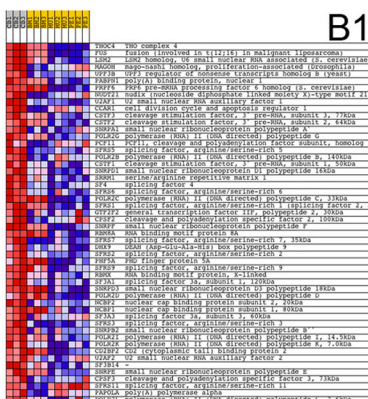
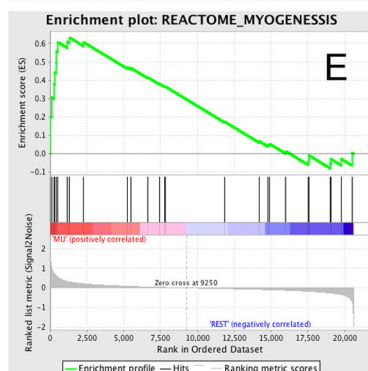
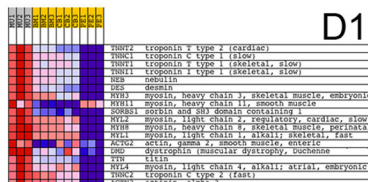
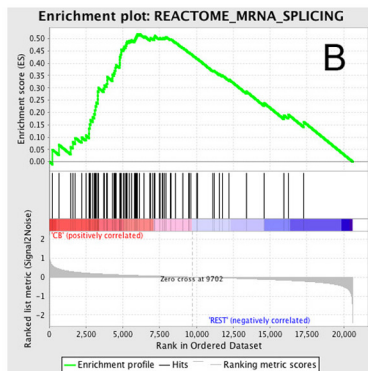
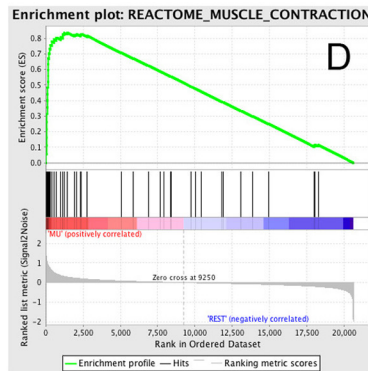
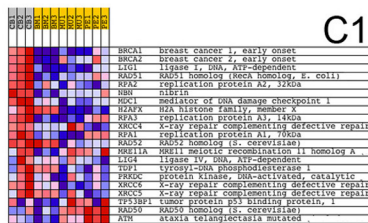
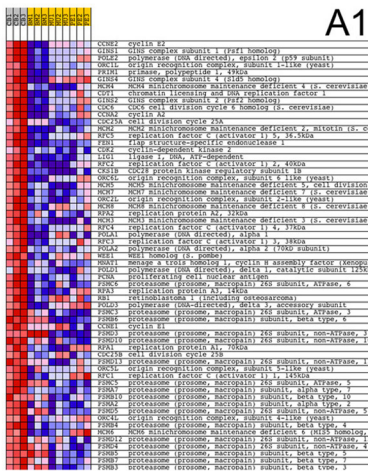
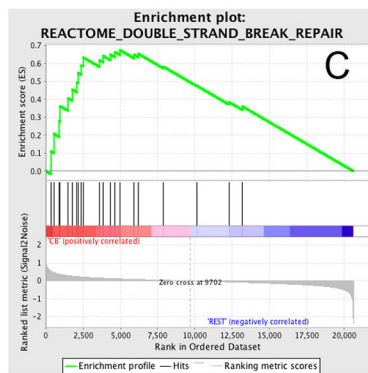
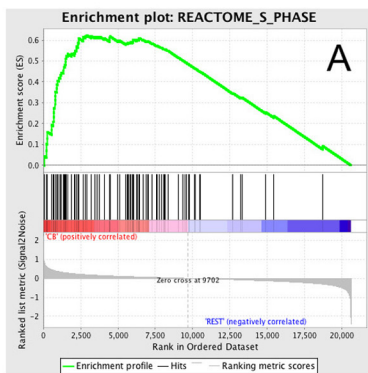
(Bar=350 μ). E) In a heterotopic transplantation assay, human CD34⁻/CD56⁻/CD146⁺/GFP⁺ MU cells suspended in growth factor-reduced MatrigelTM without endothelial cells are injected into the epifascial space of the back of SCID/beige mice, and harvested 3 wks later. Extensive formation not only of myotubes expressing human-specific myogenic markers, Desmin, CD56, MyHC, but even of striated myofibers (*black arrows*) and non-conventional muscle structures (*red arrows*) were observed. F) No myogenic differentiation was observed with BM or any non-MU cell strain. In contrast, CB CD146⁺ “MSCs” spontaneously generated hyaline cartilage when transplanted in MatrigelTM as a carrier. No ingrowth of BVs into the MatrigelTM plug was associated with the extensive cartilage differentiation observed.

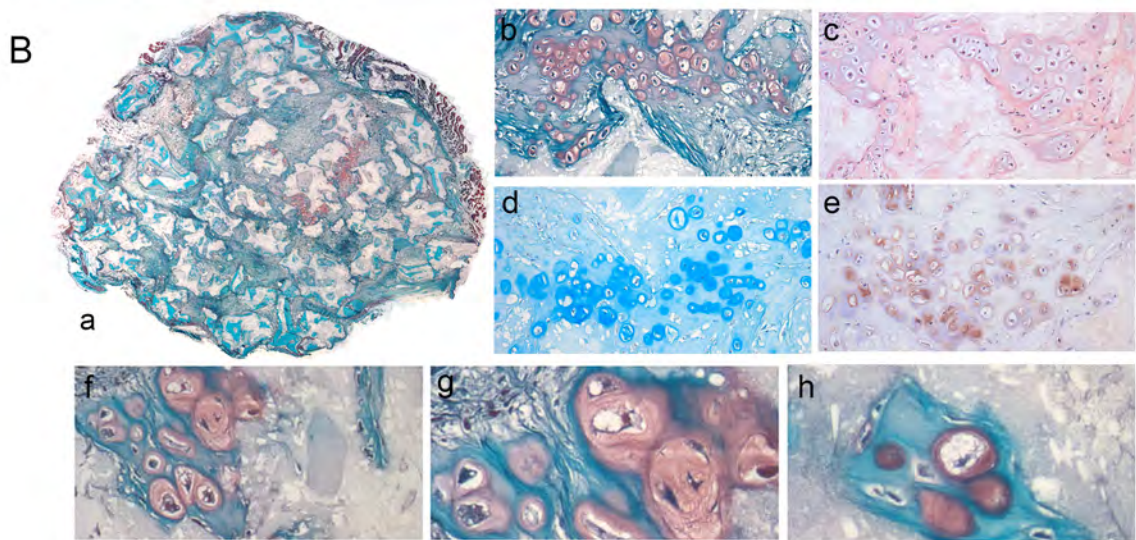
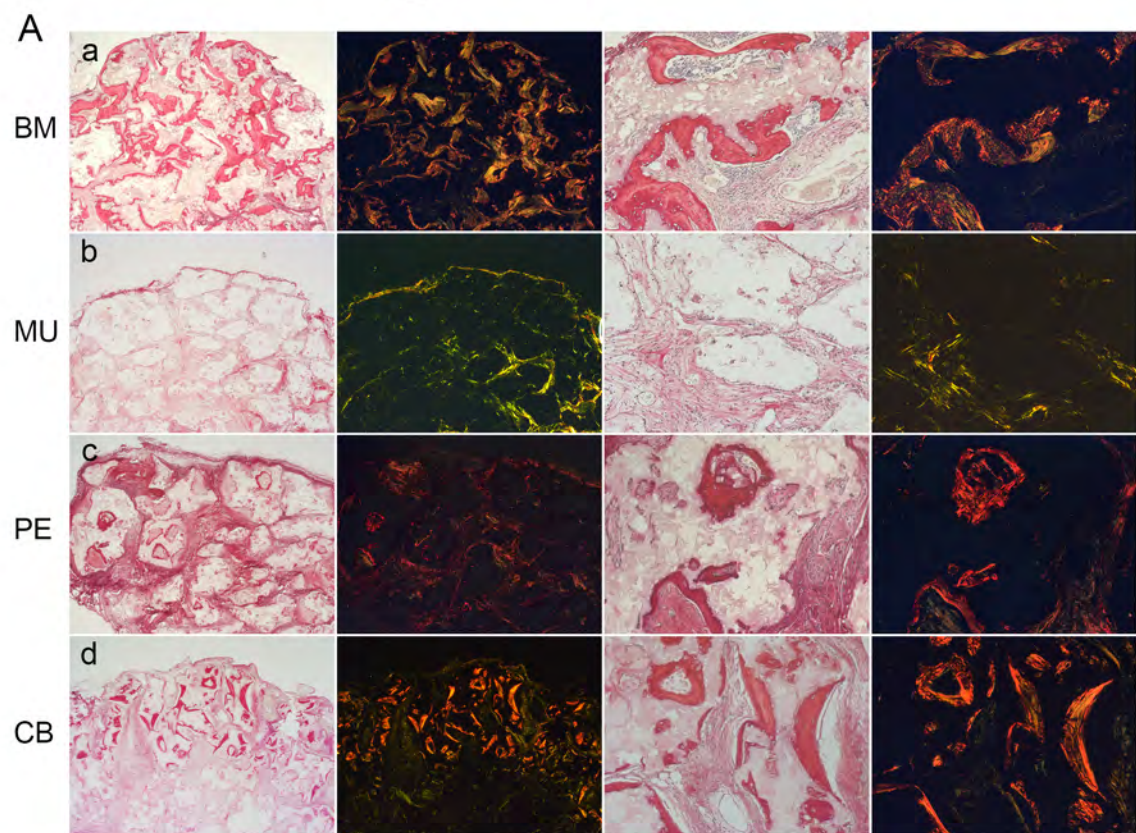
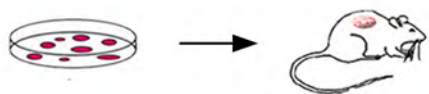
Figure 6. A) Induction of the satellite cell marker, CD56, in cultures of CD34⁻/CD56⁻/CD146⁺ cells. Co-expression of CD56 in a subset of CD146-expressing cells is detectable after 18 days in culture, and the % of CD146⁺/CD56⁺ cells increases over time. Upon replating cultured CD146⁺/CD56⁺ cells at high density, CD146 expression is eventually turned off, whereas CD56⁺ expressing cells remain detectable. Replating sub-confluent cultures (22 days in culture) at high density results in the generation of a wealth of myotubes expressing MyHC. At a terminal stage of differentiation (26-28 days in culture), CD146 expression is no longer detectable. B) FACS of collagenase-released cell suspensions of muscle. Co-expression of two pericyte markers, CD146 and ALP, in human MU cell suspensions before culture. CFE assay of FACS-sorted CD146⁻/ALP⁺ cells and CD146⁺/ALP[±] cell subsets. CD146⁺/ALP[±] and CD146⁻/ALP⁺ cells were plated at different cell densities. Numbers (upper left each panel) indicate the number of cells plated/cm². C) When unsorted cell strains, sorted CD146⁺/ALP⁻, CD146⁺/ALP⁺ and CD146⁻/ALP⁺ total collagenase-released cells at clonal density are induced to myogenic differentiation (2% HS on MatrigelTM), high numbers of myotubes expressing skeletal muscle-specific myosin heavy chain (MyHC) are found in freshly sorted cultures enriched in

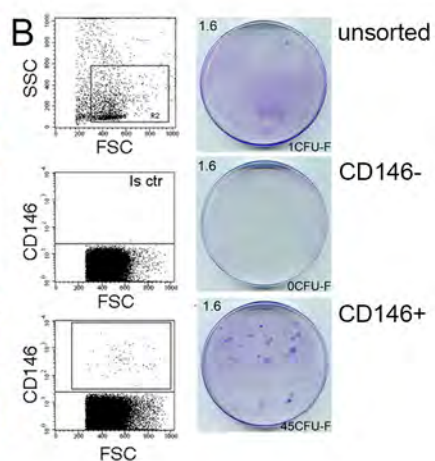
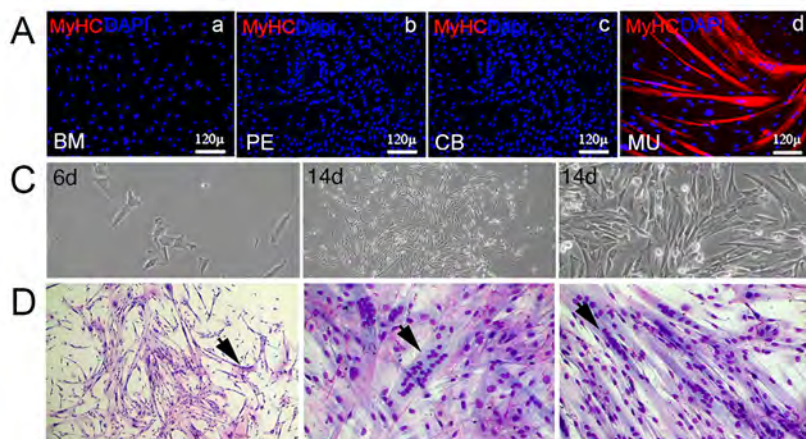
MU CD146⁺/ALP⁻ cells. Only rare myotubes are observed in explant-derived cultures (data not showed) or CD146⁺/ALP⁺ (Bar=120μ). D) Immunolocalization analysis of the distribution of CD146 and ALP expression in intact muscle revealed that while ALP cells (*green*) was predominantly expressed in precapillary arterioles, CD146 cells (*red*) was predominantly expressed in large venules (v). E) A subset of vascular wall-associated cells was found to express PAX3 and PAX7 in intact adult skeletal MU. Immunoreactivity was distributed to the surface of myofibers (MF) in a satellite cell-like position (*arrowhead*), and to BVs walls (V). Bar=10μ, 25μ. F) A subset of freshly isolated, uncultured CD146⁺ cells was found to coexpress the satellite cell marker, PAX7.

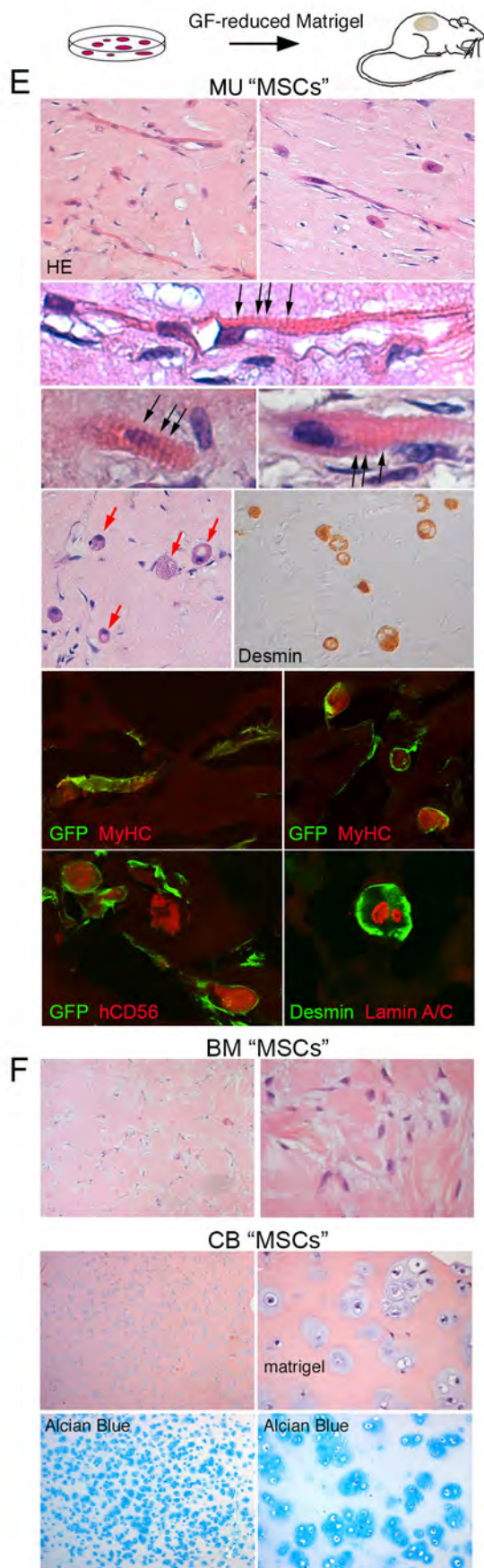
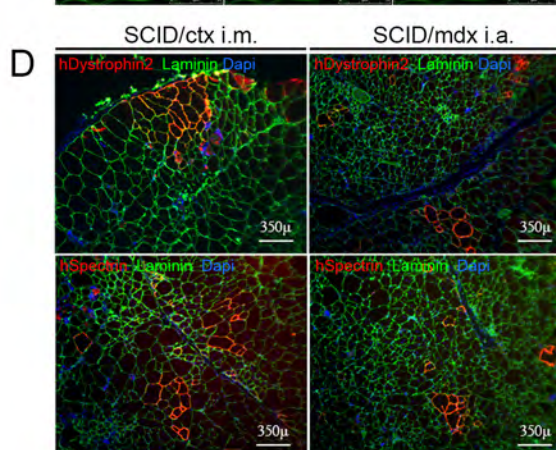
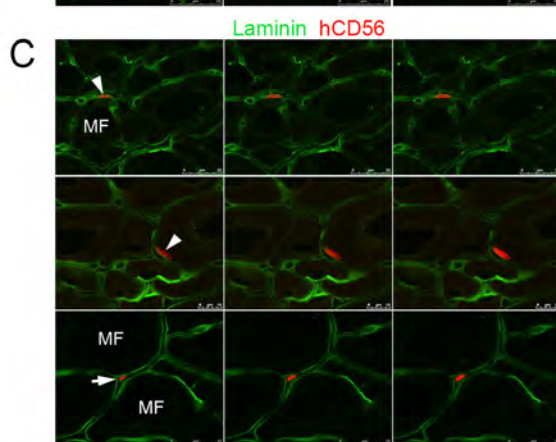
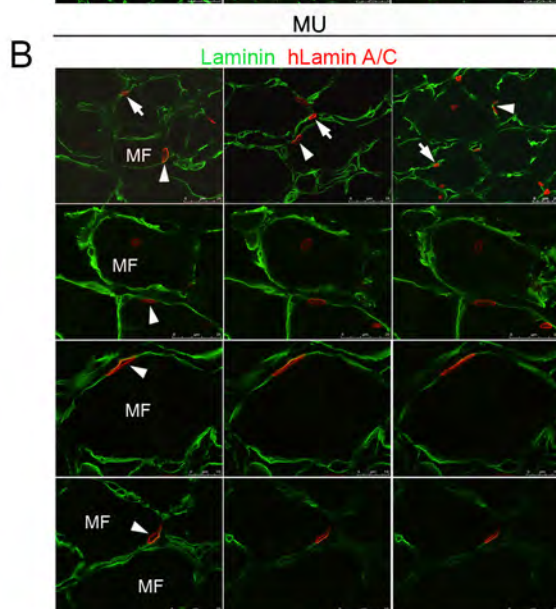
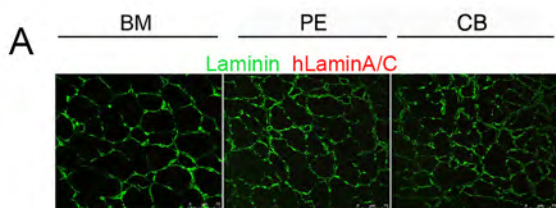
Figure 7. A) Co-transplant of BM-derived progenitors in MatrigelTM, along with HUVECs resulting in the formation of an extensive network of capillary-like BVs at 3 wks. Their wall was made by two cell layers – an inner hCD34⁺ endothelial layer, and an outer, discontinuous layer of mural cells made by transplanted, GFP-tagged BM progenitors, expressing CD146 and αSM actin. Transplants harvested at 8 wks exhibited extensive maturation of the BV wall as indicated by the formation of thick-walled artery- and vein-like BVs, with a multilayer GFP⁺, αSM actin⁺ smooth muscle coat, and were functional as indicated by perfusion with host blood. B) Similar experiments made with MU CD146⁺ progenitors also resulted in the formation of a capillary lattice, which was less extensive than with BM cells, but similarly well organize. C) Heterotopic co-transplantation of CB progenitors in MatrigelTM, along with HUVECs resulted in the formation of an extensive network of capillary-like BVs at 3 wks, which were functional and perfused by host blood. Their wall was made by an inner continuous hCD34⁺ endothelial layer, coated by an subluminal layer of thin, hCD146⁺ mural cells, and an outer coat of differentiated chondrocytes, making these BVs a unique kind of cartilage-armored BVs.

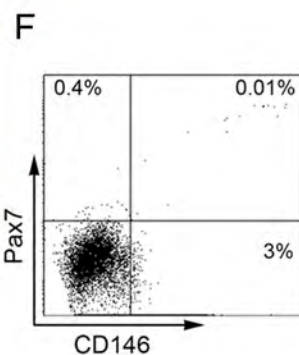
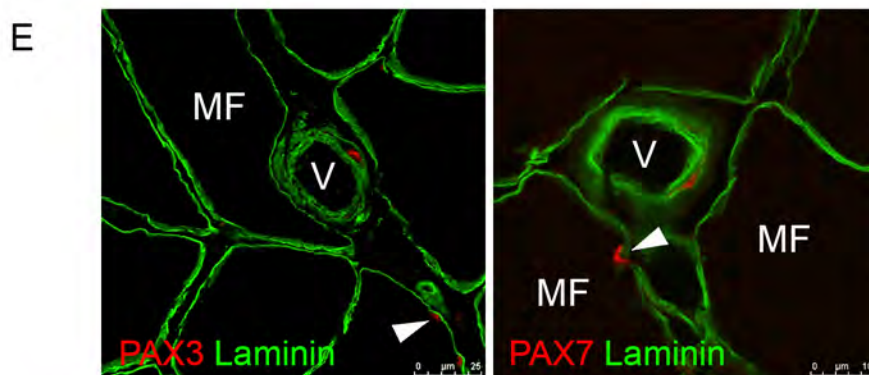
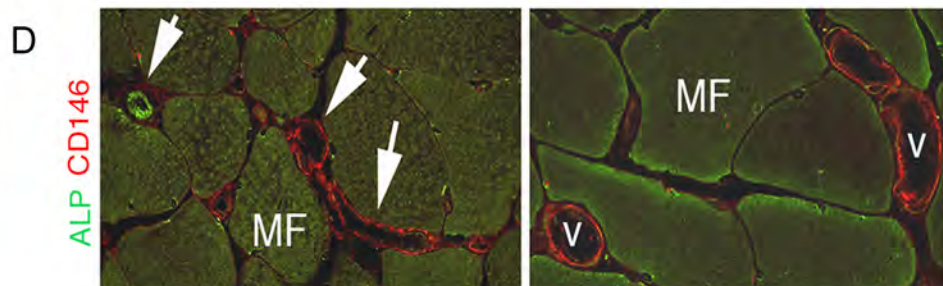
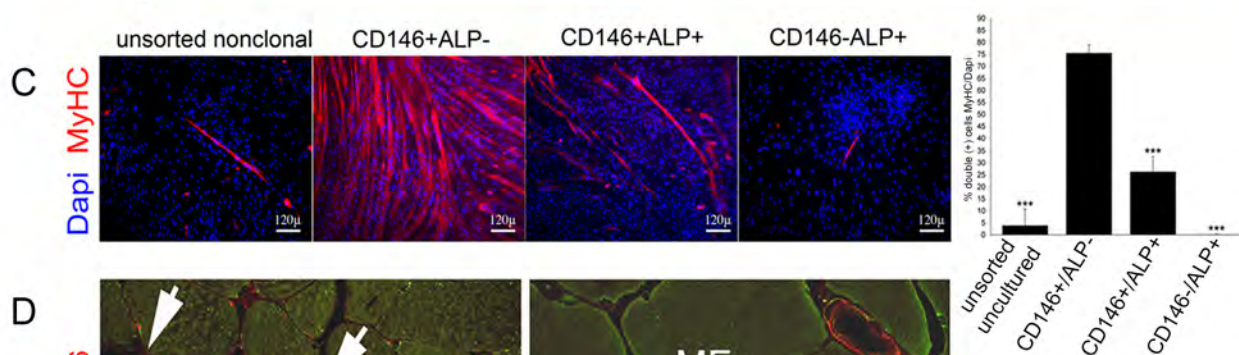
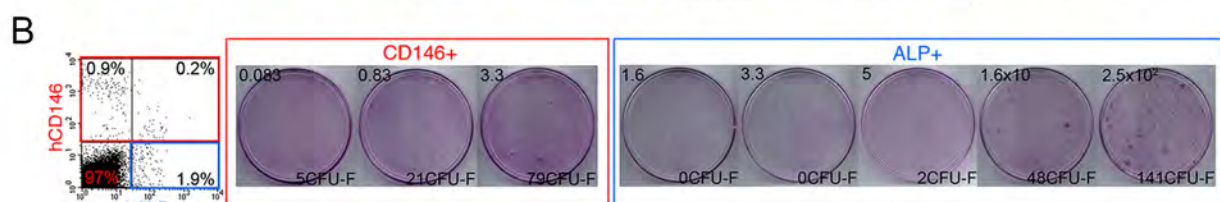
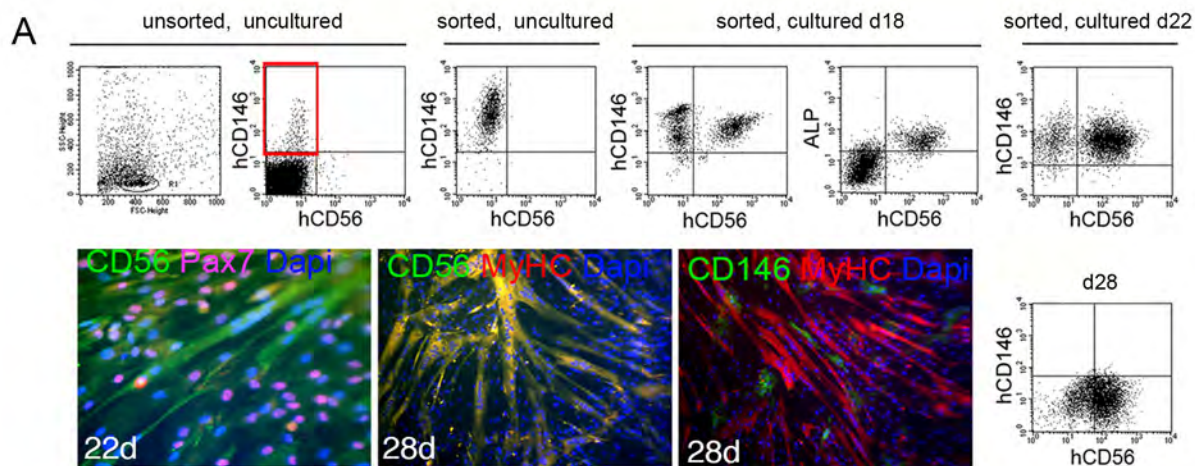




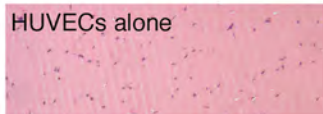




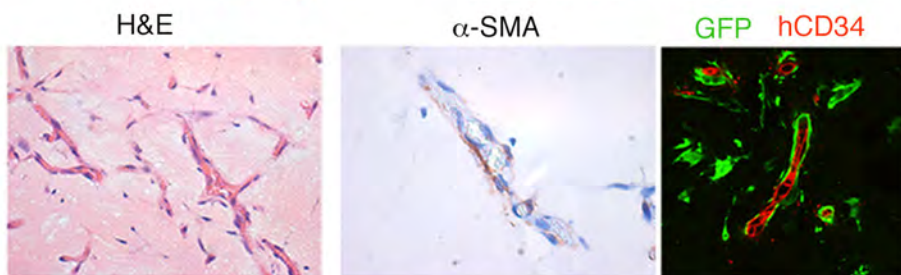




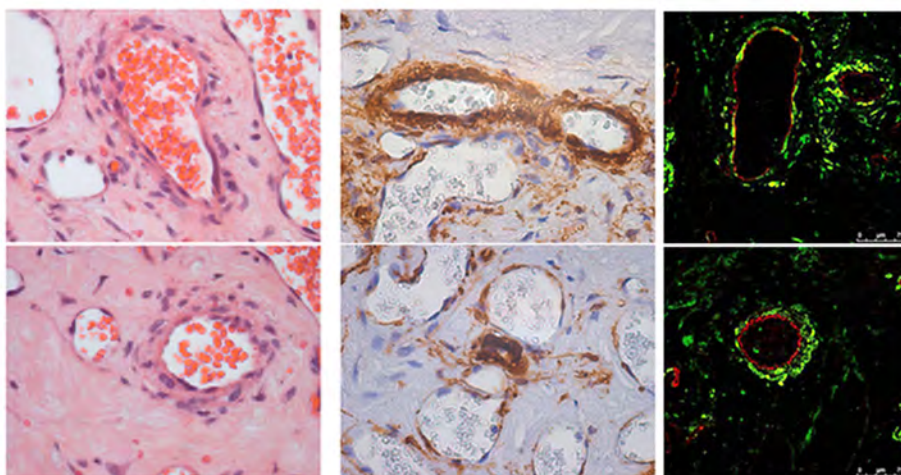
A



BM "MSCs" 3 wks

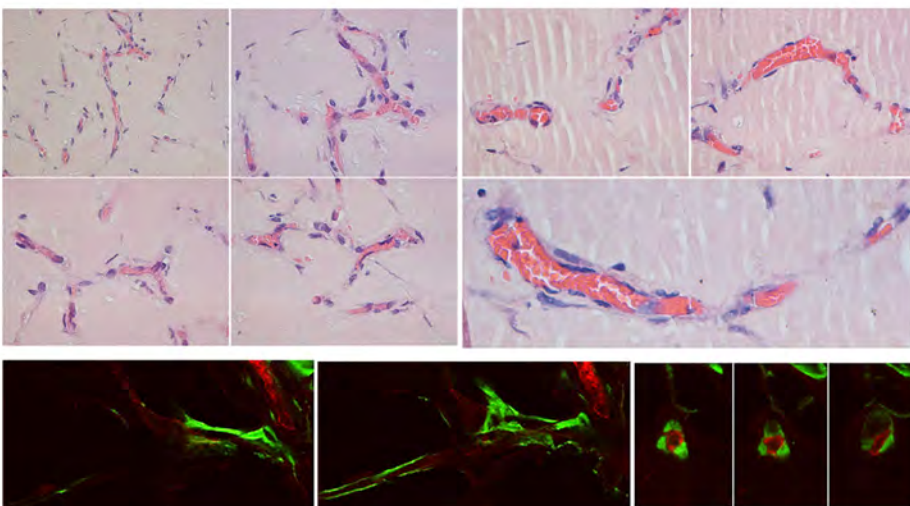


BM "MSCs" 8 wks



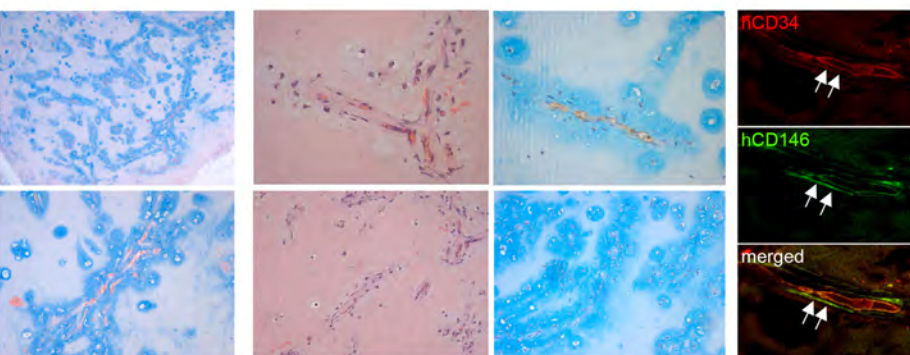
B

MU "MSCs" 3 wks



C

CB "MSCs"



INVENTORY OF SUPPLEMENTAL INFORMATION

No identical “mesenchymal stem cells” at different times and sites: Human committed progenitors of distinct origin and differentiation potential are incorporated as adventitial cells in microvessels

Benedetto Sacchetti, Alessia Funari, Cristina Remoli, Giuseppe Giannicola, Pamela G. Robey, Gesine Kogler, Stefanie Liedtke, Giulio Cossu, Marta Serafini, Maurilio Sampaolesi, Enrico Tagliafico, Elena Tenedini, Isabella Saggio, Mara Riminucci, Paolo Bianco

EXPERIMENTAL PROCEDURES AND REFERENCE

SUPPLEMENTARY FIGURES

Supplementary Figure 1. *In vivo* osteogenic differentiation of bone marrow-, dermis-, adipose- and amniotic fluid-derived cells.

Supplementary Figure 2. Expression of myogenic regulators and markers in “MSCs.”

Supplementary Figure 3. Expression of CD146, CD56 and CD34 in muscle and colony forming efficiency and myogenesis of cells sorted for these markers.

Supplementary Figure 4. Effect of knockdown of CD146 in BMSCs in vessel formation with HUVECs in an *in vivo* transplantation assay.

SUPPLEMENTARY TABLES

Supplementary Table 1. Over- and under-represented genes in BM, MU, PE and CB cells as computed by supervised analysis.

Supplementary Table 2. Gene sets enriched in CB.

Supplementary Table 3. Gene sets enriched in MU.

Supplementary Table 4. Quantification of satellite, mural cells of CD146⁺/CD34⁻ cells in vivo SCID beige/ctx.

Supplementary Table 5. Quantification of satellite, mural cells of CD146⁺/CD34⁻ cells in vivo SCID/mdx.

Supplementary Table 6. Regenerative efficiency of CD146⁺/CD34⁻ cells in vivo.

Supplementary Table 7. CFE assay for unsorted, CD146⁺ and CD146⁻ muscle cells.

Supplementary Table 8. CFE assay for sorted CD146^{+/-} and CD56^{+/-} muscle cells.

Supplementary Table 9. CFE assay for sorted CD146^{+/-} and CD34^{+/-} muscle cells.

Supplementary Table 10. CFE assay for sorted CD146⁺/ALP^{+/-} and CD146⁻/ALP⁺ muscle cells.

Supplementary Table 11. Antibodies used for flow cytometry and fluorescence-activated cell sorting.

Supplementary Table 12. Antibodies used for immunohistochemistry and immunocytochemistry.

Supplementary Table 13. Primers used for semiquantitative PCR.

SUPPLEMENTAL TEXT, FIGURES AND TABLES

No identical “mesenchymal stem cells” at different times and sites: Human committed progenitors of distinct origin and differentiation potential are incorporated as adventitial cells in microvessels

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SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Establishment of Cell Cultures

Human adipose tissue-derived cells were obtained from human adult subcutaneous adipose tissue. Fat tissue was minced with scissors, washed with $\text{Ca}^{2+}/\text{Mg}^{2+}$ -free PBS and the extracellular matrix was digested with collagenase type I (Invitrogen), at 37°C for 1 h. The samples were centrifuged at 1000 rpm for 5 min at 4°C, washed with $\text{Ca}^{2+}/\text{Mg}^{2+}$ -free PBS, resuspended in PBS, passed through 18 gauge needles to break up cell aggregates, and filtered through a 40 μm pore size cell strainer to obtain a single cell suspension. Human dermal fibroblasts were purchased from PromoCell GmbH, Heidelberg, Germany. Human amniotic cells were isolated as previously described (Pievani et al., 2014).

RT-PCR Analysis

From CD146-sorted, uncultured cells, total RNA was extracted using a PicoPureTM RNA Isolation Kit (Arcturus Bioscience), per the manufacturer's instruction. cDNA was synthesized using 9 μl of

RNA, 100 ng of random hexamers, and 50 units of SuperScriptII Reverse Transcriptase (Invitrogen) in a total volume of 20 µl. From cultured cells, total RNA was extracted using TRIZOL™ RNA isolation system (Invitrogen) per the manufacturer's instructions. cDNA was synthesized using 3 µg of RNA, 150 ng of random hexamers, and 50 units of SuperScript II Reverse Transcriptase (Invitrogen) in a total volume of 20 µl. Target cDNA sequences were amplified in standard PCR reactions using Platinum® PCR SuperMix according to the manufacturer's instructions. Primers used for RT-PCR are described in Supplementary Table 13.

SUPPLEMENTARY REFERENCES

Pievani, A., Scagliotti, V., Russo, F.M., Azario, I., Rambaldi, B., Sacchetti, B., Marzorati, S., Erba, E., Giudici, G., Riminucci, M., *et al.* (2014). Comparative analysis of multilineage properties of mesenchymal stromal cells derived from fetal sources shows an advantage of mesenchymal stromal cells isolated from cord blood in chondrogenic differentiation potential. *Cytotherapy* 16, 893-905.

SUPPLEMENTARY FIGURES

Supplementary Figure 1. *In vivo* osteogenic differentiation of bone marrow-(A), dermis-(B), adipose-(C) and amniotic fluid-derived cells (D). When cultured “MSC” cell strains were transplanted, using the same *in vivo* assays and HA/TCP as a carrier and stained with Sirius red, osteogenic potential was restricted to bone marrow-derived cells (BM). Cells derived in culture from dermis (D), adipose tissue (A) or amniotic fluid (AF), regularly failed to form any histological bone, whereas “MSCs” from BM did form bone and establish the hematopoietic microenvironment *in vivo*.

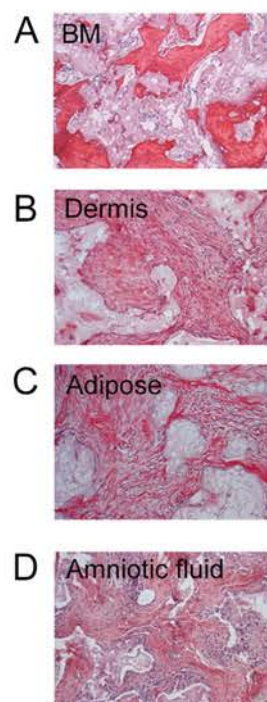
Supplementary Figure 2. A) RT-PCR analysis of myogenic regulators and markers in “MSCs,” demonstrating restriction of their expression to CD146⁺ muscle-derived cells only (sorted a and b – two independent populations of cells). B) Sorted and cultured cultures CD146⁺/CD56⁻ muscle-

derived cells progressively turn on expression of human-specific myogenic markers PAX3, Myf5 and Desmin.

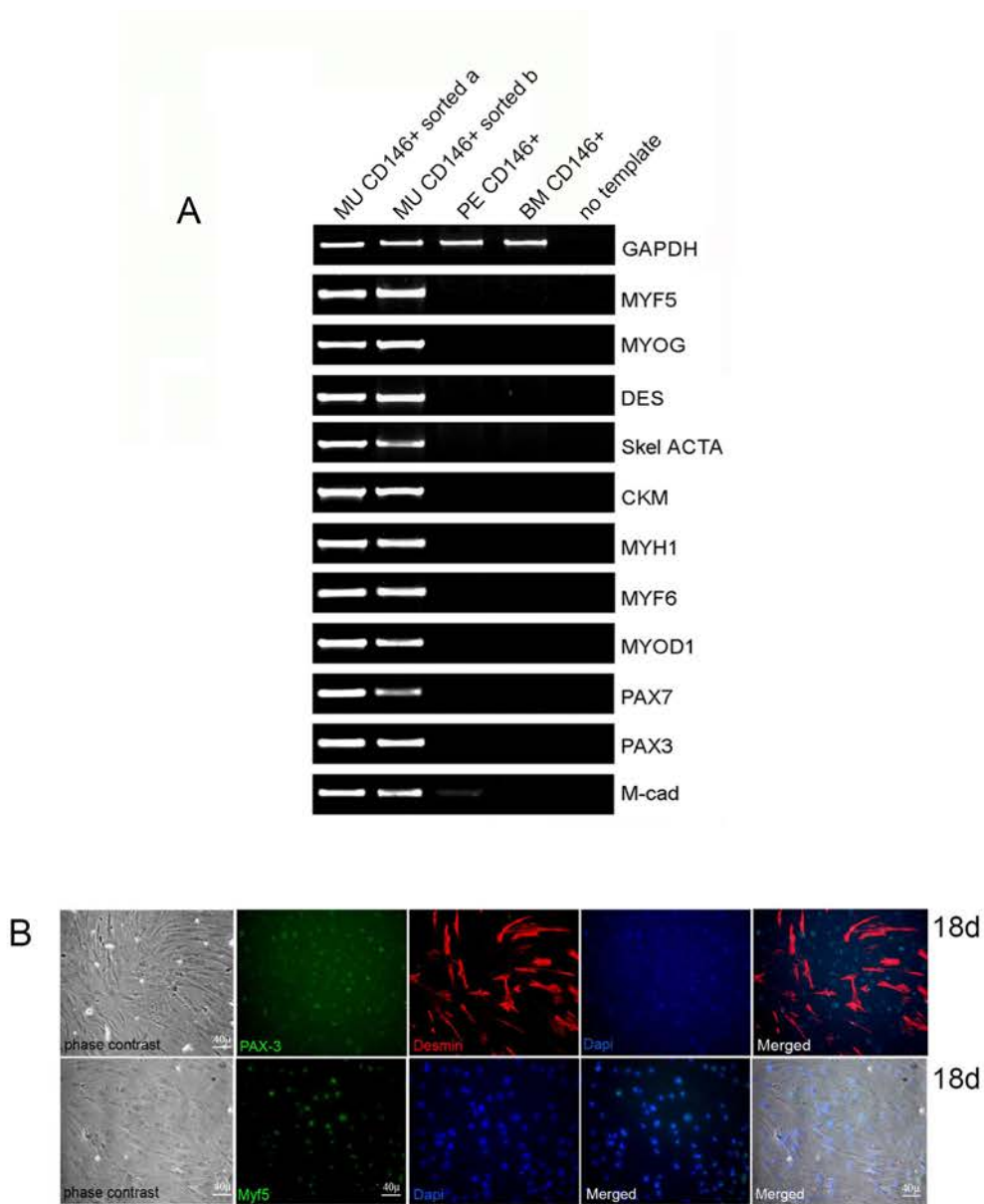
Supplementary Figure 3. A) Isotype control and dual label FACS analysis of a collagenase-released muscle cell suspension. Expression of CD146 and CD56 is mutually exclusive in distinct cell subsets, with no co-expression. B) Localization of CD146 and CD56 in muscle sections. CD56 is restricted to the surface of myofibers where satellite cells reside (*arrows* in b, *red arrows* in e). CD146 is restricted to vascular walls (*arrows* in d, *green arrows* in e). MF, myofiber. Bar=70 μ a-d, 20 μ e. C) CFE assay with CD146⁺/CD56⁺ subsets of collagenase-released cells. CFU-Fs capable of growth on plastic are found in the CD146⁺/CD56⁻ fraction. Numbers (upper left each panel) indicate the number of cells plated/cm². D) Isotype control and dual label FACS of CD146 and CD34 expression in collagenase-released muscle cells. ~25% of CD146⁺ cells co-express CD34 (ellipse), and ~12% of CD34⁺ cells express CD146. E) Localization of CD146 and CD34 in muscle sections. a) Both antigens are localized to cross-sections of pre-capillary arterioles and post-capillary venules (a, *large arrows*), whereas most capillaries (a, i, j, *small arrows*) among myofibers (MF) only label for CD34. b-d) Detail of a large pre-capillary arteriole. Endothelial cells [*e* in d] co-express CD34 and CD146; subendothelial mural cells [*peri* in d] only express CD146. e-g) Detail of a small pre-capillary arteriole. Endothelial cells express CD34 but not CD146. Subendothelial cells express CD146 but not CD34. h-j) Detail of a capillary adjacent to a myofiber (MF). Endothelial cells express CD34 but not CD146. No CD146 expression is detected. Bar = 90 μ a; 50 μ b-g; 10 μ h-j. F) When sorted CD146⁺/CD34⁻, CD146⁺/CD34⁺ and CD146⁻/CD34⁺ total collagenase-released cells plated at clonal density are induced to myogenic differentiation (2% HS on MatrigelTM), high numbers of myotubes expressing skeletal muscle-specific myosin heavy chain (MyHC) are found in freshly sorted cultures enriched in muscle-derived CD146⁺/CD34⁻ cells. Only rare myotubes are observed in CD146⁺/CD34⁺; Bar=120 μ .

Supplementary Figure 4. A) Co-transplant at 3 weeks of BM-derived progenitors (green, GFP) in MatrigelTM, along with HUVECs (red, hCD34) resulting in the formation of a capillary lattice well organized. B) Co-transplant of in BM-derived progenitors in which CD146 was knockeddown in MatrigelTM, along with HUVECs resulting in the formation of vessels of irregular size and shape (arrows), often devoid of a lumen, and devoid of a regular mural cell coat, at 3 weeks.

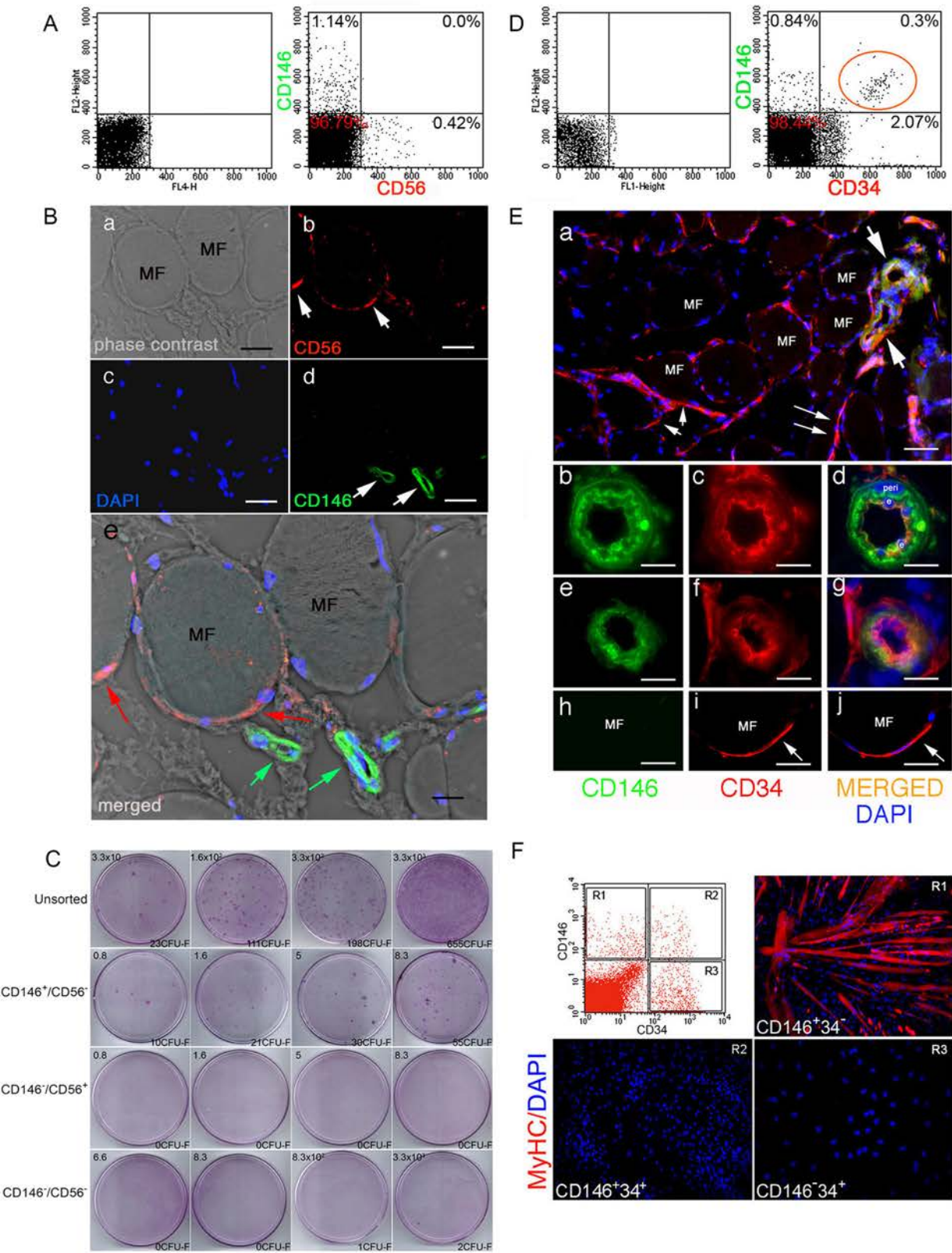
Supplementary Figure 1



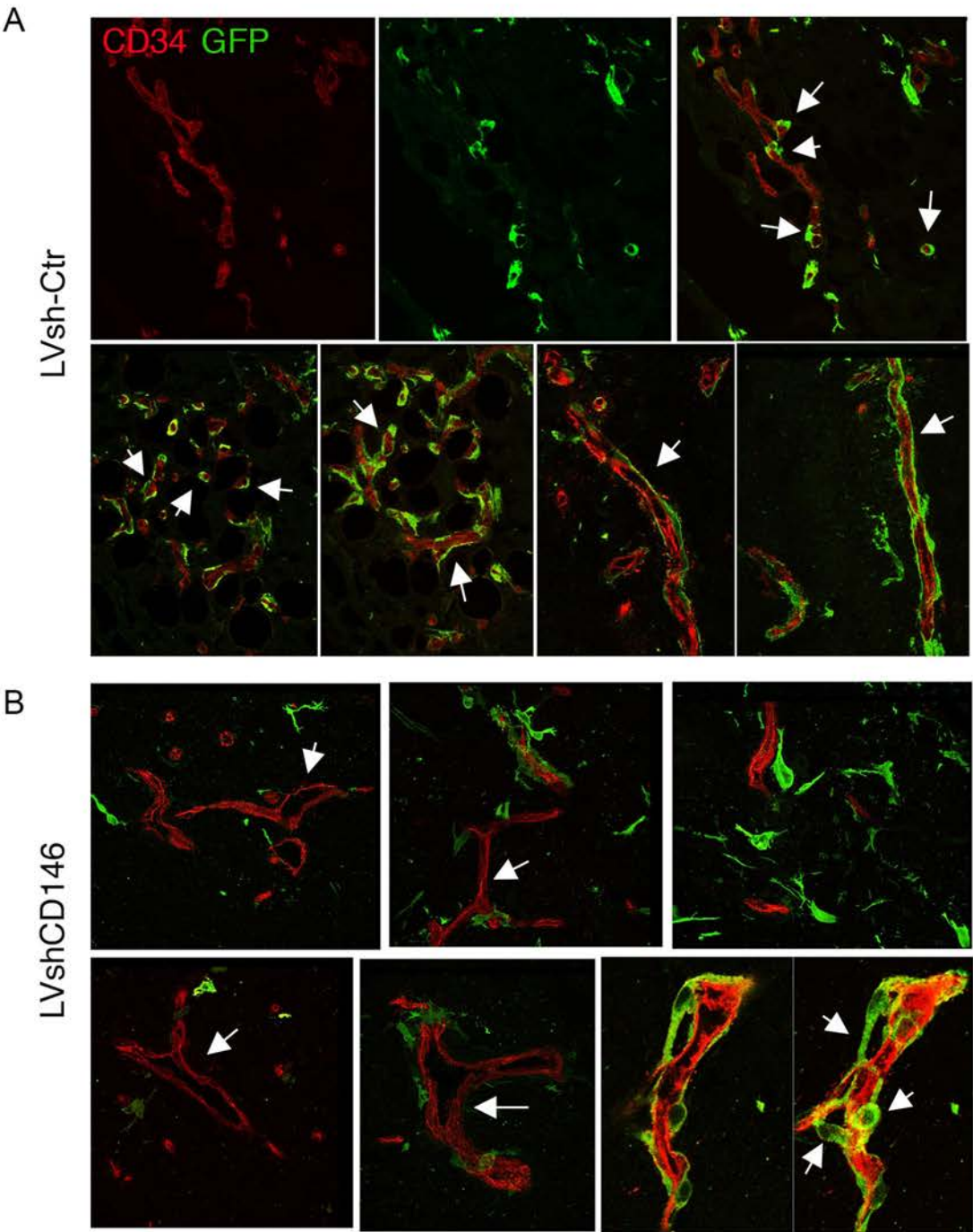
Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4



SUPPLEMENTARY TABLES

Supplementary Table 1. Up and down-regulated genes in BM, MU, PE and CB cells as computed by supervised analysis.

Probeset ID	Gene Symbol	Gene Title	p-value	Fold-Change	Fold-Change (Description)
206029_at	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	0,01474	245,53	BM up vs all others
219106_s_at	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	1,20E-06	215,395	MU up vs all others
206633_at	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	7,64E-08	180,46	MU up vs all others
210302_s_at	MAB21L2	mab-21-like 2 (C. elegans)	7,69E-07	155,268	PE up vs all others
235503_at	ASB5	ankyrin repeat and SOCS box-containing 5	3,64E-06	136,489	MU up vs all others
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	1,48E-06	133,043	MU up vs all others
205132_at	ACTC1	actin, alpha, cardiac muscle 1	7,49E-07	132,726	MU up vs all others
224646_x_at	H19	H19, imprinted maternally expressed transcript	5,52E-07	123,31	MU up vs all others
224997_x_at	H19	H19, imprinted maternally expressed transcript	9,27E-07	95,8828	MU up vs all others
203305_at	F13A1	coagulation factor XIII, A1 polypeptide	3,84E-09	83,9848	MU up vs all others
219087_at	ASPN	Asporin	0,0114985	75,0563	PE up vs all others
224588_at	XIST	X (inactive)-specific transcript (non-protein coding)	9,18E-10	53,1622	BM up vs all others
228885_at	MAMDC2	MAM domain containing 2	5,50E-05	52,3678	MU up vs all others
212843_at	NCAM1	neural cell adhesion molecule 1	5,87E-10	48,9158	MU up vs all others
205713_s_at	COMP	cartilage oligomeric matrix protein	0,000103363	45,7201	PE up vs all others
217757_at	A2M	alpha-2-macroglobulin	1,02E-05	43,6134	MU up vs all others
207424_at	MYF5	myogenic factor 5	3,85E-06	42,5978	MU up vs all others
222827_s_at	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	2,77E-06	42,0672	MU up vs all others
206375_s_at	HSPB3	heat shock 27kDa protein 3	0,000312071	40,0065	MU up vs all others
209904_at	TNNC1	troponin C type 1 (slow)	0,00236963	39,261	MU up vs all others
202157_s_at	CELF2	CUGBP, Elav-like family member 2	4,68E-07	38,8966	MU up vs all others
223940_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript1	3,63E-06	37,7316	CB up vs all others
222717_at	SDPR	serum deprivation response	3,77E-06	36,8153	MU up vs all others
227462_at	ERAP2	endoplasmic reticulum aminopeptidase 2	0,000137388	36,293	CB up vs all others
226535_at	ITGB6	integrin, beta 6	0,000481096	36,1127	MU up vs all others
235343_at	VASH2	vasohibin 2	1,69E-05	34,5985	MU up vs all others
210135_s_at	SHOX2	short stature homeobox 2	0,00120483	33,4344	PE up vs all others
230319_at	---	---	0,00136022	33,3182	PE up vs all others
238914_at	DCC	deleted in colorectal carcinoma	1,62E-11	32,0499	CB up vs all others
206932_at	CH25H	cholesterol 25-hydroxylase	0,00133248	31,6754	PE up vs all others
239468_at	MKX	mohawk homeobox	0,00279796	31,6617	PE up vs all others
225894_at	SYNPO2	synaptopodin 2	1,20E-05	31,3849	MU up vs all others
225895_at	SYNPO2	synaptopodin 2	0,000313931	31,2718	MU up vs all others
229802_at	---	---	0,00225538	31,1838	PE up vs all others
204614_at	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin)	0,00186773	30,7901	BM up vs all others
224568_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript1	1,69E-06	29,691	CB up vs all others
205054_at	NEB	Nebulin	0,0166631	29,1918	MU up vs all others
232523_at	MEGF10	multiple EGF-like-domains 10	4,89E-07	29,1084	MU up vs all others
204830_x_at	PSG5	pregnancy specific beta-1-glycoprotein 5	0,000127147	29,0356	BM up vs all others
227671_at	XIST	X (inactive)-specific transcript (non-protein coding)	5,19E-09	28,2808	BM up vs all others
219387_at	CCDC88A	coiled-coil domain containing 88A	9,31E-13	27,8005	CB up vs all others
209541_at	IGF1	insulin-like growth factor 1 (somatomedin C)	7,70E-06	27,1699	PE up vs all others

209888_s_at	MYL1	myosin, light chain 1, alkali; skeletal, fast	0,0475808	26,5369	MU up vs all others
241981_at	FAM20A	family with sequence similarity 20, member A	5,79E-05	26,1023	PE up vs all others
213909_at	LRRC15	leucine rich repeat containing 15	4,25E-06	26,0642	PE up vs all others
209742_s_at	MYL2	myosin, light chain 2, regulatory, cardiac, slow	0,0353048	25,9991	MU up vs all others
225720_at	SYNPO2	synaptopodin 2	3,97E-05	25,2145	MU up vs all others
202158_s_at	CELF2	CUGBP, Elav-like family member 2	1,96E-08	24,9742	MU up vs all others
213201_s_at	TNNT1	troponin T type 1 (skeletal, slow)	0,0031487	24,2437	MU up vs all others
239537_at	ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	5,52E-05	24,1651	MU up vs all others
226828_s_at	HEYL	hairy/enhancer-of-split related with YRPW motif-like	1,60E-07	23,5275	MU up vs all others
204364_s_at	REEP1	receptor accessory protein 1	4,60E-06	23,3454	MU up vs all others
209540_at	IGF1	insulin-like growth factor 1 (somatomedin C)	7,38E-06	23,3369	PE up vs all others
204584_at	L1CAM	L1 cell adhesion molecule	0,000284977	23,3182	MU up vs all others
205792_at	WISP2	WNT1 inducible signaling pathway protein 2	1,54E-07	22,8741	PE up vs all others
205163_at	MYLPF	myosin light chain, phosphorylatable, fast skeletal muscle	0,00764667	22,806	MU up vs all others
205177_at	TNNI1	troponin I type 1 (skeletal, slow)	0,00320341	22,8051	MU up vs all others
238332_at	ANKRD29	ankyrin repeat domain 29	2,64E-06	22,7285	PE up vs all others
224567_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1	0,000172817	22,6026	CB up vs all others
205940_at	MYH3	myosin, heavy chain 3, skeletal muscle, embryonic	0,011495	22,5842	MU up vs all others
227812_at	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	0,00011296	22,5668	PE up vs all others
204654_s_at	TFAP2A	transcription factor AP-2 alpha	9,46E-10	21,86	BM up vs all others
226804_at	FAM20A	family with sequence similarity 20, member A	0,000225613	21,7481	PE up vs all others
215389_s_at	TNNT2	troponin T type 2 (cardiac)	7,48E-05	21,5421	MU up vs all others
204529_s_at	TOX	thymocyte selection-associated high mobility group box	1,35E-06	21,0809	CB up vs all others
222278_at	---	---	1,93E-06	20,6578	MU up vs all others
226913_s_at	SOX8	SRY (sex determining region Y)-box 8	2,62E-05	20,6284	MU up vs all others
230130_at	---	---	6,86E-05	20,6242	PE up vs all others
218087_s_at	SORBS1	sorbin and SH3 domain containing 1	1,22E-05	20,5559	MU up vs all others
235821_at	---	---	0,000370946	20,5267	PE up vs all others
207010_at	GABRB1	gamma-aminobutyric acid (GABA) A receptor, beta 1	3,29E-07	20,3347	CB up vs all others
219937_at	TRHDE	thyrotropin-releasing hormone degrading enzyme	0,000860928	20,1466	CB up vs all others
228708_at	RAB27B	RAB27B, member RAS oncogene family	0,00199321	19,9117	PE up vs all others
229399_at	C10orf118	chromosome 10 open reading frame 118	5,23E-09	19,7845	CB up vs all others
202156_s_at	CELF2	CUGBP, Elav-like family member 2	1,23E-08	19,5241	MU up vs all others
235228_at	CCDC85A	coiled-coil domain containing 85A	0,00122984	19,4652	CB up vs all others
209621_s_at	PDLIM3	PDZ and LIM domain 3	3,32E-05	19,416	MU up vs all others
227394_at	NCAM1	neural cell adhesion molecule 1	1,50E-07	19,3007	MU up vs all others
209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0,000213976	19,2647	PE up vs all others
227478_at	SETBP1	SET binding protein 1	8,57E-05	18,9248	PE up vs all others
34471_at	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	0,0425744	18,9221	MU up vs all others
206717_at	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	0,0340866	18,6912	MU up vs all others
208191_x_at	PSG4	pregnancy specific beta-1-glycoprotein 4	3,89E-07	18,6412	BM up vs all others
204363_at	F3	coagulation factor III (thromboplastin, tissue factor)	1,95E-06	18,6104	MU up vs all others
235944_at	HMCN1	hemicentin 1	0,00141596	18,4189	PE up vs all others
208195_at	TTN	Titin	0,0383172	18,3901	MU up vs all others
218736_s_at	PALMD	palmdelphin	0,000392082	18,3088	MU up vs all others
203872_at	ACTA1	actin, alpha 1, skeletal muscle	0,0117013	17,9592	MU up vs all others
232238_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated	9,84E-09	17,9304	CB up vs all others

240633_at	DOK7	docking protein 7	0,000345824	17,8967	MU up vs all others
223557_s_at	TMEFF2	transm protein with EGF-like and two follistatin-like domains 2	0,000133885	17,5814	CB up vs all others
220794_at	GREM2	gremlin 2	5,83E-05	17,5589	PE up vs all others
236088_at	NTNG1	netrin G1	3,50E-06	17,5026	PE up vs all others
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	2,97E-07	17,4579	MU up vs all others
214587_at	COL8A1	collagen, type VIII, alpha 1	0,000237022	17,4108	PE up vs all others
209047_at	AQP1	aquaporin 1 (Colton blood group)	0,000517632	17,3564	MU up vs all others
219759_at	ERAP2	endoplasmic reticulum aminopeptidase 2	0,000831388	17,2613	CB up vs all others
205818_at	DBC1	deleted in bladder cancer 1	0,000272432	17,1102	PE up vs all others
209032_s_at	CADM1	cell adhesion molecule 1	1,91E-08	16,9657	PE up vs all others
212865_s_at	COL14A1	collagen, type XIV, alpha 1	7,66E-06	16,9541	MU up vs all others
200835_s_at	MAP4	microtubule-associated protein 4	5,47E-07	16,8855	CB up vs all others
226237_at	COL8A1	collagen, type VIII, alpha 1	0,000518394	16,7978	PE up vs all others
219747_at	C4orf31	chromosome 4 open reading frame 31	0,00041913	16,6634	PE up vs all others
210170_at	PDLIM3	PDZ and LIM domain 3	1,95E-05	16,6357	MU up vs all others
219740_at	VASH2	vasohibin 2	0,000103129	16,5441	MU up vs all others
210839_s_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0,000107646	16,5086	PE up vs all others
209496_at	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	5,75E-06	16,392	MU up vs all others
202409_at	IGF2///INS-IGF2	insulin-like growth factor 2 /// INS-IGF2 readthrough transcript	0,000243241	16,2376	MU up vs all others
242940_x_at	DLX6	distal-less homeobox 6	3,08E-06	16,1421	PE up vs all others
221728_x_at	XIST	X (inactive)-specific transcript (non-protein coding)	3,02E-07	16,0623	BM up vs all others
207317_s_at	CASQ2	calsequestrin 2 (cardiac muscle)	0,0292967	15,9897	MU up vs all others
204631_at	MYH2	myosin, heavy chain 2, skeletal muscle, adult	0,0739509	15,9645	MU up vs all others
218899_s_at	BAALC	brain and acute leukemia, cytoplasmic	0,00268006	15,9209	PE up vs all others
226824_at	CPXM2	carboxypeptidase X (M14 family), member 2	0,00269378	15,8979	PE up vs all others
205239_at	AREG	Amphiregulin	2,54E-08	15,8928	CB up vs all others
201860_s_at	PLAT	plasminogen activator, tissue	1,90E-08	15,8731	BM up vs all others
204040_at	RNF144A	ring finger protein 144A	2,94E-05	15,6704	PE up vs all others
230109_at	PDE7B	phosphodiesterase 7B	8,97E-05	15,6619	PE up vs all others
204035_at	SCG2	secretogranin II	0,000809164	15,5411	MU up vs all others
216840_s_at	LAMA2	laminin, alpha 2	2,08E-05	15,4402	MU up vs all others
214464_at	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	1,83E-06	15,4301	CB up vs all others
202222_s_at	DES	Desmin	2,28E-05	15,3461	MU up vs all others
226675_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1	0,00132292	15,2707	CB up vs all others
217428_s_at	COL10A1	collagen, type X, alpha 1	0,000503516	15,1812	PE up vs all others
213348_at	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	0,00042146	15,0801	MU up vs all others
219049_at	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	0,00145742	14,9776	PE up vs all others
227088_at	PDE5A	phosphodiesterase 5A, cGMP-specific	0,00146867	14,9466	PE up vs all others
202508_s_at	SNAP25	synaptosomal-associated protein, 25kDa	6,65E-08	14,7865	PE up vs all others
225721_at	SYNPO2	synaptopodin 2	1,13E-05	14,7683	MU up vs all others
204731_at	TGFBR3	transforming growth factor, beta receptor III	0,00102474	14,6611	PE up vs all others
235059_at	RAB12	RAB12, member RAS oncogene family	1,25E-07	14,5133	CB up vs all others
227609_at	EPSTI1	epithelial stromal interaction 1 (breast)	0,000219542	14,4964	PE up vs all others
1556638_at	PAX7	paired box 7	0,00014818	14,4719	MU up vs all others
209683_at	FAM49A	family with sequence similarity 49, member A	9,92E-07	14,4568	MU up vs all others
209594_x_at	PSG9	pregnancy specific beta-1-glycoprotein 9	4,98E-05	14,3212	BM up vs all others
209258_s_at	SMC3	structural maintenance of chromosomes 3	2,57E-09	14,1599	CB up vs all others

228766_at	CD36	CD36 molecule (thrombospondin receptor)	0,000204137	14,1244	MU up vs all others
230585_at	---	---	1,72E-06	14,1088	PE up vs all others
230748_at	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transp7)	3,63E-11	13,984	PE up vs all others
238091_at	---	---	4,96E-07	13,912	MU up vs all others
213541_s_at	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	0,00201095	13,8287	PE up vs all others
224215_s_at	DLL1	delta-like 1 (Drosophila)	8,02E-06	13,7432	MU up vs all others
213316_at	KIAA1462	KIAA1462	0,000816411	13,689	PE up vs all others
1563933_a_at	PLD5	phospholipase D family, member 5	2,54E-09	13,5262	MU up vs all others
1554411_at	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	9,27E-07	13,4447	CB up vs all others
235722_at	SYNJ2BP	synaptojanin 2 binding protein	1,28E-07	13,4349	CB up vs all others
212909_at	LYPD1	LY6/PLAUR domain containing 1	0,00169975	13,2418	BM up vs all others
203726_s_at	LAMA3	laminin, alpha 3	1,72E-06	13,239	PE up vs all others
238133_at	---	---	6,05E-06	13,2335	PE up vs all others
206500_s_at	C14orf106	chromosome 14 open reading frame 106	2,56E-08	12,9123	CB up vs all others
204653_at	TFAP2A	transcription factor AP-2 alpha	0,00590467	12,8509	BM up vs all others
203131_at	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	0,00040229	12,8108	PE up vs all others
229479_at	---	---	0,0125282	12,7797	BM up vs all others
214218_s_at	XIST	X (inactive)-specific transcript (non-protein coding)	3,42E-07	12,7755	BM up vs all others
207147_at	DLX2	distal-less homeobox 2	0,00543424	12,7656	CB up vs all others
209031_at	CADM1	cell adhesion molecule 1	9,50E-06	12,7653	PE up vs all others
222877_at	---	---	0,000172625	12,6265	PE up vs all others
240027_at	LIN7A	lin-7 homolog A (C. elegans)	2,10E-07	12,5036	CB up vs all others
229459_at	FAM19A5	family with sequence similarity 19, member A5	0,000907483	12,3855	PE up vs all others
208092_s_at	FAM49A	family with sequence similarity 49, member A	1,07E-06	12,3216	MU up vs all others
210997_at	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	0,00188857	12,2786	PE up vs all others
225626_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	0,000128056	12,2283	MU up vs all others
213519_s_at	LAMA2	laminin, alpha 2	1,03E-05	12,2265	MU up vs all others
222722_at	OGN	Osteoglycin	7,61E-05	12,1674	PE up vs all others
203819_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0,00373983	12,1245	CB up vs all others
239309_at	DLX6	distal-less homeobox 6	1,05E-06	12,0625	PE up vs all others
211906_s_at	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	4,95E-06	12,0427	PE up vs all others
219772_s_at	SMPX	small muscle protein, X-linked	0,0587466	12,0265	MU up vs all others
222439_s_at	THRAP3	thyroid hormone receptor associated protein 3	1,32E-07	11,9833	CB up vs all others
206796_at	WISP1	WNT1 inducible signaling pathway protein 1	0,00114458	11,9832	PE up vs all others
240509_s_at	GREM2	gremlin 2	4,17E-06	11,9593	PE up vs all others
202834_at	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	4,00E-10	11,8618	MU up vs all others
211823_s_at	PXN	Paxillin	1,62E-08	11,8526	BM up vs all others
205174_s_at	QPCT	glutaminyl-peptide cyclotransferase	3,98E-06	11,7974	PE up vs all others
204894_s_at	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	0,000139774	11,7617	MU up vs all others
210305_at	PDE4DIP	phosphodiesterase 4D interacting protein	0,00100297	11,7221	BM up vs all others
241902_at	MKX	mohawk homeobox	0,000988777	11,7138	PE up vs all others
	PCDHGA10	///			
	PCDHGA11	///			
	PCDHGA12	///			
	PCDHGA3	///			
	PCDHGA5	///			
211876_x_at	PCDHGA6	protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protoca	5,55E-09	11,6953	BM up vs all others
226145_s_at	FRAS1	Fraser syndrome 1	2,27E-05	11,6295	MU up vs all others
210317_s_at	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat	5,80E-10	11,6221	BM up vs all others

212187_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	9,90E-07	11,6191	MU up vs all others
211748_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	3,30E-07	11,6133	MU up vs all others
231766_s_at	COL12A1	collagen, type XII, alpha 1	0,00019229	11,6039	PE up vs all others
205933_at	SETBP1	SET binding protein 1	9,16E-05	11,5895	PE up vs all others
241560_at	---	---	0,000118933	11,5705	PE up vs all others
225871_at	STEAP2	six transmembrane epithelial antigen of the prostate 2	0,000367994	11,5419	PE up vs all others
209030_s_at	CADM1	cell adhesion molecule 1	9,90E-06	11,5194	PE up vs all others
206118_at	STAT4	signal transducer and activator of transcription 4	0,00216441	11,4541	PE up vs all others
235079_at	ZNF704	zinc finger protein 704	1,51E-06	11,4419	MU up vs all others
229578_at	JPH2	junctophilin 2	7,28E-05	11,4022	MU up vs all others
228218_at	LSAMP	limbic system-associated membrane protein	1,17E-05	11,305	PE up vs all others
205681_at	BCL2A1	BCL2-related protein A1	9,88E-05	11,1502	PE up vs all others
209555_s_at	CD36	CD36 molecule (thrombospondin receptor)	0,000156201	11,1006	MU up vs all others
213075_at	OLFML2A	olfactomedin-like 2°	2,95E-05	11,0306	MU up vs all others
235182_at	ISM1	isthmin 1 homolog (zebrafish)	0,00012063	11,0253	PE up vs all others
228750_at	---	---	2,56E-06	10,9045	MU up vs all others
204437_s_at	FOLR1	folate receptor 1 (adult)	2,99E-06	10,8274	MU up vs all others
206481_s_at	LDB2	LIM domain binding 2	0,00080976	10,8222	PE up vs all others
204967_at	SHROOM2	shroom family member 2	0,000282543	10,7962	PE up vs all others
208900_s_at	TOP1	topoisomerase (DNA) I	1,26E-10	10,7544	CB up vs all others
205959_at	MMP13	matrix metalloproteinase 13 (collagenase 3)	1,05E-05	10,7127	PE up vs all others
203276_at	LMNB1	lamin B1	1,47E-09	10,7088	CB up vs all others
202855_s_at	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transp 4)	0,000953278	10,6152	BM up vs all others
200795_at	SPARCL1	SPARC-like 1 (hevin)	0,000553389	10,5986	MU up vs all others
205352_at	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	0,000599461	10,5976	PE up vs all others
227760_at	IGFBPL1	insulin-like growth factor binding protein-like 1	1,75E-05	10,5662	MU up vs all others
227354_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	4,30E-06	10,552	MU up vs all others
241749_at	MURC	muscle-related coiled-coil protein	0,0506991	10,5268	MU up vs all others
209373_at	MALL	mal, T-cell differentiation protein-like	0,00113241	10,5158	BM up vs all others
209909_s_at	TGFB2	transforming growth factor, beta 2	0,00264651	10,5146	BM up vs all others
226884_at	LRRN1	leucine rich repeat neuronal 1	1,66E-07	10,512	MU up vs all others
230836_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	3,74E-06	10,4581	PE up vs all others
209343_at	EFHD1	EF-hand domain family, member D1	2,25E-05	10,449	MU up vs all others
208859_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked	6,04E-05	10,2753	CB up vs all others
204938_s_at	PLN	Phospholamban	0,000859249	10,2173	MU up vs all others
208443_x_at	SHOX2	short stature homeobox 2	5,65E-05	10,0776	PE up vs all others
205923_at	RELN	Reelin	0,000528779	10,0599	CB up vs all others
235104_at	ERAP2	endoplasmic reticulum aminopeptidase 2	0,000563169	9,99704	CB up vs all others
216627_s_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide1	7,76E-08	9,99065	BM up vs all others
211570_s_at	RAPSN	receptor-associated protein of the synapse	0,000369039	9,94518	MU up vs all others
220407_s_at	TGFB2	transforming growth factor, beta 2	0,000233223	9,89648	BM up vs all others
213498_at	CREB3L1	cAMP responsive element binding protein 3-like 1	3,35E-07	9,88768	BM up vs all others
206170_at	ADRB2	adrenergic, beta-2-, receptor, surface	0,000157388	9,87791	CB up vs all others
223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	7,50E-06	9,83508	MU up vs all others
203296_s_at	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	0,0168679	9,80512	MU up vs all others
203820_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0,00557138	9,73753	CB up vs all others
221019_s_at	COLEC12	collectin sub-family member 12	0,00178981	9,65251	PE up vs all others

216733_s_at	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0,000217742	9,63777	MU up vs all others
209908_s_at	TGFB2	transforming growth factor, beta 2	1,38E-06	9,61008	BM up vs all others
37512_at	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	1,37E-05	9,58135	MU up vs all others
236620_at	RIF1	RAP1 interacting factor homolog (yeast)	0,000347156	9,53921	CB up vs all others
230746_s_at	LOC100288985	Hypothetical protein LOC100288985	0,00109983	9,53766	PE up vs all others
206693_at	IL7	interleukin 7	4,74E-06	9,48679	PE up vs all others
209167_at	GPM6B	glycoprotein M6B	8,81E-06	9,48324	MU up vs all others
241955_at	HECTD1	HECT domain containing 1	1,17E-06	9,47724	CB up vs all others
209732_at	CLEC2B	C-type lectin domain family 2, member B	5,41E-07	9,45503	MU up vs all others
227952_at	---	---	0,00031677	9,44493	PE up vs all others
241652_x_at	---	---	8,25E-07	9,41294	CB up vs all others
204840_s_at	EEA1	early endosome antigen 1	2,96E-06	9,39124	CB up vs all others
227475_at	FOXQ1	forkhead box Q1	5,08E-08	9,34064	PE up vs all others
231842_at	KIAA1462	KIAA1462	0,00160849	9,33896	PE up vs all others
209738_x_at	PSG6	pregnancy specific beta-1-glycoprotein 6	2,53E-06	9,32637	BM up vs all others
1555480_a_at	FBLIM1	filamin binding LIM protein 1	7,29E-07	9,30814	BM up vs all others
202450_s_at	CTSK	cathepsin K	0,000850041	9,26336	PE up vs all others
209582_s_at	CD200	CD200 molecule	0,00283663	9,25442	PE up vs all others
202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	0,00657309	9,24639	BM up vs all others
1567224_at	HMGGA2	high mobility group AT-hook 2	0,00178157	9,20685	CB up vs all others
224348_s_at	---	---	9,63E-08	9,12929	MU up vs all others
217878_s_at	CDC27	cell division cycle 27 homolog (S. cerevisiae)	1,74E-09	9,12131	CB up vs all others
235276_at	EPSTI1	epithelial stromal interaction 1 (breast)	1,30E-05	9,1155	PE up vs all others
235504_at	GREM2	gremlin 2	7,82E-06	9,07362	PE up vs all others
220603_s_at	MCTP2	multiple C2 domains, transmembrane 2	3,00E-05	9,00805	PE up vs all others
243209_at	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	0,000219227	8,99969	MU up vs all others
208894_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	1,83E-07	8,98803	PE up vs all others
207570_at	SHOX	short stature homeobox	7,35E-05	8,96131	PE up vs all others
235057_at	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	0,000107172	8,89436	CB up vs all others
209257_s_at	SMC3	structural maintenance of chromosomes 3	7,24E-11	8,88794	CB up vs all others
235425_at	SGOL2	shugoshin-like 2 (S. pombe)	0,00157646	8,87123	CB up vs all others
1554803_s_at	TRIM72	tripartite motif-containing 72	0,00457505	8,84011	MU up vs all others
225173_at	ARHGAP18	Rho GTPase activating protein 18	6,33E-06	8,83099	CB up vs all others
223537_s_at	WNT5B	wingless-type MMTV integration site family, member 5B	0,000334777	8,78254	BM up vs all others
227984_at	LMF1	lipase maturation factor 1	6,10E-06	8,76985	MU up vs all others
229308_at	ANKRD29	ankyrin repeat domain 29	7,35E-08	8,75788	PE up vs all others
202546_at	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	9,37E-05	8,73311	MU up vs all others
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C	0,00272377	8,67885	PE up vs all others
223541_at	HAS3	hyaluronan synthase 3	0,000357683	8,67258	PE up vs all others
204506_at	PPP3R1	protein phosphatase 3, regulatory subunit B, alpha	4,50E-09	8,66588	CB up vs all others
203963_at	CA12	carbonic anhydrase XII	0,00164683	8,63802	PE up vs all others
206657_s_at	MYOD1	myogenic differentiation 1	8,20E-06	8,53407	MU up vs all others
205388_at	TNNC2	troponin C type 2 (fast)	0,0667018	8,52335	MU up vs all others
217901_at	DSG2	desmoglein 2	0,000918581	8,47339	PE up vs all others
222171_s_at	PKNOX2	PBX/knotted 1 homeobox 2	5,16E-05	8,47064	MU up vs all others
214767_s_at	HSPB6	heat shock protein, alpha-crystallin-related, B6	0,000408472	8,43939	BM up vs all others
213994_s_at	SPON1	spondin 1, extracellular matrix protein	0,000247855	8,3666	PE up vs all others

207558_s_at	PITX2	paired-like homeodomain 2	0,00941008	8,33045	BM up vs all others
235244_at	CCDC58	coiled-coil domain containing 58	0,00739574	8,28182	CB up vs all others
1560017_at	TMTC3	transmembrane and tetratricopeptide repeat containing 3	1,51E-08	8,26219	CB up vs all others
204483_at	ENO3	enolase 3 (beta, muscle)	0,0254451	8,25479	MU up vs all others
224590_at	XIST	X (inactive)-specific transcript (non-protein coding)	1,27E-07	8,24232	BM up vs all others
235874_at	PRSS35	protease, serine, 35	5,94E-05	8,22969	PE up vs all others
207824_s_at	MAZ	MYC-associated zinc finger protein	6,90E-09	8,22439	BM up vs all others
210303_at	MAB21L2	mab-21-like 2 (C. elegans)	6,85E-08	8,18409	PE up vs all others
201262_s_at	BGN	Biglycan	7,47E-05	8,14334	BM up vs all others
210861_s_at	WISP3	WNT1 inducible signaling pathway protein 3	0,00696522	8,1308	CB up vs all others
209170_s_at	GPM6B	glycoprotein M6B	1,88E-05	8,08489	MU up vs all others
201167_x_at	ARHGDIA CRYBB2	Rho GDP dissociation inhibitor (GDI) alpha ///	1,98E-06	8,06413	BM up vs all others
206777_s_at	CRYBB2P1	crystallin, beta B2 /// crystallin, beta B2 pseudogene 1	0,000110646	8,0421	BM up vs all others
224589_at	XIST	X (inactive)-specific transcript (non-protein coding)	8,41E-07	8,03778	BM up vs all others
200935_at	CALR	Calreticulin	6,01E-07	8,02794	BM up vs all others
243813_at	---	---	0,000961558	8,02163	PE up vs all others
202957_at	HCLS1	hematopoietic cell-specific Lyn substrate 1	0,000587211	8,01363	BM up vs all others
226213_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0,0202108	7,94978	MU up vs all others
229461_x_at	NEGR1	neuronal growth regulator 1	0,000595529	7,94432	PE up vs all others
211081_s_at	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	1,13E-08	7,93085	CB up vs all others
231841_s_at	KIAA1462	KIAA1462	0,00273551	7,9227	PE up vs all others
201072_s_at	SMARCC1	SWI/SNF related,matrixassociated, regulator chromatin subfamilyc	2,55E-08	7,91542	CB up vs all others
205700_at	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	1,34E-06	7,90471	MU up vs all others
237056_at	INSC	inscuteable homolog (Drosophila)	3,23E-05	7,90429	PE up vs all others
242138_at	DLX1	distal-less homeobox 1	0,00394837	7,86095	CB up vs all others
210457_x_at	HMGA1	high mobility group AT-hook 1	8,55E-06	7,8167	BM up vs all others
39248_at	AQP3	aquaporin 3 (Gill blood group)	0,000125255	7,81665	MU up vs all others
210632_s_at	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	0,00254085	7,79576	MU up vs all others
218730_s_at	OGN	Osteoglycin	0,000312574	7,76976	PE up vs all others
209692_at	EYA2	eyes absent homolog 2 (Drosophila)	0,0013086	7,74609	PE up vs all others
1557256_a_at	---	---	1,26E-05	7,74193	CB up vs all others
217388_s_at	KYNU	kynureninase (L-kynurenine hydrolase)	1,47E-07	7,69829	PE up vs all others
202350_s_at	MATN2	matrilin 2	0,000390085	7,68164	PE up vs all others
214374_s_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	5,17E-06	7,67332	CB up vs all others
213647_at	DNA2	DNA replication helicase 2 homolog (yeast)	1,65E-05	7,62733	CB up vs all others
201367_s_at	ZFP36L2	zinc finger protein 36, C3H type-like 2	0,0011022	7,61391	BM up vs all others
1552680_a_at	CASC5	cancer susceptibility candidate 5	0,000172844	7,60669	CB up vs all others
242352_at	NIPBL	Nipped-B homolog (Drosophila)	2,54E-06	7,55076	CB up vs all others
1553962_s_at	RHOB	ras homolog gene family, member B	1,00E-07	7,53614	BM up vs all others
227955_s_at	EFNA5	ephrin-A5	0,00138193	7,53416	CB up vs all others
228155_at	C10orf58	chromosome 10 open reading frame 58	2,44E-05	7,50056	MU up vs all others
222513_s_at	SORBS1	sorbin and SH3 domain containing 1	8,67E-05	7,4866	MU up vs all others
242945_at	FAM20A	family with sequence similarity 20, member A	0,000339878	7,41118	PE up vs all others
219304_s_at	PDGFD	platelet derived growth factor D	0,000128612	7,39236	PE up vs all others
229437_at	MIR155HG	MIR155 host gene (non-protein coding)	0,00020494	7,36695	CB up vs all others
234068_s_at	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	0,000928073	7,36582	BM up vs all others
202856_s_at	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transp4)	0,00285394	7,36159	BM up vs all others

219872_at	FAM198B	family with sequence similarity 198, member B	0,00107099	7,34682	BM up vs all others
210933_s_at	FSCN1	fascin homolog 1, actin-bundling protein(<i>Strongylocentrotus purp.</i>)	1,44E-07	7,34638	BM up vs all others
225667_s_at	FAM84A	family with sequence similarity 84, member A	0,00634186	7,32213	CB up vs all others
205116_at	LAMA2	laminin, alpha 2	4,23E-05	7,32063	MU up vs all others
1569872_a_at	LMF1	lipase maturation factor 1	0,000711677	7,30408	MU up vs all others
227188_at	C21orf63	chromosome 21 open reading frame 63	1,06E-05	7,29723	PE up vs all others
211136_s_at	CLPTM1	cleft lip and palate associated transmembrane protein 1	1,96E-09	7,27702	BM up vs all others
204679_at	KCNK1	potassium channel, subfamily K, member 1	0,000703421	7,26384	PE up vs all others
226322_at	TMTC1	transmembrane and tetratricopeptide repeat containing 1	0,000732475	7,25918	MU up vs all others
204160_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	0,000834348	7,24625	MU up vs all others
225016_at	APCDD1	adenomatosis polyposis coli down-regulated 1	0,000117181	7,23263	PE up vs all others
235696_at	---	---	0,00616404	7,22998	CB up vs all others
227948_at	FGD4	FYVE, RhoGEF and PH domain containing 4	0,000481057	7,19222	MU up vs all others
207145_at	MSTN	Myostatin	0,00842652	7,18041	MU up vs all others
228575_at	IL20RB	interleukin 20 receptor beta	0,000291871	7,17972	MU up vs all others
213247_at	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain1	0,00118451	7,17287	PE up vs all others
229011_at	---	---	2,41E-05	7,16033	PE up vs all others
217452_s_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	0,000446558	7,15135	MU up vs all others
232618_at	CYorf15A	chromosome Y open reading frame 15°	0,00529575	7,11603	CB up vs all others
235171_at	LOC100505501	hypothetical LOC100505501	7,04E-06	7,11572	CB up vs all others
214841_at	CNIH3	cornichon homolog 3 (<i>Drosophila</i>)	1,22E-06	7,10035	PE up vs all others
208483_x_at	KRT33A	keratin 33°	0,00187609	7,09496	BM up vs all others
213845_at	GRIK2	glutamate receptor, ionotropic, kainate 2	0,00164695	7,09473	BM up vs all others
1554220_a_at	---	---	6,00E-08	7,06747	PE up vs all others
219717_at	DCAF16	DDB1 and CUL4 associated factor 16	8,28E-09	7,05504	CB up vs all others
212962_at	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (<i>C. elegans</i>)	1,19E-08	7,0508	BM up vs all others
209199_s_at	MEF2C	myocyte enhancer factor 2C	0,0207183	7,04775	MU up vs all others
216563_at	ANKRD12	Ankyrin repeat domain 12	0,00526102	7,02398	CB up vs all others
231879_at	COL12A1	collagen, type XII, alpha 1	0,00228033	7,02325	PE up vs all others
205066_s_at	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	0,000219452	6,999	PE up vs all others
209990_s_at	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	7,02E-06	6,95147	BM up vs all others
235014_at	LOC147727	hypothetical LOC147727	4,59E-06	6,92135	CB up vs all others
63305_at	PKNOX2	PBX/knotted 1 homeobox 2	1,67E-05	6,90981	MU up vs all others
219064_at	ITIH5	inter-alpha (globulin) inhibitor H5	0,000171417	6,88414	MU up vs all others
209829_at	FAM65B	family with sequence similarity 65, member B	0,0138167	6,86815	MU up vs all others
210121_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	0,000657925	6,81905	MU up vs all others
227386_s_at	TMEM200B	transmembrane protein 200B	0,00302777	6,77704	PE up vs all others
203841_x_at	MAPRE3	microtubule-associated protein, RP/EB family, member 3	8,59E-07	6,77523	BM up vs all others
206825_at	OXTR	oxytocin receptor	0,004579	6,75186	BM up vs all others
1559506_x_at	FLJ35409	FLJ35409 protein	0,000187097	6,74204	CB up vs all others
209830_s_at	SLC9A3R2	solute carrier family 9, member 3 regulator 2	5,30E-08	6,73731	BM up vs all others
218824_at	PNMAL1	PNMA-like 1	4,09E-05	6,71535	MU up vs all others
227350_at	HELLS	helicase, lymphoid-specific	0,000207434	6,68577	CB up vs all others
210119_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	0,00116576	6,66741	PE up vs all others
223316_at	CCDC3	coiled-coil domain containing 3	7,53E-08	6,64638	MU up vs all others
209369_at	ANXA3	annexin A3	0,000471195	6,63304	MU up vs all others
224435_at	C10orf58	chromosome 10 open reading frame 58	1,20E-06	6,60924	MU up vs all others

225622_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	1,11E-06	6,60463	MU up vs all others
227900_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	0,000243432	6,60192	PE up vs all others
208106_x_at	PSG6	pregnancy specific beta-1-glycoprotein 6	7,19E-06	6,59553	BM up vs all others
222837_s_at	NAA15	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	0,00193731	6,59123	CB up vs all others
201150_s_at	TIMP3	TIMP metalloproteinase inhibitor 3	0,000540683	6,56876	PE up vs all others
209897_s_at	SLIT2	slit homolog 2 (Drosophila)	0,00162674	6,55551	PE up vs all others
207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	0,000366107	6,55269	MU up vs all others
1568680_s_at	YTHDC2	YTH domain containing 2	1,84E-09	6,54055	CB up vs all others
209719_x_at	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	6,89E-06	6,53725	PE up vs all others
219181_at	LIPG	lipase, endothelial	0,000158613	6,53516	CB up vs all others
1561615_s_at	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	5,27E-05	6,52617	CB up vs all others
203708_at	PDE4B	phosphodiesterase 4B, cAMP-specific	0,0074327	6,51281	PE up vs all others
230560_at	STXBP6	syntaxin binding protein 6 (amisyn)	0,000308294	6,48321	MU up vs all others
213169_at	SEMA5A	sema domain, seven thrombospondin repeats, transmembr domain	0,000921364	6,47497	PE up vs all others
210413_x_at	SERPINB3 SERPINB4	/// serpin peptidase inhibitor, clade B (ovalbumin), member 3 /// serpin peptidase inhibitor	6,67E-05	6,46798	PE up vs all others
207510_at	BDKRB1	bradykinin receptor B1	0,00158529	6,45821	BM up vs all others
216971_s_at	PLEC	Plectin	0,0169834	6,44908	BM up vs all others
214313_s_at	EIF5B	Eukaryotic translation initiation factor 5B	0,000114375	6,44343	CB up vs all others
214581_x_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0,00361861	6,42225	BM up vs all others
209996_x_at	PCM1	pericentriolar material 1	0,000249824	6,40964	CB up vs all others
229225_at	NRP2	neuropilin 2	0,000893326	6,4069	PE up vs all others
219829_at	ITGB1BP2	integrin beta 1 binding protein (melusin) 2	0,00314912	6,39991	MU up vs all others
1557129_a_at	FAM111B	family with sequence similarity 111, member B	9,66E-09	6,381	CB up vs all others
226625_at	TGFBR3	transforming growth factor, beta receptor III	0,000290161	6,36772	PE up vs all others
236270_at	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dep4	2,11E-06	6,35843	PE up vs all others
213606_s_at	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	1,30E-06	6,35035	BM up vs all others
218826_at	SLC35F2	solute carrier family 35, member F2	0,000313068	6,32775	PE up vs all others
228202_at	PLN	Phospholamban	0,00158075	6,3257	MU up vs all others
211663_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	2,93E-06	6,32285	MU up vs all others
1557051_s_at	---	---	0,000702441	6,3123	CB up vs all others
218045_x_at	PTMS	Parathyrosin	3,76E-06	6,31024	BM up vs all others
228033_at	E2F7	E2F transcription factor 7	1,28E-05	6,30962	CB up vs all others
225612_s_at	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	1,94E-06	6,25113	CB up vs all others
208937_s_at	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix	4,37E-07	6,24037	CB up vs all others
209301_at	CA2	carbonic anhydrase II	0,0012108	6,21153	PE up vs all others
224022_x_at	WNT16	wingless-type MMTV integration site family, member 16	0,000193293	6,20549	CB up vs all others
221211_s_at	C21orf7	chromosome 21 open reading frame 7	0,000726709	6,19475	BM up vs all others
202827_s_at	MMP14	matrix metalloproteinase 14 (membrane-inserted)	0,00154585	6,15661	BM up vs all others
34478_at	RAB11B	RAB11B, member RAS oncogene family	3,89E-07	6,15244	BM up vs all others
235751_s_at	VMO1	vitelline membrane outer layer 1 homolog (chicken)	8,21E-07	6,12087	PE up vs all others
235588_at	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	5,97E-08	6,0897	CB up vs all others
226304_at	HSPB6	heat shock protein, alpha-crystallin-related, B6	0,00411431	6,06765	BM up vs all others
223454_at	CXCL16	chemokine (C-X-C motif) ligand 16	3,13E-07	6,04732	PE up vs all others
214027_x_at	DES /// FAM48A	desmin /// family with sequence similarity 48, member A	0,00708532	6,04608	MU up vs all others
205908_s_at	OMD	Osteomodulin	4,19E-06	6,04557	PE up vs all others
223075_s_at	AIF1L	allograft inflammatory factor 1-like	1,01E-07	6,03161	MU up vs all others
1553810_a_at	KIAA1524	KIAA1524	1,10E-06	6,02093	CB up vs all others

242787_at	---	---	1,69E-07	6,02043	CB up vs all others
207788_s_at	SORBS3	sorbin and SH3 domain containing 3	3,81E-06	6,01904	BM up vs all others
1559397_s_at	PRR14	proline rich 14	4,09E-09	6,01709	BM up vs all others
226864_at	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	0,00711684	5,98735	CB up vs all others
1570153_at	C13orf38	chromosome 13 open reading frame 38	0,00171165	5,97906	CB up vs all others
225046_at	LOC389831	hypothetical LOC389831	0,000412659	5,97168	BM up vs all others
209710_at	GATA2	GATA binding protein 2	0,00175874	5,96717	CB up vs all others
235009_at	BOD1L	biorientation of chromosomes in cell division 1-like	2,73E-07	5,96673	CB up vs all others
214265_at	ITGA8	integrin, alpha 8	3,64E-05	5,96387	MU up vs all others
52255_s_at	COL5A3	collagen, type V, alpha 3	0,000720258	5,94839	MU up vs all others
204285_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0,000630826	5,9336	CB up vs all others
242629_at	RAB3B	RAB3B, member RAS oncogene family	0,00139419	5,92834	PE up vs all others
208204_s_at	CAV3	caveolin 3	0,000509835	5,91512	MU up vs all others
216352_x_at	PCDHGA3	protocadherin gamma subfamily A, 3	2,76E-06	5,91261	BM up vs all others
239002_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated	9,79E-06	5,89967	CB up vs all others
213006_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	0,00115501	5,88668	PE up vs all others
242005_at	LOC100506377	hypothetical LOC100506377	0,00229158	5,86631	CB up vs all others
243438_at	PDE7B	phosphodiesterase 7B	4,34E-05	5,8656	PE up vs all others
208930_s_at	ILF3	interleukin enhancer binding factor 3, 90kDa	1,08E-07	5,85687	CB up vs all others
213640_s_at	LOX	lysyl oxidase	0,00110206	5,84178	BM up vs all others
215059_at	---	---	0,00130591	5,83615	PE up vs all others
236665_at	CCDC18	coiled-coil domain containing 18	1,20E-07	5,81539	CB up vs all others
224863_at	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	1,70E-08	5,81447	CB up vs all others
210261_at	KCNK2	potassium channel, subfamily K, member 2	0,00103693	5,80935	PE up vs all others
205542_at	STEAP1	six transmembrane epithelial antigen of the prostate 1	0,00087929	5,80485	PE up vs all others
202895_s_at	SIRPA	signal-regulatory protein alpha	8,28E-06	5,8008	BM up vs all others
229199_at	SCN9A	sodium channel, voltage-gated, type IX, alpha subunit	0,00500028	5,80063	CB up vs all others
230425_at	EPHB1	EPH receptor B1	0,0026954	5,79061	CB up vs all others
204999_s_at	ATF5	activating transcription factor 5	1,69E-07	5,78882	MU up vs all others
213085_s_at	WWC1	WW and C2 domain containing 1	0,000157925	5,76784	PE up vs all others
202626_s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0,00332099	5,76294	BM up vs all others
211599_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	7,55E-05	5,75959	BM up vs all others
1553565_s_at	DDAH1	dimethylarginine dimethylaminohydrolase 1	2,09E-05	5,74702	BM up vs all others
208502_s_at	PITX1	paired-like homeodomain 1	7,08E-05	5,74636	BM up vs all others
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	6,26E-06	5,74377	PE up vs all others
202175_at	CHPF	chondroitin polymerizing factor	2,75E-05	5,73805	BM up vs all others
211039_at	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	0,00733841	5,73543	MU up vs all others
228642_at	---	---	0,000142174	5,73464	CB up vs all others
214266_s_at	PDLIM7	PDZ and LIM domain 7 (enigma)	3,05E-05	5,73098	BM up vs all others
205809_s_at	WASL	Wiskott-Aldrich syndrome-like	2,52E-06	5,7276	CB up vs all others
229127_at	JAM2	junctional adhesion molecule 2	2,94E-06	5,72705	MU up vs all others
205991_s_at	PRRX1	paired related homeobox 1	0,000222093	5,71578	PE up vs all others
204507_s_at	PPP3R1	protein phosphatase 3, regulatory subunit B, alpha	7,36E-07	5,71405	CB up vs all others
205296_at	RBL1	retinoblastoma-like 1 (p107)	7,10E-05	5,71333	CB up vs all others
243357_at	NEGR1	neuronal growth regulator 1	0,0019981	5,70685	PE up vs all others
238778_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily 7)	5,87E-06	5,70183	MU up vs all others
234701_at	ANKRD11	ankyrin repeat domain 11	3,82E-07	5,68093	CB up vs all others

1556329_a_at	---	---	0,00688673	5,67179	CB up vs all others
207535_s_at	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2	3,44E-06	5,66793	BM up vs all others
203861_s_at	ACTN2	actinin, alpha 2	0,0833558	5,666	MU up vs all others
1554018_at	GPNMB	glycoprotein (transmembrane) nmb	9,37E-05	5,66529	PE up vs all others
219367_s_at	---	---	0,000709411	5,65952	PE up vs all others
202920_at	ANK2	ankyrin 2, neuronal	0,000506264	5,65807	MU up vs all others
229669_at	LOC100507263	hypothetical LOC100507263	3,64E-05	5,6421	MU up vs all others
242592_at	GPR137C	G protein-coupled receptor 137C	0,000125199	5,64063	CB up vs all others
205941_s_at	COL10A1	collagen, type X, alpha 1	0,00201726	5,64008	PE up vs all others
224828_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	0,000131766	5,63355	CB up vs all others
210395_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	0,0133824	5,61375	MU up vs all others
227618_at	---	---	0,00150776	5,61106	PE up vs all others
202888_s_at	ANPEP	alanyl (membrane) aminopeptidase	0,000342564	5,60802	PE up vs all others
236599_at	---	---	8,80E-05	5,60793	PE up vs all others
224563_at	WASF2	WAS protein family, member 2	3,24E-08	5,60723	CB up vs all others
1552289_a_at	CILP2	cartilage intermediate layer protein 2	7,42E-05	5,60565	PE up vs all others
228986_at	OSBPL8	oxysterol binding protein-like 8	3,64E-08	5,60281	CB up vs all others
205741_s_at	DTNA	dystrobrevin, alpha	0,00751688	5,59888	CB up vs all others
204482_at	CLDN5	claudin 5	6,63E-06	5,59566	MU up vs all others
216054_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	0,0178762	5,58625	MU up vs all others
206566_at	SLC7A1	solute carrier family 7, member 1	5,40E-07	5,5789	BM up vs all others
232569_at	---	---	5,16E-05	5,57791	CB up vs all others
204693_at	CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1	0,000131584	5,55485	BM up vs all others
1558173_a_at	LUZP1	leucine zipper protein 1	8,47E-08	5,55341	CB up vs all others
231532_at	NCAM1	Neural cell adhesion molecule 1	9,67E-07	5,53566	MU up vs all others
205951_at	MYH1	myosin, heavy chain 1, skeletal muscle, adult	0,110818	5,52399	MU up vs all others
207542_s_at	AQP1	aquaporin 1 (Colton blood group)	0,00016018	5,50632	MU up vs all others
225301_s_at	MYO5B	myosin VB	2,66E-08	5,48345	MU up vs all others
215706_x_at	ZYX	Zyxin	0,000223951	5,46874	BM up vs all others
243940_at	TSHZ2	teashirt zinc finger homeobox 2	0,000659181	5,4661	PE up vs all others
204530_s_at	TOX	thymocyte selection-associated high mobility group box	2,14E-07	5,46464	CB up vs all others
1569110_x_at	LOC728613	programmed cell death 6 pseudogene	0,000216466	5,45471	MU up vs all others
91816_f_at	MEX3D	mex-3 homolog D (C. elegans)	0,00024956	5,44763	CB up vs all others
207148_x_at	MYOZ2	myozenin 2	0,140266	5,44539	MU up vs all others
207306_at	TCF15	transcription factor 15 (basic helix-loop-helix)	2,43E-09	5,44457	BM up vs all others
218975_at	COL5A3	collagen, type V, alpha 3	0,00022438	5,43502	MU up vs all others
234118_at	---	---	0,000117233	5,41987	PE up vs all others
205442_at	MFAP3L	microfibrillar-associated protein 3-like	9,03E-05	5,3987	MU up vs all others
210088_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	0,0210673	5,39611	MU up vs all others
213183_s_at	CDKN1C	Cyclin-dependent kinase inhibitor 1C (p57, Kip2)	7,08E-06	5,39121	MU up vs all others
1558924_s_at	CLIP1	CAP-GLY domain containing linker protein 1	2,33E-06	5,38239	CB up vs all others
213217_at	ADCY2	adenylate cyclase 2 (brain)	1,29E-05	5,37636	MU up vs all others
	LOC100506119				
	///				
229296_at	LOC100508342	hypothetical LOC100506119 /// hypothetical LOC100508342	0,00214462	5,36439	PE up vs all others
234951_s_at	COL12A1	collagen, type XII, alpha 1	0,000134371	5,35224	PE up vs all others
202625_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0,000200183	5,34595	BM up vs all others
227929_at	---	---	0,00105204	5,34137	CB up vs all others

225566_at	NRP2	neuropilin 2	0,000708968	5,33364	PE up vs all others
229158_at	WNK4	WNK lysine deficient protein kinase 4	0,00225817	5,32914	BM up vs all others
230543_at	USP9X	ubiquitin specific peptidase 9, X-linked	3,31E-07	5,32604	BM up vs all others
216867_s_at	PDGFA	platelet-derived growth factor alpha polypeptide	0,00273183	5,3243	CB up vs all others
230250_at	PTPRB	protein tyrosine phosphatase, receptor type, B	0,00807966	5,32167	BM up vs all others
213986_s_at	C19orf6	chromosome 19 open reading frame 6	1,15E-05	5,31679	BM up vs all others
204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0,000734807	5,31157	CB up vs all others
238763_at	RBM20	RNA binding motif protein 20	3,53E-05	5,31045	MU up vs all others
211993_at	WNK1	WNK lysine deficient protein kinase 1	3,83E-07	5,30566	CB up vs all others
230026_at	MRPL43	mitochondrial ribosomal protein L43	0,000992838	5,29607	PE up vs all others
221628_s_at	GLYR1	glyoxylate reductase 1 homolog (Arabidopsis)	6,15E-08	5,27549	BM up vs all others
227265_at	FGL2	fibrinogen-like 2	2,76E-05	5,27262	MU up vs all others
217599_s_at	MDFIC	MyoD family inhibitor domain containing	1,81E-05	5,27224	CB up vs all others
222803_at	PRTFDC1 FNIP1	phosphoribosyl transferase domain containing 1 folliculin interacting protein 1	0,00449525	5,27175	CB up vs all others
1555247_a_at	RAPGEF6	/// factor (GEF) 6	1,86E-06	5,26582	CB up vs all others
203254_s_at	TLN1	talin 1	0,000142326	5,26433	BM up vs all others
226319_s_at	THOC4	THO complex 4	0,00369424	5,26	CB up vs all others
235616_at	TSHZ2	teashirt zinc finger homeobox 2	0,00023422	5,24697	PE up vs all others
238326_at	ODF3B	outer dense fiber of sperm tails 3B	4,84E-07	5,24572	BM up vs all others
237534_at	---	---	1,82E-09	5,23812	BM up vs all others
213429_at	BICC1	bicaudal C homolog 1 (Drosophila)	0,00149428	5,23494	PE up vs all others
235653_s_at	THAP6	THAP domain containing 6	4,70E-08	5,23468	CB up vs all others
206022_at	NDP	Norrie disease (pseudoglioma)	0,000606057	5,22691	CB up vs all others
202247_s_at	MTA1	metastasis associated 1	1,24E-06	5,22584	BM up vs all others
203000_at	STMN2	stathmin-like 2	0,000453553	5,22064	PE up vs all others
226587_at	SNRPN	small nuclear ribonucleoprotein polypeptide N	3,35E-06	5,21669	MU up vs all others
214701_s_at	FN1	fibronectin 1	0,0118898	5,21609	BM up vs all others
238762_at	MTHFD2L	methylenetetrahydrofolate dehydrogenase(NADP+dependen)2-like	1,24E-05	5,21326	CB up vs all others
212007_at	UBXN4	UBX domain protein 4	1,35E-07	5,21107	CB up vs all others
203862_s_at	ACTN2	actinin, alpha 2	0,156187	5,19061	MU up vs all others
205341_at	EHD2	EH-domain containing 2	3,93E-06	5,19055	BM up vs all others
216250_s_at	LPXN	Leupaxin	0,00106159	5,18917	BM up vs all others
204420_at	FOSL1	FOS-like antigen 1	0,000126001	5,18324	BM up vs all others
238919_at	---	---	0,000101147	5,1757	CB up vs all others
1552611_a_at	JAK1	Janus kinase 1	6,70E-07	5,17113	CB up vs all others
1554579_a_at	MYO18B	myosin XVIIIIB	0,000673598	5,15837	MU up vs all others
228121_at	TGFB2	transforming growth factor, beta 2	0,00263299	5,14728	BM up vs all others
1569986_x_at	TNNT3	troponin T type 3 (skeletal, fast)	0,110632	5,14669	MU up vs all others
201673_s_at	GYS1	glycogen synthase 1 (muscle)	1,70E-05	5,14481	BM up vs all others
203239_s_at	CNOT3	CCR4-NOT transcription complex, subunit 3	1,80E-08	5,1436	BM up vs all others
203890_s_at	DAPK3	death-associated protein kinase 3	7,26E-08	5,13932	BM up vs all others
204072_s_at	FRY	furry homolog (Drosophila)	2,75E-05	5,13633	MU up vs all others
209312_x_at	HLA-DRB1 HLA-DRB4 HLA-DRB5	/// /// major histocompatibility complex, class II, DR beta 1 /// major histocompatibility comp	8,51E-08	5,12306	PE up vs all others
205304_s_at	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	3,88E-05	5,11956	PE up vs all others
227487_s_at	SERPINE2	Serpin peptidase inhibitor, clade E	0,000649533	5,11325	PE up vs all others
229655_at	FAM19A5	family with sequence similarity 19 -like, member A5	0,00148005	5,09856	PE up vs all others

223827_at	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	8,97E-07	5,09003	PE up vs all others
229305_at	MLF1IP	MLF1 interacting protein	1,35E-05	5,08298	CB up vs all others
229610_at	CKAP2L	cytoskeleton associated protein 2-like inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	1,54E-05	5,07135	CB up vs all others
211027_s_at	IKBKB		2,72E-07	5,06361	BM up vs all others
229139_at	JPH1	junctionophilin 1	0,0145572	5,05299	MU up vs all others
209542_x_at	IGF1	insulin-like growth factor 1 (somatomedin C)	1,09E-05	5,04441	PE up vs all others
230925_at	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	0,0133911	5,04078	BM up vs all others
203085_s_at	TGFB1	transforming growth factor, beta 1	0,00052557	5,03474	BM up vs all others
218711_s_at	SDPR	serum deprivation response microtubule associated monooxygenase, calponin and LIM domain containing 2	0,000165354	5,01915	MU up vs all others
206275_s_at	MICAL2		0,000337302	5,0136	BM up vs all others
235281_x_at	AHNAK	AHNAK nucleoprotein	3,65E-05	4,99996	BM up vs all others
208710_s_at	AP3D1	adaptor-related protein complex 3, delta 1 subunit	8,37E-09	4,99979	CB up vs all others
231807_at	KIAA1217	KIAA1217	2,29E-05	4,99174	PE up vs all others
200808_s_at	ZYX	Zyxin	0,000339335	4,99008	BM up vs all others
222062_at	IL27RA	interleukin 27 receptor, alpha	0,00441044	4,98087	BM up vs all others
242907_at	---	---	0,000255667	4,97768	MU up vs all others
241938_at	QKI	Quaking homolog, KH domain RNA binding (mouse)	5,72E-05	4,97516	MU up vs all others
	LOC100132247				
	LOC348162	LOC613037			
	LOC728888	LOC728888			
211996_s_at	NPIPL3	similar to Uncharacterized protein KIAA0220 /// hypothetical protein 348162 /// nuclear	0,00648276	4,95843	CB up vs all others
233109_at	COL12A1	Collagen, type XII, alpha 1	0,000254894	4,95295	PE up vs all others
204983_s_at	GPC4	glypican 4	0,000699137	4,94998	BM up vs all others
212705_x_at	PNPLA2	patatin-like phospholipase domain containing 2	1,93E-07	4,94189	BM up vs all others
227971_at	NRK	Nik related kinase	0,00562906	4,93076	CB up vs all others
210186_s_at	FKBP1A	FK506 binding protein 1A, 12kDa	5,43E-07	4,92982	BM up vs all others
209811_at	CASP2	caspase 2, apoptosis-related cysteine peptidase	3,46E-07	4,91048	CB up vs all others
223578_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1	0,00168878	4,90654	CB up vs all others
222016_s_at	ZNF323	zinc finger protein 323	0,00204927	4,89935	PE up vs all others
236356_at	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	1,83E-05	4,89869	CB up vs all others
223366_at	ZNF704	zinc finger protein 704	4,63E-07	4,88373	MU up vs all others
1559504_at	FLJ35409	FLJ35409 protein	0,000501598	4,87821	CB up vs all others
205405_at	SEMA5A	sema domain, seven thrombospondin repeats, transmembrane domain	0,000309563	4,87675	PE up vs all others
205034_at	CCNE2	cyclin E2	0,00123391	4,87447	CB up vs all others
227096_at	JOSD2	Josephin domain containing 2	2,15E-07	4,87008	BM up vs all others
220580_at	BICC1	bicaudal C homolog 1 (Drosophila)	9,55E-05	4,86613	PE up vs all others
212938_at	COL6A1	collagen, type VI, alpha 1	0,000714689	4,86474	BM up vs all others
205439_at	GSTT2	glutathione S-transferase theta 2	0,00238326	4,858	BM up vs all others
229586_at	CHD9	chromodomain helicase DNA binding protein 9	6,85E-07	4,84526	CB up vs all others
1555103_s_at	FGF7	fibroblast growth factor 7	0,00244722	4,84244	PE up vs all others
214270_s_at	MAPRE3	microtubule-associated protein, RP/EB family, member 3	2,20E-08	4,83974	BM up vs all others
235765_at	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	0,000117873	4,83473	CB up vs all others
203424_s_at	IGFBP5	insulin-like growth factor binding protein 5	0,00724629	4,82234	CB up vs all others
212611_at	DTX4	deltex homolog 4 (Drosophila)	1,27E-06	4,81944	MU up vs all others
201043_s_at	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	0,000160392	4,81772	CB up vs all others
206805_at	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3°	0,00303122	4,81434	CB up vs all others

218294_s_at	NUP50	nucleoporin 50kDa	5,31E-06	4,80556	CB up vs all others
226695_at	PRRX1	paired related homeobox 1	2,14E-05	4,7998	PE up vs all others
	HOXD3	///			
	HOXD4	///			
205522_at	MIR10B	homeobox D3 /// homeobox D4 /// microRNA 10b	0,000804416	4,79843	PE up vs all others
219463_at	C20orf103	chromosome 20 open reading frame 103	1,77E-05	4,79549	PE up vs all others
235243_at	CLIP3	CAP-GLY domain containing linker protein 3	7,31E-07	4,78699	BM up vs all others
228933_at	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	0,000110841	4,78296	PE up vs all others
201101_s_at	BCLAF1	BCL2-associated transcription factor 1	2,45E-08	4,77761	CB up vs all others
236044_at	PPAPDC1A	phosphatidic acid phosphatase type 2 domain containing 1A	0,00519989	4,75347	BM up vs all others
226189_at	ITGB8	integrin, beta 8	0,000618072	4,75099	PE up vs all others
231183_s_at	JAG1	Jagged 1 (Alagille syndrome)	0,000562086	4,74515	MU up vs all others
225407_at	MBP	myelin basic protein	0,000312793	4,73816	MU up vs all others
211958_at	IGFBP5	insulin-like growth factor binding protein 5	0,000324806	4,72027	BM up vs all others
1556009_at	PEX13	peroxisomal biogenesis factor 13	0,00103237	4,71647	CB up vs all others
237183_at	---	---	2,47E-05	4,7149	PE up vs all others
206343_s_at	NRG1	neuregulin 1	0,00463023	4,70455	CB up vs all others
214604_at	HOXD11	homeobox D11	0,0192652	4,70124	CB up vs all others
218963_s_at	KRT23	keratin 23 (histone deacetylase inducible)	0,000315192	4,70016	PE up vs all others
239678_at	---	---	0,000983972	4,69544	CB up vs all others
227209_at	CNTN1	Contactin 1	0,000387308	4,69179	MU up vs all others
201182_s_at	CHD4	chromodomain helicase DNA binding protein 4	8,14E-07	4,68962	CB up vs all others
237094_at	FAM19A5	family with sequence similarity 19 (chemokine-like), member A5	0,000248359	4,68543	PE up vs all others
40850_at	FKBP8	FK506 binding protein 8, 38kDa	2,01E-05	4,68333	BM up vs all others
225606_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	2,78E-05	4,67505	MU up vs all others
209647_s_at	SOCS5	suppressor of cytokine signaling 5	0,000125058	4,67396	PE up vs all others
202729_s_at	LTBP1	latent transforming growth factor beta binding protein 1	0,000794499	4,67073	PE up vs all others
202357_s_at	CFB	complement factor B	0,000438879	4,6582	PE up vs all others
209436_at	SPON1	spondin 1, extracellular matrix protein	0,00031561	4,65136	PE up vs all others
219655_at	C7orf10	chromosome 7 open reading frame 10	0,000102513	4,65074	PE up vs all others
226320_at	THOC4	THO complex 4	0,00368058	4,64564	CB up vs all others
	DLEU2	/// deleted in lymphocytic leukemia 2 (non-protein coding) /// deleted in			
215629_s_at	DLEU2L	lymphocytic leuke	0,00529849	4,63424	CB up vs all others
1554685_a_at	KIAA1199	KIAA1199	0,000881624	4,63188	BM up vs all others
1558678_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1	0,00067379	4,62965	CB up vs all others
230221_at	BAT5	HLA-B associated transcript 5	3,08E-07	4,62625	BM up vs all others
222101_s_at	DCHS1	dachsous 1 (Drosophila)	0,00201735	4,62461	PE up vs all others
203809_s_at	AKT2	v-akt murine thymoma viral oncogene homolog 2	3,26E-08	4,61728	BM up vs all others
1553094_at	TAC4	tachykinin 4 (hemokinin)	2,72E-05	4,6161	BM up vs all others
218717_s_at	LEPREL1	leprecan-like 1	0,00267389	4,61258	PE up vs all others
241535_at	LOC100292909	hypothetical protein LOC100292909	0,00192389	4,61258	PE up vs all others
212940_at	COL6A1	collagen, type VI, alpha 1	0,000439375	4,60655	BM up vs all others
209682_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	0,000172185	4,60288	PE up vs all others
235388_at	CHD9	chromodomain helicase DNA binding protein 9	0,000685172	4,58328	CB up vs all others
210973_s_at	FGFR1	fibroblast growth factor receptor 1	0,00435206	4,58323	BM up vs all others
1565717_s_at	FUS	fused in sarcoma	0,00533624	4,57719	CB up vs all others
217025_s_at	DBN1	drebrin 1	9,06E-08	4,57519	BM up vs all others
229176_at	ANKH	ankylosis, progressive homolog (mouse)	0,000879723	4,57279	PE up vs all others
208889_s_at	NCOR2	nuclear receptor corepressor 2	3,66E-08	4,57004	BM up vs all others

233335_at	---	---	1,77E-06	4,5617	PE up vs all others
216222_s_at	MYO10	myosin X	2,20E-07	4,55955	CB up vs all others
226838_at	TTC32	tetratricopeptide repeat domain 32	1,14E-05	4,55294	CB up vs all others
242871_at	PAQR5	progesterone and adiponectin receptor family member V	0,00394855	4,55217	CB up vs all others
229070_at	C6orf105	chromosome 6 open reading frame 105	0,00287399	4,54915	PE up vs all others
203370_s_at	PDLIM7	PDZ and LIM domain 7 (enigma)	0,0100897	4,54294	BM up vs all others
216493_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	1,05E-07	4,53989	CB up vs all others
1552914_a_at	CD276	CD276 molecule	1,10E-05	4,535	BM up vs all others
239738_at	DACH2	dachshund homolog 2 (Drosophila)	0,00083074	4,53075	CB up vs all others
220946_s_at	SETD2	SET domain containing 2	9,81E-06	4,52817	CB up vs all others
205347_s_at	TMSB15A	thymosin beta 15°	0,00173365	4,52315	CB up vs all others
211631_x_at	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,polypeptide 1	1,10E-07	4,523	BM up vs all others
205410_s_at	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	1,26E-06	4,51788	BM up vs all others
220994_s_at	STXBP6	syntaxin binding protein 6 (amisyn)	0,0001064	4,50967	MU up vs all others
214326_x_at	JUND	jun D proto-oncogene	0,000137811	4,50732	BM up vs all others
224920_x_at	MYADM	myeloid-associated differentiation marker	3,86E-08	4,49733	BM up vs all others
242051_at	---	---	0,00200896	4,49648	CB up vs all others
232119_at	SYNPO2	synaptopodin 2	0,000635368	4,49432	MU up vs all others
1555639_a_at	RBM14	RNA binding motif protein 14	5,86E-09	4,49055	BM up vs all others
213260_at	FOXC1	forkhead box C1	0,000111107	4,48374	PE up vs all others
1554795_a_at	FBLIM1	filamin binding LIM protein 1	1,12E-08	4,48121	BM up vs all others
220945_x_at	MANSC1	MANSC domain containing 1	0,00124224	4,48092	PE up vs all others
1554251_at	HP1BP3	heterochromatin protein 1, binding protein 3	8,83E-07	4,47899	CB up vs all others
207379_at	EDIL3	EGF-like repeats and discoidin I-like domains 3	0,00222038	4,47727	BM up vs all others
219511_s_at	SNCAIP	synuclein, alpha interacting protein	0,00026884	4,4736	PE up vs all others
201850_at	CAPG	capping protein (actin filament), gelsolin-like	2,73E-05	4,46717	PE up vs all others
238877_at	EYA4	eyes absent homolog 4 (Drosophila)	4,65E-05	4,4558	MU up vs all others
203295_s_at	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	0,0251986	4,45248	MU up vs all others
1559005_s_at	CNTLN	centlein, centrosomal protein	3,31E-06	4,45047	CB up vs all others
219737_s_at	PCDH9	protocadherin 9	2,62E-05	4,45027	CB up vs all others
218608_at	ATP13A2	ATPase type 13A2	1,92E-07	4,44141	BM up vs all others
230180_at	---	---	0,000294455	4,44092	CB up vs all others
224397_s_at	TMTC1	transmembrane and tetratricopeptide repeat containing 1	0,000248912	4,43969	MU up vs all others
203426_s_at	IGFBP5	insulin-like growth factor binding protein 5	1,33E-05	4,43905	BM up vs all others
238345_at	SLC38A10	Solute carrier family 38, member 10	4,99E-05	4,43778	BM up vs all others
210098_s_at	---	---	0,000435373	4,43268	CB up vs all others
1559170_at	---	---	8,72E-07	4,43025	BM up vs all others
215303_at	DCLK1	doublecortin-like kinase 1	1,77E-05	4,42548	MU up vs all others
227443_at	C9orf150	chromosome 9 open reading frame 150	0,000238053	4,42503	PE up vs all others
203001_s_at	STMN2	stathmin-like 2	0,000402246	4,4155	PE up vs all others
215092_s_at	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	4,63E-07	4,41448	CB up vs all others
223690_at	LTBP2	latent transforming growth factor beta binding protein 2	0,000661673	4,41378	PE up vs all others
231875_at	KIF21A	kinesin family member 21°	0,00085127	4,41325	CB up vs all others
219155_at	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	5,94E-05	4,40865	PE up vs all others
203751_x_at	JUND	jun D proto-oncogene	2,50E-05	4,40493	BM up vs all others
220952_s_at	PLEKHA5	pleckstrin homology domain containing, family A member 5	0,00135345	4,40224	PE up vs all others
235843_at	---	---	0,000430808	4,39903	CB up vs all others

235216_at	ESCO1	establishment of cohesion 1 homolog 1 (<i>S. cerevisiae</i>)	2,20E-05	4,39614	CB up vs all others
202465_at	PCOLCE	procollagen C-endopeptidase enhancer	0,000473615	4,38906	PE up vs all others
224762_at	SERINC2	serine incorporator 2	0,000395986	4,38844	BM up vs all others
236526_x_at	C5orf44	chromosome 5 open reading frame 44	5,62E-05	4,38623	CB up vs all others
209212_s_at	KLF5	Kruppel-like factor 5 (intestinal)	0,000610488	4,38079	MU up vs all others
214119_s_at	FKBP1A	FK506 binding protein 1A, 12kDa	1,72E-07	4,37706	BM up vs all others
242918_at	NASP	Nuclear autoantigenic sperm protein (histone-binding)	0,000387761	4,36923	CB up vs all others
208257_x_at	PSG1	pregnancy specific beta-1-glycoprotein 1	2,73E-05	4,36775	BM up vs all others
224480_s_at	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	0,00123802	4,36621	CB up vs all others
213446_s_at	IQGAP1	IQ motif containing GTPase activating protein 1	1,17E-07	4,36124	CB up vs all others
1558369_at	MPHOSPH9	M-phase phosphoprotein 9	1,56E-05	4,35983	CB up vs all others
206140_at	LHX2	LIM homeobox 2	9,24E-08	4,35838	PE up vs all others
205832_at	CPA4	carboxypeptidase A4	0,000159062	4,35833	BM up vs all others
1563947_a_at	ERC1	ELKS/RAB6-interacting/CAST family member 1	0,0001076	4,35061	CB up vs all others
215037_s_at	BCL2L1	BCL2-like 1	4,09E-07	4,34963	BM up vs all others
223340_at	ATL1	atlastin GTPase 1	0,00237523	4,34689	PE up vs all others
213957_s_at	CEP350	centrosomal protein 350kDa	5,53E-09	4,34656	CB up vs all others
228325_at	KIAA0146	KIAA0146	0,00123702	4,34543	PE up vs all others
201251_at	PKM2	pyruvate kinase, muscle	0,00140718	4,34479	BM up vs all others
217951_s_at	PHF3	PHD finger protein 3	3,72E-05	4,34278	CB up vs all others
215905_s_at	SNRNP40	small nuclear ribonucleoprotein 40kDa (U5)	1,53E-05	4,33484	CB up vs all others
222616_s_at	USP16	ubiquitin specific peptidase 16	1,61E-06	4,33373	CB up vs all others
215733_x_at	CTAG2	cancer/testis antigen 2	5,52E-06	4,3325	PE up vs all others
235086_at	THBS1	thrombospondin 1	0,000806229	4,32708	PE up vs all others
209725_at	UTP20	UTP20, small subunit processome component, homolog (yeast)	2,26E-07	4,32567	CB up vs all others
201654_s_at	HSPG2	heparan sulfate proteoglycan 2	0,000611559	4,3231	BM up vs all others
229622_at	FAM132B	family with sequence similarity 132, member B	0,000408859	4,32281	MU up vs all others
229026_at	CDC42SE2	CDC42 small effector 2	1,27E-08	4,32259	BM up vs all others
204249_s_at	LMO2	LIM domain only 2 (rhombotin-like 1)	0,00178465	4,32238	BM up vs all others
208372_s_at	LIMK1	LIM domain kinase 1	2,08E-08	4,31853	BM up vs all others
209769_s_at	GP1BB	glycoprotein Ib (platelet), beta polypeptide	4,59E-06	4,30324	BM up vs all others
221264_s_at	TARDBP	TAR DNA binding protein	6,62E-08	4,29788	CB up vs all others
233011_at	ANXA1	Annexin A1	0,000117898	4,29377	BM up vs all others
213599_at	OIP5	Opa interacting protein 5	1,17E-05	4,29287	CB up vs all others
242943_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	7,40E-07	4,28805	PE up vs all others
227892_at	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	6,95E-08	4,28798	MU up vs all others
204977_at	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	0,0011878	4,28135	CB up vs all others
225056_at	SIPA1L2	signal-induced proliferation-associated 1 like 2	4,79E-06	4,27936	MU up vs all others
227719_at	SMAD9	SMAD family member 9	0,00193563	4,27635	CB up vs all others
217274_x_at	MYL4	myosin, light chain 4, alkali; atrial, embryonic	0,0318343	4,27614	MU up vs all others
232451_at	---	---	0,00168534	4,27515	PE up vs all others
234411_x_at	CD44	CD44 molecule (Indian blood group)	7,28E-05	4,2732	BM up vs all others
236352_at	VGLL2	vestigial like 2 (<i>Drosophila</i>)	0,0100128	4,27018	MU up vs all others
228115_at	FAM59A	family with sequence similarity 59, member A	0,000341699	4,26595	MU up vs all others
244882_at	TNRC18	Trinucleotide repeat containing 18	1,68E-06	4,26513	BM up vs all others
208829_at	TAPBP	TAP binding protein (tapasin)	5,57E-08	4,26507	BM up vs all others
213985_s_at	C19orf6	Chromosome 19 open reading frame 6	0,00024552	4,26349	BM up vs all others

207765_s_at	KIAA1539	KIAA1539	4,07E-09	4,26182	BM up vs all others
214564_s_at	PCDHGC3	protocadherin gamma subfamily C, 3	7,79E-07	4,26014	BM up vs all others
202410_x_at	IGF2 /// INS-IGF2	insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	2,81E-05	4,25909	MU up vs all others
244287_at	SREK1	splicing regulatory glutamine/lysine-rich protein 1	3,44E-07	4,25845	CB up vs all others
230316_at	SEC14L2	SEC14-like 2 (S. cerevisiae)	2,67E-07	4,25472	BM up vs all others
222040_at	HNRNPA1 /// LOC100506653	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC100506653	0,00179362	4,25054	CB up vs all others
243109_at	MCTP2	multiple C2 domains, transmembrane 2	6,91E-08	4,24484	PE up vs all others
218859_s_at	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog	0,00215233	4,23591	CB up vs all others
238328_at	MPRIP	myosin phosphatase Rho interacting protein	1,05E-05	4,23446	BM up vs all others
200707_at	PRKCSH	protein kinase C substrate 80K-H	0,00637341	4,23133	BM up vs all others
213756_s_at	HSF1	heat shock transcription factor 1	2,78E-07	4,23086	BM up vs all others
218564_at	RFWD3	ring finger and WD repeat domain 3	7,12E-07	4,23003	CB up vs all others
230744_at	FSTL1	folliculin-like 1	0,00158317	4,22812	PE up vs all others
202454_s_at	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0,0616183	4,22761	MU up vs all others
201469_s_at	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	5,88E-05	4,22651	BM up vs all others
237116_at	LOC646903	hypothetical LOC646903	0,000182123	4,22589	CB up vs all others
225972_at	TMEM64	transmembrane protein 64	0,00580994	4,21864	CB up vs all others
202728_s_at	LTBP1	latent transforming growth factor beta binding protein 1	0,00112676	4,21585	PE up vs all others
227655_at	LOC100505806 /// SNORD123	hypothetical LOC100505806 /// small nucleolar RNA, C/D box 123	0,00111171	4,21132	PE up vs all others
211453_s_at	AKT2	v-akt murine thymoma viral oncogene homolog 2	6,04E-09	4,20878	BM up vs all others
1554311_a_at	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	1,23E-06	4,20604	BM up vs all others
226720_at	PWWP2A	PWWP domain containing 2°	3,09E-06	4,20551	CB up vs all others
202581_at	HSPA1A /// HSPA1B	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	0,00252076	4,20434	CB up vs all others
209088_s_at	UBN1	ubiquitin 1	1,59E-05	4,20236	CB up vs all others
212592_at	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu	0,000209674	4,19991	PE up vs all others
233819_s_at	LTN1	listerin E3 ubiquitin protein ligase 1	0,00703621	4,19858	CB up vs all others
221683_s_at	CEP290	centrosomal protein 290kDa	6,49E-08	4,19834	CB up vs all others
201808_s_at	ENG	Endoglin	0,00633319	4,19774	BM up vs all others
216967_at	GAP43	growth associated protein 43	0,00030227	4,1967	CB up vs all others
212193_s_at	LARP1	La ribonucleoprotein domain family, member 1	2,00E-05	4,19332	BM up vs all others
215535_s_at	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	4,68E-09	4,19225	BM up vs all others
236141_at	NBLA00301	Nbla00301	1,82E-09	4,18659	PE up vs all others
240686_x_at	TFRC	Transferrin receptor (p90, CD71)	8,92E-06	4,1863	BM up vs all others
202840_at	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	0,00658407	4,18624	CB up vs all others
201724_s_at	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptideN-acetylgalactosaminyltransferase 1	0,000248306	4,17921	PE up vs all others
1555609_a_at	ZMAT3	zinc finger, matrin-type 3	2,97E-05	4,17788	BM up vs all others
227178_at	CELF2	CUGBP, Elav-like family member 2	0,000269333	4,17557	MU up vs all others
228892_at	SH3RF2	SH3 domain containing ring finger 2	9,93E-08	4,16736	BM up vs all others
207530_s_at	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	4,19E-09	4,16646	BM up vs all others
213807_x_at	MET	met proto-oncogene (hepatocyte growth factor receptor)	4,56E-06	4,16296	BM up vs all others
230629_s_at	EP400	E1A binding protein p400	2,62E-07	4,16185	CB up vs all others
203792_x_at	PCGF2	polycomb group ring finger 2	7,38E-05	4,1604	BM up vs all others
219729_at	PRRX2	paired related homeobox 2	0,000636783	4,15636	PE up vs all others
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	4,90E-06	4,15548	CB up vs all others

221919_at	LOC100506653	hypothetical LOC100506653	1,16E-06	4,15455	CB up vs all others
211947_s_at	BAT2L2	HLA-B associated transcript 2-like 2	1,23E-07	4,1521	CB up vs all others
219287_at	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	7,45E-05	4,15156	MU up vs all others
1559052_s_at	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	2,08E-07	4,14481	BM up vs all others
221198_at	SCT	Secretin	0,000708176	4,14417	BM up vs all others
218010_x_at	PPDPF	pancreatic progenitor cell differentiation and proliferation factor	9,37E-05	4,14295	BM up vs all others
218086_at	NPDC1	neural proliferation, differentiation and control, 1	0,00427647	4,14263	BM up vs all others
205031_at	EFNB3	ephrin-B3	8,68E-05	4,1419	PE up vs all others
238346_s_at	TGS1	trimethylguanosine synthase 1	0,00312496	4,1371	CB up vs all others
218513_at	C4orf43	chromosome 4 open reading frame 43	0,00448736	4,13608	CB up vs all others
230276_at	FAM49A	family with sequence similarity 49, member A	9,23E-05	4,13396	MU up vs all others
231020_at	ARX	Aristaless related homeobox	2,02E-05	4,12888	BM up vs all others
211796_s_at	TRBC1 TRBC2	/// T cell receptor beta constant 1 /// T cell receptor beta constant 2	9,77E-07	4,12852	BM up vs all others
238577_s_at	TSHZ2	teashirt zinc finger homeobox 2	0,000552239	4,12846	PE up vs all others
37577_at	ARHGAP19	Rho GTPase activating protein 19	1,01E-06	4,12417	CB up vs all others
211433_x_at	KIAA1539	KIAA1539	1,93E-08	4,12373	BM up vs all others
222857_s_at	KCNMB4	potassium large conductance calcium-activated channel, subfam M	6,28E-05	4,12208	MU up vs all others
229427_at	SEMA5A	sema domain, seven thrombospondin repeats, transmembrane domain	0,00216922	4,11926	PE up vs all others
208994_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	0,000642195	4,11804	CB up vs all others
1552365_at	SCIN	Scinderin	0,00111045	4,11425	PE up vs all others
205129_at	NPM3	nucleophosmin/nucleoplasmin 3	0,00458133	4,10857	CB up vs all others
232940_s_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	1,31E-06	4,10799	CB up vs all others
214036_at	EFNA5	ephrin-A5	0,00256577	4,10309	CB up vs all others
241683_at	HECTD1	HECT domain containing 1	0,000452444	4,10308	CB up vs all others
237945_at	---	---	0,00170818	4,0952	PE up vs all others
210982_s_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	4,01E-05	4,09127	PE up vs all others
212758_s_at	ZEB1	zinc finger E-box binding homeobox 1	0,000779267	4,08735	CB up vs all others
205846_at	PTPRB	protein tyrosine phosphatase, receptor type, B	0,000826584	4,08536	BM up vs all others
214764_at	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	0,00125018	4,08015	CB up vs all others
211600_at	PTPRO	protein tyrosine phosphatase, receptor type, O	0,00301457	4,07788	BM up vs all others
225238_at	MSI2	musashi homolog 2 (Drosophila)	0,00715999	4,07245	CB up vs all others
223648_s_at	FGFRL1	fibroblast growth factor receptor-like 1	8,91E-06	4,0722	BM up vs all others
204188_s_at	RARG	retinoic acid receptor, gamma	0,000676899	4,0695	BM up vs all others
207419_s_at	RAC2	ras-related C3 botulinum toxin substrate 2	0,00237752	4,06926	BM up vs all others
222508_s_at	ARGLU1	arginine and glutamate rich 1	6,83E-05	4,06669	CB up vs all others
201261_x_at	BGN	Biglycan	0,00179732	4,0651	PE up vs all others
228314_at	LRRRC8C	leucine rich repeat containing 8 family, member C	0,00254426	4,05891	CB up vs all others
222309_at	LOC100506935	hypothetical LOC100506935	0,00547238	4,05853	CB up vs all others
241272_at	---	---	0,0012018	4,05801	PE up vs all others
	PCDHGA1	///			
	PCDHGA10	///			
	PCDHGA11	///			
	PCDHGA12	///			
	PCDHGA2	///			
	PCDHGA3	///			
	PCDHGA4	///			
	PCDHGA5	///			
	PCDHGA6	///			
	PCDHGA7	///			
215836_s_at	PCDHGA8	/// protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocad	1,53E-07	4,05766	BM up vs all others

	PCDHGA9	///				
	PCDHGB1	///				
	PCDHGB2	///				
	PCDHGB3	///				
	PCDHGB4	///				
	PCDHGB5	///				
	PCDHGB6	///				
	PCDHGB7	///				
	PCDHGC3	///				
	PCDHGC4	///				
	PCDHGC5	///				
230465_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	4,79E-10	4,05309	CB up vs all others	
204915_s_at	SOX11	SRY (sex determining region Y)-box 11	0,00162154	4,04722	CB up vs all others	
217058_at	GNAS	GNAS complex locus	5,32E-06	4,04341	BM up vs all others	
225025_at	IGSF8	immunoglobulin superfamily, member 8	6,68E-05	4,04	BM up vs all others	
211668_s_at	PLAU	plasminogen activator, urokinase	0,000457988	4,03724	MU up vs all others	
239454_at	SCARF2	scavenger receptor class F, member 2	1,66E-05	4,03713	BM up vs all others	
1557924_s_at	ALPL	alkaline phosphatase, liver/bone/kidney	3,95E-05	4,03565	BM up vs all others	
232174_at	---	---	1,19E-05	4,03481	CB up vs all others	
205511_at	FLJ10038	hypothetical protein FLJ10038	6,47E-07	4,03336	CB up vs all others	
212016_s_at	PTBP1	polypyrimidine tract binding protein 1	0,000996368	4,0298	BM up vs all others	
226767_s_at	FAHD1	fumarylacetoacetate hydrolase domain containing 1	0,0002495	4,02411	CB up vs all others	
1560573_at	LOC387895	hypothetical LOC387895	0,00253009	4,02363	PE up vs all others	
235065_at	FAM59A	family with sequence similarity 59, member A	0,000109684	4,01932	MU up vs all others	
208328_s_at	MEF2A	myocyte enhancer factor 2°	0,000482122	4,01525	CB up vs all others	
229893_at	FRMD3	FERM domain containing 3	0,00099689	4,01272	CB up vs all others	
241926_s_at	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	0,00218777	4,00937	PE up vs all others	
243135_x_at	LOC100287081	Similar to hCG1999172	0,00231923	4,00908	BM up vs all others	
1558199_at	FN1	fibronectin 1	0,00100515	4,00753	CB up vs all others	
234051_at	---	---	4,50E-05	4,00519	PE up vs all others	
201969_at	NASP	nuclear autoantigenic sperm protein (histone-binding)	2,64E-06	4,00512	CB up vs all others	
217182_at	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	2,71E-05	4,00384	BM up vs all others	
212113_at	ATXN7L3B	ataxin 7-like 3B	4,30E-05	4,00339	CB up vs all others	
241739_at	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	1,50E-08	4,00081	PE up vs all others	
203722_at	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	2,11E-08	4,00071	BM up vs all others	
218318_s_at	NLK	nemo-like kinase	2,95E-05	3,998	CB up vs all others	
1553142_at	C13orf31	chromosome 13 open reading frame 31	0,00161078	3,99606	PE up vs all others	
204670_x_at	HLA-DRB1	/// major histocompatibility complex, class II, DR beta 1 /// major				
	HLA-DRB4	histocompatibility complex	6,73E-05	3,99557	PE up vs all others	
228106_at	DCAF16	DDB1 and CUL4 associated factor 16	0,00101387	3,99481	CB up vs all others	
221956_at	LRCH4	leucine-rich repeats and calponin homology (CH) domain 4	4,93E-06	3,99354	BM up vs all others	
200922_at	KDELRL1	KDEL endoplasmic reticulum protein retention receptor 1	4,70E-06	3,99219	BM up vs all others	
1553304_at	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	0,000187306	3,98891	CB up vs all others	
211022_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked	2,12E-07	3,98875	CB up vs all others	
210823_s_at	PTPRS	protein tyrosine phosphatase, receptor type, S	2,66E-06	3,98182	BM up vs all others	
202912_at	ADM	Adrenomedullin	0,00109293	3,98126	PE up vs all others	
240460_at	---	---	0,000184057	3,97843	PE up vs all others	
1565347_s_at	TFE3	transcription factor binding to IGHM enhancer 3	1,45E-06	3,97653	BM up vs all others	
242110_at	---	---	0,00045344	3,9715	MU up vs all others	
228731_at	---	---	0,000458608	3,96994	MU up vs all others	
228821_at	ST6GAL2	ST6 beta-galactosamide alpha-2,6-sialyltransferase 2	0,00357649	3,96579	CB up vs all others	

239253_at	---	---	0,000945476	3,96057	CB up vs all others
200646_s_at	NUCB1	nucleobindin 1	0,0075298	3,95941	BM up vs all others
240551_at	ZBTB45	zinc finger and BTB domain containing 45	7,28E-06	3,95723	BM up vs all others
1553139_s_at	PLXNA3	plexin A3	0,00160936	3,94799	BM up vs all others
208255_s_at	FKBP8	FK506 binding protein 8, 38kDa	0,000233385	3,94627	BM up vs all others
219978_s_at	NUSAP1	nucleolar and spindle associated protein 1	3,82E-07	3,94446	CB up vs all others
228069_at	FAM54A	family with sequence similarity 54, member A	0,000676094	3,94185	CB up vs all others
208995_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	0,00158187	3,93902	CB up vs all others
225380_at	PKDCC	protein kinase domain containing, cytoplasmic homolog (mouse)	0,000516792	3,9341	MU up vs all others
210854_x_at	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	3,96E-05	3,93304	BM up vs all others
224821_at	ABHD14B	abhydrolase domain containing 14B	0,000445424	3,92985	BM up vs all others
1560826_at	---	---	0,000367503	3,92911	PE up vs all others
207038_at	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	2,80E-06	3,92891	PE up vs all others
243849_at	TMEM37	Transmembrane protein 37	0,000133041	3,92841	BM up vs all others
209869_at	ADRA2A	adrenergic, alpha-2A-, receptor	2,09E-07	3,92743	MU up vs all others
215685_s_at	DLX2	distal-less homeobox 2	9,55E-08	3,9256	BM up vs all others
204120_s_at	ADK	adenosine kinase	0,000209377	3,92433	CB up vs all others
201722_s_at	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide acetylgalactosaminyltransferase 1 (Gal	N-0,000519419	3,91817	PE up vs all others
216268_s_at	JAG1	jagged 1	0,000339306	3,91809	MU up vs all others
207425_s_at	09-set	septin 9	3,10E-05	3,90871	BM up vs all others
222650_s_at	SLC2A4RG	SLC2A4 regulator	2,72E-08	3,90759	BM up vs all others
203425_s_at	IGFBP5	insulin-like growth factor binding protein 5	7,81E-06	3,89834	BM up vs all others
1554574_a_at	CYB5R3	cytochrome b5 reductase 3	0,00657635	3,89756	BM up vs all others
229824_at	SHC3	SHC (Src homology 2 domain containing) transforming protein 3	0,00711814	3,89456	CB up vs all others
226674_at	SHISA4	shisa homolog 4 (Xenopus laevis)	1,98E-05	3,89385	BM up vs all others
231121_at	HPS3	Hermansky-Pudlak syndrome 3	0,000375703	3,89247	CB up vs all others
33148_at	ZFR	zinc finger RNA binding protein	2,36E-07	3,89147	CB up vs all others
1564066_at	TMEM151B	transmembrane protein 151B	8,85E-05	3,88617	BM up vs all others
201156_s_at	RAB5C	RAB5C, member RAS oncogene family	4,46E-05	3,88221	BM up vs all others
225166_at	ARHGAP18	Rho GTPase activating protein 18	7,25E-06	3,88135	CB up vs all others
244774_at	PHACTR2	phosphatase and actin regulator 2	0,00764877	3,87863	BM up vs all others
203417_at	MFAP2	microfibrillar-associated protein 2	0,00872378	3,87372	BM up vs all others
229021_at	MCTP2	multiple C2 domains, transmembrane 2	7,23E-05	3,86991	PE up vs all others
210042_s_at	CTSZ	cathepsin Z	9,23E-06	3,86699	CB up vs all others
229324_x_at	ISYNA1	inositol-3-phosphate synthase 1	8,12E-05	3,86679	BM up vs all others
221029_s_at	WNT5B	wingless-type MMTV integration site family, member 5B	0,00193326	3,86444	BM up vs all others
204994_at	MX2	myxovirus (influenza virus) resistance 2 (mouse)	0,000182322	3,85952	PE up vs all others
241720_at	ZNF326	zinc finger protein 326	1,89E-08	3,85804	CB up vs all others
201058_s_at	MYL9	myosin, light chain 9, regulatory	0,01182	3,8577	BM up vs all others
225516_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0,00612561	3,85647	CB up vs all others
230309_at	BHMT2	betaine--homocysteine S-methyltransferase 2	0,000839357	3,85619	MU up vs all others
215760_s_at	SBNO2	strawberry notch homolog 2 (Drosophila)	4,15E-08	3,85218	BM up vs all others
1555240_s_at	GNG12	guanine nucleotide binding protein (G protein), gamma 12	0,000144147	3,8514	CB up vs all others
213979_s_at	---	---	1,82E-05	3,85089	BM up vs all others
227994_x_at	PPDPF	pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)	1,17E-05	3,84919	BM up vs all others

202510_s_at	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	0,000268344	3,84785	MU up vs all others
204682_at	LTBP2	latent transforming growth factor beta binding protein 2	0,00088016	3,84764	PE up vs all others
232195_at	GPR158	G protein-coupled receptor 158	9,80E-05	3,84668	PE up vs all others
217478_s_at	HLA-DMA	major histocompatibility complex, class II, DM alpha	0,000143545	3,84639	PE up vs all others
205289_at	BMP2	bone morphogenetic protein 2	0,00034318	3,84504	MU up vs all others
241360_at	CCDC15	coiled-coil domain containing 15	3,46E-06	3,84444	CB up vs all others
236453_at	---	---	0,00390165	3,83935	CB up vs all others
208297_s_at	EVI5	ecotropic viral integration site 5	2,92E-07	3,83726	CB up vs all others
211173_at	CCKAR	cholecystokinin A receptor	0,000890456	3,83293	PE up vs all others
205907_s_at	OMD	Osteomodulin	0,00159671	3,83087	PE up vs all others
223747_x_at	WWOX	WW domain containing oxidoreductase	1,08E-07	3,82969	BM up vs all others
206327_s_at	CDH15	cadherin 15, type 1, M-cadherin (myotubule)	0,0135055	3,82713	MU up vs all others
235272_at	SBSN	Suprabasin	9,00E-09	3,82416	PE up vs all others
226612_at	UBE2QL1	ubiquitin-conjugating enzyme E2Q family-like 1	8,11E-05	3,82356	PE up vs all others
65133_i_at	INO80B	INO80 complex subunit B	1,54E-08	3,82219	BM up vs all others
238624_at	---	---	1,88E-05	3,82197	CB up vs all others
1559141_s_at	---	---	2,20E-05	3,82163	PE up vs all others
1558706_a_at	ATOH8	Atonal homolog 8 (Drosophila)	0,00157433	3,82073	CB up vs all others
204492_at	ARHGAP11A	Rho GTPase activating protein 11A	0,000203971	3,8206	CB up vs all others
207289_at	MMP25	matrix metalloproteinase 25	6,89E-05	3,81877	BM up vs all others
235028_at	---	---	0,000779037	3,81668	MU up vs all others
206652_at	ZMYM5	zinc finger, MYM-type 5	5,72E-06	3,81638	CB up vs all others
1558292_s_at	PIGW	phosphatidylinositol glycan anchor biosynthesis, class W	0,000204	3,81554	CB up vs all others
221458_at	HTR1F	5-hydroxytryptamine (serotonin) receptor 1F	6,23E-06	3,81544	BM up vs all others
230474_at	UBIAD1	UbiA prenyltransferase domain containing 1	4,09E-08	3,81381	BM up vs all others
1559993_at	SFXN3	Sideroflexin 3	1,46E-06	3,81081	CB up vs all others
211709_s_at	CLEC11A	C-type lectin domain family 11, member A	1,56E-05	3,81023	PE up vs all others
1554026_a_at	MYO10	myosin X	0,000305456	3,80906	CB up vs all others
208232_x_at	---	---	7,73E-06	3,80663	BM up vs all others
1557257_at	BCL10	B-cell CLL/lymphoma 10	3,48E-07	3,80348	CB up vs all others
52837_at	KIAA1644	KIAA1644	0,00128036	3,80336	PE up vs all others
210605_s_at	MFGE8	milk fat globule-EGF factor 8 protein	0,0150948	3,80248	BM up vs all others
203158_s_at	GLS	Glutaminase	0,0116491	3,79729	BM up vs all others
1564637_a_at	FAM98B	family with sequence similarity 98, member B	0,000150805	3,7931	CB up vs all others
223457_at	COPG2	coatamer protein complex, subunit gamma 2	1,02E-05	3,79105	CB up vs all others
233894_x_at	EMID2	EMI domain containing 2	4,40E-08	3,79087	BM up vs all others
215780_s_at	LOC642869 SET	/// SET translocation (myeloid leukemia-associated) pseudogene /// SET nuclear oncogene	0,000951346	3,7904	CB up vs all others
205397_x_at	SMAD3	SMAD family member 3	0,0062905	3,78869	BM up vs all others
1558643_s_at	EDIL3	EGF-like repeats and discoidin I-like domains 3	0,000627457	3,7865	BM up vs all others
239183_at	ANGPTL1	angiopoietin-like 1	6,70E-06	3,78526	MU up vs all others
215609_at	---	---	9,15E-07	3,78502	BM up vs all others
235073_at	SCAMP4	secretory carrier membrane protein 4	4,34E-09	3,78292	BM up vs all others
204857_at	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	2,48E-05	3,78287	BM up vs all others
219730_at	MED18	mediator complex subunit 18	0,000286526	3,78074	CB up vs all others
219412_at	RAB38	RAB38, member RAS oncogene family	0,00723795	3,77968	CB up vs all others
202724_s_at	FOXO1	forkhead box O1	7,73E-05	3,77943	MU up vs all others
207347_at	ERCC6	/// excision repair cross-complementing rodent repair deficiency,	1,40E-05	3,77115	BM up vs all others

	PGBD3	complementation group 6 /			
230929_s_at	---	---	4,36E-06	3,76818	BM up vs all others
203176_s_at	TFAM	transcription factor A, mitochondrial	0,000129647	3,76642	CB up vs all others
216604_s_at	SLC7A8	solute carrier family 7 (amino acid transporter, L-type), member 8	0,00235243	3,76591	PE up vs all others
216929_x_at	ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferas	5,42E-07	3,76583	BM up vs all others
206824_at	CES1P1	carboxylesterase 1 pseudogene 1	1,89E-06	3,76284	BM up vs all others
214975_s_at	MTMR1	myotubularin related protein 1	9,10E-06	3,75143	BM up vs all others
207935_s_at	KRT13	keratin 13	4,67E-08	3,74993	BM up vs all others
206336_at	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	0,000248457	3,74636	PE up vs all others
1553185_at	RASEF	RAS and EF-hand domain containing	0,000425453	3,74565	CB up vs all others
204916_at	RAMP1	receptor (G protein-coupled) activity modifying protein 1	0,000106941	3,74543	BM up vs all others
219414_at	CLSTN2	calsyntenin 2	0,000862553	3,74472	MU up vs all others
224982_at	AKT1S1	AKT1 substrate 1 (proline-rich)	8,39E-07	3,74436	BM up vs all others
241346_at	ARHGAP30	Rho GTPase activating protein 30	0,000666889	3,74421	BM up vs all others
230228_at	SSC5D	scavenger receptor cysteine-rich glycoprotein	8,12E-08	3,74247	BM up vs all others
241670_x_at	LOC729177	hypothetical LOC729177	1,03E-07	3,74111	BM up vs all others
217190_x_at	ESR1	estrogen receptor 1	0,00053221	3,73836	BM up vs all others
222596_s_at	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	0,000788957	3,73748	BM up vs all others
218000_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	0,00095206	3,73621	BM up vs all others
220591_s_at	EFHC2	EF-hand domain (C-terminal) containing 2	1,43E-06	3,73444	PE up vs all others
1552288_at	CILP2	cartilage intermediate layer protein 2	7,44E-06	3,73151	PE up vs all others
219094_at	ARMC8	armadillo repeat containing 8	0,00051563	3,73061	CB up vs all others
1569290_s_at	GRIA3	glutamate receptor, ionotropic, AMPA 3	0,0019857	3,72963	PE up vs all others
228399_at	OSR1	odd-skipped related 1 (Drosophila)	0,00542718	3,72805	CB up vs all others
230261_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	2,71E-05	3,72641	PE up vs all others
204541_at	SEC14L2	SEC14-like 2 (S. cerevisiae)	1,98E-05	3,72488	BM up vs all others
205602_x_at	PSG7	pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)	0,000131096	3,72417	BM up vs all others
219685_at	TMEM35	transmembrane protein 35	0,000309188	3,71794	CB up vs all others
232670_at	---	---	7,00E-05	3,71785	BM up vs all others
230013_s_at	ARHGAP23	Rho GTPase activating protein 23	1,54E-06	3,71461	BM up vs all others
222026_at	RBM3	RNA binding motif (RNP1, RRM) protein 3	0,000201253	3,71431	CB up vs all others
209653_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	1,06E-06	3,71406	BM up vs all others
217545_at	MYH14	myosin, heavy chain 14, non-muscle	0,0045882	3,71273	BM up vs all others
232078_at	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0,0102723	3,71128	BM up vs all others
241669_x_at	PRKD2	protein kinase D2	0,00276353	3,70793	BM up vs all others
238267_s_at	---	---	0,000127095	3,70623	BM up vs all others
218260_at	DDA1	DET1 and DDB1 associated 1	3,50E-06	3,70112	BM up vs all others
242671_at	---	---	0,000123138	3,70075	PE up vs all others
1555372_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	0,000283177	3,70038	MU up vs all others
223556_at	HELLS	helicase, lymphoid-specific	4,23E-05	3,69008	CB up vs all others
235718_at	SRL	Sarcalumenin	0,0103494	3,6891	BM up vs all others
211901_s_at	PDE4A	phosphodiesterase 4A, cAMP-specific	5,10E-06	3,68473	BM up vs all others
209261_s_at	NR2F6	nuclear receptor subfamily 2, group F, member 6	3,17E-07	3,68164	BM up vs all others
208127_s_at	SOCS5	suppressor of cytokine signaling 5	0,000830265	3,68082	PE up vs all others
243614_s_at	PRODH2	proline dehydrogenase (oxidase) 2	4,80E-07	3,67954	BM up vs all others
242218_at	LOC100509629	hypothetical LOC100509629	0,00150031	3,66963	CB up vs all others

244566_at	---	---	4,64E-07	3,66729	BM up vs all others
201140_s_at	RAB5C	RAB5C, member RAS oncogene family	2,09E-06	3,66719	BM up vs all others
211447_s_at	PDE4A	phosphodiesterase 4A, cAMP-specific	3,99E-05	3,66293	BM up vs all others
218737_at	SBNO1	strawberry notch homolog 1 (Drosophila)	3,58E-05	3,66287	CB up vs all others
1562294_x_at	ANKRD30B	ankyrin repeat domain 30B	6,60E-07	3,66152	BM up vs all others
228126_x_at	CTXN1	cortixin 1	1,04E-08	3,66058	BM up vs all others
48808_at	DHFR	dihydrofolate reductase	4,52E-06	3,65987	CB up vs all others
239996_x_at	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	1,45E-06	3,65704	BM up vs all others
209266_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	1,81E-06	3,65703	BM up vs all others
238325_s_at	ODF3B	outer dense fiber of sperm tails 3B	1,63E-05	3,65592	BM up vs all others
208461_at	HIC1	hypermethylated in cancer 1	1,54E-08	3,65337	BM up vs all others
223254_s_at	G2E3	G2/M-phase specific E3 ubiquitin protein ligase	2,63E-09	3,65306	CB up vs all others
201957_at	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	1,57E-06	3,65003	MU up vs all others
235163_at	MOBKL2A	MOB1, Mps One Binder kinase activator-like 2A (yeast)	1,42E-07	3,64994	BM up vs all others
212081_x_at	BAT2	HLA-B associated transcript 2	8,92E-06	3,64911	BM up vs all others
219202_at	RHBDF2	rhomboid 5 homolog 2 (Drosophila)	4,25E-07	3,6412	BM up vs all others
234694_at	CNTROB	centrobin, centrosomal BRCA2 interacting protein	3,09E-05	3,64049	BM up vs all others
203842_s_at	MAPRE3	microtubule-associated protein, RP/EB family, member 3	9,10E-10	3,64029	BM up vs all others
209581_at	PLA2G16	phospholipase A2, group XVI	0,00249807	3,63841	BM up vs all others
212090_at	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1	5,68E-07	3,63488	BM up vs all others
201324_at	EMP1	epithelial membrane protein 1	0,000225507	3,6341	PE up vs all others
229130_at	---	---	0,000133665	3,63196	MU up vs all others
204684_at	NPTX1	neuronal pentraxin I	0,00214476	3,63162	PE up vs all others
225655_at	UHRF1	ubiquitin-like with PHD and ring finger domains 1	3,21E-05	3,63084	CB up vs all others
212574_x_at	C19orf6	chromosome 19 open reading frame 6	0,00459837	3,63076	BM up vs all others
223772_s_at	TMEM87A	transmembrane protein 87A	0,000654312	3,62968	CB up vs all others
203697_at	FRZB	frizzled-related protein	0,203909	3,62888	CB up vs all others
220553_s_at	PRPF39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	0,000303724	3,62736	CB up vs all others
1554036_at	ZBTB24	zinc finger and BTB domain containing 24	5,48E-05	3,6261	CB up vs all others
232541_at	---	---	0,00098362	3,62405	PE up vs all others
219270_at	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	0,00898513	3,62328	BM up vs all others
228556_at	YTHDC1	YTH domain containing 1	0,0005327	3,62223	CB up vs all others
202755_s_at	GPC1	glypican 1	5,49E-07	3,62095	BM up vs all others
208250_s_at	DMBT1	deleted in malignant brain tumors 1	0,000120309	3,62083	MU up vs all others
238051_x_at	PWWP2B	PWWP domain containing 2B	6,35E-07	3,61902	BM up vs all others
229745_x_at	DACT3	Dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	1,95E-09	3,61855	BM up vs all others
221783_at	WIZ	widely interspaced zinc finger motifs	6,32E-10	3,61786	BM up vs all others
221031_s_at	APOLD1	apolipoprotein L domain containing 1	2,27E-05	3,61325	PE up vs all others
203215_s_at	MYO6	myosin VI	3,90E-06	3,61317	CB up vs all others
231239_at	LOC100507063	hypothetical LOC100507063	0,00344064	3,61289	CB up vs all others
235863_at	JSRP1	junctional sarcoplasmic reticulum protein 1	0,000546772	3,61153	BM up vs all others
217849_s_at	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	2,92E-05	3,61001	BM up vs all others
239675_at	LOC283143	hypothetical LOC283143	3,24E-05	3,60832	PE up vs all others
1554966_a_at	FILIP1L	filamin A interacting protein 1-like	3,16E-05	3,60732	MU up vs all others
242293_at	ING3	inhibitor of growth family, member 3	9,19E-07	3,60623	CB up vs all others
206665_s_at	BCL2L1	BCL2-like 1	1,96E-05	3,60537	BM up vs all others
206233_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	0,000857679	3,60505	PE up vs all others

212525_s_at	H2AFX	H2A histone family, member X	1,31E-05	3,60426	BM up vs all others
203811_s_at	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	0,00246487	3,60228	BM up vs all others
204146_at	RAD51AP1	RAD51 associated protein 1	0,00398654	3,6022	CB up vs all others
211141_s_at	CNOT3	CCR4-NOT transcription complex, subunit 3	4,54E-07	3,59944	BM up vs all others
241671_x_at	FLJ22536	hypothetical locus LOC401237	1,95E-05	3,59808	BM up vs all others
229310_at	KLHL29	kelch-like 29 (Drosophila)	0,000464189	3,59657	MU up vs all others
1566303_s_at	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11	6,36E-05	3,59629	BM up vs all others
210990_s_at	LAMA4	laminin, alpha 4	0,00285673	3,59235	PE up vs all others
221785_at	WIZ	widely interspaced zinc finger motifs	2,63E-05	3,59133	BM up vs all others
209878_s_at	RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	2,12E-05	3,59114	BM up vs all others
66053_at	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2	1,69E-06	3,58954	CB up vs all others
211692_s_at	BBC3	BCL2 binding component 3	1,62E-08	3,58823	BM up vs all others
224566_at	NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	0,00010105	3,58812	CB up vs all others
213808_at	ADAM23	ADAM metallopeptidase domain 23	0,000759563	3,58804	CB up vs all others
221922_at	GPSM2	G-protein signaling modulator 2	0,0032612	3,58717	CB up vs all others
1568618_a_at	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide acetylgalactosaminyltransferase 1	N- 0,000119308	3,58451	PE up vs all others
223465_at	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	1,92E-05	3,58432	CB up vs all others
227936_at	TMEM68	transmembrane protein 68	6,80E-07	3,58404	CB up vs all others
227370_at	FAM171B	family with sequence similarity 171, member B	0,000208874	3,58196	PE up vs all others
243766_s_at	TEAD2	TEA domain family member 2	6,89E-06	3,57953	BM up vs all others
225062_at	LOC389831	hypothetical LOC389831	0,000290164	3,57885	BM up vs all others
241871_at	CAMK4	calcium/calmodulin-dependent protein kinase IV	0,00152171	3,57773	CB up vs all others
1553243_at	ITIH5	inter-alpha (globulin) inhibitor H5	0,000567296	3,57718	MU up vs all others
232079_s_at	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0,00957464	3,57574	BM up vs all others
239562_at	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	0,000159909	3,57505	CB up vs all others
219861_at	DNAJC17	DnaJ (Hsp40) homolog, subfamily C, member 17	3,47E-05	3,57161	CB up vs all others
228608_at	NALCN	sodium leak channel, non-selective	0,00144034	3,57003	PE up vs all others
216345_at	KIAA0913	KIAA0913	4,78E-07	3,56996	BM up vs all others
235666_at	ITGA8	integrin, alpha 8	0,000208477	3,56859	MU up vs all others
202534_x_at	DHFR	dihydrofolate reductase	0,00150981	3,56505	CB up vs all others
204135_at	FILIP1L	filamin A interacting protein 1-like	9,28E-05	3,56505	MU up vs all others
215256_x_at	ARHGAP33	Rho GTPase activating protein 33	5,42E-05	3,56207	BM up vs all others
232874_at	DOCK9	dedicator of cytokinesis 9	5,44E-05	3,56073	MU up vs all others
204161_s_at	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative) solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	5,70E-06	3,55866	MU up vs all others
241866_at	SLC16A7	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	3,00E-05	3,55851	CB up vs all others
207137_at	NFKBIL2		4,41E-06	3,55509	BM up vs all others
235435_at	AASDH	aminoadipate-semialdehyde dehydrogenase	0,00214569	3,55401	CB up vs all others
243259_at	ATXN7	ataxin 7	0,000570791	3,55029	CB up vs all others
239011_at	PRKCE	Protein kinase C, epsilon	2,62E-07	3,54484	BM up vs all others
229304_s_at	MLF1IP	MLF1 interacting protein	2,83E-06	3,54467	CB up vs all others
218382_s_at	U2AF2	U2 small nuclear RNA auxiliary factor 2	0,000447422	3,54424	BM up vs all others
214157_at	GNAS	GNAS complex locus	0,000541874	3,54389	CB up vs all others
222777_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0,00677203	3,54387	CB up vs all others
232489_at	CCDC76	coiled-coil domain containing 76	0,000295525	3,54009	MU up vs all others
223635_s_at	SSBP3	single stranded DNA binding protein 3	1,54E-05	3,53895	BM up vs all others
225258_at	FBLIM1	filamin binding LIM protein 1	1,00E-07	3,53493	BM up vs all others

233803_s_at	MYBBP1A	MYB binding protein (P160) 1°	3,05E-06	3,53475	BM up vs all others
244656_at	RASL10B	RAS-like, family 10, member B	1,01E-07	3,53464	BM up vs all others
225428_s_at	DDX54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	5,86E-10	3,53327	BM up vs all others
218856_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0,0148151	3,53258	BM up vs all others
238856_s_at	---	---	5,02E-05	3,5306	CB up vs all others
232099_at	PCDHB16	protocadherin beta 16	4,60E-07	3,52974	MU up vs all others
211577_s_at	IGF1	insulin-like growth factor 1 (somatomedin C)	0,000266653	3,52812	PE up vs all others
1558378_a_at	AHNAK2	AHNAK nucleoprotein 2	0,00546594	3,52653	CB up vs all others
1554864_a_at	SDC3	syndecan 3	0,00010979	3,52509	BM up vs all others
229508_at	U2AF2	U2 small nuclear RNA auxiliary factor 2	3,04E-05	3,52441	BM up vs all others
230885_at	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	1,77E-05	3,52336	CB up vs all others
244546_at	CYCS	cytochrome c, somatic	1,87E-05	3,5197	CB up vs all others
243582_at	SH3RF2	SH3 domain containing ring finger 2	8,07E-06	3,51935	BM up vs all others
204641_at	NEK2	NIMA (never in mitosis gene a)-related kinase 2	0,000731013	3,51849	CB up vs all others
225203_at	PPP1R16A	protein phosphatase 1, regulatory (inhibitor) subunit 16A	8,36E-06	3,51793	BM up vs all others
209644_x_at	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	0,000219209	3,51508	BM up vs all others
219377_at	FAM59A	family with sequence similarity 59, member A	9,93E-05	3,51499	MU up vs all others
216074_x_at	WWC1	WW and C2 domain containing 1	0,00159393	3,51408	PE up vs all others
207069_s_at	SMAD6	SMAD family member 6	0,00134357	3,51289	CB up vs all others
208993_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	0,00406427	3,51214	CB up vs all others
219310_at	TMEM90B	transmembrane protein 90B	0,00264163	3,5088	PE up vs all others
219506_at	C1orf54	chromosome 1 open reading frame 54	0,000399723	3,50796	PE up vs all others
201341_at	ENC1	ectodermal-neural cortex 1 (with BTB-like domain)	3,24E-05	3,50724	BM up vs all others
235186_at	LOC388692	hypothetical LOC388692	2,87E-07	3,50471	BM up vs all others
215712_s_at	IGFALS	insulin-like growth factor binding protein, acid labile subunit	5,00E-08	3,50204	BM up vs all others
201545_s_at	PABPN1	poly(A) binding protein, nuclear 1	1,13E-05	3,5003	CB up vs all others
230341_x_at	ADAMTS10	ADAM metalloproteinase with thrombospondin type 1 motif, 10	2,20E-09	3,4995	BM up vs all others
205627_at	CDA	cytidine deaminase	6,35E-05	3,49794	BM up vs all others
238542_at	ULBP2	UL16 binding protein 2	1,49E-05	3,49306	BM up vs all others
213843_x_at	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	3,77E-06	3,49068	BM up vs all others
205050_s_at	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	5,05E-09	3,48833	BM up vs all others
218733_at	MSL2	male-specific lethal 2 homolog (Drosophila)	4,66E-10	3,48782	CB up vs all others
1555515_a_at	FAM189B	family with sequence similarity 189, member B	4,98E-05	3,48563	BM up vs all others
223425_at	RAVER1	ribonucleoprotein, PTB-binding 1	5,05E-07	3,48352	BM up vs all others
206631_at	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	0,00341267	3,48308	CB up vs all others
227781_x_at	FAM57B	family with sequence similarity 57, member B	8,07E-07	3,48284	BM up vs all others
208835_s_at	LUC7L3	LUC7-like 3 (S. cerevisiae)	4,89E-05	3,48247	CB up vs all others
1564378_a_at	---	---	7,95E-05	3,48166	CB up vs all others
1555967_at	---	---	0,000930106	3,47936	BM up vs all others
226906_s_at	ARHGAP9	Rho GTPase activating protein 9	4,32E-07	3,47428	BM up vs all others
222206_s_at	NCLN	Nicalin	3,15E-09	3,47256	BM up vs all others
211300_s_at	TP53	tumor protein p53	0,00646208	3,47202	BM up vs all others
228405_at	RHPN1	rhopilin, Rho GTPase binding protein 1	8,58E-05	3,47017	BM up vs all others
219700_at	PLXDC1	plexin domain containing 1	2,52E-06	3,46986	MU up vs all others
209456_s_at	FBXW11	F-box and WD repeat domain containing 11	7,98E-07	3,46637	BM up vs all others
218813_s_at	SH3GLB2	SH3-domain GRB2-like endophilin B2	3,21E-05	3,4658	BM up vs all others

201806_s_at	ATXN2L	ataxin 2-like	2,19E-05	3,46415	BM up vs all others
228357_at	UNK	unkempt homolog (Drosophila)	0,00343283	3,46356	CB up vs all others
235494_at	LSAMP	limbic system-associated membrane protein	1,40E-06	3,46005	PE up vs all others
204422_s_at	FGF2	fibroblast growth factor 2 (basic)	0,0018727	3,45631	PE up vs all others
211693_at	IGHA1	Immunoglobulin heavy constant alpha 1	3,79E-05	3,45561	BM up vs all others
231721_at	JAM3	junctional adhesion molecule 3	0,000734314	3,4516	BM up vs all others
229966_at	EWSR1	Ewing sarcoma breakpoint region 1	8,43E-07	3,45139	CB up vs all others
1559249_at	ATXN1	ataxin 1	1,75E-05	3,44867	CB up vs all others
227084_at	DTNA	dystrobrevin, alpha	0,000674804	3,44777	CB up vs all others
224631_at	ZFP91	zinc finger protein 91 homolog (mouse)	0,000416478	3,44735	CB up vs all others
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	7,98E-05	3,4465	CB up vs all others
238636_at	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	0,00106969	3,44509	PE up vs all others
230876_at	ZNF883	zinc finger protein 883	0,000307128	3,4431	PE up vs all others
209675_s_at	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	1,95E-05	3,44273	BM up vs all others
204986_s_at	TAOK2	TAO kinase 2	3,09E-07	3,4426	BM up vs all others
227697_at	SOCS3	suppressor of cytokine signaling 3	0,00267379	3,44259	CB up vs all others
237851_at	---	---	7,24E-06	3,44109	BM up vs all others
201551_s_at	LAMP1	lysosomal-associated membrane protein 1	4,79E-05	3,44068	BM up vs all others
212636_at	QKI	quaking homolog, KH domain RNA binding (mouse)	0,000642141	3,44067	MU up vs all others
239835_at	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	0,00243296	3,43955	CB up vs all others
220189_s_at	MGAT4B	mannosyl(alpha-1,3-)-glycoproteinbeta-1,4-N-acetylglucosaminyltransferase, isozyme B	1,20E-05	3,4395	BM up vs all others
215891_s_at	GM2A	GM2 ganglioside activator	2,36E-06	3,43929	BM up vs all others
243221_at	FAM20A	family with sequence similarity 20, member A	2,94E-05	3,43924	PE up vs all others
226934_at	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	0,00187081	3,43783	CB up vs all others
228955_at	---	---	0,000977161	3,43677	CB up vs all others
211622_s_at	ARF3	ADP-ribosylation factor 3	4,04E-06	3,43649	BM up vs all others
235671_at	---	---	7,01E-06	3,43524	BM up vs all others
222731_at	ZDHHC2	zinc finger, DHHC-type containing 2	0,00461036	3,43347	CB up vs all others
218701_at	LACTB2	lactamase, beta 2	0,00356266	3,43187	CB up vs all others
244779_at	ZDHHC2	zinc finger, DHHC-type containing 2	0,00225266	3,43075	CB up vs all others
1561500_at	CTU2	Cytosolic thiouridylase subunit 2 homolog (S. pombe)	1,49E-05	3,4305	BM up vs all others
224973_at	FAM46A	family with sequence similarity 46, member A	0,00256789	3,429	PE up vs all others
212732_at	MEG3	maternally expressed 3 (non-protein coding)	0,000417298	3,42788	CB up vs all others
228003_at	RAB30	RAB30, member RAS oncogene family	0,000215961	3,42734	PE up vs all others
201168_x_at	ARHGDI	Rho GDP dissociation inhibitor (GDI) alpha	1,11E-07	3,42707	BM up vs all others
214460_at	LSAMP	limbic system-associated membrane protein	0,00176985	3,42667	PE up vs all others
208730_x_at	RAB2A	RAB2A, member RAS oncogene family	0,000167296	3,42617	BM up vs all others
218110_at	XAB2	XPA binding protein 2	3,90E-07	3,42597	BM up vs all others
242408_at	STYX	serine/threonine/tyrosine interacting protein	9,08E-09	3,42528	CB up vs all others
1554447_at	NCRNA00183	non-protein coding RNA 183	9,55E-06	3,42444	CB up vs all others
205049_s_at	CD79A	CD79a molecule, immunoglobulin-associated alpha	2,20E-07	3,42376	BM up vs all others
213059_at	CREB3L1	cAMP responsive element binding protein 3-like 1	0,000100996	3,42309	BM up vs all others
209648_x_at	SOCS5	suppressor of cytokine signaling 5	0,000400335	3,42193	PE up vs all others
217054_at	---	---	6,22E-07	3,42071	BM up vs all others
1560746_at	C1orf118	chromosome 1 open reading frame 118	0,00210662	3,42008	CB up vs all others
237324_s_at	HKDC1	hexokinase domain containing 1	6,81E-07	3,41756	BM up vs all others
214963_at	NUP160	nucleoporin 160kDa	2,97E-06	3,41636	CB up vs all others

219742_at	PRR7	proline rich 7 (synaptic)	0,000833027	3,415	BM up vs all others
228597_at	C21orf45	chromosome 21 open reading frame 45	1,74E-05	3,41464	CB up vs all others
220748_s_at	ZNF580	zinc finger protein 580	0,000162956	3,41281	BM up vs all others
1556216_s_at	---	---	0,000448254	3,41019	CB up vs all others
219249_s_at	FKBP10	FK506 binding protein 10, 65 kDa	0,00152474	3,40969	BM up vs all others
217370_x_at	FUS	fused in sarcoma	0,000713861	3,40756	CB up vs all others
228729_at	CCNB1	cyclin B1	3,25E-05	3,40705	CB up vs all others
230165_at	SGOL2	shugoshin-like 2 (S. pombe)	0,000839472	3,40623	CB up vs all others
227055_at	METTL7B	methyltransferase like 7B	0,00214243	3,40177	BM up vs all others
209204_at	LMO4	LIM domain only 4	5,44E-05	3,40108	CB up vs all others
229747_x_at	LOC146880	Hypothetical LOC146880	0,000136967	3,3996	BM up vs all others
207629_s_at	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	0,00138016	3,39831	BM up vs all others
91703_at	EHBP1L1	EH domain binding protein 1-like 1	0,000665314	3,3982	BM up vs all others
210263_at	KCNF1	potassium voltage-gated channel, subfamily F, member 1	7,36E-05	3,39715	BM up vs all others
231899_at	ZC3H12C	zinc finger CCH-type containing 12C	0,00209007	3,39422	CB up vs all others
227738_s_at	ARMC5	armadillo repeat containing 5	9,21E-06	3,39055	BM up vs all others
207303_at	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	0,000125056	3,38911	BM up vs all others
243567_at	---	---	2,17E-07	3,38741	BM up vs all others
200796_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	2,30E-07	3,38533	BM up vs all others
232406_at	---	---	1,54E-06	3,38526	MU up vs all others
201474_s_at	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	2,77E-06	3,3842	BM up vs all others
214230_at	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	0,00081645	3,38314	CB up vs all others
201079_at	SYNGR2	synaptogyrin 2	0,0100578	3,38231	BM up vs all others
210643_at	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	9,82E-09	3,38046	PE up vs all others
1553107_s_at	C5orf24	chromosome 5 open reading frame 24	2,85E-06	3,37944	CB up vs all others
223131_s_at	TRIM8	tripartite motif-containing 8	0,000157091	3,37677	BM up vs all others
231993_at	ITGBL1	Integrin, beta-like 1 (with EGF-like repeat domains)	0,000371914	3,37652	PE up vs all others
219230_at	TMEM100	transmembrane protein 100	0,00422718	3,37476	CB up vs all others
213286_at	ZFR	zinc finger RNA binding protein	3,93E-07	3,37424	CB up vs all others
223984_s_at	NUPL1	nucleoporin like 1	0,000508953	3,37027	CB up vs all others
203491_s_at	CEP57	centrosomal protein 57kDa	0,000948028	3,36806	CB up vs all others
1555225_at	C1orf43	chromosome 1 open reading frame 43	0,000232182	3,36678	CB up vs all others
211909_x_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	5,15E-06	3,36364	BM up vs all others
238313_at	---	---	3,91E-07	3,36245	BM up vs all others
206923_at	PRKCA	protein kinase C, alpha	3,28E-06	3,36196	BM up vs all others
211716_x_at	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	4,91E-07	3,36195	BM up vs all others
207413_s_at	SCN5A	sodium channel, voltage-gated, type V, alpha subunit	0,0407494	3,35831	MU up vs all others
1553275_s_at	---	---	0,000285946	3,35523	MU up vs all others
231957_s_at	DPP9	dipeptidyl-peptidase 9	5,80E-07	3,35109	BM up vs all others
201082_s_at	DCTN1	dynactin 1	0,0124899	3,34926	BM up vs all others
204292_x_at	STK11	serine/threonine kinase 11	1,49E-05	3,34746	BM up vs all others
209099_x_at	JAG1	jagged 1	0,000541942	3,34688	MU up vs all others
228483_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	0,0019639	3,34631	PE up vs all others
204727_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0,00186169	3,34584	CB up vs all others
210120_s_at	RANBP3	RAN binding protein 3	1,44E-05	3,34359	BM up vs all others
232183_at	SERAC1	serine active site containing 1	0,000359853	3,34225	PE up vs all others

204730_at	RIMS3	regulating synaptic membrane exocytosis 3	2,00E-05	3,34144	MU up vs all others
210770_s_at	CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	0,000266139	3,34116	BM up vs all others
1564067_x_at	TMEM151B	transmembrane protein 151B	3,17E-05	3,3402	BM up vs all others
201559_s_at	CLIC4	chloride intracellular channel 4	0,00208555	3,34009	BM up vs all others
233020_at	---	---	0,00190652	3,33976	PE up vs all others
211003_x_at	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	0,00370501	3,3397	BM up vs all others
243603_at	---	---	3,40E-06	3,33847	BM up vs all others
209885_at	RHOD	ras homolog gene family, member D	0,000718156	3,33618	BM up vs all others
219051_x_at	METRN	meteorin, glial cell differentiation regulator	1,42E-06	3,33433	BM up vs all others
202145_at	LY6E	lymphocyte antigen 6 complex, locus E	0,00309214	3,33407	BM up vs all others
227372_s_at	BAIAP2L1	BAI1-associated protein 2-like 1	0,00295621	3,33271	PE up vs all others
244765_at	---	---	2,17E-05	3,33232	BM up vs all others
1555989_at	---	---	0,0125545	3,33178	BM up vs all others
212190_at	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), me	0,000855309	3,3303	PE up vs all others
228749_at	ZDBF2	zinc finger, DBF-type containing 2	1,66E-07	3,32999	CB up vs all others
219112_at	FNIP1	/// folliculin interacting protein 1 /// Rap guanine nucleotide exchange factor (GEF) 6	0,000119362	3,32882	CB up vs all others
	RAPGEF6				
205290_s_at	BMP2	bone morphogenetic protein 2	5,48E-06	3,32796	MU up vs all others
209636_at	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	1,31E-06	3,32763	BM up vs all others
207754_at	RASSF8	Ras association(RalGDS/AF-6)domain family(N-terminal) member 8	2,36E-05	3,32587	CB up vs all others
204909_at	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	1,56E-06	3,32266	CB up vs all others
212032_s_at	PTOV1	prostate tumor overexpressed 1	8,41E-07	3,32195	BM up vs all others
1557079_at	ITGBL1	Integrin, beta-like 1 (with EGF-like repeat domains)	0,00082719	3,32172	PE up vs all others
229009_at	SIX5	SIX homeobox 5	9,18E-06	3,32125	BM up vs all others
213388_at	PDE4DIP	phosphodiesterase 4D interacting protein	0,000270217	3,32007	PE up vs all others
214045_at	LIAS	lipoic acid synthetase	3,85E-05	3,3199	CB up vs all others
203718_at	PNPLA6	patatin-like phospholipase domain containing 6	9,01E-05	3,31984	BM up vs all others
217350_at	KRT19P2	keratin 19 pseudogene 2	0,000174243	3,3135	BM up vs all others
210585_s_at	TNPO2	transportin 2	2,99E-06	3,31323	BM up vs all others
201723_s_at	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide acetylgalactosaminyltransferase 1	0,000338187	3,3123	PE up vs all others
206707_x_at	FAM65B	family with sequence similarity 65, member B	0,0186125	3,31209	MU up vs all others
206986_at	FGF18	fibroblast growth factor 18	0,000124855	3,31158	BM up vs all others
1568633_a_at	---	---	0,000184534	3,30967	PE up vs all others
229700_at	ZNF738	zinc finger protein 738	2,62E-05	3,30915	CB up vs all others
214444_s_at	PVR	poliovirus receptor	0,000824335	3,30762	BM up vs all others
219046_s_at	PKNOX2	PBX/knotted 1 homeobox 2	4,03E-06	3,30725	MU up vs all others
201325_s_at	EMP1	epithelial membrane protein 1	1,49E-05	3,307	PE up vs all others
225294_s_at	TRAPPC1	trafficking protein particle complex 1	0,00906742	3,3067	BM up vs all others
240245_at	---	---	0,00070283	3,30165	MU up vs all others
223818_s_at	RSF1	remodeling and spacing factor 1	2,78E-05	3,30087	CB up vs all others
1568765_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), me	0,000630976	3,30087	PE up vs all others
232352_at	ISL2	ISL LIM homeobox 2	0,0131805	3,29835	BM up vs all others
206060_s_at	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	0,00386989	3,29824	CB up vs all others
209916_at	DHTKD1	dehydrogenase E1 and transketolase domain containing 1	2,27E-06	3,29736	CB up vs all others
200695_at	PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha	0,00502836	3,29734	BM up vs all others
1563467_at	---	---	0,00018439	3,29708	CB up vs all others

217635_s_at	POLG	polymerase (DNA directed), gamma	3,15E-06	3,29624	BM up vs all others
203795_s_at	BCL7A	B-cell CLL/lymphoma 7 ^o	1,30E-05	3,2962	BM up vs all others
222044_at	PCIF1	PDX1 C-terminal inhibiting factor 1	2,14E-06	3,29566	CB up vs all others
225847_at	NCEH1	neutral cholesterol ester hydrolase 1	0,00722075	3,29547	CB up vs all others
205932_s_at	MSX1	msh homeobox 1	0,0061867	3,29532	PE up vs all others
1557348_at	---	---	0,00374822	3,29525	CB up vs all others
218683_at	PTBP2	polypyrimidine tract binding protein 2	0,00151222	3,29388	CB up vs all others
244753_at	---	---	0,000876981	3,29324	MU up vs all others
205110_s_at	FGF13	fibroblast growth factor 13	5,05E-05	3,29175	MU up vs all others
1556361_s_at	ANKRD13C	ankyrin repeat domain 13C	2,45E-05	3,28884	CB up vs all others
205567_at	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	0,000195069	3,28681	PE up vs all others
238738_at	PSMD7	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	2,94E-05	3,28471	CB up vs all others
221661_at	SLC22A7	solute carrier family 22 (organic anion transporter), member 7	0,001329	3,28366	BM up vs all others
232287_at	PGBD3	piggyBac transposable element derived 3	0,00208046	3,28345	BM up vs all others
238427_at	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	2,95E-06	3,28333	BM up vs all others
231011_at	LARP1B	La ribonucleoprotein domain family, member 1B	6,31E-06	3,28174	CB up vs all others
219423_x_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	0,00216863	3,28041	CB up vs all others
227458_at	CD274	CD274 molecule	0,0049069	3,27905	CB up vs all others
222118_at	CENPN	centromere protein N	6,51E-05	3,27812	CB up vs all others
201211_s_at	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	2,04E-07	3,27752	BM up vs all others
203615_x_at	SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	0,000651659	3,27713	MU up vs all others
208751_at	NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha	0,00344902	3,27709	BM up vs all others
211302_s_at	PDE4B	phosphodiesterase 4B, cAMP-specific	0,00678678	3,27574	PE up vs all others
238351_x_at	---	---	3,67E-07	3,27361	BM up vs all others
225240_s_at	MSI2	musashi homolog 2 (Drosophila)	0,000735987	3,27066	MU up vs all others
217264_s_at	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	3,08E-07	3,26824	BM up vs all others
207156_at	HIST1H2AG	histone cluster 1, H2ag	4,51E-05	3,26823	CB up vs all others
223788_at	---	---	6,29E-06	3,26626	BM up vs all others
206440_at	LIN7A	lin-7 homolog A (C. elegans)	0,00292129	3,26597	CB up vs all others
242121_at	NCRNA00182	non-protein coding RNA 182	3,16E-05	3,26572	MU up vs all others
232184_at	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	0,00203258	3,26298	CB up vs all others
226160_at	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	0,00058185	3,26291	PE up vs all others
202984_s_at	BAG5	BCL2-associated athanogene 5	0,00161328	3,26282	CB up vs all others
219865_at	HSPC157	hypothetical LOC29092	4,86E-05	3,26183	CB up vs all others
234863_x_at	FBXO5	F-box protein 5	4,00E-06	3,26163	CB up vs all others
228935_at	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	0,000122855	3,25877	CB up vs all others
217278_x_at	---	---	4,24E-06	3,25774	BM up vs all others
241350_at	FBXL22	F-box and leucine-rich repeat protein 22	9,32E-06	3,25772	MU up vs all others
89476_r_at	NPEPL1	aminopeptidase-like 1	1,32E-06	3,25763	BM up vs all others
204375_at	CLSTN3	calsyntenin 3	2,36E-05	3,2567	BM up vs all others
226462_at	STXBP6	syntaxin binding protein 6 (amisyn)	0,000795536	3,25654	MU up vs all others
229884_s_at	MRPL2	mitochondrial ribosomal protein L2	9,68E-07	3,25576	BM up vs all others
231903_x_at	ARHGAP23	Rho GTPase activating protein 23	4,99E-06	3,25529	BM up vs all others
205479_s_at	PLAU	plasminogen activator, urokinase	3,20E-06	3,25487	MU up vs all others
1555920_at	CBX3	Chromobox homolog 3 (HP1 gamma homolog, Drosophila)	1,63E-06	3,2547	CB up vs all others
234495_at	KLK15	kallikrein-related peptidase 15	4,24E-06	3,25444	BM up vs all others
240512_x_at	KCTD4	potassium channel tetramerisation domain containing 4	0,00105333	3,25396	CB up vs all others

204834_at	FGL2	fibrinogen-like 2	1,55E-05	3,25299	MU up vs all others
201750_s_at	ECE1	endothelin converting enzyme 1	1,11E-06	3,25218	BM up vs all others
221584_s_at	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	0,00301656	3,25198	PE up vs all others
244503_at	---	---	0,000798312	3,24905	PE up vs all others
217793_at	RAB11B	RAB11B, member RAS oncogene family	8,29E-08	3,24832	BM up vs all others
1561123_at	---	---	1,19E-06	3,24721	PE up vs all others
209645_s_at	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	0,00660336	3,24584	BM up vs all others
209967_s_at	CREM	cAMP responsive element modulator	5,98E-07	3,24518	CB up vs all others
238125_at	ADAMTS16	ADAM metalloproteinase with thrombospondin type 1 motif, 16	0,000225629	3,24479	BM up vs all others
200649_at	NUCB1	nucleobindin 1	0,00346049	3,24478	BM up vs all others
215454_x_at	SFTPC	surfactant protein C	2,88E-06	3,24357	BM up vs all others
225601_at	HMGB3	high-mobility group box 3	1,34E-06	3,24315	CB up vs all others
203750_s_at	RARA	retinoic acid receptor, alpha	1,06E-05	3,24091	BM up vs all others
227203_at	FBXL17	F-box and leucine-rich repeat protein 17	2,29E-06	3,2401	CB up vs all others
211837_s_at	PTCRA	pre T-cell antigen receptor alpha	1,58E-05	3,2389	BM up vs all others
210089_s_at	LAMA4	laminin, alpha 4	0,00257268	3,23796	PE up vs all others
228716_at	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog	9,07E-05	3,23758	MU up vs all others
227921_at	---	---	0,00527475	3,23719	CB up vs all others
235042_at	XIRP1	xin actin-binding repeat containing 1	0,0511354	3,23563	MU up vs all others
206699_x_at	NPAS1	neuronal PAS domain protein 1	7,61E-06	3,23469	BM up vs all others
214877_at	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	0,000758286	3,23416	CB up vs all others
211681_s_at	PDLIM5	PDZ and LIM domain 5	0,0107348	3,23065	BM up vs all others
203369_x_at	PDLIM7	PDZ and LIM domain 7 (enigma)	3,16E-06	3,23015	BM up vs all others
227397_at	TPM2	tropomyosin 2 (beta)	1,25E-06	3,22887	BM up vs all others
231550_at	XYLT2	Xylosyltransferase II	0,0151419	3,22861	BM up vs all others
221755_at	EHBP1L1	EH domain binding protein 1-like 1	0,00226791	3,2285	BM up vs all others
202388_at	RGS2	regulator of G-protein signaling 2, 24kDa	0,00581406	3,22746	CB up vs all others
200787_s_at	PEA15	phosphoprotein enriched in astrocytes 15	0,00870097	3,22737	BM up vs all others
229451_at	GALNT9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide acetylgalactosaminyltransferase 9 (Gal	7,37E-07	3,22737	BM up vs all others
240468_at	---	---	1,60E-05	3,22621	BM up vs all others
221525_at	ZMIZ2	zinc finger, MIZ-type containing 2	7,61E-06	3,22552	BM up vs all others
220581_at	C6orf97	chromosome 6 open reading frame 97	3,63E-05	3,22525	PE up vs all others
205142_x_at	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	1,99E-05	3,22358	BM up vs all others
238969_at	C3orf55	chromosome 3 open reading frame 55	0,000375929	3,22285	CB up vs all others
232355_at	SNORD114-3	small nucleolar RNA, C/D box 114-3	8,47E-05	3,22192	PE up vs all others
212384_at	ATP6V1G2	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	N-B associated transcript	0,000143378	3,2213
207747_s_at	BAT1	HLA-B associated transcript			
233850_s_at	DOK4	docking protein 4	0,000151858	3,2207	BM up vs all others
208447_s_at	EBF4	early B-cell factor 4	0,000663039	3,22046	BM up vs all others
225500_x_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	0,0101278	3,21846	BM up vs all others
212218_s_at	SCAF1	SR-related CTD-associated factor 1	2,94E-07	3,21678	BM up vs all others
238335_at	FASN	fatty acid synthase	1,44E-06	3,21562	BM up vs all others
236457_at	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	1,48E-05	3,21419	CB up vs all others
216685_s_at	GTDC1	glycosyltransferase-like domain containing 1	0,000351688	3,21067	BM up vs all others
211806_s_at	MTAP	methylthioadenosine phosphorylase	0,00323663	3,20897	CB up vs all others
235572_at	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	0,000185655	3,20786	PE up vs all others
	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S.	2,88E-06	3,20572	CB up vs all others

cerevisiae)

202572_s_at	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	5,33E-09	3,20569	BM up vs all others
	PCDHGA1	///			
	PCDHGA10	///			
	PCDHGA11	///			
	PCDHGA12	///			
	PCDHGA2	///			
	PCDHGA3	///			
	PCDHGA4	///			
	PCDHGA5	///			
	PCDHGA6	///			
	PCDHGA7	///			
	PCDHGA8	///			
	PCDHGA9	///			
	PCDHGB1	///			
	PCDHGB2	///			
	PCDHGB3	///			
	PCDHGB4	///			
	PCDHGB5	///			
	PCDHGB6	///			
	PCDHGB7	///			
	PCDHGC3	///			
	PCDHGC4	///			
205717_x_at	PCDHGC5	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocad	3,94E-05	3,20391	BM up vs all others
228469_at	PPID	Peptidylprolyl isomerase D	0,00339348	3,20279	CB up vs all others
202118_s_at	CPNE3	copine III	0,00084125	3,20193	PE up vs all others
223700_at	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	9,30E-05	3,20159	CB up vs all others
216496_s_at	---	---	6,36E-08	3,201	BM up vs all others
238550_at	RUFY2	RUN and FYVE domain containing 2	0,000117958	3,20086	CB up vs all others
226037_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	9,97E-05	3,20052	CB up vs all others
1566003_x_at	---	---	1,11E-05	3,19849	BM up vs all others
235629_at	---	---	6,25E-05	3,19632	PE up vs all others
235173_at	LOC401093	hypothetical LOC401093	0,00051911	3,19619	PE up vs all others
211573_x_at	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	0,0150985	3,19535	BM up vs all others
207556_s_at	DGKZ	diacylglycerol kinase, zeta 104kDa	2,15E-07	3,19392	BM up vs all others
200623_s_at	CALM3	calmodulin 3 (phosphorylase kinase, delta)	6,90E-06	3,19345	BM up vs all others
1554821_a_at	ZBED1	zinc finger, BED-type containing 1	6,85E-07	3,19306	CB up vs all others
203942_s_at	MARK2	MAP/microtubule affinity-regulating kinase 2	5,10E-06	3,19285	BM up vs all others
217199_s_at	STAT2	signal transducer and activator of transcription 2, 113kDa	1,38E-10	3,19194	BM up vs all others
214336_s_at	COPA	coatamer protein complex, subunit alpha	0,00161072	3,19158	BM up vs all others
207039_at	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	0,0115234	3,19038	BM up vs all others
216253_s_at	PARVB	parvin, beta	2,59E-05	3,18752	BM up vs all others
1554757_a_at	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	0,00634002	3,18659	BM up vs all others
222587_s_at	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (Gal	0,0016885	3,18654	CB up vs all others
239138_at	LOC100506638	hypothetical LOC100506638	0,000159499	3,18632	CB up vs all others
231720_s_at	JAM3	junctional adhesion molecule 3	5,38E-05	3,18551	BM up vs all others
202416_at	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	0,00566102	3,18424	CB up vs all others
206020_at	SOCS6	suppressor of cytokine signaling 6	0,00208906	3,18245	CB up vs all others
224932_at	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	0,00193365	3,1819	BM up vs all others
230380_at	LOC100289049	Hypothetical protein LOC100289049	1,07E-05	3,18185	CB up vs all others
207827_x_at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	0,00159912	3,18082	BM up vs all others
238045_at	TMEM65	transmembrane protein 65	1,98E-05	3,1804	CB up vs all others

206278_at	PTAFR	platelet-activating factor receptor	1,36E-05	3,17606	BM up vs all others
210692_s_at	SLC43A3	solute carrier family 43, member 3	0,00232093	3,17398	PE up vs all others
200959_at	FUS	fused in sarcoma	0,00190452	3,1724	CB up vs all others
201045_s_at	RAB6A	RAB6A, member RAS oncogene family	2,23E-06	3,17072	BM up vs all others
210233_at	IL1RAP	interleukin 1 receptor accessory protein	3,42E-06	3,16986	CB up vs all others
244623_at	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	0,00868788	3,16965	BM up vs all others
219507_at	RSRC1	arginine/serine-rich coiled-coil 1	5,32E-05	3,16899	CB up vs all others
205153_s_at	CD40	CD40 molecule, TNF receptor superfamily member 5	0,000319433	3,16885	PE up vs all others
200964_at	UBA1	ubiquitin-like modifier activating enzyme 1	0,013679	3,16778	BM up vs all others
226341_at	---	---	0,00181171	3,16771	CB up vs all others
226902_at	USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	0,000953449	3,16747	CB up vs all others
235308_at	ZBTB20	zinc finger and BTB domain containing 20	4,07E-05	3,16693	MU up vs all others
1561633_at	HMGA2	high mobility group AT-hook 2	0,0026016	3,16441	CB up vs all others
243023_at	---	---	0,00079134	3,16237	CB up vs all others
230108_at	ERCC6 PGBD3	/// excision repair cross-complementing rodent repair deficiency, complementation group 6 /	5,27E-06	3,16216	BM up vs all others
222962_s_at	MCM10	minichromosome maintenance complex component 10	0,000360374	3,16188	CB up vs all others
230304_at	---	---	0,000130308	3,16084	CB up vs all others
221974_at	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	0,000481174	3,16052	CB up vs all others
213338_at	TMEM158	transmembrane protein 158 (gene/pseudogene)	0,000589451	3,15808	BM up vs all others
231772_x_at	CENPH	centromere protein H	6,41E-06	3,15665	CB up vs all others
206338_at	ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	2,58E-07	3,15591	BM up vs all others
229667_s_at	HOXB8	homeobox B8	0,00297572	3,15589	CB up vs all others
222885_at	EMCN	Endomucin	0,000534158	3,15506	MU up vs all others
1569472_s_at	TTC3	tetratricopeptide repeat domain 3	0,0022144	3,15298	CB up vs all others
1558636_s_at	ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif, 5	0,000241387	3,14969	MU up vs all others
230073_at	---	---	1,45E-06	3,14966	BM up vs all others
219493_at	SHCBP1	SHC SH2-domain binding protein 1	0,0075652	3,14873	CB up vs all others
226118_at	CENPO	centromere protein O	1,97E-06	3,1455	CB up vs all others
217520_x_at	LOC283683	hypothetical LOC283683	1,28E-07	3,1452	CB up vs all others
236702_at	C20orf43	Chromosome 20 open reading frame 43	0,000678429	3,14368	BM up vs all others
217270_s_at	DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	1,67E-07	3,14152	BM up vs all others
202312_s_at	COL1A1	collagen, type I, alpha 1	7,93E-08	3,14121	BM up vs all others
202071_at	SDC4	syndecan 4	0,00279381	3,14027	PE up vs all others
209127_s_at	SART3	squamous cell carcinoma antigen recognized by T cells 3	9,48E-08	3,14019	CB up vs all others
239680_at	WDR76	WD repeat domain 76	0,00547532	3,14013	CB up vs all others
1555821_a_at	AKT1S1	AKT1 substrate 1 (proline-rich)	8,23E-05	3,13992	BM up vs all others
217079_at	LOC100288679	Hypothetical protein LOC100288679	1,73E-08	3,1396	BM up vs all others
232211_at	PPP1R3F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	2,77E-07	3,13866	BM up vs all others
1568951_at	ZNF280D	zinc finger protein 280D	0,000298843	3,13797	CB up vs all others
211632_at	IGHD /// IGHG1 /// IGHM	immunoglobulin heavy constant delta /// immunoglobulin heavy constant gamma 1 (G1m mark	4,24E-05	3,13791	BM up vs all others
233939_at	REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	7,83E-08	3,13771	BM up vs all others
202935_s_at	SOX9	SRY (sex determining region Y)-box 9	0,0385478	3,13735	PE up vs all others
207198_s_at	LIMS1	LIM and senescent cell antigen-like domains 1	6,04E-06	3,13685	CB up vs all others
233734_s_at	OSBPL5	oxysterol binding protein-like 5	2,70E-05	3,13679	BM up vs all others
219355_at	CXorf57	chromosome X open reading frame 57	0,00201688	3,13627	CB up vs all others
231365_at	---	---	0,00709877	3,13602	CB up vs all others

222036_s_at	MCM4	minichromosome maintenance complex component 4	2,04E-05	3,13543	CB up vs all others
1563431_x_at	CALM3	Calmodulin 3 (phosphorylase kinase, delta)	0,00133406	3,135	PE up vs all others
206003_at	CEP135	centrosomal protein 135kDa	0,00174656	3,1345	CB up vs all others
228847_at	EXOC3	exocyst complex component 3	0,000288633	3,13269	CB up vs all others
226667_x_at	EPN1	epsin 1	7,52E-09	3,13097	BM up vs all others
241629_at	---	---	6,00E-09	3,13035	BM up vs all others
206703_at	CHRNA1	cholinergic receptor, nicotinic, beta 1 (muscle)	0,00209614	3,12876	MU up vs all others
209982_s_at	NRXN2	neurexin 2	0,00398031	3,1276	BM up vs all others
226747_at	TXNDC16	thioredoxin domain containing 16	0,00325092	3,12745	CB up vs all others
218466_at	TBC1D17	TBC1 domain family, member 17	8,58E-09	3,12641	BM up vs all others
222760_at	ZNF703	zinc finger protein 703	0,00293419	3,12541	BM up vs all others
210513_s_at	VEGFA	vascular endothelial growth factor A	0,00469361	3,12499	BM up vs all others
217066_s_at	DMPK	dystrophia myotonica-protein kinase	0,00353046	3,12138	BM up vs all others
218522_s_at	MAP1S	microtubule-associated protein 1S	2,61E-07	3,12119	BM up vs all others
224282_s_at	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	6,62E-05	3,1203	BM up vs all others
1558750_a_at	LOC100288693	Hypothetical protein LOC100288693	0,00458179	3,11883	CB up vs all others
221258_s_at	KIF18A	kinesin family member 18A	0,000350119	3,11868	CB up vs all others
209117_at	WBP2	WW domain binding protein 2	0,00017414	3,11723	BM up vs all others
223199_at	MKNK2	MAP kinase interacting serine/threonine kinase 2	0,000545013	3,11499	BM up vs all others
230833_at	ACRBP	acrosin binding protein	9,06E-06	3,11352	BM up vs all others
1558002_at	STRAP	Serine/threonine kinase receptor associated protein	7,87E-05	3,11138	CB up vs all others
242470_at	EID2B	EP300 interacting inhibitor of differentiation 2B	7,48E-05	3,11011	CB up vs all others
213668_s_at	SOX4	SRY (sex determining region Y)-box 4	0,00184576	3,10987	PE up vs all others
200772_x_at	PTMA	prothymosin, alpha	7,76E-07	3,10962	CB up vs all others
203641_s_at	COBLL1	COBL-like 1	0,000531071	3,10895	MU up vs all others
222685_at	HAUS6	HAUS augmin-like complex, subunit 6	0,00149216	3,10819	CB up vs all others
224454_at	ETNK1	ethanolamine kinase 1	2,30E-06	3,10795	CB up vs all others
224999_at	EGFR	epidermal growth factor receptor	0,000899265	3,10761	PE up vs all others
204864_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	0,00091277	3,1068	BM up vs all others
222009_at	CEMP1	cementum protein 1	2,79E-06	3,10449	BM up vs all others
212064_x_at	MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	0,000431482	3,10423	BM up vs all others
204886_at	PLK4	polo-like kinase 4	0,000519184	3,10163	CB up vs all others
243062_at	FLCN	Folliculin	5,00E-05	3,1016	BM up vs all others
	IGHA1 /// IGHG2				
	/// IGHD ///				
	IGHG1 /// IGHG3				
	/// IGHM ///				
	IGHV4-31 ///				
	IGHV4-59 ///				
211638_at	LOC100126583	immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m ma	1,79E-07	3,1013	BM up vs all others
205195_at	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	0,000963117	3,10107	CB up vs all others
239772_x_at	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	0,000164973	3,09784	BM up vs all others
212913_at	C6orf26 /// MSH5	chromosome 6 open reading frame 26 /// mutS homolog 5 (E. coli)	0,000475235	3,09685	CB up vs all others
205476_at	CCL20	chemokine (C-C motif) ligand 20	4,73E-05	3,0959	BM up vs all others
219475_at	OSGIN1	oxidative stress induced growth inhibitor 1	4,47E-09	3,09484	BM up vs all others
205766_at	TCAP	titin-cap (telethonin)	0,0107608	3,09482	BM up vs all others
205339_at	STIL	SCL/TAL1 interrupting locus	0,000208025	3,09394	CB up vs all others
230333_at	---	---	0,00230092	3,09168	PE up vs all others
217960_s_at	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	0,00288349	3,09028	CB up vs all others

202571_s_at	DLGAP4	discs, large (Drosophila) homolog-associated protein 4	1,35E-07	3,08999	BM up vs all others
217399_s_at	FOXO3	forkhead box O3	6,62E-07	3,08982	BM up vs all others
222772_at	MYEF2	myelin expression factor 2	0,00298083	3,08828	CB up vs all others
209179_s_at	MBOAT7	membrane bound O-acyltransferase domain containing 7	4,41E-07	3,0878	BM up vs all others
226569_s_at	CTF18	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	0,000450248	3,08651	CB up vs all others
205739_x_at	ZNF107	zinc finger protein 107	1,78E-05	3,08345	CB up vs all others
240813_at	---	---	1,05E-06	3,08295	BM up vs all others
227214_at	GOPC	golgi-associated PDZ and coiled-coil motif containing	0,000519248	3,07909	BM up vs all others
211924_s_at	PLAUR	plasminogen activator, urokinase receptor	0,0057524	3,07796	BM up vs all others
205519_at	WDR76	WD repeat domain 76	0,000961569	3,07751	CB up vs all others
221284_s_at	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	2,37E-07	3,07657	BM up vs all others
209502_s_at	BAIAP2	BAI1-associated protein 2	1,19E-05	3,07572	BM up vs all others
1553186_x_at	RASEF	RAS and EF-hand domain containing	0,000387266	3,07558	CB up vs all others
214122_at	PDLIM7	PDZ and LIM domain 7 (enigma)	3,15E-06	3,07548	BM up vs all others
1554986_a_at	SNX19	sorting nexin 19	0,000169071	3,07434	BM up vs all others
212437_at	CENPB	centromere protein B, 80kDa	1,18E-07	3,07364	BM up vs all others
224974_at	SUDS3	suppressor of defective silencing 3 homolog (S. cerevisiae)	0,000805316	3,07272	CB up vs all others
244163_at	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	0,00403712	3,07243	CB up vs all others
204678_s_at	KCNK1	potassium channel, subfamily K, member 1	0,000510664	3,07235	PE up vs all others
218035_s_at	RBM47	RNA binding motif protein 47	1,81E-05	3,07217	PE up vs all others
218502_s_at	TRPS1	trichorhinophalangeal syndrome I	0,000350295	3,07125	PE up vs all others
212466_at	SPRED2	sprouty-related, EVH1 domain containing 2	8,39E-05	3,07075	BM up vs all others
244491_at	---	---	5,77E-08	3,07051	BM up vs all others
234924_s_at	ZNF687	zinc finger protein 687	1,41E-06	3,06978	BM up vs all others
208776_at	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	0,000195244	3,06883	CB up vs all others
203016_s_at	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	2,49E-05	3,06777	CB up vs all others
231161_x_at	TRIM8	Tripartite motif-containing 8	5,15E-08	3,06678	BM up vs all others
1564426_x_at	LOC389634	hypothetical LOC389634	0,000575662	3,06651	BM up vs all others
207896_s_at	DLEC1	deleted in lung and esophageal cancer 1	1,50E-07	3,06634	BM up vs all others
211725_s_at	BID	BH3 interacting domain death agonist	0,000210806	3,06599	BM up vs all others
228941_at	ALG10B	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B (yeast)	0,00290431	3,06529	CB up vs all others
226458_at	---	---	3,39E-05	3,06528	CB up vs all others
1552295_a_at	SLC39A13	solute carrier family 39 (zinc transporter), member 13	0,00105146	3,06431	BM up vs all others
213253_at	SMC2	structural maintenance of chromosomes 2	0,000179238	3,06427	CB up vs all others
1569785_at	---	---	4,22E-07	3,06414	PE up vs all others
202876_s_at	PBX2	pre-B-cell leukemia homeobox 2	0,000465947	3,06334	CB up vs all others
205909_at	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	0,000900007	3,06259	CB up vs all others
208677_s_at	BSG	basigin (Ok blood group)	0,00105085	3,06241	BM up vs all others
226490_at	NHSL1	NHS-like 1	0,000907782	3,06054	PE up vs all others
238242_at	---	---	4,87E-06	3,06042	BM up vs all others
212336_at	EPB41L1	erythrocyte membrane protein band 4.1-like 1	2,95E-05	3,05943	BM up vs all others
231855_at	KIAA1524	KIAA1524	0,00162835	3,05853	CB up vs all others
236862_at	GOPC	Golgi-associated PDZ and coiled-coil motif containing	0,00233044	3,05813	PE up vs all others
208875_s_at	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	1,23E-05	3,0561	BM up vs all others
202948_at	IL1R1	interleukin 1 receptor, type I	0,000149535	3,05582	PE up vs all others
207106_s_at	LTK	leukocyte receptor tyrosine kinase	3,44E-07	3,05436	BM up vs all others

1557128_at	FAM111B	family with sequence similarity 111, member B	1,76E-05	3,05435	CB up vs all others
238532_at	DPF3	D4, zinc and double PHD fingers, family 3	0,000469703	3,0543	CB up vs all others
205104_at	SNPH	Syntaphilin	2,05E-05	3,05406	BM up vs all others
216092_s_at	SLC7A8	solute carrier family 7 (amino acid transporter, L-type), member 8	1,58E-05	3,05353	PE up vs all others
205167_s_at	CDC25C	cell division cycle 25 homolog C (S. pombe)	7,36E-05	3,05324	CB up vs all others
232576_at	---	---	1,06E-07	3,0518	CB up vs all others
236447_at	---	---	2,67E-07	3,05077	BM up vs all others
205053_at	PRIM1	primase, DNA, polypeptide 1 (49kDa)	0,000407765	3,0498	CB up vs all others
227390_at	MEG3	maternally expressed 3 (non-protein coding)	1,26E-05	3,04834	BM up vs all others
240595_at	---	---	0,000361062	3,04682	BM up vs all others
243409_at	FOXL1	forkhead box L1	0,01564	3,04672	CB up vs all others
225124_at	PPP1R9B	protein phosphatase 1, regulatory (inhibitor) subunit 9B	5,54E-09	3,04622	BM up vs all others
224218_s_at	TRPS1	trichorhinophalangeal syndrome I	0,00192013	3,04615	PE up vs all others
237227_at	NEK10	NIMA (never in mitosis gene a)- related kinase 10	3,74E-06	3,04587	BM up vs all others
222197_s_at	---	---	8,57E-08	3,04411	BM up vs all others
205359_at	AKAP6	A kinase (PRKA) anchor protein 6	0,000345225	3,04341	MU up vs all others
227014_at	ASPHD2	aspartate beta-hydroxylase domain containing 2	0,000191568	3,04339	PE up vs all others
223415_at	RPP25	ribonuclease P/MRP 25kDa subunit	4,84E-07	3,04315	BM up vs all others
202046_s_at	GRLF1	glucocorticoid receptor DNA binding factor 1	5,85E-09	3,04038	BM up vs all others
208530_s_at	RARB	retinoic acid receptor, beta	2,43E-05	3,04011	BM up vs all others
211363_s_at	MTAP	methylthioadenosine phosphorylase	0,000111321	3,03891	CB up vs all others
227954_at	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	0,000608215	3,03825	CB up vs all others
219771_at	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)	0,00156244	3,03804	PE up vs all others
221881_s_at	CLIC4	chloride intracellular channel 4	6,67E-07	3,03736	BM up vs all others
221291_at	ULBP2	UL16 binding protein 2	6,37E-06	3,03731	BM up vs all others
218169_at	VAC14	Vac14 homolog (S. cerevisiae)	2,28E-06	3,03661	BM up vs all others
236442_at	DPF3	D4, zinc and double PHD fingers, family 3	0,00108292	3,03634	CB up vs all others
202327_s_at	PKD1	polycystic kidney disease 1 (autosomal dominant)	2,01E-07	3,03593	BM up vs all others
231773_at	ANGPTL1	angiopoietin-like 1	2,87E-05	3,03529	MU up vs all others
229415_at	CYCS	cytochrome c, somatic	0,00349768	3,03518	CB up vs all others
1558803_at	---	---	5,95E-05	3,03434	PE up vs all others
213725_x_at	XYLT1	xylosyltransferase I	0,00718907	3,03412	CB up vs all others
210842_at	NRP2	neuropilin 2	1,82E-05	3,0338	PE up vs all others
212030_at	RBM25	RNA binding motif protein 25	2,08E-10	3,03254	CB up vs all others
32836_at	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase,	6,67E-11	3,03081	BM up vs all others
207018_s_at	RAB27B	RAB27B, member RAS oncogene family	0,00228938	3,03054	PE up vs all others
202219_at	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	4,74E-05	3,03036	BM up vs all others
242887_at	KCMF1	potassium channel modulatory factor 1	6,26E-05	3,02935	CB up vs all others
227666_at	DCLK2	doublecortin-like kinase 2	0,00125149	3,02906	CB up vs all others
231034_s_at	---	---	0,00125059	3,02858	PE up vs all others
206191_at	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	0,00212292	3,02853	PE up vs all others
227286_at	INO80E	INO80 complex subunit E	3,86E-07	3,02844	BM up vs all others
223484_at	C15orf48	chromosome 15 open reading frame 48	1,26E-05	3,02844	PE up vs all others
1563719_a_at	---	---	0,00012587	3,02774	MU up vs all others
242217_s_at	FBR3	Fibrosin	0,00136731	3,02749	BM up vs all others
223520_s_at	KIF13A	kinesin family member 13A	0,000432588	3,02672	CB up vs all others

1558683_a_at	HMGA2	high mobility group AT-hook 2	0,00105504	3,02567	CB up vs all others
1566603_s_at	RPUSD3	RNA pseudouridylate synthase domain containing 3	3,78E-05	3,02564	CB up vs all others
202383_at	KDM5C	lysine (K)-specific demethylase 5C	1,94E-05	3,02521	BM up vs all others
224565_at	NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	0,000319495	3,02388	CB up vs all others
244463_at	ADAM23	ADAM metalloproteinase domain 23	0,00240672	3,02247	CB up vs all others
216180_s_at	SYNJ2	synaptojanin 2	0,00586625	3,02163	BM up vs all others
241457_at	---	---	0,000517987	3,02082	MU up vs all others
235088_at	C4orf46	chromosome 4 open reading frame 46	0,000400749	3,02044	CB up vs all others
201369_s_at	ZFP36L2	zinc finger protein 36, C3H type-like 2	0,00728902	3,02018	BM up vs all others
214729_at	TWISTNB	TWIST neighbor	3,63E-06	3,02014	CB up vs all others
224734_at	HMGB1	high-mobility group box 1	0,000401224	3,01964	CB up vs all others
241364_at	TMEM57	transmembrane protein 57	0,000367424	3,01887	CB up vs all others
228092_at	CREM	cAMP responsive element modulator	0,00245672	3,01851	CB up vs all others
203698_s_at	FRZB	frizzled-related protein	0,219575	3,01845	CB up vs all others
207633_s_at	MUSK	muscle, skeletal, receptor tyrosine kinase	5,26E-06	3,01843	MU up vs all others
232795_at	---	---	0,000144699	3,01809	MU up vs all others
231724_at	MED26	mediator complex subunit 26	3,40E-06	3,01716	BM up vs all others
241972_at	LOC401588	hypothetical LOC401588	5,65E-05	3,01549	CB up vs all others
219148_at	PBK	PDZ binding kinase	0,000379468	3,01439	CB up vs all others
207555_s_at	TBXA2R	thromboxane A2 receptor	0,00116813	3,01293	BM up vs all others
210612_s_at	SYNJ2	synaptojanin 2	0,00295523	3,01201	PE up vs all others
231061_at	---	---	0,00293127	3,01171	CB up vs all others
212738_at	ARHGAP19	Rho GTPase activating protein 19	1,79E-06	3,00992	CB up vs all others
205254_x_at	TCF7	transcription factor 7 (T-cell specific, HMG-box)	2,15E-05	3,00984	BM up vs all others
221068_at	KANK2	KN motif and ankyrin repeat domains 2	0,000315674	3,00928	BM up vs all others
218965_s_at	TUT1	terminal uridylyl transferase 1, U6 snRNA-specific	5,73E-05	3,00631	BM up vs all others
203946_s_at	ARG2	arginase, type II	0,00295109	3,00628	PE up vs all others
226811_at	FAM46C	family with sequence similarity 46, member C	3,69E-06	3,00553	PE up vs all others
236278_at	HIST1H3E	Histone cluster 1, H3e	3,89E-06	3,00456	BM up vs all others
214520_at	FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	3,34E-07	3,00422	BM up vs all others
	PCDHGA1	///			
	PCDHGA10	///			
	PCDHGA11	///			
	PCDHGA12	///			
	PCDHGA2	///			
	PCDHGA3	///			
	PCDHGA4	///			
	PCDHGA5	///			
	PCDHGA6	///			
	PCDHGA7	///			
	PCDHGA8	///			
	PCDHGA9	///			
	PCDHGB1	///			
	PCDHGB2	///			
	PCDHGB3	///			
	PCDHGB4	///			
	PCDHGB5	///			
	PCDHGB6	///			
	PCDHGB7	///			
	PCDHGC3	///			
	PCDHGC4	///			
209079_x_at	PCDHGC5	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocad	1,72E-05	3,00392	BM up vs all others
1558028_x_at	LOC647979	hypothetical LOC647979	0,00132215	3,00279	CB up vs all others
235521_at	HOXA3	homeobox A3	0,129359	3,00253	CB up vs all others

241935_at	SHROOM1	shroom family member 1	0,000144143	3,00083	BM up vs all others
215626_at	---	---	4,96E-06	3,00048	MU up vs all others
213319_s_at	CSDA	Cold shock domain protein A	5,41E-05	3,00025	BM up vs all others

Supplementary Table 2. Gene sets enriched in CB.

GS follow link to MSigDB	NOM p-val	FDR q-val
KEGG TERPENOID BACKBONE BIOSYNTHESIS	0.000	0.366
REACTOME CDC20 PHOSPHO APC MEDIATED DEGRADATION OF CYCLIN A	0.000	0.327
BIOCARTA VEGF PATHWAY	0.000	0.298
REACTOME M G1 TRANSITION	0.000	0.293
REACTOME CDT1 ASSOCIATION WITH THE CDC6 ORC ORIGIN COMPLEX	0.000	0.242
KEGG RNA DEGRADATION	0.008	0.319
REACTOME RNA POLYMERASE II TRANSCRIPTION	0.010	0.322
REACTOME APCDC20 MEDIATED DEGRADATION OF CYCLIN B	0.010	0.211
REACTOME MRNA_3_END_PROCESSING	0.011	0.567
KEGG SPLICIOSOME	0.011	0.430
REACTOME ORC1 REMOVAL FROM CHROMATIN	0.013	0.283
REACTOME CONVERSION FROM APC CDC20 TO APC CDH1 IN LATE ANAPHASE	0.019	0.257
REACTOME METABOLISM OF MRNA	0.020	0.347
REACTOME INACTIVATION OF APC VIA DIRECT INHIBITION OF THE APCOMPLEX	0.023	0.223
REACTOME CYCLIN E ASSOCIATED EVENTS DURING G1 S TRANSITION	0.025	0.296
REACTOME ACTIVATION OF THE PRE REPLICATIVE COMPLEX	0.025	0.244
REACTOME RNA POLYMERASE III TRANSCRIPTION INITIATION FROM TYPE 2 PRO MOTER	0.028	0.494
REACTOME DNA STRAND ELONGATION	0.030	0.224
KEGG PROTEASOME	0.033	0.226
KEGG MISMATCH REPAIR	0.038	0.275
REACTOME GLOBAL GENOMIC NER	0.039	0.246
REACTOME SCF SKP2 MEDIATED DEGRADATION OF P27 P21	0.039	0.243
KEGG DNA REPLICATION	0.039	0.225
REACTOME FANCONI ANEMIA PATHWAY	0.039	0.227
REACTOME INFLUENZA LIFE CYCLE	0.040	0.786
REACTOME LAGGING STRAND SYNTHESIS	0.040	0.225
REACTOME G2 M CHECKPOINTS	0.040	0.243
REACTOME DNA REPAIR	0.041	0.274
REACTOME REGULATION OF ORNITHINE DECARBOXYLASE	0.041	0.262
REACTOME CELL CYCLE MITOTIC	0.042	0.231
REACTOME TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRON CONTAINING TRANSCRIPT	0.043	0.237
BIOCARTA PROTEASOME PATHWAY	0.043	0.330
BIOCARTA NGF PATHWAY	0.044	0.264
REACTOME REGULATION OF APC ACTIVATORS BETWEEN G1 S AND EARLY ANAPHASE	0.045	0.245
REACTOME METABOLISM OF RNA	0.045	0.234
REACTOME NUCLEOTIDE EXCISION REPAIR	0.046	0.304
KEGG NUCLEOTIDE EXCISION REPAIR	0.049	0.290
REACTOME AUTODEGRADATION OF CDH1 BY CDH1 APC	0.049	0.231
REACTOME ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS	0.050	0.243
REACTOME CELL CYCLE CHECKPOINTS	0.052	0.295
REACTOME REPAIR SYNTHESIS OF PATCH 27_30 BASES LONG BY DNA POLYMERASE	0.052	0.246
REACTOME TRANSCRIPTION	0.053	0.232
REACTOME EXTENSION OF TELOMERES	0.053	0.263
REACTOME PROCESSING OF CAPPED INTRON CONTAINING PRE MRNA	0.055	0.275
REACTOME MRNA SPLICING	0.056	0.214
REACTOME FORMATION AND MATURATION OF MRNA TRANSCRIPT	0.058	0.285
KEGG GLYCEROLIPID METABOLISM	0.059	0.402
REACTOME S PHASE	0.061	0.235
REACTOME SCF BETA TRCP MEDIATED DEGRADATION OF EMI1	0.061	0.244

REACTOME HIV LIFE CYCLE	0.062	0.230
KEGG LYSINE DEGRADATION	0.062	0.289
REACTOME MITOTIC M M G1 PHASES	0.063	0.226
REACTOME TRANSCRIPTION OF THE HIV GENOME	0.064	0.232
REACTOME GENE EXPRESSION	0.065	0.287
REACTOME DNA REPLICATION PRE INITIATION	0.065	0.230
REACTOME G1 S TRANSITION	0.065	0.222
REACTOME HIV INFECTION	0.066	0.222
REACTOME G2 M TRANSITION	0.069	0.234
BIOCARTA MCM PATHWAY	0.069	0.269
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	0.072	0.221
REACTOME SNRNP ASSEMBLY	0.072	0.215
KEGG RNA POLYMERASE	0.074	0.222
REACTOME TRANSPORT OF THE SLBP INDEPENDENT MATURE MRNA	0.074	0.224
REACTOME MITOTIC PROMETAPHASE	0.075	0.230
REACTOME SYNTHESIS OF DNA	0.077	0.224
REACTOME DOUBLE STRAND BREAK REPAIR	0.077	0.228
REACTOME HOMOLOGOUS RECOMBINATION REPAIR	0.077	0.238
REACTOME E2F MEDIATED REGULATION OF DNA REPLICATION	0.078	0.244
REACTOME GLUCOSE TRANSPORT	0.079	0.228
REACTOME P53 INDEPENDENT DNA DAMAGE RESPONSE	0.079	0.259
REACTOME LATE PHASE OF HIV LIFE CYCLE	0.080	0.238
REACTOME TELOMERE MAINTENANCE	0.081	0.330
REACTOME ELONGATION AND PROCESSING OF CAPPED TRANSCRIPTS	0.084	0.222
KEGG GLYOXYLATE AND DICARBOXYLATE METABOLISM	0.088	0.388
KEGG PORPHYRIN AND CHLOROPHYLL METABOLISM	0.089	0.381
BIOCARTA TNFR1 PATHWAY	0.094	0.221
KEGG VALINE LEUCINE AND ISOLEUCINE DEGRADATION	0.096	0.231
REACTOME TRANSCRIPTION COUPLED NER	0.097	0.217
REACTOME HIV1 TRANSCRIPTION INITIATION	0.098	0.224
REACTOME INTRINSIC PATHWAY FOR APOPTOSIS	0.098	0.380
REACTOME ELECTRON TRANSPORT CHAIN	0.099	0.232
REACTOME RNA POLYMERASE III TRANSCRIPTION INITIATION	0.101	0.264
REACTOME CENTROSOME MATURATION	0.104	0.262
BIOCARTA CASPASE PATHWAY	0.107	0.263
KEGG HOMOLOGOUS RECOMBINATION	0.109	0.262
REACTOME REV MEDIATED NUCLEAR EXPORT OF HIV1 RNA	0.118	0.240
REACTOME LOSS OF NLP FROM MITOTIC CENTROSOMES	0.125	0.292
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	0.127	0.225
REACTOME CHOLESTEROL BIOSYNTHESIS	0.127	0.257
KEGG ONE CARBON POOL BY FOLATE	0.127	0.312
KEGG FATTY ACID METABOLISM	0.127	0.385
REACTOME E2F TRANSCRIPTIONAL TARGETS AT G1 S	0.129	0.300
KEGG CELL CYCLE	0.132	0.376
REACTOME CAM PATHWAY	0.135	0.466
REACTOME METABOLISM OF PROTEINS	0.136	0.296
REACTOME_DUAL_INCISION_REACTION_IN_GG_NER	0.142	0.219
REACTOME RNA POL II CTD PHOSPHORYLATION AND INTERACTION WITH CE	0.145	0.296
REACTOME PURINE METABOLISM	0.147	0.293
REACTOME RNA POLYMERASE I CHAIN ELONGATION	0.149	0.377
REACTOME MICRORNA BIOGENESIS	0.149	0.387

Supplementary Table 3. Gene sets enriched in MU.

GS follow link to MSigDB	NOM p-val	FDR q-val
BIOCARTA_AGR_PATHWAY	0.000	0.266
REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_ALPHA	0.000	0.282
KEGG_RETINOL_METABOLISM	0.000	0.205
REACTOME_BIOLOGICAL_OXIDATIONS	0.000	0.810
REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUNDS	0.000	0.808
KEGG_BETA_ALANINE_METABOLISM	0.000	0.787
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	0.000	0.702
BIOCARTA_NO1_PATHWAY	0.000	0.637
REACTOME_BASIGIN_INTERACTIONS	0.009	0.736
REACTOME_RHO_GTPASE_CYCLE	0.011	0.779
BIOCARTA_AT1R_PATHWAY	0.018	0.486
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	0.021	0.648
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	0.023	0.910
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	0.028	0.709
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	0.033	0.855
BIOCARTA_ALK_PATHWAY	0.036	0.672
KEGG_STEROID_HORMONE_BIOSYNTHESIS	0.042	0.688
BIOCARTA_RAC1_PATHWAY	0.043	0.683
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	0.046	0.682
KEGG_DILATED_CARDIOMYOPATHY	0.048	0.720
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	0.048	0.748
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	0.050	0.659
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	0.053	0.724
KEGG_ARGININE_AND_PROLINE_METABOLISM	0.053	0.765
REACTOME_PHASE_II_CONJUGATION	0.057	0.629
REACTOME_SIGNALLING_BY_NGF	0.063	0.831
KEGG_CARDIAC_MUSCLE_CONTRACTION	0.064	0.645
BIOCARTA_P38MAPK_PATHWAY	0.064	0.698
BIOCARTA_CCR3_PATHWAY	0.065	0.665
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	0.065	0.691
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.065	0.768
REACTOME_MYD88_CASCADE	0.072	0.685
ST_ADRENERGIC	0.073	0.701
KEGG_GAP_JUNCTION	0.073	0.731
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	0.074	0.663
BIOCARTA_NFAT_PATHWAY	0.077	0.778
REACTOME_ACTIVATED_TLR4_SIGNALLING	0.082	0.657
KEGG_RENIN_ANGIOTENSIN_SYSTEM	0.083	0.762
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	0.088	0.654
KEGG_REGULATION_OF_AUTOPHAGY	0.091	0.653
REACTOME_TIGHT_JUNCTION_INTERACTIONS	0.093	0.773
BIOCARTA_ERK_PATHWAY	0.096	0.817
KEGG_VIRAL_MYOCARDITIS	0.099	0.794
REACTOME_HEMOSTASIS	0.103	0.788
REACTOME_TOLL LIKE RECEPTOR 9 CASCADE	0.113	0.798
KEGG_NOTCH_SIGNALING_PATHWAY	0.116	0.769
REACTOME_SMOOTH_MUSCLE_CONTRACTION	0.120	0.814
SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO_GTPASES	0.122	0.784
REACTOME_NCAM1_INTERACTIONS	0.123	0.822
BIOCARTA_ACH_PATHWAY	0.124	0.765
BIOCARTA_CARDIACEGF_PATHWAY	0.126	0.739
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	0.128	0.775

REACTOME DIABETES PATHWAYS	0.136	0.809
REACTOME MUSCLE CONTRACTION	0.139	0.812
REACTOME NRAGE SIGNALS DEATH THROUGH JNK	0.145	0.826
REACTOME METAL ION SLC TRANSPORTERS	0.147	0.741
REACTOME FORMATION OF A POOL OF FREE 40S SUBUNITS	0.149	0.675
ST INTEGRIN SIGNALING PATHWAY	0.149	0.823
REACTOME CELL DEATH SIGNALLING VIA NRAGE NRIF AND NADE	0.151	0.775
KEGG INSULIN SIGNALING PATHWAY	0.153	0.772
KEGG TYROSINE METABOLISM	0.155	0.750
BIOCARTA SPRY PATHWAY	0.161	0.829
REACTOME CREB PHOSPHORYLATION THROUGH THE ACTIVATION OF CAMKII	0.166	0.743
BIOCARTA BIOPEPTIDES PATHWAY	0.171	0.783
REACTOME P75 NTR RECEPTOR MEDIATED SIGNALLING	0.171	0.823
REACTOME PEPTIDE CHAIN ELONGATION	0.174	0.802
REACTOME PLATELET DEGRANULATION	0.178	0.766
ST MYOCYTE AD PATHWAY	0.178	0.752
REACTOME NCAM SIGNALING FOR NEURITE OUT GROWTH	0.182	0.788
BIOCARTA RHO PATHWAY	0.182	0.779
REACTOME TOLL LIKE RECEPTOR 4 CASCADE	0.183	0.759
KEGG LINOLEIC ACID METABOLISM	0.183	0.824
REACTOME PLATELET ACTIVATION	0.185	0.814
REACTOME NUCLEOTIDE LIKE PURINERGIC RECEPTORS	0.198	0.738
REACTOME SIGNALING BY NOTCH	0.201	0.755
KEGG TIGHT JUNCTION	0.205	0.740
KEGG CALCIUM SIGNALING PATHWAY	0.205	0.887
REACTOME FORMATION OF PLATELET PLUG	0.218	0.849
REACTOME CD28 CO STIMULATION	0.219	0.786
BIOCARTA MYOSIN PATHWAY	0.221	0.779
ST JNK MAPK PATHWAY	0.221	0.816
KEGG PRIMARY BILE ACID BIOSYNTHESIS	0.230	0.799
KEGG DRUG METABOLISM CYTOCHROME P450	0.232	0.828
REACTOME SIGNALING BY EGFR	0.232	0.828
BIOCARTA ECM PATHWAY	0.234	0.800
REACTOME VIRAL MRNA TRANSLATION	0.240	0.796
REACTOME LIPOPROTEIN METABOLISM	0.248	0.826
REACTOME G ALPHA Q SIGNALLING EVENTS	0.248	0.867
REACTOME METABOLISM OF AMINO ACIDS	0.251	0.884
REACTOME MYOGENESSIS	0.255	0.840
BIOCARTA HDAC PATHWAY	0.258	0.882
REACTOME GTP HYDROLYSIS AND JOINING OF THE 60S RIBOSOMAL SUBUNIT	0.260	0.842
REACTOME TRANSLATION	0.261	0.758
BIOCARTA MCALPAIN PATHWAY	0.262	0.817
REACTOME INTRINSIC PATHWAY	0.268	0.821
REACTOME RAS ACTIVATION UOPN CA2 INFUX THROUGH NMDA RECEPTOR	0.268	0.787
KEGG LEUKOCYTE TRANSENDOTHELIAL MIGRATION	0.274	0.883
REACTOME REGULATION OF INSULIN LIKE GROWTH FACTOR ACTIVITY BY INSULIN LIKE GROWTH FACTOR BINDING PROTEINS	0.280	0.813
KEGG CYTOSOLIC DNA SENSING PATHWAY	0.286	0.821
REACTOME G ALPHA 12 13 SIGNALLING EVENTS	0.288	0.873
BIOCARTA CYTOKINE PATHWAY	0.299	0.878
BIOCARTA PGC1A PATHWAY	0.300	0.830
KEGG OXIDATIVE PHOSPHORYLATION	0.300	0.880

Supplementary Table 4. Quantification of satellite, mural cells of CD146⁺/CD34⁺ cells in vivo SCID beige/ctx.

<i>Donor cell types huCD146⁺/CD34⁺</i>	<i>Strain of mice</i>	<i>delivery</i>	<i>Number of injected cells</i>	<i>days after injection</i>	<i>% positive cells (mean±dev st)</i>
huCD56 (N-CAM)	SCID beige	i.m.	1x10 ⁶	40	8.8 ± 2
huCD146 (M-CAM)	SCID beige	i.m.	1x10 ⁶	40	0.03 ± 0.01
huLamin A/C	SCID beige	i.m.	1x10 ⁶	40	9.2 ± 2.7

i.m., single intra-muscular injection into tibialis anterior; ctx, cardiotoxin.

Supplementary Table 5. Quantification of satellite, mural cells of CD146⁺/CD34⁺ cells in vivo SCID/mdx.

<i>Donor cell types huCD146⁺/CD34⁺</i>	<i>Strain of mice</i>	<i>delivery</i>	<i>Number of injected cells</i>	<i>days after injection</i>	<i>% positive cells (mean±dev st)</i>
huCD56 (N-CAM)	SCID/mdx	i.a.	2x(5x10 ⁵)	15	2.6 ± 1.8
huLamin A/C	SCID/mdx	i.a.	2x(5x10 ⁵)	15	3 ± 1.4

i.a., two consecutive intra-femoral artery injections.

Supplementary Table 6. Regenerative efficiency of CD146⁺/CD34⁺ cells in vivo.

<i>Donor cell types huCD146⁺/CD34⁺</i>	<i>Strain of mice</i>	<i>delivery</i>	<i>Number of injected cells</i>	<i>days after injection</i>	<i>N° positive fibers per muscle (mean±dev st)</i>
huSpectrin	SCID beige	i.m.	1x10 ⁶	40	406 ± 47
huDystrophin 2	SCID/mdx	i.a.	2x(5x10 ⁵)	15	543 ± 51.8
huDystrophin 3	SCID beige	i.m	1x10 ⁶	40	503 ± 28.5

i.m., single intra-muscular injection into *tibialis anterior*; i.a., two consecutive intra-femoral artery injections. In all injected animals, only the *tibialis anterior* was analysed.

Supplementary Table 7. CFE assay for unsorted, CD146⁺ and CD146⁻ muscle cells.

<i>Cells plated</i>	<i>Cell density (cells/cm²)</i>	<i>CFU-F</i>		
		Unsorted	CD146 ⁺	CD146 ⁻
1x10 ²	1.6	2 ± 1.7	24 ± 21	0
2x10 ²	3.3	ND	82 ± 2	0
1x10 ³	16	10.3 ± 0.6	confluent	0
1x10 ⁴	160	90 ± 20.5	confluent	0
1x10 ⁵	1600	293 ± 47.4	ND	0

CFU-F, Colony Forming Unit-Fibroblastic; ND, not determined. Data are expressed as mean ± SEM. n=3

Supplementary Table 8. CFE assay for sorted CD146^{+/−} and CD56^{+/−} muscle cells.

Cells plated	Cell density (cells/cm ²)	CFU-F		
		CD146 ⁺ /56 [−]	CD146 [−] /56 ⁺	CD146 [−] /56 [−]
1x10 ²	1.6	41.7 ± 4	0	ND
2x10 ²	3.3	83.5 ± 8	0	ND
3x10 ²	5	117.3 ± 0.4	0	ND
5x10 ²	8.3	195.5 ± 0.7	0	0
1x10 ³	16	ND	ND	0
1x10 ⁴	160	ND	ND	0
1x10 ⁵	1600	ND	ND	1 ± 1

CFU-F, Colony Forming Unit-Fibroblastic; ND, not determined. Data are expressed as mean ± SEM. n=2

Supplementary Table 9. CFE assay for sorted CD146^{+/−} and CD34^{+/−} muscle cells.

Cells plated	Cell density (cells/cm ²)	CFU-F			
		CD146 ⁺ /34 [−]	CD146 ⁺ /34 ⁺	CD146 [−] /34 [−]	CD146 [−] /34 ⁺
1x10 ²	1.6	16.5 ± 6.4	4 ± 1.5	0	0
3x10 ²	5	31.5 ± 2.1	12 ± 4.2	0	0
5x10 ²	8.3	52.5 ± 3.5	14 ± 1.4	0	0
1x10 ³	16	ND	ND	0	0
1x10 ⁴	160	ND	ND	0	0
1x10 ⁵	1600	ND	ND	0	1 ± 1

CFU-F, Colony Forming Unit-Fibroblastic; ND, not determined. Data are expressed as mean ± SEM. n=2

Supplementary Table 10. CFE assay for sorted CD146⁺/ALP^{+/-} and CD146⁻/ALP⁺ muscle cells.

Cells plated	Cell density (cells/cm ²)	CFU-F	
		CD146 ⁺ /ALP ^{+/-}	CD146 ⁻ /ALP ⁺
5	0.083	2 ± 0.7	0
50	0.83	21 ± 0.7	0
1x10 ²	1.6	39.8 ± 0.4	0
2x10 ²	3.3	79.5 ± 0.7	0
3x10 ²	5	ND	8.2 ± 8.8
1x10 ³	16	ND	28 ± 28

CFU-F, Colony Forming Unit-Fibroblastic; ND, not determined. Data are expressed as mean ± SEM. n=2

Supplementary Table 11. Antibodies used for flow cytometry and fluorescence-activated cell sorting.

<i>Antigen</i>	<i>Type</i>	<i>Label</i>	<i>Clone/Cat#</i>	<i>Distributor</i>
CD34 (gp 105-120)	MC	FITC	581	BD Biosciences
CD45 (LCA, T200)	MC	FITC	HI30	BD Biosciences
CD56 (NCAM)	MC	PE	MY31	R&D Systems
CD56 (NCAM)	MC	APC	B159	BD Biosciences
CD73 (ecto-5'-nucleotidase)	MC	PE	AD2	BD Biosciences
CD90 (Thy-1)	MC	PE	5E10	eBiosciences
CD105 (Endoglin)	MC	NC	266	BD Biosciences
CD146 (MUC-18, S-endo 1, MCAM)	MC	PE	P1H12	BD Biosciences
ALP (alkaline phosphatase)	MC	NC	B4-78	R&D Systems
HLAI	MC	PE	G46-2.6	BD Biosciences
HLAII	MC	PE	G46-6	BD Biosciences
PAX-7	MC	NC	EPR3353	Abcam

MC, mouse monoclonal; PE, phycoerythrin; FITC, fluorescein isothiocyanate; NC, non-conjugated; APC, allophycocyanin

Supplementary Table 12. Antibodies used for immunohistochemistry and immunocytochemistry.

<i>Antigen</i>	<i>Type</i>	<i>Clone</i>	<i>Cat#</i>	<i>Distributor</i>
Hu CD146 (MCAM)	MC	Clone N1238 IgG1	NCL-CD146	Novocastra
Hu CD56 (NCAM)	MC	Clone CD564 IgG2b	NCL-CD56-504	Novocastra
Hu CD34	MC	Clone QBEnd/10 IgG1	NCL-END	Novocastra
MyHC (MF20)	MC	IgG2b	-----	Hybridoma Bank, DSHB , NIH
Hu Lamin A/C	MC	Clone 636 IgG2b	NCL-LAM-A/C	Novocastra
Hu Dystrophin 2	MC	Clone Dy8/6C5 IgG1	NCL-DYS2	Novocastra
Hu Dystrophin 3	MC	Clone Dy10/12B2 IgG2a	NCL-DYS3	Novocastra
Hu Spectrin	MC	Clone RBC2/3D5 IgG2b	NCL-SPEC1	Novocastra
Laminin	PC	-----	L9393	Sigma
Myf-5	PC	-----	SC-302	Santa Cruz Biotech
GFP	PC	-----	A6455	Invitrogen
Desmin	MC	Clone D33 IgG1	MO760	Dako
ALP (LF-47)	PC	-----	-----	Gift from L.W. Fisher, NIDCR, NIH
PAX-7	MM	IgG1	-----	Hybridoma Bank, DSHB, NIH
PAX-3	MC	IgG2a	-----	Hybridoma Bank, DSHB, NIH
Col II	PC	-----	ab53047	Abcam

MC, mouse monoclonal; PC, rabbit polyclonal antiserum

Supplementary Table 13. Primers used for semiquantitative PCR.

Name	Sequence	Description, genbank accession number and reference	Product size
GAPDH-For	5'-CGG GAA GCT TGT GAT CAA TGG-3'	Human glyceraldehyde-3-phosphate dehydrogenase, mRNA [M17851]	358bp
GAPDH-Rev	5'-GGC AGT GAT GGC ATG GAC TG-3'		
h-β-actin For	5'-CCGACAGGATGCAGAAGGAG-3'	Homo sapiens actin, beta (ACTB), mRNA [NM_001101]; (De Bari <i>et al.</i> , 2003)	662 bp
h-β-actin Rev	5'-GGCACGAAGGCTCATCATTC-3'		
h-PCNA For	5'-GGAGAACTTGGAATGGAAAC-3'	Homo sapiens proliferating cell nuclear antigen (PCNA), transcript variant 1 and transcript variant 2, mRNA [NM_002592] [NM_182649]; (De Bari <i>et al.</i> , 2003)	548 bp
h-PCNA Rev	5'-CTGCATTTAGAGTCAAGACCC-3'		
h-Myf5 For	5'-TGAGAGAGCAGGTGGAGAACTAC-3'	Homo sapiens myogenic factor 5 (MYF5), mRNA [NM_005593]; (De Bari <i>et al.</i> , 2003)	417 bp
h-Myf5 Rev	5'-GCCTTCTTCGTCCTGTGTATTAG-3'		
h-Myogenin For	5'-GCCACAGATGCCACTACTTC-3'	Homo sapiens myogenin (myogenic factor 4) (MYOG), mRNA [NM_002479]; (De Bari <i>et al.</i> , 2003)	565 bp
h-Myogenin Rev	5'-CAACTTCAGCACAGGAGACC-3'		
h-Desmin For	5'-CCTACTCTGCCCTCAACTTC-3'	Homo sapiens desmin (DES), mRNA [NM_001927]; (De Bari <i>et al.</i> , 2003)	519 bp
h-Desmin Rev	5'-AGTATCCCAACACCCTGCTC-3'		
h-SkM-actin For	5'-CGTGGCTACTCCTTCGTGAC-3'	Homo sapiens actin, alpha 1, skeletal muscle (ACTA1) [NM_001100]; (De Bari <i>et al.</i> , 2003)	597 bp
h-SkM-actin Rev	5'-CCCATTGAGAAGATTCGTCG-3'		
h-MCK For	5'-GGCACAATGACAACAAGAGC-3'	Homo sapiens creatine kinase, muscle (CKM), mRNA [NM_001824]; (De Bari <i>et al.</i> , 2003)	721 bp
h-MCK Rev	5'-GAAAAGAAGAGGACCCTGCC-3'		
h-MyHC-IIx/d For	5'-ATAGGAACACCCAAGCCATC-3'	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA [NM_005963]; (De Bari <i>et al.</i> , 2003)	599 bp
h-MyHC-IIx/d Rev	5'-TTTGCGTAGACCCTTGACAG-3'		
MRF4(MYF6) For	5'-GATCCCACCGACCCTTCCTGG-3'	Homo sapiens myogenic factor 6 (herculin) (MYF6), mRNA [NM_002469]	215 bp
MRF4(MYF6) Rev	5'-GAGGCTAGACCTAAGCCACTCGC-3'		
MYOD For	5'-CGATATAACAGGTGCTCTGAGGG-3'	Homo sapiens myogenic differentiation 1 (MYOD1), mRNA [NM_002478]	430 bp
MYOD Rev	5'-GGGTGGGTTACGGTTACACCTGC		
PAX7 For	5'-GTACGGCCAGAGTGAGTGCCTG-3'	Homo sapiens paired box gene 7 (PAX7), transcript variant 2, mRNA [NM_013945]	245 bp
PAX7 Rev	5'-CTGTTGGAGCCATAGTACGGAAG-3'		
PAX3 For	5'-ACCACATCCGCCACAAGA-3'	Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), all the isoforms	303bp
PAX3 Rev	5'-TGGAACCTCACTGACGGCAC-3'		
M-cadherin For	5'-CCCGTGCGGGTTGGAGTACGG-3'	Homo sapiens cadherin 15, M-cadherin (myotubule) (CDH15), mRNA [NM_004933]	360 bp
M-cadherin Rev	5'-CACTGGTAGGAGGCAAAGGTGGG-3'		