DIRECTED DIFFERENTIATION OF HUMAN EMBRYONIC STEM CELLS INTO HAEMATOPOIETIC AND DEFINITIVE ENDODERMAL LINEAGES

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SUMMARY

Human embryonic stem cells (hESCs) are derived from the inner cell mass of a 5-day old blastocyst. hESCs possess the cardinal properties of unlimited self-renewal and pluripotency which enable them to give rise to the approximately 220 different cell types that comprise the human body. Theoretically, harnessing this property of hESCs could provide an inexhaustible source of cell therapy material for diseases like diabetes, Parkinson's disease, etc.

In order to assess the usefulness of hESCs in regenerative medicine, I investigated the ability of two cell lines– hES2 and hES3– to generate derivatives of mesoderm and endoderm *in vitro*. Differentiation into these particular lineages was of interest to me as hESC-derived β-like cells could be used as cell therapy for Type I Diabetes and haematopoietic cells from the same source could possibly be used to induce transplantation tolerance in a host receiving the allogeneic hESC-derived cell therapy graft. To this end, I evaluated published strategies that used stromal cell support or cytokines to differentiate hESCs or hESC-EBs into haematopoietic-like cells. Differentiation either on a cell layer of OP9 stroma or in the presence of cytokines like SCF, IL-4, TPO and Flt3L generated haematopoietic cells from both hES2 and hES3 EBs. The haematopoietic identity of these cells was established by the expression of relevant markers like CD45, CD14, CD34, CD83 and CD86 and the formation of colony forming units in methylcellulose cultures. The combination and concentrations of the cytokines used or the stroma itself seemed to bias the differentiation towards a granulocytic fate as no erythroid cells were formed at any stage. This finding might also indicate the restricted differentiation potential of hES2 and hES3. Though not efficient, the differentiation achieved in this study provides proof-of-principle that these 2 cells lines can be directed to a haematopoietic fate.

A simultaneous investigation of the endodermal potential of these cells resulted in the development of a three-dimensional differentiation strategy in which hESC-EBs embedded in Matrigel were exposed to Activin A and Bmp4 to generate definitive endoderm. Differentiation progressed in a developmentally relevant sequence with the formation of *TBRA*-expressing primitive streak-like cells followed by *FOXA2*- and *SOX17*-expressing endodermal cells. These cells differentiated further in the presence of growth factors that promote pancreatic development and maturation to generate $PDX1^{+}$ pancreatic progenitors which gave rise to insulin-secreting β-like cells albeit at a low efficiency. The unexpected combinatorial effect of Activin A and Bmp4 on the formation of endoderm was investigated in detail using molecular techniques that dissected the individual role of these factors in the differentiation. However, no clear mechanism of action was evident from these studies. A global view of the differentiation was obtained using microarray technology which revealed expression of novel genes and novel expression patterns of known genes in this system. Expression analysis of a few selected genes in the early mouse embryo showed hitherto uncharacterized expression domains some of which may be relevant to endoderm formation. The significance of these genes in the specification of endoderm will be addressed in future studies employing other model systems like *Xenopus* and Zebrafish.

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α – Alpha

β – Beta

Δ – Delta

δ – Delta

μ – Mu

° – Degree

CHAPTER 1: GENERAL INTRODUCTION

1.1. Embryonic stem cells

The isolation of mouse and human embryonic stem cells (ES cells) heralded a new era in regenerative medicine, raising hopes for effective cellular therapies to treat conditions like diabetes and heart disease. Working with the simple goal of replacing defective, diseased or lost cell types, embryonic stem cell-based therapy promised the repair of damaged tissue/s or organs of the human body. ES cells are derived from the inner cell mass (ICM) of the blastocyst-stage pre-implantation embryo which gives rise to the approximately 220 specialised cell types in the human body. ES cells possess the cardinal properties of self-renewal and pluripotency which enable them to give rise to all the cells that comprise the vertebrate body. The first successful isolation and study of pluripotent ES cells was accomplished in the mouse in 1981 (Evans and Kaufman 1981; Martin 1981). The ease with which mouse embryonic stem cells (mESCs) can be derived and manipulated has made them an ideal model system for the study of developmental biology. *In vitro* differentiation of mESCs has successfully given rise to cells of the various germ layers and provided valuable insights into the events in early development of the embryo like hemangioblast development (Keller 2005; Keller 1995). mESCs retain their pluripotency despite extended *in vitro* culture and generate all three germ layers and the germ line when re-introduced into mouse blastocysts (Bradley *et al*. 1984).

ES cell research achieved another milestone in 1994 when Bongso *et al*. (1994) reported the isolation and culture of ICM cells with stem cell-like morphology from human blastocysts (**Fig 1.1A**) though cultures failed beyond 2 passages. The first long-term culture (4-5 months) of human embryonic stem cells (hESCs) was accomplished using mouse fibroblast feeder layers by Thomson *et al*. (1998) (**Fig 1.1B**). These cells show characteristic expression of pluripotency markers like the

transcription factor *OCT4/ POU5F1*[1] and the cell surface antigen Tra1-60 (**Fig 1.1 D-E**). Unlike mESCs the pluripotent nature of hESCs cannot be demonstrated through chimera formation as there are obvious ethical concerns in generating mosaic human embryos that require development *in utero*. Therefore, *in vitro* differentiation into the three embryonic germ layers– ectoderm, mesoderm and endoderm– and *in vivo* teratoma formation assays are used to substantiate pluripotency of hESCs. For *in vitro* culture of hESCs, mouse or human primary "feeder" monolayers are still popular though substrates like Matrigel are also widely used. In addition to the traditional method of mechanical dissection, enzymes like Trypsin and Collagenase IV have been successfully used for passaging hESCs. Culture media also play an important role in maintenance of the undifferentiated state. For example, unlike mouse ES cells, hESCs do not require LIF (leukemia inhibitory factor) or Bmp4 (bone morphogenetic protein 4) for maintenance of self-renewing, undifferentiated cultures. A combination of Activin A/ Nodal and Fgf2 has been shown to be sufficient to maintain hESCs in the pluripotent state even in the absence of feeders, fetal bovine serum or Matrigel (Xiao *et al*. 2006; Vallier *et al*. 2005; James *et al*. 2005; Beattie *et al*. 2005).

If mouse ES cells are grown in suspension cultures on low-attachment surfaces in the absence of feeder support, they form aggregates of differentiating cells called embryoid bodies or EBs (**Fig 1.1C**) (Reubinoff *et al*. 2000; Doetschman *et al*. 1985; Evans 1981). Various precursors representing the three germ layers including haematopoietic and endothelial progenitors emerge as these EBs spontaneously differentiate (Keller 1995).

[1] Gene names are italicized. Human genes- all capital letters eg. *OCT4*. Mouse genes- first letter capital eg. *Oct4*.

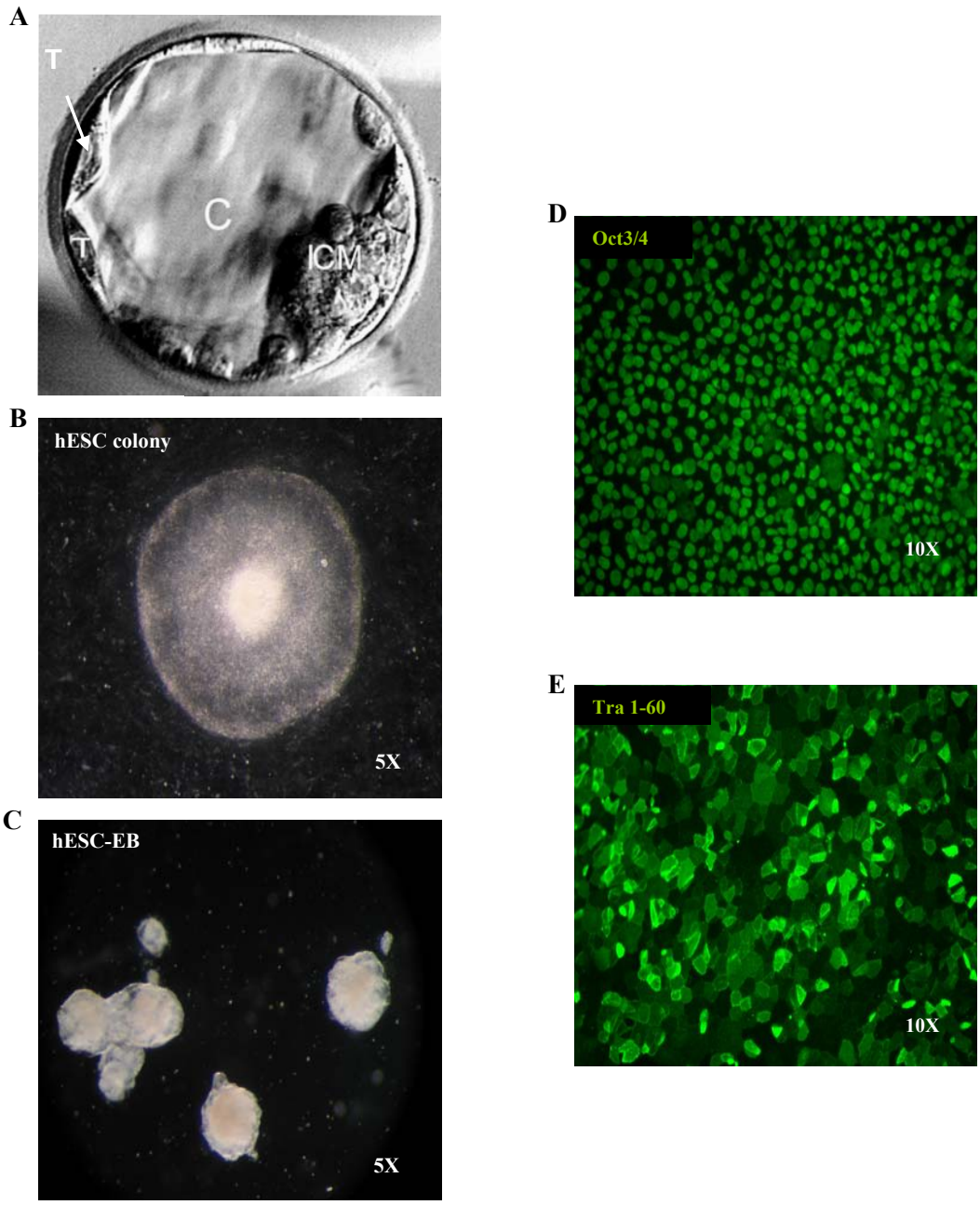


Figure 1.1. Embryonic origin of human embryonic stem cells and their in vitro characterisation. (A) 5-day human blastocyst with inner cell mass (ICM), blastocoel cavity (C) and trophectoderm (T). Image from the Advanced Fertility Centre, Chicago http://www.advancedfertility.com/blastocystimages.htm. **(B)** A single hESC colony, here hES3, maintained on a mitotically inactivated mouse embryonic fibroblast (MEF) monolayer. Typically a hESC colony grown under these conditions has the dense, white 'central button' surrounded by a thinner halo of cells with a crisp border. **(C)** hESC-derived embryoid bodies (EBs) in suspension culture. **(D, E)** Immunostaining performed on hESC colonies for pluripotency markers. Nuclear staining for transcription factor *OCT4* (**D**) and cell surface staining for Tra 1-60 **(E)** show that more than 90% of the cells in all colonies stain positive for these two markers.

Detailed investigation of the differentiating ES/ EB system suggests that it recapitulates to a limited degree the early events of embryonic development (Dvash and Benvenisty 2004; Dvash *et al*. 2004; Rust *et al*. 2006). EBs derived from hESCs organise themselves in a manner reminiscent of the early post-implantation mouse embryo, with features like an outer jacket of extraembyonic (visceral) endoderm (Rust *et al*. 2006). These similarities prompted the use of the EB system as a model to stimulate *in vitro* the early events of mammalian axis specification and germ layer patterning. Several methods of EB formation– in hanging drops, in low-attachment plates, in 3D matrices (synthetic and natural) and the use of various growth factors in all or some of these methods– are commonly used to induce differentiation.

Though they were thought to be equivalent to the ICM, it was suggested that ES cells are cell culture artefacts as they adapt well to *in vitro* growth conditions and show properties not usually associated with the embryo such as dependence on exogenous cytokines/ growth factors (Buehr *et al*. 2003; Smith 2001; Rossant 2001). Later studies provided evidence that ES cells likely bear closer resemblance to embryonic germ (EG) cells as several germ cell markers like *Dppa3* (*Stella*) were expressed in ES cells (Zwaka and Thomson 2005). Derivation of pluripotent cell lines from the mouse epiblast, called EpiSCs, brought to light similarities between these cells and hESCs (Tesar *et al*. 2007; Brons *et al*. 2007). EpiSCs and hESCs have the ability to give rise to trophectoderm in the presence of Bmp4 which mESCs do not possess (Xu *et al*. 2002; Beddington and Robertson 1989). Another similarity between these two cell types is the requirement for Activin A/ Nodal signaling to maintain pluripotency, a property that has been previously demonstrated for hESCs (Vallier *et a*l. 2005). Inhibition of Activin signaling resulted in rapid downregulation of pluripotency genes in both cell types. This may reflect the embryonic stage to which

hESCs are equivalent, since Activin/ Nodal signaling is known to be required for maintenance of pluripotency in the epiblast of the post-implantation embryo (Brennan *et al*. 2001). The importance of Activin/ Nodal signaling in the maintenance of hESC pluripotency has been re-iterated in recent studies detailing the derivation and maintenance of induced pluripotent stem (iPS) cells (Takahashi *et al*. 2007; Takahashi and Yamanaka 2006). iPS cells are generated from mouse and human adult fibroblasts by nuclear reprogramming using a few critical transcription factors like *SOX2*, *OCT3/4*, *KLF4* and *C-MYC*. Human iPS cells were found to be similar to hESCs in several aspects including morphology, growth kinetics, cell-surface antigen profile and gene expression. In addition it has been shown that iPS cells can differentiate into the three germ layers *in vivo* and form teratomas identical to hESCs. A family tree of the various embryonic and extraembryonic lineages summarises these relationships (**Fig 1.2**). The lineage tree emphasizes that as the biology of ES cells continues to be unravelled, there is mounting confidence that culture regimes can be developed which direct pluripotent ES cells toward a desired cell fate that would be therapeutically useful.

Much progress has been made towards gaining a better understanding of hESC biology and translating the technology from the bench to the bedside. However, the hESC lines on which most of these studies were performed might have restricted use in the clinic, as they have all come in contact with materials or reagents of foreign origin (Bongso *et al*. 2008; Hentze *et al*. 2007). Recently, this presumed roadblock was deemed acceptable when the Food and Drug Administration (FDA), USA granted permission for the use of oligodendrocyte cells derived from hESCs for Phase I clinical trials to treat patients with spinal cord injury. GRNOPC1, oligodendroglial progenitor cells, were derived from the H7 hESC line (Thomson *et al*. 1998) and have

been demonstrated to support re-myelination and nerve growth stimulation in animal models of acute spinal cord injury (Kierstead *et al*. 2005). The current clinical trial will be an attempt to demonstrate the safety of using these cells in humans though it has been shown to elicit a poor immune response in the immune-deficient animal model (Okamura *et al*. 2007).

The isolation of clinically compliant hESC lines was recently achieved (Crook *et al*. 2007). Six hESC lines were derived on clinical grade human fibroblasts, Ortec 143, and maintained in chemically defined medium containing Knockout Serum Replacement supplemented with basic fibroblast growth factor (bFGF). None of the reagents used during derivation and expansion were of animal origin and the entire process was carried out under cGMP (current good manufacturing practice) guidelines. Even with derivation of qualified lines and defined culture methods, the recurring challenges of directing the differentiation of hESCs to generate cell types in numbers sufficient for clinical applications and ensuring acceptance of the transplant and preventing rejection by the recipient's immune system remain. Harnessing and understanding the differentiation potential of hESCs and employing that knowledge to gain insight into mammalian development is the focus of the thesis. Such studies require experimental strategies that are guided by the knowledge of how a vertebrate embryo develops and forms a complex organism. Hence it is important to review key aspects of the mammalian developmental sequence especially, formation of the three primary germ layers in the embryo.

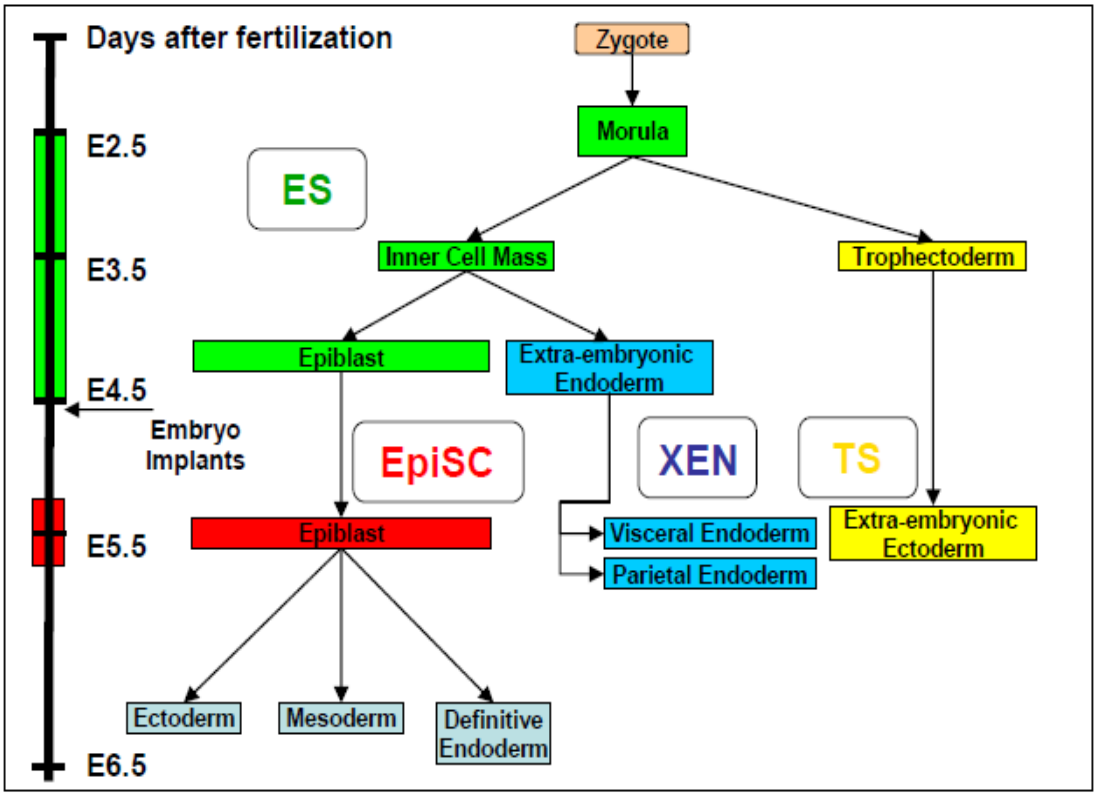
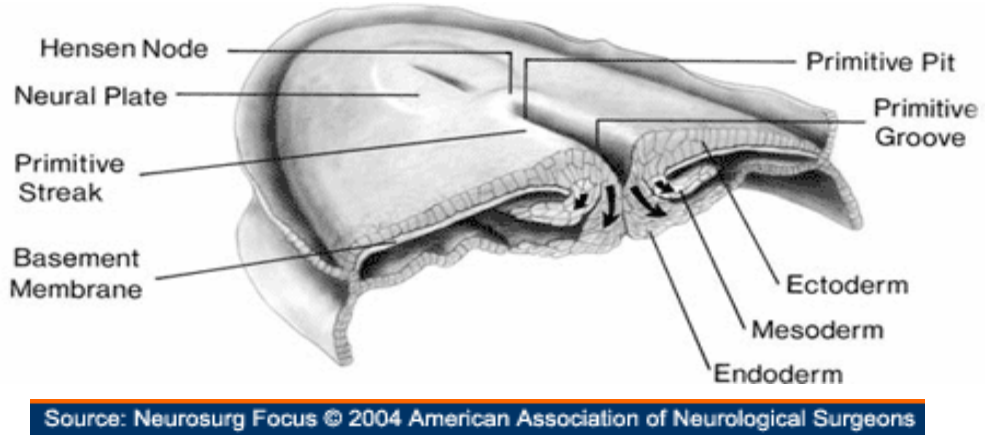


Figure 1.2. Lineage tree of embryo-derived cells and cell lines. The various stages of embryonic development from fertilization to E6.5 are represented in this image. Embryonic Stem (ES) cells are derived from the inner cell mass while epiblast stem cells (EpiSCs) are of epiblast origin. Human ES cells (hESCs) and mouse EpiSCs have been found to share several characteristics which imply that hESCs might actually be derivatives of epiblast-stage embryos. The extraembryonic endoderm is the source of XEN cells while TS cells represent the extraembryonic ectoderm lineage. Schematic used with permission from Tesar *et al*. 2007, *Nature*.

1.2. Gastrulation– formation of mesoderm and endoderm in the embryo

Gastrulation is defined by a series of complex morphogenetic events in combination with cell proliferation and differentiation that generate the three embryonic germ layers and establish a vertebrate body plan (Arnold and Robertson 2009; Tam and Loebel 2007; Rossant and Tam 2004). In the mouse embryo gastrulation is initiated by the recruitment of epiblast cells to the primitive streak around E6.5 **(Fig 1.3)**. There, epiblast cells undergo an epithelial to mesenchymal transition (EMT) as they ingress through the primitive streak, emerging as definitive endoderm (DE) and the mesoderm (Tam and Beddington 1992; Lawson *et al*. 1991). Mesoderm is formed as an epithelial sheet that expands from either side of the primitive streak (Tam and Behringer 1997). Extensive studies on cells of the cardiac mesoderm showed that the timing of ingression through the streak and the position of these cells in the epiblast determines their lineage fate (Tam and Behringer 1997; Tam and Zhou 1996; Lawson *et al*. 1991). The newly formed motile mesoderm migrates laterally between the outer visceral endoderm (VE) layer and the epiblast, while the definitive endoderm moves to the outer surface of the embryo by displacing the visceral endoderm proximally (Lawson *et al*. 1986). However, recent work from Kwon *et al*. (2008) suggests that the DE is formed by intercalation of epiblast cells with the underlying VE and not by complete displacement of the visceral layer. This work is discussed in more detail in section 1.5. Understanding the complex events that characterise gastrulation is critical for the creation of experimental strategies to generate relevant cell types for therapeutic use (discussed below).

A



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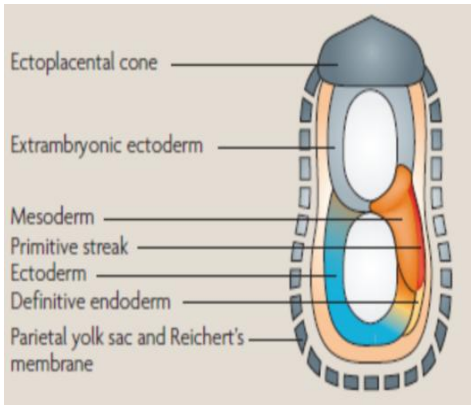

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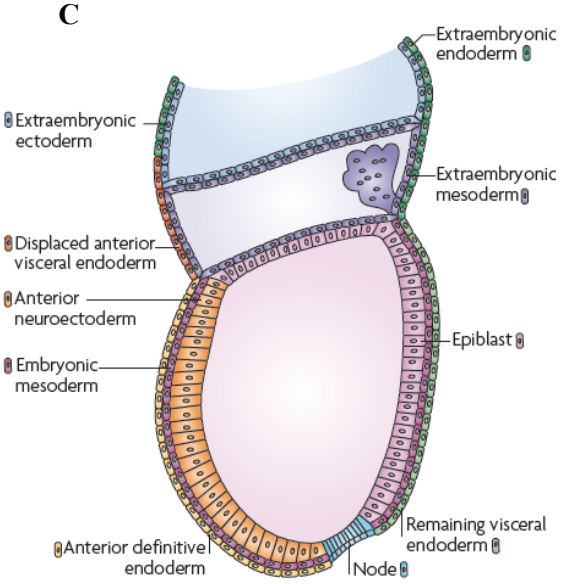


Figure 1.3. Gastrulation and specification of the germ layers. (A) Gastrulation in the human embryo results in the specification of the three germ layers. During this process, prospective endodermal and mesodermal cells ingress through the primitive streak (arrows) to form definitive endoderm and mesoderm respectively. Image used with permission from Dias *et al*. 2004 *Neurosurgical Focus*. **(B)** Gastrulation in mouse embryo occurs at E6.5 and forms the three germ layers. Image used with permission from Tam *et al*. 2007 *Nature Reviews Genetics*. **(C)** Cellular organisation of the mouse embryo after the process of gastrulation is complete. Image used with permission from Arnold *et al*. 2009 *Nature Reviews Molecular Cell Biology*.

1.3. Regenerative medicine and embryonic stem cells

1.3.1. Diabetes– a candidate disease for cell therapy

Autoimmune destruction of insulin-secreting pancreatic β-cells within the Islets of Langerhans causes Type I diabetes which makes up about 5-10% of all diagnosed cases (**Fig 1.4**). Clinical islet transplantation using cadaveric islets is to date, the most successful cell-based therapy that has been used to treat this condition (Shapiro *et al*. 2006; Robertson 2004). However, the demand for such islets far exceeds the actual supply especially, since the modern procedure called the Edmonton protocol utilises approximately 10,000 islet 'units' per kilogram of bodyweight. Therefore, alternative sources of β-cells need to be identified and hESCs are an appealing source. Pluripotent hESCs retain the capability to differentiate into cells representing all three embryonic germ layers (Keller 2005). By directing the differentiation of hESCs to generate functional beta (β) cells, one hopes to create an inexhaustible supply of these cells for the treatment of Type I Diabetes. This has led to immense interest in the differentiation of hESCs into endodermal derivatives. One part of this thesis (Chapter 4) describes my contribution to the development of *in vitro* β cell differentiation protocols, with particular emphasis on the formation of the definitive endoderm, the parental lineage of the pancreas.

1.3.2. Transplantation tolerance of hESC-derived cell therapy

As research efforts intensify towards deriving transplantable cell therapy material like insulin-secreting β-like cells from hESCs, issues pertaining to graft acceptance/ rejection must be addressed. Rejection of hESC-derived cell populations is a significant concern as their immunological signature is indisputably foreign

(Draper and Andrews 2002; Drukker *et al*. 2002). Interestingly, several studies have shown that undifferentiated hESCs and their differentiated progeny may in fact be immune-privileged or can be transplanted specifically into immune-privileged sites like the spleen (Li *et al*. 2004; Drukker *et al*. 2006**)**. Transplantation into areas like the spleen are under consideration largely due to the low expression of Major Histocompatibility Complex (MHC) class I molecules on the surface of hESCs and the resultant low immunostimulatory capacity of these cells. Though hESC-derivatives show increased expression of MHC class I, this does not alter the immune response.

Recently, it was demonstrated that mESCs and their derivatives with similar MHC I signatures can induce a potent immunological reaction even with a single difference between the donor and host Minor Histocompatibility antigen (mH) profiles (Robertson *et al*. 2007). However, these authors found that the inherent immune-privileged status of mESCs could be harnessed with minimal intervention to induce tolerance and prevent rejection. Highlighting the differences between the mouse and human systems, a very recent study shows that hESCs and their derivatives might not be as immune-privileged as previously thought and are capable of triggering a severe immune response in a xenogeneic host like the mouse (Swijnenburg *et al*. 2008). In this study, hESCs transduced with a double fusion reporter gene consisting of firefly luciferase and enhanced GFP were tracked *in viv*o using bioluminescent imaging. Severe infiltration of the graft 5 days after transplantation with immune cells and detectable levels of anti-hESC antibodies in the recipient serum together demonstrate active rejection of the graft. However, this reaction could be mitigated with the use of immunosuppressive drugs like tacrolimus (binds calcineurin and thereby inhibits T-cell signaling) and sirolimus (blocks

activation of T- and B- cells by inhibiting interleukin-2 responsiveness) that prolonged hESC graft survival up to 28 days. The disadvantage of immunosuppression is the undesirable side-effects that it triggers including nephrotoxicity, liver disease, increased risk of infections and a compromised immune system. Though much progress has been made, it is clear that more studies are required before any of the above strategies can be put to clinical use. Nevertheless, one step forward is the recently approved clinical trial for oligodendrocyte precursor cells derived from hESCs. The outcome of this safety study is eagerly anticipated as longevity of the graft within humans will pave the way for effective cell therapy.

If the inherent immune-privileged status of hESCs is inadequate to aid transplantation, one strategy is to induce tolerance with the use of hESC-derived haematopoietic cells (Drukker and Benvenisty 2004). Haematopoietic stem cells (HSC) are mesodermal derivatives that serve as progenitors to all cells that circulate in the peripheral blood and differentiate into several myeloid or lymphoid lineages during development (**Fig 1.5**). Theoretically, haematopoietic cells derived from the same exact source as the therapeutic graft, for example, a given pluripotential hESC line, could tolerise the recipient towards the incoming transplant material irrespective of its cellular nature (Kaufman and Thomson 2002). Tolerance could either be induced (1) through mixed haematopoietic chimerism or (2) through tolerogenic dendritic cells (DCs) (**Fig 1.6**) (Drukker and Benvenisty 2004; Fairchild *et al*. 2004).

Mixed haematopoietic chimerism refers to the use of haematopoietic progenitor cells to establish a resident donor population in the host. This grants donor-specific tolerance to the host and allows any other material from the same donor to be accepted with out any adverse reaction. Clinical examples of this phenomenon in humans have been reported (Alexander *et al*. 2008; Kawai *et al*. 2008).

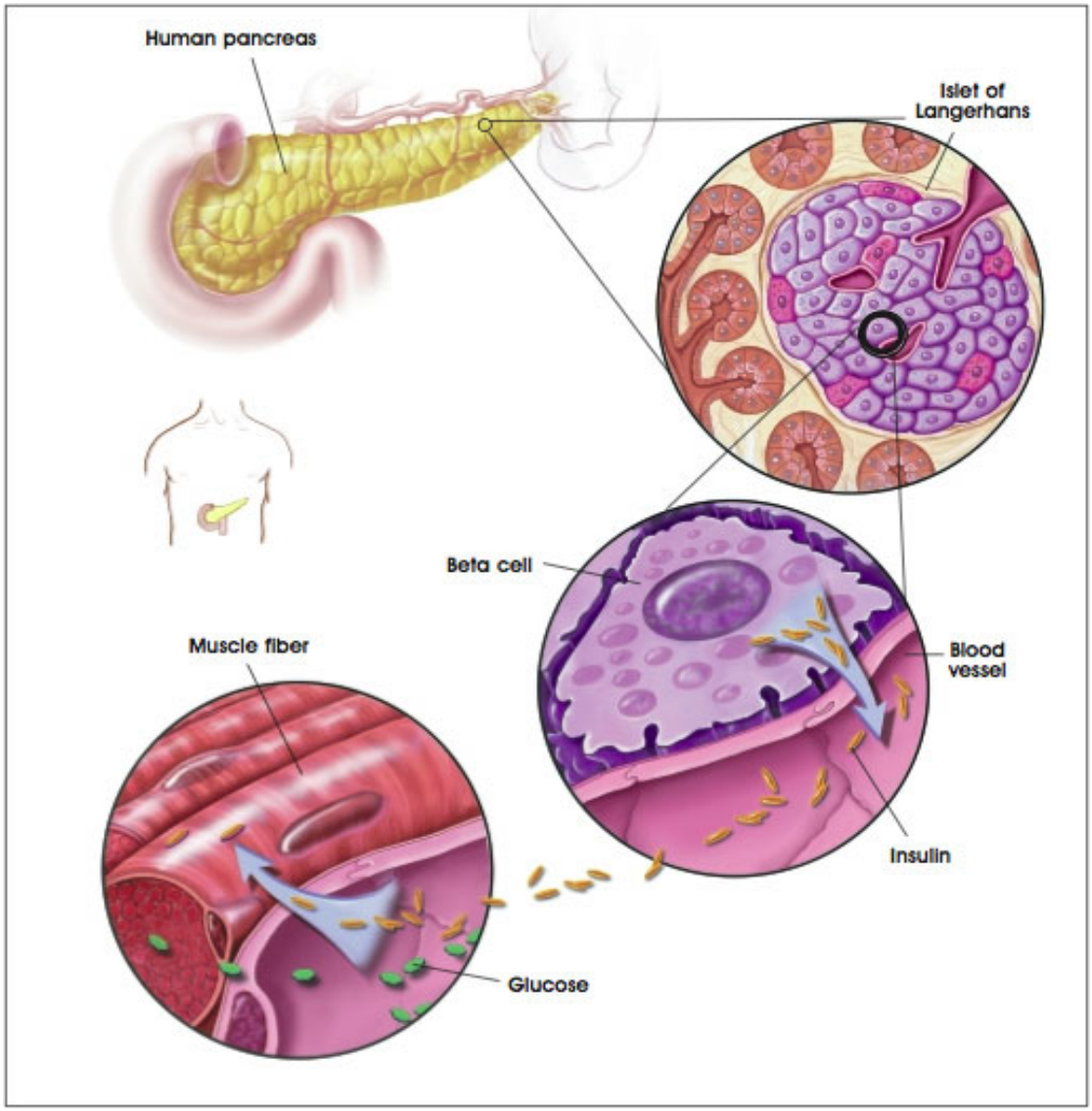


Figure 1.4. Pancreas and diabetes. The pancreas consists of Acinar cells which perform its exocrine functions and clusters of cells called Islets of Langerhans which perform its endocrine functions. Acinar cells secrete digestive enzymes like trypsin and chymotrypsin into the small intestine. Islets of Langerhans secrete various hormones into blood from its four main cell types which are (1) alpha (α) cells that secrete glucagon, (2) beta (β) cells that secrete insulin, (3) Delta (δ) cells that secrete somatostatin and (4) PP cells that secrete pancreatic polypeptide. The beta cells sense glucose levels in the blood and secrete Insulin to allow uptake of this important nutrient. Decreased production of Insulin leads to hyperglycemia and all the symptoms associated with the metabolic disease Type I Diabetes. Schematic diagram adapted from the NIH Stem Cells Information Resource at http://stemcells.nih.gov/info/scireport/chapter7.asp.

Kawai *et al*. (2008) showed that the patient's immune system accepted solid organ transplants from a donor whose haematopoietic cells were previously used to treat the same patient after myeloablative chemotherapy. A recent study describes the role of mixed chimerism in the successful treatment of type I diabetes in a mouse model transplanted with ES cell-derived haematopoietic material (Verda *et al*. 2008). Haematopoietic defects are one of the causes of autoimmune diabetes in the non-obese diabetic (NOD) mice. Therefore, these authors generated diabetic-resistant adult haematopoietic progenitor-like cells from mESCs and transplanted these into NOD mice to induce islet cell tolerance and treat diabetes. Though cell surface marker analysis showed that full donor chimerism was not established, the low level chimerism was significant enough to have an anti-diabetic effect. Importantly, no teratomas were formed in mice transplanted with the differentiated cells. Similar observations have previously been reported where highly homogenous differentiated populations failed to generate teratomas in the animal model (Kroon *et al*. 2008; Okamura *et al*. 2007).

Mixed chimerism induces tolerance through the deletion of alloreactive T cells that would otherwise activate the host immune system against the incoming graft (Sykes 2001). Recently Bonde *et al*. (2008) demonstrated that tolerance could be induced by the stimulation of regulatory T (T_{reg}) cells in the host. This mechanism in part can be attributed to the differentiation of the mixed pool of donor haematopoietic cells into allogeneic antigen-presenting cells (APCs). DCs are potent antigen presenting cells of the immune system that are responsible for priming naïve T cells (Banchereau and Steinman 1998). They are identified by the presence of co-stimulatory cell surface molecules CD80, CD86 and CD83 that enhance the activation of naive T cells.

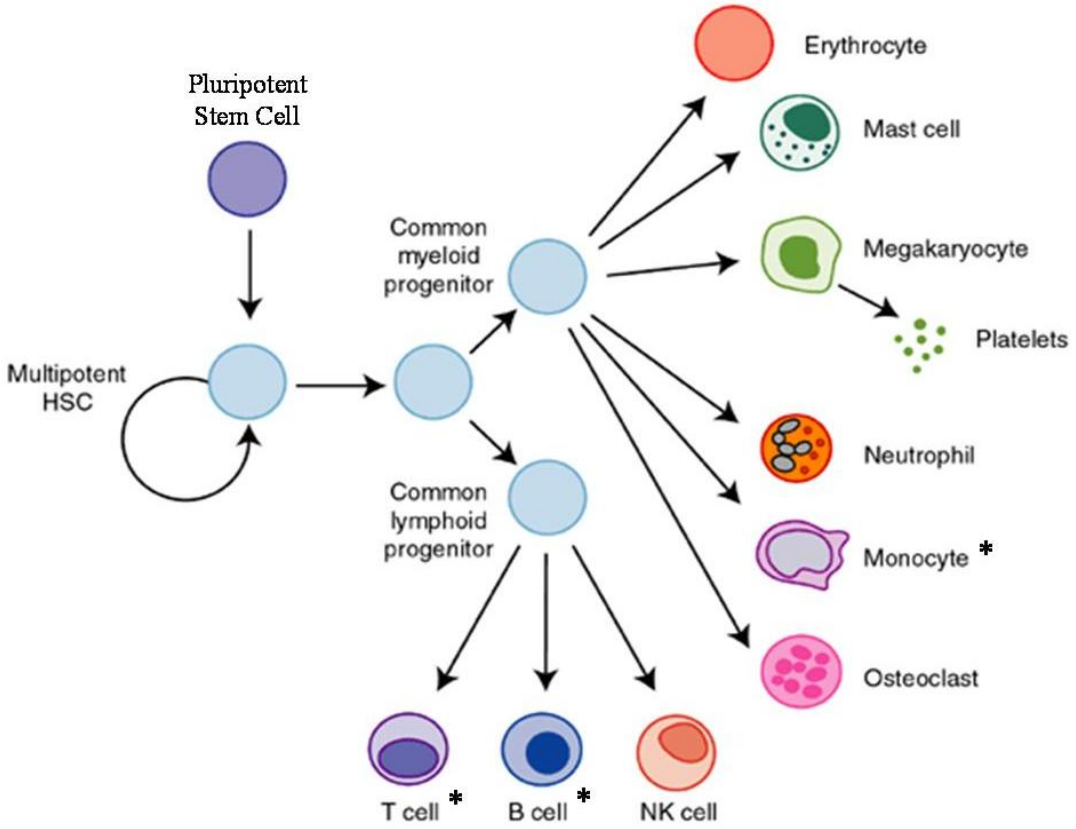


Figure 1.5. Haematopoietic development. Pluripotent stem cells give rise to multipotent haematopoietic stem cells that differentiate into lymphoid and myeloid progenitors. T-cells, B-cells and Natural killer (NK) cells form from lymphoid progenitors. Myeloid progenitors differentiate into various lineages including erythrocytes, granulocytes and monocytes. The asterisk (*) marks the cell types from which dendritic cells can be generated. Schematic diagram adapted with permission from Qasim *et al*. 2004 *Expert Reviews in Molecular Medicine*.

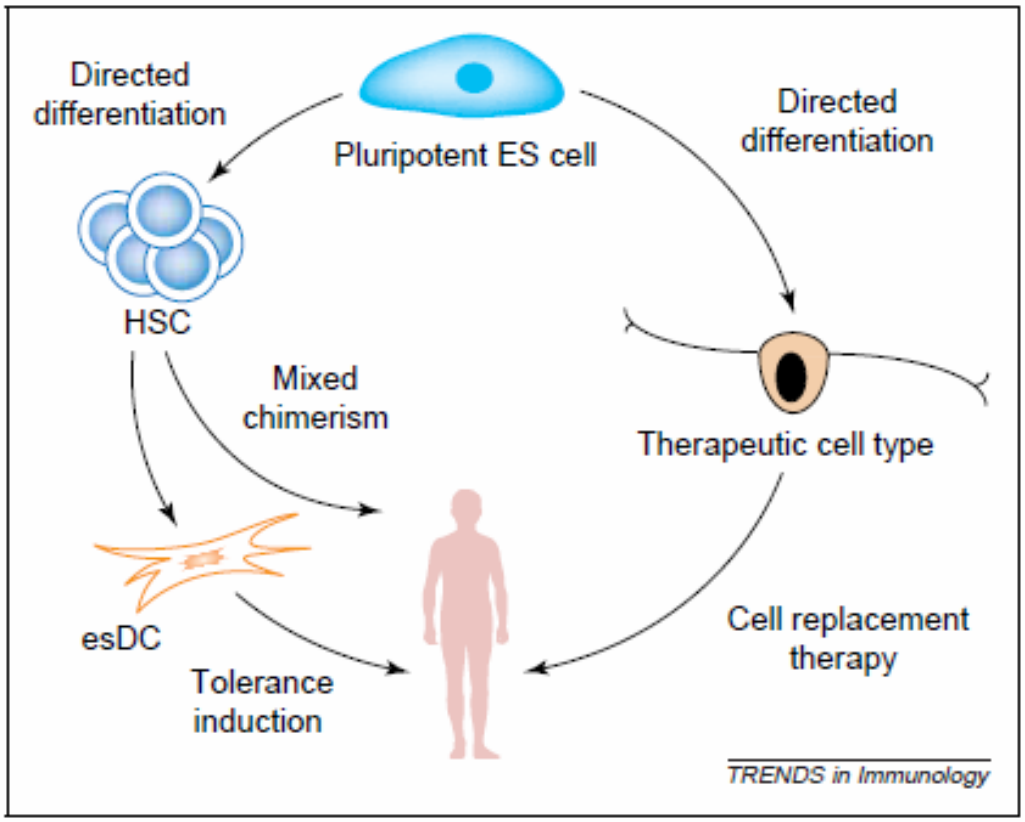


Figure 1.6. Pluripotent hESCs for cell replacement therapy. Regenerative medicine aims to produce therapeutic cell types through the directed differentiation of hESCs *in vitro*. Rejection of hESC-derived grafts is a concern that may be effectively addressed by using co-grafts derived from the exact same hESC source. Haematopoietic progenitors are known to repopulate myeloablated animals by establishing donor-specific chimerism in the host. In much the same way, haematopoietic cells differentiated from hESCs can either be used directly to achieve a state of mixed haematopoietic chimerism or can be differentiated further to generate dendritic cells (esDCs) that tolerise the host to the incoming graft. Schematic diagram used with permission from Fairchild *et al*. 2004 *Trends in Immunology*.

DCs are also involved in the maintenance of immunologic self-tolerance, inducing production of regulatory T cells or anergy/ immune unresponsiveness of autoreactive T cells (Steinbrink *et al*. 2002). Several studies have documented graft tolerance induced by donor DCs or host DCs in mice with various immunological backgrounds. Pulsing host DCs with alloantigens, using DCs to generate antigen-specific T_{reg} cells which induce tolerance, targeting DCs using monoclonal antibodies and targeting DCs using donor-derived apoptotic cells are some of the methods that were used with varying degrees of success (Morelli and Thomson 2007). If hESCs could be differentiated *in vitro* to form tolerogenic DCs, these could be presented to the host's immune system to establish a state of tolerance. Theoretically, these DCs would selectively activate T_{reg} cells that induce anergy and attenuate the host's immune response to the graft, even though the introduction of DCs into the host can be considered an allogeneic transplantation. The predicted tolerance of this graft sets the stage for the delivery and engraftment of other hESC-derived transplant material such as cardiomyocytes or beta-like cells. Ideally, this second graft would be recognized as 'self' as the host's immune system has encountered and developed prior tolerance to a similar set of antigens.

To generate functional haematopoietic-like cells *in vitro*, it is critical to understand the process of haematopoiesis *in vivo* during embryogenesis. By closely mimicking *in vitro* the sequence of haematopoietic development, one envisages that efficient differentiation of hESCs into these mesodermal derivatives can be robustly achieved.

1.4. Haematopoiesis

1.4.1. Haematopoietic development in the mouse

In the mouse, haematopoietic lineages first appear in the form of blood islands in the yolk sac, a derivative of the extraembryonic mesoderm by embryonic day E7.5 of gestation (Russell and van den Engh 1979). This is preceded by the expression of key haematopoietic genes like *Gata-2*, *Scl/ Tal-1* in the extraembryonic mesoderm which forms the visceral yolk sac (VYS), as revealed by *in situ* hybridization studies on the early embryo (Silver and Palis 1997). This yolk sac haematopoiesis was thought to seed the fetal liver and establish bone marrow haematopoiesis in the adult (Weissman *et al*. 1977; Moore and Metcalf 1970). However, this was shown otherwise by elegant grafting experiments done mainly in the chick which showed that adult haematopoiesis was established by cells from the embryo proper and the allantois (Caprioli *et al*. 2001; Cormier and Dieterlen-Lievre 1988; Dieterlen-Lievre 1975). By E10-11 of gestation, the yolk sac primitive haematopoiesis declines and haematopoietic activity shifts to the embryo proper where HSC emerge from the intraembryonic Para-Aortic Splanchnopleura (PAS/P-Sp), which is the presumptive aorta-gonad-mesonephros (AGM) (Godin *et al*. 1993; Medvinsky *et al*. 1993).

At E7.5, before circulation has connected the YS with the embryo, the PAS only contains stem cells with lymphoid potential (Cumano *et al*. 1996). Intraembryonic HSC emerge autonomously *in situ*, independently from the precursors emerging in the YS (Cumano *et al*. 1996; Medvinsky and Dzierzak 1996). Particularly, the dorsal aorta and the vitelline and umbilical arteries have been shown to contain haematopoietic cells between E9.5 to E12 (Garcia-Porrero *et al*. 1995). *In vitro* culture of segments of the embryo proper demonstrated that the haematopoietic precursors were exclusively present in the PAS (Godin *et al*. 1995). The AGM region

is the first site in the murine embryo where multipotential long term repopulating stem cells (LTRSCs) are detected (Muller *et al*. 1994). In this study, the E10 AGM injected into irradiated mice showed long-term reconstitution of the haematopoietic system. The AGM functions as a haematopoietic site until E11/E12 when it begins to degenerate; at the same time there is an increase in fetal liver haematopoietic activity (Medvinsky and Dzierzak 1996; Muller *et al*. 1994; Medvinsky *et al*. 1993). Haematopoiesis in the liver is not *de novo* but occurs by colonization from other tissues like yolk sac, placenta and AGM (Gekas *et al*. 2005; Kumaravelu *et al*. 2002; Houssaint 1981; Johnson and Moore 1975). The large number of HSC in the fetal liver could be the results of these colonisations and expansion of the population by the liver itself (Takeuchi *et al*. 2002). Beyond this point the liver functions as the site of haematopoiesis until just before birth when the bone marrow takes over and remains the only site of haematopoiesis in the adult (**Fig 1.7**).

The emergence of haematopoiesis is influenced by distinct interactions between germ layers within the embryo as well as transcription factors and other environmental factors. It has been shown that contact with visceral endoderm is required for primitive haematopoiesis in mouse yolk sac explants and that the VE can impart a haematopoietic fate to prospective neuroectoderm (Dyer *et al*. 2001; Belaoussoff *et al*. 1998). One of the signals responsible for this effect was found to be Indian Hedgehog which was then proven to be essential but not sufficient for effective primitive erythropoiesis in the mouse (Byrd *et al*. 2002). In the chick embryo, ventralising factors like vascular endothelial growth factor (VEGF) and bone morphogenetic protein 4 (BMP4) promote haematopoiesis while dorsalising factors like epidermal growth factor (EGF) and transforming growth factor α (TGF-α) antagonize the process (Pardanaud and Dieterlen-Lievre 1999). Similar activity of the

ventralising factors has been shown in the mouse through ES cell differentiation and gene targeting studies (Faloon *et al*. 2000; Shalaby *et al*. 1995; Winnier *et al*. 1995). For example, knockout studies showed that BMP4 is important for initiation of haematopoiesis in the mouse as *Bmp4–/–* embryos either die around gastrulation or have a smaller yolk sac and decreased erythropoiesis (Winnier *et al*. 1995). The critical requirement for Bmp4 in development of the cardiac mesoderm was also shown in studies on Bmp4 homozygous null mutant mice that showed abnormal heart formation (Fujiwara *et al*. 2002). These ventralising factors also regulate expression of critical haematopoietic transcription factors like *Scl* and *Gata-1* (Sadlon *et al*. 2004). In addition to these *Runx1* and *Gata-2* are known to be absolutely essential for definitive haematopoiesis that originates in the AGM region. Mice lacking *Gata-2* show a complete lack of committed progenitors and HSC and die at E10.5 as there is a severe drop in the number of AGM HSC (Tsai *et al*. 1994). *Runx1* deficiency also leads to the absence of AGM HSC and all myeloid and lympho-myeloid progenitors (Cai *et al*. 2000). Absence of both transcription factors only marginally impaired primitive erythropoiesis thus revealing the specific role of these factors in the definitive program. Thus, complex interactions within the embryonic environment establish haematopoietic identity in the developing mouse embryo.

The yolk sac blood islands in the developing embryo consist of primitive erythrocytes surrounded by differentiating endothelial cells (Risau 1991). This close developmental association of the haematopoietic and endothelial cell lineages within the blood islands of the developing embryo has led to the hypothesis that they arise from a common precursor, termed the hemangioblast.

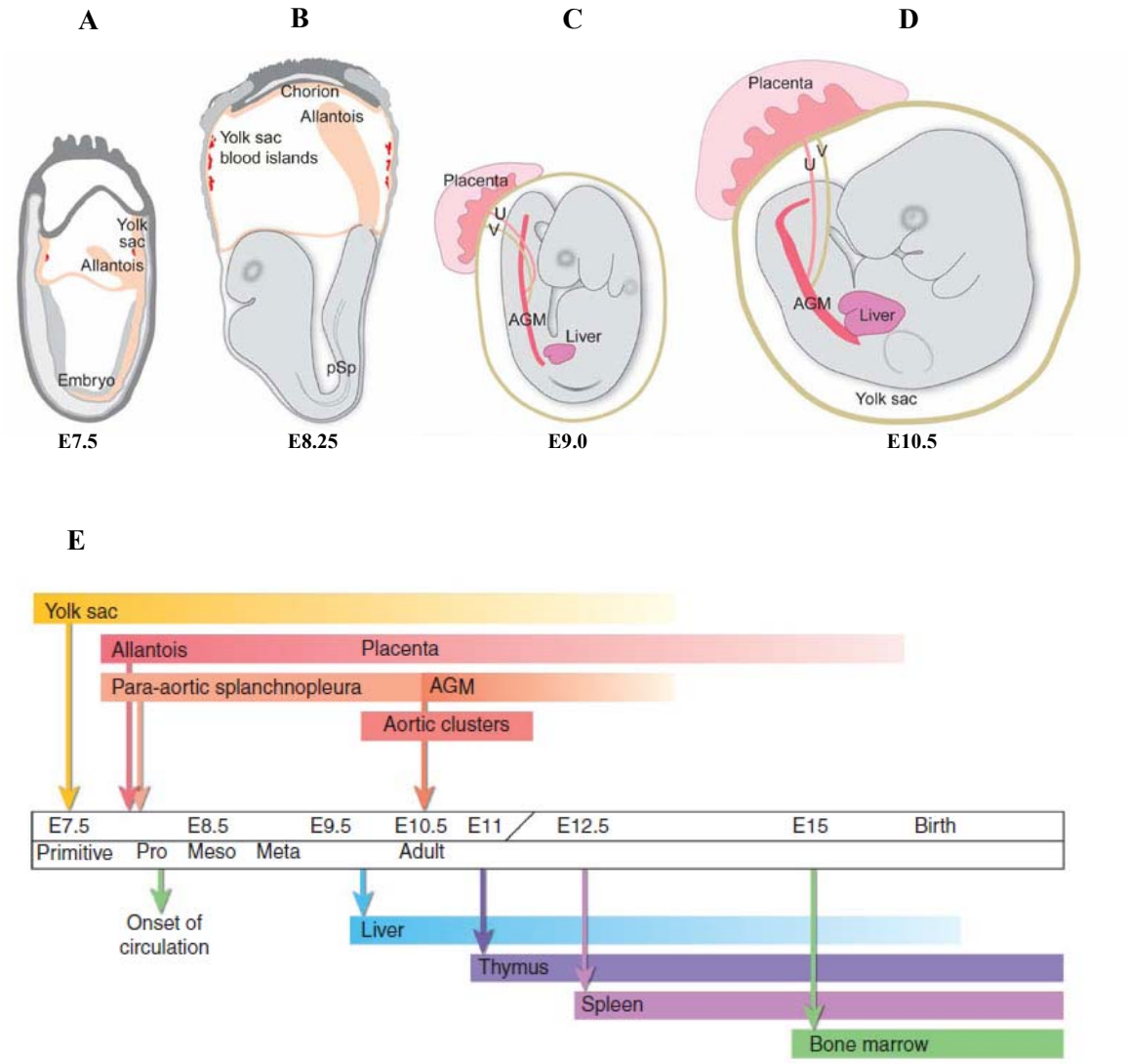


Figure 1.7. Haematopoiesis in the mouse embryo. (A) Haematopoietic cells are first visible at E7.5 in the yolk sac blood islands as primitive haematopoiesis is initiated. **(B)** At E8.25 circulation is established in the embryo. The allantois which will fuse with the chorion to form the umbilicus is seen at days E7.5 and E8.25. The para-aortic splanchnopleura (pSp) which is the prospective Aorta Gonad Mesonephros (AGM) is also indicated. **(C)** At E9.0 the embryo has turned and is enveloped in the yolk sac. Colonisation of the liver by haematopoietic progenitors begins at late E9. **(D)** The E10.5 mouse embryo contains haematopoietic clusters in the dorsal aorta in the AGM region, the vitelline (V) and umbilical (U) arteries. The first adult haematopoietic stem cells are found in these vessels. **(E)** Timeline of haematopoietic development in the mouse embryo. Arrows above indicate formation of specific haematopoietic populations. Arrows below show the colonisation of secondary sites of haematopoiesis. Schematic diagram adapted with permission from Dzierzak *et al.* 2008 *Nature Immunology*.

The concept of a bi-potent hemangioblast was supported by the observation that the expression of several genes was common to both haematopoietic and endothelial cell populations (Asahara *et al*. 1997; Kabrun *et al*. 1997; Young *et al*. 1995; Anagnostou *et al*. 1994; Kallianpur *et al*. 1994; Millauer *et al*. 1993; Yamaguchi *et al*. 1993; Fina *et al*. 1990). Studies on mice deficient in the receptor tyrosine kinase, Flk1 support the hemangioblast hypothesis as homozygous mutant embryos do not develop blood vessels or yolk sac blood islands, and die between E8.5 and E9.5 (Shalaby *et al*. 1997; Shalaby *et al*. 1995). ES cells provide a powerful tool to probe the existence of the hemangioblast population in the developing embryo. This is possible because haematopoietic and endothelial differentiation of ES cells *in vitro* is known to follow the same developmental sequence observed in the mouse embryo (Vittet *et al*. 1996; Keller 1995; Nakano *et al*. 1994; Keller *et al*. 1993; Wiles and Keller 1991; Risau *et al*. 1988). Using mESC-derived EBs, a common precursor for the primitive and definitive haematopoietic lineages was identified *in vitro* (Kennedy *et al*. 1997). When cultured in the presence of vascular endothelial growth factor (VEGF), c-Kit ligand and conditioned medium from an endothelial cell line D4T, these precursors formed colonies consisting of immature or blast-like cells that expressed a number of genes common to both the haematopoietic and endothelial lineages, including *Tal-1/Scl*, *CD34* and the VEGF receptor, *Flk-1*. This work was developed further by Choi *et al*. (1998) who established the blast colony assay using mESC-derived EBs to prove the presence of BL-CFCs (blast colony forming cells) that could clonally give rise to cells of both endothelial and haematopoietic lineages in presence of factors like VEGF. Using genetic tools, Chung *et al*. (2002) determined that haematopoietic cells develop from the $Flk1^{+}$ Scl^{+} and $Flk1^{-}$ Scl^{+} population while endothelial cells arise from the $Flk1^{+}$ Scl^{+} and $Flk1^{+}$ Scl^{-} population. Applying the blast colony assay to

early stage mouse embryos, it was demonstrated that in E7.0 embryos, the hemangioblast emerges from the posterior primitive streak and migrates to the extraembryonic mesoderm in the yolk sac (Huber *et al*. 2004). In this study, hemangioblasts were found to be most enriched in the Brachyury^{+} Flk1^{+} population within mESC-derived EBs and were determined to co-express Scl (**Fig 1.8**). Investigations in the zebrafish gastrula also provide evidence for the existence of a hemangioblast population (Vogeli *et al*. 2006). Detailed molecular characterization of hemangioblast cells has revealed an important role for the Notch pathway in differentiation of this multipotent lineage. Activation of Notch signaling in combination with inhibition of Wnt signaling was shown to be responsible in part for the formation of cardiac mesoderm from hemangioblasts while the converse was found to be important for specification of a primitive haematopoietic fate from hemangioblasts (Chen *et al*. 2008; Cheng *et al*. 2008). Recently, Lu *et al*. (2008) made improvements to the cell culture protocols to demonstrate that Bmp4 and VEGF were necessary and sufficient to induce robust differentiation of hESCs into hemangioblasts. Expression of hemangioblast-associated genes like *TBRA*, *FLK-1*, *CD31* and *LMO2* was upregulated in the differentiated cells while expression of the pluripotency gene *OCT4* was downregulated. Hemangioblasts generated using this differentiation approach were recently shown to be tripotent cells which could differentiate into endothelial cells, haematopoietic cells and smooth muscle-like cells (Lu *et al*. 2009). This shows that functional vasculatures can be developed from such differentiated progeny again demonstrating that multipotent progenitors like the hemangioblast exist in the developing embryo.

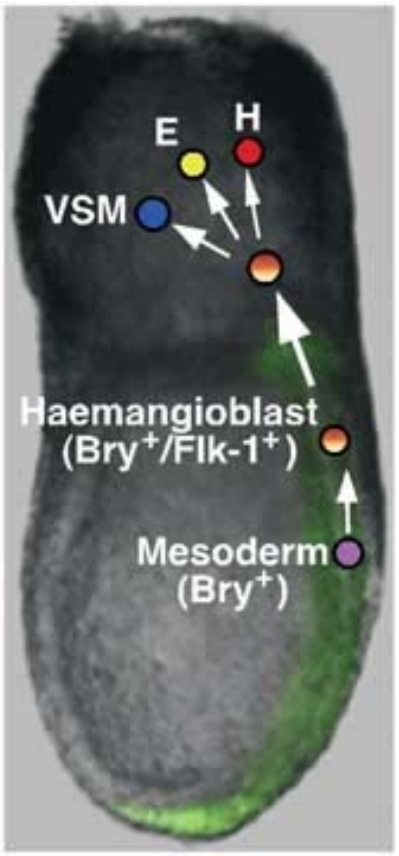


Figure 1.8. A model for hemangioblast development. Hemangioblasts are thought to arise from the *Brachyury* (Bry+) expressing mesodermal population of the developing embryo. These cells go on to express *Flk1* in addition to *T* and migrate to the yolk sac (Bry+/ Flk-1+). At this point the hemangioblast differentiates to form progenitors of haematopoietic (H), endothelial (E) and vascular smooth muscle (VSM) cell lineages. Image adapted with permission from Huber *et al*. 2004 *Nature*.

1.4.2. Haematopoiesis in the human embryo

Detectable yolk-sac haematopoiesis and expression of evolutionarily conserved haematopoietic genes in the human system closely follows the sequence in mouse (Tavian *et al*. 1999). However, the lack of detectable haematopoietic activity after day 60 of human development suggests that the duration of yolk sac haematopoiesis in human gestation is shorter than that in birds and rodents (Huyhn *et al*. 1995; Dommergues *et al*. 1992; Migliaccio *et al*. 1986). Similar to the mouse embryo, the human yolk sac is the site of primitive haematopoiesis during which nucleated erythrocytes expressing embryonic globin and the surface molecule glycophorin A are detected. Primitive haematopoiesis gives way to definitive haematopoiesis in the liver where the erythrocytes are enucleated and express fetal globin (Brotherton *et al*. 1979). As mentioned earlier studies in chick embryos provided evidence that the yolk sac gives rise predominantly to primitive haematopoiesis while the embryo proper is the site of definitive haematopoiesis. Haematopoiesis in the embryo proper occurs at the embryonic truncal arteries (homologous to the mouse AGM region) in early development (Tavian *et al*. 1996). Other components of the definitive haematopoietic lineage, like lymphoid cells, are derived from multipotential cells which can be found at either the yolk sac or the embryo proper or both.

Recently, Tavian *et al*. (2005) used an *in vitro* organ culture assay with human embryonic explants to show that the aorta as well as the P-Sp is capable of establishing long-term haematopoietic cultures. This study also differentiated the multi-lineage potential of the yolk-sac and the embryo proper: though both contributed myeloid and NK cells, only intraembryonic haematopoiesis generated lymphoid cells. As in the mouse, progenitors from the embryo proper are thought to be responsible for the establishment of definitive haematopoiesis in the human system

(Tavian *et al*. 2001). Yoder *et al*. (1997) studied and identified these precursors in the embryo as $CD34^{+}$/ c-Kit^{+} progenitor populations. CD34 is a cell-surface molecule thought to be one of the earliest markers of a haematopoietic cell/ progenitor. Another haematopoietic progenitor marker is c-Kit which is the receptor for the cytokine Stem Cell Factor (SCF/ Steel Factor). This study demonstrated that the $CD34^{+}$/ c-Kit^{+} cells isolated from the yolk sac and separately from the P-Sp at the same stage of development showed presence of long-term repopulating stem cells (LTRSCs). LTRSCs are stem cells that can establish long term haematopoietic cultures and have the potency to repopulate an entire animal post irradiation. Beginning in the yolk sac and transiting through the liver, the haematopoietic program finally arrives in the bone marrow which takes over as the major site of haematopoiesis through out the lifetime of the developing adult (**Fig 1.9**).

1.4.3. Haematopoietic differentiation from mESCs

Although many aspects of embryonic haematopoiesis have been studied in detail, early events regulating the lineage specification and maturation of stem cells are still unclear. Studying the mouse embryo immediately after gastrulation and before the appearance of blood islands has yielded important insights into these processes (Baron 2005; Baron and Fraser 2005). However, unhindered analysis of developmental events was made possible with the isolation of embryonic stem cells. Extensive investigation of the properties and capabilities of these cells has led to the development of several experimental approaches to induce haematopoietic differentiation from ES cells (**Fig 1.10**).

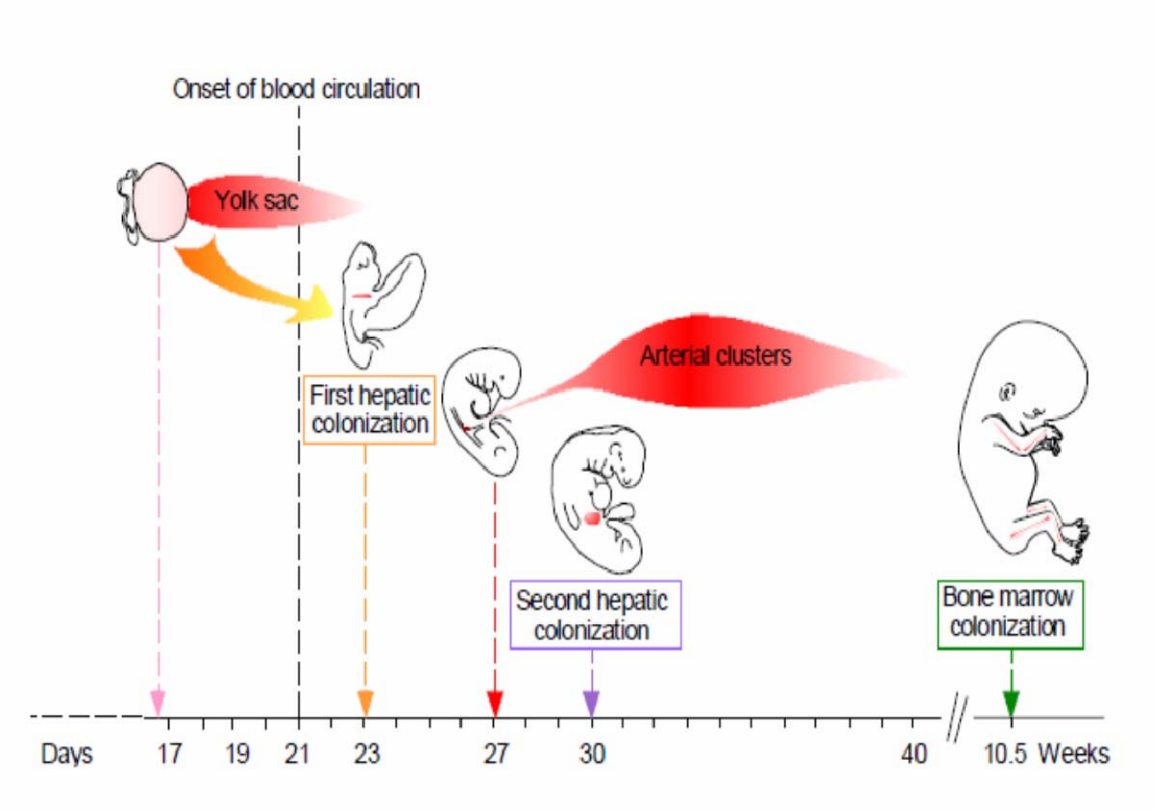


Figure 1.9. Haematopoiesis in the human embryo. Primitive haematopoiesis begins in the yolk sac around day 16 and contributes to erythroid and granulo-macrophage lineages. Circulation initiates around day 21 of development and mainly involves the nucleated erythrocytes found in the yolk sac. Around day 23, the first haematopoietic cells in the fetal liver are detected. These cells are thought to be of yolk sac origin. A second wave of haematopoiesis occurs at day 27 during which clusters of haematopoietic cells are visible in the vitelline and umbilical arteries and the AGM region. This definitive haematopoiesis seeds the fetal liver leading to the second hepatic colonisation. The fetal liver remains the main site of haematopoiesis until after birth when the bone marrow takes over and becomes the only site of haematopoiesis throughout adult life. Schematic diagram used with permission from Tavian *et al*. 2005 *International Journal of Developmental Biology*.

One favoured method is the formation of three-dimensional EBs from mESCs as described earlier (Evans and Kaufman 1981). Spontaneous mesodermal differentiation occurs quite reproducibly within mESC-EBs and has been shown to generate cardiac and haematopoietic mesodermal cells (Keller 1995; Doetschman *et al*. 1985). Co-culture on stromal feeder cells is another method employed to generate haematopoietic progeny from mESCs. Stromal cells of bone marrow or yolk sac origin are known to support the growth and maintenance of haematopoietic progenitors in culture (Lu *et al*. 1996; Wineman *et al*. 1993). One such cell line OP9 is a murine macrophage colony stimulating factor (M-CSF)- deficient cell line which has been shown extensively to support the maintenance of haematopoietic progenitors differentiated from mESCs (Senju *et al*. 2003; Kitajima *et al*. 2003; Kyba *et al*. 2002; Nakano *et al*. 1994). OP9 co-culture mainly gives rise to B lymphocytes.

Haematopoietic-like cells have also been obtained from mESCs differentiating in monolayers on extracellular matrix proteins like collagen (Nishikawa *et al*. 1998). The authors of this study used antibodies against markers like E-cadherin, Flk1/KDR, CD45, etc., to define the intermediate stages during differentiation of mESCs to blood cells. Gene targeting studies have revealed that transcription factors like *Gata-1*, *Gata-2* and *Scl* that are known to be essential for haematopoietic development in the embryo are expressed during *in vitro* differentiation of mESCs. *Gata-1* is necessary for primitive erythroid differentiation as mESCs deficient in *Gata-1* and EBs derived from these showed a complete block in the development of erythroid precursors (Weiss *et al*. 1994). Mice homozygous for *Gata-2* and mESCs derived from the same have defective primitive erythropoiesis and an absolute lack of definitive erythroid precursors (Tsai *et al*. 1994). *Scl/ Tal-1* is critical for haematopoiesis as *Tal-1* deficient mESCs were found not to differentiate into several haematopoietic lineages

(Porcher *et al*. 1996). Though developmentally relevant markers were expressed on the differentiated progeny the functional competence of these cells was unclear. Since then, several studies have documented that haematopoietic progenitors derived from mESCs are capable of long-term repopulation of myeloablated mice (Burt *et al*. 2004; Kyba *et al*. 2003; Palacios *et al*. 1995). These studies were done with differentiated cells derived using distinct strategies and all of them showed low-level repopulating ability. Though these results are highly encouraging, more investigations need to be done to determine if these cells are indeed comparable to those found in the fetal liver and adult bone marrow.

1.4.4. Haematopoietic differentiation from hESCs

Although murine haematopoiesis has been extensively described using both embryological and gene targeting strategies, knowledge of early developmental decisions in the human embryo is limited. The study of human haematopoiesis has mainly been limited to primary human tissues like bone marrow, peripheral blood and umbilical cord blood. The differentiation of hESCs provides a possible inroad into embryonic development especially given the limited availability of human embryonic material. Differences in morphology, population doubling time and growth factor requirements between mESCs and hESCs point to the likelihood that there might be differences in the factors that direct *in vitro* differentiation of hESCs. Drawing on lessons from studies on mouse and human embryos and mESCs, hESCs have been subjected to various differentiation strategies in order to develop and establish models of human embryonic and haematopoietic development. These approaches are expectedly very similar to those used with mESCs despite the differences between the two cell types and are summarized in **Figure 1.10**.

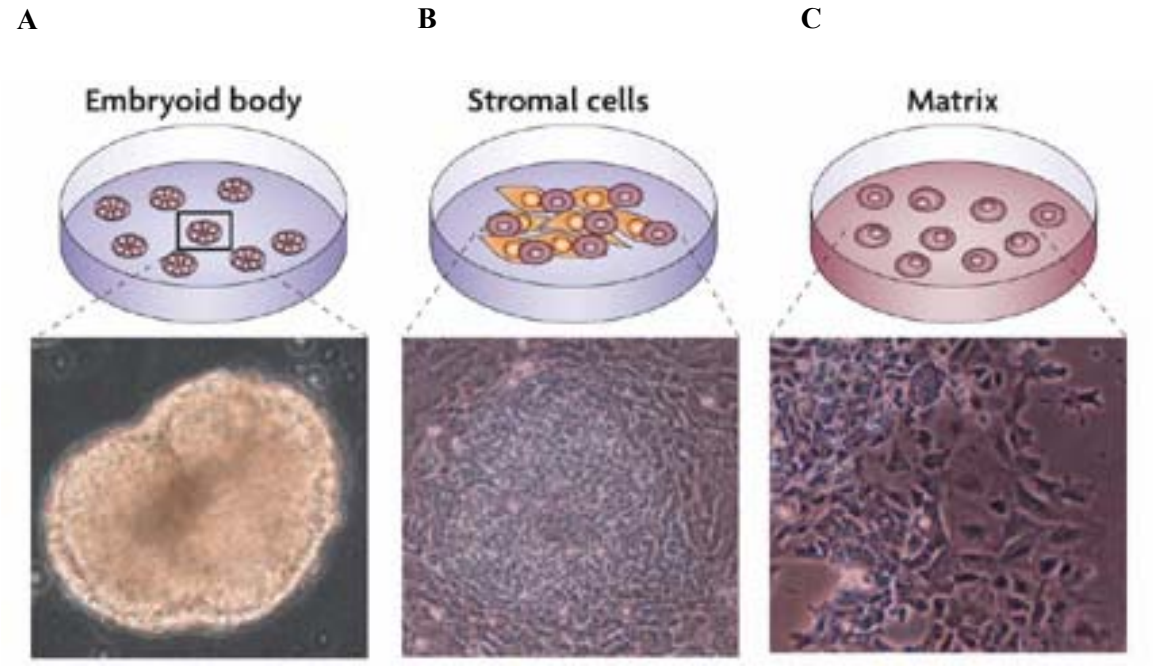


Figure 1.10. Strategies for haematopoietic differentiation from ES cells. Various successful strategies have been used in the recent years to differentiate ES cells (mouse and human) into cells of the haematopoietic lineage. **(A).** Differentiation within an EB shares similarities with vertebrate development and serves as an in vitro model system. However, the three-dimensional structure allows only minimal access to monitor selected cell types and hence to guide the differentiation. **(B)** The use of stromal cells allows better access to the differentiating cells and limited guidance of the differentiation although it is labour-intensive process. Another disadvantage is the low reproducibility as efficiency of differentiation depends on the quality of the stromal cells. **(C).** Differentiation on a matrix like collagen, fibronectin, etc., has the advantage of being a selective strategy that allows for maximum access to cells and therefore, directed differentiation. However, determination of optimal culture conditions is difficult and the cost is extremely high. Schematic diagram adapted with permission from Nishikawa *et al*. 2007 *Nature Reviews Molecular Cell Biology*.

A much reported strategy for haematopoietic differentiation from ES cells is the use of stromal cells as a supportive feeder layer which promotes the efficient production of haematopoietic derivatives *in vitro*. In addition to various murine cell lines including OP9 (described earlier), two immortalised human bone marrow stromal cell lines HS-5 and HS-27A have been shown to maintain bone marrow-derived haematopoietic progenitors in culture (Nakano *et al*. 1994; Roecklein and Torok-Storb 1995). HS-5 secretes large amounts of cytokines; conditioned medium from this line supports the *ex vivo* expansion of both immature and mature haematopoietic progenitors. In contrast HS-27A does not secrete cytokines but has been shown to support formation of typically haematopoietic "cobblestone areas" from progenitor cells of human bone marrow origin (Torok-Storb *et al*. 1999). One of the first reports of hESC-derived haematopoietic colony-forming cells was from Kaufman *et al*. who co-cultured hESCs with either S17, a mouse bone marrow cell line, or C166, a mouse endothelial cell line (Kaufman *et al*. 2001). Few resulting cells (1-2%) were $CD34^+$ $CD38^-$, which identifies early haematopoietic cells. The haematopoietic potential of these cells at various stages of differentiation was demonstrated using the clonal assay for Colony Forming Units (CFUs). In this assay, a viscous Methyl Cellulose-based medium supplemented with appropriate cytokines is used to enrich the clonal progeny of single haematopoietic progenitor cells called colony-forming cells (CFCs) or colony-forming units (CFUs). In the study from Kaufman *et al*. (2001) the expression of evolutionarily conserved genes, *GATA-2* and *TAL-1*, and the decline in their expression with a simultaneous decrease in CFU numbers confirmed the haematopoietic origin of the differentiated progeny. Although haematopoietic cells were successfully derived from hESCs and extensively characterized, some inherent problems in the process were brought to light. The

differentiation was inefficient as the number of CFUs generated from days 14 to 18 was low (0.03%). The use of selectively enriched $CD34^+$ cells from the whole population resulted in an improved CFU efficiency of 0.27% (equivalent to human bone marrow samples). However, no new CFUs (secondary or tertiary) were formed during this assay. The lack of new CFUs indicates the absence of LTRSCs that are essential for successful engraftment of an irradiated animal. Therefore, the haematopoiesis obtained by differentiation is transient and not definitive in nature. In another study, hESCs growing on OP9 monolayers were shown to give rise to $CD34^+$ $CD38^-$ primitive haematopoietic-like cells which were further induced to differentiate into a definitive population by culturing on M5 stroma in the presence of cytokines (Vodyanik *et al*. 2005). These cells were enriched in CFUs and expressed haematopoietic genes like *GATA-1*, *GATA-2*, *SCL/ TAL-1* and *FLK1*. This study was used by Slukvin *et al*. to demonstrate the efficient generation of well characterized DCs from hESCs (Slukvin *et al*. 2006). These authors used OP9 co-culture to differentiate hESCs into $CD34^+$ haematopoietic progenitors. These precursors were then treated with GM-CSF and other cytokines in a non-feeder based system to generate myeloid cells like DCs. The DCs exhibited a typical marker profile (CD80, CD86, CD40, etc.,) and gave expected readouts in biological assays *in vitro* which demonstrated that these terminally differentiated cells were functional.

Another proven method of differentiation from ES cells is the use of pro-haematopoietic cytokines. Chadwick *et al*. (2003) demonstrated the successful use of cytokines like Stem Cell Factor (SCF), Flt-3 Ligand (Flt-3L), Interleukin-3 (IL-3), Interleukin-6 (IL-6) and Granulocyte Colony Stimulating Factor (G-CSF) and Bmp4, to direct the differentiation of hESCs to haematopoietic stem cells. In this study, the differentiated cells were characterised as $CD45^+$ haematopoietic cells similar to both

committed adult haematopoietic tissue and the initial population of definitive haematopoietic cells detected within the AGM region of the human embryo around day 27 (Oberlin *et al*. 2002; Labastie *et al*. 1998). The haematopoietic transcription factors *GATA-1* and *PU.1* were upregulated in these cells, confirming their acquired identity. Though it did not significantly affect the efficiency of differentiation, Bmp4 was found to promote the self-renewal capacity of these hESC-derived haematopoietic progenitors.

An alternative strategy for haematopoietic differentiation of hESCs was developed by Zhan *et al*. (2004) where a combination of cytokines was used to generate functional antigen-presenting leukocytes in culture. Using a combination of serum stimulation and addition of haematopoietic cytokines to EBs grown in suspension, $CD34^+$ $CD45^+$ haematopoietic progenitors were generated in culture. In addition, cells expressing CD80, CD86 (dendritic-like cells) and CD40 (antigen presenting cells) were detected and confirmed to be of dendritic origin by Wright-Giemsa staining which allows identification of the different cells in blood or bone marrow samples. These immature DC-like cells were shown to be functional antigen presenting cells through a mixed leukocyte reaction (MLR). In the MLR assay, the cytotoxic T-cell response to antigens is measured as a direct result of the antigen presenting activity of the test population. Even though there is extensive proof that *in vitro* differentiation of hESCs can give rise to HSC the functionality of these cells *in vivo* needs to be demonstrated. In a recent study, either a $CD34^+$ $CD38^-$ or $CD34^+$/ lin^- cell population generated using S17 stroma was used to successfully engraft fetal sheep via haematopoietic chimerism (Narayan *et al*. 2006). This is an encouraging result that provides proof of principle that differentiated cells derived *in vitro* retain their functional behaviour after transplantation.

In Chapter 3 of this thesis, I will present preliminary results from investigations on the haematopoietic differentiation potential of two hESC lines, hES2 and hES3, which are extensively utilized in our laboratory. I employed two approaches– stromal cell co-culture and exposure to cytokines– to induce differentiation of the hESC lines. In both strategies, hESC-EBs were used as the starting material as these seemed to have a selective advantage over undifferentiated cells in generating differentiated progeny. Stromal cells are thought to promote differentiation by providing an environment that mimics *in vivo* conditions. Since the differentiation using stromal cells was sporadic it is possibly a spontaneous occurrence. Cytokine-based differentiation has the advantage of being a slightly more controlled and defined system in which pro-haematopoietic cytokines tightly control the development of the relevant cell types in contrast to the inconsistencies accompanying the use of stromal cells. This phenomenon was clearly noted in my investigations as cytokine treatment gave much more reproducible differentiation from hESCs. Though much improvement is needed to improve the efficiency of differentiated, these results provide proof that these two cell lines can be directed to a haematopoietic fate *in vitro* (Chapter 3).

1.5. Definitive endoderm formation in the vertebrate embryo

As a result of segregatory events in the embryo, the DE emerges from the anterior part of the primitive streak about 8 to 10 hours after gastrulation and incorporates into the visceral endoderm (VE) which covers the basal surface of the embryo (Grapin-Botton and Constam 2007; Tam and Beddington 1992; Lawson *et al*. 1991). This endodermal layer progressively displaces the VE to a more anterior and proximal position and closer to the extraembryonic region of the embryo (Tremblay

and Zaret 2005; Kinder *et al*. 2000; Tam *et al*. 1993; Lawson *et al*. 1986). Supporting this observation is the expression of VE markers which initially mark the cells overlying both embryonic and extraembryonic regions and are subsequently restricted to the visceral layer of the yolk sac (Weber *et al*. 1999; Beddington and Robertson 1999). By the late streak stage, the endodermal layer overlying the epiblast is exclusively DE, except for a region overlying the posterior primitive streak (Tam and Beddington 1992; Lawson and Pedersen 1987; Lawson *et al*. 1986). Soon after the emergence of DE, the gut endoderm folds and is internalized to form the gut tube from which the respiratory and digestive tracts and associated visceral organs develop (Lewis and Tam 2006; Wells and Melton 1999). This model of DE formation was arrived at through extensive fate-mapping studies using single-cell labelling and cell transplantation techniques. Advances in genetic and imaging tools available for such studies have led to a revision of this classical model. Kwon *et al*. recently put forth an 'intercalation' model in which cells of the DE get integrated into the existing VE (Kwon *et al*. 2008). These authors used three different transgenic lines that expressed either Alpha Feto Protein (*Afp*) or Transthyretin (*Ttr*), both VE markers, to track these cells *in vivo*. Several findings were made during the course of this study. (1) Cells of the VE disperse to accommodate definitive endoderm cells thus leading to cell mixing. (2) The external epithelial lining of the embryo consists of both VE and DE cells (not exclusively VE). (3) Absence of expression of VE-specific genes is due to down regulation and not cell migration. (4) VE-derived cells incorporate into the gut tube and hence contribute to the embryo proper. The proposed new model for morphogenesis of the endoderm is based on these observations (**Fig 1.11**).

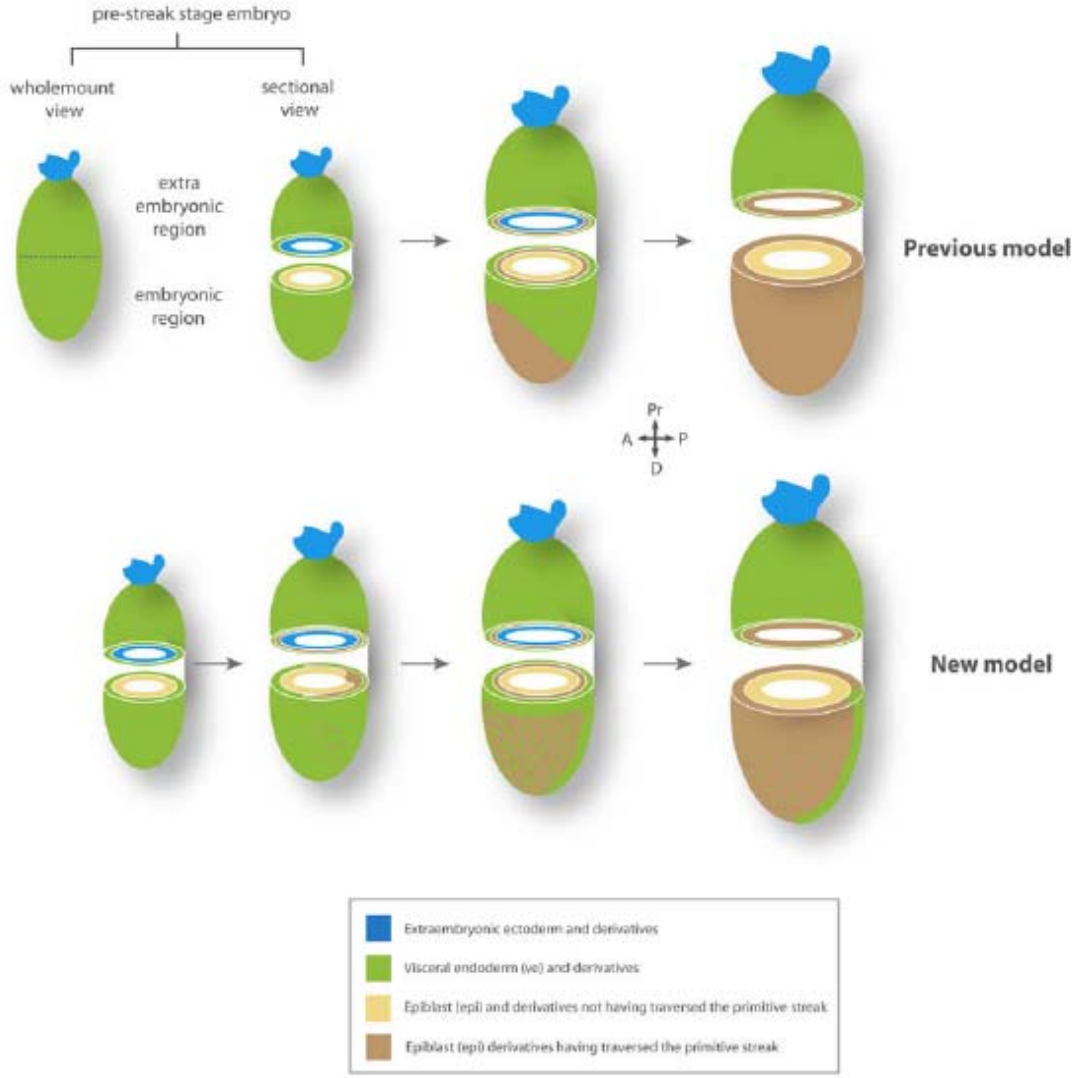


Figure 1.11. Development of endoderm in the vertebrate embryo. Historically, definitive endoderm is thought to arise at the anterior primitive streak present at the distal end of the embryo near the node. Ingression of definitive endodermal cells through the streak is accompanied by proximal movement of the visceral endoderm towards the extraembryonic region. In the new model proposed by Kwon *et al*. the visceral endoderm is not completely displaced but becomes dispersed by the intercalation of epiblast-derived definitive endodermal cells. Schematic diagram used with permission from Kwon *et al*. 2008 *Developmental Cell*.

Extensive studies in zebrafish, *Xenopus* and mouse have shown that members of the TGF-β family of molecules play critical roles in early development especially in the formation of mesoderm and endoderm (Schier 2003; Stainier 2002; Winnier *et al*. 1995; Smith *et al*. 1993). Nodal and Activin A are two such ligands that signal through phosphorylated Smad molecules to initiate transcription of genes important in development (Shi and Massague 2003; Moustakas *et al*. 2001). Receptor Smads– Smad2 and Smad3 are integral to the Nodal signalling pathway as these molecules mediate the intracellular consequences of ligand binding (**Fig 1.12**) (Arnold and Robertson 2009). Nodal has been shown to be important in determining cell fate and cell movements during early vertebrate development (Vincent *et al*. 2003; Norris *et al*. 2002; Whitman 2001; Schier and Shen 2000; Nomura and Li 1998). Its role in patterning is revealed in Nodal mutant mouse embryos that fail to form anterior visceral endoderm (AVE) and primitive streak and have no anterior-posterior identity (Brennan *et al*. 2001; Conlon *et al*. 1994). In the developing embryo, Nodal is also known to influence the formation of mesoderm and endoderm (Lewis and Tam 2006; Vincent *et al*. 2003; Lowe *et al*. 2001, Jones *et al*. 1995). Nodal establishes a gradient of expression which specifies the endoderm at higher levels and mesoderm at lower concentrations (Brennan *et al*. 2002; Stainier 2002; Chen and Schier 2001; Smith 1995). Activin A closely mimics Nodal, which is the endogenous ligand, and transduces its signals using the same receptor apparatus and Smads with the exception of Cripto, a co-receptor which is required for most Nodal signalling (Chen and Shen 2004; de Caestecker 2004; Schier 2003). This might explain why Activin can phosphorylate Smad2 faster than Nodal in *Xenopus* embryos as Nodal activity is limited by the requirement for the co-receptor (Lee *et al*. 2001). Studies on vertebrate embryos have shown that like Nodal, Activin can induce formation of both mesoderm

and endoderm in a dose-dependant manner (Okabayashi and Asashima 2003; Ninomiya *et al*. 1999; Gurdon *et al*. 1995; Gurdon *et al*. 1994; Smith *et al*. 1990). Though largely considered to be identical, differences between these two molecules have been reported. Ramis *et al*. (2007) showed that Activin and Nodal are expressed differently and regulate distinct sets of genes in *Xenopus*. While Activin was ubiquitously expressed, Nodal was restricted to the vegetal and equatorial regions of the embryo.

For *in vitro* studies the commercially available preparation of Activin A is preferred over Nodal as it is more stable and shows better induction of differentiation (Tada *et al*. 2005). The ability of Activin A to generate either mesoderm or endoderm in a dose-dependent manner has been demonstrated in ES cells with low levels generating mesoderm and a higher concentration of Activin forming endoderm (Kubo *et al*. 2004; Johansson and Wiles 1995). Kubo *et al*. developed culture conditions in which Activin A induced formation of a primitive streak-like population expressing *Brachury*, which further developed into endodermal cells. Since then extensive studies have documented the use of Activin A *in vitro* to induce endoderm formation from mESCs and hESCs (McLean *et al*. 2007; D'Amour *et al*. 2005; Shi *et al*. 2005; Tada *et al*. 2005; Yasunaga *et al*. 2005). Activin A has also been employed successfully in generating more specialised and differentiated endoderm cell types from ES cells (D'Amour *et al*. 2006; Gouon-Evans *et al*. 2006). These observations prompted the use of Activin A in our differentiation strategy to induce formation of definitive endoderm *in vitro*.

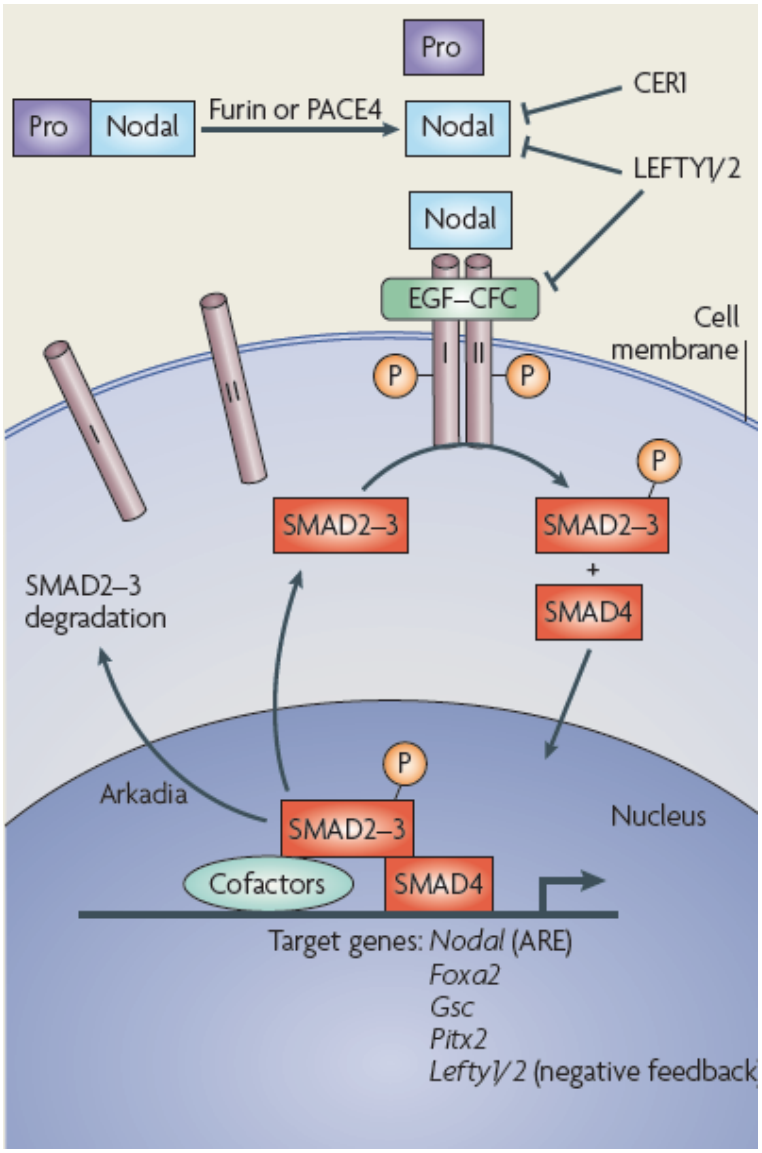


Figure 1.12. Nodal pathway. Pro Nodal is processed by convertases like Furin or PACE4 to generate Nodal which binds to the EGF-CFC co-receptor, Cripto to activate signaling. Ligand binding causes phosphorylation of Smad2/3 which enables the co-Smad, Smad4 to complex with Smad2/3. This complex then translocates to the nucleus and binds to co-factors like Foxh1/ FAST to trigger transcription of downstream target genes including *Nodal, Foxa2, Gsc, Pitx2 and Lefty1/2*. Image used with permission from Arnold *et al*. 2009 *Nature Reviews Molecular Cell Biology*.

1.5.1. Differentiation of mESCs to endodermal derivatives

Endoderm induction has been extensively studied in model systems like *Xenopus* and zebrafish while such investigations in the mouse model have been limited due to the restricted accessibility to early stages of development. mESCs provide an ideal alternative system that allows extensive interrogation of mammalian development *in vitro* if their differentiation potential can be directed to give rise to desired cell types like endodermal cells (Keller 1995). One of the first reports of endoderm induction *in vitro* was from Kubo *et al*. who used a mESC line with GFP targeted to the *Brachyury (Tbra)* locus to monitor endoderm differentiation (Kubo *et al*. 2004, Fehling *et al*. 2003). *Tbra* is a T-box transcription factor that marks the primitive streak and nascent mesoderm in vertebrate embryos (Wilkinson *et al*. 1990). These authors used Activin A in serum-free conditions to differentiate mESCs into *Foxa2* and *Sox17*-expressing endoderm and *Tbra*-expressing mesoderm at the expense of *Gata1*-expressing haematopoietic cells and neuroectoderm marked by *Pax6*. *Foxa2* (Forkhead box a2) is a marker of the anterior primitive streak (APS) and early endoderm, and is essential for the formation of foregut and midgut endoderm (Ang *et al*. 1993; Monaghan *et al*. 1993; Sasaki and Hogan 1993). *Sox17* (Sry-related HMG box transcription factor) is expressed in the APS and DE, and is known to be essential for endoderm development as *Sox17* null mice show severe depletion of definitive endoderm (Kanai-Azuma *et al*. 2002). The marker genes used most commonly to monitor endodermal differentiation as summarized in **Table 1.1**.

Kubo *et al*. (2004) observed, rather unexpectedly, that the endodermal cells were specified from $Tbra^{+}$ cells which also exhibited mesoderm potential at the appropriate concentration of Activin A. When used at a high concentration Activin A induced endoderm and very little mesoderm, while at lower concentrations only

mesoderm formed from *Tbra*$^{+}$ cells. In the embryo, *Tbra* is exclusively expressed in the PS and since both mesoderm and endoderm emerge from the PS, these cell types would have been *Tbra*$^{+}$ at some point during their development. This was demonstrated in mouse studies using differentiated mESCs which showed development of both mesoderm and endoderm from mESC-derived *Tbra*$^{+}$ cells (Kubo *et al*. 2004). The formation of mesoderm and endoderm from the same cell population under relevant culture conditions lends support to the existence of the mesendoderm. Though the concept of a common progenitor for mesoderm and endoderm, termed mesendoderm, had earlier been shown in *C. elegans* and *Xenopus*, no direct evidence had been found in the mouse system (Rodaway and Patient 2001). In Zebrafish the existence of cells expressing markers of both mesoderm (*Tbra*) and endoderm (*Gata5*) that generate all endoderm but only some part of mesoderm has been shown (Rodaway *et al*. 1999; Kimelman and Griffin 2000). Cell fate studies in the mouse have previously pointed to the possible mesendodermal potential of the organizer region of the anterior primitive streak as it gives rise to both anterior definitive endoderm and axial mesoderm (Kinder *et al*. 1999; Lawson *et al*. 1991). Therefore, it seems likely that the *Tbra*$^{+}$ *Foxa2*$^{+}$ cells generated by Kubo *et al*. are similar to cells of the anterior primitive streak that express these markers and give rise to the first endodermal cells and may possibly represent mesendoderm (Wilkinson *et al*. 1990; Monaghan *et al*. 1993; Sasaki and Hogan 1993; Wells and Melton 1999). Though *Tbra* expression was used to define a bi-potent population by Kubo *et al*. it is not an exclusive marker of the mesendoderm. *Tbra* is expressed in the node and early mesodermal cells and does not distinguish between mesendoderm and other cells of the mesoderm (Showell *et al*. 2004).

Working on the hypothesis that *Goosecoid* (*Gsc*) might be a better marker of the mesendoderm, Tada *et al*. (2005) generated a mESC line with a GFP reporter knocked into the *Gsc* locus and showed that a bi-potent mesendoderm population exists during Activin-induced mesodermal and endodermal differentiation of mESCs. *Gsc* is a homeobox transcription factor expressed in the organizer region that forms definitive endoderm in the developing mouse embryo (Blum *et al*. 1992). Using Gsc-GFP knock-in mESCs these authors were able to define a Gsc^+ E-cadherin$^+$ $PDGFR^+$ mesendoderm population that subsequently diverges into Gsc^+ E-cadherin$^+$ $PDGFR^-$ definitive endoderm precursors and Gsc^+ E-cadherin$^-$ $PDGFR^+$ mesodermal precursors. E-cadherin functions as a cell adhesion protein and is expressed in the epiblast and endoderm of the early mouse embryo (Takeichi 1995; Damjanov *et al*. 1986). The development of mesoderm from the Ecadherin$^-$ precursors in the study outline above is consistent with the downregulation of E-cadherin expression during EMT which is essential for the differentiation and development of mesoderm at gastrulation (Burdsal *et al*. 1993). PDGFRα (platelet-derived growth factor receptor α) is expressed in the presumptive mesoderm of the vertebrate embryo and is induced during mesoderm formation by high doses of Activin (Jones *et al*. 1993; Symes *et al*. 1994). The Gsc^+ Ecadherin$^+$ $PDGFR^-$ endoderm precursors and the Gsc^+ Ecadherin$^-$ $PDGFR^+$ mesoderm precursors defined in this study further developed into *Foxa2* and *Sox17*-expressing definitive endoderm and some mesoderm lineages respectively.

Though much progress was made in the derivation of endoderm induction *in vitro* it was still difficult to judge whether these differentiated endodermal cells represent definitive or visceral endoderm owing to the lack of molecular markers that distinguish between the two endodermal lineages (Grapin-Botton and Melton 2000; Tam *et al*. 2003).

Gene Name	Embryonic Expression	Relevance
Tbra	Primitive streak, Nascent Mesoderm	Required for posterior mesoderm movement and somite differentiation
Gsc	Primitive streak, Anterior mesoderm	Role in cell fate specification and craniofacial development
Foxa2	Anterior Primitve Streak, Early Endoderm	Required for formation of foregut and midgut endoderm
Sox17	Anterior Primitve Streak, Definitive Endoderm	Required for formation of definitive endoderm

Table 1.1. Marker genes expressed during the differentiation of mouse and human ES cells to definitive endoderm.

However, the expression of *Tbra* (which does not mark the VE) and lack of expression of VE markers like *Sox7* in the above differentiation strategies suggests that it is DE and not VE that is being specified from the $Tbra^{+}$ and Gsc^{+} populations (Kanai-Azuma *et al*. 2002). In order to distinguish between formation of DE and VE *in vitro*, Yasunaga *et al*. (2005) exploited the following observations: (1) *Gsc* is expressed in the anterior visceral endoderm of the mouse embryo (Filosa *et al*. 1997) and (2) *Sox17* is expressed in the DE and not in the anterior VE (Kanai-Azuma *et al*. 2002). The authors proposed that it will be possible to distinguish between VE-derived and DE-derived cells by monitoring appearance of mesendoderm markers during differentiation, as the DE forms through an intermediate mesendodermal state while the VE is derived directly from the ICM. In this study, a mESC line with a double knock-in– GFP into the *Gsc* locus and the human *IL2Rα* gene (*CD25*) into the *Sox17* locus– was generated and used to define and characterize the differentiated populations *in vitro* (Yasunaga *et al*. 2005). These authors were able to define mesendoderm-derived DE as Gsc^{+} $Sox17^{+}$ and VE as Gsc^{-} $Sox17^{+}$ and used this marker profile to identify culture conditions that selectively induced formation of either DE (Activin in serum-free medium) or VE (serum-free medium without Activin) and not both tissues. An unexpected observation from this study was that the cells designated as DE also expressed *Tbra*, an expression pattern that has rarely been described (Kispert and Herrmann 1994). This suggests that the mESCs progress through a gastrulation-like stage during differentiation as *Tbra* is a known marker of the same. Activin A could be responsible for this developmental sequence as it is known to induce expression of *Tbra* (D'amour *et al*. 2006; Rust *et al*. 2006; Kubo *et al*. 2004; Kimelman and Griffin 2000). To characterize the DE and VE populations, further microarray analysis of the differentiations was done to identify cell surface

markers. Nine surface markers with 10-fold difference in expression between DE and VE were identified. One of these, Cxcr4, is a chemokine receptor for Sdf-1 (stromal cell-derived factor 1) which is expressed in the DE and mesoderm but not in the VE (McGrath *et al*. 1999). Under conditions that support DE formation, Yasunaga *et al*. found that Cxcr4 expression was induced simultaneously with Gsc while the Gsc^{-} population showed no Cxcr4 expression. As Cxcr4 is not detected in VE or on undifferentiated ES cells, it can be used in combination with DE-specific markers to designate cells from the DE. These studies and others on mESCs encouraged and guided efforts to induce endoderm from hESCs, some of which are described below.

1.5.2. Endodermal differentiation from hESCs

Encouraged by the success of Activin A in generating definitive endodermal derivatives from mESCs when used at a high concentration, this Nodal mimic has been used widely to differentiate hESCs into DE. In one such strategy D'Amour *et al*. (2005) induced endodermal differentiation from hESCs in presence of high Activin A concentration (100 ng/ml) and low levels of serum. This differentiation resulted in the elevated expression of definitive endodermal marker genes like *GSC*, *FOXA2*, *SOX17* and *CXCR4* (described earlier) while markers of primitive, visceral and parietal endoderm like *SOX7*, *Alpha feto protein* (*AFP*) and *Thrombomodulin* (*THBD*) were not detected (Kanai-Azuma *et al*. 2002; Weiler-Guettler *et al*. 1996; Dziadek and Andrews 1983). *FOXA2* and *SOX17* double-positive cells were shown to be derived exclusively from the $TBRA^{+}$ population thus confirming formation of DE as *TBRA* is not detected in the primitive endoderm (Wilkinson *et al*. 1990). The decreasing expression of E-cadherin followed by increasing expression of N-cadherin pointed to an EMT-like event and formation of a primitive streak-like intermediate during

differentiation. Testing the *in vivo* potential of these cells showed partial differentiation into endodermal derivatives. These authors subsequently extended this differentiation strategy to produce pancreatic hormone-expressing endocrine-like cells from hESCs (D'Amour *et al*. 2006).

In the modified protocol, DE was formed by treating cells with Activin A (high) and Wnt3 in serum-free conditions, which eliminated the requirement for serum stimulation. Sequential exposure of the DE to various other reagents like fibroblast growth factor 10 (FGF10), cyclopamine and Retionic Acid resulted in the formation of $PDX1^{+}$ (pancreatic and duodenal homeobox 1) pancreatic endocrine progenitor cells which were further differentiated into hormone-expressing cells. Expression of the transcription factor *Pdx1* in the ventral and dorsal endoderm first specifies the pancreatic fate in the embryonic foregut and this precedes the progressive expression of more mature markers of the endocrine lineage, including *Neurogenin 3* (*Ngn3*) and *Islet 1* (*Isl1*) (Habener *et al*. 2005; Ashizawa *et al*. 2004; Jensen 2004). The hormone-expressing cells formed during the differentiation described by D'Amour *et al*. (2006) responded to a variety of insulin secretagogues, but only showed limited glucose responsiveness. In addition, a significant proportion of the $insulin^{+}$ cells curiously displayed immunoreactivity for the additional islet endocrine hormones glucagon and/or somatostatin. Thus, these cells resemble the infrequent, doubly hormone-positive cells observed in the mouse and human embryo that have been shown by lineage analysis in the mouse to never give rise to adult endocrine cells (Piper *et al*. 2004; Herrera 2002). This emphasized the need for improved protocols for the generation of glucose-sensing insulin-secreting cells from hESCs.

Our lab used a novel hESC differentiation strategy that combines an initial three-dimensional (3D) endoderm induction phase with a series of culture conditions

originally optimized to trigger formation of endocrine *β*-cells from adult pancreatic epithelial duct cells (Phillips *et al*. 2007). Unlike the strategies described above, this differentiation exploited the hESC-EB system as we hypothesized that effective cell-cell interactions within the three-dimensional EB may promote better lineage specification and cell type allocation in a manner reminiscent of human development. Even with the predicted drawbacks of (1) random EB sizes and (2) stochastic internal architecture, which may promote counter-productive cell-cell interactions, this system was effective in reproducibly generating pancreatic endoderm. Genes characteristic of definitive endoderm formation were induced within the first 4 days of differentiation, and this was followed by activation of *PDX1* on day 12. With extended differentiation, a portion of *PDX1*-expressing pancreatic progenitors became further restricted to the endocrine lineage, uniquely expressing the *INSULIN* gene and releasing C-peptide into the culture medium. These *β*-like cells do not produce other pancreatic hormones, show modest glucose responsiveness, and retain their endocrine identity when transplanted into diabetic severe combined immunodeficiency (SCID) mice.

In this protocol Activin A and Bmp4 (bone morphogenetic protein 4) were shown to synergistically enhance the formation of *PDX1*-expressing pancreatic endoderm in a Matrigel-based medium. Matrigel, a mouse EHS sarcoma-derived basement membrane matrix, can function as a supportive scaffold for cellular maintenance by mimicking *in vivo* conditions (Kleinman and Martin 2005). The endoderm-inducing effect of Bmp4 when used with Activin A is unexpected as it has been previously shown to induce formation of trophoblast, extraembryonic endoderm, primordial germ cells, and mesoderm-derived haematopoietic progenitors from hESCs but not definitive endoderm (Kee *et al*. 2006; Valdimarsdottir and Mummery

2005; Xu *et al*. 2002). This ability of Bmp4 to form endoderm is entirely reproducible within the EB-based differentiation and can also be implemented to promote endoderm differentiation of hESCs in a monolayer (Y. Ali, A. Teo, H. Chipperfield– unpublished results). Individually, both Activin A and Bmp4 are known to have critical functions in the embryo around the same period of development. However, synergistic activity between the two that enables the induction of endoderm has not been reported.

Activin A transduces its signal through a complex of Smad2/3 and Smad4 that translocates to the nucleus and binds to *FOXH1 (FAST)* which activates transcription of genes like *Goosecoid* (*GSC*), *NODAL*, *PITX2*, etc. This leads to downstream signaling that results in the formation of mesoderm or endoderm (Schier 2003). In the developing mouse embryo, Bmp4 is first expressed in the extraembryonic region adjacent to the posterior epiblast at gastrulation (Lawson *et al*. 1999; Waldrip *et al*. 1998). Later in development expression is detectable at the junction of the amnion with the posterior PS. Bmp4 signals through Smad1/5/8 to initiate transcription of genes that specify its downstream functions (Wu and Hill 2009; Massague and Gomis 2006; Massague *et al*. 2005). The requirement for extraembryonic Bmp4 in the formation of the node and primitive streak and for epiblast-derived Bmp4 in maintaining left-right patterning in the mouse embryo has been clearly shown using Bmp4 mutant mice that had defects in these processes (Fujiwara *et al*. 2002). However, not much is known about the relevance of Bmp4 in the formation of DE. One study provides evidence that Bmp receptor 1A (Bmpr1a) is required for endodermal morphogenesis in mouse embryos as mutants lacking Bmpr1a in the epiblast form mosaic embryos showing abnormal expression of definitive endoderm markers (Davis *et al*. 2004). Though the endoderm cell identity was not affected, the

distribution of definitive endoderm was defective as seen by the patchy expression of *Foxa1* (marks definitive endoderm) and the formation of the gut tube was incomplete. In a very recent report Bmp4 has been shown to be necessary and sufficient for the specification of ventral endoderm in *Xenopus* (Wills *et al*. 2008). In this study, Bmp4 was overexpressed in *Xenopus* embryos which resulted in the specific induction of ventral endoderm marked by *Sox17β*, *Mixer, VegT,* etc., and not dorsal endoderm. The importance of Bmp signaling for the formation of ventral and not dorsoanterior endoderm was reiterated in experiments employing Bmp antagonists Chordin and Noggin, and morpholino knockdown of Bmp2, Bmp4 and Bmp7. A quadruple knockdown of Bmp2, Bmp4, Bmp7 and β-Catenin resulted in complete abrogation of all endoderm in the embryos, indicating that Bmp and Wnt pathways are essential for endoderm formation in *Xenopus*. These studies suggested that Bmp4 might be acting early in endoderm specification. Therefore, a significant focus of this dissertation is investigation of the role of Bmp4 in the initial part of this differentiation.

It is possible that our differentiation protocol creates an environment that reveals the effect of Bmp4 on primitive streak patterning and endoderm specification as has been reported in other vertebrate systems (Tiso *et al*. 2002; Song *et al*. 2007). It has been demonstrated that differentiating hESC-EBs form a VE-like layer around themselves (Conley *et al*. 2004). In the mouse embryo, the anterior VE (AVE) is known to antagonize formation of the primitive streak by secreting Bmp antagonists (Lewis and Tam 2006). Our lab recently demonstrated that Matrigel inhibits VE formation during *in vitro* differentiation of hESCs (Rust *et al*. 2006). Loss of this tissue might therefore be creating an environment which relieves the Bmp4 antagonism and facilitates its action during differentiation.

A more direct effect of Bmp4 could be due to its induction of *Tbra* expression which has been reported in mESCs (Johansson and Wiles 1995). Since definitive endoderm derived during *in vitro* differentiation of mESCs has been shown to arise from *Tbra*$^{+}$ cells this might be a possible mechanism of Bmp4 action during hESC differentiation (Tada *et al*. 2005; Yasunaga *et al*. 2005; Kubo *et al*. 2004). The three-dimensional differentiation described in Chapter 4 employs extended exposure of EBs to Bmp4 which raises the possibility that Bmp4 could act later in the differentiation on committed endodermal progenitors, possibly mimicking pancreas-promoting signals emanating from the lateral plate mesoderm (Kumar *et al*. 2003). This is supported by a recent study using mESCs which showed that isolating Activin A-induced endodermal progenitors by cell sorting and subsequently culturing them at high density in the presence of Activin A and Bmp4 (and bFGF) promoted both hepatocyte differentiation and activation of *Pdx1* (Gouon-Evans *et al*. 2006). However, this might not be relevant to my differentiation scheme as Bmp4 seems to be acting early to exert an endoderm-specifying effect on the hESCs in Matrigel and does not have a similar effect if added later (data not shown). In addition to probing the how Bmp4 facilitates or directly influences the formation of definitive endoderm it is also important to assess the actual mechanism of endoderm induction by Activin A in hESCs. In Chapter 4 of this thesis, I will describe my efforts towards a) the detailed characterization of differentiation in the 3D Matrigel system and b) the identification of a mechanism for the synergy shown by Activin A and Bmp4 in inducing endoderm from hESCs.

Broad Aims of the Thesis

1. **Test haematopoietic potential of human embryonic stem cells lines– hES2 and hES3– maintained on various culture platforms.**

2. **Characterise the early lineage specification events that occur during *in vitro* endoderm differentiation from human embryonic stem cells.**

3. **Identify a mechanism of action for the observed Activin A and Bmp4 synergy during differentiation by screening for expression of novel genes.**

CHAPTER 2: MATERIALS and METHODS

2.1. Cell culture

2.1.1. Human embryonic stem cell culture

Human embryonic stem cells lines (hESCs), hES2 and hES3, were cultured as described (Reubinoff *et al*. 2000). Briefly, hESC lines were grown on a feeder layer of mitotically inactivated mouse embryonic fibroblasts (MEFs) derived from day 13.5 129/Sv mouse embryos and plated at a density of 5 x 10^4 cells/cm^2 in hESC medium containing Dulbecco's Modified Eagle's Medium (DMEM), 20% Fetal Bovine Serum (FBS), 100 μM non-essential amino acids (NEAA), 2 mM L-glutamine, 1% v/v Insulin Transferrin Selenium (ITS), 0.5% v/v penicillin/streptomycin, and 0.1 mM β-mercaptoethanol (β-ME) (ES Cell Culture Lab Manual, ES Cell International Pte Ltd). Alternatively, hESCs were grown on gamma-irradiated human fibroblasts CCD919 (ATCC) or Ortec (Crook *et al*. 2007) fibroblasts in KO medium containing Knock-out DMEM (KO-DMEM), 20% Knock-out Serum Replacement (KOSR), 2 mM L-glutamine, 100 μM NEAA and 25 ng/ml basic Fibroblast Growth Factor (bFGF) (Strathmann). For routine passaging, hESC colonies were cut into small clumps using a combination of manual and enzymatic methods. The plate was rinsed with Phosphate Buffered Saline (PBS) and treated with 1 mg/ml Type IV Collagenase in PBS for 5 minutes at 37°C. Collagenase was rinsed away with PBS and replaced with hESC/ KO medium. The entire surface area of the plate was streaked with a micropipette tip at approximately 2mm intervals. Cells were then harvested with a cell scraper and transferred to fresh feeder plates previously conditioned in hESC/ KO medium. Typical splitting ratios were between 1:3 and 1:6 depending on the density of the starting culture. Morphologically differentiated colonies or cystic regions were

removed by aspiration prior to dissociation. All tissue culture reagents were purchased from Invitrogen (Gibco) unless otherwise stated.

2.1.2. Stromal feeder cells

Human feeder cells HS-5 and HS-27A were obtained from ATCC and cultured according to manufacturer's recommendations. Briefly, HS-5 cells were thawed and cultured in growth medium composed of DMEM, 4 mM L-glutamine, 4.5 mg/ml Glucose, 1.5 mg/ml Sodium bicarbonate (Na_2CO_3) and 10% FBS. Splitting ratio was 1: 3 to 1: 9. HS-27A cells were grown in medium composed of RPMI 1640, 2 mM L-glutamine, 10 mM HEPES, 1 mM Sodium pyruvate ($C_3H_3NaO_3$), 4.5 mg/ml Glucose, 1.5 mg/ml Na_2CO_3 and 10% FBS. Split ratio was 1: 4 to 1: 5. Mouse stromal cell line OP9 was grown in medium composed of Alpha Minimum Essential Medium without ribonucleosides and deoxyribonucleosides, 2 mM L-glutamine, 1.5 mg/ml Na_2CO_3 and 20% FBS (Nakano *et al*. 1994). Split ratio was 1: 4 to 1: 5.

2.2. Differentiation protocols

2.2.1. Haematopoietic differentiation: Co-culture with stromal cell lines

Human stromal cell lines HS-5 and HS-27A were seeded onto tissue culture dishes at a cell density of 5 $x10^4$ cells/ cm^2. The next day, hESCs or EBs (defined in Chapter 1) were seeded onto the feeder cells. Briefly, hES2 and hES3 cells grown on MEFs were dissociated using Collagenase IV (1 mg/ml). The hESC layer was sectioned into small clumps (3-4 mm) and scrapped off using a cell scraper into hESC medium. Clumps were spun down at 1200 rpm for 3 minutes and resuspended in the appropriate medium, DMEM-based HS-5 medium, RPMI-based HS-27A medium or

hESC medium. Clumps in hESC medium were seeded into 6-well Ultra low attachment plates (Corning Lifesciences) for EB formation for 2 weeks with medium changes every 2 days. Clumps in feeder medium or day 14 EBs were seeded on feeder layers at the seeding density used in routine culture of hESCs. Medium changes were done every 2 days and culture continued for 2 weeks. By day 3, most hESC clumps attached and some seemed to differentiate (change in cell morphology) while others remained undifferentiated. By day 10 almost all clumps seemed to have differentiated. EBs attached by day 2 and seemed to grow out on the feeders. On day 14, cells were detached from the dishes using 0.25% Trypsin and seeded into Methocult H+4435 (Stem Cell Technologies) for the CFU assay described later. Methocult-containing plates were monitored for the appearance of haematopoietic colonies over the next 4 weeks.

OP9, a mouse MCF-deficient stromal cell line, was seeded in tissue culture dishes at 5 x 10^4 cells/ cm^2. hESCs or day 14 hESC EBs were seeded onto the monolayers in OP9 or hESC medium as outlined above. Cultures were continued for 2 weeks with medium changes every 2 days. At the end of culture, cells were dissociated using 0.25% Trypsin and seeded in Methocult for CFU assay as described. If cells with dendritic-like protrusions were observed in culture, 20 ng/ml Tumor Necrosis Factor alpha (TNF-α) and 1 μg/ml Lipo Poly Saccharide (LPS) were added for 90 minutes at 37°C to stimulate maturation of any dendritic-like cells before using the cells for immunostaining.

2.2.2. Haematopoietic differentiation: Use of cytokines

hESC-derived EBs were differentiated in presence of cytokines that are known to be functional during haematopoiesis (Zhan *et al*. 2004). Briefly, hESCs were

dissociated using Collagenase IV and EBs were generated in 6-well ultra low attachment plates. EBs were formed in hESC medium supplemented with 0.1 mM β-ME and 20% FBS. After 2 weeks, EBs were transferred to 6-well tissue culture plates in a differentiation medium containing KO-DMEM, 2 mM L-glutamine, 0.1 mM NEAA, 0.1 mM β-ME and 20% FBS for another 2 weeks. The following cytokines were added to the differentiation medium: 100 ng/ml Stem Cell Factor (SCF), 50 ng/ml Flt3 ligand (Flt3L), and 20 ng/ml Thrombopoietin (TPO) to maintain haematopoietic stem cells and to expand committed progenitor cells; 20 ng/ml Interleukin 3 (IL-3), 100 ng/ml Granulocyte-Macrophage Colony-Stimulating Factor (GM-CSF), and 20 ng/ml Interleukin 4 (IL-4) to enhance maturation of lymphoid cells and dendritic cells (Cytokines from Peprotech). After 4 weeks of differentiation cells were dissociated using 0.25% Trypsin and either immunostained for flow cytometry or seeded in Methocult for CFU assay as described below. If cells with dendritic-like protrusions were observed in culture, these were stimulated with 20 ng/ml TNF-α and 1 μg/ml LPS for 90 minutes at 37°C to induce maturation of any dendritic-like cells before dissociating the cells.

2.2.3. Endodermal differentiation: 3D Matrigel protocol

hESCs cultures were washed with PBS+ (with Ca++, Mg++) and incubated with Collagenase IV (1 mg/ml) for 5 minutes at 37°C. Cells were washed again with PBS+ after removing the Collagenase IV and growth medium was added. Cell layer was sectioned/ streaked into 3-4 mm-sized clumps using a micropipette tip. Differentiated regions were aspirated out before Collagenase treatment. Cell clumps were scrapped off in the medium and spun down at 1500 rpm for 3 minutes. Clumps were resuspended in ice-cold RPMI + 20% KOSR medium containing 1:6 dilution of

Growth Factor reduced Matrigel (BD Biosciences, USA). Early factors (EF) Activin A and Bmp4 (50 ng/ml each; R & D Systems) were added to the relevant aliquot of cells. Clumps were distributed evenly between required number of wells in 6-well ultra low attachment plates (day 0) and incubated at 37°C for the duration of the experiment. Clumps started aggregating and rounding up by day 1 and were compact embryoid bodies by day 2. To accommodate medium evaporation and growth factor depletion and to maintain the semi-solid matrix over extended culture, the culture medium was supplemented on days 3 and 6 by adding 0.5 ml/well of basal RPMI medium (without Matrigel) containing 100 ng/ml Activin A and 100 ng/ml Bmp4. On day 10, EBs embedded in Matrigel were treated with the late factors (LF) - HGF (50 ng/ml), β-cellulin (50 ng/ml) and Exendin-4 (10 ng/ml) (growth factors from R & D Systems). Briefly, 2 ml RPMI+ 20% KOSR basal medium was added to each well and incubated for 1 hour to wash out the early factors. Without disrupting the Matrigel layer 2 ml medium was removed carefully from each well. Medium (0.5 ml) containing the appropriate amount of late factors was added to all wells. The culture medium was similarly supplemented with these late factors on days 13 and 16. One set of EBs did not receive any growth factors. Cultures were harvested every other day till day 20, unless otherwise stated, for expression analysis of *PDX1* and other assorted markers by Q-PCR.

A variation of the above protocol was used to investigate in detail the role of Activin A and Bmp4 in this system. hESCs were dissociated using Collagenase IV and clumps were seeded in RPMI+KOSR medium containing Matrigel as described. Early factors were used to create four different conditions for differentiation- (1) Activin A (50 ng/ml), (2) Bmp4 (50 ng/ml), (3) Activin A + Bmp4 (50 ng/ml each) and (4) No growth factors. The same scheme was followed for medium top-up on

days 3 and 6. The second phase of differentiation was identical for all 4 conditions with the addition of all three Late Factors. EBs were harvested every other day for expression analysis using undifferentiated hESCs as control. Selected samples from this differentiation were used for Microarray analysis described later.

To study the effect of Matrigel on the differentiation, free-floating EBs were generated exactly as above without the supporting Matrigel matrix. Growth factors were used at a concentration of 50 ng/ml. Differentiation of free-floating EBs was done only up to day 10, unless otherwise indicated.

2.3. CFU assay

CFU assay allows generation of clonal colonies from haematopoietic progenitors in a viscous methyl cellulose-based medium supplemented with stimulatory cytokines. Cells/ EBs were dissociated using 0.25% Trypsin and seeded in Methocult (H+4435, Stem Cell Technologies) to allow formation of haematopoietic colonies. Briefly, between 1 x 10^4 and 2 x 10^5 cells in 300 µl KO-DMEM was added to 2.7 ml Methocult and vortexed. After allowing the cell suspension to settle for 5 minutes, 1 ml each was seeded into three 35 mm non-treated culture dishes (Stem Cell Technologies) specifically designed for CFU assays and incubated at 37°C. These plates were monitored over 4 weeks for the appearance of haematopoietic colonies. A cluster of at least 50 cells was counted as a colony, and identification was based on descriptions given in the Atlas of Human Haematopoietic Colonies (Stem Cell Technologies). Since CFU colony morphology was identical for hES2 and hES3, images of colonies shown are from either cell line.

2.4. Flow Cytometry

Cells from the differentiating adherent culture or colonies from the CFU assay were immunostained and subjected to Fluorescence Activated Cell Sorting (FACS) using a FACScalibur (BD Biosciences). Adherent cells were dissociated using 0.25% Trypsin and washed in PBS. Colonies from CFU assays were progressively diluted with PBS to allow easy aspiration of the colonies. Colonies were resuspended and washed in PBS. Cells in PBS were transferred to FACS tubes and fixed using Cytofix/ Cytoperm reagent (BD Biosciences) for 20 minutes on ice. Fixed cells were washed and stained with primary antibody for 40 minutes on ice. All washes post- fixation were done in 1 x washing solution (BD Biosciences) and cells were spun at 1220 rpm for 5 minutes at 4°C. One aliquot of cells was treated with the appropriate isotype control or used as control with no primary antibody addition. After 2 washes appropriate secondary antibodies were added and incubated for 30 minutes on ice. Cells were washed to remove excess secondary antibody and resuspended in PBS + 1% FBS. Samples were analysed on FACScalibur and quantitated using Cellquest Pro software. Normalisation was against the isotype or no primary antibody control. The following primary antibodies were used at 1:100 dilutions: CD83-FITC, CD45-PE, CD14-PerCP-Cy5.5, CD34- FITC and CD86-Biotin (all from BD Biosciences). Isotype controls IgG1k-FITC, IgG1k-PE, IgG2ak-PerCP-Cy5.5 and IgG1k-Biotin (BD Biosciences, USA) were used at 1:100 dilutions.

2.5. Immunocytochemistry

Plated cells/ EBs were washed 2x with PBS and fixed in 4% paraformaldehyde (PFA) for 30 minutes at room temperature. After 2 washes, cells/ EBs were blocked using blocking solution (10% FBS, 0.05% Triton X-100 in PBS) for 1 hour at room

temperature. Diluted primary antibody was added to the cells after removing the blocking solution and incubated overnight at 4°C. Cells were washed 3x with PBS. Diluted secondary antibody was then added and incubated for 1 hour at room temperature. Cells were washed 3x with PBS and incubated for 3 minutes at room temperature with 1:10,000 diluted Hoechst 33342 (Molecular Probes). Cells were washed 2x in PBS and either observed immediately or the next day using a Zeiss Axiovert microscope. All antibody dilutions were performed with blocking solution. For haematopoietic cells, fluorophore-conjugated primary antibodies CD34-FITC and CD45-PE were diluted 1:100 for use. For endodermal differentiation primary antibodies Sox-17, Foxa2 (R&D systems) and Oct4 (Santa Cruz Biotech) were diluted 1:100 for use. Alexa 488 was the secondary antibody used at a dilution of 1:200.

2.6. Differential staining

May-Grünwald and Giemsa staining is a differential staining procedure done to distinguish between various types of cells in blood. Methocult cultures were progressively diluted with PBS to allow easy removal of colonies for staining. Colonies collected were pooled and washed in PBS. Cells in 100 µl PBS was spun on to poly-lysine-coated slides at 500 rpm for 5 minutes with low acceleration. Slides were fixed in absolute Methanol for 20 minutes. Staining solutions were diluted using 0.2 M phosphate buffer or Sorenson's buffer (**Appendix I**). Without washing or drying, slides were stained with May-Grünwald stain (diluted 1:1 with Sorenson's buffer) for 10 minutes followed by Giemsa stain (1:10 using Sorenson's buffer) for 30 minutes. Slides were rinsed once with Sorenson's buffer (0.2 M phosphate buffer) and washed in running deionised water. Air-dried slides were examined using a Zeiss Axiovert Microscope. Blood cell types were identified using published images of

stained blood films (slides 1-6) from the following webpage as reference. http://www1.imperial.ac.uk/medicine/about/divisions/is/haemo/morphology/bain/images/default.html

2.7. RNA extraction

EBs or cells collected at different time points were washed in PBS to remove medium and lysed in Trizol (Invitrogen) or RLT buffer (RNeasy Kit, Qiagen) for RNA extraction. To ensure complete lysis, cells in RLT buffer were first spun through Qiashredder columns (Qiagen) at 13,000 rpm for 2 minutes. Lysates from either method were stored at -80°C till use. Trizol lysates (500 µl) were thawed on ice, mixed well with 150 µl Chloroform and incubated at room temperature for 3 minutes. Lysates were spun at 12,000 rpm for 15 minutes at 4°C and the aqueous phase was transferred to a fresh tube. RNA was precipitated by adding 375 µl of Isopropanol and incubating at room temperature for 10 minutes followed by centrifugation at 12,000 rpm for 10 minutes at 4°C. The supernatant was discarded and the pellet resuspended in 1 ml 70% Ethanol, vortexed and spun at 7,500 rpm for 5 minutes at 4°C. After removing the supernatant, the pellet was air-dried and re-suspended in 30 µl RNase-free water for quantification using Nanodrop. Ethanol, Chloroform and Isopropanol were from Sigma Aldrich. RLT buffer lysates were processed using the RNeasy kit (Qiagen) according to manufacturer's instructions. RNA was eluted in 30 µl RNase-free H_2O and quantitated using the Nanodrop.

2.8. Quantitative RT-PCR

5 μg RNA was reverse transcribed to generate cDNA for quantitative PCR. For cDNA preparation, 60 μg/ml Random Primers (Invitrogen), 1x MMLV RT Buffer (NEBL) and 0.5 mM dNTP mix (Invitrogen) was added to each sample and mixed well. An aliquot was removed as the RT negative control (-RT). 1 μl MMLV Reverse Transcriptase (NEBL) was added to each sample and incubated at 37°C for 1 hour after mixing well. RT was inactivated by heating samples at 95°C for 5 minutes. Each Q-PCR consisted of 50 ng cDNA, 2x Sybergreen master mix and 10 mM primer mix (forward and reverse). PCR was performed using the iCycler MyiQ (Biorad). Quantitation was performed either against a standard curve or according to ΔCt relative to β-actin amplification. Primer pairs are listed in **Appendix II.**

2.9. Western blotting

EBs were harvested and washed in PBS to remove all traces of media. Pellet was snap frozen in liquid nitrogen and stored at -80°C till use. For protein extraction, the pellet was thawed and lysed in RIPA (Radio Immuno Precipitation Assay) buffer with freshly added 1 mM PMSF (phenylmethanesulphonylfluoride) (Sigma) and 1X protease inhibitor cocktail (Roche). Lysate was triturated to lyse the EBs efficiently and spun down at 13,000 rpm for 10 minutes to remove debris. Supernatant was collected and spun a second time at 13,000 rpm for 5 minutes. Total protein content of the supernatant was estimated using the BCA protein assay (Pierce) following manufacturer's recommendations. Colorimetric measurements were done using the Fluorostar Optima plate reader. For western blot, 20-30 μg total cellular protein was loaded in each well along with 1X Laemmli sample buffer.

Using the Biorad mini-Protean System, 1.5 mm thick gels (3% stacking and 8% running) were run at 100 V for 90 minutes in 1x Tris Glycine SDS (Sodium Dodecyl Sulphate) buffer (Biorad). Pre-stained molecular marker (Biorad) was used to identify and assign sizes to the protein bands on the gel. Gels were blotted onto Hybond-P PVDF or Hybond C-extra nitrocellulose membrane (Amersham Biosciences) under semi-dry conditions in Transfer buffer for 45 minutes at 10 V. Blots were stained with Ponceau S to check for transfer and before blocking in either 5% w/v non-fat dry milk or 5% Bovine Serum Albumin (BSA) (Sigma) in 1X Tris Buffered Saline (TBS) + 0.1% Tween-20 (Sigma) (TBST). After one hour of blocking, blots were incubated overnight at 4°C with the primary antibody diluted appropriately in blocking buffer. Blots were washed 5 times in TBST to remove excess and unbound primary antibody. Secondary antibody incubation was performed for one hour at room temperature and blots were washed 5 times to remove excess secondary antibody. Gel and buffer compositions are given in **Appendix I**.

Chemiluminescent detection of proteins was done using the ECL Plus system (Amersham Biosciences) according to manufacturer's recommendations. Protein signal was captured on Hyperfilm (Amersham Biosciences) and developed using a Kodak film processor. Rabbit polyclonal primary antibodies pSmad2/3 and pSmad1/5/8 were diluted 1:1000 before use (Cell Signaling). Monoclonal anti- human Actin antibody was diluted 1:4000 for use (Chemicon). Secondary antibodies, anti-rabbit IgG-HRP (Cell Signaling) was used for the Smad antibodies at 1:1000 dilution. Actin was detected using anti-mouse Ig-HRP (Dako) at 1:4000 dilution.

2.10. Microarray

hESCs were differentiated using a variation of the 3D Matrigel protocol in 4 different conditions- (1) Activin A (50 ng/ml), (2) Bmp4 (50 ng/ml), (3) Activin A + Bmp4 (50 ng/ml each) and (4) No growth factors. RNA from undifferentiated hESCs on day 0 and hESC-EBs harvested on days 4 and 6 was used for microarray using the Illumina Sentrix® BeadChip Human Reference 8 Version 2. Two biological replicates of each sample were performed. An aliquot of each RNA sample (500 ng) was converted to complementary RNA with the Illumina TotalPrep™ RNA Amplification Kit (Ambion) according to manufacturer's recommendations. Purified cRNA samples were added to the Illumina BeadChips and loaded into the Hybridization Chamber. After overnight incubation at 58ºC on a rocker BeadChips were washed thoroughly, blocked and stained with Streptavidin-Cy3. Once the chips were thoroughly washed and dried, the staining was detected and measured using an Illumina Bead scanner. Data was generated using Illumina Bead Studio software and analysed using Genespring software. Statistically relevant data were generated using the paired T-Test ($p \leq 0.17$).

2.11. Whole Mount *In Situ* Hybridisation (WISH)

2.11.1. Cloning of genes

Total Mouse embryonic RNA from E7.5, E8.5 and E9.5 was used for cDNA preparation as described earlier. A partial cDNA fragment was amplified by PCR using primers spanning the 3' UTR (variable) region of each specific gene. The PCR product was resolved on a 1% agarose gel run at 100V for 40 minutes and visualized using 0.5ug/ml Ethidium Bromide added in the gel. Once product size was confirmed,

the DNA fragment was cloned into the TOPO PCR II vector according to manufacturer's recommendations (TOPO TA Cloning Kit, Invitrogen). The plasmid preparation was used to transform TOP10 (Invitrogen) or XL-Gold (Stratagene) cells according to manufacturer's recommendations. Clones, after selection for Ampicillin resistance and lack of X-gal staining were grown up and plasmid DNA was extracted subsequently using the Qiaprep Miniprep kit (Qiagen) according to manufacturer's recommendations. DNA was quantitated using Nanodrop and 1 μg of each sample was used for restriction enzyme (RE) digest analysis to confirm insertion of specific gene fragment.

RE digest was done using appropriate enzymes that would cut the plasmid at sites such that the DNA insert is released as a single fragment. Reactions were carried out in recommended buffers at 37°C for 90 minutes. Digested DNA was run on 1% agarose gels at 100V for 40 minutes to confirm proper digestion and fragment release. Clones containing the correct insert were subsequently sequenced and aligned against the expected PCR product gene sequence to confirm the 5' to 3' orientation of insert in the pCRII vector.

2.11.2. Riboprobe synthesis

For riboprobe synthesis, 2 μg of the plasmid prep was linearised using an RE that cuts only once at the 5' end of the insert. RE digest was done as described earlier in a total volume of 40 μl at 37°C for 2 hours. 2ul of the RE reaction was run on a 1% agarose gel to confirm for complete linearization. The remainder was purified using the QIAquick PCR Purification kit according to manufacturer's recommendations (Qiagen) and eluted in 40 μl RNase-free H_2O. 500 ng of DNA was used for subsequent RNA synthesis using either the T7 or SP6 RNA polymerases (Stratagene).

RNA synthesis was done in 5X reaction buffer (Roche) + Digoxigenin-NTP (Dig-NTP) (Roche) + RNasin (Stratagene) + Dithiothreitol (DTT) (Promega) + DNA template + appropriate polymerase at 37°C. After 2 hours, 2 µl of the reaction was run on a 1.5% agarose gel (90V for 45 mins) to check for the RNA synthesis product. .Upon RNA product confirmation, RNA was treated with 2 µl DNase I (Qiagen) at 37°C for 15 minutes to remove residual DNA template. RNA was precipitated at -20°C for 30 minutes in 4 M Lithium Chloride (LiCl; 10 µl) and 100% Ethanol (300 µl). Precipitate was spun down at 16,000 g for 15 minutes at 4°C and washed once in 100% Ethanol (500 µl). RNA pellet, air-dried and thereafter resuspended in 30 µl H_2O, was stored at -80°C till use.

2.11.3 Whole-mount In Situ Hybridisation (WISH)

Mouse embryos previously harvested, fixed and stored in Methanol at E7, E7.5, E8.5 and E9.5 were used for WISH. Embryos were rehydrated using a Methanol + PBT (PBS + 1% Tween-20) series with decreasing concentration of Methanol. After 2 rinses in PBT, embryos were bleached in freshly prepared H_2O_2 in PBT for 1 hour. Embryos were washed 3x in PBT and treated with 10 µg/ml Proteinase K/ PBT: 3 minutes for E7 and E7.5, 4 minutes for E8.5 and 5 minutes for E9.5. Embryos were washed in 2 mg/ml Glycine/ PBT for 5 minutes followed by 2 washes in PBT. At this point embryos were sorted such that there were at least 2 embryos of each stage per in-situ probe. After proteinase K treatment, 4% PFA + 0.2% glutaraldehyde (Sigma) was used to re-fix the embryos for 20 minutes at room temperature. After 2 washes in PBT, the embryos were rinsed in pre-warmed Hybridisation solution (Hyb). Embryos were incubated in Hyb for 2 hours at 70°C. 50 - 100 ng of the earlier synthesized RNA in-situ probe was added to the embryos in fresh Hyb and incubated overnight at

70°C with gentle rotating. The next day, embryos were first washed in pre-warmed Hyb for 5 minutes at 70°C, followed by washes in Formamide wash buffers: Solutions I and II at 70°C and 65°C respectively. Embryos were washed 3x in MAB buffer + 1% Levamisole before blocking for 90 minutes at room temperature in embryo blocking solution. Embryo blocking solution was MAB + 2% Boehringer Mannheim Blocking Reagent (BBR) + 10% Heat Inactivated Sheep Serum (HIS) + 1% Levamisole. This was followed by treatment with the pre-absorbed anti-Dig antibody overnight at 4°C with gentle shaking. Pre-absorption was done in antibody block solution using acetone powder prepared from grounded E12.5 embryos to block non-specific hybridisations. Briefly, MAB + 2% BBR + 1% Levamisole + 1 mg mouse embryo acetone powder (per probe) were mixed and heated at 70°C for 30 minutes. After cooling on ice and vortexing for 5 minutes, 10 µl HIS and 1 µl anti-Dig antibody (per probe) were added and samples kept at 4°C for 1 hour with gentle shaking. Acetone powder residue was spun down at 13,000 rpm for 10 minutes and the supernatant was diluted in embryo block for use. The next day, embryos were washed extensively in MAB + 1% Levamisole followed by 3 washes in Alkaline Phosphatase (NTMT) buffer. BM Purple staining solution (Roche) was added to the embryos and incubated in the dark at room temperature till colour develops. Colour reaction was stopped using 2 mM EDTA in PBT and stained embryos were stored at 4°C indefinitely. Images were obtained on the Olympus MVX10 inverted Microscope. Buffer compositions are given in **Appendix I**.

CHAPTER 3: HAEMATOPOIETIC DIFFERENTIATION

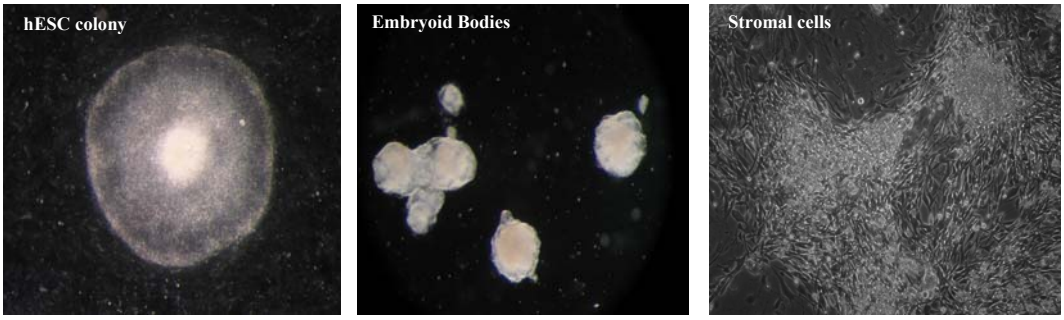
INTRODUCTION

As described in Chapter 1, the rejection of hESC-derived cell transplant material is a significant concern in regenerative medicine as their immunological profile will be recognized as foreign (Draper and Andrews 2002; Drukker *et al*. 2002). Suggested strategies to reduce the immunogenicity of such cells include (1) transplanting into immune-privileged sites in the body, (2) exploiting the immune-privileged status of hESCs imparted by the low expression of MHC class I molecules on their cell surface and (3) inducing transplantation tolerance using hESC-derived haematopoietic cells (Drukker *et al*. 2006; Drukker and Benvenisty 2004; Li *et al*. 2004). Theoretically, haematopoietic cells derived from the same exact source as the therapeutic graft, specifically a given hESC line, could tolerise the recipient towards the incoming transplant material irrespective of its cellular nature (Kaufman and Thomson 2002). Existing reports of haematopoietic differentiation from hESCs at the time I initiated my dissertation research used either stromal cell co-culture or cytokine treatment to induce formation of these mesodermal derivatives (Kaufman *et al*. 2001, Chadwick *et al*. 2003). Kaufman *et al*. co-cultured hESCs with a human stromal cell line S17 to generate CD34 expressing haematopoietic progenitors. These cells had the capacity to form more differentiated cell types like erythroid, myeloid and megakaryocytic lineages as evidenced by marker expression. In contrast, Chadwick *et al*. used a selection of cytokines and Bone Morphogenetic Protein 4 (Bmp4) to derive haematopoietic progenitors expressing the pan-haematopoietic marker CD45 from hESCs. These studies provided the experimental framework for my investigation in this chapter into the ability of hESC lines, hES2 and hES3, to undergo haematopoietic differentiation. The need for embarking on this series of experiments is further

elaborated in Chapter 4, which chronicles my experimental contribution toward our laboratory's overarching goal of generating insulin-secreting beta cells from hESCs. This clinical goal prompted concurrent work on haematopoietic differentiation of hESCs which could provide a transplantation tool to allow successful engraftment of therapeutic grafts (**Figure 1.3**). In this chapter I will describe the preliminary results obtained for differentiation of hESC lines, hES2 and hES3, into cells of the haematopoietic lineage using the following two experimental strategies:

1. Co-culture of hESCs with stromal cell lines OP9, HS-5 and HS-27A (**Fig 3.1B**).
2. Exposure of hESC-EBs to cytokines SCF, G-CSF, IL-3, IL-6 and Flt3L (**Fig 3.1C**).

A



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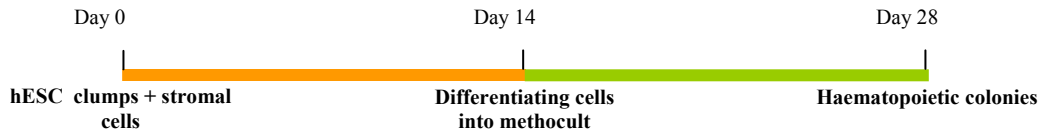

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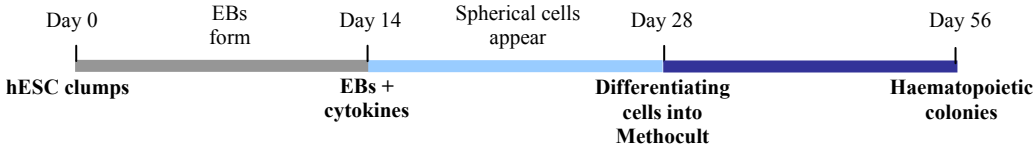


Figure 3.1. Summary of various protocols tested. (A) Representative images of a hESC colony (hES3), day 14 EBs and stromal cell lines (OP9). **(B)** Schematic of differentiation strategy using stromal cell lines OP9, HS-5 and HS-27A. hESC clumps seeded onto stromal monolayers were differentiated for 14 days and plated in Methocult for CFU assay (Nakano 1994, Kaufman 2001). **(C)** Schematic of haematopoietic differentiation in presence of cytokines. Day 14 hESC-EBs were seeded in tissue culture plates with SCF, GM-CSF, TPO, Flt3L, IL-3 and IL-4 and cultured for 2 weeks before plating into Methocult for CFU assay (Zhan *et al*. 2004).

RESULTS

3.1. hESC-derived embryoid bodies (EBs) give rise to haematopoietic-like cells when co-cultured with stromal cell lines

Stromal cells of bone marrow or yolk sac origin are known to support the growth and maintenance of haematopoietic progenitors in culture (Lu *et al*. 1996; Wineman *et al*. 1993). In a prior study, the mouse bone marrow-derived cell line S17 was used successfully to generate mixed populations of haematopoietic cells *in vitro* from hESCs (Kaufman *et al*. 2001). In contrast, I investigated the ability of OP9, a murine macrophage colony stimulating factor (M-CSF)-deficient cell line to promote haematopoietic differentiation from hESCs. OP9 has been shown extensively to support the maintenance of haematopoietic progenitors differentiated from mESCs *in vitro* (Nakano *et al*. 1994; Kyba *et al*. 2002; Kitajima *et al*. 2003). In addition, I co-cultured hESCs with immortalised human bone marrow stromal cell lines HS-5 and HS-27A, which are known to maintain bone marrow-derived haematopoietic progenitors in culture (Roecklein and Torok-Storb 1995). HS-5 secretes large amounts of cytokines; conditioned medium from this line supports the *ex vivo* expansion of both immature and mature haematopoietic progenitors. HS-27A does not secrete cytokines but has been shown to support formation of typically haematopoietic "cobblestone areas" from progenitor cells of human bone marrow origin (Torok-Storb *et al*. 1999). hESC lines and stromal cell lines were maintained as described in Chapter 2.1. Briefly, hES2 and hES3 maintained on MEFs were dissociated and hESC clumps were seeded on stromal cells OP9, HS-5 and HS-27A (Chapter 2.2.1). Previous reports suggested that haematopoietic differentiation of mESCs and hESCs is initiated around day 5 and continues for more than 2 weeks

(Kaufman *et al*. 2001; Kitajima *et al*. 2003). Anticipating a similar timeframe, I monitored the morphological changes during differentiation over a period of 2 weeks. However, none of the typical colony or haematopoietic cell morphologies were detectable in culture over this period (Kitajima *et al*. 2003). Given the possibility that the cell lines used in this study might not yield identical results to those described in the prior reports, the differentiation was prolonged for another week. Though no haematopoietic-like morphological changes were obvious at the end of 3 weeks, the differentiation was continued and cells were seeded in Methocult for the CFU assay (Chapter 2.3). Plates were monitored for the appearance of colony forming units over the next 28 days. Disappointingly, no haematopoietic colonies were observed in this first of four independent experiments. Subsequent attempts at this protocol– hESC co-culture with stromal cells– did not yield any haematopoietic-like cells or colonies in Methocult (data not shown).

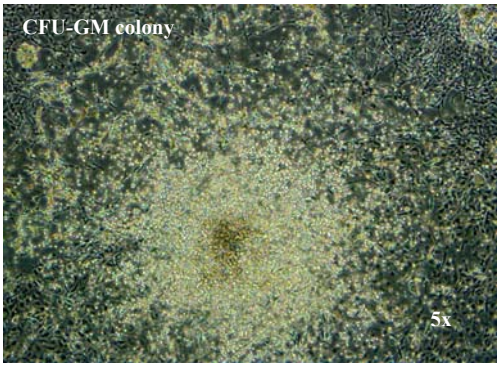
Therefore, I employed an alternative approach using the EB system which has been shown to generate progenitors of all three germ layers by spontaneous differentiation (Schuldiner *et al*. 2000; Keller 1995). Our lab previously reported that the architecture of a human EB bears some resemblance to the pre-gastrulation mammalian embryo; it forms an outer layer of visceral (extraembryonic) endoderm (VE) and expresses known markers of the VE (Rust *et al*. 2006). I hypothesized that the appropriate combinations of cell culture conditions and cytokines could act on spontaneously differentiating EBs and guide the differentiation to form predominantly mesoderm. hESC clumps in growth medium were seeded into Ultra low attachment plates for EB formation over the next 14 days. This particular time frame was chosen based on existing reports of haematopoietic differentiation. After 14 days of spontaneous differentiation, EBs were plated on stromal cell monolayers. Co-culture

was carried out over the next 14 days during which the EBs readily attached and grew out. Following co-culture, cells were seeded in Methocult for the CFU assay. Unlike what was seen during the co-culture of hESCs on stromal cells, haematopoietic-like colonies of the CFU-GM (colony forming unit-granulocyte macrophage) type were visible by day 14 in plates seeded with cells from hES3-EBs co-cultured on OP9 (**Fig 3.2A**). CFU-GM colonies were large and relatively homogenous, though some colonies had more cells concentrated in the centre. Pooled cells from these colonies were cytospun on to slides for Giemsa and May-Grünwald staining. Neutrophils were clearly distinguishable by their segmented nuclei (**Fig 3.2B**).

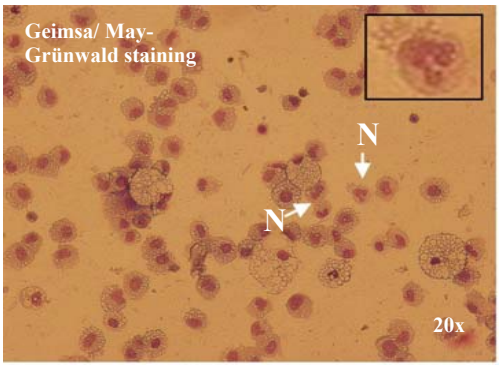
In addition, immunostaining of cells from the Methocult colonies was performed for CD45 (pan-haematopoietic), CD14 (monocytic), CD86 (antigen presenting cells) and CD83 (mature DCs) antigens. The DC-specific marker was chosen since many cells showed dendrite-like protrusions. Cells were stimulated with LPS and TNF-α prior to staining. Flow cytometry revealed significantly high numbers of haematopoietic cells (**Fig 3.2C**). Staining was detected in the gated population (excludes dead cells) of which 66% were $CD45^+$ haematopoietic cells. $CD14^+$ monocytes and $CD86^+$ macrophages or antigen presenting cells were also abundant. CD83 expression was low indicating the absence of mature dendritic cells. The marker profile shows that stromal co-culture induced haematopoietic differentiation in cells derived from hESC-EBs but not in differentiating hESCs.

The presence of haematopoietic colonies in the CFU assay and the marker expression profile of these colonies indicate that haematopoietic differentiation has occurred from the hESC-EBs. These differentiated cells, which form colonies in semi-solid media and express CD45, represent committed progenitors with limited development and differentiation potential.

A


CFU-GM colony
5x

B


Geimsa/ May-
Grünwald staining
N
N
20x

C

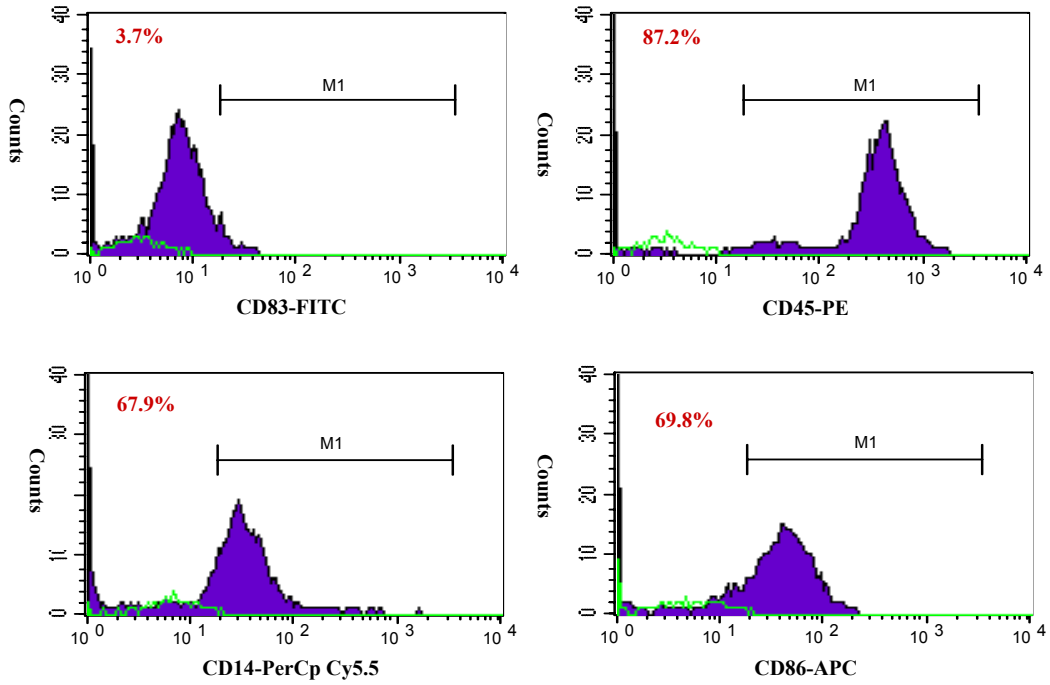

3.7%
M1
Counts
CD83-FITC
87.2%
M1
Counts
CD45-PE
67.9%
M1
Counts
CD14-PerCp Cy5.5
69.8%
M1
Counts
CD86-APC

Figure 3.2. hESC-EBs co-cultured with OP9 stromal cells give rise to haematopoietic colony forming units. Day 14 hESC-EBs were co-cultured on OP9 stromal layers for 14 days. On day 14, EBs were plated in Methocult for CFU assay and incubated for 28 days. **(A**) Phase contrast image of a CFU-GM (Colony Forming Unit-Granulocyte Macrophage) formed in Methocult (5x magnification). These colonies were tightly packed. **(B)** Giemsa and May-Grünwald staining of cells pooled from various colonies formed in Methocult (20x magnification). Neutrophils were the most common cell type observed (white arrows labelled N). Inset shows magnified image of a neutrophil. **(C)** FACS analysis of pooled cells immunostained for CD45, CD14, CD83 and CD86. The green line represents isotype control while the purple filled area indicates stained cells. Expression of each marker within the marker region (M1) is indicated as percentage of the gated live population. Expression of the pan-leukocyte marker CD45 and the monocytic marker CD14 was high. This is not surprising since colonies in Methocult were mainly of granulocytic origin. CD86 (marker of antigen presenting cells) was extremely high suggesting that some of the cells were terminally differentiated and formed a macrophage or antigen presenting cell population.

Stromal Cell Line	Source	Salient Feature/s	Summary of Results
HS-5 (**Roecklein 1995, Blood**)	Human	•E6/E7 Papilloma Virus-transformed cells •Secretes haematopoietic cytokines	NO haematopoietic differentiation using hESCs or hESC-EBs
HS-27A (**Torok-Storb 1999, Ann N Y Acad Sci.**)	Human	•E6/E7 Papilloma Virus-transformed cells •Supports formation of haematopoietic "cobblestone areas"	NO haematopoietic differentiation using hESCs or hESC-EBs
OP9 (**Nakano 1994, Science**)	Mouse	•Macrophage Colony Stimulating Factor (M-CSF) deficient cell line •Known to support haematopoietic differentiation of mESCs	Spontaneous and sporadic myeloid differentiation from hESC-EBs only.

Table 3.1. Various stromal feeders used, their features and outcome of differentiation.

It is possible that this strategy does not support the formation of more versatile multi-potent progenitors with a wider differentiation capability due to culture conditions including the choice of cytokines. Most of the differentiated haematopoietic cells were monocytic ($CD14^+$) with a significant percentage becoming antigen presenting cells or macrophages ($CD86^+$), though few were mature dendritic-like cells (CD83). Therefore the differentiation seems to be biased towards the formation of leukocytes ($CD45^+$), most of which are monocytic and immature antigen-presenting cells. The human stromal cell lines HS-5 and HS-27A did not support haematopoietic differentiation of hES2 and hES3 in any of the conditions described above. The results are summarized in **Table 3.1**.

3.2. hESCs form haematopoietic-like cells when differentiated in presence of pro-haematopoietic- cytokines

The use of haematopoietic cytokines to promote haematopoietic differentiation from hESCs has been clearly demonstrated in the literature. In one of the earliest successful studies, Chadwick *et al*. used cytokines SCF, G-CSF, Flt3L, IL-3, and IL-6 in the presence of Bmp4 to generate self-renewing $CD45^+$ $CD34^+$ haematopoietic progenitor cells *in vitro* (Chadwick *et al*. 2003). A slightly different combination of haematopoietic cytokines was used by Zhan *et al*. to produce functional antigen presenting cells and leucocytes from hESCs (Zhan *et al*. 2004). As mentioned earlier, antigen-presenting cells (APCs; DC-like cells) may be preferable over a mixed pool of haematopoietic cells for transplantation studies. This prompted me to adapt this strategy for the *in vitro* differentiation of hES2 and hES3 into cells of the haematopoietic lineage. The cytokines used in this study and their known functions are summarized in **Table 3.2**.

EBs were generated from hES2 and hES3 cells in Ultra low attachment plates as described in Chapter 2.2.2. After 14 days, EBs were plated onto tissue culture plates in Differentiation medium with the addition of SCF, Flt3L, TPO, IL-4, GM-CSF and IL-3. Most EBs attached in two days and generated cellular outgrowths (day 6) in culture. After two weeks of culture two wells of cells were used for CFU assay while the rest were left to differentiate further. Extended differentiation generated floating or loosely attached spherical cells (**Fig 3.3A**) and cells with dendrite-like protrusions (**Fig 3.3B**) on day 20 of culture. Interestingly, these cells were only observed in hES2 cultures, alluding to differences between hESC lines in their potential to differentiate into haematopoietic cells. The two cell types observed in culture increased in number over the next 4 days. To confirm their haematopoietic identity, cells were immunostained for haematopoietic, monocytic and dendritic markers after stimulation with TNF-α and LPS. Flow cytometric analysis of immunostaining showed 44% $CD45^+$ cells in the gated live population (**Fig 3.3C**). CD14 expression was high indicating the presence of monocytes. Low CD83 staining shows that mature dendritic cells were not formed in culture. The marker expression profile suggests that haematopoietic differentiation in the presence of these particular cytokines generates cells which are very similar to those seen when OP9 was used as stromal support.

As described earlier, 2 wells of cells from the adherent culture (day 14) were seeded in Methocult for the CFU assay (~150,000 cells per plate). Colony forming units appeared in these plates by day 17– mainly CFU-GM (**Fig 3.4A**) and CFU-M (**Fig 3.4B**) types. While CFU-GM colonies were large and tightly packed with small sized cells, CFU-M colonies were smaller and consisted of sparsely arranged cells. Colonies pooled from the CFU assay plates were used for immunostaining and for Giemsa and May Grünwald staining.

Cytokines	Function(s)
Stem Cell Factor (SCF) or c-kit ligand	Required for self-renewal, growth and differentiation of the more primitive haematopoietic progenitors and for some early lineage progenitors.
Granulocyte Macrophage Colony Stimulating Factor (GM-CSF)	Growth factor for several lineage progenitors and differentiation factor acting on granulocytes, macrophages and dendritic cells.
Thrombopoietin (TPO)	Regulates the production of platelets by bone marrow by stimulating the production and differentiation of megakaryocytes.
Flt3 Ligand (Flt3L)	Ligand for the FLT3 tyrosine kinase receptor. Belongs to a small group of growth factors that regulate proliferation of early haematopoietic cells.
Interleukin- 3 (IL-3)	Multipotent haematopoietic growth factor; induces proliferation, maturation and probably self-renewal of pluripotent haematopoietic stem cells and cells of myeloid, erythroid and megakaryocytic lineages.
Interleukin- 4 (IL-4)	Stimulates activated B-cell and T-cell proliferation. Induces the differentiation of naive helper T cells (Th0 cells) to Th2 cells.

Table 3.2. Cytokines used in haematopoietic differentiation of hESC-derived EBs and their known functions.

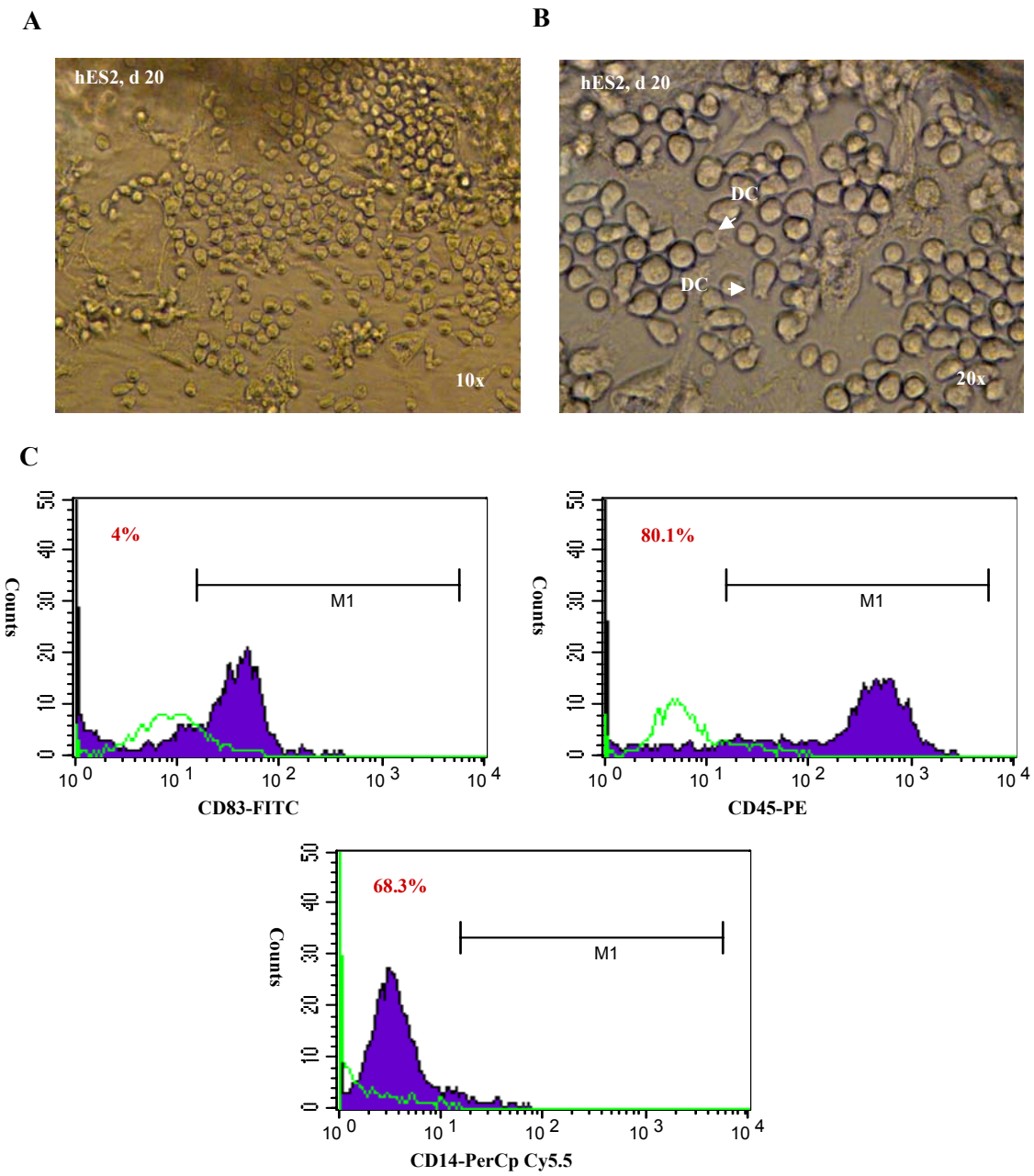


Figure 3.3. hESC-EBs treated with cytokines give rise to haematopoietic-like cells in culture. Day 14 hESC-EBs were differentiated for 14 days in presence of haematopoietic cytokines. **(A, B)** Distinct areas with spherical haematopoietic-like cells and cells with dendrite-like projections (white arrows labelled DC in **B**) were observed in culture (10x and 20x magnification respectively). **(C)** FACS analysis of these cells immunostained for CD45, CD14 and CD83. Cells were stimulated with LPS and TNF-α for 90 minutes prior to staining to induce maturation of DCs. The green line represents isotype control while the purple filled area indicates stained cells. Expression of each marker within the marker region (M1) is indicated as percentage of the gated live population. High expression of CD45 and CD14 shows that granulocytic differentiation has occurred in the cultures. CD83 staining was not significant enough to conclude the presence of mature DCs. CD86 was not used due to lack of cells.

Differential staining showed the presence of neutrophils, eosinophils, basophils and monocytes (**Fig 3.4C**). Flow cytometric analysis of immunostaining with antibodies to CD45, CD14, CD83 and CD86 revealed an expression profile similar to that of cells in adherent culture. Ninety-six percent of the gated live cell population was found to be $CD45^{+}$. Presence of $CD14^{high}$ cells indicates significant monocytic differentiation (**Fig 3.4D**).

Using cytokines to differentiate hESCs gave rise mainly to $CD45^{+}$ leukocytes, which included a high number of $CD14^{+}$ monocytic cells. Expression of co-stimulatory molecules CD86 and CD83 (specific to dendritic cells) was low indicating that differentiation did not progress beyond a certain progenitor stage. In contrast to the OP9-based differentiation, CD86 expression was very low indicating that antigen presenting cells or macrophages were more efficiently formed in the stromal co-culture. Though Zhan *et al*. (2004) generated very high numbers of haematopoietic cells using the combination of EB formation and cytokines, hES2 produced relatively low numbers of these cells in a similar protocol. hES3 did not form CFUs or stain for haematopoietic markers. The reasons for this are unclear, but tailoring the protocol to the specific differentiation requirements of hES2 and hES3, for example, optimising the concentration of cytokines, would likely help to address this shortfall.

3.3. hESCs maintained on human feeder cells are amenable to haematopoietic differentiation

Historically hESCs have been grown on feeder cells of murine origin. This particular culture platform can have an impact on the differentiation potential of these hESCs.

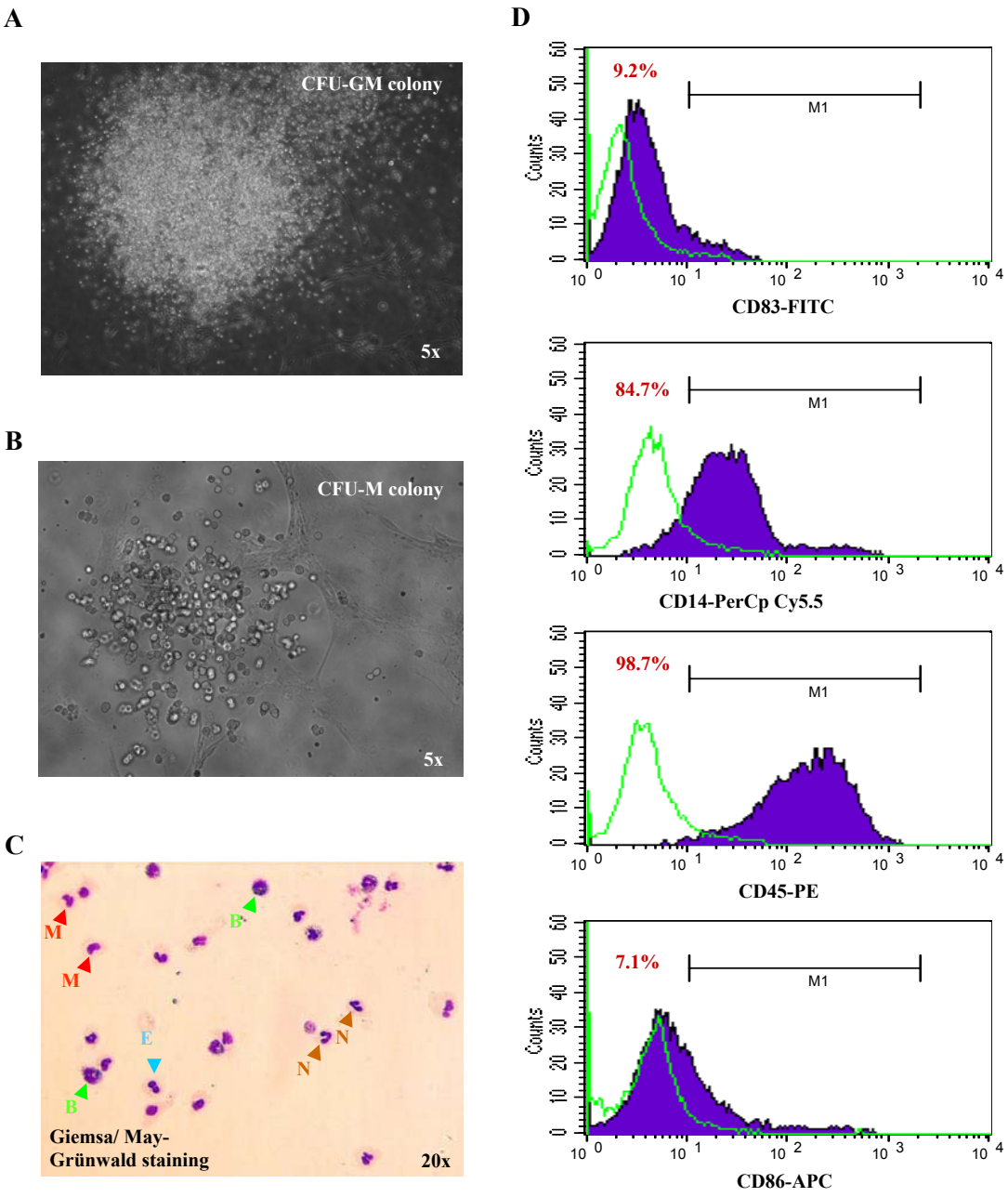


Figure 3.4. hESC-EBs differentiated in presence of cytokines generate haematopoietic colony forming units in Methocult. hESC-EBs differentiating in presence of cytokines (shown in Fig. 6) were plated in Methocult for CFU assay. **(A, B)** Representative images of CFU-GM (Granulocyte Macrophage) and CFU-M (Monocyte) colonies (5x magnification). **(C)** Giemsa and May-Grünwald staining of pooled cells from colonies (20x magnification). Neutrophils (brown arrow heads), eosinophils (blue arrowheads), basophils (green arrowheads) and monocytes (red arrowheads) are shown. **(D)** FACS analysis of pooled cells immunostained for CD45, CD14, CD86 and CD83. The green line represents the isotype control while the purple filled area indicates the stained cells. Expression within the marker region (M1) is indicated as percentage of the gated live population. As seen in the OP9 differentiation, CD45 and CD14 expression was high, though the CD86 expression was extremely low.

Studies in our lab have shown that hESCs tend to form largely stable cultures on human feeder cells (Crook *et al*. 2007) compared to mouse feeders. For example, the rate and frequency of spontaneous differentiation are comparatively lower when human feeders like CCD919 and Ortec143 are used. To analyse the impact of the human feeder culture platform on the haematopoietic potential of the hESCs, EBs derived from hES2 and hES3 cells grown on either CCD919 or Ortec143 were differentiated in presence of cytokines.

3.3.1. hESCs maintained on CCD919 cells

CCD919 is a fibroblast cell line derived from normal human adult mammary epithelial tissue and has been proven to support undifferentiated growth of hESCs (Crook *et al*. 2007). For differentiation, hESC-EBs were formed in ultra low attachment plates. At days 5, 11 and 15, EBs were plated onto tissue culture plates in Differentiation medium containing SCF, Flt3L, TPO, IL-4, GM-CSF and IL-3. Most EBs attached in 2 days and generated outgrowths (day 6) in culture. After 2 weeks of culture 2 wells of cells were seeded in Methocult for CFU assay (50,000 cells/ plate). Only cells from EBs treated with cytokines on days 5 and 11 of differentiation gave rise to haematopoietic colonies in Methocult. Colonies were CFU-GM (**Fig 3.5A**) and CFU-M (**Fig 3.5B**) types, similar to those obtained using MEF-based hESCs for differentiation. Giemsa and May Grünwald staining showed presence of neutrophils, eosinopihls and monocytes (**Fig 3.5C**). Unlike MEF-grown hESCs which gave rise to CFUs only from day 14 EBs, human feeder-grown hESCs generated CFUs even from 5-day old EBs. However, the frequency of colony formation– 0.008% for CFU-GM and 0.005% for CFU-M- was quite low.

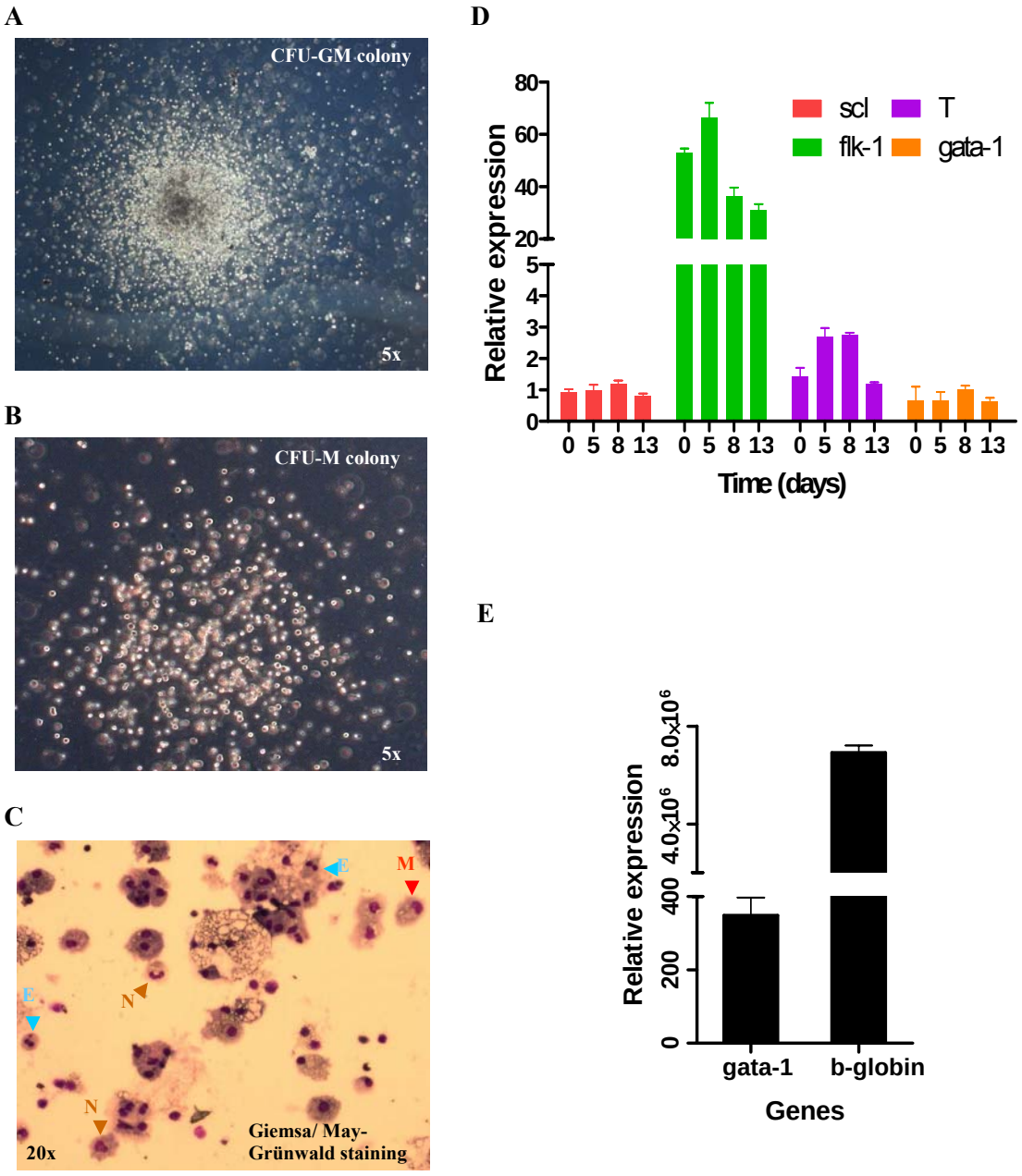


Figure 3.5. hESC grown on CCD919 human feeders differentiate in presence of cytokines to generate haematopoietic colonies. (A, B) Representative images of CFU-GM (Granulocyte Macrophage) and CFU-M (Monocyte) colonies (5x magnification). **(C)** Giemsa and May-Grünwald staining of pooled cells from colonies (20x magnification). Neutrophils (brown arrow heads), eosinophils (blue arrowheads) and monocytes (red arrowheads) are shown. **(D)** Gene expression during differentiation. Only *Brachyury* (*T*) showed an increase which could be due to spontaneous differentiation since its activation preceded addition of cytokines. *FLK-1*, was expressed in undifferentiated cells and persisted through out the differentiation. *β-GLOBIN* was not expressed. Exposure to cytokines does not seem to have a significant effect on expression of these genes. **(E)** Human adult bone marrow RNA was used as positive control for gene expression; only *GATA-1* and *β-GLOBIN* were detected in the BM-RNA sample (high Y-axis values necessitated a separate graph).

Though inefficient, the data suggests that hESCs grown on CCD919 show slightly better haematopoietic differentiation than hESCs maintained on MEFs. This could be due to a variety of reasons including (1) a more homogeneous culture platform provided by the human feeders, which ensures that a higher percentage of cells are pluripotent at the onset and are poised to differentiate, (2) differences in medium formulation, (3) expression of cell surface receptors specific to the cytokines used and (4) expression of developmentally relevant genes in the differentiating cells.

A more thorough characterization of the differentiation especially with regards to gene expression will not only help to precisely establish the differentiation status but also to identify areas that could be targeted to improve efficiency. It is also of interest to study whether the *in vitro* differentiation regime, especially in the early commitment stages, follows patterns that are established in embryonic development. To this end expression of haematopoietic genes including *SCL*, *FLK1* and *GATA-1* was determined in the differentiating cells. hES3 which showed better CFU formation than hES2 was differentiated as described and hES3-EBs were treated with cytokines from day 5 of differentiation. Samples were collected at various time points during EB differentiation and adherent culture. Trizol was used to generate RNA from the samples and quantitative RT-PCR was performed as described. Expression of the haematopoietic transcription factors *SCL* (Elefanty *et al*. 1997, Robb *et al*. 1996) and *GATA-1* (Suwabe *et al*. 1998; Fujiwara *et al*. 1996), mesodermal/ hemangioblast markers *FLK1* and T/*BRACHYURY (TBRA)* (Kennedy *et al*. 2007; Huber *et al*. 2004), and *β-GLOBIN* (Lanyon *et al*. 1975) was compared to control commercially available bone marrow total RNA (Clontech). Curiously, *FLK1* expression was high in undifferentiated hESCs and did not vary much over the entire duration of differentiation (**Fig 3.5D**). However, this is not surprising as there are studies which

have clearly demonstrated that *FLK1* is expressed in undifferentiated hESCs (Zambidis *et al*. 2005; Wang *et al*. 2004). This is in contrast to undifferentiated mESCs that do not express *FLK1* until the cells progressively differentiate into the mesodermal/ hemangioblast population (Chung *et al*. 2002; Choi *et al*. 1998). *TBRA* levels which increased by day 5, remained steady through day 8 and then dropped precipitously. *SCL*, *GATA-1* and *β-GLOBIN* were not significantly upregulated at any point in the differentiation. Human adult bone marrow RNA used as control, showed the predicted expression of *GATA-1* and *β-GLOBIN* but not of any of the other genes (**Fig 3.5E**). Since *TBRA* levels increased before the addition of cytokines, this can be attributed to gastrulation-like events triggered within the spontaneously differentiating EBs. However, the differentiation seems not to have progressed beyond this point as the addition of cytokines did not have any significant effect on expression of the other genes. Perhaps it is not surprising then that an aliquot of these differentiating cells seeded in Methocult did not generate any colonies. Therefore, if the relevant genes are not activated at the right stages, differentiation does not progress beyond a certain developmental point. The above data suggest that CFUs seen in earlier experiments might have been the result of a spontaneous differentiation event.

3.3.2. hESCs maintained on Ortec143 cells

Though CCD919 cells promote haematopoietic differentiation from hESCs, the low efficiency and poor reproducibility prompted further trials using alternative culture platforms. Ortec143 is a human feeder cell line derived under clinically compliant conditions from neo-natal foreskin tissue (Ortec International). These cells support undifferentiated culture of hESCs over numerous passages with an extremely low frequency of spontaneous differentiation (Crook *et al*. 2007). To assess the

haematopoietic potential hESCs grown on Ortec cells, hES2 and hES3 were differentiated in the presence of cytokines.

Briefly, hESC-EBs were formed in Ultra low attachment plates. On day 14, EBs were plated onto tissue culture plates in Differentiation medium containing SCF, Flt3L, TPO, IL-4, GM-CSF and IL-3. After 2 weeks of culture an aliquot of the differentiating population was seeded in Methocult for CFU assay while some were left to differentiate further. On day 29 of differentiation, both hES2 and hES3 showed presence of numerous spherical cells restricted to certain areas in the plates (**Fig 3.6A**). To confirm the haematopoietic nature of these cells, plate-based immunostaining was done for CD34 (haematopoietic progenitors) and CD45 (pan-haematopoietic) markers. Almost all the spherical cells were positive for CD45 (**Fig 3.6B**) and negative for CD34. This suggests that these cells are more mature progenitors expressing only CD45 and not early precursor cells which are $CD34^{+}$ $CD45^{-}$. A merged image of cells stained for CD45 (red) and DAPI (blue) to mark the nuclei is shown (**Fig 3.6C**). An aliquot of the differentiating culture was also immunostained for CD45, CD14, CD83 and CD86 and analysed by flow cytometry. Only CD45 was expressed at very low levels– 17% of the gated live population (**Fig 3.6D**). All other markers were negative. This suggests that differentiation was inefficient and did not progress beyond the $CD45^{+}$ progenitor stage.

As mentioned earlier, two wells of differentiating cells were seeded in Methocult for the CFU assay. These cells generated haematopoietic colonies mainly of CFU-GM (**Fig 3.7A**) and CFU-M (**Fig 3.7B**) types. The frequency of colony formation was 0.02% for CFU-GM and 0.05% for CFU-M respectively. Giemsa and May Grünwald staining of cells from the colonies showed presence of neutrophils, eosinophils and monocytes (**Fig 3.7C**).

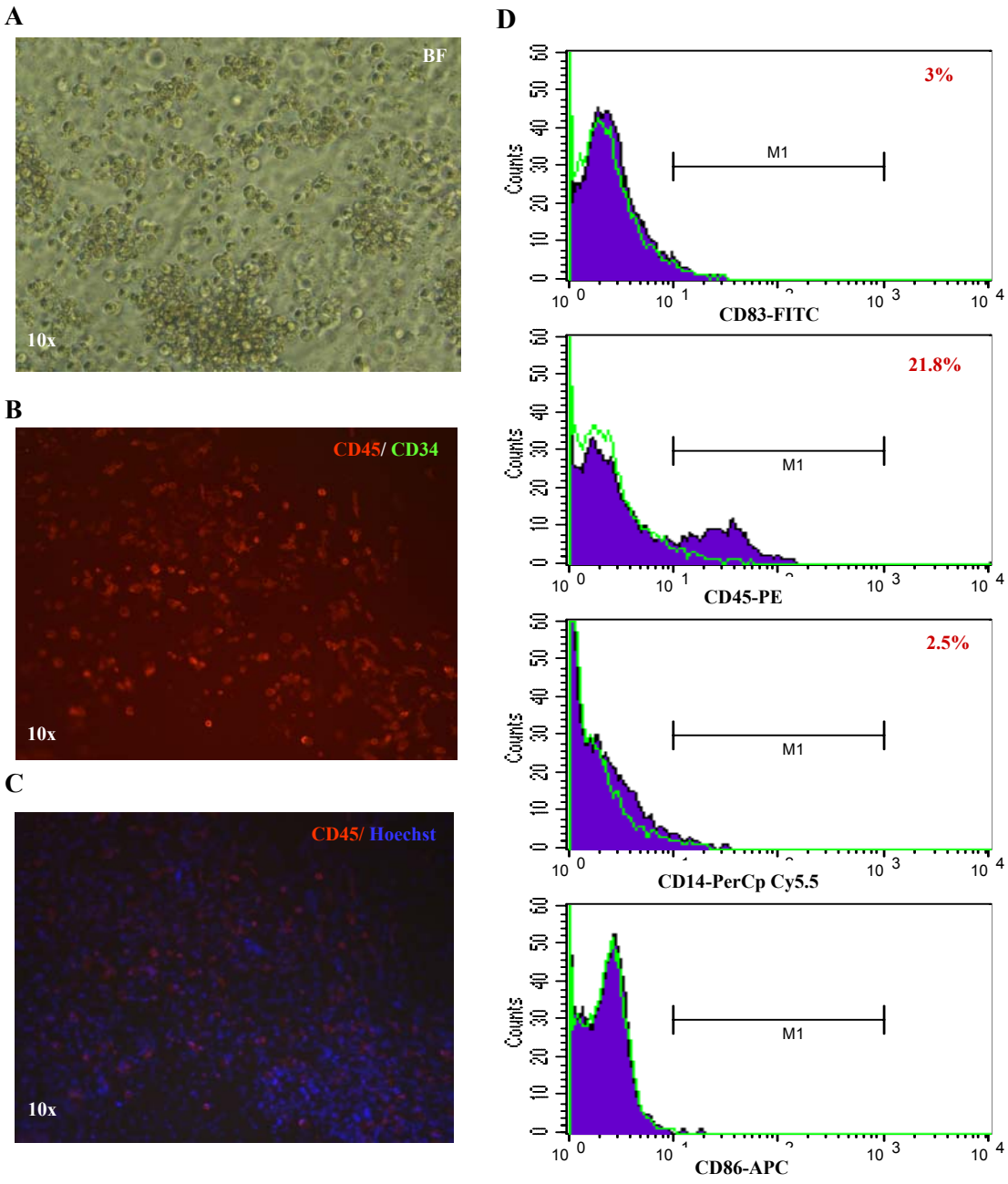


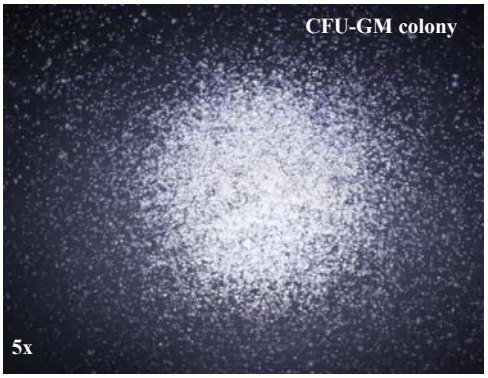
Figure 3.6. hESCs cells grown on Ortec143 differentiated in presence of cytokines to give rise to haematopoietic-like cells. (A) Distinct areas with spherical haematopoietic-like observed in culture (10x magnification). (B, C) Cells shown in (A) stained with CD45-PE, CD34-FITC and Hoechst (10x magnification). (B) Cells stained positive for CD45 while no CD34 was detected. (C) Hoechst was used to mark the nuclei of stained cells. (D) FACS analysis of pooled cells immunostained for CD45, CD14, CD86 and CD83. The green line represents isotype control while the purple filled area indicates stained cells. Expression within the marker region (M1) is indicated as percentage of the gated live population. Only CD45 was detected and at extremely low levels even though the culture had high numbers of spherical cells which were expected to be positive for CD45.

hES3-derived cells showed more efficient differentiation and formed 4 times more colonies than hES2 cells. hESCs grown on Ortec cells generated 40 times more CFU-GM and 10 times more CFU-M colonies than the CCD919-based cultures. These results suggest that Ortec cells provide a culture platform more supportive of efficient haematopoietic differentiation than even the CCD919 human feeders.

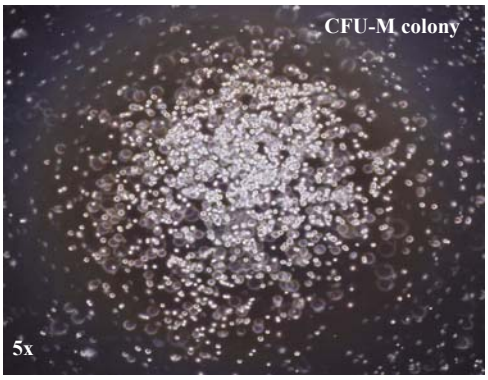
For a detailed characterisation of haematopoietic differentiation obtained using hESCs maintained on Ortec cells, gene expression analysis was performed. EBs/ cells harvested every 4 days during differentiation were processed using the RNAeasy kit according to the manufacturer's recommendations. Quantitative RT-PCR was performed to detect expression of assorted marker genes (**Fig 3.7D**). As seen in the case of hESCs maintained on CCD919 cells, *FLK1* was expressed even in the undifferentiated cells and showed a very slight increase on exposure to cytokines (day 18). *TBRA* was low through out the EB differentiation phase and was upregulated transiently upon cytokine treatment. *MIXL1*, an early marker of the developing mesoderm (Willey *et al*. 2006; Hart *et al*. 2002) and *PU.1* a haematopoietic transcription factor (Fisher and Scott 1998) did not show any variation in expression compared to undifferentiated control. *GATA-2* is a mesodermal marker known to be expressed in haematopoietic progenitors (Tsai *et al*. 1994) and is expressed at high levels through out the differentiation. *HOXB4*, a critical haematopoiesis-specific transcription factor (Kyba *et al*. 2002; Antonchuk *et al*. 2001) responded specifically to the addition of cytokines and showed increased levels of expression. However, the expression of *GATA-2* and *HOXB4* in the untreated control (–GF) was also high suggesting that this might not be a specific response to the cytokines. *GATA-1*, *SCL* and *LMO2* were not expressed at any stage tested.

Though *TBRA* was upregulated upon cytokine treatment, the very slight increase in *FLK1* expression might not be significant enough to infer the presence of a hemangioblast-like (common progenitor for haematopoietic and endothelial cells) population. The high levels of *GATA-2* and *HOXB4* in the untreated control indicates that expression of these genes is not triggered exclusively by the cytokines. Due to these reasons, the gene expression analysis was not conclusive enough to show if differentiation is a specific response to the addition of cytokines. As seen in the case of CCD919-based hESCs, differentiation does not seem to activate developmentally relevant genes. This roadblock in differentiation is also evident from the immunostaining seen in **Figure 3.6D** which shows extremely low levels of only $CD45^+$ expression. It would seem that the CFUs generated in Methocult (**Fig 3.7A and 3.7B**) were merely the result of spontaneous differentiation.

A


CFU-GM colony
5x

B


CFU-M colony
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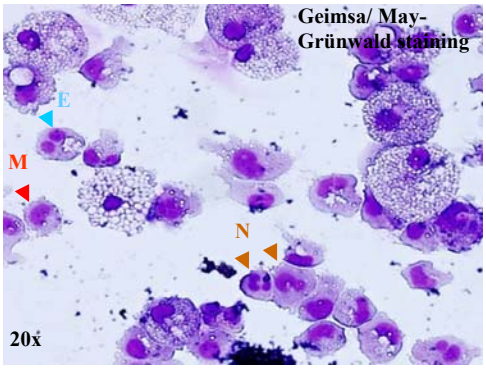
C


Geimsa/ May-
Grünwald staining
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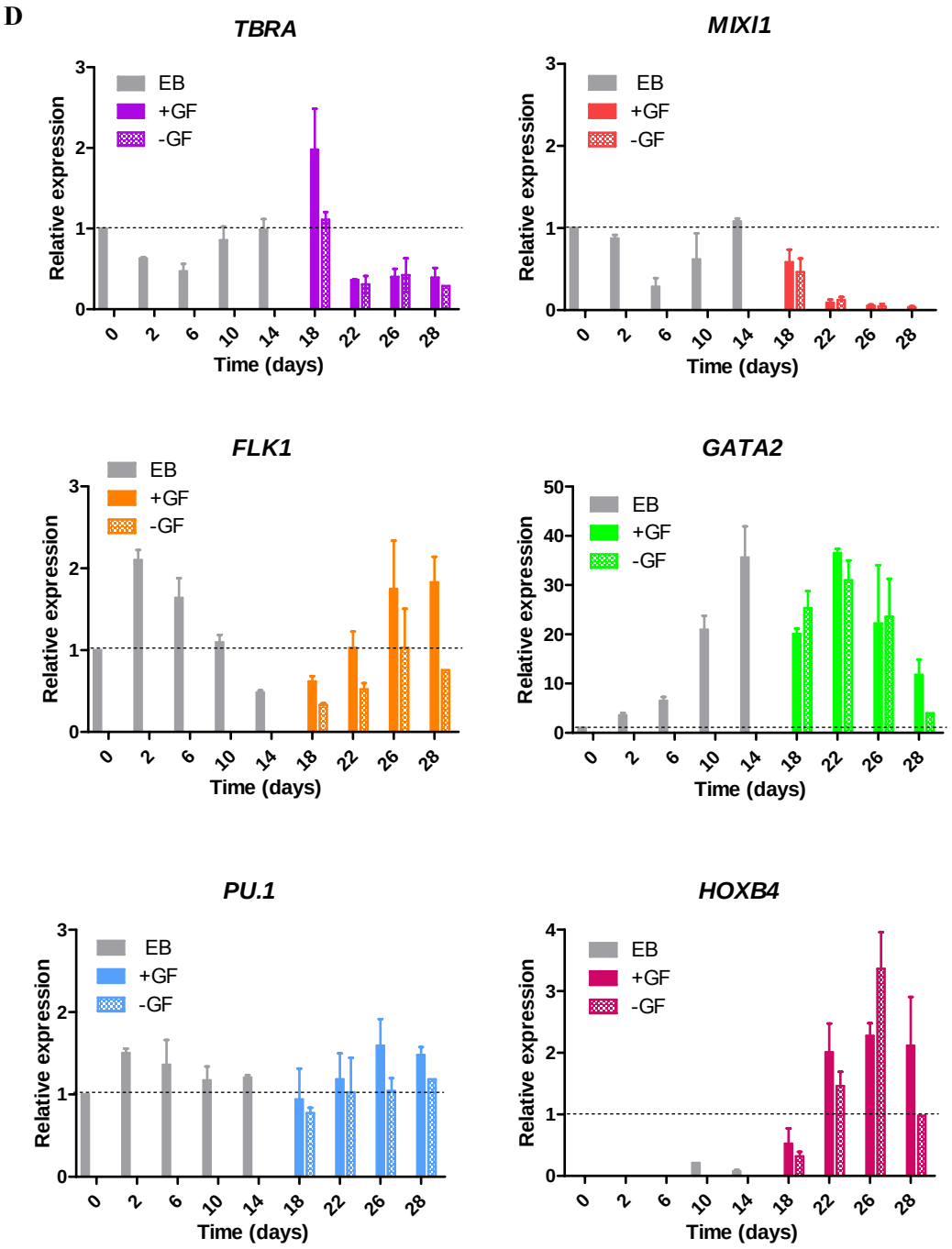


Figure 3.7. hESCs grown on Ortec feeders differentiate in presence of cytokines to generate haematopoietic colonies. (A, B) Representative images of CFU-GM (Granulocyte Macrophage) and CFU-M (Monocyte) colonies formed in Methocult. **(C)** Giemsa and May-Grünwald staining of pooled cells from colonies. Neutrophils (brown arrow heads), eosinophils (blue arrowheads) and monocytes (red arrowheads) are shown. **(D)** Increased expression of marker genes *TBRA*, *FLK1* and *HOXB4* in response to cytokine treatment (day 18 onwards) shows the induction of a low degree of mesodermal differentiation in this system. Surprisingly, *PU.1* is not significantly upregulated even though granulocytic differentiation is known to be characterised by the expression of this gene. Grey bars indicate differentiation during the EB formation phase in absence of cytokines. Dotted line represents day 0 normalisation.

CONCLUSION and DISCUSSION

Several factors including the derivation, feeders used, epigenetic status, etc., can influence the amenability of hESCs to differentiate (Pekkanen-Mattila *et al*. 2009; Aiba *et al*. 2008; Catalina *et al*. 2008; Chang *et al*. 2008; Adewumi *et al*. 2007). As part of my preliminary studies to test the multipotential differentiation capability of hESC lines, hES2 and hES3, I used strategies that were known to induce haematopoietic differentiation.

Using bone marrow-derived cell lines as supportive stroma, hESC-EBs could be differentiated to generate haematopoietic-like cells. However, hESCs did not show a similar capacity, suggesting that differentiation needed to be 'kick started' as a spontaneous event within EBs. The source and support capability of the stroma were also important factors as only OP9, a murine cell line, supported haematopoietic differentiation from hESCs while human stromal cell lines HS-5 and HS-27A did not. Reproducibility of differentiation using co-culture was quite low indicating that it may be a spontaneous event or that the outcome may be easily affected by slight changes in culture conditions. Efficient differentiation may also be hESC line dependent as hES2 subjected to identical conditions did not yield similar results as hES3. The use of OP9 for haematopoietic differentiation from hESC lines H1 and H9 was reported by Vodyanik *et al*. (2005) around the same time as my work was underway. In contrast to results obtained with hES3, these authors reported generation of haematopoietic cells from hESCs in a monolayer differentiation and not from hESC-EBs. They reported low CD45 (3.4%) and high CD34 (19.3%) expression and a wider range of colonies in the CFU assay. This suggests that the haematopoietic cells they obtained in culture are more naïve and have a wider developmental capacity in contrast to the more differentiated $CD45^{+}$ population I obtained. These differences

could be attributed to several factors including hESC line variation, quality of OP9 monolayers and sampling points within experiments.

Differentiation in presence of human recombinant cytokines was another favoured strategy as this approach eliminates the foreign (murine) stromal cells in culture. A cocktail of haematopoiesis-promoting cytokines acted on hESC-derived EBs to give cells mainly of the granulocytic lineage. No erythroid differentiation was detected at any time. The bias towards granulocytes was expected since the cytokines used are known to promote differentiation of this particular lineage (Zhan *et al.* 2004). An interesting observation was that hES3 did not seem to differentiate as well as hES2 in the presence of cytokines. This is in contrast to the OP9-based differentiation where only hES3 gave rise to differentiated haematopoietic-like cells. Though these two cell lines were derived under identical conditions, inherent differences between the two are highlighted by such observations.

With the aim of adapting hESCs to clinically compliant culture regimes, our lab began using human feeder cells to maintain hESCs in the undifferentiated state. Since hESC culture platforms can significantly affect the differentiation capability of these cells, I decided to test if the new culture conditions alter this potential. EBs derived from hESCs grown on CCD919 or Ortec feeders were differentiated in presence of cytokines in a manner similar to hESCs grown on MEFs. In general, expression of haematopoietic cell surface markers was not as dramatic or high in the human feeder based differentiation as it was with the use of MEFs (FACS data). Another difference seems to be the efficiency of differentiation. Though Ortec-based hESCs formed a significantly higher number of colonies in the CFU assay than the CCD919 cultures, the frequency was much lesser than in the MEF-based cultures. Since the protocol used was optimized for hESCs grown on MEFs, slight modifications may be required

to adapt this protocol to hESCs grown on human feeders. Though the human feeder-based hESC system generated CFUs in Methocult, they did not seem to activate expression of genes known to be important in haematopoietic development. *TBRA* upregulation shows that a gastrulation-like event initiated but this did not advance to give rise to haematopoietic mesoderm in this system. The lack of *GATA-1* expression in the differentiating population supports the observation that no erythroid colonies were formed in the CFU assay, since *GATA-1* is critical for the formation of the erythroid lineage (Suwabe *et al.* 1998). The extremely low percentage of CFUs and lack of corroborative gene expression data suggests that the CFUs formed in Methocult were most likely the result of spontaneous differentiation events. It is also possible that the sampling points chosen for my gene expression analysis might have missed important events in the differentiation. This emphasizes the need for more thorough analysis of the differentiation process by increasing the frequency of sampling.

My experimental observations point towards a certain degree of haematopoietic differentiation albeit spontaneous, occurring in this system. Immunostaining revealed that cells formed were mainly haematopoietic progenitors which did not develop further into more terminally differentiated cell types. Differentiation was mainly towards cells of the myeloid lineage which is not surprising since the cytokines used were pro-granulocytic. Gene expression analysis proved inconclusive as either genes were not expressed or did not show specific response to cytokine treatment. This makes it almost impossible to conclude if *in vitro* differentiation using hES2 and hES3 with the strategies described, mirrors haematopoietic development in the embryo (Kennedy *et al.* 2007). However, these results constitute proof-of-principle that haematopoietic differentiation from hESCs can be obtained with the use of

cytokines on differentiating embryoid bodies. Better tailoring of this differentiation strategy might help resolve the current issues.

Since this work was done numerous innovations have been reported resulting in improved methods for generation of haematopoietic cells from ES cells. One particular gene of interest is HOXB4 which has been reported to be expressed in haematopoietic progenitors and has been shown to enhance the repopulating ability of haematopoietic stem cells (Sauvageau *et al*. 1995; Sauvageau *et al*. 1994). In addition, recombinant HOXB4 protein has been used to achieve expansion of human and murine haematopoietic stem cell populations (Amsellem *et al*. 2003; Krosl *et al*. 2003). Taking cues from these studies Bowles *et al*. reported that over-expression of HOXB4 in hESCs led to the expansion of haematopoietic progenitors and their derivative populations (Bowles *et al*. 2006). Clonogenic progenitors expressing markers like CD34, CD45 and Glycophorin A were generated in this differentiation. Another recent study demonstrated that HOXB4, and not Bmp4, confers self-renewal properties to haematopoietic progenitors derived from ES cells (Bonde *et al*. 2008). These authors found that the ES-derived haematopoiesis induced by Bmp4 leads only to transient mixed chimerism. However, HOXB4 transduced mESCs generated haematopoietic progenitors with enhanced self-renewal and long-term engraftment capability. This latest study is encouraging as it provides a strategy to generate a source of haematopoietic cells that could induce transplantation tolerance.

Concurrent investigations on endodermal differentiation from hESCs proved to be more successful than the mesodermal differentiation. These experiments yielded differentiated progeny with a much greater efficiency. Therefore, studies of endodermal differentiation constitute the bulk of my dissertation work and are presented in Chapter 4 of this thesis.

CHAPTER 4: ENDODERMAL DIFFERENTIATION

INTRODUCTION

In Chapter 3, I described my results on differentiation of hESCs into haematopoietic-like cells which could theoretically be used as a transplantation aid for hESC-derived cell therapy products. In this chapter, I focus on the efficient differentiation of hESCs into definitive endoderm as a first step towards the *in vitro* production of insulin-secreting β cells for the treatment of diabetes. As outlined in Chapter 1, our lab developed an EB-based differentiation strategy that begins with an initial endoderm induction phase and is followed by pancreatic and endocrine cell specification phases (Phillips *et al*. 2007). In this protocol, a known inducer of endoderm, Activin A was used to initiate differentiation towards a definitive endodermal fate. Genes characteristic of definitive endoderm (DE) formation are induced within the first 4 days of differentiation, with activation of the pancreatic homeobox gene *PDX1* about one week later.

During the course of developing our EB-based differentiation regime, we discovered that the combined use of Activin A and Bmp4 led to greater expression of genes characteristic of definitive endoderm. The extent of endoderm induction was found to be concentration-dependent as only a certain range of growth factor concentrations efficiently gave rise to the desired progeny from differentiating hESCs. The enhanced induction of endoderm in the presence of Bmp4 is surprising as this growth factor is known to be involved in a variety of developmental events including bone formation, mesoderm induction and primordial germ cell generation, but is not a well-established endoderm inducer.

Several models can be proposed and tested for the unexpected role of Bmp4 during DE formation *in vitro*. (1) Bmp4 might signal directly to cells that receive the

Activin A patterning signal and potentiate their endodermal differentiation. (2) Bmp4 may facilitate the transduction of locally produced Nodal signals emanating from the hESCs by directly impacting the signaling pathway. (3) Bmp4 may induce the formation of an unrelated cell type that indirectly, for example, influences DE formation and expansion. In this Chapter, I will describe my efforts to characterize DE differentiation in detail and to arrive at a possible mechanism for the collaborative effect of Activin A and Bmp4, using a variety of molecular methods. In depth analysis of the differentiation revealed that Activin A induces formation of DE in Matrigel-embedded EBs and this induction is augmented with the addition of Bmp4 to the differentiation. Detailed investigation of the Activin A and Bmp4 signaling pathways and the pleiotropic roles of Bmp4 did not bring to light a clear mechanism for the combinatorial activity of these two growth factors. By studying changes in global gene expression during differentiation, I identified novel genes that were upregulated during the formation of DE. The expression domains of these genes during mouse embryonic development were investigated to establish their relevance to the generation of DE.

RESULTS

4.1. Formation of definitive endoderm within embryoid bodies derived from hESCs

Our lab previously developed an empirical protocol for the differentiation of hESCs into pancreatic progenitor cells. A summary of this Matrigel-based three-dimensional differentiation is given in **Figure 4.1**. Briefly, hESC clumps grown on mouse feeders (MEFs) were embedded in Matrigel-containing medium either with or without Activin A and Bmp4, as described in Chapter 2.2.3 (**Fig 4.1A**). Spherical EBs of various sizes were formed by day 2 of differentiation. As differentiation progressed some of the EBs developed cystic areas, while a few fused to form larger structures. On day 10, the early factors were replaced with the late factors Exendin-4, β-cellulin and HGF. Differentiation was discontinued on day 20, since from previous trials it was known that pancreatic progenitors are formed by this time. *PDX1,* the earliest marker of the pancreas, is detectable by day 12 (**Fig 4.1B**) and decreases thereafter with a simultaneous increase in markers of mature pancreatic progenitors like *INSULIN*, *NGN3* and *PTF1a* (**Fig 4.1B and C**). Therefore, in the presence of Matrigel, an initial stimulus of Activin A and Bmp4 seems to induce formation of a pancreatic progenitor population from hESCs.

As pancreatic tissue is known to arise from DE during development, I examined if markers of DE could be detected in the differentiation cultures by immunostaining. Briefly, EBs embedded in Matrigel with the early factors were plated on fibronectin-coated plates to enable staining against endodermal markers Sox17 and Foxa2 and the pluripotency marker Oct4. Addition of Activin A and Bmp4 triggered downregulation of the pluripotency marker Oct4, while simultaneously upregulating the expression of

endodermal markers Foxa2 and Sox17 (**Fig 4.2**). In the absence of growth factors, Oct4 expression remained high in all EBs. There were a few cells in some untreated EBs that stained for Foxa2 and Sox17, which suggests that a certain degree of spontaneous differentiation occurs in this differentiation system. These results suggest that DE cells form during hESC differentiation in response to growth factor treatment and most likely give rise to $PDX1^{+}$ pancreatic progenitors.

4.1.1. Bmp4 enhances the endoderm-inducing potential of Activin A in Matrigel

Since they have distinct roles in development, Activin A and Bmp4 acting together to specify or enhance the formation of endoderm *in vitro* came as a surprise. In the 3D Matrigel differentiation, the combination of these growth factors reproducibly gives enhanced endoderm differentiation (N=7). This effect was irrespective of the hESC culture platform used, as hESCs grown on MEFs and HFs gave similar results. Since HFs and KOSR-based culture medium provide a stable culture platform for hESCs in our hands, I adopted this method for all experiments described henceforth (Crook *et al*. 2007). To investigate molecularly the Activin A and Bmp4 collaboration in detail, I used the following iterations of the 3D differentiation protocol. In the standard Matrigel embedding conditions, I added either Activin A alone (AA) or Bmp4 alone (Bmp4) or both (+GF) or neither (–GF) and allowed differentiation to proceed through the endoderm phase onto the pancreatic progenitor phase (d20).

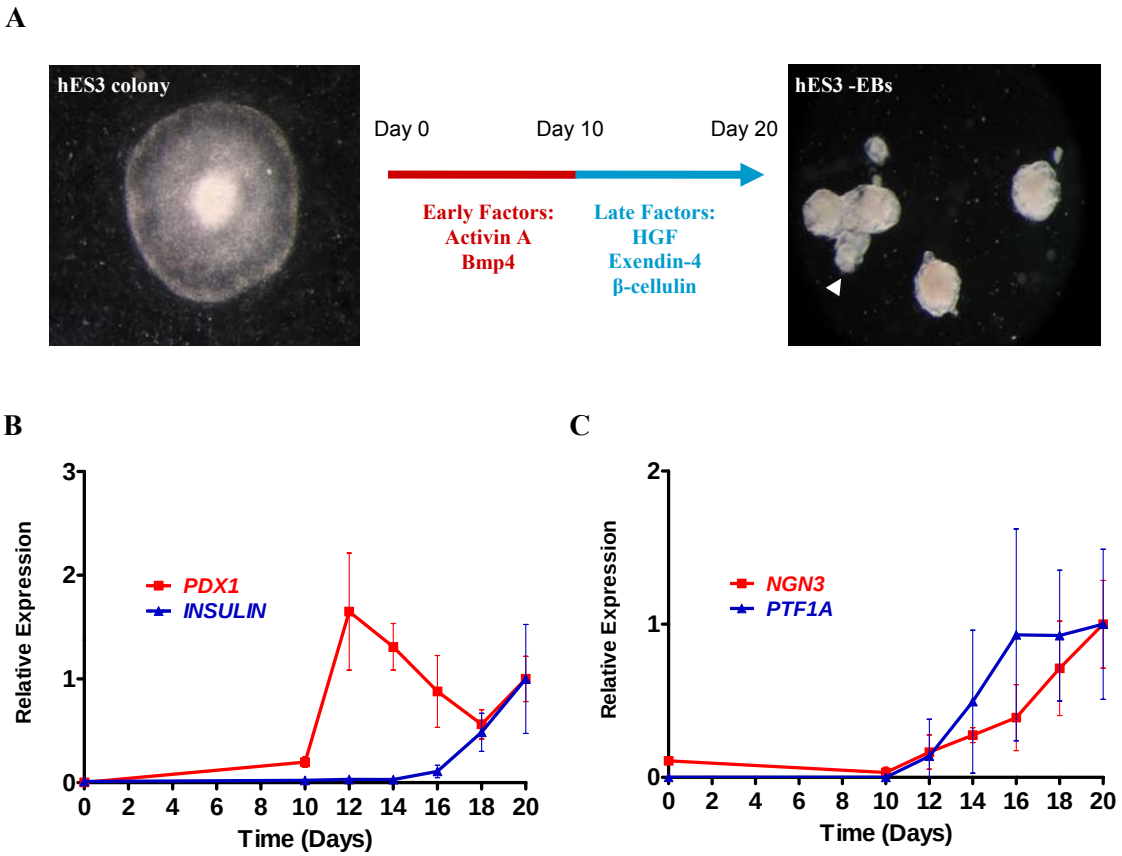


Figure 4.1. Three dimensional differentiation in the presence of Activin A and Bmp4. (A) Schematic representation of differentiation strategy. hESC colonies were enzymatically dissociated to create clumps that formed EBs of various sizes in Matrigel-containing medium. Differentiation was carried out in the presence of the indicated growth factors. As differentiation progressed many EBs formed cystic areas, giving them a bubble-like appearance (white arrowhead). **(B)** A critical marker of pancreatic differentiation, *Pdx1* (red), is activated around day 10 of differentiation. *Insulin* expression (blue) is detected by day 16 and continues to rise with a simultaneous decrease in the levels of *Pdx1*, which is consistent with the known pattern of *Pdx1* expression during pancreatic development (Jensen 2004). **(C)** Other pancreatic markers like *Ngn3* (red) and *Ptf1a* (blue) are detected following *Pdx1* expression. This work was published in Philips *et al*. 2007.

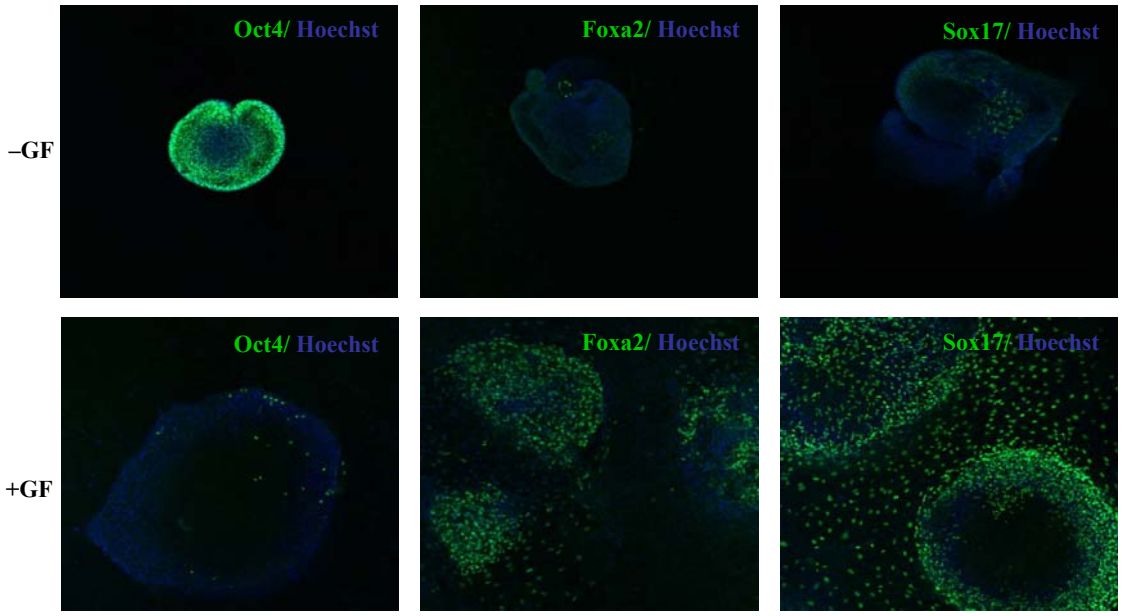


Figure 4.2. Activin A and Bmp4 induce upregulation of endodermal markers and simultaneous downregulation of pluripotency markers. hESCs were differentiated using the 3D Matrigel protocol either with (+GF) or without (–GF) both Activin A and Bmp4. On day 4 of differentiation, EBs were seeded on Fibronectin-coated plates and allowed to attach for 2 days before staining. Oct4, Foxa2 and Sox17 were detected using Alexa 488 conjugated secondary antibodies. The number of $Oct4^+$ cells in the –GF condition were significantly greater than EBs exposed to growth factors. Few $Foxa2^+$ and $Sox17^+$ cells were observed in the –GF EBs but the population increased dramatically in EBs treated with Activin A and Bmp4. The low number of endodermal cells in the –GF condition can be attributed to spontaneous differentiation, which is consistent with the RT-PCR results shown in Figure 1.

Markers of pluripotency, *OCT4* and *NANOG*, were rapidly downregulated in +GF and Bmp4 (**Fig 4.3A and 4B**). However, Activin A when added alone sustained expression of *OCT4* and *NANOG* for a short time. This finding supports the reported role of Activin A in maintaining the pluripotency of hESCs and mEpiSCs (Tesar *et al.* 2007; Vallier *et al.* 2005). In the absence of growth factor stimulation (–GF), expression of these markers was maintained for a few days before being downregulated. This decrease in expression is expected as spontaneous differentiation occurs even when EBs are cultured in differentiation medium rich in KOSR (20%).

Directed differentiation was measured as changes in the expression of *TBRA*, *FOXA2* and *SOX17*. In general, all three genes were upregulated in presence of Activin A + Bmp4 (+GF) and Activin A; the expression was always higher in the +GF condition (**Fig 4.3C-E**). The lack of expression of all three genes in –GF suggests that there was little spontaneous differentiation toward DE in this system. As expected from what is known from previous work, Bmp4 alone induced expression of *TBRA* (Johansson and Wiles 1995). No expression of *FOXA2* and *SOX17* was detected in the presence of Bmp4 alone. Taken together these observations imply that the growth factors used here specifically and rapidly downregulate pluripotency genes and set the stage for differentiation. The progress of differentiation was measured by *PDX1* expression, which was detected by day 10 in the presence +GF and Activin A (**Fig 4.3F**). The significantly higher PDX1 expression in +GF suggests that the endoderm-inducing synergistic activity of Activin A and Bmp4 might significantly impact the pancreatic differentiation phase of the protocol, most likely by providing a greater initial pool of DE that can undergo pancreatic commitment.

Detailed analysis of the differentiation under the 4 different conditions stated above has revealed that both conditions, Activin A and Activin A + Bmp4 (+GF), specifically induce endoderm differentiation. However, the +GF condition always elicited a higher expression of the marker genes than Activin A alone. This confirms the earlier observation that the presence of Bmp4 enhances the ability of Activin A to promote endodermal differentiation.

4.1.2. Matrigel affects the extent, not the outcome of differentiation

The 3D differentiation protocol uses the growth factor-reduced formulation of Matrigel to induce endoderm differentiation from hESC-EBs. Since Matrigel contains biologically active components, including trace amounts of potent growth factors, it is important to examine the influence of this substrate on differentiation. hESCs were dissociated using collagenase as described and seeded in RPMI/KOSR medium without Matrigel. EBs formed by day 2 and were more varied in size than in Matrigel-based culture. Differentiation was initiated identically to the 3D protocol described earlier. Quantitative RT-PCR analysis was performed on free-floating EBs harvested every other day and compared against those embedded in Matrigel (adapted from Figure 4.3). In free-floating EBs, growth factor addition caused only a slight decrease in *OCT4* expression, which was similar to the –GF condition (**Fig 4.4A**). This is in contrast to the Matrigel-based differentiation where addition of growth factors triggers a rapid drop in *OCT4* levels, while expression is maintained in the –GF condition (**Fig 4.4E**). In the free-floating EBs, expression of *TBRA*, *FOXA2* and *SOX17* was induced in the +GF condition, though the levels of expression were roughly 10 times lower than in the Matrigel-based platform (**Fig 4.4B-D and F-H**). As expected, Bmp4 when used alone induced expression of *TBRA* but not *FOXA2* and *SOX17*.

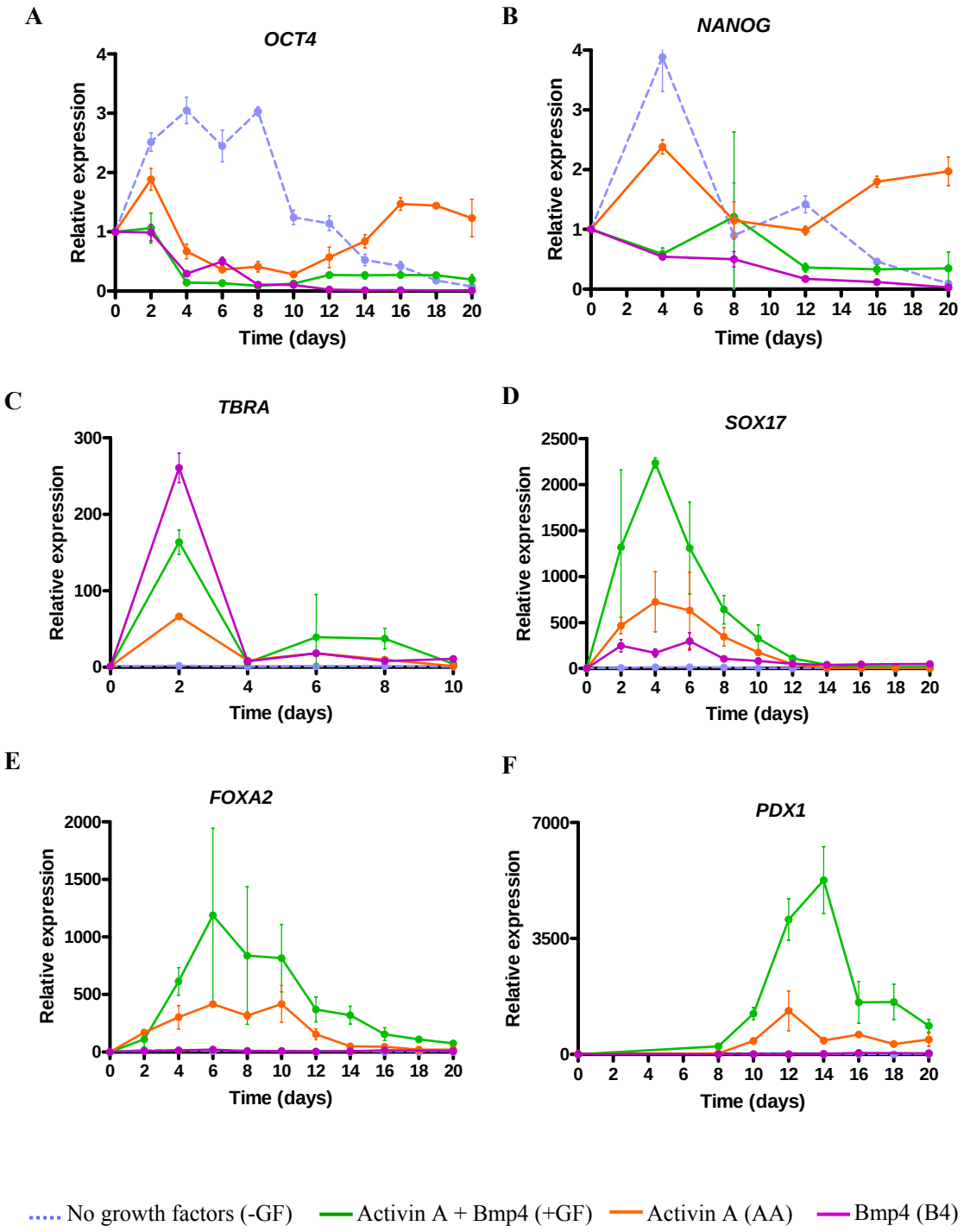

A
OCT4
Relative expression
Time (days)
B
NANOG
Relative expression
Time (days)
C
TBRA
Relative expression
Time (days)
D
SOX17
Relative expression
Time (days)
E
FOXA2
Relative expression
Time (days)
F
PDX1
Relative expression
Time (days)
No growth factors (-GF)
Activin A + Bmp4 (+GF)
Activin A (AA)
Bmp4 (B4)

Figure 4.3. Activin A and Bmp4 together are more effective in inducing endodermal differentiation than either growth factor alone. hESCs were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data were generated by quantitative RT-PCR with samples collected every other day from day 0 to day 20. **(A, B)** Expression of pluripotency markers *OCT4* **(A)** and *NANOG* **(B)** decreases during the course of differentiation as expected. The continued expression of these markers in the –GF condition shows that decreasing expression in all other conditions is a direct effect of growth factor addition. **(C)** The gastrulation marker *BRACHYURY (TBRA)* is expressed in response to all growth factor treatments. Bmp4, which is known to induce *TBRA*, stimulated the highest expression followed by +GF and Activin A. **(D, E)** Genes specific to the endodermal lineage, *FOXA2* and *SOX17,* are expressed in response to the growth factors and seem to follow the known developmental sequence of gene expression. Activin A alone does expectedly induce some amount of endodermal differentiation but much lower than +GF (~3 fold). Bmp4 when used alone does not seem to efficiently differentiate hESCs into endoderm. **(F)** To confirm if the differentiation progressed as expected to generate pancreatic progenitors, *PDX1* expression was determined. *PDX1* is detectable by day 10 and shows higher expression in +GF than in Activin A alone. These expression data suggest that undifferentiated cells downregulate pluripotency markers, undergo a gastrulation-like event and form DE and pancreatic progenitors in culture.

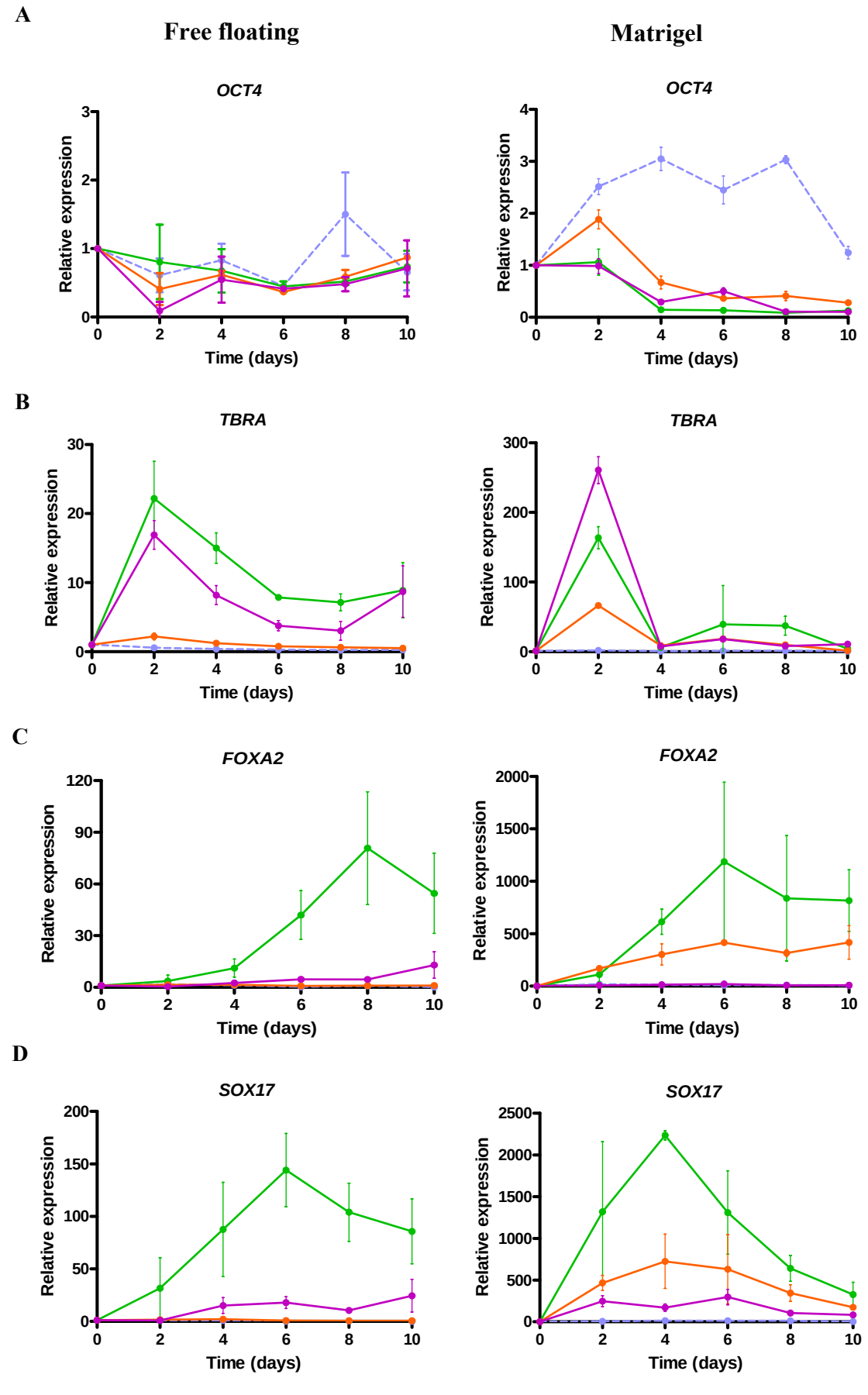

A
Free floating
Matrigel
OCT4
OCT4
Relative expression
Time (days)
B
TBRA
TBRA
C
FOXA2
FOXA2
D
SOX17
SOX17
No growth factors (-GF)
Activin A + Bmp4 (+GF)
Activin A (AA)
Bmp4 (B4)

Figure 4.4. Absence of Matrigel adversely affects the extent of endodermal differentiation. hESCs were differentiated using the 3D protocol without Matrigel under the 4 conditions indicated. Gene expression data were generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10 and compared against the data from Matrigel-embedded EBs (adapted from Figure 4.3). **(A, E)** Expression of *OCT4* was low but persistent in the free-floating EBs. In presence of Matrigel, all conditions except –GF showed rapid downregulation of *OCT4*, while expression remained constant in –GF. **(B-D, F-H)** In the absence of Matrigel, Activin A alone does not seem to induce endodermal differentiation. When free-floating EBs are treated with both Activin A and Bmp4, there is expression of the gastrulation marker *TBRA,* followed by the endodermal genes *SOX17* and *FOXA2*, though 10 times lower than in the Matrigel-based differentiation. Induction of endoderm seems to be slower than in the Matrigel differentiation as expression of *SOX17* and *FOXA2* is delayed. Bmp4 alone has no effect on gene expression except in the case of *TBRA* as expected. EBs in –GF show no endodermal differentiation.

Strikingly, Activin A alone did not seem to induce endodermal differentiation in the absence of Matrigel (**Figure 4.4**). This suggests that Matrigel enhances the ability of Activin A to bring about differentiation. There could be a Bmp4-like activity in Matrigel, which causes an effect similar to the +GF condition. Eliminating Matrigel possibly abrogates this Bmp4-like activity thus rendering recombinant Activin A inefficient in inducing endodermal differentiation in this system. Alternatively, Activin A when used alone could be acting to maintain pluripotency or to resist differentiation and the addition of Matrigel possibly overcomes this block.

An alternative explanation for this observation is the potent anti-differentiation activity present in KOSR which can be attributed mainly to Insulin/ IGF-like activity (Bendall *et al*. 2007). Since Matrigel- and free-floating- EBs are differentiated in KOSR-containing medium, this IGF-like activity is present in all conditions. However, the presence of Matrigel seems to serve as a protective barrier to the anti-differentiation effect of KOSR. In the absence of this buffer, free-floating EBs are exposed to extremely high concentrations of IGF which hampers and delays the differentiation or even eliminates it when Activin A is used alone. Another interesting observation is that the absence of Matrigel seems to prolong the gastrulation-like phase (*TBRA* expression) and delay the expression of *FOXA2* and *SOX17*. This suggests that Matrigel renders the EB more amenable to differentiation. These data also reiterate the importance of Bmp4 in inducing endodermal differentiation.

4.1.3. Cells expressing FOXA2 and SOX17 are of definitive endodermal origin as visceral endoderm is suppressed during differentiation

Both *FOXA2* and *SOX17* are known to be expressed in the definitive and visceral endoderm (Dufort *et al*. 1998, Kanai-Azuma *et al*. 2002). Therefore, it is

important to verify that *FOXA2* and *SOX17* expression during *in vitro* differentiation specifically identifies DE-like cells. This is especially relevant in light of experimental evidence that hESC-EBs form a VE-like layer during *in vitro* differentiation (Conley *et al*. 2004).

Since the outer VE-like layer is expected to form quite rapidly during EB organization, the expression of VE genes is predicted during the earliest stages of *in vitro* differentiation. Molecular analysis of the differentiation shows that the expression of *FOXA2* and *SOX17* always follows *TBRA* expression (**Fig 4.3**). This indicates that the differentiation closely mimics development and gives rise to a $TBRA^{+}$ primitive streak-like population from which the $FOXA2^{+}$ $SOX17^{+}$ DE cells emerge. In addition, RT-PCR analysis of samples from Matrigel-based and free-floating differentiations shows that gene expression of markers unique to the VE like Transthyretin (*TTR*), Alpha Feto Protein (*AFP*) and *H19* expression is suppressed in the early part of differentiation (**Fig 4.5A-D**). The effect on gene expression seemed to be irrespective of Matrigel unlike what has been reported previously. *H19* expression was insignificant in all conditions except in the presence of Bmp4 alone. *TTR* and *AFP* expression is detectable later in differentiation and is coincident with the expression of *PDX1* (**Fig 4.3**). As *TTR* and *AFP* resolve to the liver later in development, the similar timeline of expression of these genes suggests that multiple derivatives of the DE are being generated during differentiation. Taken together, these data strongly suggest that *FOXA2* and *SOX17* expression marks cells of the DE that are derived from a primitive streak-like population and are therefore not indicative of substantial formation of VE.

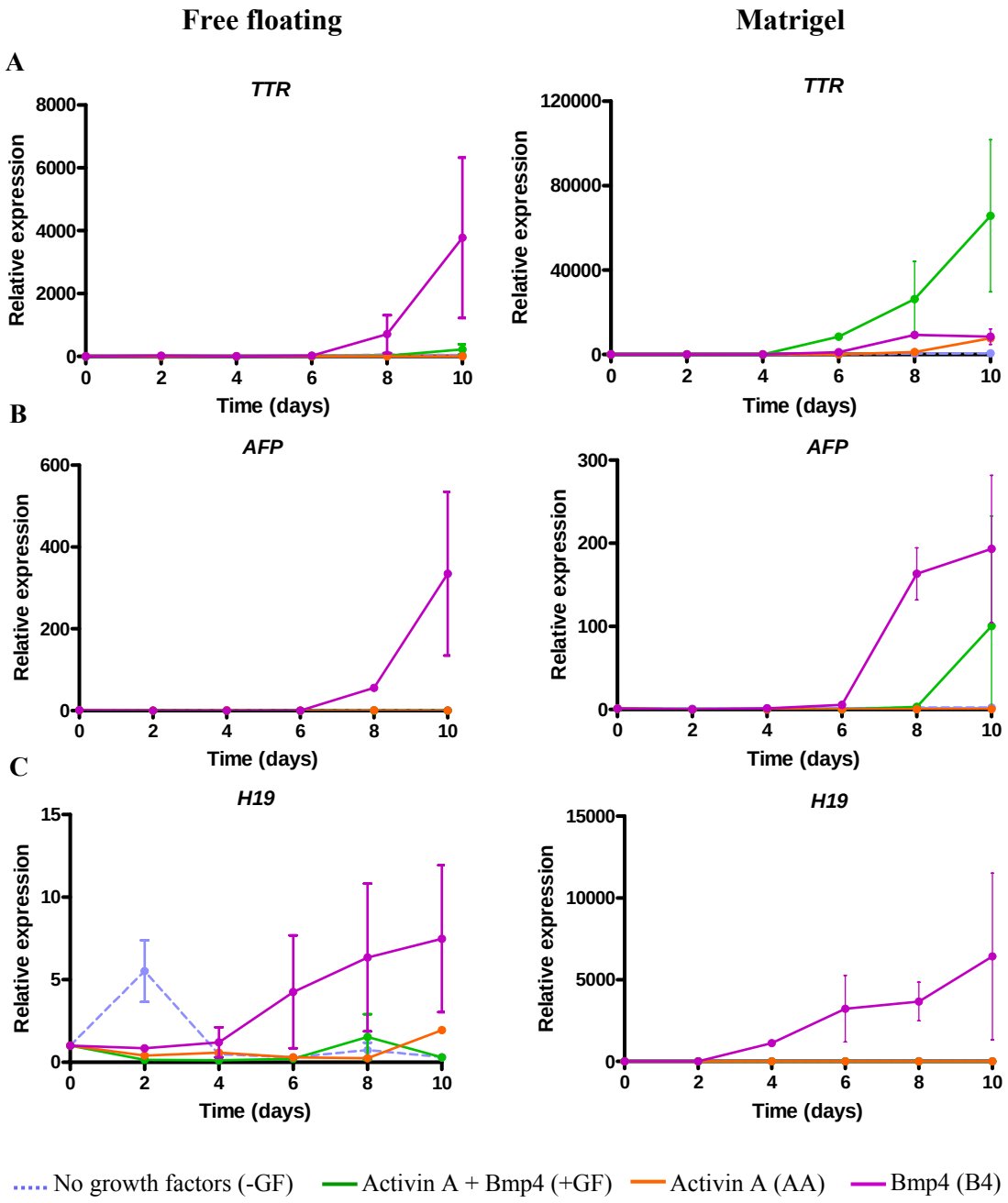


Figure 4.5. Markers of visceral endoderm are suppressed during the definitive endoderm formation phase of differentiation. Cells were differentiated using the 3D protocol with or without Matrigel under the 4 conditions indicated. Gene expression data were generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. In general, markers of visceral endoderm– *TTR*, *AFP* and *H19*– are suppressed in endoderm-forming conditions irrespective of the presence of Matrigel. **(A, B)** *TTR* and *AFP* are specifically suppressed during the initial endoderm-forming phase of differentiation in both free-floating and Matrigel-EBs. +GF and Bmp4 alone induce gene expression later in the differentiation following the activation of *TBRA*, *FOXA2* and *SOX17* (between days 2 and 6 in **Fig 3**). These data strongly argue that these markers have resolved to the definitive endoderm. **(C)** *H19* was expressed only when Bmp4 was used alone.

The above data (Section 4.1) show that reproducible, directed differentiation of hESCs to DE can be achieved by exposing EBs embedded in Matrigel to Activin A and that this induction can be enhanced with the addition of Bmp4. Analysis of gene expression suggests that the growth factors generate specifically DE and suppress the formation of VE *in vitro*. However, it is entirely possible that certain VE-like cells exist in these cultures and this has been shown later in this chapter. It is important to note that by day 20 of differentiation a variety of cell types reside within the EBs– not every cell is $Pdx1^{+}$. This observation is consistent with QPCR analysis of the differentiation which is given in the various sections of this chapter.

4.2. Detailed analysis of the role played by Bmp4 in the formation of definitive endoderm *in vitro*

The initial investigations outlined in Section 4.1 show that in our differentiation strategy, Activin A expectedly induces the formation of DE in Matrigel-embedded EBs. Strikingly, the addition of Bmp4 to this differentiation significantly increases the expression of DE-specific genes. This unexpected synergy is consistent between various hESC culture platforms and is highly reproducible. To address the role of Bmp4 in the formation of DE *in vitro*, it is important to draw lessons from Bmp4's role during vertebrate development.

As alluded to in the general introduction and earlier in this chapter, Bmp4 is known to play pleiotropic roles in development but is not known to be an inducer of endoderm. However, there are a few possible mechanisms by which Bmp4 could enhance endodermal differentiation *in vitro*. (1) Activin A utilizes the Nodal signaling machinery and potentially induces transcription of *Nodal* and other genes that locally influence the formation of DE. Binding of Activin A to its receptor initiates

phosphorylation of Smad2, which in a complex with Smad4 induces transcription. Phosphorylated Smad2 (p-Smad2) is known to activate transcription of *Nodal* by binding to the Asymmetric Enhancer (ASE) element within the *Nodal* gene (Saijoh *et al*. 2005; Adachi *et al*. 1999). It is therefore conceivable that endogenous Nodal production also leads to transcription of genes essential for generation of DE. Both signaling events could result in increased Nodal activity as the *Nodal* gene is known to establish a positive feedback loop for its own induction. Consequently there might be greater levels of DE formation in the differentiation. Bmp4 might be enhancing this differentiation (Activin A-induced + Nodal-induced endoderm formation) by activating expression of *Cripto*, the co-receptor required for Nodal function. Bmp4 is known to induce Cripto in embryonic explants (Beck *et al*. 2002) which mirrors hESC differentiation *in vitro*. The above hypothesis is represented in **Figure 4.6**. (2) Bmp4 induces expression of brachyury (*Tbra*) during endodermal differentiation from mESCs and could be acting similarly in hESCs to exert a direct effect on differentiation (Johansson and Wiles 1995). The expression of *TBRA* indicates the presence of a primitive streak-like population which forms DE. This is supported by gene expression data that shows the expression of *TBRA* followed by *FOXA2* and *SOX17* (**Fig 4.3**). As is evident from the data, Bmp4 induces expression of *TBRA* which could increase the pool of primitive streak-like cells primed for allocation to the DE lineage. (3) Our lab has previously demonstrated that Matrigel inhibits VE formation associated with *in vitro* differentiation of hESCs. Since the VE is known to secrete Bmp antagonists like Noggin and Chordin, the use of Matrigel might create an environment that reveals a previously masked function of Bmp4 in endoderm specification *in vitro* (Song *et al*. 2007; Rust *et al*. 2006; Tiso *et al*. 2002). It is also

important to note that the formation of anterior primitive streak derivatives such as the node is impaired in *Bmp4* mutant mouse embryos (Fujiwara *et al*. 2002).

In order to address these possibilities and interrogate the collaborative activity of Activin A and Bmp4 during DE formation from hESC, I undertook the studies outlined below.

4.2.1. Activin A signaling leads to the expression of known target genes during differentiation

Activin A binding to its receptor initiates phosphorylation of Smad2/3, which ultimately leads to transcriptional activation of target genes. Gene expression analysis showed that *NODAL* was upregulated specifically in response to Activin A treatment as the –GF and Bmp4 alone conditions did not show any change in expression levels (**Fig 4.7)**. This shows that Activin A is able to induce *NODAL* transcription over and above the endogenous levels seen at day 0 and in the –GF condition. When Activin A and Bmp4 were added together, there was only a slight upregulation of *NODAL* expression which disappeared by day 6 of differentiation, indicating a rapid signaling event in the presence of these two growth factors. This is in contrast to the sustained expression of *NODAL* in the presence of Activin A alone. The effector Smad molecules phosphorylated by Activin A and Bmp4 compete for the same co-Smad (Smad4) which might affect gene expression. This could be an alternative explanation for the lower expression of *NODAL* in the presence of both growth factors. If this were true, it would suggest that both signaling pathways are active in the same cell and that Bmp4 has a direct effect on DE formation. Along with several other targets, *NODAL* is known to induce transcription of its own inhibitor *LEFTYA* (*LEFTY2*) in a regulatory negative feedback loop (Meno *et al*. 1999).

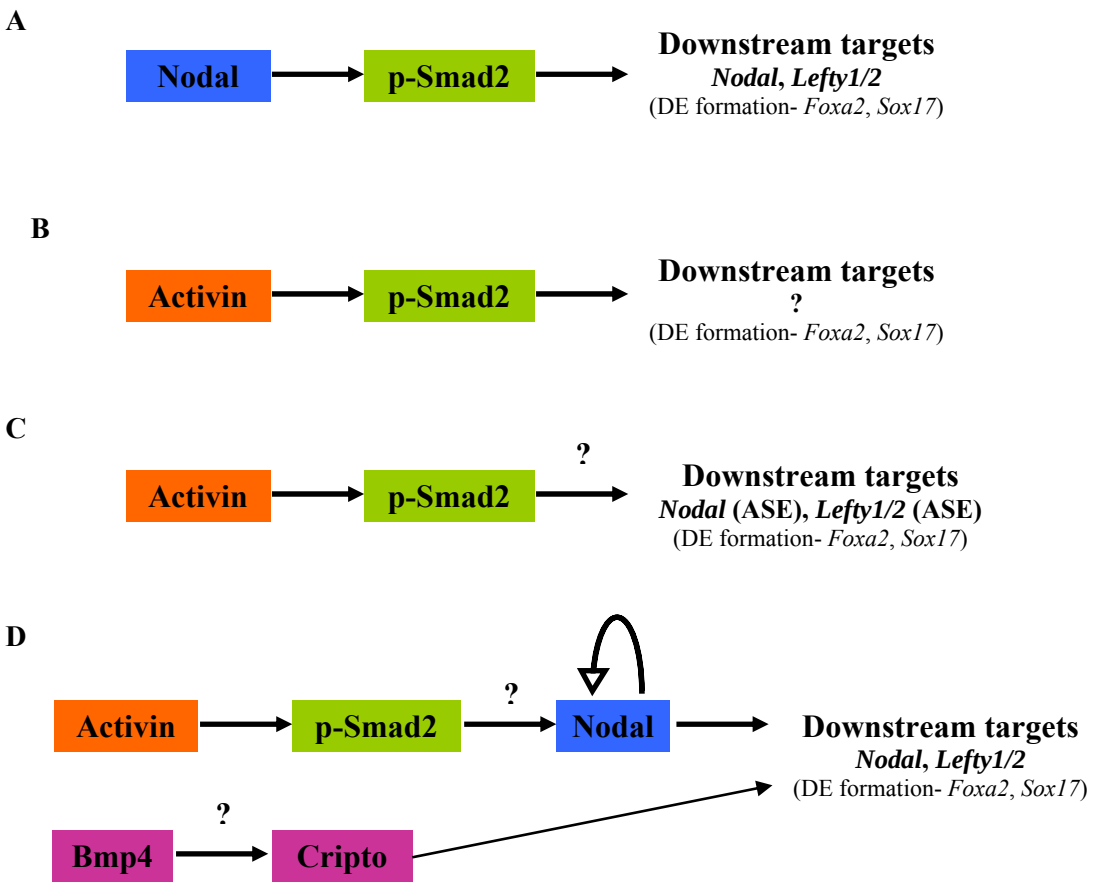


Figure 4.6. Proposed model for synergistic activity of Activin A and Bmp4.

(A) Nodal binding to its receptor causes phosphorylation of Smad2, which complexes with Smad4 and translocates to the nucleus to initiate transcription of downstream target genes including *Nodal* itself and *Lefty1/2*. **(B)** Activin mimics Nodal signaling *in vitro* and results in the expression of genes like *Foxa2* and *Sox17* which are required for DE formation. **(C)** Activin A signaling potentially leads to the expression of genes like *Nodal* as p-Smad2 is known to activate *Nodal* expression through the Asymmetric Enhancer (ASE) element within the *Nodal* gene. This addition activation of *Nodal* transcription could lead to increased expression of genes essential for DE formation. **(D)** A combinatorial effect of these various events is highly likely in the Matrigel-based differentiation in which Activin and p-Smad2 separately induce expression of genes including *Nodal*. This along with the positive feedback loop induced by *Nodal* increases the endogenous pool of *Nodal* that leads to activation of genes that influence DE formation *in vitro*. Bmp4 might be enhancing Nodal signaling locally by inducing Cripto, a co-receptor essential for Nodal function. The net result of these various processes would be robust generation of DE in the *in vitro* system.

In the differentiation, expression of *LEFTYA* followed the peak expression of *NODAL* in the presence of Activin A alone and in the +GF condition (**Fig 4.7B**). This pattern suggests that *NODAL* could be inducing *LEFTYA* at levels relative to its own expression. In addition to this, Smad2 could be directly activating *LEFTY* as there is a Smad-responsive ASE element within the *LEFTY* gene (Saijoh *et al*. 2000; Adachi *et al*. 1999). The Nodal co-receptor *CRIPTO* was expressed at low levels in –GF and in both conditions where Activin A was present (**Fig 4.7C**). Since –GF represents the expression, if any, in the spontaneously differentiating population any equivalent expression cannot be considered significant. Interestingly, Bmp4, which is known to induce *CRIPTO* in explant cultures did not exhibit the same effect in this Matrigel-based differentiation when Bmp4 was used alone. The homeobox transcription factor *Goosecoid* (*GSC*) is expressed in the epiblast region that later forms DE and is a known target of Nodal/ Activin signaling (**Schier 2003**). As expected, *GSC* is activated specifically in response to the addition of Activin A alone or Activin A + Bmp4, and not Bmp4 alone (**Fig 4.7D**). These data indicate that Activin A might be inducing transcription of Nodal through p-Smad2, resulting in endoderm formation as proposed in **Figure 4.5D**. It is important to note that though Activin A was supplemented during the course of differentiation this did not seem to have any specific effect on gene expression. The above data indicate that induction of CRIPTO might not be the mechanism by which Bmp4 enhances endodermal differentiation.

Activin A transduces its signal by phosphorylating Smad2 to mediate the downstream effects. Therefore, I monitored phosphorylation of Smad proteins by SDS PAGE and western blotting as detailed in Chapter 2.9. Phosphorylated Smad2 (pSmad2) was detected in all conditions though sustained expression was seen only in presence of Activin A alone (**Fig 4.8A**). The sustained pSmad2 expression in the

presence of Activin A alone could be attributed to the robust endogenous *NODAL* expression seen in the QPCR analysis. Supplementing Activin A at various time points during the differentiation did not seem to increase or sustain the p-Smad2 expression in any other condition including Activin A + Bmp4. This was inconsistent with the QPCR data which shows induction of *Nodal* at those time points. High p-Smad2 expression on day 2 and a sharp drop in expression by day 4 is consistent with the idea of a short but rapid signaling in the presence of both growth factors.

As phosphorylation of Smad2 is a relatively quick response to ligand binding, I tested early time points during growth factor treatment. Samples were collected as indicated and phosphorylation status analysed (**Fig 4.8B**). Smad2 phosphorylation levels were almost identical for all conditions tested; starting at 15 minutes there was a clear increase which continued up to 3 hours after which it decreased. This suggests that Activin A is depleted by this time in the differentiation resulting in lower levels of pSmad2. This aligns with the reported kinetics of Smad2 phosphorylation in response to Activin A treatment (Mavrakis *et al*. 2007). However, identical pSmad2 levels in all conditions indicate that any specific response to growth factor addition does not occur this early in the differentiation. Taken together these data strongly argue that Activin A triggers a signaling cascade that involves phosphorylated Smads and *NODAL* gene expression to induce endoderm formation. Sustained phosphorylation of Smad2 in the presence of Activin A alone might be a consequence of *NODAL* expression, which possibly increases the pool of p-Smad2 protein. The increased expression of endodermal genes in the presence of Activin A and Bmp4 is most likely the consequence of a rapid and short signaling event induced by these factors as there is no sustained expression of NODAL or p-Smad2 in this condition.

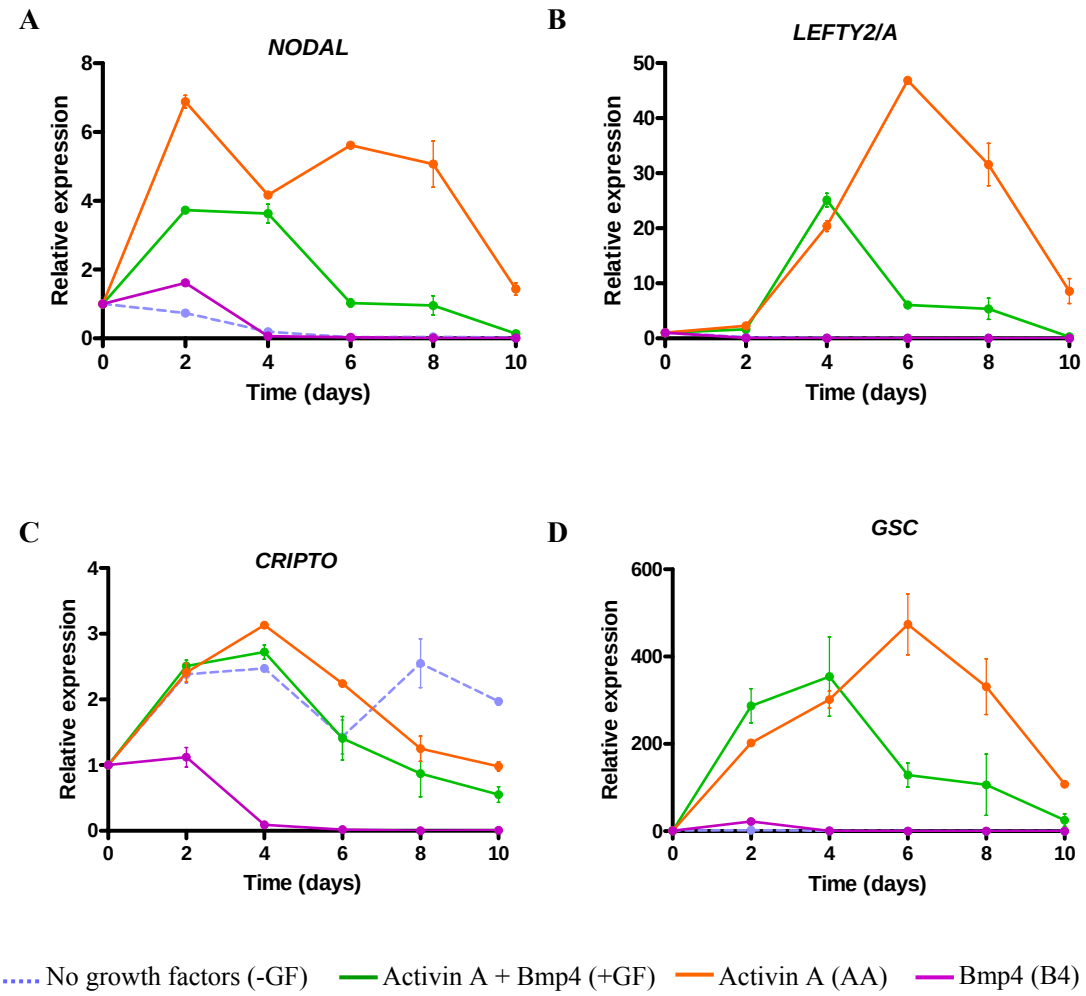


Figure 4.7. Genes characteristic of Nodal/ Activin A signaling.

Cells were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data was generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. **(A)** *NODAL* is expressed during differentiation and is upregulated as a specific response to Activin A. The presence of Bmp4 seems to be dampening *Nodal* expression in the +GF condition. **(B)** A potent inhibitor of *NODAL*, *LEFTY A* is highly expressed in presence of Activin A and both growth factors. The more *NODAL* in the system, the more *LEFTY A* is generated, indicating a self-regulatory negative feedback loop that is induced by *NODAL*. **(C)** The *Nodal* co-receptor, *Cripto*, shows a modest upregulation in all conditions except in presence of Bmp4 alone. The expression is possibly insignificant since –GF represents the background levels of differentiation. Though Bmp4 is a known inducer of *Cripto*, there does not seem to be a specific effect of Bmp4 on the same in this instance. **(D)** *Goosecoid* (*GSC*) is a direct target of Activin signaling and is robustly expressed in both conditions where Activin A is added.

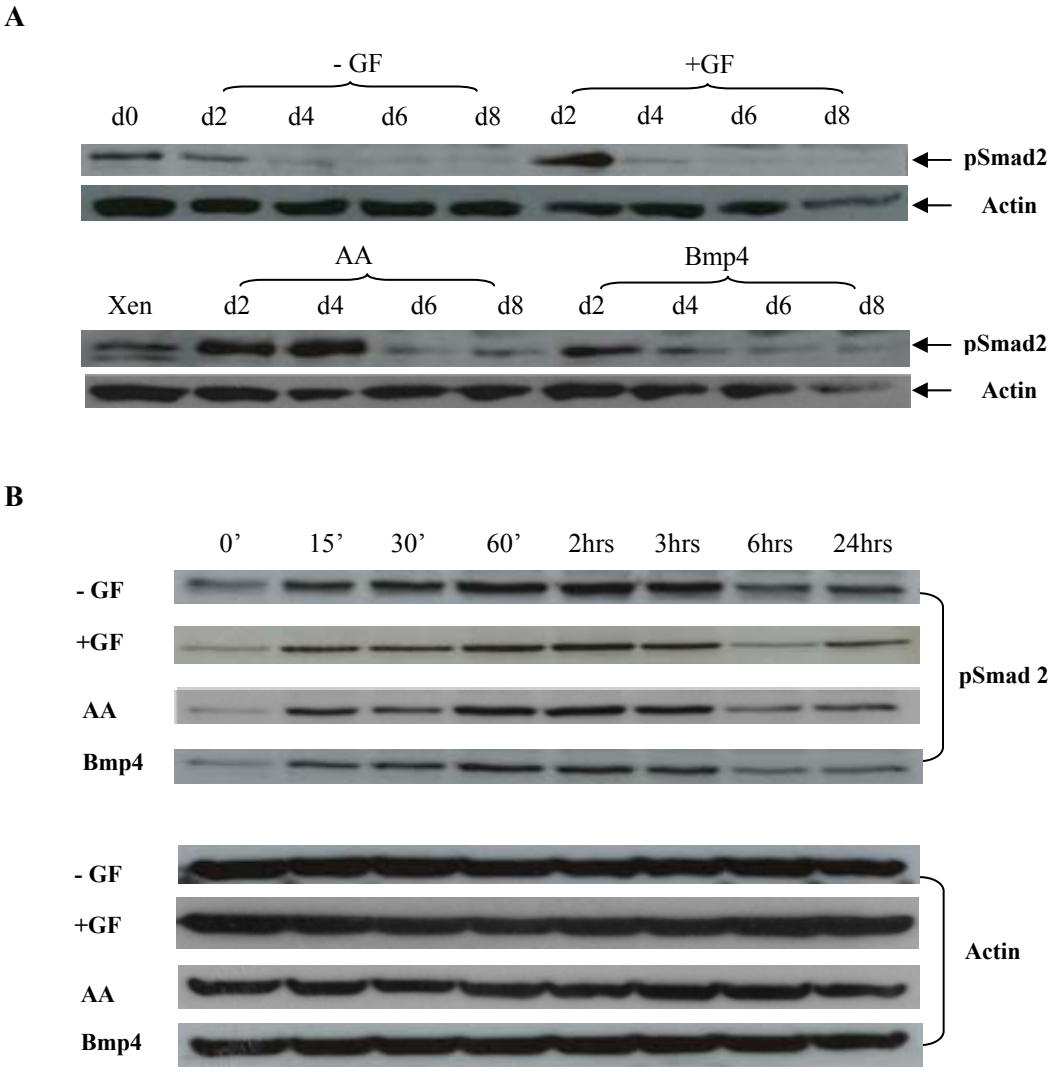


Figure 4.8. Phosphorylation of Smad2/3 in response to the Activin A signal.

Cells were differentiated using the 3D Matrigel protocol under the 4 conditions indicated and SDS-PAGE performed as described. **(A)** Western blot for pSmad2 which is phosphorylated specifically in response to Activin A/ Nodal. In Activin A alone, there is sustained phosphorylation of the Smad2. In all the other conditions, the expression is significantly high only till day 2 and seems to decrease/ disappear thereafter. Bmp4 seems to be squelching the phosphorylation of Smad2 which could result in lower Nodal levels. Xen denotes stage 10 *Xenopus* embryos lysed and run as control. Blots were stained for Actin as the loading control. **(B)** Western blot to assess the timing of Smad phosphorylation upon exposure to differentiating conditions. Samples were collected at the times indicated ('– minutes, hrs – hours). Smad2 showed almost identical pattern of phosphorylation in all conditions indicating that any specific response to growth factor addition was not occurring this early in the differentiation. Since the same activity is seen even in absence of all growth factor treatment, this could be considered background levels of phosphorylation.

4.2.3. Bmp4 signaling and its downstream effects

Bmp4 phosphorylates Smad1/5/8 to initiate a signaling cascade which results in transcription of relevant genes like the inhibitor of differentiation (*Id*) genes in ES cells (Ying *et al*. 2003; Hollnagel *et al*. 1999). To check whether components of this pathway were induced during differentiation, I employed RT-PCR analysis and western blotting. All three *ID* genes *ID1*, *ID2* and *ID3* were expressed in the presence of Activin A + Bmp4 and Bmp4 alone. *ID2* expression was significantly higher than the other two genes and seems to be a specific response to growth factor treatment (**Fig 4.9B**). However, *ID1* and *ID3* were also expressed in the –GF condition which indicates that these genes were induced irrespective of growth factor addition thus rendering the data inconclusive (**Fig 4.9A, C**). The homeobox genes *MSX1* and *MSX2* are functional in multiple tissues during embryogenesis and are important in craniofacial development and limb patterning (Chen *et al*. 2008; Han *et al*. 2007; Ishii *et al*. 2005; Brugger *et al*. 2004; van den Boogaard *et al*. 2000; Bei and Mas 1998). Since these genes are known downstream targets of Bmp4 signaling, I monitored their expression during differentiation. In the presence of Activin A + Bmp4 only *MSX2* was expressed, at very low levels (**Fig 4.9D, E**). As the MSX genes are expressed in the primitive streak, this data supports the presence of a primitive streak-like population as identified by *TBRA* expression earlier. When cells were exposed to Bmp4 alone, both *MSX1* and *MSX2* were significantly upregulated as expected. The inhibitory Smads (I-Smads) *SMAD6* and *SMAD7* are induced by TGF-β signaling and regulate both Activin and Bmp4 signals differently (Imamura *et al*. 1997; Nakao *et al*. 1997). While Smad7 regulates both Activin and Bmp4 signaling, Smad6 is more effective in inhibiting the Bmp4 pathway (Hanyu *et al*. 2001; Hata *et al*. 1998; Itoh *et al*. 1998). Analysis of gene expression during *in vitro* differentiation shows that

SMAD7 is not significantly upregulated (**Fig 4.9G**). Curiously, SMAD6 is significantly high in the +GF condition while low level expression is detected in the presence of either growth factor (**Fig 4.9F**). This is an unexpected observation as only p-Smad1/5 is known to induce SMAD6 and expression was anticipated to be high in the presence of Bmp4 alone with low level expression in the +GF condition (Ishida *et al*. 2000).

Phosphorylation of Smad1/5/8 molecules as a consequence of Bmp4 signaling was detected employing western blotting. Phosphorylated Smad1/5/8 (p-Smad1/5/8) expression was high in all conditions throughout the differentiation and even in undifferentiated hESCs (**Fig 4.10A**). Expression of p-Smad1/5/8 was high even at very early time points and identical between the 4 differentiation conditions (**Fig 4.10B**). These data suggest that Smad1/5/8 phosphorylation occurs in undifferentiated cells and is not a direct and exclusive response to growth factor addition in this differentiation. This supports the speculation that a Bmp4-like activity exists in Matrigel which is responsible for the p-Smad1/5/8 expression.

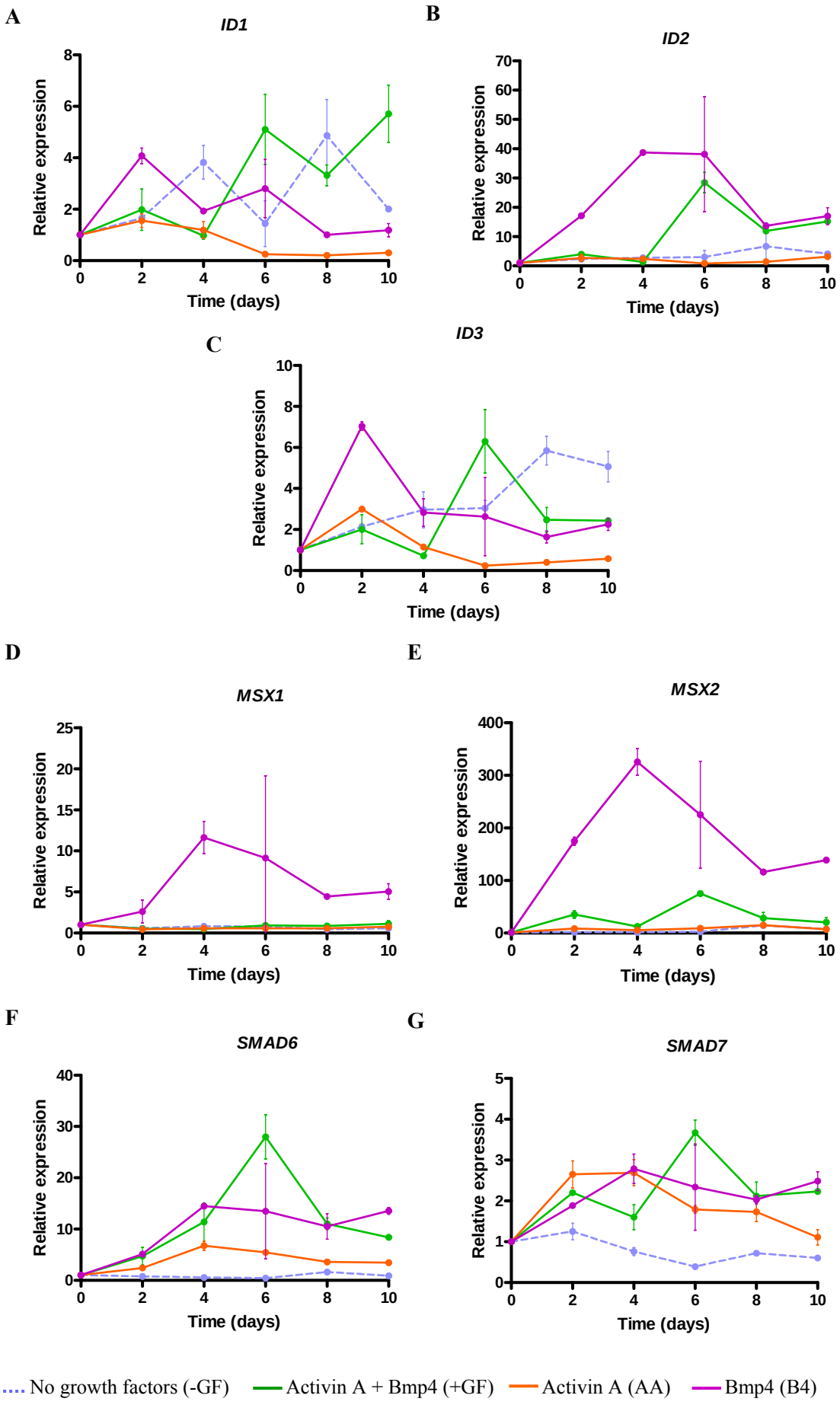

A
ID1
Relative expression
Time (days)
B
ID2
Relative expression
Time (days)
C
ID3
Relative expression
Time (days)
D
MSX1
Relative expression
Time (days)
E
MSX2
Relative expression
Time (days)
F
SMAD6
Relative expression
Time (days)
G
SMAD7
Relative expression
Time (days)
No growth factors (-GF)
Activin A + Bmp4 (+GF)
Activin A (AA)
Bmp4 (B4)

Figure 4.9. Genes expressed in response to Bmp4 signaling. Cells were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data were generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. **(A-C)** A direct consequence of Bmp4 binding its receptor is the induction of *Id* genes. *ID2* is expressed robustly when Bmp4 alone is added to the culture system. In presence of Activin A and Bmp4, the *ID2* expression is delayed and short-lived. Expression patterns of *ID1* and *ID3* were inconclusive. **(D, E)** *MSX* genes, which are induced by Bmp4, are not expressed at significantly high levels during endoderm differentiation (+GF). However these genes are induced specifically in response to Bmp4 addition. **(F, G)** *SMAD6* and *SMAD7* are inhibitory Smads induced by TGF-β signaling. *SMAD6* is expressed in presence of Activin A and Bmp4 individually but highest levels are seen in presence of both growth factors showing a combinatorial effect on gene expression. Higher SMAD6 expression could be the result of induction by p-Smad1/5.

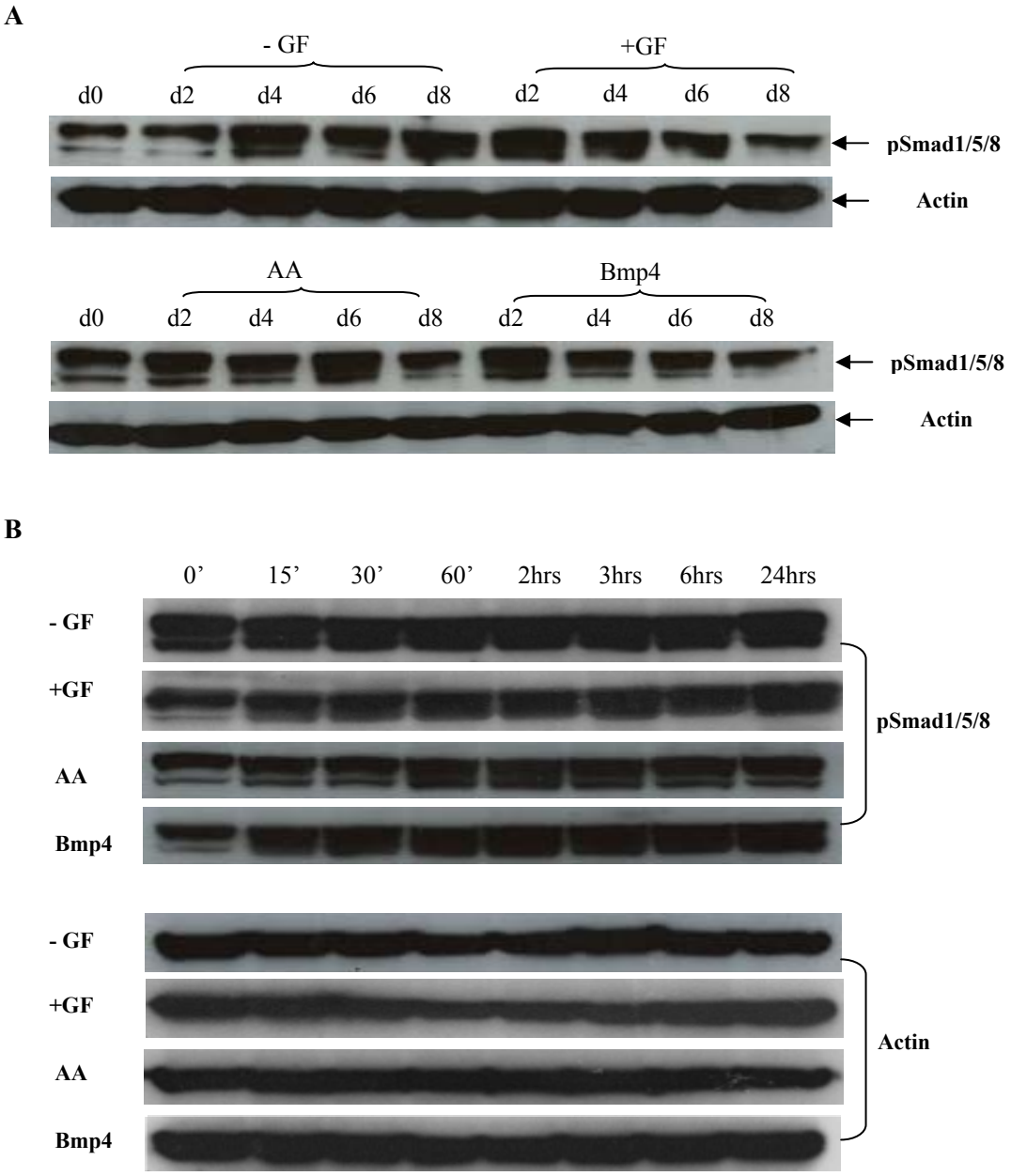


Figure 4.10. Phosphorylation status of Smad1/5/8 in response to the Bmp4 signal.
(A) Western blot for p-Smad1/5/8. Phosphorylation of the Smad protein is high in all conditions, irrespective of growth factor addition. **(B)** Western blot to estimate the timeline of Smad phosphorylation upon exposure to differentiating conditions. Samples were collected at the times indicated (' – minutes, hrs – hours). P-Smad1/5/8 showed almost identical pattern of phosphorylation in all conditions with no specific response to growth factor treatment. Since the same activity is seen even in absence of all growth factor treatment, this could be considered background levels of phosphorylation.

4.2.4. Bmp4 shows inefficient formation of cell types associated with its pleiotropic activities

Bmp4 is known for its pleiotropic activities during development including its roles in the formation of primordial germ cells and mesoderm. In addition, Bmp4 is known to induce trophoblast differentiation from ES cells *in vitro*. I used a candidate gene approach to evaluate the expression of these lineage markers in order to assess if Bmp4 functions along known pathways and induces expression of known target genes.

Primordial Germ Cells (PGCs)

It has been shown that Bmp4 is an absolute requirement for the formation of PGCs in the mouse embryo (Lawson *et al*. 1999). Bmp4 and other related proteins have also been implicated in germ cell differentiation from hESCs *in vitro* (Kee *et al*. 2006). *BLIMP1*, *STELLA*, *FRAGILIS* and *VASA* were chosen as the markers to test for the presence of the germ cell lineage during differentiation. In conditions favouring endodermal differentiation (Activin A + Bmp4 and Activin A) only *STELLA* and *BLIMP1* were upregulated slightly (**Fig 4.11A and C**). *VASA* and *FRAGILIS* did not show any significant expression (**Fig 4.11B and D**). Interestingly, Bmp4 alone did not induce expression of any of these genes. Therefore, a germ cell-like population is not a significant part of the differentiating milieu in Matrigel. Moreover, no cells were found that show the characteristics of PGCs after staining for endogenous alkaline phosphatase activity (N. R. Dunn, unpublished observations).

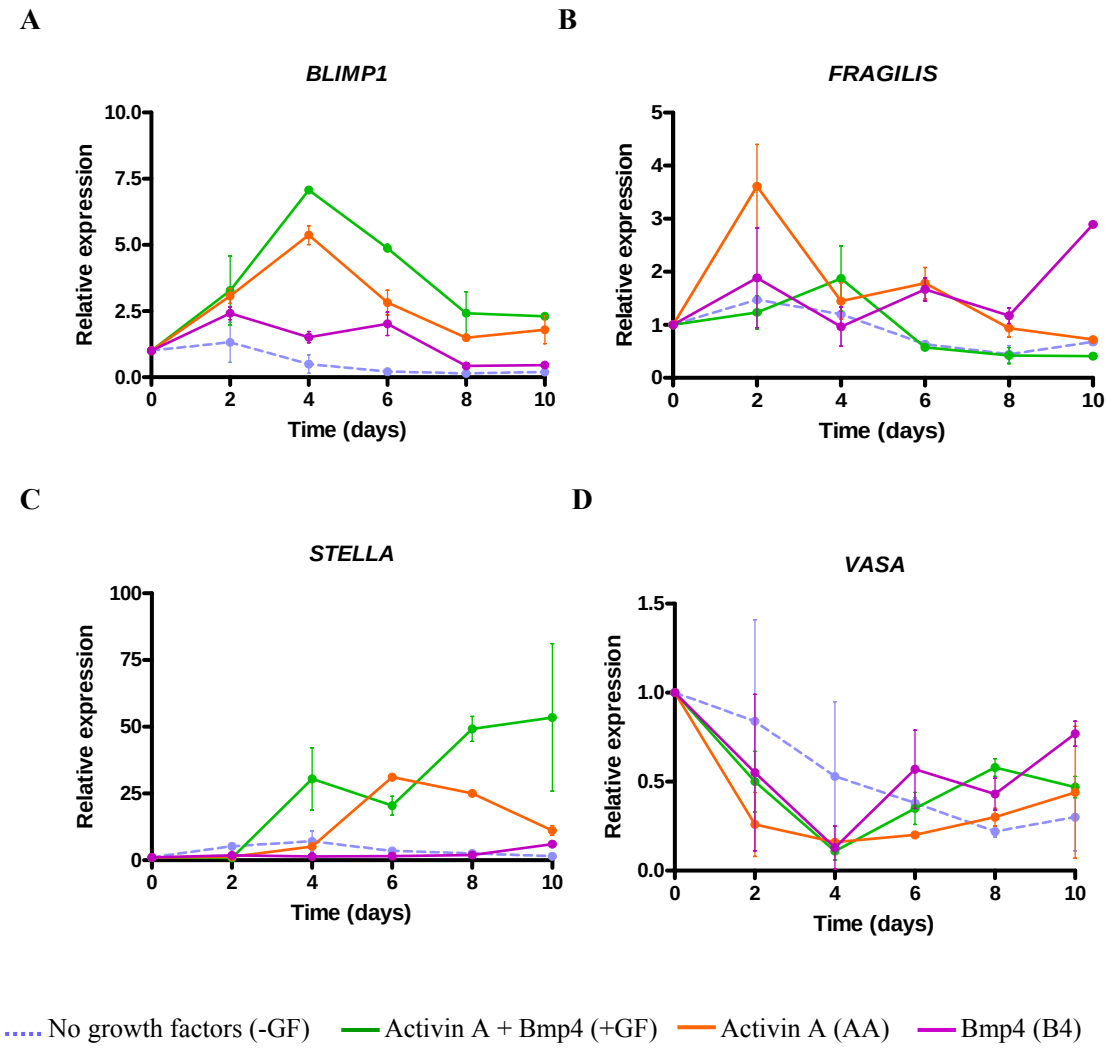


Figure 4.11. Primordial Germ Cell markers are expressed transiently at extremely low levels. Cells were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data was generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. **(A-D)** *Blimp1* and *Stella* are expressed in presence of Activin A and when the growth factor combination is used. *Fragilis* is induced slightly in presence of Activin A alone. *VASA* does not show any induction. Therefore, the germ cell lineage does not seem to be induced as the overall expression of germ cell markers is very low.

Trophoblast

Bmp4 has also been successfully used to generate trophoblast cells *in vitro* from hESCs (Xu *et al*. 2002). Quantitative RT-PCR for marker genes *BMP4*, *ELF5*, *CDX2*, *SPC4*, *FGFR2* and *ESRRB* was used to investigate for signs of trophoblast differentiation. These markers are all detected in the extraembryonic ectoderm (ExE) of the developing mouse embryo between E6.5 and E7.5 (Donnison *et al*. 2005; Pettersson *et al*. 1996). All genes showed significant upregulation when Bmp4 was the only growth factor (**Fig 4.12A-F**). No gene expression was detected when Activin A and Bmp4 were added together. From this data it would seem that conditions that give rise to endoderm do not encourage trophoblast differentiation.

Haematopoietic Cells

Bmp4 is known to induce formation of self-renewing haematopoietic cells from hESCs (Chadwick *et al*. 2003). Haematopoietic markers *SCL* (stem cell leukemia gene) and *PU.1* (purine-rich box.1) were significantly upregulated during differentiation in presence of Bmp4 alone (**Fig 4.12C and D**). *SCL* was also induced in the +GF condition which shows that whenever Bmp4 was added, it led to low level haematopoietic differentiation in this system. In presence of Activin A alone there was only a modest increase in *SCL*. The coincident expression of *SCL* and *TBRA* in Activin A + Bmp4 and Activin A suggests that there might be a hemangioblast-like population forming in the differentiating culture (Chung *et al*. 2002). Hemangioblasts cells are multipotent precursors that can give rise to haematopoietic and endothelial cells. The presence of this bi-potent population might explain the expression of the endothelial cell marker, *VWF* (Von Willebrand Factor) in cells differentiating in the +GF condition and in the presence of Activin A alone (**Fig 4.12E**).

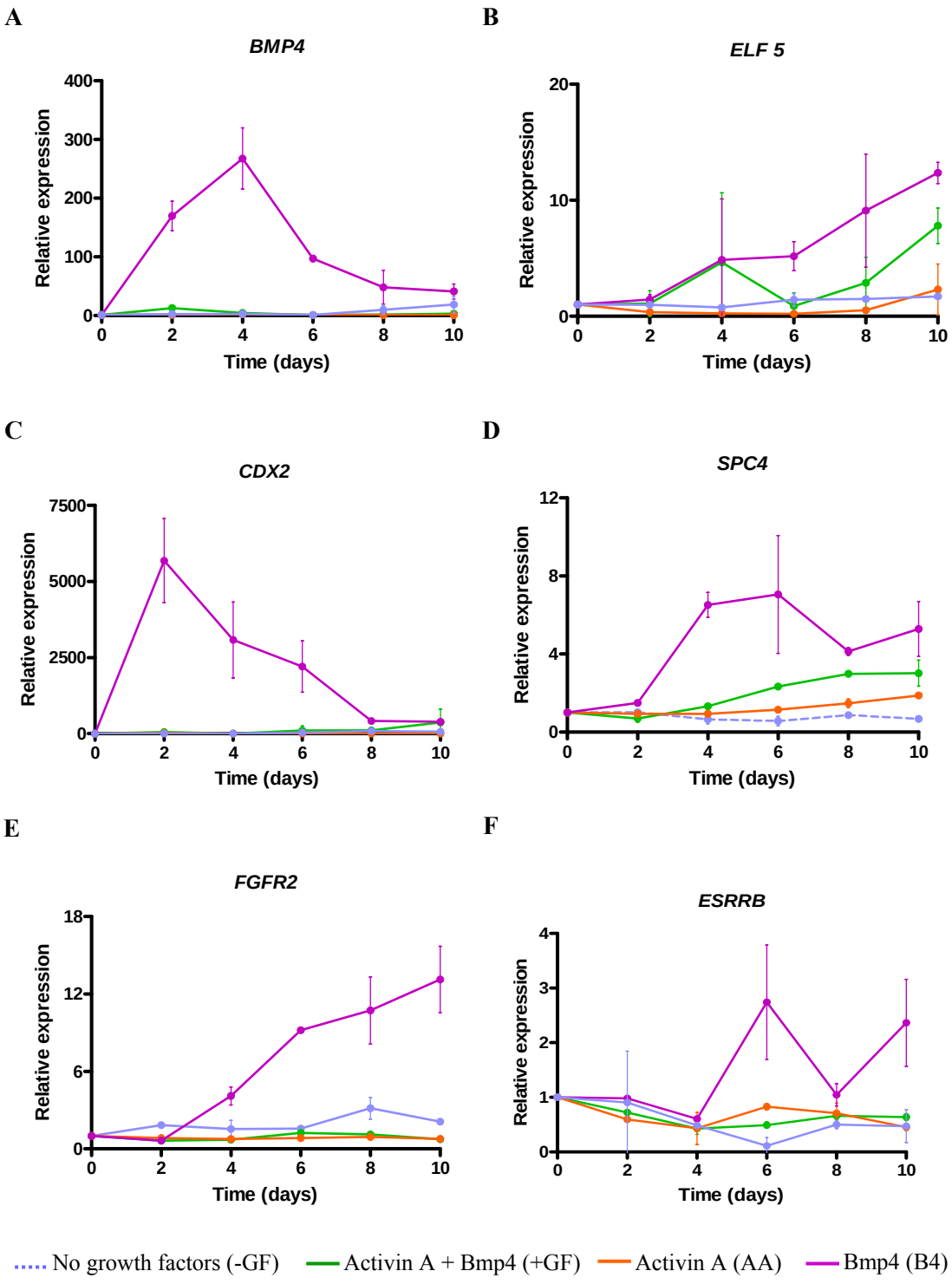


Figure 4.12. Trophoblast markers are expressed at extremely low levels, mainly in response to Bmp4. Cells were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data was generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. **(A-F)** All six markers, including Bmp4 itself, were expressed specifically in response to Bmp4 treatment only. None of the other conditions induced significant expression of the markers.

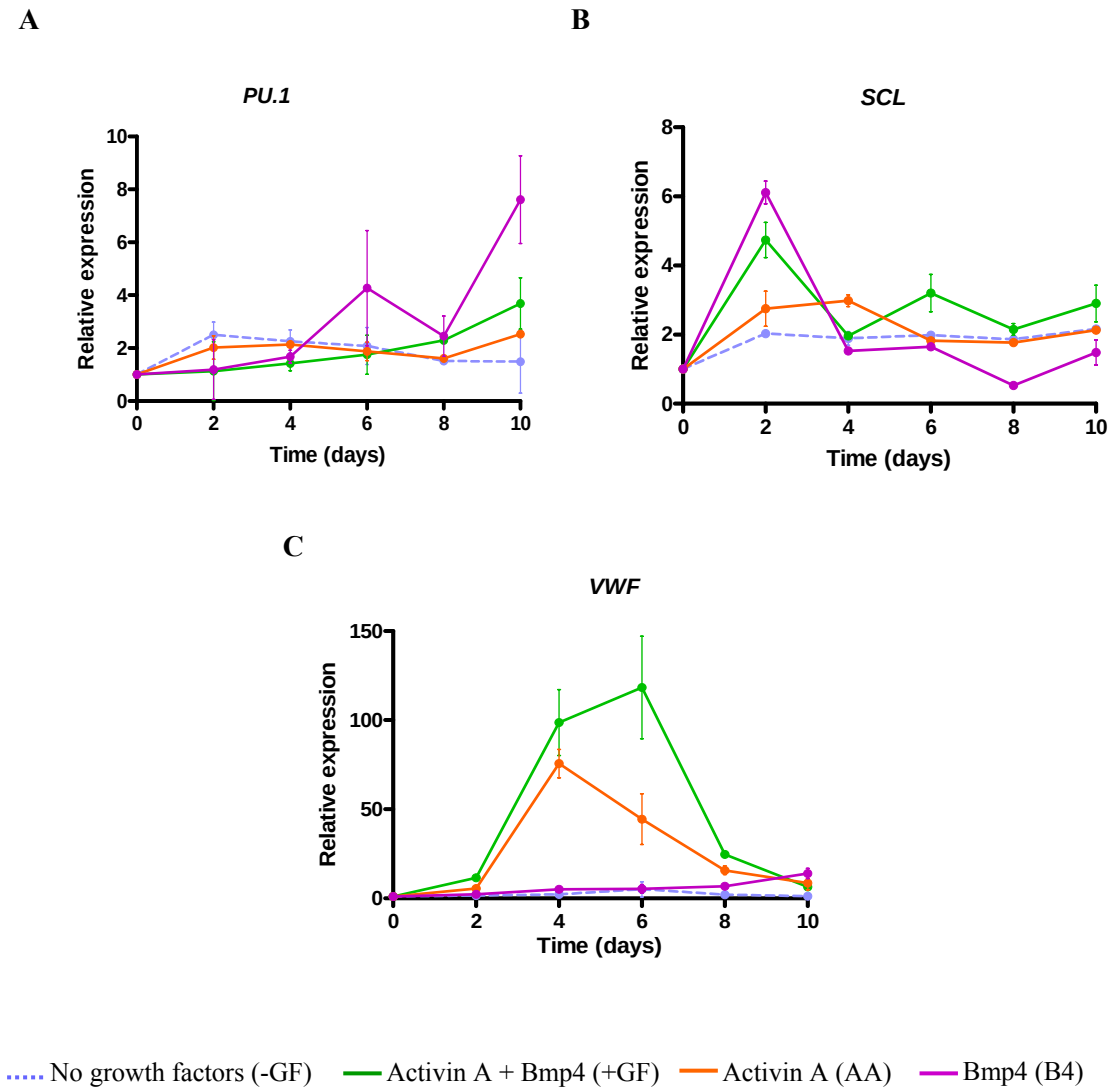


Figure 4.13. Differentiation does not induce significant mesodermal gene expression. hESCs were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data was generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. **(A, B)** Haematopoietic markers *PU.1* and *Scl* were induced in presence of Bmp4 alone as expected. Scl was upregulated transiently in presence of both growth factors but in general haematopoietic differentiation was negligible. **(C)** Endothelial cell marker *VWF* was significantly upregulated in presence of Activin A and when both Activin A and Bmp4 were added. This is not entirely unexpected as endothelial cells are known to be closely associated with the developing endoderm. These cells may be differentiating from the *Scl*- expressing hemangioblast-like population in this system.

4.2.5. Negligible formation of alternate lineages during DE differentiation

Given the sub-optimal efficiency of pancreatic differentiation it must be assumed that other lineages are also being formed in the differentiating cultures. These cell types could arise as a result of spontaneous differentiation or as a direct response to growth factor treatment.

hESCs are known to readily form cells with a neuronal phenotype either through directed or spontaneous differentiation *in vitro* (Itskovitz-Eldor *et al*. 2000). However, in this system, little neuronal differentiation was observed, as evidenced by negligible levels of *NESTIN, TUBB4*, *OTX2*, *SOX1* and *SOX2* (**Fig 4.14A-D**). High *SOX2* expression in the –GF condition is similar to the expression of OCT4 and NANOG shown earlier (**Fig. 4.3**). This is not entirely unexpected as these genes are expressed in the epiblast and might be maintained in hESCs that are not exposed to differentiation signals (Wood and Episkopou 1999). *OTX2* was specifically upregulated to significant levels in presence of Activin A alone and Activin A + Bmp4 as early as day 2 and expression was maintained till day 10 (**Fig 4.14E**). This expression might indicate the persistence of epiblast-like cells in the differentiation as *OTX2* is known to be expressed in the epiblast (Ang *et al*. 1994). Another alternative is that Activin signaling triggers a synthetic induction of *OTX2* as Smad2 is known to regulate the expression of *OTX2* (supported by microarray data shown later in the chapter).

The mesenchyme is known to be important for pancreatic development and has recently been shown to regulate beta cell differentiation in rat embryonic explants (Attali *et al*. 2007; Gittes *et al*. 1996). I tested the differentiation for expression of *VIMENTIN* a marker of mesenchyme but found that there is a meagre response only to Bmp4 addition (**Fig 4.14F**).

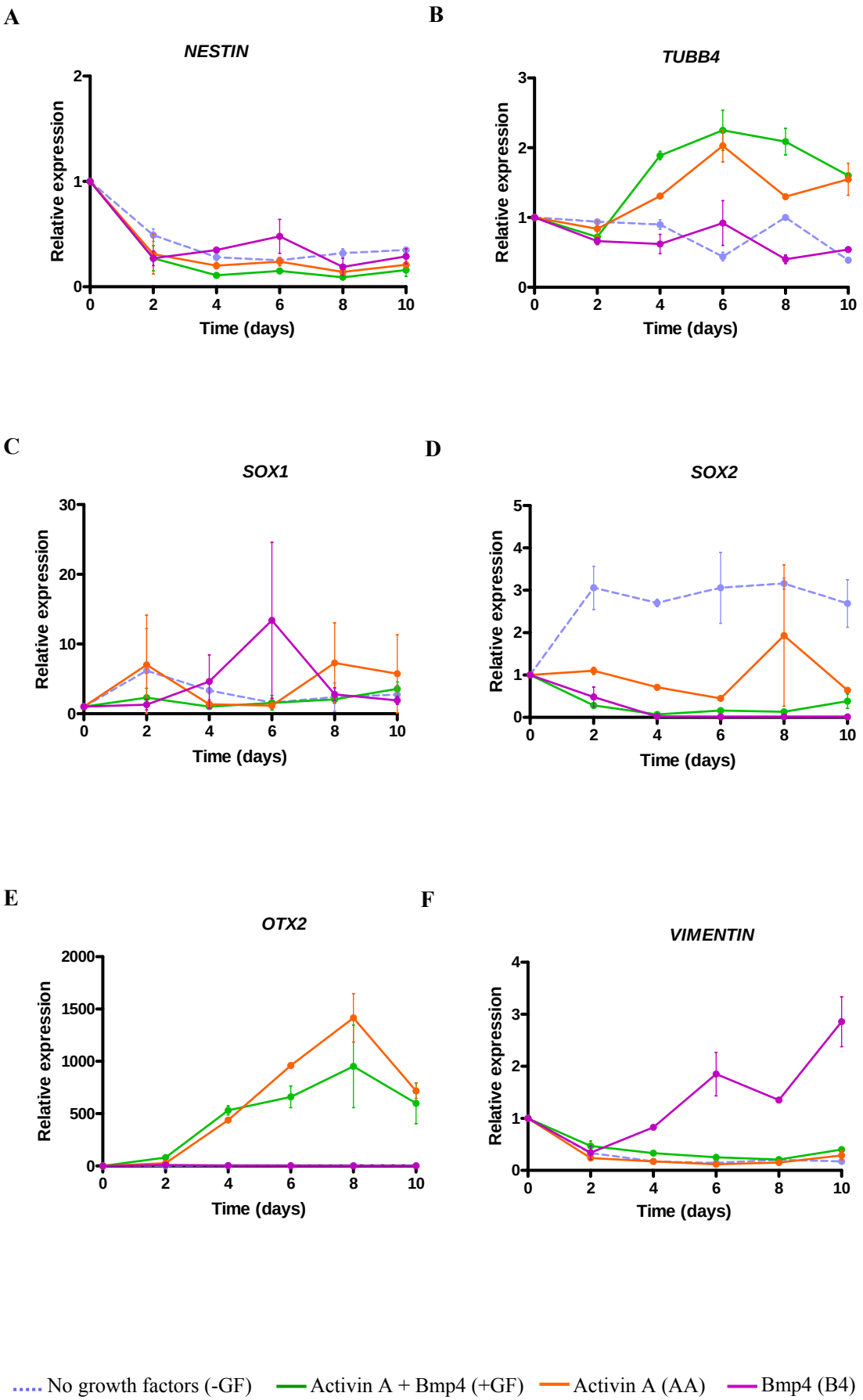

A
NESTIN
Relative expression
Time (days)
B
TUBB4
Relative expression
Time (days)
C
SOX1
Relative expression
Time (days)
D
SOX2
Relative expression
Time (days)
E
OTX2
Relative expression
Time (days)
F
VIMENTIN
Relative expression
Time (days)
No growth factors (-GF)
Activin A + Bmp4 (+GF)
Activin A (AA)
Bmp4 (B4)

Figure 4.14. No significant expression of neuronal markers during differentiation. hESCs were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data was generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. **(A-D)** Markers of the neurectodermal lineage *NESTIN*, *TUBB4*, *SOX1* and *SOX2* were not significantly upregulated in conditions that gave rise to endoderm during the differentiation. High *SOX2* expression in the –GF is consistent with expression of this marker in the epiblast. As cells in the –GF condition do not encounter massive differentiation signals there might be persistence of epiblast-like characteristics. **(E)** *OTX2* was specifically upregulated to high levels in presence of Activin A alone and Activin A + Bmp4. As *OTX2* is known to be expressed in epiblast tissue this expression might indicate persistence of epiblast-like cells in the differentiation. Another explanation is that Activin A-induced p-Smad2 causes synthetic regulation of gene expression as Smad2 is known to regulate *OTX2*. **(F)** *Vimentin* which marks mesenchymal cells or intermediate filaments is not expressed significantly though there is some response to Bmp4 addition.

In an effort to understand the differentiation process and to define a mechanism for the combinatorial activity of Activin A and Bmp4 that leads to reproducible formation of DE from hESCs, I undertook the investigations detailed in sections *4.2.1* to *4.2.5*. These studies showed that the endoderm induction by Activin A was enhanced significantly by Bmp4. However, monitoring gene expression and Smad phosphorylation status of members of Activin and Bmp4 signaling pathways did not reveal a direct impact of Bmp4 on the Activin pathway to potentiate DE formation. Supplementing Activin A in the differentiation did not seem to have a pronounced effect on the expression of target genes and p-Smad2. This suggests that Activin A might not be inducing significantly higher levels of *NODAL* as suggested, that results in increased formation of DE. Gene expression analysis of markers indicative of Bmp4's known pleiotropic activities showed that there was little formation of those specific lineages known to be induced by Bmp4. Taken together these data suggest that Bmp4 impacts DE formation in a novel manner which is not captured in any of the above experimental strategies. In light of these observations, I chose to adopt a global view of the differentiation which is outlined below.

4.2.6. Gene Expression Analysis of Differentiation Using Microarray Technology

My quest to deduce a potential mechanism for the synergistic activity of Activin A and Bmp4 led me to undertake the studies described in Sections 4.2.1 to 4.2.**5**. Since these strategies did not yield any significant clues about the role of Bmp4, I analysed global gene expression patterns during differentiation using microarray technology. Briefly, hES3 cells were differentiated as Matrigel-embedded EBs in presence of Activin A and Bmp4 either individually or in combination. RNA samples were generated at various time points as described earlier and found to express genes

indicative of efficient DE formation by QPCR analysis (**Fig 4.3**). Complementary RNA (cRNA) was synthesized from these samples as detailed in Chapter 2.10. cRNA from selected time points were hybridized to Illumina BeadChips as shown in **Figure 4.15**. Days 4 and 6 were chosen as the preferred sampling points as the expression of key endodermal genes like *SOX17* and *FOXA2* was high on these particular days of the differentiation (**Fig 4.3**). After normalizations and statistical analysis, genes whose expression was altered in comparison to day 0 undifferentiated cells on day 4 were chosen for further investigation. Heat map shows changing expression of genes when treated with the relevant growth factor (s) (**Fig 4.16**). Genes upregulated in undifferentiated hESCs are significantly downregulated in cells treated with Activin A alone (AA) or with Activin A + Bmp4 (+GF). Alterations in gene expression are similar between the treated samples though the +GF condition shows robust expression as seen by the colour intensity (*). Gene list is given in **Appendix III**.

To assess if the microarray is a true representation of the *in vitro* differentiation I analysed the expression of genes known to be upregulated during endoderm formation and previously characterized by QPCR analysis in the day 4 samples. Key indicators of endodermal development in the vertebrate embryo including *FOXA2*, *SOX17*, *EOMES* and *CXCR4* were detected in the presence of Activin A alone and in the presence of Activin A + Bmp4 thus validating the endoderm induction mediated by these two conditions in the differentiation (**Table 4.1**). As was seen in the QPCR analysis, expression of key genes was significantly higher in Activin A + Bmp4 than when Activin A was used alone as evident from the fold change data (**Appendix III**). There was evidence of some mesendodermal and ectodermal differentiation as genes representing these two germ layers including *MIXL1*, *VWF*, *GSC* and *FGF17* were also detected.

Day 0 undiff: Undifferentiated cells

-GF: No growth factors

+GF: Activin A + Bmp4

AA: Activin A

B4: Bmp4

Figure 4.15. Samples loaded on Illumina BeadChip for microarray analysis. hESCs were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. RNA samples from days 0, 4 and 6 of differentiation were converted to cRNA and subjected to microarray analysis using the Illumina Human genome array (N=2).

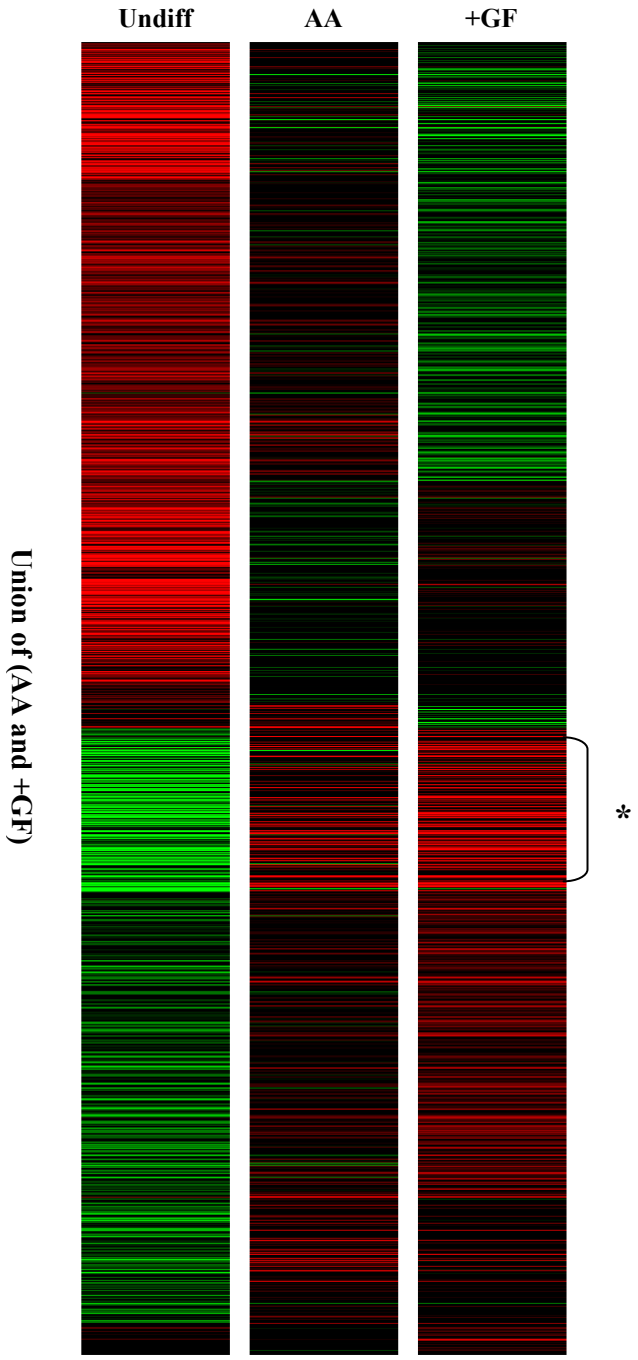


Figure 4.16. Heat map shows global changes in gene expression corresponding to growth factor treatment. Heat map shows clustering of genes expressed differentially between undifferentiated hESCs (Undiff), Activin A treated cells (AA) and Activin A + Bmp4 treated cells (+GF). Genes upregulated in undifferentiated cells (red) are significantly downregulated upon growth factor treatment (green) and vice versa. Gene expression changes are similar between AA and +GF as expected since these two conditions give rise to endoderm during differentiation. However, there is a more robust induction of gene expression in the +GF condition as seen by the difference in colour intensity (representative area indicated by *).

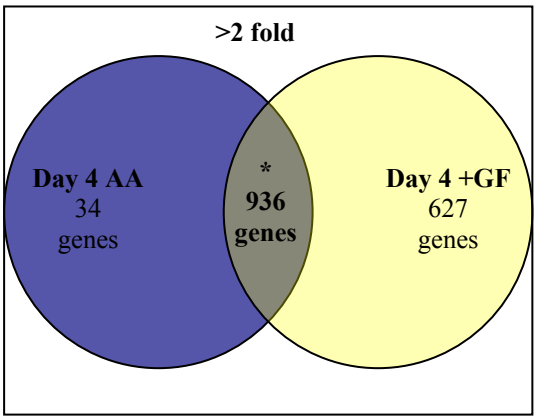
Gene Name	Fold Change (+GF)	Fold Change (AA)
CYP26A1	**90.12**	**60.53**
EOMES	**81.1**	**70.9**
CXCR4	**79.35**	**65.16**
CER1	**71.97**	**56.35**
FOXA2	**71.79**	**56.62**
FGF17	**61.28**	**40.56**
SOX17	**54.05**	**38.06**
FOXQ1	**31.93**	**21.35**
FRZB	**30.38**	**21.99**
GSC	**26.62**	**20.9**
FLRT3	**22.63**	**19.93**
LHX1	**16.62**	**14.69**
BMP2	**13.1**	**8.584**
LEFTY2	**9.403**	**8.651**
PITX2	**4.762**	**3.969**
LEFTY1	**4.607**	**4.332**
PRDM1	**3.677**	**3.739**
FGF8	**3.068**	**3.516**

Table 4.1. Genes expressed during gastrulation in the mouse and/ or associated with the formation of DE. Genes known to be expressed during gastrulation and others known to be critical for endoderm formation are upregulated as expected in day 4 Activin A alone and day 4 Activin + Bmp4. Most genes showed higher expression in presence of both factors than in presence of Activin A alone. The induction of relevant genes validates the sensitivity of the microarray technique for this particular study.

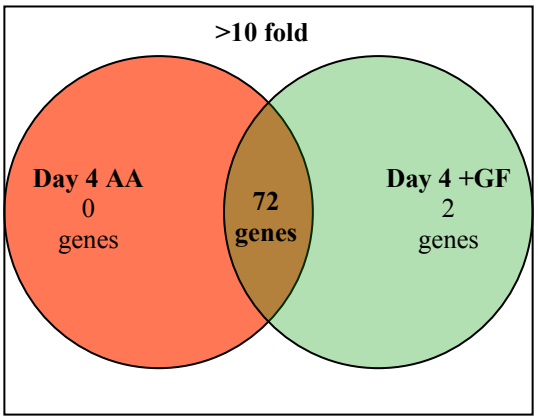
The presence of other germ layers was not clearly captured in the QPCR analysis described earlier as only a small subset of genes was chosen for analysis. Among the various data sets, I chose to look more closely at conditions that promote endoderm formation, i.e. Activin A alone and Activin A + Bmp4 on day 4 of differentiation as that is my primary area of interest (**Fig 4.17 A, B**). Genes altered by 2-fold or above and 10-fold or above were compared between the treated conditions in Venn diagrams. Gene lists are given in **Appendix III**. Gene Ontology analysis was performed to distinguish these gene lists on the basis of molecular function. The pie charts show that in general, genes altered during differentiation fall into the following main categories– binding, catalytic activity, signal transducer activity, transcription regulator activity and transporter activity (**Fig 4.17C**).

Genes in the data set d4 [AA] + [+GF] that showed a difference in expression of 2-fold or more compared to undifferentiated cells were chosen for further analysis (**Fig 4.17 A***). In these conditions, several genes **not** previously associated with or characterized in the context of the endoderm and its formation were highly upregulated. These genes were interrogated in two ways (1) expression analysis of the murine homologues in the developing embryo and (2) QPCR corroboration of candidate gene expression in an independent hESC differentiation experiment. Though these genes were upregulated under conditions that specify endoderm it is important to establish their expression domain (s) in the developing embryo and to analyse if it is relevant to the formation of endoderm. I chose to use the mouse as a model system to study gene expression during development. After eliminating those genes known to be related to endoderm formation and those that are well characterized in other contexts, I chose a total of 26 genes to test in the mouse system (**Table 4.2**).

A


>2 fold
Day 4 AA
34
genes
*
936
genes
Day 4 +GF
627
genes

B


>10 fold
Day 4 AA
0
genes
72
genes
Day 4 +GF
2
genes

C

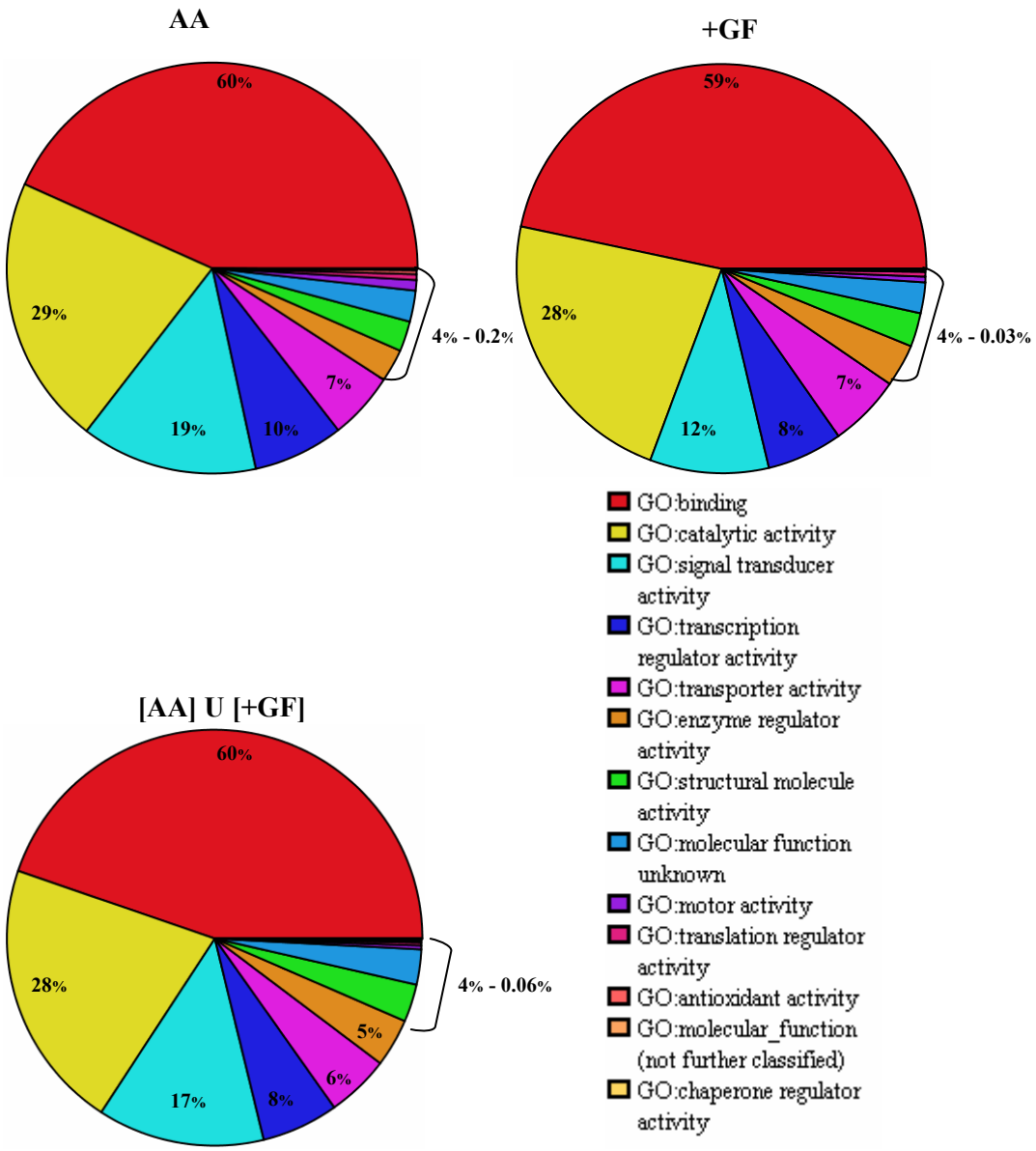

AA
60%
29%
19%
10%
7%
4% - 0.2%
+GF
59%
28%
12%
8%
7%
4% - 0.03%
[AA] U [+GF]
60%
28%
17%
8%
6%
5%
4% - 0.06%
GO:binding
GO:catalytic activity
GO:signal transducer activity
GO:transcription regulator activity
GO:transporter activity
GO:enzyme regulator activity
GO:structural molecule activity
GO:molecular function unknown
GO:motor activity
GO:translation regulator activity
GO:antioxidant activity
GO:molecular_function (not further classified)
GO:chaperone regulator activity

Figure 4.17. Genes expressed in conditions that form DE were chosen for further analysis. **(A, B)** The conditions that gave rise to endoderm– Activin A alone (AA) and Activin A + Bmp4 (+GF) – were compared in a Venn diagram. **(A)** The number of genes altered by 2 fold or more in these conditions is shown. **(B)** The number of genes altered by 10 fold or more is shown. As the subset of genes available for analysis was not significant in the +GF list, genes common to both conditions which were altered by 2 fold or more (936 in the intersect marked by *) were studied in detail. This represents the subset of genes that induce formation of DE. **(C)** Gene Ontology analysis was performed for the indicated conditions taken from (A) and results are represented as pie charts. Distribution of genes was similar between the conditions with significant changes in +GF in signal transducer activity.

APOC1	**KCNF1**
APOA1	**LRRC3**
BHLHB5	**MANEA**
CALCR	**MGST2**
CMKOR1	**MYCT1**
COL9A2	**NPPB**
DDIT4L	**NR0B1**
EDG3	**NUAK1**
FLJ23514	**PCDH7**
GATM	**RCOR3**
HAS2	**RHOBTB3**
HOMER2	**SLC5A9**
IRX3	**SLCO2A1**

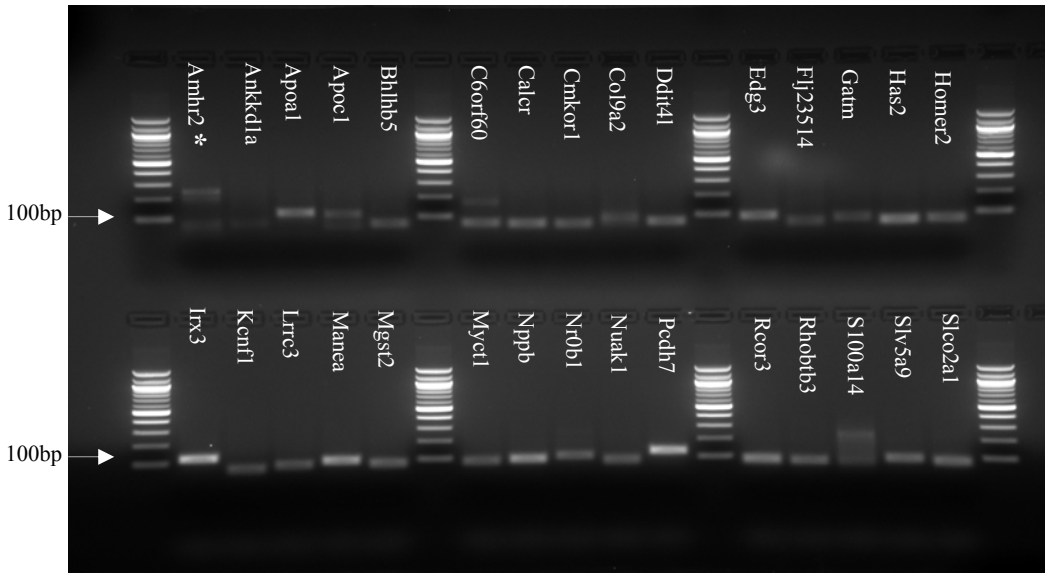
Table 4.2. Preliminary list of genes for detailed analysis. After eliminating genes that are known to be associated with gastrulation, endoderm formation and those novel genes that are common between two very distinct differentiation strategies– 3D and monolayer differentiation (mentioned later in this chapter), a selection of genes hitherto uncharacterised in the context of definitive endoderm formation was chosen for further analysis.

As mentioned in Chapter 1 endoderm development in the mouse commences around E6.5. Therefore, I chose embryos at early stages of development for the studies outlined below. Since these genes were shortlisted on the basis of expression in differentiating hESCs, it was important to establish that genes are indeed expressed in the mouse system. This was by performing Q-PCR analysis on mouse embryo samples at embryonic days E7.5, E8.5 and E9.5. cDNA preparation and PCR conditions are described in Chapter 2.7 and 2.8 respectively. Expression values were normalized to Actin using the ΔΔCt method and PCR product size was confirmed by agarose gel electrophoresis (**Fig 4.18A**). Results show that some of the genes are either not expressed at all or are expressed in a pattern that does not seem relevant to my investigation (**Fig 4.18B**). After careful analysis of these results, 15 genes were chosen for Whole mount In Situ Hybridisation (WISH) (**Table 4.3**). WISH was performed to obtain knowledge about the expression of these genes in the developing mouse embryo. Cloning of these genes, riboprobe synthesis and the WISH protocol are described in Chapter 2.11. Of the 15 genes only one, *Rcor3*, did not yield a PCR product for cloning and is therefore not included in the WISH analysis.

Among the 14 genes tested, 8 showed tissue-specific staining and are described below (**Table 4.4)**. (1) As the major component of high density lipoprotein (HDL), apolipoprotein 1 (*Apoa1*) promotes cholesterol efflux from tissues to the liver for excretion. A recent study showed the expression of *Apoa1* in the extraembryonic hypoblast and endoblast and restricted expression in the endoderm of the developing chick embryo (Bertocchini and Stern 2008). A similar expression pattern was seen in the mouse embryo as hybridisation with *in situ* probes shows that *Apoa1* strongly marks the extraembryonic visceral endoderm between E7.0 and E9.5 (**Fig 4.19A**). However, *Apoa1* is restricted entirely to the extraembryonic tissue in the mouse

unlike in the chick embryo. (2) Edg3 (sphingolipid G-protein coupled receptor 3/ S1P3) is known to mediate the effects of its ligand, sphingosine-1-phosphate (S1P), during embryonic angiogenesis and bone homeostasis (Ishii *et al*. 2009; Kono *et al*. 2004). A recent report shows that S1P activity indirectly promotes budding of the pancreatic endoderm by stimulating pancreatic mesenchymal cell proliferation by (Edsbagge *et al*. 2005). This ligand is also known to induce proliferation and morphological changes in neural progenitor cells (Harada *et al*. 2004). Expression in the mouse embryo was mainly in the somites, neural tissue and the allantois (**Fig 4.19B**). (3) *Gatm* (glycine amidinotranferase) is a creatine synthesis enzyme which is known to be imprinted in the mouse placenta and the yolk sac but not in embryonic tissues (Sandell *et al*. 2003). However, here I show expression in the somites, the brachial arch and possibly in neural tissue (**Fig 4.19C**). (4) Previously known to be expressed in neural tissue, *Homer2*, was strongly expressed in the developing heart and in the 1st brachial arch (**Fig 4.19D**). *Homer2* expression in cardiac tissue was previously reported in adult rats but not in embryonic tissue (Schweitzer *et al*. 2006). This is the first report of *Homer2* expression in the developing vertebrate heart. (5) Another gene that was expressed in the extraembryonic/ chorionic ectoderm is *Irx3* (Iroquois related homeobox 3) which progressively resolved to the anterior region of the embryo (**Fig 4.19E**). *Irx3* belongs to a family of genes involved in patterning and regionalization of differentiation within the embryo. It has been implicated in neural development and is known to be expressed in the foregut at E10.5 in the epithelial layer of lung buds and bronchia (Houweling *et al*. 2001). In the stained embryos, *Irx3* was also seen in the anterior neuroectoderm and the neural tube from E7.0 to E9.5. In addition, this gene seems to be expressed in the early DE which resolves to the foregut pocket in the later stage embryos.

A



B

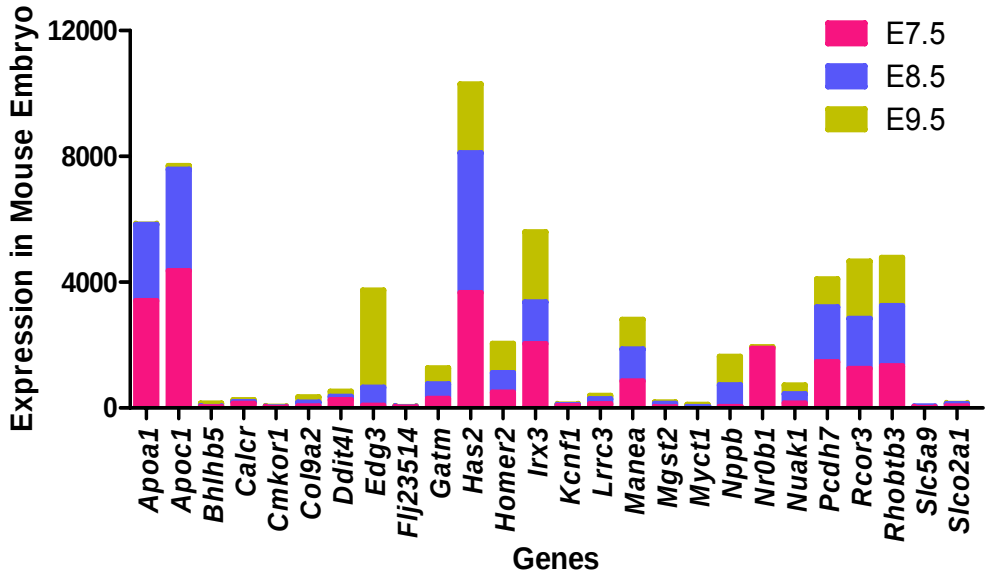


Figure 4.18. Quantitative PCR in mouse embryo samples for genes shortlisted from microarray. (A) PCR product sizes of the genes were confirmed by agarose gel electrophoresis. Some genes like *Amhr2* in lane 1 (*) were eliminated from further analysis as their expression patterns are known and might not be relevant to my investigation. **(B)** Q-PCR revealed varied expression patterns of the selected genes in mouse embryo samples at embryonic days E7.5, E8.5 and E9.5. Some genes like *Has2* showed high but sustained expression while others like *Apoa1* showed differential expression between the samples tested.

APOA1	**IRX3**
APOC1	**LRRC3**
CALCR	**MANEA**
DDIT4L	**NR0B1**
EDG3	**NUAK1**
GATM	**PCDH7**
HOMER2	**RHOBTB3**

Table 4.3. Genes chosen for riboprobe synthesis and whole mount in situ hybridisation. Based on expression in the mouse embryo 14 genes were selected for detailed characterisation. These were cloned into bacterial vector to generate DNA template for riboprobe synthesis. Probes were used for whole mount in situ hybridisation (WISH).

Extraembryonic	Neural tissue	Endoderm	Mesoderm
APOA1	***EDG3***	***IRX3***	***HOMER2***
IRX3	***GATM***	***NUAK1***	***RHOBTB3***
NR0B1	***IRX3***	***GATM***	
EDG3	***RHOBTB3***	***HOMER2***	

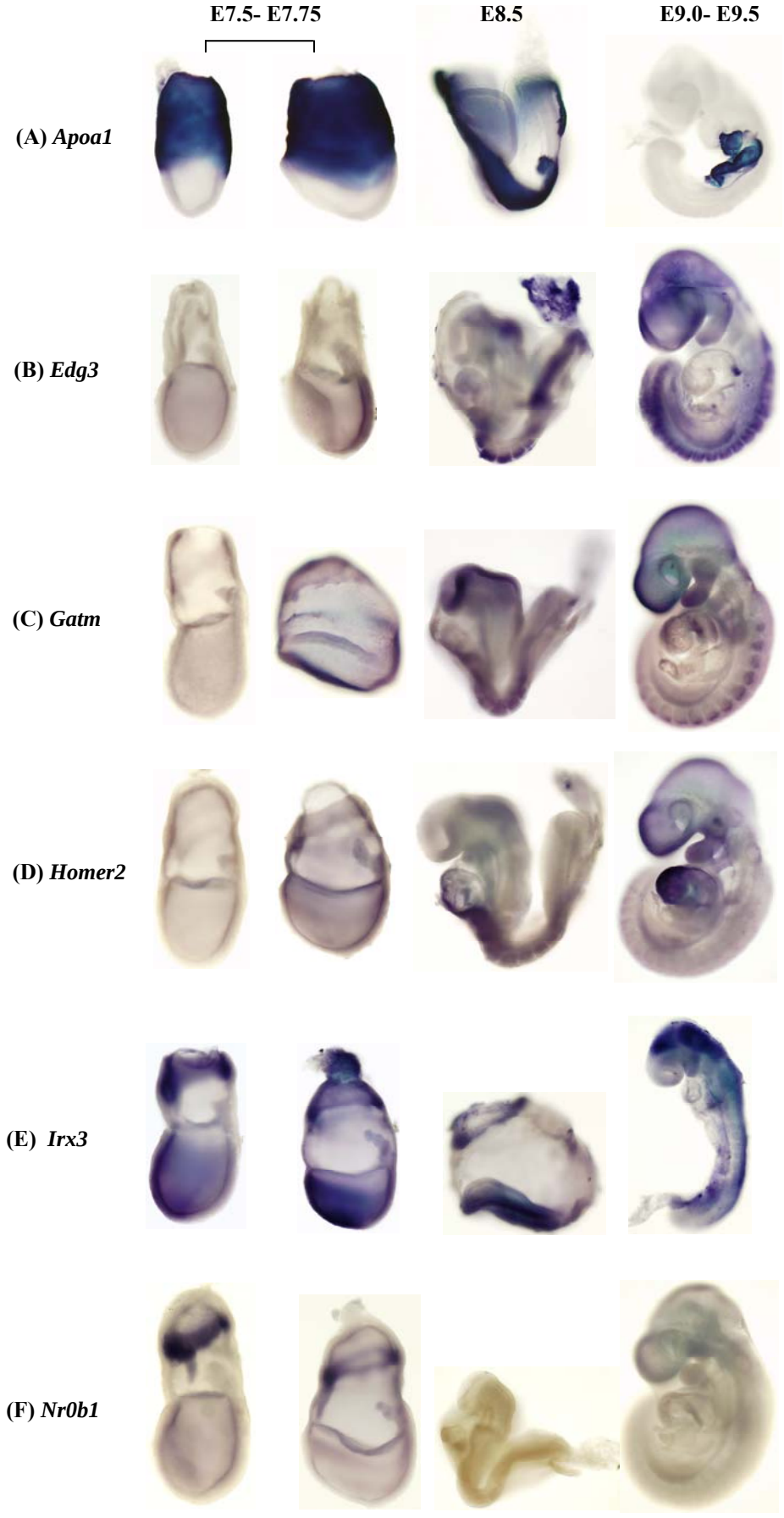
Table 4.4. Expression domains of key genes identified by WISH in the mouse embryo. While some genes like *Apoa1* showed restricted areas of expression, others like *Irx3* showed widespread tissue distribution in their staining.

(6) *Nr0b1* (Nuclear receptor subfamily 0, group B, member 1) is the gene that encodes *DAX1* (dosage sensitive sex-reversal (DSS), adrenal hypoplasia congenita (AHC)), a nuclear receptor protein which is essential for vertebrate development. *DAX1* is expressed on preimplantation mouse blastocysts and mouse ES cells and is known to be regulated by *Oct3/4* and *Stat3* to promote maintenance of the undifferentiated state of ES cells (Sun *et al*. 2008; Niakan *et al*. 2006; Clipsham and McCabe 2003). *Nr0b1* has recently been identified as one of the possible target genes of the homeodomain protein *Hex*, which marks the anterior DE and anterior VE (Zamparini *et al*. 2006; Thomas *et al*. 1998). In support of this observation, *Nr0b1* was strongly expressed in the chorionic/ extraembryonic ectoderm only in early embryos at E7.0 and E7.5 in a pattern reminiscent of *Hex* expression (**Fig 4.19F**). (7) *Nuak1* is an SNF1-like kinase known to be suppressor of apoptosis induced by nutrient starvation (Suzuki *et al*. 2005; Suzuki *et al*. 2003). This kinase promotes survival by triggering the Akt/ PKB (protein kinase B) pathway upon encountering metabolic stress. In early mouse embryos there seems to be weak primitive streak expression that becomes progressively restricted to the foregut and then to the pharyngeal endoderm (**Fig 4.19**). *Nuak1* was also detected in the brachial arches and brain. (8) *Rhobtb3* (Rho related BTB domain containing 3) is a member of the Rho GTPase family known to be expressed strongly in adult mouse neural and cardiac tissues by Northern blot analysis (Ramos *et al*. 2002). The *in situ* data shows for the first time expression of this gene in the embryonic component of the early embryo and in the neural tissue of the later stage embryo (**Fig 4.19H**). Five genes– *Edg3*, *Gatm*, *Homer2*, *Nuak1* and *Rhobtb3*– were also expressed in the primitive streak (PS) and may impact DE formation as this germ layer arises from the PS. These will be studied in detail in further experiments outlined in Chapter 5. Three genes– *Apoa1*, *Irx3* and

Nr0b1– showed specific expression in the extraembryonic ectoderm. Of these, *Apoa1* was robustly expressed in the extraembryonic VE indicating the formation of low levels of VE for which Bmp4 could be solely responsible. Six other probes that were used for WISH either showed no tissue-specific expression or were not expressed at all. These need to be re-visited to resolve the discrepancy between QPCR data and WISH observations.

The second approach to validate the microarray results was QPCR analysis of gene expression during *in vitro* differentiation (**Fig 4.20**). Samples from an independent Matrigel-based differentiation were used to assess gene expression. In general, all genes tested showed increased expression in conditions favouring endodermal differentiation (AA and +GF) compared to untreated control (–GF). *APOA1*, *GATM*, *IRX3*, *NR0B1* and *RHOBTB3* showed significant upregulation in the +GF condition compared to the other conditions while *EDG3*, *HOMER2* and *NUAK1* showed higher expression when Activin A was used alone (**Fig 4.20 A-H**). In addition, some genes like *EDG3*, *RHOBTB3* and *NR0B1* were also upregulated in the presence of Bmp4 alone. *APOA1* in particular was significantly upregulated only when both Activin A and Bmp4 were used (**Fig 4.20A**). The late expression (post day 4) of *APOA1* was similar to that of *AFP* and *TTR* (**Fig 4.4**). As these markers resolve to the liver, it is possible that the *APOA1* expression detected here marks the precocious formation of hepatic cell types during differentiation. *IRX3* expression in the +GF condition shows that it is involved in endodermal development (**Fig 4.20E**). This is consistent with the staining seen in the early DE and the foregut of the mouse embryo. Upregulation of *NUAK1* in the +GF and AA conditions, validates the staining observed in the foregut and pharyngeal endoderm (**Fig 4.20G**). Significant levels of *IRX3*, *NR0B1* and *RHOBTB3* on day 2 of differentiation aligns with the

expression seen in the early embryo (**Fig 4.20E, F, H**). However, *APOA1* is an exception as it is detected in the early embryo but not in initial part of differentiation. It is possible that *APOA1* specifically marks the VE unlike the other early markers and is inhibited along with the other VE markers like *H19* during the differentiation. As the QPCR analysis was done on an independent hESC differentiation, these data serve to validate the microarray results. Concurrent to this work our lab developed a differentiation strategy in monolayer culture using the combination of Activin A and Bmp4 to generate in phases, definitive endoderm and pancreatic progenitors. Microarray analysis of this two-dimensional differentiation revealed genes that were common between the two experimental regimes (**Table 4.5**). These genes are currently being investigated in detail and are not included in this thesis.


E7.5- E7.75
E8.5
E9.0- E9.5
(A) Apoa1
(B) Edg3
(C) Gatm
(D) Homer2
(E) Irx3
(F) Nr0b1

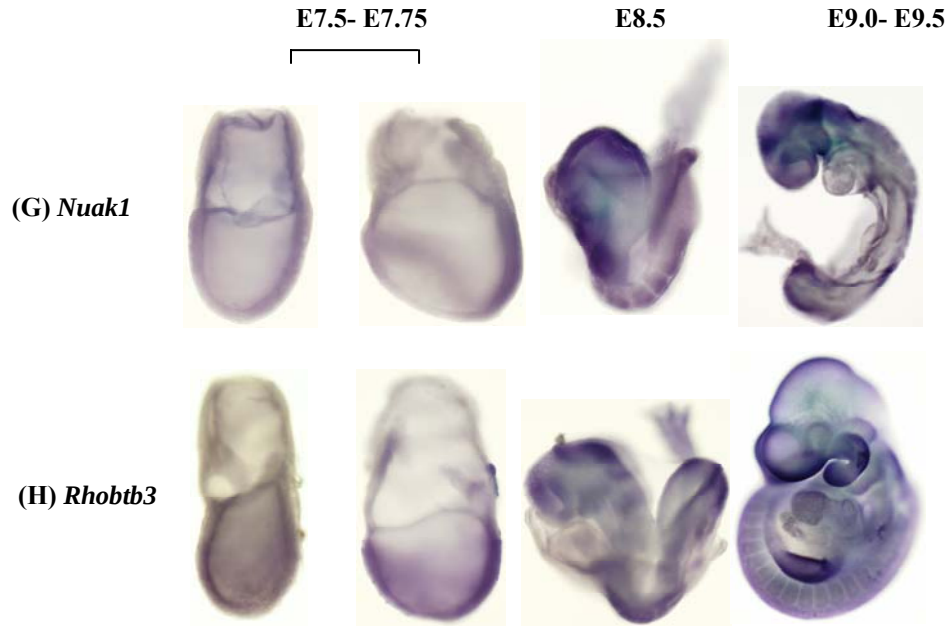


Figure 4.19. Whole mount in-situ hybridisation in mouse embryos. Mouse embryos at E7.0-E7.5, E8.5 and E9.5-10.5 were used for WISH using specific RNA probes created against genes of interest. **(A)** *Apoa1* exclusively marks the extraembryonic visceral endoderm. In the E9.5 embryo staining is clearly visible only in the remnants of the allantois (black arrowhead). **(B)** *Edg3* is not detected in the early stage embryos which is consistent with the PCR data. Expression in the later stage embryos seems restricted to the somites, anterior and posterior neural tissues. In E8.5 the allantois retains some staining. **(C)** *Gatm* was expressed in the somites and neural tissue in the E8.5 and in the somites, first brachial arch and possibly heart traberculae in E9.5. **(D)** *Homer2* is first detected in E8.5 embryos where it stains the somites and the forming heart. By E9.5 staining is clearly visible in the heart and in the first brachial arch. **(E)** *Irx3* is expressed in the hat/ bonnet of the extraembryonic (chorionic) ectoderm in early allantoic bud (EB+), late allantoic bud (LB) and late head fold stage embryos. Between E7.5 to E8.0 the expression resolves to the anterior region and is excluded from the node and the posterior primitive streak. In the late head fold embryo (E8.0), *Irx3* was also detected in the neural folds, midline (notochordal plate) and possibly in the definitive endoderm. At the 1-2 somite stage, *Irx3* resolves to the anterior neuroectoderm (hindbrain, midbrain and forebrain) and the anterior endoderm represented by the foregut pocket. In E10.5 embryos staining is detectable in the midbrain, hindbrain, midline neural tissue and lateral plate mesoderm. **(F)** *Nr0b1* is expressed in a ring-like form at the junction where the visceral endoderm meets the chorionic ectoderm. Expression is highest in the early embryos, decreases by E7.5 and is not present in E8.5 and E9.5 embryos. **(G)** *Nuak1* weakly stains the posterior primitive streak in E7.5 embryos and shows specific staining at the foregut entrance in E8.5 embryos. By E10.5 this gene is expressed in the brachial arches and the limb bud. **(H)** *Rhobtb3* is weakly expressed through out the embryonic component of the early stage embryos (E7.5 to E8.5). In E8.5 expression is also detectable in the anterior and posterior neural tissue.

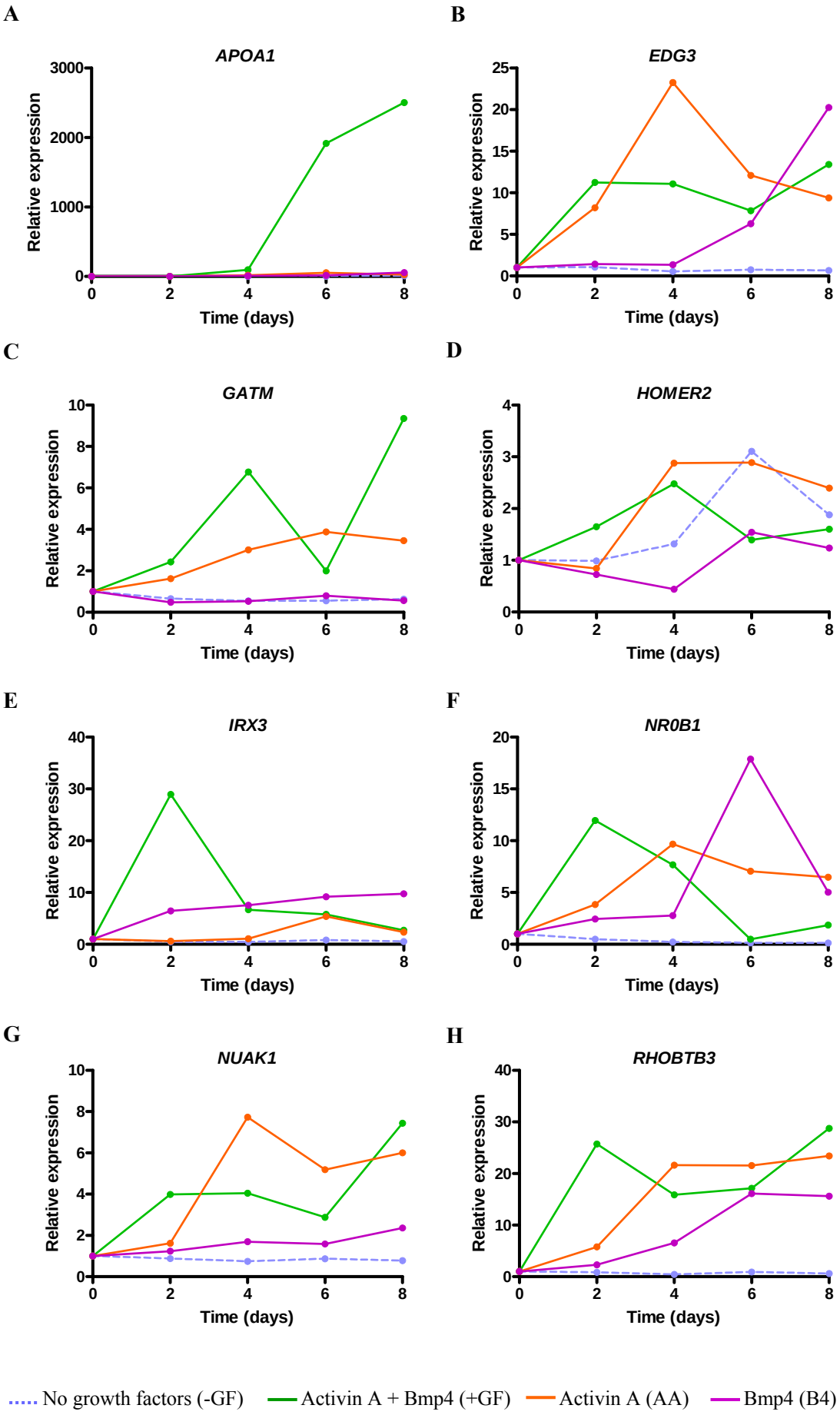

A
APOA1
Relative expression
Time (days)
B
EDG3
Relative expression
Time (days)
C
GATM
Relative expression
Time (days)
D
HOMER2
Relative expression
Time (days)
E
IRX3
Relative expression
Time (days)
F
NR0B1
Relative expression
Time (days)
G
NUAK1
Relative expression
Time (days)
H
RHOBTB3
Relative expression
Time (days)
No growth factors (-GF)
Activin A + Bmp4 (+GF)
Activin A (AA)
Bmp4 (B4)

Figure 4.20. Expression of genes characterised by WISH during in vitro differentiation of hESCs. Cells were differentiated using the 3D Matrigel protocol under the 4 conditions indicated. Gene expression data was generated by quantitative RT-PCR with samples collected every other day from day 0 to day 10. All genes analysed here show increased expression in conditions favouring endoderm formation when compared to untreated control (–GF). A subset of the genes showed higher expression in response to Activin A alone and some to Bmp4 alone. **(E, F, H)** *IRX3*, *NR0B1* and *RHOBTB3* gene expression was detected in the first few days of differentiation mirroring the staining in very early stage embryos. **(A)** *APOA1* was the exception as gene expression was absent early in the differentiation while strong staining was seen in the early stage embryos. The specific response to +GF condition and the late expression suggests that *APOA1* might be an endodermal marker which resolves to the liver similar to *TTR* and *AFP*.

GRP	SERHL2
FREM1	HAK
SEMA3E	AGTRL1
COLEC12	ANKS1B
PDZK1	DKK4
UPK1B	LRIG3
DIO3	LEPREL1
IL18R1	APOA2
EPSTI1	EPHA4
SAMD3	CUGBP2
SMARCD3	CRIP1
CPE	RTDRD7
CCKBR	MCC
PCDH10	DACT2
ROR2	SAMD11
IGFBP5	KCNK12
EPHB3	KCNG1
PPAPDC1	ADAM19
PCDH20	MX1
DEPDC6	TXNIP

Table 4.5. Novel genes potentially involved in endoderm differentiation of hESCs. Several novel genes that showed altered expression were common between the 3D approach and a parallel monolayer differentiation strategy developed in our lab for the generation of pancreatic progenitors from hESCs. These are currently being investigated in detail.

CONCLUSION and DISCUSSION

In an effort to develop effective cell therapy for diabetes our lab devised an *in vitro* differentiation strategy that allows the sequential formation of DE and pancreatic progenitor cells from hESCs. This differentiation employed the combination of a known endoderm inducer Activin A and the pleiotropic factor, Bmp4 to generate DE-like cells marked by *FOXA2* and *SOX17*. These cells further developed into *PDX1*$^{+}$ pancreatic progenitors which gave rise to more mature cell types that expressed *INSULIN*, *NGN3* and *PTF1A* in the presence of appropriate growth and maturation factors. Though inefficient with regard to β cell output, this three-dimensional protocol reproducibly led to the production of definitive endoderm and pancreatic progenitors (Phillips *et al*. 2007). Detailed investigation of the differentiation revealed that the gene activation pattern closely mimics what is known in the vertebrate embryo. The onset of differentiation led to an increase in expression of the gastrulation marker *TBRA*. This was followed by sequential expression of *FOXA2* and *SOX17* (DE) and *PDX1* and other endocrine markers. Immunocytochemistry showed that as differentiation progresses, there are reciprocal changes in the expression of pluripotency and differentiation markers.

Though Activin A is a known endoderm inducer, Bmp4 is better known for its pleiotropic activities like mesoderm induction and PGC formation. The unexpected synergy between Activin A and Bmp4 that induces endoderm prompted detailed characterization of the differentiation in the presence of either factor singly or together. Gene expression profiles of *TBRA*, *FOXA2*, *SOX17* and *PDX1* suggested that Activin A either used alone or with Bmp4 gave rise to endodermal derivatives though the combination of the two factors always induced higher levels of

differentiation. However, removal of Matrigel from the system abrogated this ability of Activin A to induce endoderm formation. This suggests that a Bmp4-like activity exists in Matrigel that might be mimicking the environment created by the combination of Activin A and Bmp4. An alternative explanation is that Activin A used in the differentiation maintains the pluripotency of the hESCs and only the differentiation signals from Matrigel/ Bmp4 allow it to overcome that block. Another possibility is that Matrigel buffers the EBs against the anti-differentiation activity of IGF in the medium formulation, thereby allowing differentiation to proceed. Delayed and lower level gene expression in free-floating EBs even in the presence of both growth factors also support the observation that removal of Matrigel creates sub-optimal conditions for differentiation.

In order to elucidate the mechanism of Activin A + Bmp4 synergy, I investigated the expression of components of the individual signaling pathways. Since Activin is an able mimic of Nodal signaling, it is possible that recombinant Activin activates transcription of genes relevant to DE formation through the phosphorylation of Smad2. Since Smad2 is known to activate *Nodal* directly through the ASE element in the *Nodal* gene, p-Smad2 could increase the endogenous levels of *Nodal* leading to enhanced DE formation. To test this hypothesis, I monitored p-Smad2 levels and expression of target genes. Disappointingly, there seemed to be no specific upregulation of pSmad2 levels as a direct response to Activin addition. Expression analysis of target genes also did not yield any clues to deciphering the mechanism of the Activin A + Bmp4 synergy. Similar analysis of the Bmp4 pathway did not generate significant findings. These results strongly argue that there is no direct impact of Bmp4 on the Activin signaling machinery to influence DE formation. Bmp4 does not seem to facilitate the transduction of the Activin patterning signal either

directly or by enhancing local Nodal signaling. Since Bmp4 is known to have pleiotropic effects in the developing embryo and in ES cells I tested the ability of this growth factor to execute these functions during the differentiation. Using a candidate gene approach, I found that though there was low level expression of some markers, none were significantly high to conclude the presence of any other major cell lineage including trophoblast, mesodermal or primordial germ cell lineages. Since the differentiation only generates between 5-20% *PDX1*$^{+}$ cells, it is possible that there are other lineages being formed in the differentiating population. Using a candidate gene approach, I determined that neural or mesenchymal cells were also not generated robustly. Curiously, the expression of *OTX2* was high in conditions where Activin A was present, suggesting that there is persistence of some epiblast-like cells in the differentiating culture. The studies outlined above suggest that Bmp4 enhances DE formation by Activin A through a novel mechanism. None of my investigations have shed light on a possible mode of action. It is important to note that gene expression analysis was the preferred method of investigation in the studies summarized above, as immunostaining and flow cytometry were extremely difficult to perform on the extracellular matrix-rich EBs.

An entirely different role for Bmp4 was suggested by a recent study using mESCs showed that Activin A and Bmp4 (and bFGF) promoted both hepatocyte differentiation and activation of *Pdx1* from endoderm progenitors (Gouon-Evans *et al*. 2006). Though this indicates a possible role for Bmp4 later in pancreatic development, my focus was on the impact of Bmp4 in the early developmental stages as seen using the three-dimensional Matrigel-based differentiation.

Since none of the above experimental approaches yielded significant clues about the mechanism of the synergy between these growth factors, I chose to obtain a more

global view of the differentiation using genetic tools like Microarray technology to analyse gene expression. Expression of genes known to be important for endodermal development established the validity of this technique. Among the various data sets, I chose to look closely at a subset of these genes upregulated on day 4 of differentiation in presence of Activin A alone and Activin A + Bmp4 i.e. conditions that favour endoderm differentiation. In this data set there were numerous genes strongly upregulated which have not been characterized in the context of endoderm formation; some relatively unknown. A few of these genes were chosen for further analysis. Validation of results from the microarray screen was done by (1) *in vivo* analysis in the mouse embryo using whole mount in situ hybridization after establishing expression in the early mouse embryo by QPCR and (2) *in vitro* endoderm differentiation of hESCs. Analysis of embryos subjected to WISH revealed tissue-restricted and stage-specific expression of several genes. *Irx3* and *Nuak1* were expressed in the foregut region which suggests that these might be markers of the definitive endoderm. Though some reports exist that associate these markers with the endoderm, detailed studies are required to characterize these further. Five of the genes– *Edg3*, *Gatm*, *Homer2, Nuak1* and *Rhobtb3* were expressed in the primitive streak, and although not exclusive to DE, may impact the formation of this lineage. Various genetic strategies that will be used to define the role of these genes in the development of DE are outlined in Chapter 5. Several genes like *Gatm*, *Edg3*, *Irx3* and *Rhobtb3* were expressed in neural tissue which indicates that some neural differentiation occurs in the three-dimensional strategy. This is not entirely unexpected as the low efficiency of pancreatic differentiation suggests that other lineages are being formed from the differentiating hESCs. *Nr0b1*, *Apoa1* and *Irx3* were expressed in the extraembryonic component of the embryo while *Homer2*

specifically marked the heart. These genes have not been previously associated with the mentioned embryonic regions and might serve as novel markers of the same. *Apoa1* specifically marked the VE and indicates that there is a low percentage of VE formed during differentiation which might be due to Bmp4 signaling. In addition to these genes that showed specific domains of expression, there were others that showed non-specific or no expression. This discrepancy between the expression detected in Q-PCR and in WISH could be due to sub-optimal PCR primers or riboprobes and will be addressed in future experiments.

Genes that showed specific patterns of expression were validated in the hESC differentiation system that confirmed significant induction of most of these genes in presence of both Activin A and Bmp4 compared to the other conditions on day 4. While some were significantly upregulated in the presence of Activin A alone, other showed a similar response to the presence of Bmp4 alone. Interestingly all the genes that showed expression in the early embryo were upregulated during the first 2 days of differentiation with the exception of *APOA1* which was only detected later. The gene expression pattern of *APOA1* was similar to that of VE-specific markers like *AFP*, *TTR* and *H19* which are suppressed during the early stages of *in vitro* differentiation. Though QPCR analysis showed that formation of VE was suppressed during differentiation, it is not entirely eliminated. This is evident from the microarray data as genes like *Apoa1* were upregulated in differentiation conditions that formed endoderm but marked the extraembryonic VE in the mouse embryo. The differentiation creates a synthetic environment by suppressing VE formation. This possibly allows Bmp4, which is restricted to the node, to impact the formation and specification of another lineage like the DE.

Though significant progress has been made in understanding the *in vitro* differentiation programme that generates definitive endoderm from hESCs, an actual mechanism of action for Activin A and Bmp4 is still not obvious. In depth analysis of the microarray data might help to resolve this quest.

CHAPTER 5- FUTURE DIRECTION

INTRODUCTION

The inner cell mass of a developing embryo gives rise to all organs and tissues in the adult vertebrate. Embryonic stem cells are derivatives of the ICM which recapitulate this pluripotent ability *in vitro*. The isolation of these cells from the developing blastocyst has added a new dimension to the field of regenerative medicine. Various strategies have been proposed and used successfully to differentiate ES cells into derivatives of the three germ layers as part of efforts to develop cell replacement therapy for various diseases or conditions like diabetes, heart disease, Parkinson's disease etc. Our lab aims to derive effective cell therapy reagents by differentiating human embryonic stem cells (hESCs) into mesoderm-derived cardiomyocytes and definitive endoderm-derived β-like cells. Increasing concerns about the immunogenicity of such therapeutic grafts has focused attention on the development of immunotolerance mechanisms which could prevent outright rejection of the transplant. Immunotolerance can be induced either using a pool of haematopoietic cells to create a state of mixed haematopoietic chimerism in the host or using terminally differentiated dendritic cells (DCs) to induce a state of tolerance towards the donor antigens. Deriving such tolerance-inducing cells from the exact same source (hESCs) as the cardiomyocyte or β-cell graft would help to minimize the immune reaction. Therefore I focused my research efforts on the directed differentiation of hESCs into cells of the haematopoietic and definitive endodermal lineages employing adaptations of various published strategies used to differentiate either mouse or human ES cells.

5.1. Haematopoietic Differentiation

At the time I initiated work on this dissertation, there were few reports of haematopoietic differentiation from hESCs. I sought to obtain the cell types of my interest by a step-wise differentiation of hESCs first into haematopoietic progenitor cells and then into terminally differentiated dendritic-like cells. As described in Chapter 3 of this thesis, I chose to use either stromal feeder cells or pro-haematopoietic cytokines which have been shown to support the differentiation and maintenance of haematopoietic cells derived from peripheral blood and/or bone marrow to induce differentiation. Both approaches gave rise to cells of the granulocytic and monocytic lineages marked by the pan leukocyte marker CD45 and the monocyte marker CD14. No erythroid differentiation was detected in any of the conditions. This was not surprising as the successful differentiation strategies were originally reported to promote formation of granulocytic cells. Employing various markers to characterize the cells further I observed that differentiation did not progress much beyond this stage of progenitor cells. Sporadically immature dendritic-like cells expressing CD86 were detected when stromal feeder cells were used for differentiation. However, these did not seem to mature into functional DCs as their marker profile remained unchanged upon stimulation with maturation factors. Though several alternate and additional approaches could be used to refine these differentiations, I limited my investigations to the generation of progenitor cells. These serve as proof-of-principle experiments which show that hESCs could be differentiated into haematopoietic progenitor cells in presence of stromal feeder cells or appropriate cytokines. Recent work in this field, e.g., overexpression of developmentally relevant genes like HOXB4, has led to vast improvements in the generation of functional haematopoietic cells from hESCs.

5.2. Endoderm Differentiation

The major focus of my dissertation work was on the differentiation of hESCs into definitive endodermal cells and further into pancreatic β-like cells. At the time our lab had developed a strategy to differentiate hESCs into *PDX1*$^{+}$ pancreatic progenitor cells with the sequential use of factors known to 1) promote formation of definitive endoderm and 2) promote differentiation and maturation of these cells into an endocrine fate. In order to characterize the differentiation in detail and to obtain a better understanding of the developmentally relevant events, if any, that occur during the process, I used a candidate gene approach. As detailed in Chapter 4, gene expression studies showed that hESCs rapidly downregulated pluripotency markers and upregulated markers of differentiation when treated with factors like Activin A and Bmp4. Expression of gastrulation and definitive endodermal markers in a sequential manner showed that hESCs were closely mimicking a developmentally relevant pattern during the differentiation. These cells further developed into pancreatic progenitor cells which matured into the endocrine lineage as seen by marker analysis. Differentiation was most efficient in presence of both Activin A and Bmp4 though Activin A alone also seemed to induce endoderm formation. Since a candidate gene approach to define active members of the Activin and Bmp4 signaling pathways did not yield any clues, an overview of gene expression was obtained using microarray technology.

Along with the known and expected genes that showed altered expression, there were numerous genes that were previously not known to be associated with endoderm formation. I investigated the expression of these in the vertebrate embryo using mouse as the model system. Whole mount in situ hybridization studies revealed the varied expression domains of these genes including extraembryonic ectoderm, mesoderm,

endoderm, primitive streak, etc. Expression of these genes was analysed in differentiation samples which validated the microarray data. Five genes– *Edg3*, *Gatm*, *Homer2, Nuak1* and *Rhobtb3*– that were expressed in the primitive streak are of interest to our lab as these could impact DE formation. Available data on the mouse knock-out (KO) phenotypes for these genes are given in **Table 5.1**. Future studies involving these four genes will include the following approaches. (1) Analysis of expression in early embryos (E6.5) employing whole mount in-situ hybridisation (2) gain of function studies in independent model systems like *Xenopus* and Zebrafish and (3) loss of function studies in *Xenopus* and Zebrafish.

Though my primary aim was to elucidate a role for Bmp4 in promoting endoderm formation, the gene list (+GF) – (AA), which should have been the most informative, did not highlight many genes of interest (based on the available data from various databases). Hence, I chose to conduct detailed studies on genes upregulated only in conditions favouring endoderm formation which are outlined in this dissertation. There are several clusters of genes that could be investigated further including 1) genes downregulated during endoderm formation, 2) genes differentially expressed between Activin A alone and Activin A + Bmp4 and 3) genes expressed differentially as differentiation progresses. Detailed study of these data could reveal novel genes involved in the negative regulation of endoderm formation. In addition, charaterisation of genes expressed during various stages of differentiation could enhance the study of endoderm development in the embryo.

Ultimately, extensive analysis of the microarray data may provide clues to investigate and reveal a mechanism for the synergy between Activin A and Bmp4 that induces endoderm formation.

Gene Name	Knock-Out Phenotype	Reference
Edg3	lethality/prenatal-perinatal, cardiovascular, reproductive, nervous system, behaviour, hearing/vestibular/ear, homeostasis, skin/coat/nails	Ishii *et al*. 2001 *J Biol Chem* Ishii *et al*. 2002 *J Biol Chem* Kono *et al*. 2004 *J Biol Chem*
Gatm	None	None
Homer2	None	None
Nuak1	None	None
Rhobtb3	None	None

Table 5.1. Available information on knock-out phenotypes in the mouse. Whole mount in-situ hybridization (WISH) of mouse embryos showed the expression of *Edg3*, *Gatm*, *Homer2, Nuak1* and *Rhobtb3* in the primitive streak. Since the expression pattern suggests that these might impact DE formation, detailed studies will be performed on the five genes. Currently knock-out (KO) phenotype information is available only for *Edg3* which does not seem to correlate with the primitive streak expression seen in mouse embryos.

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APPENDICES

I. Buffers and Gels

Sorenson's Buffer pH 6.8

24.5 ml 0.2M dibasic sodium phosphate
25.5 ml 0.2M monobasic sodium phosphate

Make volume up to 100 ml with distilled water.

Radio Immuno Precipitation Assay (RIPA) Buffer

20 mM Tris, pH 8.0
1 mM EDTA
0.1% NP-40
10% Glycerol
1 mM Sodium orthovanadate ($Na_3VO_{4)}$
1 mM PMSF
1X Protease Inhibitor (Roche)

Polyacrylamide gels

8% resolving gel (10 ml)

Distilled H_2O	4.6 ml
30% Acrylamide	2.7 ml
1.5 M Tris pH 8.8	2.5 ml
10% Sodium Dodecyl Sulphate (SDS)	100 µl
10% Ammonium per Sulphate (APS)	100 µl
Tetramethylethylenediamine (TEMED)	6 µl

Stacking gel (3 ml)

Distilled H_2O	2.1 ml
30% Acrylamide	500 µl
1 M Tris pH 6.8	380 µl
10% SDS	30 µl
10% APS	30 µl
TEMED	3 µl

Sample buffer- 5X Laemmli Buffer

1 M Tris, pH 6.8	15.6 ml
Glycerol	25 ml
β-mercaptoethanol	12.5 ml

SDS	5 g
Bromophenol Blue	0.05%

Protein Transfer Buffer

For nitrocellulose membranes

Trizma Base	6 g
Glycine	3 g
Methanol	100 ml
10% Triton X	2 ml
10% SDS	2 ml

Make volume up to 1 Litre with distilled water.

For PVDF membranes

Trizma base	6 g
Glycine	3 g
Methanol	100 ml

Make volume up to 1 Litre with distilled water.

Tris Buffered Saline with Tween-20 (TBST)

Tris base	12.1 g
Sodium Chloride (NaCl)	8.76 g
Tween-20	1 ml

Make volume up to 1 Litre with distilled water and adjust pH to 7.4.

Buffers for Whole-mount In Situ Hybridisation

Paraformaldehyde (4%)

Paraformaldehyde	4 g
Phosphate Buffered Saline (PBS)	100 ml

In a water bath, warm solution to 65°C to dissolve the powder.

Phosphate Buffered Saline with Tween-20 (PBT)

10x PBS	100 ml
Tween-20	1 ml
H_2O	898 ml
DEPC	1 ml

Stir for 12 hours and autoclave.

Hybridisation solution

Deionised Formamide	250 ml
20x SSC (DEPC)	125 ml
Tween-20	500 µl
20% SDS	2.5 ml
50 mg/ml Heparin (in 4x SSC)	0.5 ml
10 mg/ml Yeast tRNA	2.5 ml
1 M Citric acid	30 ml

Make volume up to 500 ml with DEPC-treated distilled water.

Solution I

Formamide	75 ml
20x SSC	37.5 ml
1 M Citric acid	9 ml
20% SDS	7.5 ml
DEPC- H_2O	21 ml

Solution II

Formamide	75 ml
20x SSC	15 ml
1 M Citric acid	3.6 ml
20% SDS	1.5 ml
Tween-20	150 µl
DEPC- H_2O	55 ml

200 mM Levamisole (100x)

Dissolve 0.5 g Levamisole in 10 ml H_2O.

MAB buffer

Maleic Acid	11.61 g
NaCl	17.4 g
Sodium Hydroxide (NaOH) pellets	7 g
Tween-20	1 ml

Adjust pH to 7.5 using NaOH pellets and 5M NaOH. Add 1% v/v 100x Levamisole prior to use.

Boehringer Mannheim Blocking Reagent (BBR) (2%)

Boehringer blocking reagent (DIG detection kit)	1 g
MAB	50 ml

Heat solution to 70°C to dissolve powder. Add 1% v/v Levamisole prior to use.

Alkaline Phosphatase (NTMT) Buffer

1 M Tris-HCl pH 9.5	10 ml
5 M NaCl	2 ml
1 M MgCl2	5 ml
Tween-20	0.1 ml
H2O	82.9 ml

Add 1% v/v 100x Levamisole prior to use.

II. PCR Primer Sequences

HUMAN Q-PCR

PRIMERS	**FORWARD**	**REVERSE**
ACTIN	caatgtggccgaggactttg	cattctccttagagagaagtgg
PDX1	cctttcccatggatgaagtc	ggaactccttctccagctcta
NGN3	ctattcttttgcgccggtag	ctccctcttccgcctctg
INSULIN	ggggaacgaggcttcttcta	cacaatgccacgcttctg
PTF1A	tgagtttgtgtcctgagaagtcc	acatgtacaatatgcacagagacataa
BRACHYURY	aattggtccagccttggaat	cgttgctcacagaccacag
FOXA2	ggagcggtgaagatggaa	tacgtgttcatgccgttcat
SOX17	cagaatccagacctgcacaa	ctctgcctcctccacgaa
OCT4	ggcaacctggagaatttgtt	gccggttacagaaccacact
NANOG	tacctcagcctccagcagat	tgcgtcacaccattgctatt
TTR	tagatgctgtccgaggcagt	ccatgcagctctccagactc
AFP	gtagcgctgcaaacaatgaa	tccaacaggcctgagaaatc
ALBUMIN	tcagctctggaagtcgatga	ttcacgagctcaacaagtgc
H19	ttacttcctccacggagtcg	gctgggtagcaccatttctt
NODAL	agggcgagtgtcctaatcct	caacaagtggaagggactcg
CRIPTO	agatggcccgcttctctta	gagatggacgagcaaattcc
LEFTY2	aggttcagccagagcttcc	caccagcaggtgtgtgct
ID2	atatcagcatcctgtccttgc	aaagaaatcatgaacaccgctta
FRAGILIS	ccctgttcaacaccctcttc	gccaaccatcttcctgtcc
BLIMP1	acgtgtgggtacgaccttg	ctgccaatccctgaaacct
STELLA	gttactgggcggagttcgta	tgaagtggcttggtgtcttg
SPC4	ggtggtacagacctcgaagc	gccatatgagtggctcacttt
FGFR2	cctgcggagacaggtaacag	cggggtgttggagttcat
BMP4	ctgcaaccgttcagaggtc	tgctcgggatggcactac
CDX2	atcaccatccggaggaaag	tgcggttctgaaaccagatt
ELF5	cctcctctttggacctagcc	acatcaggggatcgcaga
ESRRB	agagaggcaggcagatctca	gtgagccagagatgctttcc
CSH2	tagaggaaggcatccaaacg	tcagcgccttactgctaaaa
SCL (TAL-1)	cctatgagatggagattactgatgg	gtgtggggatcagcttgc
PU.1	caggggatctgaccgactc	aggtcttctgatggctgagg
VWF	agtgcagacccaacttcacc	gtggggacactcttttgcac
VIMENTIN	aaagtgtggctgccaagaac	agcctcagagaggtcagcaa
NESTIN	gccctgaccactccagttta	ggagtcctggatttccttcc
TUBB4	gcggatcagcgtctactaca	atgtccaaaggcccctgag
APOA1	ccttgggaaaacagctaaacc	ccagaactcctgggtcaca
EDG3	tgatgagatgaaacctatttgtaagg	caagaaggcaacagaaatgct
GATM	tgaccgaccatgtcacca	ggatgatcgtctgggatga
HOMER2	gacctcaagtaatcattcccaag	tgagaggccttttcatcgtc
IRX3	aaaagttactcaagacagctttcca	ggatgaggagagagccgata
NR0B1	aagccatcaagtgctttctttc	cctgaatgtacttcacgcactg
NUAK1	gtcaatgggagaccttaccg	ccataaacaagagtgtaaagcaaca
RHOBTB3	gccgatgttgtcttcgaaat	ggctgccatcacttcacaa
GSC	gcgaggagaaagtggaggt	cgttctccgactcctctgat
ID3	catctccaacgacaaaaggag	cttccggcaggagaggtt
ID1	ccagaaccgcaaggtgag	ggtccctgatgtagtcgatga
OTX2	ctggctatttggaatttaaaggat	ggtttggagcagtggaactt

SOX1	gagattcatctcaggattgagattcta	ggcctactgtaatcttttctccact
SOX2	ttgctgcctctttaagactagga	ctggggctcaaacttctctc
MSX1	ctcgtcaaagccgagagc	cggttcgtcttgtgtttgc
MSX2	tcggaaaattcagaagatgga	caggtggtagggctcatatgtc
SMAD6	tgcaacccctaccacttca	cgaggagacagccgagagt
SMAD7	cgatggattttctcaaaccaa	attcgttccccctgtttca
FLK1	gaacatttgggaaatctcttgc	cggaagaacaatgtagtctttgc
GATA-1	cactgagcttgccacatcc	atggagcctctggggatta
GATA-2	aaggctcgttcctgttcaga	ggcattgcacaggtagtgg
β-*GLOBIN*	acacaactgtgttcactagc	agtgatgggccagcacacag
HOXB4	tggatgcgcaaagttcac	gaaattccttctccagctcca
MIXL1	ggtaccccgacatccactt	gcctgttctggaaccatacct

MOUSE Q-PCR PRIMERS

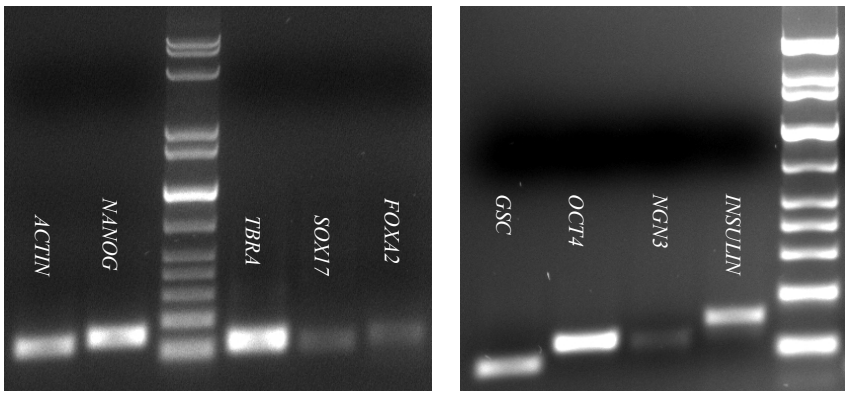
Amhr2	cccaacatcccatccact	cttccaggagctccctcag
Ankkd1a	tgtggacgacgtggactc	tctgcaagtggccaaacc
Apoa1	tatgtggatgcggtcaaaga	tgaacccagagtgtcccagt
Apoc1	tgggaacactttggaagaca	actttgccaaatgcctctga
Bhlhb5	acacttgcagggcaaacaa	gaatgtccggtttgtctctga
C6orf60	ccaaagagcccaagacattt	gggtctggagaagccactg
Calcr	ggttccttctcgtgaacaggt	agaactggagttgggctcac
Cmkor1	cagccacatgtccatcagac	cacagctcgctgacacctaa
Col9a2	agggcagtgcaggacaagt	tccttttgttccaggctgac
Ddit4l	gagcaagatccactttgccta	aggcgggtacaataacagca
Edg3	agatgcgccttgcagaac	agagtggtggtgggttcct
Flj23514	agttgatggaccgcttgg	gagctctttgtgcagcaagtt
Gatm	ttttcaagaaagcaggatgga	tgacatccagaggggatgat
Has2	ggcggaggacgagtctatg	acacatagaaacctctcacaatgc
Homer2	ggaacagctatcggatcatca	tcggggtgatagtgctgttt
Irx3	aaaagttactcaagacagctttcca	cgatttaaaaatggttgaaaagttaag
Kcnf1	caacaagcttccaggtacagc	gttcaaagccatttttgtggatt
Lrrc3	accccgacttgagtgttcc	gagccatgtggcaaaaataaa
Manea	agatgatcaaaacatgcatcaaa	gcccagtcctggtcttgtat
Mgst2	acatatacgcccgtcacaagta	cagtcggaaaccggtgat
Myct1	tgggaatgaaaaccgttcc	gccaaacagctaaatgaacca
Nppb	gtcagtcgtttgggctgtaac	agacccaggcagagtcagaa
Nr0b1	accgtgctctttaacccaga	ccggatgtgctcagtaagg
Nuak1	ccttaccgagggccagag	gaagggcatcgttccataaa
Pcdh7	ctaccaccagccaacacattt	tgtatggatgtacacgcatctg
Rcor3	agtcctgtttgaacaagccttt	tgcaattgtcttatctggaagc
Rhobtb3	cagctccttccatgggatt	tgatgcctcagctttcaaga
S100a14	atgggacagtgtcggtcag	gtgtctcaatggccctctct
Slc5a9	agtcgagggaccgttggt	ccacattgctggacattagaga
Slco2a1	ctttatgggatgttccacacc	ggctgcggatgtatagaacttg

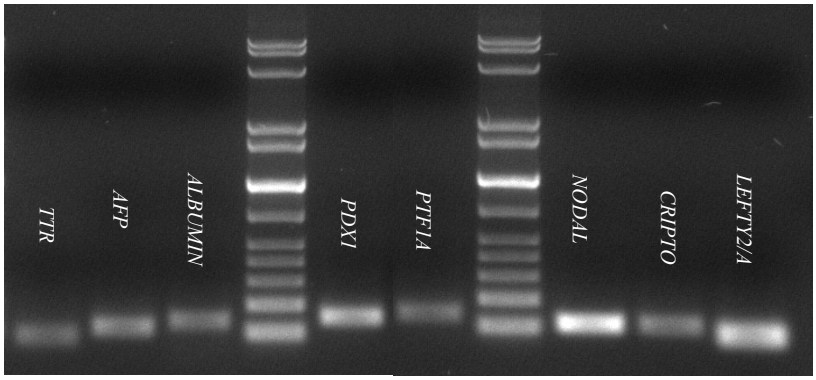
MOUSE 3' UTR PRIMERS

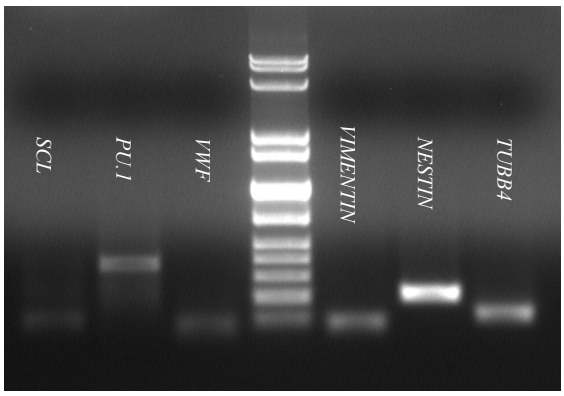
Apoa1	acccagactgtcggagagc	ggtttattgtaagaaagccaatgc
Apoc1	cctcctgagagatccttagatcc	ttttattggtctgtgatgaagagg
Calcr	atactctgattgtcatggctgtgt	aagcacatacaaggttcagatcaa
Ddit4l	actgtctgtccagatcaaagca	tcattgcagtaagaggcacact
Edg3	tgtgttcattgcctgttggt	ctggcttttctgtggctttc
Gatm	ttctttgagtaccgagcgtaca	aaggttaggaccgacatctcaa
Homer2	cttctatgatgtcaccaggaacag	tttttgagtgtgaactttgtggtt
Irx3	catcaccaagatgaccctca	acagacatgcttgcaactcg
Lrrc3	tctgaaactagacgccaacaga	cttcagtccctcctctttctga
Manea	acactcagaacacccggaac	ctctggctgtcctggaactc
Nr0b1	tcctgtaccgcagctatgtg	tttatttggcggggttaatg
Nuak1	gaaaaagacccagcagagagaa	aaggtccaggagcaaattaaca
Pcdh7	tacagtgttagcgacagacagtga	tttgcacataaagccaaaatctta
Rhobtb3	tgctcaaaaaggccaagttt	gaactgggggagtgtttcaa

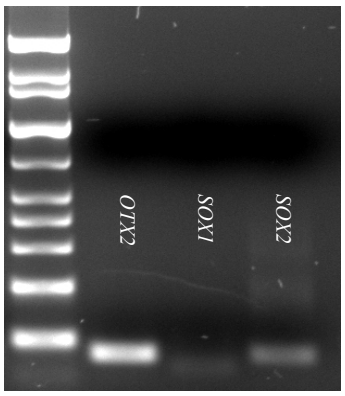
Gel Images

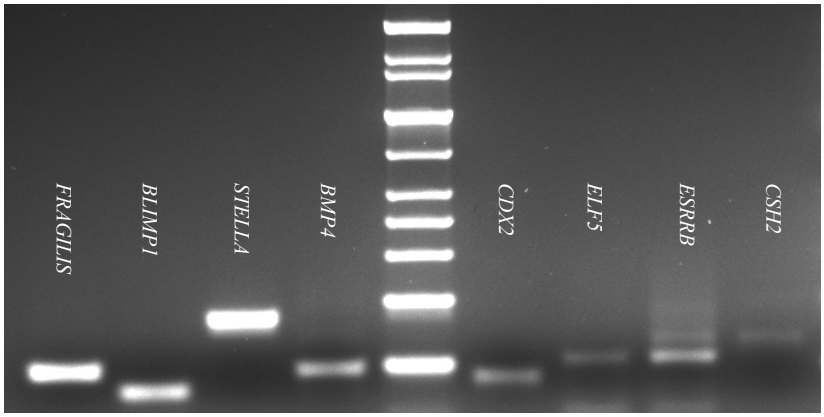
Q-PCR products resolved on 2% Agarose gels to confirm product sizes. The lowest band on the 1kb plus DNA Ladder used is 100bp.

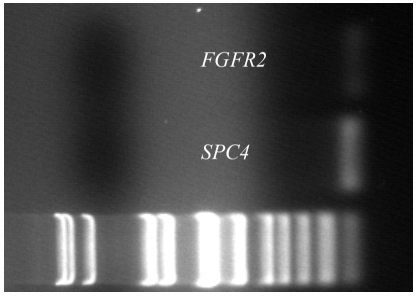








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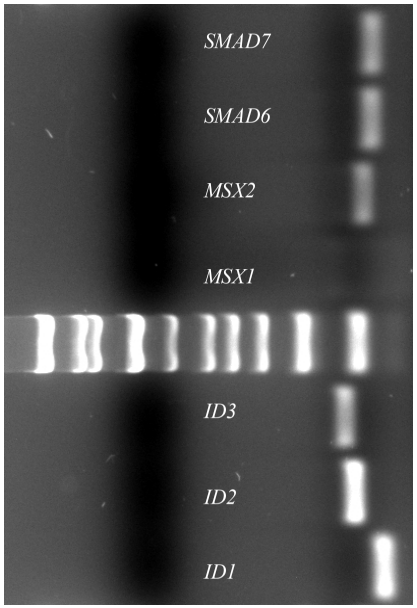
SPC4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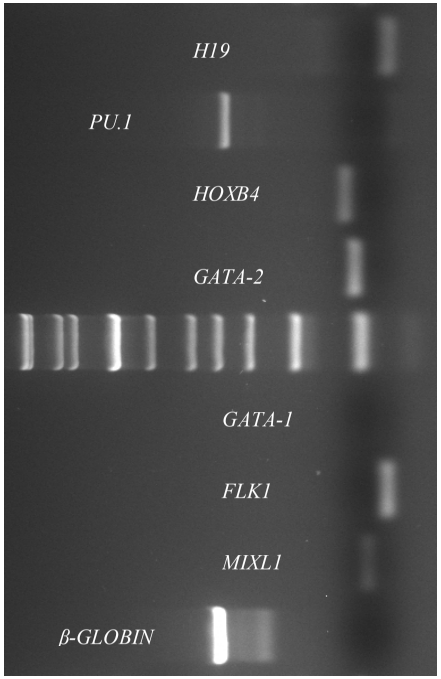
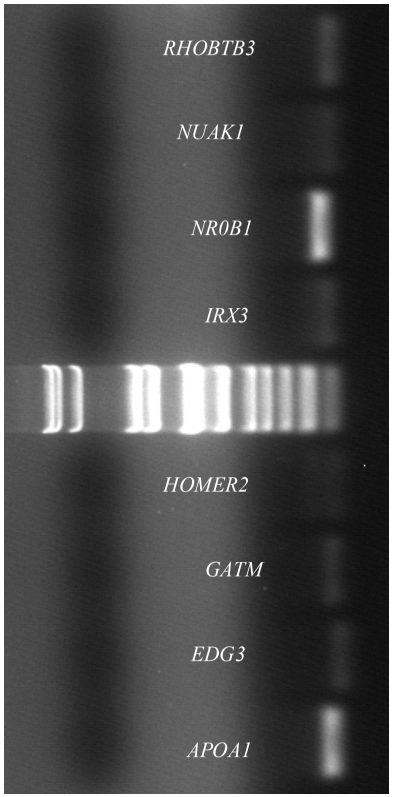
SMAD6
MSX2
MSX1
ID3
ID2
ID1


H19
PU.1
HOXB4
GATA-2
GATA-1
FLK1
MIXL1
ß-GLOBIN


RHOBTB3
NUAK1
NR0B1
IRX3
HOMER2
GATM
EDG3
APOA1

III. Microarray Gene Lists

Intersect of (d4AA and d4+GF)

Gene Name	Fold Change	Common	Genbank	Description
CYP26A1	90.12	CP26; CYP26; P450RAI; P450RAI1	NM_000783	cytochrome P450, family 26, subfamily A, polypeptide 1
EOMES	81.1	TBR2	NM_005442	eomesodermin homolog (Xenopus laevis)
CXCR4	79.35	FB22; HM89; LAP3; LCR1; NPYR; WHIM; CD184; LESTR; NPY3R; NPYRL; HSY3RR; NPYY3R; D2S201E	NM_003467	chemokine (C-X-C motif) receptor 4
CXCR4	74.17	FB22; HM89; LAP3; LCR1; NPYR; WHIM; CD184; LESTR; NPY3R; NPYRL; HSY3RR; NPYY3R; D2S201E	NM_001008540	chemokine (C-X-C motif) receptor 4
CER1	71.97	DAND4; MGC96951; MGC119894; MGC119895	NM_005454	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)
FOXA2	71.79	HNF3B; TCF3B; MGC19807	NM_021784	forkhead box A2
APOA2	65.95	APOA2	NM_001643	apolipoprotein A-II
FGF17	61.28	FGF-13	NM_003867	fibroblast growth factor 17
SOX17	54.05	FLJ22252	NM_022454	SRY (sex determining region Y)-box 17
CYP26A1	52.32	CP26; CYP26; P450RAI; P450RAI1	NM_057157	cytochrome P450, family 26, subfamily A, polypeptide 1
GYPE	52.25	GPE; MNS; MiIX	NM_002102	glycophorin E
CCKBR	43.4	GASR; CCK-B	NM_176875	cholecystokinin B receptor
FLJ23514	43.05	FLJ16339; FLJ23514	NM_021827	coiled-coil domain containing 81
FREM1	41.77	QBRICK; C9orf154; FLJ25461; RP11-439N12.3	NM_144966	FRAS1 related extracellular matrix 1
GYPB	39.64	SS; GPB; MNS; GYPA; CD235b; GPB.NY; GYPHe.NY	NM_002100	glycophorin B (MNS blood group)
APOA1	33.79	MGC117399	NM_000039	apolipoprotein A-I
FOXQ1	31.93	HFH1	NM_033260	forkhead box Q1
LRIG3	31.01	FLJ26573; FLJ90440; KIAA3016	NM_153377	leucine-rich repeats and immunoglobulin-like domains 3
FRZB	30.38	FRE; FZRB; hFIZ; FRITZ; FRP-3; FRZB1; SFRP3; SRFP3; FRZB-1; FRZB-PEN	NM_001463	frizzled-related protein
MIXL1	27.57	MIX; MIXL; MILD1; MGC138179	NM_031944	Mix1 homeobox-like 1 (Xenopus laevis)
SLCO2A1	27.55	PGT; OATP2A1; SLC21A2	NM_005630	solute carrier organic anion transporter family, member 2A1
GSC	26.62	GSC	NM_173849	goosecoid
EPSTI1	26.6	BRESI1; MGC29634	NM_033255	epithelial stromal interaction 1 (breast)
TMOD1	25.98	TMOD; ETMOD; D9S57E	NM_003275	tropomodulin 1
FLRT3	22.63	FLRT3	NM_013281	fibronectin leucine rich transmembrane protein 3
NPPB	22.17	BNP	NM_002521	natriuretic peptide precursor B
VWF	20.32	VWD; F8VWF	NM_000552	von Willebrand factor
CALCR	19.91	CRT; CTR; CTR1	NM_001742	calcitonin receptor
GRP	19.53	BN; GRP-10; proGRP; preproGRP	NM_002091	gastrin-releasing peptide
OTX2	18.26	MCOPS5; MGC45000	NM_172337	orthodenticle homolog 2 (Drosophila)
DACT2	18.04	DAPPER2; C6orf116; FLJ31232; MGC133141; MGC133142; bA503C24.7; RP11-503C24.7	NM_214462	dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis)
LHX1	16.62	LIM1; LIM-1; MGC126723; MGC138141	NM_005568	LIM homeobox 1
CRIP1	16.6	CRHP; CRIP; CRP1	NM_001311	cysteine-rich protein 1 (intestinal)
ANKS1B	14.81	AIDA; EB-1; ANKS2; AIDA-1; MGC26087; cajalin-2	NM_181670	ankyrin repeat and sterile alpha motif domain containing 1B
PDZK1	14.4	CAP70; CLAMP; PDZD1	NM_002614	PDZ domain containing 1
CPE	13.44	CPE	NM_001873	carboxypeptidase E
COL9A2	13.26	MED; EDM2; DJ39G22.4	NM_001852	collagen, type IX, alpha 2
BMP2	13.1	BMP2A	NM_001200	bone morphogenetic protein 2
RHOBTB3	12.5	KIAA0878	NM_014899	Rho-related BTB domain containing 3
ERBB4	12.35	HER4; MGC138404; p180erbB4	NM_005235	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
MGST2	12.28	GST2; MGST-II; FLJ27438; MGC14097	NM_002413	microsomal glutathione S-transferase 2
HHEX	12.07	HEX; PRH; HMPH; PRHX; HOX11L-PEN	NM_002729	homeobox, hematopoietically expressed
ST8SIA4	12.03	PST; PST1; SIAT8D; MGC34450; MGC61459; ST8SIA-IV	NM_175052	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
C6ORF60	12	FLJ13942	NM_024581	chromosome 6 open reading frame 60
C1ORF61	11.95	CROC4; FLJ38303; RP11-139I14.3	NM_006365	chromosome 1 open reading frame 61
ROR2	11.53	BDB; BDB1; NTRKR2	NM_004560	receptor tyrosine kinase-like orphan receptor 2
HP	11.44	MGC111141; hp2-alpha	NM_005143	haptoglobin
EDG3	11.39	LPB3; S1P3; EDG-3; S1PR3; FLJ37523; MGC71696	NM_005226	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3
KCNK12	11.39	THIK2; THIK-2	NM_022055	potassium channel, subfamily K, member 12
CMKOR1	11.11	RDC1; GPR159	NM_020311	chemokine orphan receptor 1
KCNG1	10.63	K13; kH2; KCNG; KV6.1; MGC12878	NM_002237	potassium voltage-gated channel, subfamily G, member 1
OXTR	10.54	OT-R	NM_000916	oxytocin receptor
COLEC12	10.43	CLP1; NSR2; SRCL; SCARA4	NM_130386	collectin sub-family member 12
GATA4	10.41	MGC126629	NM_002052	GATA binding protein 4
ACOX3	10.39	HBA2	NM_003501	acyl-Coenzyme A oxidase 3, pristanoyl
HAS2	10.33	MGC126241; MGC126242	NM_005328	hyaluronan synthase 2
LEPREL1	10.25	P3H2; MLAT4; FLJ10718	NM_018192	leprecan-like 1
OTX2	10.12	MCOPS5; MGC45000	NM_021728	orthodenticle homolog 2 (Drosophila)
MYL7	10.05	MYL2A; MYLC2A	NM_021223	myosin, light polypeptide 7, regulatory

BHLHB5	9.742	Beta3; CAGL85; TNRC20	NM_152414	basic helix-loop-helix domain containing, class B, 5
ADAM19	9.66	MLTNB; FKSG34; MADDAM	NM_033274	ADAM metallopeptidase domain 19 (meltrin beta)
MFAP4	9.529	MFAP4	NM_002404	microfibrillar-associated protein 4
GATM	9.516	AGAT	NM_001482	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
LEFTY2	9.403	EBAF; LEFTA; TGFB4; LEFTYA; MGC46222	NM_003240	left-right determination factor 2
MXRA5	9.365	DKFZp564I1922	NM_015419	matrix-remodelling associated 5
ANKDD1A	9.185	FLJ25870; MGC120305; MGC120306; MGC120307	NM_182703	ankyrin repeat and death domain containing 1A
FZD8	9.061	FZ-8; hFZ8	NM_031866	frizzled homolog 8 (Drosophila)
ST8SIA4	9.055	PST; PST1; SIAT8D; MGC34450; MGC61459; ST8SIA-IV	NM_005668	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
AMHR2	8.828	AMHR; MISRII	NM_020547	anti-Mullerian hormone receptor, type II
AGTRL1	8.811	APJ; FLJ90771; MGC45246	NM_005161	angiotensin II receptor-like 1
KRT19	8.679	K19; CK19; K1CS; MGC15366	NM_002276	keratin 19
C1ORF97	8.674	FLJ27347; FLJ27348; MGC14801; RP11-318L16.3	NM_032705	chromosome 1 open reading frame 97
HLXB9	8.43	HB9; SCRA1; HOXHB9	NM_005515	homeobox HB9
SFRP1	8.336	FRP; FRP1; FrzA; FRP-1; SARP2	NM_003012	secreted frizzled-related protein 1
S100A14	8.249	BCMP84; S100A15	NM_020672	S100 calcium binding protein A14
TMEM46	8.239	C13orf13; PRO28631; WGAR9166; bA398O19.2	NM_001007538	transmembrane protein 46
SLITRK2	8.22	CXorf2; SLITL1; KIAA1854; MGC129912; MGC129913; DKFZp451E1911	NM_032539	SLIT and NTRK-like family, member 2
DIO3	8.202	D3; 5DIII; TXDI3; DIOIII	NM_001362	deiodinase, iodothyronine, type III
RNASE1	8.176	RIB1; RNS1; MGC12408	NM_198232	ribonuclease, RNase A family, 1 (pancreatic)
FOXA1	8.161	HNF3A; TCF3A; MGC33105	NM_004496	forkhead box A1
GATA6	8.042	GATA6	NM_005257	GATA binding protein 6
STMN2	7.99	SCG10; SGC10; SCGN10	NM_007029	stathmin-like 2
DDIT4L	7.93	REDD2; Rtp801L	NM_145244	DNA-damage-inducible transcript 4-like
LRRC3	7.757	C21orf102	NM_030891	leucine rich repeat containing 3
SERHL2	7.715	MGC149508; dJ222E13.1	NM_014509	serine hydrolase-like 2
MYCT1	7.469	MTLC; FLJ21269	NM_025107	myc target 1
KCNF1	7.426	IK8; kH1; KCNF; KV5.1; MGC33316	NM_002236	potassium voltage-gated channel, subfamily F, member 1
APOC1	7.089	TOMM40	NM_001645	apolipoprotein C-I
S100Z	7.039	Gm625; S100-zeta	NM_130772	S100 calcium binding protein Z
TDRD7	7.003	TRAP; KIAA1529; PCTAIRE2BP; RP11-508D10.1	NM_014290	tudor domain containing 7
SLC5A9	6.982	SGLT4; MGC132517; MGC132523	NM_001011547	solute carrier family 5 (sodium/glucose cotransporter), member 9
GPR37	6.865	PAELR; EDNRBL; hET(B)R-LP	NM_005302	G protein-coupled receptor 37 (endothelin receptor type B-like)
SEMA3E	6.862	SEMAH; coll-5; M-SEMAH; M-SemaK; KIAA0331; M-sema H	NM_012431	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E
NR0B1	6.818	AHC; AHX; DSS; GTD; HHG; AHCH; DAX1; DAX-1; NROB1	NM_000475	nuclear receptor subfamily 0, group B, member 1
H2AFY2	6.816	macroH2A2	NM_018649	H2A histone family, member Y2
GCNT1	6.778	G6NT; C2GNT; C2GNT1; NACGT2; NAGCT2; C2GNT-L; MGC126335; MGC126336	NM_001490	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)
MANEA	6.673	hEndo; FLJ12838; DKFZp686D20120	NM_024641	mannosidase, endo-alpha
MATN3	6.615	HOA; EDM5	NM_002381	matrilin 3
MAPK10	6.484	JNK3; JNK3A; PRKM10; p493F12; FLJ12099; FLJ33785; MGC50974; p54bSAPK	NM_138980	mitogen-activated protein kinase 10
FZD5	6.444	HFZ5; C2orf31; MGC129692; DKFZP434E2135	NM_003468	frizzled homolog 5 (Drosophila)
SMAD6	6.434	MADH6; MADH7; HsT17432	NM_005585	SMAD, mothers against DPP homolog 6 (Drosophila)
DNMT3L	6.399	MGC1090	NM_175867	DNA (cytosine-5-)-methyltransferase 3-like
ELOVL2	6.307	Ssc2; FLJ20334	NM_017770	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
ITGA9	6.086	RLC; ITGA4L; ALPHA-RLC	NM_002207	integrin, alpha 9
IRX3	6.079	IRX-1	NM_024336	iroquois homeobox protein 3
PCDH7	6.06	BHPCDH; BH-Pcdh	NM_002589	BH-protocadherin (brain-heart)
FZD4	5.91	EVR1; FEVR; Fz-4; FzE4; GPCR; FZD4S; MGC34390	NM_012193	frizzled homolog 4 (Drosophila)
ENC1	5.788	NRPB; CCL28; ENC-1; PIG10; TP53I10; FLJ39259	NM_003633	ectodermal-neural cortex (with BTB-like domain)
IL18R1	5.695	IL1RRP; CDw218a; IL-1Rrp	NM_003855	interleukin 18 receptor 1
VIPR2	5.66	VPAC2; FLJ16511	NM_003382	vasoactive intestinal peptide receptor 2
CLDN1	5.652	CLD1; SEMP1; ILVASC	NM_021101	claudin 1
RCOR3	5.644	FLJ10876; RP11-318L16.1	NM_018254	REST corepressor 3
EPHA4	5.634	SEK; HEK8; TYRO1	NM_004438	EPH receptor A4
ANKRD1	5.631	ALRP; CARP; C-193; CVARP; MCARP; bA320F15.2	NM_014391	ankyrin repeat domain 1 (cardiac muscle)
HAS2	5.625	MGC126241; MGC126242	NM_005328	hyaluronan synthase 2
NUAK1	5.586	ARK5; KIAA0537	NM_014840	NUAK family, SNF1-like kinase, 1
C9ORF66	5.479	FLJ31158; RP11-59O6.1	NM_152569	chromosome 9 open reading frame 66
FAM89A	5.416	C1orf153; MGC15887; RP11-423F24.2	NM_198552	family with sequence similarity 89, member A
HOMER2	5.415	CPD; ACPD; Vesl-2; HOMER-2; HOMER2A; HOMER2B	NM_004839	homer homolog 2 (Drosophila)
SP8	5.384	BTD	NM_182700	Sp8 transcription factor
CDH2	5.362	CDHN; NCAD; CDw325	NM_001792	cadherin 2, type 1, N-cadherin (neuronal)
ARSE	5.355	CDPX; CDPX1; CDPXR	NM_000047	arylsulfatase E (chondrodysplasia punctata 1)
COL4A6	5.35	MGC88184	NM_001847	collagen, type IV, alpha 6
PRSS2	5.328	TRY2; TRY8; TRYP2; MGC111183; MGC120174	NM_002770	protease, serine, 2 (trypsin 2)
ST6GALNAC2	5.298	STHM; SIAT7; SIAT7B; SIATL1; ST6GalNAII	NM_006456	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
TNNC1	5.287	TNC; TNNC	NM_003280	troponin C type 1 (slow)
VIL1	5.262	VIL; D2S1471	NM_007127	villin 1
CST1	5.257	CST4	NM_001898	cystatin SN
SP5	5.212	FAM5B	NM_001003845	Sp5 transcription factor
MGC39900	5.183	MGC39900	NM_194324	hypothetical protein MGC39900
AGL	5.149	GDE	NM_000645	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)

ARHGAP28	5.147	FLJ10312; DKFZp686A2038	NM_001010000	Rho GTPase activating protein 28
SLC2A14	5.12	GLUT14	NM_153449	solute carrier family 2 (facilitated glucose transporter), member 14
BHLHB2	5.119	DEC1; STRA13; Stra14; SHARP-2	NM_003670	basic helix-loop-helix domain containing, class B, 2
CA2	5.084	CAII; Car2; CA II; CA-II	NM_000067	carbonic anhydrase II
SMARCD3	5.036	Rsc6p; BAF60C; CRACD3; MGC111010	NM_003078	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
IGFBP5	5.006	IBP5	NM_000599	insulin-like growth factor binding protein 5
BCAR3	4.949	NSP2; SH2D3B; KIAA0554	NM_003567	breast cancer anti-estrogen resistance 3
COL4A5	4.922	ATS; ASLN; CA54; MGC42377	NM_033381	collagen, type IV, alpha 5 (Alport syndrome)
ARL4D	4.909	ARL6; ARF4L	NM_001661	ADP-ribosylation factor-like 4D
OR52A1	4.869	HPFH1OR	NM_012375	olfactory receptor, family 52, subfamily A, member 1
CNTNAP2	4.851	CDFE; NRXN4; CASPR2; DKFZp781D1846	NM_014141	contactin associated protein-like 2
LZTS1	4.844	F37; FEZ1	NM_021020	leucine zipper, putative tumor suppressor 1
FLJ38451	4.844	FLJ38451; MGC117233; MGC119731	NM_175872	zinc finger protein 792
SAMD11	4.838	MGC45873	NM_152486	sterile alpha motif domain containing 11
EYA2	4.837	EAB1; MGC10614	NM_172112	eyes absent homolog 2 (Drosophila)
MOBP	4.794		NM_006501	
LOC56901	4.764	NUOMS; FLJ26118	NM_020142	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2
PITX2	4.762	RS; RGS; ARP1; Brx1; IDG2; IGDS; IHG2; PTX2; RIEG; IGDS2; IRID2; Otlx2; RIEG1; MGC20144; MGC111022	NM_153426	paired-like homeodomain transcription factor 2
ARMC7	4.76	FLJ22160	NM_024585	armadillo repeat containing 7
TCF2	4.734	FJHN; HNF2; LFB3; HNF1B; MODY5; VHNF1; HNF1beta	NM_000458	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor
CAPN12	4.734	MGC20576	NM_144691	calpain 12
KEL	4.705	ECE3; CD238	NM_000420	Kell blood group, metalloendopeptidase
NDRG4	4.678	SMAP-8; FLJ30586; FLJ42011; KIAA1180; MGC19632; DKFZp686I1615	NM_022910	NDRG family member 4
FBXO34	4.653	Fbx34; CGI-301; FLJ20725; MGC126434; MGC126435; DKFZp547C162	NM_017943	F-box protein 34
LAMA1	4.644	LAMA	NM_005559	laminin, alpha 1
GATS	4.617	GATS; DKFZp686B07267	NM_178831	opposite strand transcription unit to STAG3
JUP	4.608	DP3; PDGB; PKGB; CTNNG; DPIII	NM_021991	junction plakoglobin
LEFTY1	4.607	LEFTB; LEFTYB	NM_020997	left-right determination factor 1
GPX2	4.592	GPRP; GI-GPx; GSHPx-2; GSHPX-GI	NM_002083	glutathione peroxidase 2 (gastrointestinal)
AJAP1	4.55	MOT8; SHREW1; SHREW-1; RP3-426F10.1	NM_018836	adherens junction associated protein 1
SPHK2	4.531	DBP	NM_020126	sphingosine kinase 2
RARB	4.499	HAP; RRB2; NR1B2	NM_000965	retinoic acid receptor, beta
LIFR	4.494	SWS; SJS2; STWS; CD118	NM_002310	leukemia inhibitory factor receptor alpha
KIT	4.457	SCFR; C-Kit; CD117	NM_000222	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
C5	4.457	CPAMD4; MGC142298	NM_001735	complement component 5
ELMO1	4.435	CED12; CED-12; ELMO-1; KIAA0281; MGC126406	NM_014800	engulfment and cell motility 1
TSPAN12	4.397	NET-2; TM4SF12	NM_012338	tetraspanin 12
DSCR6	4.357	RIPPLY3	NM_018962	Down syndrome critical region gene 6
ABCC4	4.348	MRP4; MOATB; MOAT-B; EST170205	NM_005845	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
LGALS12	4.328	GRIP1; GALECTIN-12	NM_033101	lectin, galactoside-binding, soluble, 12 (galectin 12)
PDZK1	4.323	CAP70; CLAMP; PDZD1	NM_002614	PDZ domain containing 1
DUSP4	4.311	TYP; HVH2; MKP2; MKP-2	NM_001394	dual specificity phosphatase 4
PRSS1	4.31	TRP1; TRY1; TRY4; TRYP1; MGC120175	NM_002769	protease, serine, 1 (trypsin 1)
ST8SIA1	4.275	GD3S; SIAT8; SIAT8A; ST8SiaI; ST8Sia I	NM_003034	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
PLCG2	4.209	PLCG2	NM_002661	phospholipase C, gamma 2 (phosphatidylinositol-specific)
NBLA10383	4.199	FLJ36674; MGC33988; NBLA10383	NM_173622	CMT1A duplicated region transcript 4
SORCS1	4.189	FLJ41758; FLJ43475; FLJ44957	NM_001013031	sortilin-related VPS10 domain containing receptor 1
SLC3A2	4.148	4F2; CD98; MDU1; 4F2HC; 4T2HC; NACAE; CD98HC	NM_001013251	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
NOG	4.144	SYM1; SYNS1	NM_005450	noggin
MGC13057	4.118	MGC13057	NM_032321	hypothetical protein MGC13057
MCC	4.106	MCC1; FLJ46755	NM_002387	mutated in colorectal cancers
SAMD3	4.105	FLJ34563; MGC35163	NM_001017373	sterile alpha motif domain containing 3
EPHB3	4.076	ETK2; HEK2; TYRO6	NM_004443	EPH receptor B3
CUGBP2	4.03	ETR-3; NAPOR; BRUNOL3	NM_006561	CUG triplet repeat, RNA binding protein 2
WDR22	4.029	BCRG2; BCRP2; KIAA1824; D14S1461E; DKFZp434A035	NM_003861	WD repeat domain 22
LOC349136	3.988	MGC129839	NM_198285	WD repeat domain 86
RNASE4	3.976	RNS4; MGC9306	NM_194430	ribonuclease, RNase A family, 4
FAM18B2	3.966	MGC8763	NM_145301	family with sequence similarity 18, member B2
RBM24	3.959	RNPC6; FLJ26355; FLJ30829; FLJ37697; dJ259A10.1	NM_153020	RNA binding motif protein 24
LOC400451	3.943	LOC400451; MGC102891	NM_207446	hypothetical gene supported by AK075564; BC060873
ANKS1B	3.939	AIDA; EB-1; ANKS2; AIDA-1; MGC26087; cajalin-2	NM_020140	ankyrin repeat and sterile alpha motif domain containing 1B
SLC35A3	3.938	DKFZp781P1297	NM_012243	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3
PLCE1	3.938	PLCE; FLJ23659; KIAA1516	NM_016341	phospholipase C, epsilon 1
FRAS1	3.922	FLJ14927; FLJ22031; KIAA1500; DKFZp686I05113; DKFZp686P08111	NM_025074	Fraser syndrome 1
RGS11	3.886	RS11	NM_183337	regulator of G-protein signalling 11
RAP2A	3.881	KREV; RAP2; K-REV; RbBP-30	NM_021033	RAP2A, member of RAS oncogene family
EDA	3.876	ED1; HED; EDA1; EDA2; XHED; XLHED; ED1-A1; ED1-A2	NM_001005615	ectodysplasin A
GJA4	3.876	CX37	NM_002060	gap junction protein, alpha 4, 37kDa

				(connexin 37)
APOBEC3G	3.826	ARP9; CEM15; MDS019; FLJ12740; bK150C2.7; dJ494G10.1	NM_021822	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G
IGFBP3	3.823	IBP3; BP-53	NM_001013398	insulin-like growth factor binding protein 3
EPHA2	3.82	ECK	NM_004431	EPH receptor A2
FGFR3	3.795	ACH; CEK2; JTK4; CD333; HSFGFR3EX	NM_000142	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
UPK1B	3.792	UPIB; UPK1; TSPAN20	NM_006952	uroplakin 1B
KCNG1	3.779	K13; kH2; KCNG; KV6.1; MGC12878	NM_172318	potassium voltage-gated channel, subfamily G, member 1
C12ORF34	3.776	FLJ14721	NM_032829	chromosome 12 open reading frame 34
PFKFB4	3.748	PFKFB4	NM_004567	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
KIAA1409	3.72	FLJ43337	NM_020818	KIAA1409
NT5DC3	3.72	FLJ11266; TU12B1-TY	NM_016575	5'-nucleotidase domain containing 3
DENND2C	3.696	FLJ37099; dJ1156J9.1; RP5-1156J9.1; DKFZp686G0351; DKFZp686N1631; DKFZp779P1149	NM_198459	DENN/MADD domain containing 2C
PCDH20	3.691	PCDH13; FLJ22218	NM_022843	protocadherin 20
PRDM1	3.677	BLIMP1; PRDI-BF1; MGC118922; MGC118923; MGC118924; MGC118925	NM_001198	PR domain containing 1, with ZNF domain
FAM89A	3.664	C1orf153; MGC15887; RP11-423F24.2	NM_198552	family with sequence similarity 89, member A
SULF2	3.612	HSULF-2; FLJ90554; KIAA1247; MGC126411; DKFZp313E091	NM_018837	sulfatase 2
CTXN1	3.605	CTXN; FLJ25968	NM_206833	cortexin 1
LRRN1	3.587	NLRR-1; KIAA1497	NM_020873	leucine rich repeat neuronal 1
ATPAF2	3.56	ATP12; ATP12p; LP3663; MGC29736	NM_145691	ATP synthase mitochondrial F1 complex assembly factor 2
DACH1	3.553	DACH; FLJ10138	NM_080759	dachshund homolog 1 (Drosophila)
SLC1A1	3.54	EAAC1; EAAT3	NM_004170	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
LOC441268	3.528	LOC441268	NM_001013725	hypothetical gene supported by BC044942
CFLAR	3.503	CASH; FLIP; MRIT; CLARP; FLAME; Casper; c-FLIP; FLAME-1; I-FLICE; USURPIN; c-FLIPL; c-FLIPR; c-FLIPS; CASP8AP1	NM_003879	CASP8 and FADD-like apoptosis regulator
VASH1	3.502	KIAA1036	NM_014909	vasohibin 1
FXYD6	3.5	FXYD6	NM_022003	FXYD domain containing ion transport regulator 6
APBB3	3.488	SRA; FE65L2; MGC87674	NM_006051	amyloid beta (A4) precursor protein-binding, family B, member 3
C10ORF114	3.475	bA418C1.3	NM_001010911	chromosome 10 open reading frame 114
ANKRD6	3.474	VAPA	NM_014942	ankyrin repeat domain 6
BTG2	3.46	PC3; TIS21; MGC126063; MGC126064	NM_006763	BTG family, member 2
ANKRD37	3.44	Lrp2bp; MGC111507	NM_181726	ankyrin repeat domain 37
RAB20	3.422	FLJ20429	NM_017817	RAB20, member RAS oncogene family
MERTK	3.394	MER; c-mer; MGC133349	NM_006343	c-mer proto-oncogene tyrosine kinase
PPAPDC1A	3.374	PPAPDC1; MGC120300	NM_001030059	phosphatidic acid phosphatase type 2 domain containing 1A
GREM2	3.373	PRDC; DAND3; CKTSF1B2	NM_022469	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)
KIAA1688	3.336	KIAA1688	NM_025251	KIAA1688 protein
ZNF664	3.291	ZFOC1; MGC126579; DKFZp761B128	NM_152437	zinc finger protein 664
ABCA1	3.288	TGD; ABC1; CERP; ABC-1; HDLDT1; FLJ14958	NM_005502	ATP-binding cassette, sub-family A (ABC1), member 1
KIAA1161	3.284	BCORL2	NM_020702	KIAA1161
KCNH8	3.266	ELK; ELK1; Kv12.1	NM_144633	potassium voltage-gated channel, subfamily H (eag-related), member 8
TMEM100	3.233	FLJ10970; FLJ37856	NM_018286	transmembrane protein 100
KIAA1729	3.226	KIAA1729	NM_053042	KIAA1729 protein
EFS	3.226	SIN; EFS1; EFS2; HEFS	NM_005864	embryonal Fyn-associated substrate
RTN4RL1	3.212	NgR3; NGRH2; DKFZp547J144	NM_178568	reticulon 4 receptor-like 1
CAP2	3.203	RAB11FIP1	NM_006366	CAP, adenylate cyclase-associated protein, 2 (yeast)
B3GNT1	3.202	B3GNT; B3GNT1; B3GN-T1; B3GN-T2; B3GNT-2; BETA3GNT	NM_006577	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
SAMD3	3.19	FLJ34563; MGC35163	NM_152552	sterile alpha motif domain containing 3
AIRE	3.186		NM_000659	
PCDH10	3.178	PCDH19; OL-PCDH; KIAA1400; MGC133344; DKFZP761O2023	NM_032961	protocadherin 10
HSPB8	3.174	H11; HMN2; CMT2L; DHMN2; E2IG1; HSP22	NM_014365	heat shock 22kDa protein 8
SERPINB9	3.143	PI9; CAP3; CAP-3	NM_004155	serpin peptidase inhibitor, clade B (ovalbumin), member 9
WWOX	3.136		NM_018560	
MLLT6	3.134	AF17; FLJ23480	NM_005937	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6
PPT2	3.13	G14; NG3; C6orf8; DKFZp564P1516	NM_138717	palmitoyl-protein thioesterase 2
CEP70	3.107	BITE; FLJ13036	NM_024491	centrosomal protein 70kDa
ZNF702	3.106	FLJ12985	NM_024924	zinc finger protein 702
FAM84B	3.101	NSE2; BCMP101	NM_174911	family with sequence similarity 84, member B
PARP6	3.099		NM_020213	
AADAT	3.093	KAT2; KATII	NM_182662	aminoadipate aminotransferase
RNF125	3.074	FLJ20456; MGC21737	NM_017831	ring finger protein 125
FGF8	3.068	AIGF; HBGF-8	NM_033164	fibroblast growth factor 8 (androgen-induced)
PPM1K	3.004	PTMP; UG0882E07; DKFZp667B084; DKFZp761G058	NM_152542	protein phosphatase 1K (PP2C domain containing)
GMPR	2.988	GMPR	NM_006877	guanosine monophosphate reductase
DSCR5	2.988	DCRC; DSRC; DSCR5; DCRC-S	NM_153682	phosphatidylinositol glycan anchor biosynthesis, class P
WSB1	2.986		NM_134264	
CHST3	2.985	C6ST; C6ST1	NM_004273	carbohydrate (chondroitin 6) sulfotransferase 3
PLEKHB1	2.984	KPL1; PHR1; PHRET1	NM_021200	pleckstrin homology domain containing, family B (evectins) member 1
KIAA1443	2.983	HOMEZ	NM_020834	KIAA1443

ZNF614	2.982	FLJ21941; MGC120638	NM_025040	zinc finger protein 614
AD031	2.971	AD031; MGC138255	NM_032021	transmembrane protein 133
CAMK2D	2.97	CAMKD; MGC44911	NM_172115	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta
LYPD2	2.968	LYPDC2; UNQ430; MGC148106	NM_205545	LY6/PLAUR domain containing 2
PIK3CB	2.968	PI3K; PIK3C1; PI3Kbeta; MGC133043; p110-BETA; DKFZp779K1237	NM_006219	phosphoinositide-3-kinase, catalytic, beta polypeptide
BTK	2.958	AT; ATK; BPK; XLA; IMD1; AGMX1; PSCTK1; MGC126261; MGC126262	NM_000061	Bruton agammaglobulinemia tyrosine kinase
PKP2	2.95	ARVD9	NM_004572	plakophilin 2
PCTP	2.945	STARD2	NM_021213	phosphatidylcholine transfer protein
TLN2	2.93	ILWEQ; KIAA0320; DKFZp451B1011	NM_015059	talin 2
GPC4	2.91	K-glypican	NM_001448	glypican 4
GRM2	2.897	GLUR2; mGlu2; GPRC1B; MGLUR2	NM_000839	glutamate receptor, metabotropic 2
ITLN2	2.888	HL2; HL-2	NM_080878	intelectin 2
PAX6	2.885	AN; AN2; MGDA; WAGR; D11S812E; MGC17209	NM_000280	paired box gene 6 (aniridia, keratitis)
TMEM27	2.881	NX17; NX-17	NM_020665	transmembrane protein 27
DOCK8	2.864	ZIR8; FLJ00026; FLJ00152; FLJ00346	NM_203447	dedicator of cytokinesis 8
FAM11A	2.856	CXorf13; MGC118844; MGC118845	NM_032508	family with sequence similarity 11, member A
TYRO3	2.85	BYK; Brt; Dtk; RSE; Sky; Tif	NM_006293	TYRO3 protein tyrosine kinase
AMOT	2.842	KIAA1071	NM_133265	angiomotin
TPK1	2.84	PP20; HTPK1	NM_022445	thiamin pyrophosphokinase 1
LGR5	2.837	FEX; HG38; GPR49; GPR67; GRP49; MGC117008	NM_003667	leucine-rich repeat-containing G protein-coupled receptor 5
BTBD3	2.829	KIAA0952; MGC130038; MGC130039; dJ742J24.1	NM_014962	BTB (POZ) domain containing 3
C3ORF32	2.823	C3orf32	NM_015931	chromosome 3 open reading frame 32
GNAL	2.817	GNAL	NM_182978	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type
GATA3	2.814	HDR; MGC2346; MGC5199; MGC5445	NM_002051	GATA binding protein 3
DPPA3	2.811	STELLA	NM_199286	developmental pluripotency associated 3
CTSH	2.804	CPSB; MGC1519; minichain; DKFZp686B24257	NM_004390	cathepsin H
CDKN1B	2.802	KIP1; CDKN4; P27KIP1	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
TMEM88	2.77	FLJ20025; MGC71744	NM_203411	transmembrane protein 88
MDK	2.768	MK; NEGF2; FLJ27379	NM_002391	midkine (neurite growth-promoting factor 2)
TLE2	2.763	ESG; ESG2; GRG2; FLJ41188	NM_003260	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
PAQR5	2.744	MPRG; FLJ20190	NM_017705	progestin and adipoQ receptor family member V
GNG2	2.742	G protein	NM_053064	guanine nucleotide binding protein (G protein), gamma 2
YPEL2	2.742	FKSG4; DKFZp761C2021	NM_001005404	yippee-like 2 (Drosophila)
CUGBP2	2.737	ETR-3; NAPOR; BRUNOL3	NM_001025077	CUG triplet repeat, RNA binding protein 2
ZNF124	2.728	HZF16; HZF-16; MGC117046	NM_003431	zinc finger protein 124
ARHGAP28	2.726	FLJ10312; DKFZp686A2038	NM_030672	Rho GTPase activating protein 28
FST	2.723	FS	NM_006350	follistatin
KIFC2	2.716	C19orf25	NM_145754	kinesin family member C2
APOBEC3F	2.707	KA6; ARP8; MGC74891; BK150C2.4.MRNA	NM_145298	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F
ARHGAP28	2.706	FLJ10312; DKFZp686A2038	NM_030672	Rho GTPase activating protein 28
DDX58	2.702	RIG-I; FLJ13599; DKFZp434J1111; DKFZp686N19181	NM_014314	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
CTDSP1	2.7	SCP1; NLIIF	NM_021198	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
NPL	2.699	NPL1; c112; C1orf13	NM_030769	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)
C9ORF52	2.687	FLJ33868	NM_152574	chromosome 9 open reading frame 52
CEP55	2.646	URCC6; C10orf3; FLJ10540	NM_018131	centrosomal protein 55kDa
FBN2	2.644	CCA	NM_001999	fibrillin 2 (congenital contractural arachnodactyly)
C18ORF19	2.635	HsT2329; MGC24180	NM_152352	chromosome 18 open reading frame 19
MEIS3	2.63	MRG2; DKFZp547H236	NM_001009813	Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)
ZIC2	2.628	HPE5	NM_007129	Zic family member 2 (odd-paired homolog, Drosophila)
PRND	2.622	DPL; PrPLP; DOPPEL; MGC41841; dJ1068H6.4	NM_012409	prion protein 2 (dublet)
C16ORF57	2.62	FLJ13154	NM_024598	chromosome 16 open reading frame 57
FLJ11155	2.619	FLJ11155	NM_018342	transmembrane protein 144
COL23A1	2.611	DKFZp434K0621	NM_173465	collagen, type XXIII, alpha 1
TRAF5	2.61	RNF84; MGC:39780	NM_004619	TNF receptor-associated factor 5
PRSS3	2.609	MTG; TRY3; TRY4; PRSS4	NM_002771	protease, serine, 3 (mesotrypsin)
DTWD2	2.605	FLJ33977; MGC138579; MGC138580	NM_173666	DTW domain containing 2
HRBL	2.589	RABR	NM_006076	HIV-1 Rev binding protein-like
FBN3	2.578	KIAA1776	NM_032447	fibrillin 3
PCDH10	2.567	PCDH19; OL-PCDH; KIAA1400; MGC133344; DKFZP761O2023	NM_020815	protocadherin 10
OGT	2.566		NM_003605	
SSBP3	2.562	CSDP; SSDP; SSDP1; FLJ10355	NM_145716	single stranded DNA binding protein 3
LAMA1	2.557	LAMA	NM_005559	laminin, alpha 1
C15ORF17	2.555	FLJ00005	NM_020447	chromosome 15 open reading frame 17
MBNL3	2.553	CHCR; MBLX; MBXL; MBLX39; FLJ11316	NM_133486	muscleblind-like 3 (Drosophila)
RIPK4	2.549	DIK; PKK; RIP4; ANKK2; ANKRD3; MGC129992; MGC129993	NM_020639	receptor-interacting serine-threonine kinase 4
FMO5	2.546	FMO5	NM_001461	flavin containing monooxygenase 5
RNF19	2.533	DORFIN; DKFZp566B1346	NM_015435	ring finger protein 19
TANC1	2.523	TANC; ROLSB; KIAA1728	NM_033394	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1
ZNF342	2.507	MAF	NM_145288	zinc finger protein 342
NGFRAP1	2.495	Bex; BEX3; NADE; HGR74; DXS6984E	NM_014380	nerve growth factor receptor (TNFRSF16) associated protein 1
TMEM74	2.491	FLJ30668	NM_153015	transmembrane protein 74
GSTA1	2.488	GST2; GTH1; GSTA1-1; MGC131939	NM_145740	glutathione S-transferase A1
LOC442578	2.475	LOC442578	NM_001013739	similar to Cohesin subunit SA-3 (Stromal

				antigen 3) (Stromalin 3) (SCC3 homolog 3)
RGS16	2.455	RGS-R; A28-RGS14; A28-RGS14P	NM_002928	regulator of G-protein signalling 16
SLC25A29	2.452	CACL; C14orf69; FLJ38975	NM_152333	solute carrier family 25, member 29
HAK	2.446	HAK; FLJ34875; FLJ43253	NM_052947	alpha-kinase 2
SORCS1	2.398	FLJ41758; FLJ43475; FLJ44957	NM_052918	sortilin-related VPS10 domain containing receptor 1
HOXD13	2.396	BDE; SPD; HOX4I	NM_000523	homeobox D13
UTX	2.385	MGC141941; bA386N14.2; DKFZp686A03225	NM_021140	ubiquitously transcribed tetratricopeptide repeat, X chromosome
PIP5K1B	2.374	MSS4; STM7	NM_003558	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
PLSCR1	2.372	MMTRA1B	NM_021105	phospholipid scramblase 1
SULF2	2.356	HSULF-2; FLJ90554; KIAA1247; MGC126411; DKFZp313E091	NM_018837	sulfatase 2
DDIT3	2.355	CHOP; CEBPZ; CHOP10; GADD153; MGC4154	NM_004083	DNA-damage-inducible transcript 3
ZBTB40	2.348	KIAA0478; MGC133098	NM_014870	zinc finger and BTB domain containing 40
BSPRY	2.345	FLJ20150	NM_017688	B-box and SPRY domain containing
MAPK7	2.34	BMK1; ERK4; ERK5; PRKM7	NM_139034	mitogen-activated protein kinase 7
SLC36A1	2.337	PAT1; LYAAT1; TRAMD3	NM_078483	solute carrier family 36 (proton/amino acid symporter), member 1
AMMECR1	2.337	AMMERC1	NM_015365	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1
TMEM56	2.335	FLJ31842; MGC102912	NM_152487	transmembrane protein 56
SLC4A2	2.328	AE2; HKB3; BND3L; NBND3; EPB3L1	NM_003040	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)
LRRC54	2.322	TSK; E2IG4	NM_015516	leucine rich repeat containing 54
ZNF160	2.318	F11; HZF5; KR18; HKr18; FLJ00032; KIAA1611; DKFZp686B16128	NM_033288	zinc finger protein 160
VCX2	2.316	VCXB; VCX2R; VCX-2r; MGC118977; MGC125729; MGC125794; MGC125795	NM_016378	variable charge, X-linked 2
FLJ45187	2.313	FLJ45187; DLN-1; DKFZp761J229	NM_207371	hypothetical protein LOC387640
ICOSLG	2.312	B7H2; GL50; B7-H2; B7RP1; CD275; ICOSL; LICOS; B7RP-1; ICOS-L; KIAA0653	NM_015259	inducible T-cell co-stimulator ligand
NCR1	2.31	LY94; CD335; NKP46; NK-p46	NM_004829	natural cytotoxicity triggering receptor 1
FLJ35725	2.304	FLJ12891; FLJ35725	NM_152544	chromosome 4 open reading frame 23
ACVR1B	2.293	ALK4; SKR2; ACTRIB; ACVRLK4	NM_004302	activin A receptor, type IB
C1ORF63	2.281		NM_207035	
AXIN2	2.268	AXIL; MGC126582; DKFZp781B0869	NM_004655	axin 2 (conductin, axil)
C22ORF8	2.264	C22orf8; FLJ20635	NM_017911	family with sequence similarity 118, member A
MDK	2.253	MK; NEGF2; FLJ27379	NM_001012333	midkine (neurite growth-promoting factor 2)
MGC33302	2.246	MGC33302	NM_152778	hypothetical protein MGC33302
GSTA2	2.244	GST2; GTA2; GTH2; GSTA2-2; MGC10525	NM_000846	glutathione S-transferase A2
ATHL1	2.244	FLJ22635; MGC129858; MGC129859	NM_025092	ATH1, acid trehalase-like 1 (yeast)
ZNF358	2.238	ZFEND; FLJ10390	NM_018083	zinc finger protein 358
UBAP2	2.227	FLJ22435; KIAA1491; bA176F3.5	NM_018449	ubiquitin associated protein 2
KIAA0980	2.217	KIAA0980; NLP; FLJ11792; dJ691N24.1	NM_025176	KIAA0980 protein
C1QTNF6	2.211	CTRP6; ZACRP6	NM_031910	C1q and tumor necrosis factor related protein 6
NRXN3	2.206	KIAA0743	NM_004796	neurexin 3
COL4A6	2.203	MGC88184	NM_033641	collagen, type IV, alpha 6
DLK1	2.199	FA1; ZOG; pG2; PREF1; Pref-1	NM_003836	delta-like 1 homolog (Drosophila)
SNX16	2.199	DKFZp666H147	NM_022133	sorting nexin 16
HS6ST1	2.195	HS6ST; MGC116899; MGC116901	NM_004807	heparan sulfate 6-O-sulfotransferase 1
PICALM	2.195	LAP; CALM; CLTH	NM_007166	phosphatidylinositol binding clathrin assembly protein
H2AFY	2.194	H2A.y; H2A/y; H2AFJ; mH2A1; H2AF12M; MACROH2A1.1; macroH2A1.2	NM_004893	H2A histone family, member Y
TRO	2.187		NM_177557	
IGSF4	2.172	BL2; ST17; NECL2; RA175; TSLC1; IGSF4A; Necl-2; SYNCAM; sTSLC-1; synCAM1; DKFZp686F1789	NM_014333	immunoglobulin superfamily, member 4
PLEKHG2	2.17	CLG; FLJ00018; FLJ22458	NM_022835	pleckstrin homology domain containing, family G (with RhoGef domain) member 2
GP1BB	2.17	CD42c	NM_000407	glycoprotein Ib (platelet), beta polypeptide
C8ORF34	2.167	VEST1; vest-1; FLJ36872; DKFZp547E186	NM_052958	chromosome 8 open reading frame 34
MAGED2	2.164	11B6; BCG1; HCA10; JCL-1; MAGED; MAGE-D2; MGC8386	NM_177433	melanoma antigen family D, 2
RCOR2	2.163	RCOR2	NM_173587	REST corepressor 2
SLC9A5	2.159	NHE5	NM_004594	solute carrier family 9 (sodium/hydrogen exchanger), member 5
ZNF193	2.158	PRD51; ZSCAN9	NM_006299	zinc finger protein 193
ARL6IP2	2.158	ATL2; ARL3IP2; FLJ23293; atlastin2	NM_022374	ADP-ribosylation factor-like 6 interacting protein 2
LPGAT1	2.155	FAM34A; FAM34A1	NM_014873	lysophosphatidylglycerol acyltransferase 1
FMN2	2.152	ROR2	NM_020066	formin 2
PTP4A3	2.132	PRL3; PRL-3; PRL-R	NM_007079	protein tyrosine phosphatase type IVA, member 3
MAGED4	2.131	MAGE1; MAGE-E1; MGC3210; MGC88639	NM_177535	melanoma antigen family D, 4
FEZ1	2.123	FEZ1	NM_022549	fasciculation and elongation protein zeta 1 (zygin I)
EFNB3	2.119	EFL6; EPLG8; LERK8	NM_001406	ephrin-B3
PCBP4	2.114	LIP4; MCG10	NM_033008	poly(rC) binding protein 4
ISOC1	2.113	CGI-111	NM_016048	isochorismatase domain containing 1
AGPAT4	2.107	1-AGPAT4; dJ473J16.2; LPAAT-delta; RP3-473J16.2	NM_001012734	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)
WDR72	2.1	FLJ38736; MGC126663; MGC126665	NM_182758	WD repeat domain 72
SETBP1	2.098	SEB; KIAA0437	NM_015559	SET binding protein 1
MTSS1	2.087	MIM; MIMA; MIMB; FLJ44694; KIAA0429	NM_014751	metastasis suppressor 1
SOX10	2.076	DOM; WS4; MGC15649	NM_006941	SRY (sex determining region Y)-box 10
LASS6	2.073	MGC129949; MGC129950	NM_203463	LAG1 longevity assurance homolog 6 (S. cerevisiae)
LOC91461	2.065	LOC91461; MGC125960	NM_138370	hypothetical protein BC007901

C9ORF47	2.064	C9orf108; FLJ37523; bA791O21.3	NM_001001938	chromosome 9 open reading frame 47
ELAVL4	2.056	HUD; PNEM	NM_021952	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)
C3ORF58	2.051	MGC33365	NM_173552	chromosome 3 open reading frame 58
DDHD2	2.041	SAMWD1; KIAA0725	NM_015214	DDHD domain containing 2
CAMTA1	2.035	KIAA0833	NM_015215	calmodulin binding transcription activator 1
DKK4	2.034	DKK-4; MGC129562; MGC129563	NM_014420	dickkopf homolog 4 (Xenopus laevis)
KIAA0895	2.034	KIAA0895	NM_015314	KIAA0895 protein
LONRF1	2.02	RNF191; FLJ23749	NM_152271	LON peptidase N-terminal domain and ring finger 1
TMC7	2.019	FLJ21240; DKFZp781O2274	NM_024847	transmembrane channel-like 7
PILRB	2.017	FDFACT1; FDFACT2	NM_175047	paired immunoglobin-like type 2 receptor beta
GCNT2	2.013	II; IGNT; ULG3; GCNT5; GCNT2C; NACGT1; NAGCT1; bA421M1.1; bA360O19.2	NM_145655	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
ZNF615	2.012	FLJ33710; FLJ39372; DKFZp686O1554	NM_198480	zinc finger protein 615
COL22A1	2.011	COL22A1	NM_152888	collagen, type XXII, alpha 1
ERF	2.008	PE-2	NM_006494	Ets2 repressor factor
ZNF608	2.006	NY-REN-36; DKFZp781C0723	NM_020747	zinc finger protein 608
DHCR24	1.999	KIAA0018; SELADIN1; Nbla03646; seladin-1	NM_014762	24-dehydrocholesterol reductase
ZNF611	1.997	MGC5384	NM_030972	zinc finger protein 611
MOBP	1.995	MGC87379	NM_182935	myelin-associated oligodendrocyte basic protein
SLC16A5	1.991	MCT5; MCT6	NM_004695	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)
AHSA2	1.989	Hch1; DKFZp564C236	NM_152392	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
ARHGEF2	1.989	GEF; P40; GEFH1; LFP40; GEF-H1; KIAA0651; DKFZp547L106; DKFZp547P1516	NM_004723	rho/rac guanine nucleotide exchange factor (GEF) 2
RAX	1.983	RX	NM_013435	retina and anterior neural fold homeobox
MLLT10	1.982	AF10; MGC75086; DKFZp686E10210	NM_004641	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10
PDLIM7	1.979	PDLIM7	NM_213636	PDZ and LIM domain 7 (enigma)
C6ORF213	1.977	C6orf212; bA160A10.4	NM_001010852	chromosome 6 open reading frame 213
PPP1R13B	1.973	p85; ASPP1; KIAA0771; p53BP2-like	NM_015316	protein phosphatase 1, regulatory (inhibitor) subunit 13B
SRRP35	1.972	SRrp35; RP11-63L7.3	NM_080743	serine-arginine repressor protein (35 kDa)
MMP15	1.968	MTMMP2; SMCP-2; MT2-MMP	NM_002428	matrix metallopeptidase 15 (membrane-inserted)
DNAJB9	1.967	MDG1; ERdj4; MST049; MSTP049; DKFZP564F1862	NM_012328	DnaJ (Hsp40) homolog, subfamily B, member 9
RXRG	1.962	RXRC; NR2B3	NM_006917	retinoid X receptor, gamma
TRIM36	1.955	RNF98; HAPRIN; RBCC728	NM_018700	tripartite motif-containing 36
ZCCHC3	1.952	C20orf99; MGC104290	NM_033089	zinc finger, CCHC domain containing 3
GALNT10	1.944	FLJ00205; FLJ11715; GalNAcT10; DKFZp586H0623; pp-GalNAc-T10	NM_198321	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)
DKFZP761I2123	1.936	DKFZp761I2123; KIAA1886	NM_031449	hypothetical protein DKFZp761I2123
SPATA6	1.933	SRF1; SRF-1; FLJ10007	NM_019073	spermatogenesis associated 6
LASS4	1.933	Trh1; FLJ12089	NM_024552	LAG1 longevity assurance homolog 4 (S. cerevisiae)
LOC130576	1.93	LOC130576	NM_177964	hypothetical protein LOC130576
RUNDC1	1.922	DKFZp761H0421	NM_173079	RUN domain containing 1
ZNF154	1.918		NM_003444	
CDK5RAP3	1.911	C53; IC53; HSF-27; MST016; OK/SW-cl.114	NM_176095	CDK5 regulatory subunit associated protein 3
RP3-473B4.1	1.908	RP3-473B4.1	NM_138819	family with sequence similarity 122C
KLF12	1.908	AP2REP; AP-2rep; HSPC122	NM_007249	Kruppel-like factor 12
ENTPD7	1.903	LALP1; FLJ30978; RP11-483F11.1	NM_020354	ectonucleoside triphosphate diphosphohydrolase 7
ID1	1.901	ID	NM_181353	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
RNF122	1.899	FLJ12526; MGC126622	NM_024787	ring finger protein 122
LCMT2	1.895	PPM2; TYW4; MGC9534; KIAA0547	NM_014793	leucine carboxyl methyltransferase 2
RAB15	1.89	RAB15	NM_198686	RAB15, member RAS onocogene family
MSI1	1.888	MSI1	NM_002442	musashi homolog 1 (Drosophila)
TRIM2	1.887	RNF86; KIAA0517	NM_015271	tripartite motif-containing 2
WDR27	1.885	MGC43690	NM_182552	WD repeat domain 27
PHACTR2	1.883	C6orf56; KIAA0680; DKFZp686F18175	NM_014721	phosphatase and actin regulator 2
COBLL1	1.88	KIAA0977	NM_014900	COBL-like 1
MRPS25	1.879	RPMS25; MRP-S25; FLJ00023; DKFZp313H0817	NM_022497	mitochondrial ribosomal protein S25
PIP5K1B	1.876	MSS4; STM7	NM_003558	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
GPM6A	1.87	M6A; GPM6	NM_201592	glycoprotein M6A
STRN3	1.853	SG2NA	NM_014574	striatin, calmodulin binding protein 3
DPP10	1.848	DPL2; DPPY; DPRP3	NM_001004360	dipeptidyl-peptidase 10
DVL2	1.845	DVL2	NM_004422	dishevelled, dsh homolog 2 (Drosophila)
TRIM17	1.845	RBCC; terf; RNF16	NM_016102	tripartite motif-containing 17
ACVR2A	1.839	ACVR2; ACTRII	NM_001616	activin A receptor, type IIA
ZC3HAV1	1.835	ZAP; ZC3H2; FLB6421; ZC3HDC2; FLJ13288; MGC48898; DKFZp686F2052; DKFZp686H1869; DKFZp686O19171	NM_024625	zinc finger CCCH-type, antiviral 1
RFFL	1.835	RNF189; RNF34L	NM_001017368	ring finger and FYVE-like domain containing 1
UNG2	1.833	UDG2; FLJ22422	NM_021147	uracil-DNA glycosylase 2
LMX1A	1.833	LMX1; LMX-1; LMX1.1; MGC87616	NM_177398	LIM homeobox transcription factor 1, alpha
TSPAN14	1.833	TM4SF14; DC-TM4F2; MGC11352	NM_030927	tetraspanin 14
C9ORF7	1.83	D9S2135	NM_017586	chromosome 9 open reading frame 7
E2F5	1.83	E2F-5	NM_001951	E2F transcription factor 5, p130-binding
MIDN	1.823	DKFZp547M072	NM_177401	midnolin
MGC39518	1.812	MGC39518	NM_173822	family with sequence similarity 126, member B
TMEM92	1.811	FLJ33318	NM_153229	transmembrane protein 92
SORCS1	1.805	FLJ41758; FLJ43475; FLJ44957	NM_001013031	sortilin-related VPS10 domain containing receptor 1

FLJ39155	1.805	FLJ39155	NM_152403	EGF-like, fibronectin type III and laminin G domains
MAPK10	1.804	JNK3; JNK3A; PRKM10; p493F12; FLJ12099; FLJ33785; MGC50974; p54bSAPK	NM_002753	mitogen-activated protein kinase 10
C1ORF91	1.799	AASL548; PRO1105; FLJ90779; RP4-622L5; dJ622L5.7; RP4-622L5.3	NM_019118	chromosome 1 open reading frame 91
FARP1	1.798	CDEP; PLEKHC2; MGC87400	NM_001001715	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
WNT3	1.795	INT4; MGC131950; MGC138321; MGC138323	NM_030753	wingless-type MMTV integration site family, member 3
OVOL1	1.794	HOVO1	NM_004561	ovo-like 1(Drosophila)
TSC1	1.793	LAM; TSC; KIAA0243; MGC86987	NM_000368	tuberous sclerosis 1
RXRG	1.79	RXRC; NR2B3	NM_001009598	retinoid X receptor, gamma
USP49	1.788	MGC20741	NM_018561	ubiquitin specific peptidase 49
VEGF	1.788	VPF; VEGFA; MGC70609	NM_001025366	vascular endothelial growth factor
UNC93A	1.785	MGC119395; MGC119397; dJ366N23.1; dJ366N23.2	NM_018974	unc-93 homolog A (C. elegans)
C8ORF72	1.766	FAM110B; MGC39325	NM_147189	chromosome 8 open reading frame 72
TREM1	1.764	TREM-1	NM_018643	triggering receptor expressed on myeloid cells 1
C14ORF101	1.762	FLJ20392	NM_017799	chromosome 14 open reading frame 101
WNK3	1.761	PRKWNK3; KIAA1566	NM_001002838	WNK lysine deficient protein kinase 3
ELMO1	1.76	CED12; CED-12; ELMO-1; KIAA0281; MGC126406	NM_014800	engulfment and cell motility 1
MESP1	1.758	MGC10676	NM_018670	mesoderm posterior 1 homolog (mouse)
EML4	1.756	C2orf2; ELP120; ROPP120; FLJ10942; FLJ32318; DKFZp686P18118	NM_019063	echinoderm microtubule associated protein like 4
LOC283932	1.756		NM_175901	
LOC389289	1.756	LOC389289	NM_001014279	similar to annexin II receptor
CRHBP	1.755	CRFBP; CRF-BP	NM_001882	corticotropin releasing hormone binding protein
MUS81	1.748	FLJ21012; FLJ44872	NM_025128	MUS81 endonuclease homolog (S. cerevisiae)
RFP2	1.744	CAR; LEU5; DLEU5; RNF77; TRIM13	NM_001007278	ret finger protein 2
TAL2	1.743	TAL2	NM_005421	T-cell acute lymphocytic leukemia 2
SPAG4	1.742	SPAG4	NM_003116	sperm associated antigen 4
ESRRG	1.741	ERR3; NR3B3; FLJ16023; KIAA0832; DKFZp781L1617	NM_206595	estrogen-related receptor gamma
ZNF513	1.74	FLJ32203; HMFT0656	NM_144631	zinc finger protein 513
ZNF558	1.74	FLJ30932	NM_144693	zinc finger protein 558
LOC388969	1.738	LOC388969; FLJ14112; FLJ35653; MGC131675	NM_001013649	hypothetical LOC388969
ZNF135	1.737	pT3; ZNF61; pHZ-17; ZNF78L1	NM_003436	zinc finger protein 135
ALPK3	1.735	MAK; MIDORI; FLJ21176; KIAA1330	NM_020778	alpha-kinase 3
ZBTB10	1.721	RINZF; FLJ12752	NM_023929	zinc finger and BTB domain containing 10
LAMC3	1.72	DKFZp434E202	NM_006059	laminin, gamma 3
TMEM50B	1.717	C21orf4; HCVP7TP3; DKFZp686C2482	NM_006134	transmembrane protein 50B
ZC3H12B	1.717	CXorf32	NM_001010888	zinc finger CCCH-type containing 12B
ABHD4	1.716	FLJ12816	NM_022060	abhydrolase domain containing 4
LOC125893	1.713	LOC125893; MGC125619	NM_001031665	hypothetical protein LOC125893
ZNF436	1.712	ZNF; KIAA1710	NM_030634	zinc finger protein 436
C1ORF63	1.71	NPD014; DJ465N24.2.1; RP3-465N24.4	NM_020317	chromosome 1 open reading frame 63
RFPL3	1.71	RFPL3	NM_006604	ret finger protein-like 3
C9ORF40	1.709	FLJ10110; FLJ25795	NM_017998	chromosome 9 open reading frame 40
DGCR8	1.705	Gy1; DGCRK6; C22orf12	NM_022720	DiGeorge syndrome critical region gene 8
LMOD3	1.703	DKFZp313F0135	NM_198271	leiomodin 3 (fetal)
FOXA2	1.703	HNF3B; TCF3B; MGC19807	NM_021784	forkhead box A2
ZNF662	1.701	FLJ45880	NM_207404	zinc finger protein 662
SLC22A15	1.699	FLIPT1; PRO34686; DKFZp761G0313	NM_018420	solute carrier family 22 (organic cation transporter), member 15
ALG14	1.699	MGC19780	NM_144988	asparagine-linked glycosylation 14 homolog (yeast)
LMBRD1	1.698	C6orf209; FLJ11240; bA810I22.1; RP11-810I22.1	NM_018368	LMBR1 domain containing 1
HSD11B2	1.697	AME; AME1; HSD2; HSD11K	NM_000196	hydroxysteroid (11-beta) dehydrogenase 2
LOC399744	1.696	LOC399744	NM_001013665	hypothetical LOC399744
NETO2	1.695	NEOT2; FLJ10430; FLJ14724; FLJ90456	NM_018092	neuropilin (NRP) and tolloid (TLL)-like 2
ZNF235	1.694	HZF6; ZFP93; ANF270; ZNF270	NM_004234	zinc finger protein 235
LIPG	1.686	EL; EDL; PRO719	NM_006033	lipase, endothelial
SNAI1	1.685	SNA; SNAH; SLUGH2; dJ710H13.1	NM_005985	snail homolog 1 (Drosophila)
FLJ13236	1.681	FLJ13236	NM_024902	hypothetical protein FLJ13236
MED12	1.677	HOPA; OPA1; CAGH45; TNRC11; TRAP230; KIAA0192	NM_005120	mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)
EFNA4	1.675	EFL4; EPLG4; LERK4; MGC125826	NM_005227	ephrin-A4
PTPRD	1.675	HPTP; PTPD; HPTPD; MGC119750; MGC119751; MGC119752; MGC119753; HPTP-DELTA; R-PTP-DELTA	NM_130391	protein tyrosine phosphatase, receptor type, D
DDX17	1.674	P72; RH70; DKFZp761H2016	NM_030881	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
SLC5A3	1.673	SMIT; SMIT2	NM_006933	solute carrier family 5 (inositol transporters), member 3
RBM33	1.672	KIAA1604	NM_001008408	RNA binding motif protein 33
ZDHHC11	1.669	ZNF399; FLJ13153	NM_024786	zinc finger, DHHC-type containing 11
MDM4	1.663	MDMX; MRP1; MGC132766; DKFZp781B1423	NM_002393	Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mouse)
CHD7	1.663	FLJ20357; FLJ20361; KIAA1416	NM_017780	chromodomain helicase DNA binding protein 7
CDC42	1.662	G25K; CDC42Hs	NM_044472	cell division cycle 42 (GTP binding protein, 25kDa)
STK32A	1.661	YANK1; MGC22688	NM_145001	serine/threonine kinase 32A
FLJ39827	1.657	FLJ39827; RP11-403E24.2	NM_152424	family with sequence similarity 123B
MSMB	1.656	MSP; PSP; IGBF; MSPB; PN44; PRPS; PSP57; PSP94; PSP-94	NM_002443	microseminoprotein, beta-
FLJ38717	1.654	FLJ38717; FLJ40915	NM_001004322	FLJ38717 protein
AFG3L1	1.653	AFG3; FLJ45200	NM_001031805	AFG3 ATPase family gene 3-like 1 (S. cerevisiae)
SH3BGRL2	1.651	FLJ90025	NM_031469	SH3 domain binding glutamic acid-rich protein like 2

SLC25A24	1.65	APC1; SCAMC-1; DKFZp586G0123	NM_013386	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24
AGXT2L1	1.65	GALC	NM_031279	alanine-glyoxylate aminotransferase 2-like 1
MCF2L2	1.649	FLJ42509; KIAA0861; DKFZp686K0690	NM_015078	MCF.2 cell line derived transforming sequence-like 2
MGC35048	1.647	FLJ20115; FLJ36575; MGC35048	NM_153208	IQ motif containing K
ZFX	1.646	ZFX	NM_003410	zinc finger protein, X-linked
PFKFB3	1.645	PFK2; IPFK2	NM_004566	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
C17ORF80	1.643	MIG3; HLC-8; FLJ20721	NM_017941	chromosome 17 open reading frame 80
ANKFY1	1.641	ANKHZN; ZFYVE14; KIAA1255; DKFZp686M19106	NM_020740	ankyrin repeat and FYVE domain containing 1
ZNF446	1.633	ZSCAN30; FLJ20626	NM_017908	zinc finger protein 446
ARHGEF11	1.631	GTRAP48; KIAA0380; PDZ-RHOGEF	NM_014784	Rho guanine nucleotide exchange factor (GEF) 11
RFXAP	1.626	RFXAP	NM_000538	regulatory factor X-associated protein
EMB	1.625	MGC71745	NM_198449	embigin homolog (mouse)
ST8SIA2	1.624	STX; SIAT8B; HsT19690; MGC116854; MGC116857; ST8SIA-II	NM_006011	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2
COL4A3BP	1.62	CERT; GPBP; CERTL; STARD11	NM_005713	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
GPR89A	1.615	GPR89; SH120	NM_016334	G protein-coupled receptor 89A
C1ORF106	1.609	FLJ10901; MGC125608	NM_018265	chromosome 1 open reading frame 106
CAMK2D	1.606	CAMKD; MGC44911	NM_001221	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta
DKFZP547C195	1.603	DKFZp547C195	NM_207343	hypothetical protein DKFZp547C195
DKFZP781I1119	1.6	FLJ35954; DKFZP781I1119; DKFZp781G1119; DKFZp781I1119; DKFZp686L09111	NM_152622	mesoderm induction early response 1, family member 3
VIPR1	1.598	II; HVR1; RDC1; VIPR; VIRG; VAPC1; VPAC1; PACAP-R-2	NM_004624	vasoactive intestinal peptide receptor 1
ICA1	1.598		NM_022308	
SEMA6D	1.593	FLJ11598; KIAA1479	NM_024966	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D
OCLN	1.592	OCLN	NM_002538	occludin
ATP1B1	1.59	ATP1B; MGC1798	NM_001677	ATPase, Na+/K+ transporting, beta 1 polypeptide
PIP5K2B	1.586	Pip4k2B; PIP5KIIB	NM_138687	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
FUT8	1.585	MGC26465	NM_178154	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
NBLA04196	1.585	C7orf12; FLJ21213; FLJ21879; FLJ41901; NBLA04196	NM_022900	CAS1 domain containing 1
GGT2	1.583	GGT	NM_002058	gamma-glutamyltransferase 2
ETV3	1.58	PE1; METS; PE-1; bA110J1.4	NM_005240	ets variant gene 3
GTPBP3	1.578	MSS1; MTGP1; THDF1; GTPBG3; FLJ14700	NM_133644	GTP binding protein 3 (mitochondrial)
HOOK3	1.577	HK3	NM_032410	hook homolog 3 (Drosophila)
PARP6	1.573		NM_020213	
MGC21830	1.569	MGC21830	NM_182563	chromosome 16 open reading frame 79
C17ORF55	1.563	FLJ39421; MGC120553; MGC120556	NM_178519	chromosome 17 open reading frame 55
GPHN	1.563	GPH; GEPH; GPHRYN; KIAA1385	NM_020806	gephyrin
FLJ10815	1.562	FLJ10815; FLJ12724	NM_018231	amino acid transporter
LBR	1.558	PHA; LMN2R; DHCR14B; MGC9041	NM_002296	lamin B receptor
IQCA	1.557	FLJ22527; 4930465P12Rik	NM_024726	IQ motif containing with AAA domain
DBN1	1.557	D0S117E; DKFZp434D064	NM_004395	drebrin 1
KIAA1618	1.557	SPAG16	NM_020954	KIAA1618
LOC349338	1.555	FLJ00038	NM_182905	CXYorf1-related protein
WAC	1.551	Wwp4; BM-016; PRO1741; MGC10753; bA48B24.1	NM_100264	WW domain containing adaptor with coiled-coil
ZNF343	1.547	FLJ39592; MGC10715; MGC20504; dJ734P14.5	NM_024325	zinc finger protein 343
SOAT1	1.547	ACAT; SOAT; STAT; ACACT; ACAT1; RP11-215I23.2	NM_003101	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
TFF1	1.544	pS2; BCEI; HPS2; HP1.A; pNR-2; D21S21	NM_003225	trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in)
ZNF33A	1.543	KOX2; KOX5; KOX31; ZNF11; ZNF33; ZZAPK; ZNF11A; FLJ23404; KIAA0065	NM_006974	zinc finger protein 33A
EFNA4	1.539	EFL4; EPLG4; LERK4; MGC125826	NM_182690	ephrin-A4
LRCH3	1.537	MGC4126	NM_032773	leucine-rich repeats and calponin homology (CH) domain containing 3
SLC30A1	1.53	ZNT1; ZRC1	NM_021194	solute carrier family 30 (zinc transporter), member 1
ATP2B1	1.529	PMCA1	NM_001001323	ATPase, Ca++ transporting, plasma membrane 1
RBM8A	1.529	Y14; RBM8; ZNRP; RBM8B; ZRNP1; BOV-1A; BOV-1B; BOV-1C; MDS014	NM_005105	RNA binding motif protein 8A
LOC440925	1.528	LOC440925	NM_001013712	hypothetical gene supported by AK123485
HSA277841	1.524	ELG; HSA277841	NM_018553	chromosome 17 open reading frame 85
ZNF548	1.523	FLJ32932	NM_152909	zinc finger protein 548
PLEKHO1	1.522	OC120; CKIP-1; RP11-458I7.3	NM_016274	pleckstrin homology domain containing, family O member 1
MSX2	1.521	FPP; MSH; PFM; CRS2; HOX8; PFM1	NM_002449	msh homeobox homolog 2 (Drosophila)
CTGLF1	1.521	MRIP2; CTGLF5	NM_133446	centaurin, gamma-like family, member 1
RGS8	1.519	MGC119067; MGC119068; MGC119069	NM_033345	regulator of G-protein signalling 8
MAP2K4	1.519	JNKK; MEK4; MKK4; SEK1; JNKK1; SERK1; MAPKK4; PRKMK4	NM_003010	mitogen-activated protein kinase kinase 4
PDLIM5	1.513	L9; ENH; LIM	NM_006457	PDZ and LIM domain 5
ASAM	1.509	ASAM; ACAM; CLMP; FLJ22415	NM_024769	adipocyte-specific adhesion molecule
SMARCE1	1.507	BAF57	NM_003079	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
C21ORF66	1.505	GCFC; BM-020; FLJ90561	NM_016631	chromosome 21 open reading frame 66
WBSCR18	1.505	MGC12943	NM_032317	Williams Beuren syndrome chromosome region 18
PCDHA12	1.502	MGC138485; MGC141932; PCDH-ALPHA12	NM_031864	protocadherin alpha 12
ING3	1.5	Eaf4; ING2; p47ING3; FLJ20089	NM_198267	inhibitor of growth family, member 3
TRIM6	1.5	RNF89	NM_058166	tripartite motif-containing 6
FGF13	1.494	FGF2; FHF2	NM_033642	fibroblast growth factor 13

CYP4X1	1.494	MGC40051	NM_178033	cytochrome P450, family 4, subfamily X, polypeptide 1
ZNF660	1.49	FLJ36870	NM_173658	zinc finger protein 660
AACS	1.488	SUR-5; FLJ12389; FLJ41251	NM_023928	acetoacetyl-CoA synthetase
SLC25A34	1.483	RP11-169K16.2; DKFZp781A10161	NM_207348	solute carrier family 25, member 34
ARMC8	1.483	S863-2; HSPC056; MGC4880; MGC10058	NM_015396	armadillo repeat containing 8
BIRC2	1.482	API1; MIHB; HIAP2; RNF48; cIAP1; Hiap-2	NM_001166	baculoviral IAP repeat-containing 2
YTHDC1	1.48	YT521; YT521-B; KIAA1966	NM_133370	YTH domain containing 1
PLAC8	1.48	C15; onzin	NM_016619	placenta-specific 8
BRD2	1.476	NAT; RNF3; FSRG1; RING3; D6S113E; FLJ31942; KIAA9001; DKFZp686N0336	NM_005104	bromodomain containing 2
OLR1	1.474	LOX1; CLEC8A; SCARE1	NM_002543	oxidised low density lipoprotein (lectin-like) receptor 1
STAT4	1.473	STAT4	NM_003151	signal transducer and activator of transcription 4
CCDC45	1.47	DKFZp667E1824	NM_138363	coiled-coil domain containing 45
HSD17B7	1.467	PRAP; MGC12523; MGC75018	NM_016371	hydroxysteroid (17-beta) dehydrogenase 7
PDZRN3	1.465	LNX3; SEMACAP3	NM_015009	PDZ domain containing RING finger 3
CSNK1G1	1.465	FIBP	NM_022048	casein kinase 1, gamma 1
CNR1	1.465	CB1; CNR; CB-R; CB1A; CANN6; CB1K5	NM_016083	cannabinoid receptor 1 (brain)
PARD3	1.463	ASIP; PAR3; SE2-5T2; FLJ21015; SE2-5L16; SE2-5LT1; PAR3alpha	NM_019619	par-3 partitioning defective 3 homolog (C. elegans)
AHR	1.459	AHR	NM_001621	aryl hydrocarbon receptor
MFSD7	1.457	LP2561; FLJ22269	NM_032219	major facilitator superfamily domain containing 7
MAX	1.45	orf1; MGC10775; MGC11225; MGC18164; MGC34679; MGC36767	NM_197957	MYC associated factor X
NPY1R	1.45	NPYR	NM_000909	neuropeptide Y receptor Y1
GUCY2D	1.449	LCA; CYGD; LCA1; CORD5; CORD6; GUC2D; retGC; GUC1A4; RETGC-1; ROS-GC1	NM_000180	guanylate cyclase 2D, membrane (retina-specific)
CYP20A1	1.447	CYP-M; MGC22229	NM_177538	cytochrome P450, family 20, subfamily A, polypeptide 1
FLJ40113	1.446	FLJ40113; FLJ35171	NM_198079	golgi autoantigen, golgin subfamily a-like
RICS	1.445	RICS; GRIT; GC-GAP; MGC1892; p250GAP; KIAA0712; p200RhoGAP	NM_014715	Rho GTPase-activating protein
ZNF480	1.434	MGC32104	NM_144684	zinc finger protein 480
ZNF223	1.434	ZNF223	NM_013361	zinc finger protein 223
ZNF740	1.431	Zfp740; MGC61706	NM_001004304	zinc finger protein 740
LAMP3	1.427	LAMP; CD208; DCLAMP; TSC403; DC-LAMP	NM_014398	lysosomal-associated membrane protein 3
RABL2A	1.427	MGC117180	NM_013412	RAB, member of RAS oncogene family-like 2A
GNL3	1.423	NS; E2IG3; C77032; MGC800	NM_206825	guanine nucleotide binding protein-like 3 (nucleolar)
MLR2	1.422	MLR2; FLJ38026; KIAA1795; RP11-175O19.1	NM_032440	ligand dependent nuclear receptor corepressor
RNF19	1.417	DORFIN; DKFZp566B1346	NM_015435	ring finger protein 19
FLJ34443	1.417	FLJ34443	NM_175918	cysteine-rich PAK1 inhibitor
PIP5K2B	1.417	Pip4k2B; PIP5KIIB	NM_138687	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
FRAS1	1.415		NM_206841	
NSUN3	1.412	MST077; MSTP077; FLJ22109; FLJ22609	NM_022072	NOL1/NOP2/Sun domain family, member 3
TBC1D2	1.41	PARIS1; PARIS-1; TBC1D2A; FLJ10702; FLJ16244; FLJ42782; DKFZp761D1823	NM_018421	TBC1 domain family, member 2
PHF21B	1.41	PHF4; BHC80L; FLJ34161	NM_138415	PHD finger protein 21B
FLJ13946	1.407	FLJ13946	NM_152275	tetratricopeptide repeat domain 30A
DMD	1.406	BMD; CMD3B; DXS142; DXS164; DXS206; DXS230; DXS239; DXS268; DXS269; DXS270; DXS272	NM_004019	dystrophin (muscular dystrophy, Duchenne and Becker types)
RIPK1	1.403	RIP; FLJ39204	NM_003804	receptor (TNFRSF)-interacting serine-threonine kinase 1
TAF9L	1.398	DN7; DN-7; TAF9L; TAFII31L; TFIID-31	NM_015975	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa
SLC29A2	1.396	ENT2; DER12; HNP36	NM_001532	solute carrier family 29 (nucleoside transporters), member 2
TTC10	1.39	TG737; TTC10; hTg737; MGC26259; D13S1056E; RP11-172H24.2	NM_175605	intraflagellar transport 88 homolog (Chlamydomonas)
ZNF579	1.388	FLJ35453	NM_152600	zinc finger protein 579
CXORF1	1.388	MGC142160; MGC142164	NM_004709	chromosome X open reading frame 1
TDRD1	1.38	FLJ21082	NM_198795	tudor domain containing 1
PDIA2	1.378	PDI; PDA2; PDIP; PDIR	NM_006849	protein disulfide isomerase family A, member 2
EGLN2	1.369	EIT6; PHD1; HIFPH1; DKFZp434E026	NM_080732	egl nine homolog 2 (C. elegans)
ZNF311	1.368	zf31	NM_001010877	zinc finger protein 311
ZNF184	1.368	ZNF184	NM_007149	zinc finger protein 184
TUBB4Q	1.364	TUBB4Q	NM_020040	tubulin, beta polypeptide 4, member Q
ZNF690	1.362	Zfp690; ZSCAN29; FLJ35867; MGC129894; MGC129895	NM_152455	zinc finger protein 690
MYRIP	1.362	SLAC2C; SLAC2-C; FLJ44025; MGC130034; MGC130035; DKFZp586F1018	NM_015460	myosin VIIA and Rab interacting protein
LANCL2	1.361	TASP; GPR69B; MGC87139	NM_018697	LanC lantibiotic synthetase component C-like 2 (bacterial)
FLJ30990	1.359	FLJ30990	NM_152517	tetratricopeptide repeat domain 30B
PBX2	1.354	G17; HOX12; PBX2MHC	NM_002586	pre-B-cell leukemia transcription factor 2
PLEKHA6	1.35	PEPP3; KIAA0969	NM_014935	pleckstrin homology domain containing, family A member 6
DDX26	1.345	HDB; INT6; DBI-1; DDX26; DICE1; DDX26A; Notchl2; DKFZP434B105	NM_012141	integrator complex subunit 6
DKFZP564K142	1.343	DKFZp564K142; PRO0756; FLJ14726; MGC64926; bA217H1.1; RP11-217H1.1	NM_032121	implantation-associated protein
PIP5K2C	1.341	FLJ22055	NM_024779	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
KCNV1	1.339	HNKA; KCNB3; KV2.3; KV8.1	NM_014379	potassium channel, subfamily V, member 1
FLJ36874	1.33	FLJ36874; MGC125671; MGC125672	NM_152716	FLJ36874 protein
PMFBP1	1.328	FLJ40146; DKFZP434G131	NM_031293	polyamine modulated factor 1 binding protein 1
ADAR	1.326	DSH; G1P1; IFI4; p136; ADAR1; DRADA;	NM_001025107	adenosine deaminase, RNA-specific

		DSRAD; IFI-4; K88dsRBP		
NR6A1	1.325	RTR; GCNF; NR61; GCNF1	NM_033334	nuclear receptor subfamily 6, group A, member 1
STK31	1.317	TDRD8; FLJ16102	NM_031414	serine/threonine kinase 31
MLSTD1	1.317	FAR2; FLJ10462	NM_018099	male sterility domain containing 1
ZNF45	1.312	KOX5; ZNF13	NM_003425	zinc finger protein 45
RHBDD3	1.31	PTAG; C22orf3; HS984G1A	NM_012265	rhomboid domain containing 3
CEP350	1.31	gm133; CAP350; FLJ38282; FLJ44058; KIAA0480	NM_014810	centrosomal protein 350kDa
RBM9	1.309	RTA; HRNBP2	NM_014309	RNA binding motif protein 9
ZNF79	1.308	pT7	NM_007135	zinc finger protein 79
CD200	1.307	MRC; MOX1; MOX2; OX-2	NM_001004196	CD200 molecule
NFASC	1.303		NM_001005389	
BARX1	1.3	BARX1	NM_021570	BarH-like homeobox 1
FNBP1L	1.299	TOCA1; C1orf39	NM_001024948	formin binding protein 1-like
PGBD1	1.298	SCAND4; HUCEP-4; dJ874C20.4	NM_032507	piggyBac transposable element derived 1
POGZ	1.298	SUHW5; ZNF635; KIAA0461; MGC71543	NM_145796	pogo transposable element with ZNF domain
TGIF2	1.294	TGIF2	NM_021809	TGFB-induced factor 2 (TALE family homeobox)
ZNF670	1.287	FLJ12606; MGC12466	NM_033213	zinc finger protein 670
FLJ40504	1.284	FLJ40504; MGC138231; MGC138233	NM_173624	hypothetical protein FLJ40504
BTAF1	1.283	MOT1; TAF172; KIAA0940; TAFII170; MGC138406; TAF(II)170	NM_003972	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)
ATP11A	1.283	ATPIH; ATPIS	NM_015205	ATPase, Class VI, type 11A
IIP45	1.282	IIP45; FLJ12438; FLJ38609	NM_001025374	invasion inhibitory protein 45
ZNF345	1.281	HZF10	NM_003419	zinc finger protein 345
CHMP6	1.28	VPS20; FLJ11749	NM_024591	chromatin modifying protein 6
TIAM1	1.279	DTNA	NM_003253	T-cell lymphoma invasion and metastasis 1
GOLGA8A	1.273	GM88	NM_181077	golgi autoantigen, golgin subfamily a, 8A
ABCC3	1.271		NM_020038	
CDAN1	1.266	CDA1; CDAI; CDA-I; PRO1295; codanin	NM_138477	congenital dyserythropoietic anemia, type I
USF2	1.265	FIP	NM_003367	upstream transcription factor 2, c-fos interacting
CC2D1B	1.264	KIAA1836; RP11-155O18.2	NM_032449	coiled-coil and C2 domain containing 1B
GPR111	1.264	PGR20; hGPCR35	NM_153839	G protein-coupled receptor 111
LOC149134	1.264	LOC149134; MGC120210; MGC120211; MGC120212; MGC120213	NM_207326	hypothetical protein LOC149134
ZNF137	1.259	pHZ-30; MGC119990; MGC119991	NM_003438	zinc finger protein 137
ZFP95	1.257	FLJ39233; KIAA1015; MGC33710	NM_014569	zinc finger protein 95 homolog (mouse)
RANBP6	1.256	FREM2	NM_012416	RAN binding protein 6
ZDHHC13	1.252	HIP14L; HIP3RP; FLJ10852; FLJ10941; MGC64994	NM_019028	zinc finger, DHHC-type containing 13
HYAL4	1.252	HYAL4	NM_012269	hyaluronoglucosaminidase 4
LHB	1.251	CGB4; hLHB; LSH-B	NM_000894	luteinizing hormone beta polypeptide
EPIM	1.25	EPM; EPIM; STX2A; STX2B; STX2C; MGC51014	NM_194356	syntaxin 2
PCDHA10	1.24	CNR8; CNRN8; CNRS8; CRNR8; PCDH-ALPHA10	NM_031859	protocadherin alpha 10
FLJ35801	1.238	FLJ35801	NM_153044	chromosome 22 open reading frame 27
ZNF510	1.238	KIAA0972; MGC33740	NM_014930	zinc finger protein 510
BRD9	1.236	PRO9856; LAVS3040; DKFZp686L0539	NM_023924	bromodomain containing 9
DHX57	1.235		NM_144995	
AADAT	1.234	KAT2; KATII	NM_016228	aminoadipate aminotransferase
GAD1	1.232	GAD	NM_013445	glutamate decarboxylase 1 (brain, 67kDa)
ZNF306	1.23	ZF47; Zfp47; ZFP306; ZSCAN13; FLJ33906; KIAA0426	NM_024493	zinc finger protein 306
SON	1.228	SON3; BASS1; DBP-5; NREBP; C21orf50; FLJ21099; FLJ33914; KIAA1019	NM_032195	SON DNA binding protein
ZNF140	1.228	pHZ-39	NM_003440	zinc finger protein 140
ZNF582	1.227	FLJ30927	NM_144690	zinc finger protein 582
FLJ39653	1.224	FLJ39653	NM_152684	hypothetical protein FLJ39653
ZNF473	1.221	ZN473; HZFP100	NM_015428	zinc finger protein 473
MLH3	1.22	HNPCC7; MGC138372	NM_014381	mutL homolog 3 (E. coli)
KCNAB1	1.218	hKvb3; AKR6A3; KCNA1B; Kvb1.3; hKvBeta3; KV-BETA-1	NM_003471	potassium voltage-gated channel, shaker-related subfamily, beta member 1
NXF5	1.217	NXF5	NM_033155	nuclear RNA export factor 5
JUB	1.215	Ajuba; MGC15563	NM_032876	jub, ajuba homolog (Xenopus laevis)
MGC24975	1.212	MGC24975	NM_153359	hypothetical protein MGC24975
GAD1	1.205	GAD	NM_013445	glutamate decarboxylase 1 (brain, 67kDa)
PNMA6A	1.204	MGC15827	NM_032882	paraneoplastic antigen like 6A
DUSP10	1.201	MKP5; MKP-5	NM_144728	dual specificity phosphatase 10
MDC1	1.197	NFBD1; KIAA0170; DKFZp781A0122	NM_014641	mediator of DNA damage checkpoint 1
DNMT3A	1.188	DNMT3A2; M.HsaIIIA	NM_153759	DNA (cytosine-5-)-methyltransferase 3 alpha
LPP	1.185	LPP	NM_005578	LIM domain containing preferred translocation partner in lipoma
MAOA	1.183	MAOA	NM_000240	monoamine oxidase A
MVK	1.178	LRBP; MVLK	NM_000431	mevalonate kinase (mevalonic aciduria)
ASB7	1.176	FLJ22551	NM_024708	ankyrin repeat and SOCS box-containing 7
RAPGEF6	1.172	PDZGEF2; KIA001LB; PDZ-GEF2; RA-GEF-2; DKFZp686I15116	NM_016340	Rap guanine nucleotide exchange factor (GEF) 6
SLC13A3	1.17	NADC3; SDCT2	NM_022829	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
ADAMTS7	1.168	ADAM-TS7; DKFZp434H204	NM_014272	ADAM metallopeptidase with thrombospondin type 1 motif, 7
PRPF4B	1.167	PR4H; PRP4; PRP4H; PRP4K; KIAA0536; dJ1013A10.1	NM_003913	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
SHPRH	1.166	FLJ37625; FLJ45012; FLJ90837; KIAA2023; MGC134886; bA545I5.2	NM_173082	SNF2 histone linker PHD RING helicase
DPY19L3	1.165	DKFZp686J17135	NM_207325	dpy-19-like 3 (C. elegans)
TRPV6	1.161	CAT1; CATL; ZFAB; ECAC2; ABP/ZF; LP6728; HSA277909	NM_018646	transient receptor potential cation channel, subfamily V, member 6
UBE2J2	1.16		NM_194316	
C14ORF49	1.159	FLJ25605; c14_5734	NM_152592	chromosome 14 open reading frame 49
PARP8	1.158	FLJ21308; MGC42864	NM_024615	poly (ADP-ribose) polymerase family, member 8
RAB12	1.157	FLJ45927; MGC104724	NM_001025300	RAB12, member RAS oncogene family
RECQL5	1.155	RECQ5; FLJ90603	NM_004259	RecQ protein-like 5
CASC5	1.153	D40; AF15Q14; KIAA1570	NM_170589	cancer susceptibility candidate 5

FLJ45445	1.15	FLJ45445	NM_001004321	FLJ45445 protein
ZNF285	1.148	FLJ30747	NM_152354	zinc finger protein 285
PTEN	1.141	BZS; MHAM; TEP1; MMAC1; PTEN1; MGC11227	NM_000314	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
CLEC9A	1.141	UNQ9341	NM_207345	C-type lectin domain family 9, member A
PMS2L3	1.141	PMS5; PMSR3; PMS2L9; MGC126647	NM_001003686	postmeiotic segregation increased 2-like 3
FLJ23322	1.138	FLJ23322; FLJ33734	NM_024955	FAD-dependent oxidoreductase domain containing 2
MSH5	1.132	G7; NG23; MutSH5; MGC2939; DKFZp434C1615	NM_002441	mutS homolog 5 (E. coli)
ZNF96	1.129		NM_014724	
FLJ46688	1.122	FLJ46688	NM_001004330	FLJ46688 protein
TMED8	1.105	FAM15B; MGC126559	NM_213601	transmembrane emp24 protein transport domain containing 8
ZNF74	1.101	Cos52; ZNF520; Zfp520	NM_003426	zinc finger protein 74
LOC388692	1.087	LOC388692	NM_001013644	hypothetical gene supported by AK123662
ZNF20	1.085	KOX13; FLJ39241	NM_021143	zinc finger protein 20
ANKRD5	1.08	FLJ21669; dJ839B4.6	NM_022096	ankyrin repeat domain 5
SMARCC2	1.07	Rsc8; BAF170; CRACC2	NM_003075	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2
SLC35C2	1.069	CGI-15; OVCOV1; C20orf5; FLJ37039; MGC20633; MGC32079; MGC39183; BA394O2.1	NM_173179	solute carrier family 35, member C2
PCDHA3	1.057	PCDH-ALPHA3	NM_031497	protocadherin alpha 3
FGFBP1	1.056	FGFBP; HBP17	NM_005130	fibroblast growth factor binding protein 1
FABP2	1.052	FABPI; I-FABP; MGC133132	NM_000134	fatty acid binding protein 2, intestinal
GIPC1	0.944	NIP; GIPC; IIP-1; TIP-2; SEMCAP; C19orf3; Hs.6454; MGC3774; GLUT1CBP; MGC15889; RGS19IP1; SYNECTIIN	NM_202468	GIPC PDZ domain containing family, member 1
KIAA1005	0.922	KIAA1005; DKFZp686C0668	NM_015272	KIAA1005 protein
HOXB2	0.916	K8; HOX2; HOX2H; Hox-2.8	NM_002145	homeobox B2
ANK1	0.915	ANK; SPH1; SPH2	NM_020480	ankyrin 1, erythrocytic
ZCCHC5	0.902	Mar3; ZHC5; Mart3; FLJ38865	NM_152694	zinc finger, CCHC domain containing 5
DGKI	0.897	DGK-IOTA	NM_004717	diacylglycerol kinase, iota
NPTXR	0.89	NPTXR	NM_058178	Neuronal pentraxin receptor
ATG12	0.889	APG12; APG12L; HAPG12	NM_004707	ATG12 autophagy related 12 homolog (S. cerevisiae)
GABRB3	0.888	MGC9051	NM_000814	gamma-aminobutyric acid (GABA) A receptor, beta 3
LSS	0.885	OSC	NM_001001438	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
TEKT3	0.872	LRRC23	NM_031898	tektin 3
STXBP1	0.861	UNC18; hUNC18; rbSec1; MUNC18-1	NM_003165	syntaxin binding protein 1
ZFHX2	0.861	KIAA1762	NM_033400	zinc finger homeobox 2
CPSF3L	0.856	RC68; INT11; RC-68; INTS11; CPSF73L; FLJ13294; FLJ20542	NM_032179	cleavage and polyadenylation specific factor 3-like
NRGN	0.854	RC3; hng	NM_006176	neurogranin (protein kinase C substrate, RC3)
ZNF706	0.85	HSPC038; PNAS-106; PNAS-113	NM_016096	zinc finger protein 706
TINAGL1	0.849	ARG1; LCN7; LIECG3; TINAGRP	NM_022164	tubulointerstitial nephritis antigen-like 1
NR2F1	0.844	EAR3; EAR-3; NR2F2; SVP44; ERBAL3; TFCOUP1; COUP-TFI; TCFCOUP1	NM_005654	nuclear receptor subfamily 2, group F, member 1
OGDH	0.841	E1k; OGDC; AKGDH	NM_001003941	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
MRE11A	0.836	ATLD; HNGS1; MRE11; MRE11B	NM_005590	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
BIRC5	0.835	API4; EPR-1	NM_001012271	baculoviral IAP repeat-containing 5 (survivin)
WDR76	0.834	FLJ12973	NM_024908	WD repeat domain 76
SHD	0.829	MAP2	NM_020209	Src homology 2 domain containing transforming protein D
BOLA1	0.828	CGI-143; MGC75015; RP11-196G18.18	NM_016074	bolA-like 1 (E. coli)
ZNRF2	0.827	RNF202	NM_147128	zinc and ring finger 2
BTD	0.827	BTD	NM_000060	biotinidase
PXK	0.824	MONaKA; FLJ20335	NM_017771	PX domain containing serine/threonine kinase
SPESP1	0.824	SP-ESP; MGC24663	NM_145658	sperm equatorial segment protein 1
TIE1	0.821	TIE; JTK14	NM_005424	tyrosine kinase with immunoglobulin-like and EGF-like domains 1
FLJ33167	0.817	FLJ33167	NM_152683	coiled-coil domain containing 111
EZH2	0.816	EZH1; ENX-1; MGC9169	NM_004456	enhancer of zeste homolog 2 (Drosophila)
LYPD5	0.814	PRO4356; FLJ30469	NM_001031749	LY6/PLAUR domain containing 5
PIGZ	0.811	SMP3; FLJ12768; MGC52163	NM_025163	phosphatidylinositol glycan anchor biosynthesis, class Z
SUHW4	0.81	ZNF634; MGC21637; MGC61687	NM_001002844	suppressor of hairy wing homolog 4 (Drosophila)
MPG	0.806	AAG; MDG; APNG; Mid1; anpg; PIG11; PIG16; CRA36.1	NM_001015054	N-methylpurine-DNA glycosylase
CTSF	0.802	CATSF	NM_003793	cathepsin F
DKFZP686K16132	0.801	DKFZp686K16132	NM_001012987	similar to BMP2 inducible kinase
UEV3	0.8	ATTP; UEV3; FLJ11068	NM_018314	UEV and lactate/malate dehyrogenase domains
MUC1	0.8	EMA; PEM; PUM; MAM6; PEMT; CD227; H23AG	NM_001018021	mucin 1, cell surface associated
THAP10	0.8	THAP10	NM_020147	THAP domain containing 10
SCYL1	0.796	GKLP; NKTL; NTKL; P105; TAPK; TEIF; TRAP; HT019	NM_020680	SCY1-like 1 (S. cerevisiae)
LOC88523	0.796	LOC88523	NM_033111	CG016
GCK	0.795	GK; GLK; HK4; HHF3; HKIV; HXKP; MODY2	NM_033508	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)
EPB41L1	0.794	4.1N; KIAA0338; MGC11072; DKFZp686H17242	NM_012156	erythrocyte membrane protein band 4.1-like 1
C6ORF204	0.791	NY-BR-15; MGC131785; bA57K17.2; RP11-57K17.2	NM_206921	chromosome 6 open reading frame 204
WDR70	0.791	FLJ10233	NM_018034	WD repeat domain 70
WHSC1	0.791	WHS; NSD2; TRX5; MMSET; REIIBP; FLJ23286; KIAA1090	NM_133331	Wolf-Hirschhorn syndrome candidate 1
WFDC1	0.784	PS20	NM_021197	WAP four-disulfide core domain 1
SEMA4F	0.783	SEMAM; SEMAW; M-SEMA; PRO2353; m-Sema M; m-Sema-M	NM_004263	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F
SMOX	0.783		NM_019025	

LRRC3B	0.78	LRP15; MGC102927	NM_052953	leucine rich repeat containing 3B
LOC92691	0.78	FLJ34263; DKFZp781L2456	NM_138390	transmembrane protein 169
GPR175	0.779	TPRA40; FLJ32197	NM_016372	G protein-coupled receptor 175
PCDH11Y	0.779	PCDHY; PCDH22; PCDH11X	NM_032971	protocadherin 11 Y-linked
PTER	0.778	RPR-1	NM_030664	phosphotriesterase related
FSD1	0.777	MIR1; GLFND; MGC3213	NM_024333	fibronectin type III and SPRY domain containing 1
GRTP1	0.776	TBC1D6; FLJ22474; MGC138328; MGC138330	NM_024719	growth hormone regulated TBC protein 1
KIAA1244	0.772	RP3-422G23.4	NM_020340	KIAA1244
GBP2	0.771	PRDM2	NM_004120	guanylate binding protein 2, interferon-inducible
KLHDC1	0.769	MST025; MGC126644; MGC126646	NM_172193	kelch domain containing 1
KIF17	0.769	KIF3X; KIF17B; KIAA1405	NM_020816	kinesin family member 17
TNFRSF10B	0.767	DR5; CD262; KILLER; TRICK2; TRICKB; ZTNFR9; TRAILR2; TRICK2A; TRICK2B; TRAIL-R2; KILLER/DR5	NM_003842	tumor necrosis factor receptor superfamily, member 10b
DOPEY2	0.767	C21orf5	NM_005128	dopey family member 2
TNFAIP8L3	0.767	FLJ41287	NM_207381	tumor necrosis factor, alpha-induced protein 8-like 3
TGM2	0.765	TG2; TGC	NM_198951	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
ABCC2	0.763	DJS; MRP2; cMRP; ABC30; CMOAT; KIAA1010	NM_000392	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
TRIM3	0.763	BERP; HAC1; RNF22; RNF97	NM_006458	tripartite motif-containing 3
PLK3	0.762	CNK; FNK; PRK	NM_004073	polo-like kinase 3 (Drosophila)
ATPBD1C	0.761	MGC14560; MGC32810	NM_016301	ATP binding domain 1 family, member C
IL19	0.76	MDA1; NG.1; ZMDA1; IL-10C	NM_153758	interleukin 19
GTF2H2	0.758	BTF2; TFIIH; BTF2P44; MGC102806; T-BTF2P44	NM_001515	general transcription factor IIH, polypeptide 2, 44kDa
PDCD6IP	0.756	AIP1; Alix; HP95; DRIP4; MGC17003	NM_013374	programmed cell death 6 interacting protein
MFAP5	0.756	MP25; MAGP2	NM_003480	microfibrillar associated protein 5
FAM14A	0.754	TLH29; MGC44913	NM_032036	family with sequence similarity 14, member A
C10ORF72	0.754	FLJ31737; MGC44086	NM_001031746	chromosome 10 open reading frame 72
QTRTD1	0.754	FLJ12960	NM_024638	queuine tRNA-ribosyltransferase domain containing 1
ADAMTSL1	0.753	ADAMTSR1; MGC40193	NM_139238	ADAMTS-like 1
ARL4	0.753	ARL4	NM_005738	ADP-ribosylation factor-like 4A
C2ORF11	0.75	FLJ30574; MGC117313	NM_144629	chromosome 2 open reading frame 11
NGB	0.75	NGB	NM_021257	neuroglobin
CCDC51	0.749	FLJ12436	NM_024661	coiled-coil domain containing 51
ANXA4	0.748	ANX4; PIG28; MGC75105; DKFZp686H02120	NM_001153	annexin A4
ADCY4	0.748	ADCY4	NM_139247	adenylate cyclase 4
GNB1L	0.746	GY2; FKSG1; WDR14; WDVCF; DGCRK3; KIAA1645	NM_053004	guanine nucleotide binding protein (G protein), beta polypeptide 1-like
C9ORF72	0.745	MGC23980; RP11-27J8.2	NM_145005	chromosome 9 open reading frame 72
AK5	0.745	AK6; MGC33326	NM_012093	adenylate kinase 5
INHBB	0.745	INHBB	NM_002193	inhibin, beta B (activin AB beta polypeptide)
POLD4	0.745	p12; POLDS	NM_021173	polymerase (DNA-directed), delta 4
ARSJ	0.744	FLJ23548	NM_024590	arylsulfatase family, member J
SLC25A16	0.743	GDA; GDC; ML7; hML7; HGT.1; D10S105E; MGC39851	NM_152707	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16
CYLD	0.743	EAC; CDMT; CYLD1; CYLDI; USPL2; HSPC057; FLJ20180; FLJ31664; KIAA0849	NM_015247	cylindromatosis (turban tumor syndrome)
PEX6	0.741	PAF2; PAF-2; PXAAA1	NM_000287	peroxisomal biogenesis factor 6
C1QTNF5	0.74	LORD; CTRP5; DKFZp586B0621	NM_015645	C1q and tumor necrosis factor related protein 5
ITPKA	0.74	ITPKA	NM_002220	inositol 1,4,5-trisphosphate 3-kinase A
ASPH	0.738	BAH; HAAH; JCTN; junctin; CASQ2BP1	NM_004318	aspartate beta-hydroxylase
NME1-NME2	0.737	NME1-NME2; NME2	NM_001018136	NM23-LV
CITED1	0.735	MSG1	NM_004143	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1
PTPN22	0.735	LYP; PEP; Lyp1; Lyp2; PTPN8	NM_012411	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
C9ORF85	0.734	MGC61599; RP11-346E17.2	NM_182505	chromosome 9 open reading frame 85
ACSM3	0.733	SA; SAH	NM_005622	acyl-CoA synthetase medium-chain family member 3
CSGLCA-T	0.733	CSGlcA-T; KIAA1402	NM_019015	chondroitin sulfate glucuronyltransferase
HERC4	0.733	KIAA1593; DKFZP564G092	NM_022079	hect domain and RLD 4
PLEKHH3	0.733	FLJ21019	NM_024927	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3
PHF19	0.729	PCL3; MGC23929; MGC131698	NM_001009936	PHD finger protein 19
PPP2R5C	0.729	B56G; MGC23064	NM_002719	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
CCDC3	0.728	FLJ20925; DKFZP761F241; RP11-347I22.1	NM_031455	coiled-coil domain containing 3
TAF13	0.727	TAF2K; TAFII18; MGC22425	NM_005645	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa
REEP2	0.727	C5orf19; SGC32445	NM_016606	receptor accessory protein 2
PRDM8	0.727	PFM5	NM_020226	PR domain containing 8
NDP	0.725	ND; EVR2; FEVR	NM_000266	Norrie disease (pseudoglioma)
C10ORF67	0.724	MGC46732; RP11-792P23.2	NM_153714	chromosome 10 open reading frame 67
ARNTL	0.722	TIC; JAP3; MOP3; BMAL1; PASD3; BMAL1c; MGC47515	NM_001178	aryl hydrocarbon receptor nuclear translocator-like
PLCB2	0.722	FLJ38135	NM_004573	phospholipase C, beta 2
TMEM117	0.722	DKFZp434K2435	NM_032256	transmembrane protein 117
HIST1H4K	0.721	H4/d; H4FD; dJ160A22.1	NM_003541	histone 1, H4k
LOC51334	0.718	DSC54; MGC104614	NM_016644	proline rich 16
ANXA2	0.718	P36; ANX2; LIP2; LPC2; CAL1H; LPC2D; ANX2L4; PAP-IV	NM_001002857	annexin A2
FBXO4	0.717	FBX4; FLJ10141; DKFZp547N213	NM_012176	F-box protein 4
PIP	0.716	GPIP4; GCDFP15; GCDFP-15	NM_002652	prolactin-induced protein
RDH12	0.716	LCA3; FLJ30273	NM_152443	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)
LMTK2	0.715	BREK; KPI2; LMR2; cprk; KPI-2; AATYK2; KIAA1079	NM_014916	lemur tyrosine kinase 2

FBXO2	0.715	FBG1; FBX2; Fbs1; NFB42	NM_012168	F-box protein 2
HPCAL1	0.713	BDR1; HLP2; VILIP-3	NM_134421	hippocalcin-like 1
FBXL17	0.711	Fbl17; Fbx13; FBXO13; DKFZp434C1715	NM_022824	F-box and leucine-rich repeat protein 17
HOXA9	0.71	HOX1; ABD-B; HOX1G; HOX1.7; MGC1934	NM_152739	homeobox A9
SERPIND1	0.71	HC2; LS2; HCF2; HCII; HLS2; D22S673	NM_000185	serpin peptidase inhibitor, clade D (heparin cofactor), member 1
XG	0.709	PBDX; MGC118758; MGC118759; MGC118760; MGC118761	NM_175569	Xg blood group
SHC4	0.707	RaLP; MGC34023	NM_203349	SHC (Src homology 2 domain containing) family, member 4
ELF4	0.707	MEF; ELFR	NM_001421	E74-like factor 4 (ets domain transcription factor)
RET	0.705	PTC; MTC1; HSCR1; MEN2A; MEN2B; RET51; CDHF12; RET-ELE1	NM_020630	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)
TOX	0.704	TOX; KIAA0808	NM_014729	thymus high mobility group box protein TOX
C17ORF76	0.703	FLJ35696	NM_207387	chromosome 17 open reading frame 76
FREQ	0.703	FLUP; NCS1; NCS-1; DKFZp761L1223	NM_014286	frequenin homolog (Drosophila)
TAC3	0.701	NKB; NKNB; PRO1155; ZNEUROK1	NM_001006667	tachykinin 3 (neuromedin K, neurokinin beta)
OGDH	0.7	E1k; OGDC; AKGDH	NM_001003941	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
PANX2	0.698	hPANX2; MGC119432	NM_052839	pannexin 2
RLTPR	0.697	RLTPR	NM_001013838	RGD, leucine-rich repeat, tropomodulin and proline-rich containing protein
CDKN2A	0.696	ARF; MLM; p14; p16; p19; CMM2; INK4; MTS1; TP16; CDK4I; CDKN2; INK4a; p14ARF; p16INK4; p16INK4a	NM_058197	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
LMO2	0.694	TTG2; RBTN2; RHOM2; RBTNL1	NM_005574	LIM domain only 2 (rhombotin-like 1)
ZFP64	0.693	MGC940; ZNF338	NM_199427	zinc finger protein 64 homolog (mouse)
UBE2H	0.693	UBC8; UBCH; UBCH2; E2-20K	NM_182697	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
LOC161931	0.693	LOC161931	NM_139174	testis nuclear RNA-binding protein-like
HSPB2	0.692	MKBP; HSP27; Hs.78846; MGC133245	NM_001541	heat shock 27kDa protein 2
ALDH3B1	0.691	ALDH4; ALDH7; FLJ26433	NM_001030010	aldehyde dehydrogenase 3 family, member B1
KIAA0247	0.691	TMEM101	NM_014734	KIAA0247
STOML1	0.691	SLP-1; STORP; hUNC-24; FLJ36370	NM_004809	stomatin (EPB72)-like 1
ZMYND15	0.69	DKFZp434N127	NM_032265	zinc finger, MYND-type containing 15
PODN	0.69	PCAN; SLRR5A; MGC24995	NM_153703	podocan
MSRA	0.686	MSRA	NM_012331	methionine sulfoxide reductase A
TAGLN3	0.686	NP22; NP25	NM_001008273	transgelin 3
SYTL4	0.684	FLJ40960; DKFZp451P0116	NM_080737	synaptotagmin-like 4 (granuphilin-a)
COG5	0.684	GTC90; GOLTC1	NM_006348	component of oligomeric golgi complex 5
CINP	0.683	CINP; MGC849	NM_032630	cyclin-dependent kinase 2-interacting protein
DKFZP686O24166	0.681	DKFZp686O24166; DKFZp686I21167	NM_001009913	hypothetical protein DKFZp686O24166
ICAM2	0.68	CD102	NM_000873	intercellular adhesion molecule 2
HLA-F	0.679	HLAF; HLA-5.4; HLA-CDA12	NM_018950	major histocompatibility complex, class I, F
FBXL16	0.678	Fbl16; C16orf22; FLJ33735; MGC33974; c380A1.1	NM_153350	F-box and leucine-rich repeat protein 16
FLJ14054	0.677	FLJ14054	NM_024563	chromosome 5 open reading frame 23
IFIT1	0.676	G10P1; IFI56; IFI-56; IFNAI1; RNM561; GARG-16	NM_001548	interferon-induced protein with tetratricopeptide repeats 1
CARD9	0.676	hCARD9	NM_052813	caspase recruitment domain family, member 9
CACNA2D3	0.676	HSA272268	NM_018398	calcium channel, voltage-dependent, alpha 2/delta 3 subunit
GABRB3	0.676	MGC9051	NM_000814	gamma-aminobutyric acid (GABA) A receptor, beta 3
RNH1	0.675	RAI; RNH; MGC4569; MGC18200; MGC54054	NM_203384	ribonuclease/angiogenin inhibitor 1
NLGN4Y	0.675	KIAA0951	NM_014893	neuroligin 4, Y-linked
ACTN4	0.674	FSGS; FSGS1; DKFZp686K23158	NM_004924	actinin, alpha 4
FLJ35258	0.673	FLJ35258	NM_182571	hypothetical protein 284297
MGC35212	0.673	gs129; MGC35212	NM_152764	chromosome 16 open reading frame 73
FIBCD1	0.673	FLJ14810	NM_032843	fibrinogen C domain containing 1
C3	0.671	ASP; CPAMD1	NM_000064	complement component 3
IL1R1	0.671	P80; IL1R; IL1RA; CD121A; D2S1473; IL-1R-alpha	NM_000877	interleukin 1 receptor, type I
ASB13	0.67	FLJ13134; MGC19879	NM_024701	ankyrin repeat and SOCS box-containing 13
FLJ20273	0.67	FLJ20273; DKFZp686F02235	NM_019027	RNA-binding protein
SGCD	0.669	SGD; DAGD; 35DAG; CMD1L; SGCDP; MGC22567; SG-delta	NM_000337	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
KITLG	0.668	SF; MGF; SCF; KL-1; Kitl; DKFZp686F2250	NM_000899	KIT ligand
TPCN1	0.668	TPC1; FLJ20612; KIAA1169	NM_017901	two pore segment channel 1
HSD3B7	0.667	PFIC4	NM_025193	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
ACOT7	0.667	ACT; ACH1; BACH; LACH; LACH1; hBACH; CTE-II; MGC1126; RP1-120G22.10	NM_181864	acyl-CoA thioesterase 7
ABHD14B	0.667	CIB; MGC15429	NM_032750	abhydrolase domain containing 14B
KRTHA4	0.666	HA4; Ha-4; hHa4; KRTHA4	NM_021013	keratin 34
C13ORF21	0.666	MGC35505; bA269C23.1; RP11-269C23.1	NM_001010897	chromosome 13 open reading frame 21
AKAP1	0.665	AKAP; PRKA1; AKAP84; AKAP121; AKAP149; D-AKAP1; MGC1807; SAKAP84	NM_003488	A kinase (PRKA) anchor protein 1
TAPBPL	0.664	TAPBPR; TAPBP-R; FLJ10143	NM_018009	TAP binding protein-like
MNS1	0.664	FLJ11222	NM_018365	meiosis-specific nuclear structural 1
SPFH1	0.664	KE04; KEO4; C10orf69; RP11-316M21.1	NM_006459	SPFH domain family, member 1
CPEB4	0.663	KIAA1673	NM_030627	cytoplasmic polyadenylation element binding protein 4
CALB2	0.662	CAL2	NM_001740	calbindin 2, 29kDa (calretinin)
CBX7	0.661	STOML1	NM_175709	chromobox homolog 7
C1ORF45	0.661	KATNAL1	NM_001025231	chromosome 1 open reading frame 45
SERINC2	0.66	TDE2; TDE2L; FKSG84; PRO0899; MGC90340	NM_178865	serine incorporator 2
C16ORF52	0.66		NM_173501	
PPAPDC3	0.658	C9orf67; FLJ14662; KIAA0515; MGC12921; RP11-643E14.1	NM_032728	phosphatidic acid phosphatase type 2 domain containing 3
Mar-04	0.657	RNF174; MARCH-IV; MGC104908	NM_020814	membrane-associated ring finger (C3HC4) 4
PLA2G10	0.656	SPLA2; GXPLA2; GXSPLA2; MGC119918; MGC119919; MGC133367	NM_003561	phospholipase A2, group X
NFKBIZ	0.652	IKBZ; INAP; MAIL; FLJ30225; FLJ34463	NM_031419	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta

GLRB	0.652	MDM2	NM_000824	glycine receptor, beta
LOC200810	0.652	LOC200810	NM_001015050	similar to beta-1,4-mannosyltransferase; beta-1,4 mannosyltransferase
ME3	0.652	FLJ34862	NM_006680	malic enzyme 3, NADP(+)-dependent, mitochondrial
ERN1	0.65	IRE1; IRE1P; FLJ30999	NM_152461	endoplasmic reticulum to nucleus signalling 1
FCHSD2	0.65	NWK; SH3MD3; KIAA0769	NM_014824	FCH and double SH3 domains 2
CDC25C	0.65	CDC25	NM_001790	cell division cycle 25C
IFT57	0.649	HIPPI; MHS4R2; ESRRBL1; FLJ10147	NM_018010	intraflagellar transport 57 homolog (Chlamydomonas)
MGC52057	0.649	MGC52057	NM_194317	LY6/PLAUR domain containing 6
CYB5R3	0.648	B5R; DIA1	NM_007326	cytochrome b5 reductase 3
NAP1L5	0.648	DRLM	NM_153757	nucleosome assembly protein 1-like 5
PCNXL2	0.648	FLJ11383; KIAA0435	NM_024938	pecanex-like 2 (Drosophila)
PLD3	0.647	HU-K4	NM_001031696	phospholipase D family, member 3
IL1F7	0.646	FIL1; FIL1Z; IL1H4; IL-1F7; IL-1H4; IL1RP1; IL-1RP1; FIL1(ZETA)	NM_014439	interleukin 1 family, member 7 (zeta)
TRHDE	0.645	PAP-II; PGPEP2; TRH-DE; FLJ22381	NM_013381	thyrotropin-releasing hormone degrading enzyme
FUBP1	0.644	FBP; FUBP	NM_003902	far upstream element (FUSE) binding protein 1
C5ORF14	0.644	UNQ335; FLJ22625	NM_024715	chromosome 5 open reading frame 14
C3ORF52	0.644	TTMP; FLJ23186	NM_024616	chromosome 3 open reading frame 52
FGF5	0.641	HBGF-5; Smag-82	NM_004464	fibroblast growth factor 5
FAM70B	0.64	MGC20579; RP11-199F6.1	NM_182614	family with sequence similarity 70, member B
RAB27A	0.64	GS2; RAM; RAB27; HsT18676; MGC117246	NM_004580	RAB27A, member RAS oncogene family
DOCK5	0.637	DKFZp451J181; DKFZp779M164; DKFZp781J211	NM_024940	dedicator of cytokinesis 5
MYO1E	0.636	MYO1C; MGC104638	NM_004998	myosin IE
SDCBP2	0.636	ST-2; SITAC18	NM_080489	syndecan binding protein (syntenin) 2
SERPINB3	0.636	SCC; T4-A; SCCA1; SCCA-1; HsT1196; SCCA-PD	NM_006919	serpin peptidase inhibitor, clade B (ovalbumin), member 3
DNPEP	0.635	DAP; ASPEP	NM_012100	aspartyl aminopeptidase
NEDD4	0.635	KIAA0093	NM_198400	neural precursor cell expressed, developmentally down-regulated 4
GNG3	0.635	GNG3	NM_012202	guanine nucleotide binding protein (G protein), gamma 3
CCT3	0.635	CCTG; PIG48; TRIC5; CCT-gamma; TCP-1-gamma	NM_001008800	chaperonin containing TCP1, subunit 3 (gamma)
TANK	0.634	TRAF2; I-TRAF	NM_004180	TRAF family member-associated NFKB activator
COL2A1	0.633	AOM; SEDC; COL11A3; MGC131516	NM_001844	collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)
ILDR1	0.633	MGC50831; ILDR1beta; ILDR1alpha	NM_175924	immunoglobulin-like domain containing receptor 1
NOTCH2	0.632	hN2; AGS2	NM_024408	Notch homolog 2 (Drosophila)
MMAA	0.632	MGC120010; MGC120011; MGC120012; MGC120013	NM_172250	methylmalonic aciduria (cobalamin deficiency) cblA type
TIP39	0.632	TIP39	NM_178449	tuberoinfundibular 39 residue protein precursor
SH2D4A	0.632	SH2A; FLJ20967	NM_022071	SH2 domain containing 4A
EDN1	0.631	ET1	NM_001955	endothelin 1
STEAP3	0.63	STMP3; TSAP6; dudlin-2	NM_018234	STEAP family member 3
AR	0.629	KD; AIS; TFM; DHTR; SBMA; NR3C4; SMAX1; HUMARA	NM_000044	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
URB	0.629	URB; DRO1; SSG1; MGC131805; MGC134851	NM_199511	coiled-coil domain containing 80
HES3	0.629	LOC339977	NM_001024598	hairy and enhancer of split 3 (Drosophila)
STK39	0.627	DCHT; SPAK; DKFZp686K05124	NM_013233	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
FLJ10178	0.626	FLJ10178; FLJ14191; RP11-647M7.1	NM_018015	chromosome X open reading frame 57
MCTP1	0.626	FLJ22344	NM_001002796	multiple C2 domains, transmembrane 1
AKR1A1	0.625	ALR; ALDR1; MGC1380; MGC12529	NM_006066	aldo-keto reductase family 1, member A1 (aldehyde reductase)
SNCA	0.624	PD1; NACP; PARK1; PARK4; MGC110988	NM_000345	synuclein, alpha (non A4 component of amyloid precursor)
C6ORF65	0.623	FLJ30162; bA203B9.1	NM_152731	chromosome 6 open reading frame 65
CHURC1	0.623	chch; My015; C14orf52; FLJ33064	NM_145165	churchill domain containing 1
C1ORF78	0.623	FLJ10647; RP11-268J15.2	NM_018166	chromosome 1 open reading frame 78
PPARD	0.622	FAAR; NUC1; NUCI; NR1C2; NUCII; PPARB; MGC3931; PPAR-beta	NM_006238	peroxisome proliferative activated receptor, delta
PDGFC	0.622	SCDGF	NM_016205	platelet derived growth factor C
ANTXR1	0.62	ATR; TEM8; FLJ10601; FLJ11298; FLJ21776	NM_032208	anthrax toxin receptor 1
EIF1AX	0.62	EIF1A; EIF4C; eIF-1A; eIF-4C	NM_001412	eukaryotic translation initiation factor 1A, X-linked
DYRK4	0.618	RPGRIP1	NM_003845	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
PH-4	0.617	PH-4	NM_177939	hypoxia-inducible factor prolyl 4-hydroxylase
SYN2	0.616	SYNII; SYNIIa; SYNIIb	NM_133625	synapsin II
MDFIC	0.616	HIC	NM_199072	MyoD family inhibitor domain containing
WNT2	0.616	IRP; INT1L1	NM_003391	wingless-type MMTV integration site family member 2
SCNN1G	0.615	PHA1; ENaCg; SCNEG; ENaCgamma	NM_001039	sodium channel, nonvoltage-gated 1, gamma
C16ORF45	0.615	FLJ32618	NM_033201	chromosome 16 open reading frame 45
TFB1M	0.615	CGI75; mtTFB; CGI-75	NM_016020	transcription factor B1, mitochondrial
MGC13040	0.615	MGC13040	NM_032930	chromosome 11 open reading frame 70
NEXN	0.614	NELIN; MGC138865; MGC138866	NM_144573	nexilin (F actin binding protein)
PHKA1	0.613	PHKA; MGC132604	NM_002637	phosphorylase kinase, alpha 1 (muscle)
ERCC1	0.613	UV20	NM_202001	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
MAGEH1	0.612	APR1; APR-1	NM_014061	melanoma antigen family H, 1
RGS4	0.612	RGP4; SCZD9; MGC2124; MGC60244	NM_005613	regulator of G-protein signalling 4
IER3IP1	0.61	HSPC039; PRO2309	NM_016097	immediate early response 3 interacting protein 1
FLJ21062	0.61		NM_024788	

OPN3	0.609	ECPN	NM_014322	opsin 3 (encephalopsin, panopsin)
PPIF	0.608	CYP3; Cyp-D; FLJ90798; MGC117207	NM_005729	peptidylprolyl isomerase F (cyclophilin F)
MR1	0.607	HLALS	NM_001531	major histocompatibility complex, class I-related
ST3GAL3	0.607	ST3N; SIAT6; ST3GALII; ST3GalIII; ST3Gal III	NM_006279	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
PDE7B	0.606	MGC88256; bA472E5.1	NM_018945	phosphodiesterase 7B
HIVEP2	0.605	MBP-2; MIBP1; HIV-EP2	NM_006734	human immunodeficiency virus type I enhancer binding protein 2
MFN2	0.605	HSG; MARF; CMT2A; CPRP1; CMT2A2; KIAA0214	NM_014874	mitofusin 2
LOXL1	0.603	LOL; LOXL	NM_005576	lysyl oxidase-like 1
ARFIP1	0.603	HSU52521; MGC117369	NM_001025595	ADP-ribosylation factor interacting protein 1 (arfaptin 1)
TRIM55	0.602	RNF29; MURF-2	NM_184086	tripartite motif-containing 55
KHK	0.602	TRAP1	NM_000221	ketohexokinase (fructokinase)
FLJ10159	0.601	FLJ10159	NM_018013	hypothetical protein FLJ10159
CNTN1	0.601	F3; GP135	NM_001843	contactin 1
ARHGAP9	0.601	10C; RGL1; MGC1295; FLJ16525	NM_032496	Rho GTPase activating protein 9
HIST1H2BC	0.601	H2B.1; H2B/l; H2BFL; dJ221C16.3	NM_003526	histone 1, H2bc
LOC196394	0.6	LOC196394	NM_207337	hypothetical protein LOC196394
SLC7A10	0.598	asc-1; HASC-1; FLJ20839	NM_019849	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10
DDX46	0.598	MGC9936; FLJ25329; KIAA0801	NM_014829	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
ZNF451	0.598	COASTER; FLJ90693; KIAA0576; MGC26701; dJ417I1.1	NM_001031623	zinc finger protein 451
ATP6V1G2	0.598	NG38; ATP6G; VMA10; ATP6G2	NM_130463	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2
LOC92689	0.598	LOC92689	NM_138389	hypothetical protein BC001096
SCIN	0.597	KIAA1905	NM_033128	scinderin
JAG1	0.597	AGS; AHD; AWS; HJ1; CD339; JAGL1; MGC104644	NM_000214	jagged 1 (Alagille syndrome)
SYN3	0.597	SYN3	NM_133633	synapsin III
ASCC3L1	0.595	BRR2; HELIC2; U5-200KD	NM_014014	activating signal cointegrator 1 complex subunit 3-like 1
ADAM9	0.595	MCMP; MDC9; Mltng; KIAA0021	NM_003816	ADAM metallopeptidase domain 9 (meltrin gamma)
IGF2	0.595	INSIGF; pp9974; C11orf43; FLJ22066; FLJ44734	NM_000612	insulin-like growth factor 2 (somatomedin A)
SERPINF1	0.594	PEDF; EPC-1; PIG35	NM_002615	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
ETFDH	0.593	MADD; ETFQO	NM_004453	electron-transferring-flavoprotein dehydrogenase
SH2D3C	0.593	CHAT; NSP3; FLJ39664; PRO34088	NM_170600	SH2 domain containing 3C
Mar-06	0.592	TEB4; RNF176; KIAA0597; MARCH-VI	NM_005885	membrane-associated ring finger (C3HC4) 6
NIP30	0.592	NIP30; CDA10; CDA018; FLJ21799; MGC74898	NM_024946	NEFA-interacting nuclear protein NIP30
IFNAR2	0.592	IFN-R; IFNABR; IFNARB; IFN-alpha-REC	NM_207584	interferon (alpha, beta and omega) receptor 2
EFEMP1	0.591	DHRD; DRAD; FBNL; MLVT; MTLV; S1-5; FBLN3; FLJ35535; MGC111353	NM_004105	EGF-containing fibulin-like extracellular matrix protein 1
LRRC8C	0.591	AD158; FAD158; MGC138551; DKFZp586J1119	NM_032270	leucine rich repeat containing 8 family, member C
RASGRP2	0.59	CDC25L; CALDAG-GEFI	NM_005825	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
GRIN1	0.59	NR1; NMDA1; NMDAR1	NM_007327	glutamate receptor, ionotropic, N-methyl D-aspartate 1
SNAP23	0.589	SNAP23A; SNAP23B; HsT17016	NM_130798	synaptosomal-associated protein, 23kDa
NRXN2	0.589	KIAA0921	NM_015080	neurexin 2
CAST	0.589	BS-17; MGC9402	NM_173060	calpastatin
C9ORF123	0.589	MGC4730	NM_033428	chromosome 9 open reading frame 123
CAMK2N2	0.589	CAM-KIIN	NM_033259	calcium/calmodulin-dependent protein kinase II inhibitor 2
STARD5	0.588	MGC10327	NM_181900	START domain containing 5
ACSBG1	0.588	BG1; BGM; hBG1; hsBG; GR-LACS; FLJ30320; KIAA0631; MGC14352	NM_015162	acyl-CoA synthetase bubblegum family member 1
RNF39	0.587	HZF; HZFW; LIRF; HZFw1	NM_025236	ring finger protein 39
FCHO1	0.586	KIAA0290	NM_015122	FCH domain only 1
BCAP29	0.585	BAP29; DKFZp686M2086	NM_001008406	B-cell receptor-associated protein 29
TRPV2	0.585	VRL; VRL1; VRL-1; MGC12549	NM_016113	transient receptor potential cation channel, subfamily V, member 2
ADAMTS2	0.584	NPI; PCINP; PCPNI; hPCPNI; ADAM-TS2; ADAMTS-3	NM_021599	ADAM metallopeptidase with thrombospondin type 1 motif, 2
DUSP16	0.583	MKP7; MKP-7; KIAA1700; MGC129701; MGC129702	NM_030640	dual specificity phosphatase 16
GPC3	0.583	SGB; DGSX; SDYS; SGBS; SGBS1	NM_004484	glypican 3
KIAA1033	0.583	KIAA1033	NM_015275	KIAA1033
VPS24	0.583	NEDF; CHMP3; CGI-149	NM_016079	vacuolar protein sorting 24 homolog (S. cerevisiae)
KCTD8	0.582	C3orf57	NM_198353	potassium channel tetramerisation domain containing 8
ABLIM3	0.582	HMFN1661	NM_014945	actin binding LIM protein family, member 3
C1QTNF1	0.581	GIP; CTRP1; ZSIG37; FLJ90694	NM_030968	C1q and tumor necrosis factor related protein 1
P2RX5	0.579	P2X5; P2X5R; MGC47755	NM_175081	purinergic receptor P2X, ligand-gated ion channel, 5
HESX1	0.579	RPX; MGC138294	NM_003865	homeobox, ES cell expressed 1
PCAF	0.579	CAF; GCN5; GCN5L; P/CAF; GCN5L1	NM_003884	p300/CBP-associated factor
SYNGR1	0.578	MGC:1939	NM_145731	synaptogyrin 1
PRRX1	0.578	PMX1; PRX1; PHOX1	NM_006902	paired related homeobox 1
HMFN0839	0.577	LPAAT-THETA; MGC11324	NM_032717	lysophosphatidic acid acyltransferase theta
FLJ32028	0.577	FLJ32028	NM_152680	transmembrane protein 154
PTHR2	0.576	PTHR2	NM_005048	parathyroid hormone receptor 2
ABHD7	0.576	EPHXRP; FLJ90341	NM_173567	abhydrolase domain containing 7
EGFL9	0.576	MGC2487; MGC111055	NM_023932	EGF-like-domain, multiple 9
FOXF1	0.576	FKHL5; FREAC1; MGC105125	NM_001451	forkhead box F1
MAF	0.575	MGC71685	NM_005360	v-maf musculoaponeurotic fibrosarcoma

				oncogene homolog (avian)
CD99L2	0.575	MIC2L1; DKFZp761H2024	NM_134446	CD99 molecule-like 2
CORO1A	0.574	p57; TACO; CLABP; HCORO1; CLIPINA; FLJ41407; MGC117380	NM_007074	coronin, actin binding protein, 1A
LOC492311	0.574	LOC492311	NM_001007189	similar to bovine IgA regulatory protein
HRASLS	0.573	A-C1; HSD28; HRASLS1; H-REV107	NM_020386	HRAS-like suppressor
OSMR	0.573	OSMRB; MGC75127	NM_003999	oncostatin M receptor
COL16A1	0.572	447AA; FP1572	NM_001856	collagen, type XVI, alpha 1
QSCN6	0.572	Q6; QSOX1	NM_002826	quiescin Q6
NOV	0.572	CCN3; NOVH; IGFBP9	NM_002514	nephroblastoma overexpressed gene
GABRA5	0.569	MGC138184	NM_000810	gamma-aminobutyric acid (GABA) A receptor, alpha 5
CDS1	0.568	CDS	NM_001263	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1
MMP24	0.567	MMP25; MT-MMP5; MT5-MMP	NM_006690	matrix metallopeptidase 24 (membrane-inserted)
SYT4	0.567	HsT1192; KIAA1342	NM_020783	synaptotagmin IV
RAB40B	0.566	RAR; SEC4L; FLJ42385	NM_006822	RAB40B, member RAS oncogene family
GDF15	0.566	PDF; MIC1; PLAB; MIC-1; NAG-1; PTGFB; GDF-15	NM_004864	growth differentiation factor 15
CLYBL	0.565	CLB; bA134O15.1	NM_206808	citrate lyase beta like
EMR2	0.565	CD312; DKFZp781B135	NM_013447	egf-like module containing, mucin-like, hormone receptor-like 2
IL13RA1	0.564	NR4; CD213A1; IL-13Ra	NM_001560	interleukin 13 receptor, alpha 1
C20ORF19	0.564	HT013; MGC102941; MGC141930; DKFZP586H021	NM_018474	chromosome 20 open reading frame 19
KYNU	0.563	DLK1	NM_003937	kynureninase (L-kynurenine hydrolase)
AIG1	0.563	AIG-1; FLJ10485; dJ95L4.1; RP1-95L4.1; DKFZp686F03136	NM_016108	androgen-induced 1
MTHFD2L	0.563	FLJ13105; MGC45532; MGC72244	NM_001004346	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
METRN	0.562	MGC2601; C16orf23; c380A1.2	NM_024042	meteorin, glial cell differentiation regulator
MAP2K5	0.562	MEK5; MAPKK5; PRKMK5; HsT17454	NM_002757	mitogen-activated protein kinase kinase 5
LPPR4	0.562	LPPR4; PHP1; PRG1; PRG-1; KIAA0455; RP4-788L13.1	NM_014839	plasticity related gene 1
SPHK1	0.562	SPHK	NM_021972	sphingosine kinase 1
SYT15	0.562	sytXV; CHR10SYT; syt XV-a	NM_181519	synaptotagmin XV
DOCK11	0.56	ZIZ2; FLJ32122; FLJ43653; bB128O4.1	NM_144658	dedicator of cytokinesis 11
IRAK3	0.559	IRAK-M	NM_007199	interleukin-1 receptor-associated kinase 3
PPAP2B	0.557	LPP3; VCIP; Dri42; PAP-2b; PAP2-b; MGC15306; PAP2-beta	NM_003713	phosphatidic acid phosphatase type 2B
TMEM42	0.557	MGC29956	NM_144638	transmembrane protein 42
HAGHL	0.557	MGC2605	NM_032304	hydroxyacylglutathione hydrolase-like
CX3CL1	0.556	NTN; NTT; CXC3; CXC3C; SCYD1; ABCD-3; C3Xkine; fractalkine; neurotactin	NM_002996	chemokine (C-X3-C motif) ligand 1
GPR176	0.555	GPR; Gm1012	NM_007223	G protein-coupled receptor 176
LY96	0.554	MD-2	NM_015364	lymphocyte antigen 96
ZNF25	0.554	Zfp9; KOX19; FLJ31890; DKFZp564C206	NM_145011	zinc finger protein 25
TMEM54	0.553	BCLP; CAC1; CAC-1; MGC10137	NM_033504	transmembrane protein 54
NALP1	0.553	CARD7; DEFCAP; PP1044; KIAA0926; DEFCAP-L/S; DKFZp586O1822	NM_001033053	NACHT, leucine rich repeat and PYD (pyrin domain) containing 1
FKBP5	0.553	P54; FKBP51; FKBP54; PPIase; Ptg-10; MGC111006	NM_004117	FK506 binding protein 5
GNE	0.552	NM; DMRV; IBM2; Uae1; GLCNE	NM_005476	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
TMEM106C	0.552	MGC5576; MGC111210	NM_024056	transmembrane protein 106C
TNFRSF14	0.551	TR2; ATAR; HVEA; HVEM; LIGHTR	NM_003820	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)
NEK6	0.55	SID6-1512	NM_014397	NIMA (never in mitosis gene a)-related kinase 6
LOC221091	0.549	LOC221091; MGC61707	NM_203422	similar to hypothetical protein
XPO6	0.549	EXP6; RANBP20; FLJ22519; KIAA0370	NM_015171	exportin 6
CNIH3	0.549	FLJ38993	NM_152495	cornichon homolog 3 (Drosophila)
PRAF2	0.549	JM4	NM_007213	PRA1 domain family, member 2
CDH13	0.549	CDHH	NM_001257	cadherin 13, H-cadherin (heart)
VEPH1	0.548	FLJ12604; KIAA1692; MGC111426; MGC126709; MGC142115	NM_024621	ventricular zone expressed PH domain homolog 1 (zebrafish)
EBF3	0.547	COE3; O/E-2	NM_001005463	early B-cell factor 3
CXCL12	0.547	PBSF; SDF1; SDF1A; SDF1B; TPAR1; SCYB12; SDF-1a; SDF-1b; TLSF-a; TLSF-b	NM_000609	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
RECQL	0.543	RecQ1; RECQL1	NM_032941	RecQ protein-like (DNA helicase Q1-like)
BLVRA	0.543	BLVR; BVRA	NM_000712	biliverdin reductase A
ATP8B3	0.542	ATPIK	NM_138813	ATPase, Class I, type 8B, member 3
C12ORF23	0.541	FLJ11721; FLJ13959; MGC17943	NM_152261	chromosome 12 open reading frame 23
PRRG1	0.541	PRGP1	NM_000950	proline rich Gla (G-carboxyglutamic acid) 1
TPBG	0.541	5T4; M6P1; 5T4-AG	NM_006670	trophoblast glycoprotein
NFIC	0.541	CTF; NFI; CTF5; NF-I; MGC20153	NM_005597	nuclear factor I/C (CCAAT-binding transcription factor)
BCAN	0.54	BEHAB; CSPG7; MGC13038	NM_021948	brevican
GPRC5B	0.539	RAIG2; RAIG-2	NM_016235	G protein-coupled receptor, family C, group 5, member B
C6ORF117	0.539	RP11-51G5.2	NM_138409	chromosome 6 open reading frame 117
LDHD	0.538	MGC57726	NM_194436	lactate dehydrogenase D
UNQ3045	0.538	UNQ3045	NM_207409	AAAL3045
C1R	0.537	VIM	NM_001733	complement component 1, r subcomponent
HEY1	0.535	CHF2; OAF1; HERP2; HESR1; HRT-1; MGC1274	NM_012258	hairy/enhancer-of-split related with YRPW motif 1
NIFUN	0.535	ISCU; ISU2; NIFU; MGC74517; 2310020H20Rik	NM_014301	NifU-like N-terminal domain containing
LOC285989	0.535	LOC285989	NM_001013258	zinc finger protein 789
KCTD10	0.535	ULRO61; MSTP028; FLJ41739	NM_031954	potassium channel tetramerisation domain containing 10
FKBP10	0.535	FKBP65; hFKBP65; FLJ22041	NM_021939	FK506 binding protein 10, 65 kDa
PTX3	0.534	TSG-14; TNFAIP5	NM_002852	pentraxin-related gene, rapidly induced by IL-1 beta
RBP7	0.534	CRBP4; CRBPIV; MGC70641	NM_052960	retinol binding protein 7, cellular

STAT5A	0.534	MGF; STAT5	NM_003152	signal transducer and activator of transcription 5A
KNTC2	0.534	HEC; HEC1	NM_006101	kinetochore associated 2
CYP27B1	0.533	VDR; CP2B; CYP1; PDDR; VDD1; VDDR; VDDRI; CYP27B; P450c1; CYP1alpha	NM_000785	cytochrome P450, family 27, subfamily B, polypeptide 1
RUNX1	0.533	AML1; CBFA2; EVI-1; AMLCR1; PEBP2aB; AML1-EVI-1	NM_001754	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)
EGFR	0.531	ERBB; mENA; ERBB1	NM_201283	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
TEX14	0.531	TEX14	NM_031272	testis expressed sequence 14
GPR177	0.531	MRP; WLS; C1orf139; FLJ23091; MGC14878; MGC131760	NM_001002292	G protein-coupled receptor 177
CUZD1	0.53	ERG-1; UO-44	NM_022034	CUB and zona pellucida-like domains 1
CRAT	0.529	CAT1	NM_000755	carnitine acetyltransferase
CPNE3	0.527	CPN3; PRO1071; KIAA0636	NM_003909	copine III
OSBPL5	0.527	ORP5; OBPH1; FLJ42929	NM_020896	oxysterol binding protein-like 5
SEMA3C	0.526	SemE; SEMAE	NM_006379	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
CD36	0.525	FAT; GP4; GP3B; GPIV; PASIV; SCARB3	NM_001001548	CD36 molecule (thrombospondin receptor)
VAMP4	0.525		NM_201994	
FLJ20105	0.524	FLJ20105; MGC131695	NM_017669	FLJ20105 protein
KIAA0367	0.524	BMCC1; BNIPXL; A214N16.3; bA214N16.3	NM_015225	KIAA0367
ANTXR1	0.522	ATR; TEM8; FLJ10601; FLJ11298; FLJ21776	NM_053034	anthrax toxin receptor 1
SPOCK2	0.522	testican-2	NM_014767	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2
NINJ1	0.521	NIN1; NINJURIN	NM_004148	ninjurin 1
NAV3	0.52	POMFIL1; unc53H3; KIAA0938; STEERIN3	NM_014903	neuron navigator 3
ZDHHC19	0.518		NM_144637	
MGLL	0.518	MGL; HU-K5	NM_001003794	monoglyceride lipase
MGC72104	0.518	MGC72104	NM_207350	similar to FRG1 protein (FSHD region gene 1 protein)
DUSP6	0.518	MKP3; PYST1	NM_001946	dual specificity phosphatase 6
CYBASC3	0.517	MGC20446	NM_153611	cytochrome b, ascorbate dependent 3
PRG2	0.515	MBP; BMPG; MGC14537	NM_002728	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)
DGKA	0.513	DAGK; DAGK1; MGC12821; MGC42356; DGK-alpha	NM_201554	diacylglycerol kinase, alpha 80kDa
SNTB2	0.513	SNT3; SNTL; SNT2B2; EST25263; D16S2531E	NM_006750	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)
ARHGAP22	0.512	RhoGAP2	NM_021226	Rho GTPase activating protein 22
DIDO1	0.511	BYE1; DIO1; DATF1; DIDO2; DIDO3; DIO-1; FLJ11265; KIAA0333; MGC16140; C20orf158; dJ885L7.8; DKFZp434P1115	NM_080796	death inducer-obliterator 1
TLOC1	0.511	HTP1; Dtrp1; SEC62; FLJ32803	NM_003262	translocation protein 1
EVI5L	0.511	EVI5L	NM_145245	ecotropic viral integration site 5-like
EMILIN1	0.51	gp115; EMILIN; EMILIN-1; DKFZP586M121	NM_007046	elastin microfibril interfacer 1
C14ORF149	0.51	FLJ25436	NM_144581	chromosome 14 open reading frame 149
CHST8	0.51	CDKN2C	NM_022467	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8
RGL1	0.509	RGL; KIAA0959	NM_015149	ral guanine nucleotide dissociation stimulator-like 1
BCL6	0.509	BCL5; LAZ3; BCL6A; ZNF51; ZBTB27	NM_001706	B-cell CLL/lymphoma 6 (zinc finger protein 51)
CAPN2	0.509	mCANP; CANPL2; CANPml	NM_001748	calpain 2, (m/II) large subunit
PCSK9	0.509	FH3; NARC1; NARC-1; HCHOLA3	NM_174936	proprotein convertase subtilisin/kexin type 9
CLIC6	0.508	CLIC1L	NM_053277	chloride intracellular channel 6
SSSCA1	0.508	p27	NM_006396	Sjogren's syndrome/scleroderma autoantigen 1
GPR177	0.508	MRP; WLS; C1orf139; FLJ23091; MGC14878; MGC131760	NM_001002292	G protein-coupled receptor 177
SGCD	0.507	SGD; DAGD; 35DAG; CMD1L; SGCDP; MGC22567; SG-delta	NM_172244	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
CALCB	0.506	CALC2; CGRP2; CGRP-II; FLJ30166	NM_000728	calcitonin-related polypeptide, beta
ATCAY	0.506	CLAC; BNIP-H; KIAA1872	NM_033064	ataxia, cerebellar, Cayman type (caytaxin)
C9ORF125	0.506	MGC12992	NM_032342	chromosome 9 open reading frame 125
ATP6V0A4	0.506	A4; STV1; VPH1; VPP2; RTA1C; RTADR; ATP6N2; RDRTA2; ATP6N1B; MGC130016; MGC130017	NM_130840	ATPase, H+ transporting, lysosomal V0 subunit a4
SFXN3	0.505	SFX3; BA108L7.2	NM_030971	sideroflexin 3
EHD2	0.505	PAST2	NM_014601	EH-domain containing 2
MOBKL2C	0.504	MOB3C; MGC26743	NM_201403	MOB1, Mps One Binder kinase activator-like 2C (yeast)
FUCA2	0.503	MGC1314; dJ20N2.5; RP1-20N2.5	NM_032020	fucosidase, alpha-L- 2, plasma
PRICKLE2	0.503	DKFZp686D143; DKFZp686M031; DKFZp686H1748	NM_198859	prickle-like 2 (Drosophila)
DDEF2	0.503	PAP; PAG3; AMAP2; SHAG1; KIAA0400; Pap-alpha	NM_003887	development and differentiation enhancing factor 2
TJP3	0.503	ZO-3; MGC119546	NM_014428	tight junction protein 3 (zona occludens 3)
MORC4	0.502	ZCW4; ZCWCC2; FLJ11565; dJ75H8.2	NM_024657	MORC family CW-type zinc finger 4
ACSL3	0.502	ACS3; FACL3; PRO2194	NM_004457	acyl-CoA synthetase long-chain family member 3
HSD11B1	0.501	HDL; 11-DH; HSD11; HSD11B; HSD11L; MGC13539; 11-beta-HSD1	NM_005525	hydroxysteroid (11-beta) dehydrogenase 1
CFH	0.501	FH; HF; HF1; HF2; HUS; FHL1; CFHL3; MGC88246	NM_001014975	complement factor H
ZAK	0.5	ZAK; AZK; MLT; MRK; MLK7; MLTK; mlklak	NM_133646	sterile alpha motif and leucine zipper containing kinase AZK
PARP12	0.5	ZC3H1; PARP-12; ZC3HDC1; FLJ22693	NM_022750	poly (ADP-ribose) polymerase family, member 12
PNCK	0.5		NM_198452	
HTR7	0.499	5-HT7	NM_000872	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)
FLJ34922	0.498	SLFN8/9; FLJ34922	NM_152270	schlafen family member 11
MGC15476	0.498	MGC15476	NM_145056	thymus expressed gene 3-like
NPY	0.496	PYY4	NM_000905	neuropeptide Y

CALCA	0.494	CT; KC; CGRP; CALC1; CGRP1; CGRP-I; MGC126648	NM_001033953	calcitonin/calcitonin-related polypeptide, alpha
FHOD3	0.493	FHOS2; Formactin2	NM_025135	formin homology 2 domain containing 3
FLJ20160	0.492	FLJ20160	NM_017694	FLJ20160 protein
PPM2C	0.492	PDH; PDP; PDP1; PDPC; FLJ32517; MGC119646	NM_018444	protein phosphatase 2C, magnesium-dependent, catalytic subunit
FBLN5	0.491	EVEC; UP50; ARMD3; DANCE; FLJ90059	NM_006329	fibulin 5
CRYL1	0.491	MGC149525; MGC149526	NM_015974	crystallin, lambda 1
PIP5K2A	0.491	PIPK; PIP5KII-alpha	NM_005028	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha
TXNDC5	0.491	ERP46; UNQ364; EndoPDI; MGC3178	NM_030810	thioredoxin domain containing 5
SIRT1	0.49	SIR2L1	NM_012238	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)
GNPDA2	0.49	SB52	NM_138335	glucosamine-6-phosphate deaminase 2
C14ORF106	0.49	FLJ11186; KIAA1903; HSA242977	NM_018353	chromosome 14 open reading frame 106
GNLY	0.49	519; LAG2; NKG5; LAG-2; D2S69E; TLA519; lymphokine	NM_012483	granulysin
MATN2	0.489	MATN2	NM_030583	matrilin 2
FLJ22746	0.488	FLJ22746	NM_024785	family with sequence similarity 124B
RGC32	0.487	RGC32; KIAA0564; MGC87338; bA157L14.2	NM_014059	response gene to complement 32
HPCAL1	0.487	BDR1; HLP2; VILIP-3	NM_002149	hippocalcin-like 1
Sep-03	0.486	SEP3; MGC133218; bK250D10.3	NM_019106	septin 3
GALNT5	0.486	GALNAC-T5	NM_014568	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)
SLC15A3	0.485	OCTP; PHT2; PTR3; hPTR3; FLJ26631	NM_016582	solute carrier family 15, member 3
ABTB1	0.485	BPOZ; EF1ABP; PP2259; MGC20585	NM_172027	ankyrin repeat and BTB (POZ) domain containing 1
SP110	0.485	VODI; IFI41; IFI75; FLJ22835	NM_004510	SP110 nuclear body protein
C7ORF10	0.485	ORF19; DERP13; FLJ11808	NM_024728	chromosome 7 open reading frame 10
MCOLN2	0.484	TRPML2; FLJ36691	NM_153259	mucolipin 2
TMEM30A	0.484	CDC50A; C6orf67; FLJ10856	NM_018247	transmembrane protein 30A
RGS3	0.483	C2PA; RGP3; FLJ20370; FLJ31516; FLJ90496; PDZ-RGS3	NM_144489	regulator of G-protein signalling 3
FAM19A3	0.482	TAFA3; TAFA-3; MGC138473; RP11-426L16.6	NM_182759	family with sequence similarity 19 (chemokine (C-C motif)-like), member A3
NTNG1	0.481	Lmnt1; KIAA0976	NM_014917	netrin G1
SH3GL3	0.48	CNSA3; EEN-B2; SH3D2C; SH3P13; HsT19371; EEN-2B-L3	NM_003027	SH3-domain GRB2-like 3
EGFR	0.479	ERBB; mENA; ERBB1	NM_005228	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
MEF2D	0.479	DKFZp686I1536	NM_005920	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)
FNDC6	0.479	MGC34923	NM_144717	fibronectin type III domain containing 6
CELSR2	0.479	EGFL2; MEGF3; CDHF10; FLJ34118; FLJ42737; FLJ45143; KIAA0279; Flamingo1	NM_001408	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)
BPGM	0.478	BPGM	NM_001724	2,3-bisphosphoglycerate mutase
NPDC1	0.477	CAB; CAB-; CAB1; CAB-1; DKFZP586J0523	NM_015392	neural proliferation, differentiation and control, 1
SIPA1	0.474	SPA1; MGC17037; MGC102688	NM_153253	signal-induced proliferation-associated gene 1
PHLDA3	0.474	TIH1	NM_012396	pleckstrin homology-like domain, family A, member 3
TEX2	0.474	HT008; TMEM96; KIAA1738; DKFZp781G0721	NM_018469	testis expressed sequence 2
LGALS3	0.473	GAL3; MAC2; CBP35; GALBP; LGALS2	NM_002306	lectin, galactoside-binding, soluble, 3 (galectin 3)
PLCL2	0.473	PLCE2; FLJ13484; KIAA1092	NM_015184	phospholipase C-like 2
ARL4	0.473	ARL4	NM_005738	ADP-ribosylation factor-like 4A
RBPSUH	0.472	csl; CBF1; KBF2; RBP-J; RBPJK; IGKJRB; IGKJRB1; MGC61669	NM_005349	recombining binding protein suppressor of hairless (Drosophila)
NMNAT2	0.472	PNAT2; PNAT-2; C1orf15; MGC2756; KIAA0479	NM_015039	nicotinamide nucleotide adenylyltransferase 2
ACSM3	0.469	SA; SAH	NM_202000	acyl-CoA synthetase medium-chain family member 3
CARD11	0.469	BIMP3; CARMA1; MGC133069	NM_032415	caspase recruitment domain family, member 11
ELAVL2	0.468	HUB; HELN1; HEL-N1	NM_004432	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)
TCEAL7	0.468	MGC23947; MPMGp800C04260Q003	NM_152278	transcription elongation factor A (SII)-like 7
DEPDC6	0.466	DEP.6; FLJ12428; FLJ13854; DKFZp564B1778	NM_022783	DEP domain containing 6
GLI3	0.465	PHS; ACLS; GCPS; PAPA; PAPB; PAP-A; PAPA1; PPDIV	NM_000168	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
FYCO1	0.464	RUFY3; ZFYVE7; FLJ13335; MGC126517; MGC126519	NM_024513	FYVE and coiled-coil domain containing 1
C14ORF138	0.464	FLJ13920	NM_024558	chromosome 14 open reading frame 138
EVC	0.463		NM_014556	
BTN3A2	0.463	BTF4; BT3.2; BT3.3	NM_007047	butyrophilin, subfamily 3, member A2
AMPH	0.463	AMPH1	NM_001635	amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen)
SCARA3	0.463	CSR; APC7; CSR1; MSLR1; MSRL1	NM_016240	scavenger receptor class A, member 3
GLI2	0.462	THP2	NM_005270	GLI-Kruppel family member GLI2
DKFZP586H2123	0.461	DKFZP586H2123; RAMP; FP938	NM_001001991	regeneration associated muscle protease
TSPAN33	0.461	PEN; MGC50844	NM_178562	tetraspanin 33
COL6A3	0.461	FLJ34702; DKFZp686D23123; DKFZp686K04147	NM_057164	collagen, type VI, alpha 3
ACVRL1	0.461	HHT; ALK1; HHT2; ORW2; SKR3; ALK-1; ACVRLK1	NM_000020	activin A receptor type II-like 1
PSG2	0.461	CEA; PSG1; PSBG2; PSGGB	NM_031246	pregnancy specific beta-1-glycoprotein 2
HSA9761	0.46	DIMT1; HSA9761	NM_014473	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)
GALNTL2	0.46	GALNT7; GALNT13; GALNT15; DKFZp686H1113	NM_054110	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2
HIST1H2AC	0.459	H2A/l; H2AFL; MGC99519; dJ221C16.4	NM_003512	histone 1, H2ac
ERAF	0.459	AHSP; EDRF	NM_016633	erythroid associated factor
PGBD5	0.459	FLJ11413; DKFZp761A0620	NM_024554	piggyBac transposable element derived 5
HSPB6	0.459	Hsp20; FLJ32389	NM_144617	heat shock protein, alpha-crystallin-related,

				B6
HIST2H2BE	0.458	H2B; GL105; H2B.1; H2B/q; H2BFQ; MGC129733; MGC129734	NM_003528	histone 2, H2be
SDSL	0.458	SDS-RS1	NM_138432	serine dehydratase-like
C5ORF21	0.457	DKFZP564D172	NM_032042	chromosome 5 open reading frame 21
NCALD	0.457	MGC33870; MGC74858	NM_032041	neurocalcin delta
INPP1	0.456	MGC110984	NM_002194	inositol polyphosphate-1-phosphatase
WIG1	0.455	WIG1; WIG-1; PAG608; FLJ12296; MGC10613	NM_152240	zinc finger, matrin type 3
LRCH2	0.455	KIAA1495; dA204F4.4	NM_020871	leucine-rich repeats and calponin homology (CH) domain containing 2
BDNF	0.455	MGC34632	NM_001709	brain-derived neurotrophic factor
PRSS23	0.455	SIG13; SPUVE; ZSIG13; MGC5107	NM_007173	protease, serine, 23
APOD	0.454	APOD	NM_001647	apolipoprotein D
PBX1	0.454	MGC126627; DKFZp686B09108	NM_002585	pre-B-cell leukemia transcription factor 1
GAS1	0.452	HAS3	NM_002048	growth arrest-specific 1
CLIPR-59	0.452	CLIPR-59; CLIPR59; FLJ33413; DKFZp586N1922	NM_015526	CLIP-170-related protein
SLC16A10	0.451	TAT1; PRO0813	NM_018593	solute carrier family 16, member 10 (aromatic amino acid transporter)
SLC25A12	0.45	ARALAR; ARALAR1	NM_003705	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
OBFC2A	0.45		NM_022837	
LTBP2	0.45	LTBP3; MSTP031; C14orf141	NM_000428	latent transforming growth factor beta binding protein 2
C9ORF127	0.45	NGX6; NAG-5; MGC120460; RP11-112J3.10	NM_016446	chromosome 9 open reading frame 127
PRG1	0.45	PPG; PRG; MGC9289; FLJ12930; SERGLYCIN	NM_002727	proteoglycan 1, secretory granule
SPG3A	0.45	ATL1; FSP1; GBP3; SPG3; AD-FSP; atlastin1	NM_181598	spastic paraplegia 3A (autosomal dominant)
FOSL1	0.449	FRA1; fra-1	NM_005438	FOS-like antigen 1
KLK6	0.449	hK6; Bssp; Klk7; SP59; ZYME; PRSS9; PRSS18; MGC9355; NEUROSIN	NM_002774	kallikrein 6 (neurosin, zyme)
RAB13	0.448	GIG4	NM_002870	RAB13, member RAS oncogene family
FADS3	0.447	CYB5RP; LLCDL3	NM_021727	fatty acid desaturase 3
C1ORF94	0.446	MGC15882	NM_032884	chromosome 1 open reading frame 94
SHC3	0.446	NSHC; SHCC; N-Shc	NM_016848	SHC (Src homology 2 domain containing) transforming protein 3
GRIA3	0.445	GLUR3; GLURC; gluR-C; GLUR-K3	NM_181894	glutamate receptor, ionotrophic, AMPA 3
CAPN5	0.445	HTRA3; nCL-3; FLJ46245	NM_004055	calpain 5
NUDT6	0.445	gfg; bFGF; FGF-2; gfg-1; ASFGF2; FGF-AS; FGF2AS	NM_007083	nudix (nucleoside diphosphate linked moiety X)-type motif 6
LACTB2	0.444	CGI-83	NM_016027	lactamase, beta 2
ALOX5	0.444	5-LO; 5LPG; LOG5	NM_000698	arachidonate 5-lipoxygenase
MYO5A	0.444	GS1; MYO5; MYH12; MYR12; MYOXIN; myosin V; myosin Va	NM_000259	myosin VA (heavy polypeptide 12, myoxin)
NRIP3	0.443	C11orf14; NY-SAR-105	NM_020645	nuclear receptor interacting protein 3
RABGAP1L	0.443	HHL; EVI5; TBC1D18; RP1-102G20.1; DKFZp686E1450	NM_014857	RAB GTPase activating protein 1-like
LRFN5	0.443	FLJ30803; C14orf146; DKFZp686G0210	NM_152447	leucine rich repeat and fibronectin type III domain containing 5
FLJ21986	0.441	FLJ21986; FLJ26813	NM_024913	hypothetical protein FLJ21986
KISS1R	0.441	GPR54; AXOR12; HOT7T175	NM_032551	KISS1 receptor
PHLDA1	0.439	PHRIP; TDAG51; DT1P1B11; MGC131738	NM_007350	pleckstrin homology-like domain, family A, member 1
UBE2E2	0.439	UBCH8; FLJ25157	NM_152653	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
NPAL3	0.437	DJ462O23.2; RP3-462O23.3; DKFZp686E22155	NM_020448	NIPA-like domain containing 3
C6ORF192	0.436	dJ55C23.6	NM_052831	chromosome 6 open reading frame 192
HSPA4	0.434	RY; APG-2; hsp70; hsp70RY; HS24/P52; MGC131852	NM_002154	heat shock 70kDa protein 4
RECQL	0.434	RecQ1; RECQL1	NM_002907	RecQ protein-like (DNA helicase Q1-like)
PAPPA	0.434	PAPA; DIPLA1; PAPP-A; PAPPA1; ASBABP2; IGFBP-4ase	NM_002581	pregnancy-associated plasma protein A, pappalysin 1
SV2A	0.433	SV2; KIAA0736	NM_014849	synaptic vesicle glycoprotein 2A
ITGA2	0.432	BR; GPIa; CD49B; VLA-2; VLAA2	NM_002203	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
KIAA1913	0.432	TTMC	NM_052913	KIAA1913
COPZ2	0.432	COPZ2	NM_016429	coatomer protein complex, subunit zeta 2
GLS2	0.431	GA; GLS; LGA; hLGA; MGC71567	NM_013267	glutaminase 2 (liver, mitochondrial)
AFP	0.431	FETA; HPAFP	NM_001134	alpha-fetoprotein
MGC17330	0.431	MGC17330; HGFL; hHGFL(S)	NM_052880	HGFL gene
GOLPH4	0.43	P138; GIMPC; GPP130	NM_014498	golgi phosphoprotein 4
GPR137B	0.428	TM7SF1	NM_003272	G protein-coupled receptor 137B
CAST	0.428	BS-17; MGC9402	NM_001750	calpastatin
HYAL1	0.427	NAT6; LUCA1; HYAL-1; MGC45987	NM_153281	hyaluronoglucosaminidase 1
ARHGDIB	0.427	D4; GDIA2; GDID4; LYGDI; Ly-GDI; RAP1GN1	NM_001175	Rho GDP dissociation inhibitor (GDI) beta
CASP1	0.426	ICE; P45; IL1BC	NM_033294	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
STS-1	0.426	STS-1; p70; KIAA1959; MGC15437	NM_032873	Cbl-interacting protein Sts-1
LPPR2	0.425	LPPR2; PRG-4; FLJ13055; DKFZp761E1121	NM_022737	lipid phosphate phosphatase-related protein type 2
NIN	0.425	KIAA1565	NM_020921	ninein (GSK3B interacting protein)
KCNS3	0.425	KV9.3; MGC9481	NM_002252	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
UGCG	0.424	GCS	NM_003358	UDP-glucose ceramide glucosyltransferase
OSBPL10	0.424	ORP10; OSBP9; FLJ20363	NM_017784	oxysterol binding protein-like 10
CCND3	0.423	CCND3	NM_001760	cyclin D3
KDELR3	0.423	ERD2L3	NM_016657	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
TNFRSF1B	0.422	p75; TBPII; TNFBR; TNFR2; CD120b; TNFR80; TNF-R75; p75TNFR; TNF-R-II	NM_001066	tumor necrosis factor receptor superfamily, member 1B
PPP1R3C	0.422	PPP1R5	NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C
ACOX2	0.421	BCOX; BRCOX; THCCox; BRCACOX	NM_003500	acyl-Coenzyme A oxidase 2, branched chain
SLC16A2	0.421	AHDS; MCT7; MCT8; XPCT; DXS128; DXS128E	NM_006517	solute carrier family 16, member 2 (monocarboxylic acid transporter 8)
MASP1	0.419	MASP; RaRF; CRARF; PRSS5; CRARF1; FLJ26383; MGC126283; MGC126284;	NM_001031849	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive

		DKFZp686I01199		factor)
TAP2	0.418	APT2; PSF2; ABC18; ABCB3; RING11; D6S217E	NM_000544	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
G0S2	0.417	RP1-28O10.2	NM_015714	G0/G1switch 2
TBC1D23	0.417	NS4ATP1; FLJ11046; DKFZp667G062	NM_018309	TBC1 domain family, member 23
SLC30A3	0.417	ZNT3 | NM_003459 | solute carrier family 30 (zinc transporter), member 3		
FCRLM2	0.416	FcRY; FCRL2; FCRLY; FREB-2; RP11-474I16.6	NM_001002901	Fc receptor-like and mucin-like 2
SDC1	0.415	SDC; CD138; SYND1	NM_002997	syndecan 1
DDB2	0.415	DDB2	NM_000107	damage-specific DNA binding protein 2, 48kDa
DIRAS3	0.414	ARHI; NOEY2	NM_004675	DIRAS family, GTP-binding RAS-like 3
SLIT3	0.413	MEGF5; SLIL2; SLIT1; slit2; Slit-3; FLJ10764	NM_003062	slit homolog 3 (Drosophila)
GLS	0.413	GLS1; FLJ10358; KIAA0838; DKFZp686O15119	NM_014905	glutaminase
ISG20	0.412	CD25; HEM45	NM_002201	interferon stimulated exonuclease gene 20kDa
FOLR3	0.41	FR-G; FR-gamma; gamma-hFR	NM_000804	folate receptor 3 (gamma)
FAM43A	0.41	FLJ90022	NM_153690	family with sequence similarity 43, member A
CREB5	0.407	CRE-BPA	NM_182898	cAMP responsive element binding protein 5
ANTXR2	0.407	ISH; JHF; CMG2; CMG-2; FLJ31074; MGC45856; MGC111533	NM_058172	anthrax toxin receptor 2
EXO1	0.406	HEX1; hExoI	NM_003686	exonuclease 1
NRP1	0.406	NRP; CD304; VEGF165R; DKFZp781F1414; DKFZp686A03134	NM_003873	neuropilin 1
IRX2	0.406	MARK2	NM_033267	iroquois homeobox protein 2
GNG12	0.405	FLJ31352; FLJ34695	NM_018841	guanine nucleotide binding protein (G protein), gamma 12
C9ORF88	0.405	OC58; MEG-3; FLJ13518; FLJ22151; FLJ22298; bA356B19.6; DKFZP434H0820; RP11-356B19.6	NM_022833	chromosome 9 open reading frame 88
MYLK	0.404	KRP; MLCK; MLCK108; MLCK210; MSTP083; FLJ12216; DKFZp686I10125	NM_005965	myosin, light polypeptide kinase
CDCP1	0.402	CD318; TRASK; SIMA135	NM_022842	CUB domain containing protein 1
PEA15	0.402	PED; MAT1; HMAT1; MAT1H; PEA-15; HUMMAT1H	NM_003768	phosphoprotein enriched in astrocytes 15
C6ORF32	0.4	PL48; DIFF40; DIFF48; FAM65B; KIAA0386	NM_015864	chromosome 6 open reading frame 32
TGFBR2	0.399	AAT3; FAA3; MFS2; RIIC; TAAD2; HNPCC6; TGFR-2; TGFbeta-RII	NM_001024847	transforming growth factor, beta receptor II (70/80kDa)
RPS26	0.399	MGC104292	NM_001029	ribosomal protein S26
CTHRC1	0.399	GIMAP5	NM_138455	collagen triple helix repeat containing 1
PDSS2	0.399	hDLP1; C6orf210; bA59I9.3	NM_020381	prenyl (decaprenyl) diphosphate synthase, subunit 2
MASP1	0.397	MASP; RaRF; CRARF; PRSS5; CRARF1; FLJ26383; MGC126283; MGC126284; DKFZp686I01199	NM_001031849	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)
NID2	0.397	NID2	NM_007361	nidogen 2 (osteonidogen)
IRXL1	0.396	IFRX; IRXL1; C10orf48; MGC39616	NM_173576	mohawk homeobox
IL32	0.396	NK4; TAIF; TAIFa; TAIFb; TAIFc; TAIFd; IL-32beta; IL-32alpha; IL-32delta; IL-32gamma	NM_001012632	interleukin 32
C21ORF7	0.396	TAK1L	NM_020152	chromosome 21 open reading frame 7
ITGB1	0.394	CD29; FNRB; MDF2; VLAB; GPIIA; MSK12	NM_133376	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
CCBL1	0.393	GTK; KATI; MGC29624	NM_004059	cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase)
TNFRSF19	0.392	TAJ; TROY; TRADE; TAJ-alpha	NM_148957	tumor necrosis factor receptor superfamily, member 19
ART5	0.391	MGC22848	NM_053017	ADP-ribosyltransferase 5
TBC1D4	0.39	AS160; DKFZp779C0666	NM_014832	TBC1 domain family, member 4
CADPS2	0.389	FLJ40851; KIAA1591	NM_017954	Ca2+-dependent activator protein for secretion 2
LAYN	0.389	FLJ30977; FLJ31092	NM_178834	layilin
MAP3K5	0.389	ASK1; MEKK5; MAPKKK5	NM_005923	mitogen-activated protein kinase kinase kinase 5
SNCAIP	0.388	SYPH1; MGC39814	NM_005460	synuclein, alpha interacting protein (synphilin)
LRRC33	0.388	GARPL1; UNQ3030; MGC50789	NM_198565	leucine rich repeat containing 33
IL12A	0.387	CLMF; NFSK; NKSF1; IL-12A	NM_000882	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
PSG6	0.387	PSG10	NM_001031850	pregnancy specific beta-1-glycoprotein 6
MAFF	0.386	U-MAF	NM_012323	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
CPT1A	0.384	CPT1; CPT1-L; L-CPT1	NM_001876	carnitine palmitoyltransferase 1A (liver)
C9ORF26	0.384	IL33; DVS27; NF-HEV; NFEHEV; DKFZp586H0523; RP11-575C20.2	NM_033439	chromosome 9 open reading frame 26 (NF-HEV)
DKFZP564O0823	0.384	DKFZP564O0823	NM_015393	DKFZP564O0823 protein
S100A3	0.383	S100E	NM_002960	S100 calcium binding protein A3
ASAHL	0.383	PLT; NAAA	NM_014435	N-acylsphingosine amidohydrolase (acid ceramidase)-like
ACTN3	0.382	MGC117002; MGC117005	NM_001104	actinin, alpha 3
AKR1C3	0.381	DD3; HAKRB; HAKRe; HA1753; HSD17B5; hluPGFS; KIAA0119	NM_003739	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
SHRM	0.381	SHRM; APXL3; ShrmL; MSTP013; KIAA1481	NM_020859	shroom family member 3
ST7	0.381	HELG; RAY1; SEN4; TSG7; ETS7q; FAM4A1; DKFZp762O2113	NM_021908	suppression of tumorigenicity 7
MAP1A	0.38	MAP1L; MTAP1A	NM_002373	microtubule-associated protein 1A
ENG	0.38	END; ORW; HHT1; ORW1; CD105; FLJ41744	NM_000118	endoglin (Osler-Rendu-Weber syndrome 1)
CYBRD1	0.378	DCYTB; FRRS3; FLJ23462	NM_024843	cytochrome b reductase 1
HPS3	0.377	SUTAL; FLJ22704; DKFZp686F0413	NM_032383	Hermansky-Pudlak syndrome 3
SCHIP1	0.377	SCHIP-1; FLJ39160	NM_014575	schwannomin interacting protein 1
MAT2B	0.376	TGR; MAT-II; MGC12237; MATIIbeta; Nbla02999	NM_182796	methionine adenosyltransferase II, beta
CTSB	0.376	APPS; CPSB	NM_001908	cathepsin B
PLAUR	0.376	CD87; UPAR; URKR	NM_001005376	plasminogen activator, urokinase receptor
ATP5G2	0.375	RNASE1	NM_001002031	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)
LMNA	0.375	FPL; IDC; LFP; CDDC; EMD2; FPLD; HGPS; LDP1; LMN1; LMNC; PRO1; CDCD1; CMD1A;	NM_005572	lamin A/C

		CMT2B1; LGMD1B		
RGS10	0.374	RGS10	NM_001005339	regulator of G-protein signalling 10
COL12A1	0.374	COL12A1L; BA209D8.1; DJ234P15.1	NM_080645	collagen, type XII, alpha 1
SLC1A5	0.374	R16; AAAT; ATBO; M7V1; RDRC; ASCT2; M7VS1; FLJ31068	NM_005628	solute carrier family 1 (neutral amino acid transporter), member 5
LMNA	0.374	FPL; IDC; LFP; CDDC; EMD2; FPLD; HGPS; LDP1; LMN1; LMNC; PRO1; CDCD1; CMD1A; CMT2B1; LGMD1B	NM_005572	lamin A/C
RRM2B	0.373	p53R2; MGC42116; MGC102856; DKFZp686M05248	NM_015713	ribonucleotide reductase M2 B (TP53 inducible)
PVRL3	0.373	PPR3; PRR3; PVRR3; CDw113; FLJ90624; nectin-3; DKFZP566B0846	NM_015480	poliovirus receptor-related 3
ACSL4	0.371	ACS4; FACL4; LACS4; MRX63; MRX68	NM_004458	acyl-CoA synthetase long-chain family member 4
PTGS1	0.371	COX1; COX3; PHS1; PCOX1; PGHS1; PTGHS; PGG/HS; PGHS-1	NM_000962	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
FLJ43339	0.37	FLJ43339; DKFZp686N1468	NM_207380	FLJ43339 protein
ERBB3	0.37	HER3; ErbB-3; c-erbB3; erbB3-S; MDA-BF-1; MGC88033; c-erbB-3; p180-ErbB3; p45-sErbB3; p85-sErbB3	NM_001982	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
TACC1	0.37	Ga55; KIAA1103; DKFZp686K18126	NM_006283	transforming, acidic coiled-coil containing protein 1
SELM	0.37	SELM; SEPM; MGC40146	NM_080430	selenoprotein M
CDH11	0.37	OB; CAD11; CDHOB; OSF-4	NM_001797	cadherin 11, type 2, OB-cadherin (osteoblast)
ARNT2	0.369	KIAA0307	NM_014862	aryl-hydrocarbon receptor nuclear translocator 2
KIAA0773	0.368	KIAA0773	NM_014690	KIAA0773 gene product
RHBDL3	0.368	VRHO; RHBDL4; FLJ45582; MGC119300; MGC119301	NM_138328	rhomboid, veinlet-like 3 (Drosophila)
SOCS1	0.367	JAB; CIS1; SSI1; TIP3; CISH1; SSI-1; SOCS-1	NM_003745	suppressor of cytokine signaling 1
LHFP	0.366	MGC22429	NM_005780	lipoma HMGIC fusion partner
WNT5B	0.366	MGC2648	NM_032642	wingless-type MMTV integration site family, member 5B
CBX6	0.366	ALDOA	NM_014292	chromobox homolog 6
ZNF483	0.366	ZNF483	NM_001007169	zinc finger protein 483
LITAF	0.365	PIG7; CMT1C; SIMPLE; TP53I7; FLJ38636; MGC116698; MGC116700; MGC116701; MGC125274; MGC125275; MGC125276	NM_004862	lipopolysaccharide-induced TNF factor
PPM1E	0.364	POPX1; PP2CH; KIAA1072; DKFZp781F1422	NM_014906	protein phosphatase 1E (PP2C domain containing)
CD68	0.364	GP110; SCARD1; DKFZp686M18236	NM_001251	CD68 molecule
IL15	0.363	IL-15; MGC9721	NM_172174	interleukin 15
BZRP	0.363	DBI; IBP; MBR; PBR; BZRP; PKBS; PTBR; mDRC; pk18	NM_000714	translocator protein (18kDa)
NFIX	0.362	NF1A	NM_002501	nuclear factor I/X (CCAAT-binding transcription factor)
DDR2	0.362	TKT; NTRKR3; TYRO10	NM_006182	discoidin domain receptor family, member 2
SYT13	0.362	KIAA1427	NM_020826	synaptotagmin XIII
HCP5	0.362	P5-1; D6S2650E	NM_006674	HLA complex P5
RRAGD	0.361	RAGD; bA11D8.2.1; DKFZP761H171	NM_021244	Ras-related GTP binding D
SYTL2	0.361	SLP2; SGA72M; CHR11SYT; KIAA1597; MGC102768	NM_206930	synaptotagmin-like 2
DOCK2	0.361	KIAA0209	NM_004946	dedicator of cytokinesis 2
SAMD4A	0.361	SMG; SMGA; SAMD4; Smaug; Smaug1; KIAA1053; DKFZp434H0350	NM_015589	sterile alpha motif domain containing 4A
MGC20983	0.36	MGC20983; FLJ31801	NM_145045	hypothetical protein MGC20983
C18ORF17	0.36	HsT2697; FLJ33761	NM_153211	chromosome 18 open reading frame 17
CXCL16	0.359	SRPSOX; CXCLG16; SR-PSOX	NM_022059	chemokine (C-X-C motif) ligand 16
KDELR3	0.359	ERD2L3	NM_016657	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
SLC1A3	0.356	EA6; EAAT1; GLAST; GLAST1; FLJ25094	NM_004172	solute carrier family 1 (glial high affinity glutamate transporter), member 3
LTBR	0.356	CD18; TNFCR; D12S370; TNFR-RP; TNFRSF3; TNFR2-RP; LT-BETA-R; TNF-R-III	NM_002342	lymphotoxin beta receptor (TNFR superfamily, member 3)
ITGA3	0.356	VL3A; CD49C; GAPB3; MSK18; VCA-2; VLA3a; GAP-B3; FLJ34631	NM_002204	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
OPN3	0.355	ECPN	NM_001030012	opsin 3 (encephalopsin, panopsin)
INA	0.355	NEF5; NF-66; TXBP-1; MGC12702	NM_032727	internexin neuronal intermediate filament protein, alpha
TUBA1	0.354	FLJ30169; H2-ALPHA	NM_006000	tubulin, alpha 1
TSRC1	0.354	TSRC1	NM_025008	ADAMTS-like 4
LCE2C	0.354	LEP11	NM_178429	late cornified envelope 2C
LRRC20	0.354	FLJ10751; FLJ10844	NM_207119	leucine rich repeat containing 20
PAM	0.353	PAL; PHM	NM_138821	peptidylglycine alpha-amidating monooxygenase
ATP1A2	0.352	FHM2; MHP2; MGC59864	NM_000702	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide
ZDHHC22	0.351	C14orf59	NM_174976	zinc finger, DHHC-type containing 22
HEBP1	0.351	HBP; HEBP	NM_015987	heme binding protein 1
HCLS1	0.35	HS1	NM_005335	hematopoietic cell-specific Lyn substrate 1
TBX2	0.349	FLJ10169	NM_005994	T-box 2
CHGB	0.349	SCG1	NM_001819	chromogranin B (secretogranin 1)
RGS20	0.348	RGSZ1; ZGAP1	NM_170587	regulator of G-protein signalling 20
DHDH	0.348	HUM2DD	NM_014475	dihydrodiol dehydrogenase (dimeric)
KCTD12	0.348	PFET1; C13orf2; KIAA1778	NM_138444	potassium channel tetramerisation domain containing 12
BNC2	0.348	BSN2; FLJ20043; FLJ34928; DKFZp686A01127	NM_017637	basonuclin 2
CLEC11A	0.348	P47; SCGF; LSLCL; CLECSF3	NM_002975	C-type lectin domain family 11, member A
GRIA3	0.347	GLUR3; GLURC; gluR-C; GLUR-K3	NM_181894	glutamate receptor, ionotrophic, AMPA 3
MRGPRF	0.344	RTA; mrgF; GPR140; GPR168; MGC21621	NM_145015	MAS-related GPR, member F
GAP43	0.343	B-50; PP46	NM_002045	growth associated protein 43
EDIL3	0.343	DEL1; MGC26287	NM_005711	EGF-like repeats and discoidin I-like domains 3
EFEMP1	0.343	DHRD; DRAD; FBNL; MLVT; MTLV; S1-5; FBLN3; FLJ35535; MGC111353	NM_004105	EGF-containing fibulin-like extracellular matrix protein 1

ST6GALNAC4	0.342	SIAT3C; SIAT7D; ST6GALNACIV	NM_175040	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
ADORA2A	0.341	RDC8; hA2aR; ADORA2	NM_000675	adenosine A2a receptor
LAMC2	0.34	B2T; EBR2; BM600; EBR2A; LAMB2T; LAMNB2; MGC138491; MGC141938	NM_005562	laminin, gamma 2
PHLDA2	0.34	IPL; BRW1C; BWR1C; HLDA2; TSSC3	NM_003311	pleckstrin homology-like domain, family A, member 2
LOXL4	0.34	LOXC; FLJ21889	NM_032211	lysyl oxidase-like 4
MYBPH	0.34	MYBPH	NM_004997	myosin binding protein H
BNC1	0.338	BNC; BSN1; HsT19447	NM_001717	basonuclin 1
PLA2G4A	0.337	PLA2G4; MGC126350; cPLA2-alpha	NM_024420	phospholipase A2, group IVA (cytosolic, calcium-dependent)
PTHB1	0.337	PTHB1; B1; D1; C18; BBS9; MGC118917	NM_001033604	parathyroid hormone-responsive B1
IGFBP7	0.337	PSF; FSTL2; MAC25; IGFBP-7; IGFBP-7v	NM_001553	insulin-like growth factor binding protein 7
DUSP1	0.337	HVH1; CL100; MKP-1; PTPN10	NM_004417	dual specificity phosphatase 1
ASB9	0.336	MGC4954; FLJ20636; DKFZp564L0862	NM_024087	ankyrin repeat and SOCS box-containing 9
GPR19	0.335	GPR19	NM_006143	G protein-coupled receptor 19
ZNF537	0.334	TSH3; ZNF537; KIAA1474	NM_020856	teashirt family zinc finger 3
DAZL	0.334	DAZH; DAZL1; DAZLA; SPGYLA; MGC26406	NM_001351	deleted in azoospermia-like
KCNS1	0.334	KV9.1	NM_002251	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1
TXNRD2	0.334		NM_145748	
NPTX1	0.332	NP1; MGC105123; DKFZp686J2446	NM_002522	neuronal pentraxin I
TRERF1	0.331	RAPA; TReP-132; HSA277276; dJ139D8.5; RP1-139D8.5	NM_033501	transcriptional regulating factor 1
RPS4Y1	0.33	RPS4Y; MGC5070; MGC119100	NM_001008	ribosomal protein S4, Y-linked 1
ASMTL	0.33	ASTML; ASMTLX; ASMTLY	NM_004192	acetylserotonin O-methyltransferase-like
EEF2K	0.329	eEF-2K; HSU93850; MGC45041	NM_013302	eukaryotic elongation factor-2 kinase
KDELR3	0.329	ERD2L3	NM_006855	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
PRKCA	0.328	AAG6; PKCA; PRKACA; MGC129900; MGC129901; PKC-alpha	NM_002737	protein kinase C, alpha
MGC34830	0.327	MGC34830	NM_152314	chromosome 11 open reading frame 69
FILIP1	0.327	FILIP; KIAA1275	NM_015687	filamin A interacting protein 1
CYFIP2	0.326	PIR121	NM_014376	cytoplasmic FMR1 interacting protein 2
LOC205251	0.326		NM_174925	
Sep-03	0.325	SEP3; MGC133218; bK250D10.3	NM_019106	septin 3
CD59	0.324	EJ16; EJ30; EL32; G344; MIN1; MIN2; MIN3; MIC11; MSK21; 16.3A5; p18-20; MGC2354; PROTECTIN	NM_203329	CD59 molecule, complement regulatory protein
HIST2H2AC	0.324	H2A; H2A/q; H2AFQ; MGC74460; H2A-GL101	NM_003517	histone 2, H2ac
DOCK10	0.324	ZIZ3; DRIP2; Nbla10300; DKFZp781A1532	NM_014689	dedicator of cytokinesis 10
ARRDC4	0.323	FLJ36045	NM_183376	arrestin domain containing 4
HGF	0.322	SF; HGFB; HPTA; F-TCF	NM_001010931	hepatocyte growth factor (hepapoietin A; scatter factor)
CD47	0.322		NM_001025080	
TAPBP	0.322	TPN; TAPA; TPSN; NGS17	NM_003190	TAP binding protein (tapasin)
MSRB3	0.321	FLJ36866; DKFZp686C1178	NM_198080	methionine sulfoxide reductase B3
HIST1H1C	0.32	H1.2; H1F2; MGC3992	NM_005319	histone 1, H1c
UGT8	0.319	CGT	NM_003360	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
TSRC1	0.319	TSRC1	NM_025008	ADAMTS-like 4
SRPX2	0.318	SRPX; SRPUL	NM_014467	sushi-repeat-containing protein, X-linked 2
VAMP4	0.317	VAMP24	NM_003762	vesicle-associated membrane protein 4
CSEN	0.317	CSEN; DREAM; KCHIP3; MGC18289	NM_013434	Kv channel interacting protein 3, calsenilin
CD82	0.317	R2; 4F9; C33; IA4; ST6; GR15; KAI1; SAR2; TSPAN27	NM_001024844	CD82 molecule
PLXDC2	0.315	TEM7R; FLJ14623	NM_032812	plexin domain containing 2
STAMBPL1	0.314	AMSH-FP; AMSH-LP; ALMalpha; FLJ31524; KIAA1373; bA399O19.2	NM_020799	STAM binding protein-like 1
ZDHHC14	0.314	NEW1CP; FLJ20984	NM_024630	zinc finger, DHHC-type containing 14
FLJ11259	0.313	DRAM; FLJ11259	NM_018370	damage-regulated autophagy modulator
GLT8D2	0.313	FLJ31494	NM_031302	glycosyltransferase 8 domain containing 2
AXL	0.312	UFO	NM_001699	AXL receptor tyrosine kinase
LIPA	0.311	LAL; CESD	NM_000235	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)
DPYSL3	0.31	DRP3; ULIP; CRMP4; DRP-3; CRMP-4	NM_001387	dihydropyrimidinase-like 3
CSRP1	0.31	CRP; CRP1; CSRP; CYRP; D1S181E; DKFZp686M148	NM_004078	cysteine and glycine-rich protein 1
LIF	0.31	CDF; HILDA; D-FACTOR	NM_002309	leukemia inhibitory factor (cholinergic differentiation factor)
MGLL	0.31	MGL; HU-K5	NM_007283	monoglyceride lipase
NR4A2	0.307	NOT; RNR1; HZF-3; NURR1; TINUR	NM_006186	nuclear receptor subfamily 4, group A, member 2
PLAU	0.305	ATF; UPA; URK; u-PA	NM_002658	plasminogen activator, urokinase
NMI	0.304	NMI	NM_004688	N-myc (and STAT) interactor
COL1A1	0.304	OI4	NM_000088	collagen, type I, alpha 1
CAT	0.303	MGC138422; MGC138424	NM_001752	catalase
PROCR	0.302	CCCA; EPCR; CCD41; CD201; MGC23024; bA42O4.2	NM_006404	protein C receptor, endothelial (EPCR)
THBS1	0.302	TSP; THBS; TSP1	NM_003246	thrombospondin 1
GPD1L	0.301	KIAA0089	NM_015141	glycerol-3-phosphate dehydrogenase 1-like
SLC22A4	0.3	OCTN1; MGC34546; MGC40524	NM_003059	solute carrier family 22 (organic cation transporter), member 4
MBNL1	0.3	EXP; MBNL; EXP35; EXP40; EXP42; KIAA0428; DKFZp686P06174	NM_207293	muscleblind-like (Drosophila)
TFAP2C	0.3	ERF1; TFAP2G; hAP-2g; AP2-GAMMA	NM_003222	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)
TXNDC5	0.3	ERP46; UNQ364; EndoPDI; MGC3178	NM_030810	thioredoxin domain containing 5
WNT5A	0.3	hWNT5A	NM_003392	wingless-type MMTV integration site family, member 5A
TERF1	0.3	TRF; PIN2; TRF1; TRBF1; t-TRF1; hTRF1-AS	NM_003218	telomeric repeat binding factor (NIMA-interacting) 1
TGM3	0.299	TGE; MGC126249; MGC126250	NM_003245	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)

PRRX2	0.298	PMX2; PRX2; MGC19843	NM_016307	paired related homeobox 2
LCE2A	0.297	LEP9	NM_178428	late cornified envelope 2A
SP110	0.297	VODI; IFI41; IFI75; FLJ22835	NM_004510	SP110 nuclear body protein
SPOCD1	0.297	FLJ25348; FLJ39908; RP11-84A19.1	NM_144569	SPOC domain containing 1
SLC16A6	0.297	MCT6; MCT7	NM_004694	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)
MOCOS	0.296	MOS; HMCS; FLJ20733	NM_017947	molybdenum cofactor sulfurase
ENPP1	0.295	M6S1; NPP1; NPPS; PC-1; PCA1; PDNP1	NM_006208	ectonucleotide pyrophosphatase/phosphodiesterase 1
TAP1	0.293	APT1; PSF1; ABC17; ABCB2; RING4; TAP1N; D6S114E; FLJ26666; TAP1*0102N	NM_000593	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
FLJ90805	0.293	FLJ90805	NM_173633	transmembrane protein 145
TMEM22	0.291	MGC3295; DKFZp564K2464	NM_025246	transmembrane protein 22
FAM101B	0.291	MGC45871	NM_182705	family with sequence similarity 101, member B
ZNF488	0.289	FLJ32104	NM_153034	zinc finger protein 488
MME	0.288	NEP; CD10; CALLA; MGC126681; MGC126707; DKFZp686O16152	NM_007288	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
MOBKL2B	0.287	MOB3B; FLJ13204; FLJ23916; MGC32960	NM_024761	MOB1, Mps One Binder kinase activator-like 2B (yeast)
HLA-E	0.285	MHC; EA1.2; EA2.1; HLA-6.2; DKFZp686P19218	NM_005516	major histocompatibility complex, class I, E
SGNE1	0.285	7B2; SgV; P7B2; SGNE1	NM_003020	secretogranin V (7B2 protein)
KLF9	0.285	BTEB; BTEB1	NM_001206	Kruppel-like factor 9
S100A6	0.285	2A9; PRA; 5B10; CABP; CACY	NM_014624	S100 calcium binding protein A6
STEAP2	0.284	STMP; IPCA1; PUMPCn; STAMP1; PCANAP1	NM_152999	six transmembrane epithelial antigen of the prostate 2
COTL1	0.283	CLP; FLJ43657; MGC19733	NM_021149	coactosin-like 1 (Dictyostelium)
PRPS2	0.283	PRSII; PRS II	NM_002765	phosphoribosyl pyrophosphate synthetase 2
CD97	0.282	TM7LN1	NM_078481	CD97 molecule
TFPI2	0.282	PP5; TFPI-2; FLJ21164	NM_006528	tissue factor pathway inhibitor 2
ITGB1	0.281	CD29; FNRB; MDF2; VLAB; GPIIA; MSK12	NM_133376	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
APOBEC3B	0.281	ARP4; ARCD3; PHRBNL; APOBEC1L; FLJ21201; bK150C2.2; DJ742C19.2	NM_004900	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
DSCR1	0.28	CSP1; DSC1; RCN1; MCIP1; ADAPT78	NM_203417	Down syndrome critical region gene 1
CTSK	0.28	CTSO; PKND; PYCD; CTS02; CTSO1; CTSO2; MGC23107	NM_000396	cathepsin K (pycnodysostosis)
METTL7A	0.279	AAM-B; DKFZP586A0522	NM_014033	methyltransferase like 7A
CXCL12	0.279	PBSF; SDF1; SDF1A; SDF1B; TPAR1; SCYB12; SDF-1a; SDF-1b; TLSF-a; TLSF-b	NM_199168	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
PRKCB1	0.277	PKCB; PRKCB; PRKCB2; MGC41878; PKC-beta	NM_002738	protein kinase C, beta 1
FLJ13391	0.276	FLJ13391	NM_032181	transmembrane protein 166
ANKRD35	0.275	FLJ25124; MGC126667; MGC126669	NM_144698	ankyrin repeat domain 35
SOX3	0.274	MRGH; SOXB	NM_005634	SRY (sex determining region Y)-box 3
FGF2	0.274	BFGF; FGFB; HBGH-2	NM_002006	fibroblast growth factor 2 (basic)
SQRDL	0.272	CGI-44	NM_021199	sulfide quinone reductase-like (yeast)
RCN3	0.271	RLP49	NM_020650	reticulocalbin 3, EF-hand calcium binding domain
UNC5A	0.27	UNC5H1; FLJ16449; KIAA1976	NM_133369	unc-5 homolog A (C. elegans)
ARID5B	0.27	MRF2; FLJ21150; RP11-341A19.1	NM_032199	AT rich interactive domain 5B (MRF1-like)
COL3A1	0.269	EDS4A	NM_000090	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
PRNP	0.269	CJD; GSS; PrP; ASCR; PRIP; PrPc; CD230; MGC26679; PrP27-30; PrP33-35C	NM_183079	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
STEAP1	0.268	STEAP; PRSS24; MGC19484	NM_012449	six transmembrane epithelial antigen of the prostate 1
FLNC	0.267	ABPA; ABPL; FLN2; ABP-280; ABP280A; FLJ10186	NM_001458	filamin C, gamma (actin binding protein 280)
PRRX1	0.267	PMX1; PRX1; PHOX1	NM_022716	paired related homeobox 1
MX1	0.267	MX; MxA; IFI78; IFI-78K	NM_002462	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
DPP4	0.266	CD26; ADABP; ADCP2; DPPIV; TP103	NM_001935	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)
PSMB8	0.266	LMP7; D6S216; RING10; D6S216E; MGC1491	NM_004159	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
SRPX	0.265	DRS; ETX1	NM_006307	sushi-repeat-containing protein, X-linked
CYP26B1	0.265	CYP26A2; MGC129613; P450RAI-2; DKFZp686G0638	NM_019885	cytochrome P450, family 26, subfamily B, polypeptide 1
EIF1AY	0.262	EIF1AY	NM_004681	eukaryotic translation initiation factor 1A, Y-linked
RND3	0.262	ARHE; Rho8; RhoE; memB	NM_005168	Rho family GTPase 3
OAF	0.262	MGC52117; NS5ATP13TP2	NM_178507	OAF homolog (Drosophila)
CDC42EP5	0.261	CEP5; Borg3; MGC21945; MGC71153	NM_145057	CDC42 effector protein (Rho GTPase binding) 5
GPR114	0.26	PGR27	NM_153837	G protein-coupled receptor 114
LAMA4	0.259	LAMA3; DKFZp686D23145	NM_002290	laminin, alpha 4
G1P3	0.259	6-16; G1P3; FAM14C; IFI616; IFI-6-16	NM_002038	interferon, alpha-inducible protein 6
SMARCA2	0.256	BRM; hBRM; Sth1p; BAF190; SNF2L2; SNF2LA; hSNF2a; FLJ36757; MGC74511	NM_139045	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
PMAIP1	0.255	APR; NOXA	NM_021127	phorbol-12-myristate-13-acetate-induced protein 1
HERC5	0.255	CEB1; CEBP1	NM_016323	hect domain and RLD 5
TRIM22	0.254	RNF94; STAF50; GPSTAF50	NM_006074	tripartite motif-containing 22
CHST4	0.254	LSST	NM_005769	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4
CDKN1A	0.254	P21; CIP1; SDI1; WAF1; CAP20; CDKN1; MDA-6; p21CIP1	NM_078467	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
RGS10	0.254	RGS10	NM_002925	regulator of G-protein signalling 10
SERPINE1	0.254	PAI; PAI1; PAI-1; PLANH1	NM_000602	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
GLIPR1	0.253	GLIPR; RTVP1; CRISP7	NM_006851	GLI pathogenesis-related 1 (glioma)

GNG11	0.251	GNGT11	NM_004126	guanine nucleotide binding protein (G protein), gamma 11
CD248	0.251	TEM1; CD164L1; MGC119478; MGC119479	NM_020404	CD248 molecule, endosialin
MGLL	0.25	MGL; HU-K5	NM_007283	monoglyceride lipase
KIAA1576	0.249	KIAA1576	NM_020927	KIAA1576 protein
PNPO	0.249	PDXPO; FLJ10535	NM_018129	pyridoxamine 5'-phosphate oxidase
SLIT2	0.247	SLIL3; Slit-2; FLJ14420	NM_004787	slit homolog 2 (Drosophila)
CBR3	0.247	hCBR3	NM_001236	carbonyl reductase 3
EBI3	0.246	MSX2	NM_005755	Epstein-Barr virus induced gene 3
PCSK5	0.246	PC5; PC6; PC6A; SPC6	NM_006200	proprotein convertase subtilisin/kexin type 5
COMT	0.246	COMT	NM_000754	catechol-O-methyltransferase
LUM	0.245	LDC; SLRR2D	NM_002345	lumican
MVP	0.245	LRP; VAULT1	NM_005115	major vault protein
TNFRSF11B	0.245	OPG; TR1; OCIF; MGC29565	NM_002546	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
CAMK2N1	0.245	PRO1489; MGC22256; ICAP-1alpha; CaMKIINalpha; RP11-401M16.1	NM_018584	calcium/calmodulin-dependent protein kinase II inhibitor 1
C20ORF108	0.243	5A3; dJ1167H4.1; DKFZP434A1114	NM_080821	chromosome 20 open reading frame 108
CAV2	0.239	CAV; MGC12294	NM_001233	caveolin 2
CLDN10	0.239	OSP-L; CPETRL3	NM_006984	claudin 10
LRAT	0.236	MGC33103	NM_004744	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)
MLKL	0.234	FLJ34389	NM_152649	mixed lineage kinase domain-like
NNMT	0.234	NNMT	NM_006169	nicotinamide N-methyltransferase
CAV2	0.234	CAV; MGC12294	NM_001233	caveolin 2
CCL8	0.234	HC14; MCP2; MCP-2; SCYA8; SCYA10	NM_005623	chemokine (C-C motif) ligand 8
POU2F2	0.232	OCT2; OTF2; Oct-2	NM_002698	POU domain, class 2, transcription factor 2
GLS2	0.23	GA; GLS; LGA; hLGA; MGC71567	NM_013267	glutaminase 2 (liver, mitochondrial)
CITED4	0.23	CITED4	NM_133467	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
C20ORF42	0.23	URP1; KIND1; DTGCU2; FLJ20116; FLJ23423	NM_017671	chromosome 20 open reading frame 42
ACTA2	0.228	ACTSA	NM_001613	actin, alpha 2, smooth muscle, aorta
VEGFC	0.227	VRP; Flt4-L	NM_005429	vascular endothelial growth factor C
DAB2	0.226	DOC2; DOC-2	NM_001343	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
C2ORF32	0.224	DKFZp566K1924	NM_015463	chromosome 2 open reading frame 32
MASP1	0.222	MASP; RaRF; CRARF; PRSS5; CRARF1; FLJ26383; MGC126283; MGC126284; DKFZp686I01199	NM_139125	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)
PTGS1	0.222	COX1; COX3; PHS1; PCOX1; PGHS1; PTGHS; PGG/HS; PGHS-1	NM_080591	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
COL8A1	0.221	MGC9568	NM_020351	collagen, type VIII, alpha 1
PIPOX	0.22	LPIPOX	NM_016518	pipecolic acid oxidase
SERPINB7	0.218	MEGSIN; MGC120014; MGC120015; DKFZp686D06190	NM_003784	serpin peptidase inhibitor, clade B (ovalbumin), member 7
CHN1	0.218	CHN; ARHGAP2; RHOGAP2	NM_001822	chimerin (chimaerin) 1
GK	0.216	GKD	NM_000167	glycerol kinase
FLJ20647	0.215	FLJ20647	NM_017918	coiled-coil domain containing 109B
UTF1	0.214	UTF1	NM_003577	undifferentiated embryonic cell transcription factor 1
LPXN	0.212	LDPL	NM_004811	leupaxin
CSF3	0.209	GCSF; G-CSF; MGC45931	NM_000759	colony stimulating factor 3 (granulocyte)
MT1JP	0.209		NM_175622	
DSCR1	0.206	CSP1; DSC1; RCN1; MCIP1; ADAPT78	NM_203418	Down syndrome critical region gene 1
FOXD1	0.204	FKHL8; FREAC4	NM_004472	forkhead box D1
HIST2H2AA	0.203	H2A; H2A.2; H2A/O; H2A/q; H2AFO; H2a-615; HIST2H2AA	NM_003516	histone 2, H2aa3
MMP12	0.203	HME; MME; MGC138506	NM_002426	matrix metallopeptidase 12 (macrophage elastase)
NPTX2	0.201	NP2; NARP; NP-II	NM_002523	neuronal pentraxin II
HSPB3	0.201	HSPL27	NM_006308	heat shock 27kDa protein 3
NT5E	0.198	NT; eN; NT5; NTE; eNT; CD73; E5NT	NM_002526	5'-nucleotidase, ecto (CD73)
EGR1	0.198	TIS8; AT225; G0S30; NGFI-A; ZNF225; KROX-24; ZIF-268	NM_001964	early growth response 1
PTRF	0.194	FKSG13	NM_012232	polymerase I and transcript release factor
SERPINB4	0.192	PI11; SCCA1; SCCA2; LEUPIN; SCCA-2	NM_002974	serpin peptidase inhibitor, clade B (ovalbumin), member 4
KIAA1199	0.191	CCSP1; TMEM2L	NM_018689	KIAA1199
CA4	0.191	CAIV; Car4	NM_000717	carbonic anhydrase IV
THBS2	0.191	TSP2	NM_003247	thrombospondin 2
RAFTLIN	0.19	RAFTLIN; MIG2; PIG9; PIB10; KIAA0084	NM_015150	raft-linking protein
MICA	0.19	PERB11.1; MGC111087; truncated	NM_000247	MHC class I polypeptide-related sequence A
C20ORF127	0.189		NM_080757	
RDH5	0.188	RDH1	NM_002905	retinol dehydrogenase 5 (11-cis/9-cis)
CXCL6	0.187	GCP2; CKA-3; GCP-2; SCYB6	NM_002993	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
NFKBIZ	0.186	IKBZ; INAP; MAIL; FLJ30225; FLJ34463	NM_001005474	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
EPAS1	0.184	HLF; MOP2; HIF2A; PASD2	NM_001430	endothelial PAS domain protein 1
PSG4	0.183	PSG9	NM_002780	pregnancy specific beta-1-glycoprotein 4
CRADD	0.18	RAIDD; MGC9163	NM_003805	CASP2 and RIPK1 domain containing adaptor with death domain
PROM1	0.18	AC133; CD133; PROML1; MSTP061	NM_006017	prominin 1
EMP1	0.179	TMP; CL-20; EMP-1	NM_001423	epithelial membrane protein 1
CAV1	0.179	CAV; VIP21; MSTP085	NM_001753	caveolin 1, caveolae protein, 22kDa
INDO	0.176	IDO; CD107B	NM_002164	indoleamine-pyrrole 2,3 dioxygenase
CLDN10	0.174	OSP-L; CPETRL3	NM_006984	claudin 10
PSG9	0.174	PSG11	NM_002784	pregnancy specific beta-1-glycoprotein 9
LOX	0.172	MGC105112	NM_002317	lysyl oxidase
FCRLM1	0.171	FCRL; FREB; FCRLX; FCRLa; FCRLb; FCRLd; FCRLe; FCRLc1; FCRLc2; MGC4595; RP11-474I16.5	NM_032738	Fc receptor-like and mucin-like 1
C10ORF116	0.169	APM2	NM_006829	chromosome 10 open reading frame 116

D4S234E	0.166	D4S234E; P21; NSG1; D4S234; NEEP21	NM_014392	DNA segment on chromosome 4 (unique) 234 expressed sequence
UGP2	0.161	UDPG; UGPP2; UDPGP2; pHC379	NM_006759	UDP-glucose pyrophosphorylase 2
PSG7	0.159	PSG1	NM_002783	pregnancy specific beta-1-glycoprotein 7
PSG1	0.157	SP1; B1G1; PBG1; CD66f; PSBG1; PSGGA; DHFRP2; PSGIIA; FLJ90598; FLJ90654	NM_006905	pregnancy specific beta-1-glycoprotein 1
MT1H	0.155	MT1; MGC70702	NM_005951	metallothionein 1H
COL10A1	0.154	COL10A1	NM_000493	collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia)
MOXD1	0.152	MOX; PRO5780; dJ248E1.1; DKFZP564G202	NM_001031699	monooxygenase, DBH-like 1
PSG5	0.149	PSG; FL-NCA-3	NM_002781	pregnancy specific beta-1-glycoprotein 5
ANPEP	0.143	APN; CD13; LAP1; PEPN; gp150	NM_001150	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)
DDAH1	0.142	DDAH; FLJ21264; FLJ25539	NM_012137	dimethylarginine dimethylaminohydrolase 1
MT1F	0.141	MT1; MGC32732	NM_005949	metallothionein 1F (functional)
IL13RA2	0.14	IL-13R; IL13BP; CD213A2	NM_000640	interleukin 13 receptor, alpha 2
OLFML3	0.137	OLF44; HNOEL-iso	NM_020190	olfactomedin-like 3
SGK	0.13	SGK1	NM_005627	serum/glucocorticoid regulated kinase
CYR61	0.125	CCN1; GIG1; IGFBP10	NM_001554	cysteine-rich, angiogenic inducer, 61
SERPINB2	0.124	PAI; PAI2; PAI-2; PLANH2; HsT1201	NM_002575	serpin peptidase inhibitor, clade B (ovalbumin), member 2
ANXA1	0.124	ANX1; LPC1	NM_000700	annexin A1
CXCL5	0.124	SCYB5; ENA-78	NM_002994	chemokine (C-X-C motif) ligand 5
FLJ14834	0.12	FLJ14834; MGC126673; MGC126675	NM_032849	chromosome 13 open reading frame 33
CAMKV	0.115	1G5; MGC8407; VACAMKL	NM_024046	CaM kinase-like vesicle-associated
GNA14	0.112	GNA14	NM_004297	guanine nucleotide binding protein (G protein), alpha 14
CXCL2	0.108	GRO2; GROb; MIP2; MIP2A; SCYB2; MGSA-b; MIP-2a; CINC-2a; MGSA beta	NM_002089	chemokine (C-X-C motif) ligand 2
LECT1	0.105	CHM1; CHM-I; BRICD3	NM_007015	leukocyte cell derived chemotaxin 1
PSG11	0.0956	PSG13; PSG14; MGC22484	NM_002785	pregnancy specific beta-1-glycoprotein 11
PLAT	0.0947	TPA; T-PA; DKFZp686I03148	NM_000930	plasminogen activator, tissue
MT1M	0.0929	MT1; MT1K; MGC40498; MGC118949	NM_176870	metallothionein 1M
THY1	0.0901	CD90; FLJ33325	NM_006288	Thy-1 cell surface antigen
MOXD1	0.0888	MOX; PRO5780; dJ248E1.1; DKFZP564G202	NM_015529	monooxygenase, DBH-like 1
CSF2	0.0836	GMCSF; MGC131935; MGC138897	NM_000758	colony stimulating factor 2 (granulocyte-macrophage)
VGF	0.0781	VGF	NM_003378	VGF nerve growth factor inducible
CCL7	0.07	FIC; MARC; MCP3; NC28; MCP-3; SCYA6; SCYA7; MGC138463; MGC138465	NM_006273	chemokine (C-C motif) ligand 7
ACTG2	0.0613	ACT; ACTE; ACTA3; ACTL3; ACTSG	NM_001615	actin, gamma 2, smooth muscle, enteric
TM4SF1	0.0455	L6; H-L6; M3S1; TAAL6	NM_014220	transmembrane 4 L six family member 1
SPP1	0.0419	OPN; BNSP; BSPI; ETA-1; MGC110940	NM_000582	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)
MT1G	0.0401	MT1; MT1K; MGC12386	NM_005950	metallothionein 1G
TXNIP	0.0271	THIF; VDUP1; HHCPA78; EST01027	NM_006472	thioredoxin interacting protein

d4+GF only

Gene Name	Fold Change	Common	Genbank	Description
HAND1	12.38	Hxt; eHand; Thing1	NM_004821	heart and neural crest derivatives expressed 1
C20ORF75	10.26	NLRR4; FLJ23994; MGC25027; dJ1056H1.1	NM_152611	chromosome 20 open reading frame 75
GYPE	9.316	GPE; MNS; MiIX	NM_002102	glycophorin E
ANGPT2	8.428	ANG2; AGPT2	NM_001147	angiopoietin 2
HAPLN1	6.167	CRTL1	NM_001884	hyaluronan and proteoglycan link protein 1
PPFIBP2	5.367	Cclp1; MGC42541; DKFZp781K06126	NM_003621	PTPRF interacting protein, binding protein 2 (liprin beta 2)
HES4	5.147	FGF23	NM_021170	hairy and enhancer of split 4 (Drosophila)
ANG	5.135	RNASE4; RNASE5; MGC71966	NM_001145	angiogenin, ribonuclease, RNase A family, 5
LTB4DH	5.129	MGC34943	NM_012212	leukotriene B4 12-hydroxydehydrogenase
MANEA	4.855	hEndo; FLJ12838; DKFZp686D20120	NM_024641	mannosidase, endo-alpha
CDC42EP4	4.714	CEP4; BORG4; MGC3740; KAIA1777; MGC17125	NM_012121	CDC42 effector protein (Rho GTPase binding) 4
MYL4	4.588	GT1; ALC1; AMLC; PRO1957	NM_002476	myosin, light polypeptide 4, alkali; atrial, embryonic
KRT8	4.515	K8; KO; CK8; CYK8; K2C8; CARD2	NM_002273	keratin 8
SIPA1L2	4.383	SPAL2; FLJ23126; FLJ23632; KIAA1389	NM_020808	signal-induced proliferation-associated 1 like 2
DLK1	4.217	FA1; ZOG; pG2; PREF1; Pref-1	NM_003836	delta-like 1 homolog (Drosophila)
CYP27A1	4.153	CTX; CP27; CYP27	NM_000784	cytochrome P450, family 27, subfamily A, polypeptide 1
BST2	4.127	CD317	NM_004335	bone marrow stromal cell antigen 2
GREB1	3.952	GREB1; KIAA0575	NM_014668	GREB1 protein
SOX21	3.797	SOX25	NM_007084	SRY (sex determining region Y)-box 21
CTSL2	3.763	CTSU; CTSV; CATL2; MGC125957	NM_001333	cathepsin L2
HLA-DRB4	3.73	DRB4; HLA DRB1; HLA-DR4B	NM_021983	major histocompatibility complex, class II, DR beta 4
GAB2	3.616	KIAA0571	NM_080491	GRB2-associated binding protein 2
HDC	3.616	HDC	NM_002112	histidine decarboxylase
SLC7A5	3.603	E16; CD98; LAT1; 4F2LC; MPE16; hLAT1; D16S469E	NM_003486	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
GPSM2	3.582	LGN; Pins	NM_013296	G-protein signalling modulator 2 (AGS3-like, C. elegans)
RAB17	3.553	FLJ12538	NM_022449	RAB17, member RAS oncogene family
DAAM1	3.544	KIAA0666	NM_014992	dishevelled associated activator of morphogenesis 1
VAMP8	3.483	EDB; VAMP5	NM_003761	vesicle-associated membrane protein 8 (endobrevin)
FEZ1	3.43	FEZ1	NM_005103	fasciculation and elongation protein zeta 1 (zygin I)
PDLIM3	3.385	ALP; DKFZp686L0362	NM_014476	PDZ and LIM domain 3
KCNK1	3.373	DPK; HOHO; TWIK1; TWIK-1	NM_002245	potassium channel, subfamily K, member 1
PCBP4	3.354	LIP4; MCG10	NM_033008	poly(rC) binding protein 4
DUSP4	3.351	TYP; HVH2; MKP2; MKP-2	NM_057158	dual specificity phosphatase 4
FUT2	3.311	SE; Se2; sej	NM_000511	fucosyltransferase 2 (secretor status included)
CAMKK2	3.299	CAMKK; CAMKKB; KIAA0787; MGC15254	NM_172215	calcium/calmodulin-dependent protein kinase kinase 2, beta
ARHGEF16	3.281	NBR; GEF16	NM_014448	Rho guanine exchange factor (GEF) 16
ARHGEF4	3.248	ASEF; GEF4; STM6	NM_032995	Rho guanine nucleotide exchange factor (GEF) 4
AMMECR1	3.232	AMMERC1	NM_001025580	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1
CLDN18	3.23	CLDN18	NM_016369	claudin 18
HIPK2	3.184	PRO0593	NM_022740	homeodomain interacting protein kinase 2
RNU3IP2	3.183	U3-55K	NM_004704	RNA, U3 small nucleolar interacting protein 2
MBD6	3.171	KIAA1887	NM_052897	methyl-CpG binding domain protein 6
APOE	3.138	AD2; MGC1571; apoprotein	NM_000041	apolipoprotein E
FOXA3	3.121	FKHH3; HNF3G; TCF3G; MGC10179	NM_004497	forkhead box A3
AHNAK	3.088	AHNAKRS; MGC5395	NM_001620	AHNAK nucleoprotein (desmoyokin)
ZNF521	3.081	EHZF; Evi3; MGC142182; MGC142208; DKFZp564D0764	NM_015461	zinc finger protein 521
FLJ22471	3.042	FLJ22471	NM_025140	coiled-coil domain containing 92
DDAH2	3.01	G6a; DDAH; NG30; DDAHII	NM_013974	dimethylarginine dimethylaminohydrolase 2
RASL12	2.999	RIS	NM_016563	RAS-like, family 12
ZFP260	2.973	ozrf1; ZFP260	NM_001012756	zinc finger protein 260
CMTM3	2.971	BNAS2; CKLFSF3; FLJ31762; MGC51956	NM_181555	CKLF-like MARVEL transmembrane domain containing 3
SLC9A3R1	2.966	EBP50; NHERF	NM_004252	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
DSCR5	2.959	DCRC; DSRC; DSCR5; DCRC-S	NM_153681	phosphatidylinositol glycan anchor biosynthesis, class P
NFKBIA	2.95	IKBA; MAD-3; NFKBI	NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
LIX1L	2.947	MGC46719; DKFZp762F237	NM_153713	Lix1 homolog (mouse) like
SRC	2.945	ASV; SRC1; c-SRC; p60-Src	NM_005417	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
RHPN2	2.944	RhoBP; p76RBE	NM_033103	rhophilin, Rho GTPase binding protein 2
HK2	2.935	HKII; HXK2; DKFZp686M1669	NM_000189	hexokinase 2
SOX18	2.923	HLTS	NM_018419	SRY (sex determining region Y)-box 18
MXI1	2.913	MXI; MAD2; MXD2; MGC43220	NM_001008	MAX interactor 1

			541	
FLJ46072	2.913	FLJ46072	NM_198488	family with sequence similarity 83, member H
COL5A2	2.901	MGC105115	NM_000393	collagen, type V, alpha 2
BNIP3	2.889	NIP3	NM_004052	BCL2/adenovirus E1B 19kDa interacting protein 3
WARS	2.861	IFI53; IFP53; GAMMA-2	NM_213646	tryptophanyl-tRNA synthetase
ZD52F10	2.859	UNQ729; ZD52F10	NM_033317	dermokine
YRDC	2.854	IRIP; SUA5; DRIP3; FLJ23476; FLJ26165; RP11-109P14.4	NM_024640	yrdC domain containing (E. coli)
C3ORF36	2.847	FLJ22173; MGC125760; MGC125761	NM_025041	chromosome 3 open reading frame 36
C9ORF61	2.839	X123; MGC142243; MGC142245; RP11-548B3.1	NM_004816	chromosome 9 open reading frame 61
FARP1	2.828	CDEP; PLEKHC2; MGC87400	NM_005766	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
NMU	2.815	NMU	NM_006681	neuromedin U
OTX1	2.81	FLJ38361; MGC15736	NM_014562	orthodenticle homolog 1 (Drosophila)
DSC2	2.788	DG2; DSC3; CDHF2; DGII/III; DKFZp686I11137	NM_004949	desmocollin 2
DHRS10	2.781	retSDR3	NM_016246	dehydrogenase/reductase (SDR family) member 10
EHHADH	2.781	LBP; ECHD; LBFP; PBFE; MGC120586	NM_001966	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
SERPINE2	2.78	GDN; PI7; PN1; PNI	NM_006216	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
TNFRSF21	2.767	DR6; BM-018; MGC31965	NM_014452	tumor necrosis factor receptor superfamily, member 21
PDLIM7	2.766	PDLIM7	NM_213636	PDZ and LIM domain 7 (enigma)
MLYCD	2.753	MCD; MGC59795	NM_012213	malonyl-CoA decarboxylase
MRPL22	2.749	RPML25; HSPC158; MRP-L25; DKFZp781F1071	NM_001014990	mitochondrial ribosomal protein L22
SOX11	2.748	SOX11	NM_003108	SRY (sex determining region Y)-box 11
FZD7	2.744	FzE3	NM_003507	frizzled homolog 7 (Drosophila)
ZNF467	2.723	EZI; Zfp467	NM_207336	zinc finger protein 467
HIC2	2.721	HRG22; ZBTB30; KIAA1020	NM_015094	hypermethylated in cancer 2
TMSL8	2.716	TMSNB	NM_021992	thymosin-like 8
NPPA	2.696	ANF; ANP; PND; CDD-ANF	NM_006172	natriuretic peptide precursor A
PALM	2.695	KIAA0270	NM_002579	paralemmin
B4GALT4	2.682	B4Gal-T4; beta4Gal-T4	NM_003778	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4
FEZ1	2.677	FEZ1	NM_022549	fasciculation and elongation protein zeta 1 (zygin I)
COL4A1	2.676	arresten	NM_001845	collagen, type IV, alpha 1
SALL1	2.676	TBS; HSAL1; ZNF794	NM_002968	sal-like 1 (Drosophila)
MCCC1	2.659	MCCA; MCC-B; FLJ25545; DKFZp686B20267	NM_020166	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
GRB10	2.65	RSS; IRBP; MEG1; GRB-IR; KIAA0207	NM_005311	growth factor receptor-bound protein 10
DNAJB2	2.649	HSJ1; HSPF3	NM_006736	DnaJ (Hsp40) homolog, subfamily B, member 2
PKM2	2.643	PK3; PKM; TCB; OIP3; CTHBP; THBP1; MGC3932	NM_002654	pyruvate kinase, muscle
CAPN13	2.631	FLJ23523	NM_144575	calpain 13
TP53BP2	2.628	BBP; 53BP2; ASPP2; p53BP2; PPP1R13A	NM_001031685	tumor protein p53 binding protein, 2
UNC50	2.605	URP; GMH1; UNCL; HSD23; hGMH1p; DKFZp564G0222	NM_014044	unc-50 homolog (C. elegans)
STX3A	2.59	STX3A	NM_004177	syntaxin 3
REEP6	2.584	DP1L1; TB2L1; C19orf32; FLJ25383	NM_138393	receptor accessory protein 6
ST6GALNAC5	2.578	SIAT7E; MGC3184; ST6GalNAcV	NM_030965	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5
SERTAD2	2.577	TRIP-Br2; MGC126688; MGC126690	NM_014755	SERTA domain containing 2
KCTD15	2.554	MGC2628; MGC25497	NM_024076	potassium channel tetramerisation domain containing 15
ST3GAL5	2.547	SIAT9; ST3GalV; SIATGM3S	NM_003896	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
KIF13B	2.529	GAKIN; KIAA0639	NM_015254	kinesin family member 13B
C17ORF59	2.52	PRO2472; FLJ20014	NM_017622	chromosome 17 open reading frame 59
LHX2	2.518	LH2; hLhx2; MGC138390	NM_004789	LIM homeobox 2
ALAD	2.505	PBGS; ALADH; MGC5057	NM_001003945	aminolevulinate, delta-, dehydratase
ZNF395	2.502	PBF; PRF1; HDBP2; PRF-1; Si-1-8-14; DKFZp434K1210	NM_018660	zinc finger protein 395
FHOD1	2.492	FHOS	NM_013241	formin homology 2 domain containing 1
S100A16	2.469	AAG13; S100F; DT1P1A7; MGC17528	NM_080388	S100 calcium binding protein A16
CRB3	2.461	DEFB106A	NM_139161	crumbs homolog 3 (Drosophila)
USP3	2.451	UBP; SIH003; MGC129878; MGC129879	NM_006537	ubiquitin specific peptidase 3
NXN	2.449	TRG-4; FLJ12614	NM_022463	Nucleoredoxin
RARB	2.446	HAP; RRB2; NR1B2	NM_000965	retinoic acid receptor, beta
MAP3K9	2.444	MLK1; PRKE1	NM_033141	mitogen-activated protein kinase kinase kinase 9
BCAT2	2.423	BCAM; BCT2	NM_001190	branched chain aminotransferase 2, mitochondrial
TRIM32	2.42	HT2A; BBS11; TATIP; LGMD2H	NM_012210	tripartite motif-containing 32
H2AFY	2.418	H2A.y; H2A/y; H2AFJ; mH2A1; H2AF12M; MACROH2A1.1; macroH2A1.2	NM_004893	H2A histone family, member Y
MST1	2.409	MSP; HGFL; NF15S2; D3F15S2; DNF15S2	NM_020998	macrophage stimulating 1 (hepatocyte growth factor-like)
CNKSR3	2.405	MAGI1; FLJ31349; RP11-486M3.1	NM_173515	CNKSR family member 3
ACSL1	2.403	ACS1; LACS; FACL1; FACL2; LACS1; LACS2	NM_001995	acyl-CoA synthetase long-chain family member 1
PLEKHC1	2.402	MIG2; KIND2; mig-2; UNC112	NM_006832	pleckstrin homology domain containing, family C (with FERM domain) member 1
DIABLO	2.4	SMAC; SMAC3; DIABLO-S; FLJ10537; FLJ25049	NM_138930	diablo homolog (Drosophila)
ANKMY2	2.398	ZMYND20; DKFZP564O043	NM_020319	ankyrin repeat and MYND domain containing 2
GPR161	2.395	RE2; FLJ33952	NM_007369	G protein-coupled receptor 161
NUDT14	2.383	UGPP	NM_177533	nudix (nucleoside diphosphate linked moiety X)-type motif 14
NODAL	2.378	MGC138230	NM_018055	nodal homolog (mouse)

ZFPM2	2.374	DIH3; FOG2; ZNF89B; hFOG-2; MGC129663; MGC129664	NM_012082	zinc finger protein, multitype 2
TCP11L1	2.371	FLJ11336; FLJ11386; dJ85M6.3	NM_018393	t-complex 11 (mouse) like 1
CGNL1	2.368	JACOP; FLJ14957; KIAA1749; MGC138254	NM_032866	cingulin-like 1
WSB1	2.361		NM_134264	
KLF6	2.36	GBF; ZF9; BCD1; CPBP; PAC1; ST12; COPEB; DKFZp686N0199	NM_001008490	Kruppel-like factor 6
CYGB	2.36	HGB; STAP	NM_134268	Cytoglobin
PTPRM	2.355	RPTPM; RPTPU; PTPRL1; hR-PTPu; R-PTP-MU	NM_002845	protein tyrosine phosphatase, receptor type, M
AES	2.353	GRG; ESP1; GRG5; TLE5; AES-1; AES-2	NM_198969	amino-terminal enhancer of split
GADD45G	2.351	CR6; DDIT2; GRP17; GADD45gamma	NM_006705	growth arrest and DNA-damage-inducible, gamma
RAB25	2.35	CATX-8	NM_020387	RAB25, member RAS oncogene family
MASK	2.349	MST4; MASK	NM_016542	serine/threonine protein kinase MST4
CDH15	2.348	CDH3; CDHM; MCAD; CDH14	NM_004933	cadherin 15, M-cadherin (myotubule)
C8ORF58	2.34	FLJ34715	NM_001013842	chromosome 8 open reading frame 58
STT3B	2.338	SIMP; STT3-B; FLJ90106	NM_178862	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)
MDK	2.336	MK; NEGF2; FLJ27379	NM_001012334	midkine (neurite growth-promoting factor 2)
BMPR2	2.336	BMR2; BMPR3; BRK-3; T-ALK; BMPR-II	NM_001204	bone morphogenetic protein receptor, type II (serine/threonine kinase)
IL17R	2.334	IL17R; CDw217; IL-17RA; hIL-17R; MGC10262	NM_014339	interleukin 17 receptor A
DYNC1I1	2.329	DNCI1; DNCIC1	NM_004411	dynein, cytoplasmic 1, intermediate chain 1
COCH	2.326	DFNA9; DFNA31; COCH5B2; COCH-5B2	NM_004086	coagulation factor C homolog, cochlin (Limulus polyphemus)
PTPN21	2.321	PTPD1; PTPRL10	NM_007039	protein tyrosine phosphatase, non-receptor type 21
SLC26A11	2.317	MGC46523	NM_173626	solute carrier family 26, member 11
TMEM51	2.317	C1orf72; FLJ10199	NM_018022	transmembrane protein 51
PLXNA2	2.312	OCT; PLXN2; FLJ11751; FLJ30634; KIAA0463	NM_025179	plexin A2
ZNF319	2.305	ZFP319; MGC126816	NM_020807	zinc finger protein 319
ZNF69	2.304	Cos5; MGC59928	NM_021915	zinc finger protein 69
BAMBI	2.304	NMA	NM_012342	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)
ISL1	2.299	Isl-1	NM_002202	ISL1 transcription factor, LIM/homeodomain, (islet-1)
CGI-38	2.284	CGI-38	NM_015964	brain specific protein
C21ORF91	2.281	YG81; C21orf14; C21orf38; DKFZp781D1223	NM_017447	chromosome 21 open reading frame 91
SNAPC3	2.28		NM_003084	
RASSF7	2.278	HRC1; HRAS1; C11orf13; MGC126069; MGC126070	NM_003475	Ras association (RalGDS/AF-6) domain family 7
RPRM	2.276	REPRIMO; FLJ90327	NM_019845	reprimo, TP53 dependent G2 arrest mediator candidate
INPPL1	2.274	SHIP2	NM_001567	inositol polyphosphate phosphatase-like 1
PRSS35	2.274	C6orf158; MGC46520; dJ223E3.1	NM_153362	protease, serine, 35
SERTAD3	2.272	RBT1	NM_203344	SERTA domain containing 3
SERAC1	2.268	FLJ14917; FLJ30544	NM_032861	serine active site containing 1
MXI1	2.267	MXI; MAD2; MXD2; MGC43220	NM_130439	MAX interactor 1
FZD2	2.266	FZD2	NM_001466	frizzled homolog 2 (Drosophila)
SPRED2	2.264	Spred-2; FLJ21897; FLJ31917	NM_181784	sprouty-related, EVH1 domain containing 2
SLC3A2	2.262	4F2; CD98; MDU1; 4F2HC; 4T2HC; NACAE; CD98HC	NM_001012661	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
C11ORF56	2.254	FLJ22665; KIAA1759; DKFZP566M1046	NM_032127	chromosome 11 open reading frame 56
PELI1	2.254	MGC50990	NM_020651	pellino homolog 1 (Drosophila)
ZIC3	2.249	HTX; HTX1; ZNF203	NM_003413	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)
S100A13	2.248	S100A13	NM_001024211	S100 calcium binding protein A13
EDG4	2.248	LPA2; EDG-4; LPAR2	NM_004720	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4
MLLT11	2.244	AF1Q; RP11-316M1.10	NM_006818	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11
LBX2	2.243	LP3727	NM_001009812	ladybird homeobox homolog 2 (Drosophila)
TBC1D9	2.24	MDR1; KIAA0882	NM_015130	TBC1 domain family, member 9 (with GRAM domain)
ETFB	2.24	MADD; FP585	NM_001014763	electron-transfer-flavoprotein, beta polypeptide
MORN2	2.239	MOPT; BLOCK27; MGC126130; MGC126131; MGC126132	NM_194270	MORN repeat containing 2
C9ORF19	2.232	GAPR-1; GLIPR2	NM_022343	chromosome 9 open reading frame 19
PDLIM1	2.231	CLIM1; CLP36; ELFIN; CLP-36; hCLIM1	NM_020992	PDZ and LIM domain 1 (elfin)
GATA5	2.23	bB379O24.1	NM_080473	GATA binding protein 5
MYO3A	2.229	DFNB30	NM_017433	myosin IIIA
DIRC2	2.229	RCC4; FLJ14784	NM_032839	disrupted in renal carcinoma 2
PREX1	2.228	PREX1; KIAA1415	NM_020820	phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1
C6ORF129	2.228	HSPC265; MGC131656	NM_138493	chromosome 6 open reading frame 129
KRAS	2.222	NS3; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-RAS2B; K-RAS4A; K-RAS4B	NM_004985	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
PLEKHG4	2.215	DKFZP434I216; puratrophin1	NM_015432	pleckstrin homology domain containing, family G (with RhoGef domain) member 4
ARHGEF3	2.215	GEF3; STA3; XPLN; MGC118905; DKFZP434F2429	NM_019555	Rho guanine nucleotide exchange factor (GEF) 3
FOLR1	2.214	FBP; FOLR; MOv18; FR-alpha	NM_016724	folate receptor 1 (adult)
GADD45A	2.214	DDIT1; GADD45	NM_001924	growth arrest and DNA-damage-inducible, alpha
SPATA7	2.209	HSD3; HSD-3.1; MGC102934;	NM_018418	spermatogenesis associated 7

		DKFZp686D07199		
CLDN23	2.207	CLDNL	NM_194284	claudin 23
SH3MD2	2.206	POSH; RNF142; SH3MD2; FLJ21602; KIAA1494	NM_020870	SH3 domain containing ring finger 1
B3GALT6	2.206	beta3GalT6	NM_080605	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6
EGF	2.198	URG	NM_001963	epidermal growth factor (beta-urogastrone)
DNAL4	2.193	PIG27	NM_005740	dynein, axonemal, light chain 4
ENSA	2.193	MGC4319; MGC8394; MGC78563	NM_207168	endosulfine alpha
C21ORF2	2.191	A2; YF5	NM_004928	chromosome 21 open reading frame 2
PNMA1	2.183	MA1	NM_006029	paraneoplastic antigen MA1
ARHGAP24	2.182	p73; FLJ33877; RC-GAP72; p73RhoGAP; DKFZP564B1162	NM_001025616	Rho GTPase activating protein 24
C6ORF211	2.182	FLJ12910; DKFZp566I174	NM_024573	chromosome 6 open reading frame 211
SLC25A13	2.177	CTLN2; CITRIN; ARALAR2	NM_014251	solute carrier family 25, member 13 (citrin)
PPP1R3B	2.172	GL; PPP1R4; FLJ14005	NM_024607	protein phosphatase 1, regulatory (inhibitor) subunit 3B
SGPL1	2.168	SPL; FLJ13811; KIAA1252	NM_003901	sphingosine-1-phosphate lyase 1
MSMB	2.167	MSP; PSP; IGBF; MSPB; PN44; PRPS; PSP57; PSP94; PSP-94	NM_002443	microseminoprotein, beta-
NFASC	2.164		NM_001005389	
SH3BP4	2.16	TTP; BOG25	NM_014521	SH3-domain binding protein 4
CDH12	2.156	CDHB; FLJ34857	NM_004061	cadherin 12, type 2 (N-cadherin 2)
PTPLA	2.154	APOBEC3F	NM_014241	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A
NFATC1	2.152	NFAT2; NFATc; NF-ATC; MGC138448	NM_172390	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
ZAP70	2.151	SRK; STD; TZK; ZAP-70	NM_207519	zeta-chain (TCR) associated protein kinase 70kDa
PIK3R5	2.15	FOAP-2; P101-PI3K; F730038I15Rik	NM_014308	phosphoinositide-3-kinase, regulatory subunit 5, p101
TEAD2	2.144	ETF; TEF4; TEF-4	NM_003598	TEA domain family member 2
ZHX2	2.138	KIAA0854	NM_014943	zinc fingers and homeoboxes 2
SEMA5B	2.136	SemG; SEMAG; FLJ10372; KIAA1445	NM_001031702	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B
TM7SF2	2.135	ANG1; DHCR14A	NM_003273	transmembrane 7 superfamily member 2
LOC375133	2.13	LOC375133	NM_199345	similar to phosphatidylinositol 4-kinase alpha
DUSP18	2.128	DUSP20; LMWDSP20; MGC32658; bK963H5.1	NM_152511	dual specificity phosphatase 18
DSCR1L2	2.127	RCN3; MCIP3; hRCN3	NM_013441	Down syndrome critical region gene 1-like 2
PROS1	2.115	PSA; PROS; PS21; PS22; PS23; PS24; PS25; PS26; Protein S; protein Sa	NM_000313	protein S (alpha)
RPIA	2.115	RPI	NM_144563	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)
LGR6	2.114	GPCR; FLJ14471; VTS20631	NM_001017403	leucine-rich repeat-containing G protein-coupled receptor 6
RFWD2	2.112	COP1; RNF200; FLJ10416; RP11-318C24.3	NM_022457	ring finger and WD repeat domain 2
MGC26885	2.102	MGC26885	NM_152339	chromosome 16 open reading frame 76
PGM1	2.099	PGM1	NM_002633	phosphoglucomutase 1
CLCNKA	2.098	CLCK1; ClC-K1; hClC-Ka; MGC61490	NM_004070	chloride channel Ka
KLF6	2.098	GBF; ZF9; BCD1; CPBP; PAC1; ST12; COPEB; DKFZp686N0199	NM_001300	Kruppel-like factor 6
LOC124491	2.098	FLJ37611	NM_145254	transmembrane protein 170
REC8L1	2.088	REC8; Rec8p	NM_005132	REC8-like 1 (yeast)
DSP	2.087	DPI; DPII	NM_001008844	Desmoplakin
PLD5	2.087	FLJ40773; MGC120565; MGC120566; MGC120567	NM_152666	phospholipase D family, member 5
SEMA5A	2.08	semF; SEMAF	NM_003966	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A
ENPEP	2.077	APA; CD249; gp160	NM_001977	glutamyl aminopeptidase (aminopeptidase A)
NEDD9	2.071	CASL; HEF1; CAS-L; dJ49G10.2; dJ761I2.1	NM_182966	neural precursor cell expressed, developmentally down-regulated 9
EFHD2	2.071	MGC4342; RP3-467K16.3	NM_024329	EF-hand domain family, member D2
GUCA2A	2.069	GUCA2; STARA; GUANYLIN	NM_033553	guanylate cyclase activator 2A (guanylin)
PTMS	2.064	PTMS	NM_002824	Parathymosin
BMP4	2.062	ZYME; BMP2B; BMP2B1	NM_001202	bone morphogenetic protein 4
ASXL1	2.062	KIAA0978; MGC71111; MGC117280	NM_015338	additional sex combs like 1 (Drosophila)
CDC42EP1	2.06	CEP1; BORG5; MSE55; MGC15316	NM_007061	CDC42 effector protein (Rho GTPase binding) 1
DERA	2.058	DEOC; CGI-26	NM_015954	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)
RGMA	2.053	RGM	NM_020211	RGM domain family, member A
GPR161	2.053	RE2; FLJ33952	NM_153832	G protein-coupled receptor 161
CDK6	2.05	PLSTIRE; MGC59692	NM_001259	cyclin-dependent kinase 6
PRG2	2.05	PRG2	NM_024888	plasticity-related gene 2
ZC3HAV1	2.042	ZAP; ZC3H2; FLB6421; ZC3HDC2; FLJ13288; MGC48898; DKFZp686F2052; DKFZp686H1869; DKFZp686O19171	NM_020119	zinc finger CCCH-type, antiviral 1
PKM2	2.039	PK3; PKM; TCB; OIP3; CTHBP; THBP1; MGC3932	NM_182470	pyruvate kinase, muscle
SERTAD3	2.034	RBT1	NM_203344	SERTA domain containing 3
ANKFY1	2.032	ANKHZN; ZFYVE14; KIAA1255; DKFZp686M19106	NM_016376	ankyrin repeat and FYVE domain containing 1
RORA	2.026	ROR1; ROR2; ROR3; RZRA; NR1F1; MGC119326; MGC119329	NM_002943	RAR-related orphan receptor A
STMN1	2.025	Lag; SMN; OP18; PP17; PP19; PR22; LAP18	NM_203401	stathmin 1/oncoprotein 18
ENTPD4	2.023	LAP70; LALP70; LYSAL1; UDPase; KIAA0392;	NM_004901	ectonucleoside triphosphate diphosphohydrolase 4

		NTPDase-4		
LOC349114	2.014	LOC349114	NM_198284	hypothetical protein LOC349114
RXRA	2.009	NR2B1; MGC102720	NM_002957	retinoid X receptor, alpha
GTF2IRD1	2.005	GTF3; RBAP2; CREAM1; MUSTRD1; WBSCR11; WBSCR12; hMusTRD1alpha1	NM_005685	GTF2I repeat domain containing 1
CREBBP	2.004	CBP; RTS; RSTS	NM_004380	CREB binding protein (Rubinstein-Taybi syndrome)
FRS3	2.001	SNT2; FRS2B; SNT-2; FRS2beta; MGC17167	NM_006653	fibroblast growth factor receptor substrate 3
LRRC56	1.998	FLJ00101; DKFZp761L1518	NM_198075	leucine rich repeat containing 56
EGLN3	1.997	PHD3; HIFPH3; FLJ21620; MGC125998; MGC125999	NM_022073	egl nine homolog 3 (C. elegans)
CHL1	1.987	CALL; L1CAM2; FLJ44930; MGC132578	NM_006614	cell adhesion molecule with homology to L1CAM (close homolog of L1)
ZNF553	1.984	FLJ31751; MGC43952; DKFZp762K013	NM_152652	zinc finger protein 553
SALL4	1.977	DRRS; HSAL4; ZNF797; MGC133050; dJ1112F19.1	NM_020436	sal-like 4 (Drosophila)
NELL1	1.976	NRP1; IDH3GL	NM_006157	NEL-like 1 (chicken)
TCN2	1.972	TC2; D22S676; D22S750	NM_000355	transcobalamin II; macrocytic anemia
LOC220686	1.971	LOC220686	NM_199283	hypothetical protein LOC220686
ZNF114	1.969	MGC17986	NM_153608	zinc finger protein 114
ANKRD13	1.965	ANKRD13; NY-REN-25	NM_033121	ankyrin repeat domain 13A
CDKN1C	1.965	BWS; WBS; p57; BWCR; KIP2	NM_000076	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
SCT	1.964	SCT	NM_021920	Secretin
C10ORF39	1.954	FLJ37857	NM_194303	chromosome 10 open reading frame 39
KCNN1	1.947	SK1; hSK1; SKCA1; KCa2.1	NM_002248	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1
DKFZP434I1020	1.945	FLJ45937; DKFZp434I1020	NM_194295	chromosome 15 open reading frame 51
CDS2	1.944	STMN1	NM_003818	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2
AQP11	1.94	AQPX1	NM_173039	aquaporin 11
C8ORF61	1.939	FLJ39417	NM_001034061	chromosome 8 open reading frame 61
TMEM28	1.939	TED; bB57D9.1	NM_015686	transmembrane protein 28
PAPLN	1.938	MGC50452; DKFZp434F053	NM_173462	papilin, proteoglycan-like sulfated glycoprotein
KIAA1598	1.936	MGC40476; DKFZp686A0439	NM_018330	KIAA1598
BRDT	1.934	BRD6	NM_001726	bromodomain, testis-specific
FLNB	1.932	AOI; FH1; SCT; TAP; LRS1; TABP; FLN1L; ABP-278; filamin B; DKFZp686O033; DKFZp686A1668	NM_001457	filamin B, beta (actin binding protein 278)
PCYT2	1.93	ET	NM_002861	phosphate cytidylyltransferase 2, ethanolamine
BRPF3	1.93	VKORC1L1	NM_015695	bromodomain and PHD finger containing, 3
SEC14L2	1.927	SPF; TAP; TAP1; C22orf6; KIAA1186; KIAA1658; MGC65053	NM_012429	SEC14-like 2 (S. cerevisiae)
FLJ35934	1.927	FLJ35934	NM_207453	FLJ35934 protein
FGF11	1.923	FHF3; FLJ16061; MGC45269; MGC102953	NM_004112	fibroblast growth factor 11
LOC55565	1.92	LOC55565	NM_017530	hypothetical protein LOC55565
LOC113179	1.919	LOC113179; FWP005; MST121; S863-5; MSTP121	NM_138422	hypothetical protein BC011824
ZNF364	1.918	RNF115	NM_014455	zinc finger protein 364
USP54	1.916	C10orf29; FLJ37318; bA137L10.3; bA137L10.4	NM_152586	ubiquitin specific peptidase 54
APLP2	1.916	APPH; APPL2; CDEBP	NM_001642	amyloid beta (A4) precursor-like protein 2
RKHD1	1.915	TINO; RNF193; KIAA2031; OK/SW-cl.4	NM_203304	ring finger and KH domain containing 1
APOBEC3F	1.912	KA6; ARP8; MGC74891; BK150C2.4.MRNA	NM_001006666	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F
DSCAM	1.912	CHD2-42; CHD2-52	NM_206887	Down syndrome cell adhesion molecule
RAB5B	1.912	RAB5B	NM_002868	RAB5B, member RAS oncogene family
TP53BP1	1.911	p202; 53BP1; MGC138366	NM_005657	tumor protein p53 binding protein, 1
C1ORF51	1.911	FLJ25889	NM_144697	chromosome 1 open reading frame 51
INPP5E	1.907	PPI5PIV; MGC117201	NM_019892	inositol polyphosphate-5-phosphatase, 72 kDa
NCOA5	1.905	CIA; bA465L10.6	NM_020967	nuclear receptor coactivator 5
TFG	1.901	TF6; TRKT3	NM_006070	TRK-fused gene
PPP1R15A	1.9	GADD34	NM_014330	protein phosphatase 1, regulatory (inhibitor) subunit 15A
C14ORF58	1.897	FLVCR2; FLJ20371	NM_017791	chromosome 14 open reading frame 58
TMC6	1.896	EV1; EVER1; EVIN1; LAK-4P	NM_007267	transmembrane channel-like 6
C10ORF125	1.893	FLJ26016	NM_198472	chromosome 10 open reading frame 125
C8ORF49	1.892	FLJ30972	NM_001031839	chromosome 8 open reading frame 49
CRMP1	1.886	DRP1; DRP-1; DPYSL1	NM_001313	collapsin response mediator protein 1
LOC285989	1.884	LOC285989	NM_213603	zinc finger protein 789
EFHD1	1.883	MST133; PP3051; MSTP133; FLJ13612; DKFZp781H0842	NM_025202	EF-hand domain family, member D1
PRKCQ	1.877	PRKCT; MGC126514; MGC141919; nPKC-theta	NM_006257	protein kinase C, theta
NRCAM	1.876	KIAA0343; MGC138845; MGC138846	NM_005010	neuronal cell adhesion molecule
ENO3	1.875	MSE	NM_001976	enolase 3 (beta, muscle)
ABR	1.872	MDB; FLJ45954	NM_021962	active BCR-related gene
MBD2	1.871	DMTase; NY-CO-41; DKFZp586O0821	NM_015832	methyl-CpG binding domain protein 2
OBSCN	1.87	UNC89; FLJ14124; KIAA1556; MGC120409; MGC120410; MGC120411; MGC120412; MGC138590; DKFZp666E245	NM_052843	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
BCORL	1.87	FLJ11362; B930011H20Rik	NM_021946	BCL6 co-repressor-like 1

1				
RNF165	1.866	RNF165	NM_152470	ring finger protein 165
FLJ35773	1.865	FLJ35773	NM_152599	hypothetical protein FLJ35773
LOC389432	1.863	LOC389432	NM_001030060	SAM domain containing 1
LOC388886	1.861	LOC388886; MGC131773	NM_207644	similar to hypothetical protein LOC192734
VEZT	1.858	VEZATIN; DKFZp761C241	NM_017599	vezatin, adherens junctions transmembrane protein
ARID1A	1.853	B120; P270; BM029; BAF250; C1orf4; BAF250a; SMARCF1	NM_139135	AT rich interactive domain 1A (SWI- like)
SLC7A6	1.85	LAT3; LAT-2; y+LAT-2; KIAA0245; DKFZp686K15246	NM_003983	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
ZMYM3	1.85	MYM; XFIM; ZNF261; DXS6673E; KIAA0385; ZNF198L2	NM_005096	zinc finger, MYM-type 3
SLC7A7	1.849	LPI; LAT3; Y+LAT1; y+LAT-1	NM_003982	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7
ABCA7	1.847	ABCX; ABCA-SSN; FLJ40025	NM_019112	ATP-binding cassette, sub-family A (ABC1), member 7
NCOA6	1.846	NRC; AIB3; ASC2; PRIP; TRBP; RAP250; KIAA0181	NM_014071	nuclear receptor coactivator 6
ARHGEF15	1.846	ARGEF15; FLJ13791; KIAA0915; MGC44868; Vsm-RhoGEF	NM_173728	Rho guanine nucleotide exchange factor (GEF) 15
MGC42630	1.844		NM_175923	
FARP1	1.837	CDEP; PLEKHC2; MGC87400	NM_001001715	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
FLJ10916	1.837	FLJ10916	NM_018271	hypothetical protein FLJ10916
REP15	1.835	REP15	NM_001029874	Rab15 effector protein
JUP	1.834	DP3; PDGB; PKGB; CTNNG; DPIII	NM_002230	junction plakoglobin
LOC128439	1.834	AKAP13	NM_139016	chromosome 20 open reading frame 198
CLCN2	1.834	CLC2; ECA3; EGI3; EGMA; CIC-2	NM_004366	chloride channel 2
CRB3	1.831	DEFB106A	NM_139161	crumbs homolog 3 (Drosophila)
PDE6B	1.828	rd1; PDEB; CSNB3	NM_000283	phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant)
DUSP5	1.825	DUSP; HVH3	NM_004419	dual specificity phosphatase 5
TNNT1	1.824	ANM; MGC104241	NM_003283	troponin T type 1 (skeletal, slow)
PIGQ	1.821	GPI1; hGPI1; MGC12693; c407A10.1	NM_004204	phosphatidylinositol glycan anchor biosynthesis, class Q
ZC3HAV1	1.821	ZAP; ZC3H2; FLB6421; ZC3HDC2; FLJ13288; MGC48898; DKFZp686F2052; DKFZp686H1869; DKFZp686O19171	NM_024625	zinc finger CCCH-type, antiviral 1
HSPA1A	1.82	HSP72; HSPA1; HSPA1B; HSP70-1	NM_005345	heat shock 70kDa protein 1A
PPFIA1	1.819	LIP1; LIP.1; LIPRIN; MGC26800	NM_003626	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
PCDHB5	1.819	PCDH-BETA5; DKFZP586B0217	NM_015669	protocadherin beta 5
SERINC3	1.819	TDE; TDE1; AIGP1; TMS-1; DIFF33; SBBI99	NM_006811	serine incorporator 3
LOC400657	1.816	LOC400657; FLJ10991	NM_001008234	hypothetical gene supported by BC036588
JMJD1A	1.814	TSGA; JMJD1; JHMD2A; KIAA0742; DKFZp686A24246; DKFZp686P07111	NM_018433	jumonji domain containing 1A
RAD54L2	1.814	HSPC325; FLJ21396; FLJ22400; KIAA0809; SRISNF2L	NM_015106	RAD54-like 2 (S. cerevisiae)
ZNF613	1.811	FLJ13590	NM_001031721	zinc finger protein 613
SKI	1.811	SKV	NM_003036	v-ski sarcoma viral oncogene homolog (avian)
ENTPD1	1.81	CD39; ATPDase; NTPDase-1	NM_001776	ectonucleoside triphosphate diphosphohydrolase 1
DDX17	1.81	P72; RH70; DKFZp761H2016	NM_006386	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
MLCK	1.81	MLCK; MLCK2; MGC126319; MGC126320	NM_182493	MLCK protein
LOC283537	1.81	LOC283537; FKSG16	NM_181785	hypothetical protein LOC283537
FLJ14154	1.81	FLJ14154	NM_024845	hypothetical protein FLJ14154
AKAP13	1.808	BRX; LBC; HA-3; Ht31; c-lbc; AKAP-Lbc; FLJ11952; FLJ43341; PROTO-LB; PROTO-LBC	NM_007200	A kinase (PRKA) anchor protein 13
TUBB3	1.806	MC1R; TUBB4; beta-4	NM_006086	tubulin, beta 3
GCH1	1.806	GCH; DYT5; GTPCH1; GTP-CH-1	NM_001024024	GTP cyclohydrolase 1 (dopa-responsive dystonia)
SLC25A18	1.803	GC2	NM_031481	solute carrier family 25 (mitochondrial carrier), member 18
LHFPL2	1.798	KIAA0206; DKFZp781E0375	NM_005779	lipoma HMGIC fusion partner-like 2
ITGB5	1.798	FLJ26658	NM_002213	integrin, beta 5
HYAL3	1.795	LUCA3; LUCA-3; LUCA14; Minna14	NM_003549	hyaluronoglucosaminidase 3
FAM105B	1.792	FLJ34884	NM_138348	family with sequence similarity 105, member B
SUHW2	1.791	ZNF279; ZNF632; 5'OY11.1; D87009.C22.3	NM_080764	suppressor of hairy wing homolog 2 (Drosophila)
GAL3ST4	1.789	FLJ12116; GAL3ST-4	NM_024637	galactose-3-O-sulfotransferase 4
PER2	1.787	FASPS; KIAA0347	NM_022817	period homolog 2 (Drosophila)
CNNM1	1.782	ACDP1; FLJ31632	NM_020348	cyclin M1
C12ORF49	1.781	FLJ21415	NM_024738	chromosome 12 open reading frame 49
ATP12A	1.781	ATP1AL1	NM_001676	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
ALDH2	1.779	ALDM; ALDHI; ALDH-E2; MGC1806	NM_000690	aldehyde dehydrogenase 2 family (mitochondrial)
DAPK1	1.778	DAPK; DKFZp781I035	NM_004938	death-associated protein kinase 1
GYPE	1.778	GPE; MNS; MiIX	NM_198682	glycophorin E
COL9A3	1.777	IDD; MED; EDM3; DJ885L7.4.1	NM_001853	collagen, type IX, alpha 3
BRD1	1.773	BRL; BRPF1; BRPF2; DKFZp686F0325	NM_014577	bromodomain containing 1
FOXI1	1.771	HFH3; FKHL10; FREAC6; MGC34197	NM_012188	forkhead box I1
EXOC6	1.766	SEC15L; Sec15p; FLJ1125; SEC15L1; FLJ11251; MGC33397; DKFZp761I2124	NM_001013848	exocyst complex component 6
C10ORF	1.764	MGC33547	NM_144661	chromosome 10 open reading frame 82

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ZNF694	1.759	ZSCAN31; FLJ23199	NM_001012981	zinc finger protein 694
FOXJ2	1.758	FHX	NM_018416	forkhead box J2
FAM89B	1.756	MTVR1	NM_152832	family with sequence similarity 89, member B
RAD51L3	1.755	Trad; R51H3; HsTRAD; RAD51D	NM_002878	RAD51-like 3 (S. cerevisiae)
RASGRP1	1.755	V; RASGRP; hRasGRP1; MGC129998; MGC129999; CALDAG-GEFI; CALDAG-GEFII	NM_005739	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
MCM8	1.754	MGC4816; MGC12866; C20orf154; MGC119522; MGC119523; dJ967N21.5	NM_032485	MCM8 minichromosome maintenance deficient 8 (S. cerevisiae)
SELI	1.753	SELI; KIAA1724	NM_033505	selenoprotein I
OPLAH	1.752	OPLA; 5-Opase; DKFZP434H244	NM_017570	5-oxoprolinase (ATP-hydrolysing)
GPR128	1.75	FLJ14454; FLJ29035; MGC142011	NM_032787	G protein-coupled receptor 128
KIFC3	1.749	DKFZp686D23201	NM_005550	kinesin family member C3
DRD1IP	1.747	RP11-122K13.5	NM_015722	dopamine receptor D1 interacting protein
FLJ25222	1.742	FLJ25222	NM_199163	CXYorf1-related protein
DKFZP434A0131	1.741	DKFZP434A0131; MGC40269	NM_018991	DKFZp434A0131 protein
GALC	1.74	TRIM5	NM_000153	Galactosylceramidase
ITGA4	1.74	IA4; CD49D; MGC90518	NM_000885	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
C9ORF28	1.739	C9orf28; FLJ00001	NM_033446	family with sequence similarity 125, member B
PFKL	1.738	PFK-B; FLJ30173; DKFZp686G1648; DKFZp686L2097	NM_002626	phosphofructokinase, liver
GPRC5C	1.737	RAIG3; RAIG-3; MGC131820	NM_018653	G protein-coupled receptor, family C, group 5, member C
LOC389634	1.736	LOC389634	NM_001012988	hypothetical LOC389634
TXNDC3	1.735	NME8; SPTRX2; Sptrx-2	NM_016616	thioredoxin domain containing 3 (spermatozoa)
TMPRSS2	1.735	PRSS10	NM_005656	transmembrane protease, serine 2
TTC3	1.735	DCRR1; RNF105; TPRDIII; DKFZp686M0150	NM_003316	tetratricopeptide repeat domain 3
ADCY8	1.733	ADCY3; HBAC1	NM_001115	adenylate cyclase 8 (brain)
HTR1E	1.733	5-HT1E	NM_000865	5-hydroxytryptamine (serotonin) receptor 1E
RALGDS	1.731	RGF; RalGEF; FLJ20922	NM_006266	ral guanine nucleotide dissociation stimulator
CRMP1	1.73	DRP1; DRP-1; DPYSL1	NM_001014809	collapsin response mediator protein 1
NKX2-5	1.729	CSX; CSX1; NKX2E; NKX2.5	NM_004387	NK2 transcription factor related, locus 5 (Drosophila)
ZFPM1	1.728	FOG; FOG1; ZNF408; ZNF89A	NM_153813	zinc finger protein, multitype 1
CDK5R1	1.728	p23; p25; p35; CDK5R; NCK5A; CDK5P35; MGC33831; p35nck5a	NM_003885	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
ATP1B1	1.727	ATP1B; MGC1798	NM_001001787	ATPase, Na+/K+ transporting, beta 1 polypeptide
TMEM97	1.726	MAC30	NM_014573	transmembrane protein 97
STK38	1.724	NDR; NDR1	NM_007271	serine/threonine kinase 38
RELN	1.724	RL	NM_005045	Reelin
ADNP	1.722	KIAA0784	NM_181442	activity-dependent neuroprotector
ZCCHC12	1.72	SIZN; FLJ16123	NM_173798	zinc finger, CCHC domain containing 12
LYL1	1.719	LYL1	NM_005583	lymphoblastic leukemia derived sequence 1
TRIP10	1.719	STP; CIP4; HSTP; STOT	NM_004240	thyroid hormone receptor interactor 10
INPP4A	1.718	INPP4	NM_001566	inositol polyphosphate-4-phosphatase, type I, 107kDa
FLJ20054	1.715	FLJ20054; DKFZp547O0715	NM_019049	hypothetical protein FLJ20054
EPHX1	1.712	MEH; EPHX; EPOX	NM_000120	epoxide hydrolase 1, microsomal (xenobiotic)
SACM1L	1.708	SAC1; KIAA0851; DKFZp686A0231	NM_014016	SAC1 suppressor of actin mutations 1-like (yeast)
AP3B2	1.706	NAPTB; DKFZp686D17136	NM_004644	adaptor-related protein complex 3, beta 2 subunit
SH3BGR	1.705	21-GARP	NM_007341	SH3 domain binding glutamic acid-rich protein
RUSC1	1.704	NESCA; DKFZp761A1822	NM_014328	RUN and SH3 domain containing 1
GRIN3B	1.703	NR3B	NM_138690	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B
FBLIM1	1.702	CAL; FBLP1; FBLP-1; DKFZp434G171; RP11-169K16.5	NM_001024215	filamin binding LIM protein 1
MGC70863	1.7	MGC70863	NM_203302	similar to RPL23AP7 protein
PLCD1	1.7	NCOA3	NM_006225	phospholipase C, delta 1
FLJ37538	1.7	FLJ37538	NM_173564	hypothetical protein FLJ37538
MAGED2	1.699	11B6; BCG1; HCA10; JCL-1; MAGED; MAGE-D2; MGC8386	NM_201222	melanoma antigen family D, 2
ZNF432	1.699	ZNF432	NM_014650	zinc finger protein 432
KIAA0232	1.698	KIAA0232	NM_014743	KIAA0232 gene product
TLE6	1.697	GRG6; FLJ14009; MGC14966	NM_024760	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)
FOXC1	1.697	ARA; IGDA; IHG1; FKHL7; IRID1; FREAC3	NM_001453	forkhead box C1
LOC158318	1.697	FAM27E1	NM_001024608	family with sequence similarity 27, member E1
VENTX	1.696	NA88A; HPX42B; VENTX2; MGC119910; MGC119911	NM_014468	VENT homeobox homolog (Xenopus laevis)
BMP5	1.695	MGC34244	NM_021073	bone morphogenetic protein 5
SEMA6C	1.693	SEMAY; m-Sema Y; m-Sema Y2	NM_030913	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C
CACNA1E	1.689	BII; CACH6; Cav2.3; CACNL1A6	NM_000721	calcium channel, voltage-dependent, alpha 1E subunit
JAG2	1.685	HJ2	NM_002226	jagged 2
ZNF181	1.683	HHZ181; MGC44316	NM_001029997	zinc finger protein 181
RAI17	1.681	MIZ; Zimp10; FLJ13541; KIAA1224	NM_020338	retinoic acid induced 17

LZIC	1.68	MGC15436	NM_032368	leucine zipper and CTNNBIP1 domain containing
TRIM11	1.678	BIA1; RNF92	NM_145214	tripartite motif-containing 11
PPFIA4	1.678	PPFIA4	NM_015053	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4
ITPKB	1.677	IP3K; PIG37; IP3K-B	NM_002221	inositol 1,4,5-trisphosphate 3-kinase B
LOH11CR2A	1.674	BCSC-1	NM_014622	loss of heterozygosity, 11, chromosomal region 2, gene A
ARHGAP27	1.671	CAMGAP1; FLJ43547; MGC120624	NM_199282	Rho GTPase activating protein 27
MLLT10	1.67	AF10; MGC75086; DKFZp686E10210	NM_004641	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10
ZDHHC2	1.668	ZNF372	NM_016353	zinc finger, DHHC-type containing 2
SLPI	1.667	ALP; MPI; ALK1; BLPI; HUSI; WAP4; WFDC4; HUSI-I	NM_003064	secretory leukocyte peptidase inhibitor
PLOD2	1.664	LH2; TLH	NM_182943	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2
TNFRSF25	1.664		NM_148973	
THRAP2	1.663	MED13L; FLJ21627; KIAA1025; TRAP240L; PROSIT240; DKFZp781D0112	NM_015335	thyroid hormone receptor associated protein 2
C14ORF79	1.662	C14orf79	NM_174891	chromosome 14 open reading frame 79
JUND	1.661	JUND	NM_005354	jun D proto-oncogene
HYPB	1.661		NM_012271	
TLE1	1.658	ESG; ESG1; GRG1	NM_005077	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
C1ORF165	1.658	FLJ11588	NM_024603	chromosome 1 open reading frame 165
C8ORF48	1.655		NM_001007090	
NME5	1.655	NM23H5; NM23-H5	NM_003551	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
NCOA1	1.654	SRC1; NCoA-1; RIP160; F-SRC-1; MGC129719; MGC129720	NM_147223	nuclear receptor coactivator 1
PPP1R3F	1.654	Hb2E	NM_033215	protein phosphatase 1, regulatory (inhibitor) subunit 3F
LOC196752	1.652	LOC196752; FLJ34302	NM_001010864	similar to CG32542-PA
TBL2	1.651		NM_032988	
MTNR1A	1.649	MT1; MEL-1A-R	NM_005958	melatonin receptor 1A
KIAA2026	1.649	FLJ20366	NM_001017969	KIAA2026
RTN1	1.648	NSP; MGC133250	NM_206857	reticulon 1
ACVR2B	1.647	ActR-IIB; MGC116908	NM_001106	activin A receptor, type IIB
GCGR	1.645	GGR; MGC138246	NM_000160	glucagon receptor
UBE2Q1	1.644	GTAP; UBE2Q; NICE-5; PRO3094	NM_017582	ubiquitin-conjugating enzyme E2Q (putative) 1
ARSD	1.642	ARSD	NM_009589	arylsulfatase D
KCNJ13	1.642	KIR1.4; KIR7.1; MGC33328	NM_002242	potassium inwardly-rectifying channel, subfamily J, member 13
LBH	1.642	LBH; MGC104312; DKFZP566J091	NM_030915	hypothetical protein DKFZp566J091
CECR6	1.642	GATS	NM_031890	cat eye syndrome chromosome region, candidate 6
SUHW1	1.641	ZNF280; ZNF636; 3'OY11.1	NM_080740	suppressor of hairy wing homolog 1 (Drosophila)
PTPN13	1.64	PNP1; FAP-1; PTP1E; PTPL1; PTPLE; PTP-BL; PTP-BAS; DKFZp686J1497	NM_080685	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
FLJ16542	1.639	FLJ16542; FLJ34141	NM_001004301	FLJ16542 protein
LAPTM4A	1.639	MBNT; Mtrp; LAPTM4; HUMORF13; KIAA0108	NM_014713	lysosomal-associated protein transmembrane 4 alpha
PLA2G4B	1.638	FLJ42498; HsT16992; cPLA2-beta	NM_005090	phospholipase A2, group IVB (cytosolic)
CA9	1.636	MN; CAIX	NM_001216	carbonic anhydrase IX
ZNF578	1.635		NM_152472	
PIK3R1	1.633	GRB1; p85-ALPHA	NM_181504	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)
NCAM1	1.629	CD56; NCAM; MSK39	NM_181351	neural cell adhesion molecule 1
L1CAM	1.628	S10; HSAS; MASA; MIC5; SPG1; CAML1; CD171; HSAS1; N-CAML1	NM_000425	L1 cell adhesion molecule
TBL1XR1	1.628	C21; DC42; IRA1; TBLR1; FLJ12894	NM_024665	transducin (beta)-like 1X-linked receptor 1
TMEM37	1.627	PR; PR1; CACNG5	NM_183240	transmembrane protein 37
TMPO	1.627	TP; LAP2; CMD1T; PRO0868; MGC61508	NM_003276	Thymopoietin
C1ORF188	1.627	FLJ32096	NM_173795	chromosome 1 open reading frame 188
IGSF3	1.626	V8; EWI-3; MGC117164	NM_001542	immunoglobulin superfamily, member 3
DGKB	1.626	DGK; DAGK2; DGK-BETA; KIAA0718	NM_004080	diacylglycerol kinase, beta 90kDa
ZNF653	1.626	ZIP67; E430039K05Rik	NM_138783	zinc finger protein 653
MGC13138	1.626	MGC13138	NM_033410	zinc finger protein 764
PCBD1	1.625		NM_001001939	
CENTA2	1.625	cent-b; HSA272195	NM_018404	centaurin, alpha 2
ZNF701	1.624	FLJ10891	NM_018260	zinc finger protein 701
ELF1	1.624	ELF1	NM_172373	E74-like factor 1 (ets domain transcription factor)
CAMK1	1.623	CAMKI; MGC120317; MGC120318	NM_003656	calcium/calmodulin-dependent protein kinase I
GAL3ST1	1.622	CST	NM_004861	galactose-3-O-sulfotransferase 1
TIGD5	1.622	FLJ14926; MGC44883	NM_032862	tigger transposable element derived 5
DOPEY1	1.622	FLJ35610; KIAA1117; dJ202D23.2	NM_015018	dopey family member 1
FBXO11	1.62	VIT1; FBX11; PRMT9; FLJ12673; MGC44383; UG063H01	NM_018693	F-box protein 11
MGC52000	1.62	MGC52000; CXYorf1; MGC90409; MGC104889; MGC111476; MGC117230	NM_198943	CXYorf1-related protein
ADD3	1.619	ADDL	NM_016824	adducin 3 (gamma)
KIAA01	1.617	KIAA0182	NM_014615	KIAA0182

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LOC113386	1.617	LOC113386; FLJ44718; FLJ46452	NM_138781	similar to envelope protein
ZBTB33	1.617	ZNF348; ZNF-kaiso	NM_006777	zinc finger and BTB domain containing 33
TGIF	1.616	HPE4; MGC5066; MGC39747	NM_003244	TGFB-induced factor (TALE family homeobox)
ZNF14	1.616	KOX6; GIOT-4	NM_021030	zinc finger protein 14
MYT1	1.615	MTF1; MYTI; PLPB1; C20orf36	NM_004535	myelin transcription factor 1
COL4A2	1.615	FLJ22259; DKFZp686I14213	NM_001846	collagen, type IV, alpha 2
B3GNT5	1.615	B3GN-T5; beta3Gn-T5	NM_032047	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
TNFRSF13B	1.614	CVID; TACI; CD267; FLJ39942; MGC39952; MGC133214; TNFRSF14B	NM_012452	tumor necrosis factor receptor superfamily, member 13B
CLDN11	1.614	OSP; OTM	NM_005602	claudin 11 (oligodendrocyte transmembrane protein)
KLKB1	1.614	KLK3	NM_000892	kallikrein B, plasma (Fletcher factor) 1
CEP192	1.612	CEP192	NM_032142	centrosomal protein 192kDa
RGS19	1.61	GAIP; RGSGAIP	NM_005873	regulator of G-protein signalling 19
DMTF1	1.606	DMP1; DMTF; hDMP1; FLJ41265	NM_021145	cyclin D binding myb-like transcription factor 1
HNF4A	1.604	TCF; HNF4; MODY; MODY1; NR2A1; TCF14; HNF4a7; HNF4a8; HNF4a9; NR2A21; FLJ39654	NM_178850	hepatocyte nuclear factor 4, alpha
RTKN	1.604	AURKA	NM_001015055	Rhotekin
TOMM70A	1.603	FLJ90470	NM_014820	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
FLJ39599	1.603	MLPH1; MLPH2; FLJ39599; MGC70356	NM_173803	MPV17 mitochondrial membrane protein-like
S100A13	1.6	S100A13	NM_001024212	S100 calcium binding protein A13
C1ORF53	1.599	LOC554235	NM_001024594	chromosome 1 open reading frame 53
LOC128977	1.597	LOC128977; MGC74441	NM_173793	hypothetical protein LOC128977
CACNA1H	1.595	CACNA1HB; FLJ90484	NM_021098	calcium channel, voltage-dependent, alpha 1H subunit
FGFRL1	1.592	FHFR; FGFR5	NM_001004358	fibroblast growth factor receptor-like 1
P2RY11	1.591	P2Y11	NM_002566	purinergic receptor P2Y, G-protein coupled, 11
DIP	1.588	DIP; KIAA0767; MGC90497; dA59H18.1; dJ439F8.1	NM_015124	death-inducing-protein
STK36	1.587	FU; KIAA1278; DKFZp434N0223	NM_015690	serine/threonine kinase 36 (fused homolog, Drosophila)
NIPSNAP3A	1.585	HSPC299; FLJ13953; MGC14553; DKFZp564D177	NM_015469	nipsnap homolog 3A (C. elegans)
EXOC7	1.585	EX070; EXO70; EXOC1; 2-5-3p; Exo70p; YJL085W; FLJ46415; DKFZp686J04253	NM_015219	exocyst complex component 7
DDEFL1	1.585	UPLC1; FLJ20199	NM_017707	development and differentiation enhancing factor-like 1
NEO1	1.584	NGN; HsT17534	NM_002499	neogenin homolog 1 (chicken)
LOC388389	1.583	FLJ13094; FLJ34211	NM_213607	coiled-coil domain containing 103
DYRK1B	1.582	MIRK	NM_006484	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B
DUSP8	1.58	HB5; HVH8; HVH-5	NM_004420	dual specificity phosphatase 8
CSNK2A1	1.578	CKII; CK2A1; CKII alpha	NM_177559	casein kinase 2, alpha 1 polypeptide
ZNF91	1.578	HPF7; HTF10	NM_003430	zinc finger protein 91
SEMA3F	1.577	SEMA4; SEMAK; SEMA-IV; sema IV	NM_004186	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F
POGK	1.575	BASS2; LST003; KIAA1513; KIAA15131	NM_017542	pogo transposable element with KRAB domain
C15ORF39	1.572	FLJ46337; MGC117209; DKFZP434H132	NM_015492	chromosome 15 open reading frame 39
SMAD5	1.571	Dwfc; JV5-1; MADH5; DKFZp781C1895; DKFZp781O1323	NM_005903	SMAD, mothers against DPP homolog 5 (Drosophila)
KIAA1984	1.568		NM_032874	
ATP8A1	1.568	ATPIA; ATPP2; ATPASEII; MGC26327; MGC130042; MGC130043	NM_006095	ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1
LIMS2	1.567	PINCH-2; FLJ10044	NM_017980	LIM and senescent cell antigen-like domains 2
POGZ	1.567	SUHW5; ZNF635; KIAA0461; MGC71543	NM_145796	pogo transposable element with ZNF domain
NUDT18	1.566	FLJ22494	NM_024815	nudix (nucleoside diphosphate linked moiety X)-type motif 18
ZNF42	1.565	MZF-1; MZF1B; ZNF42; Zfp98; ZSCAN6	NM_198055	myeloid zinc finger 1
ZNF236	1.561	ZNF236A; ZNF236B	NM_007345	zinc finger protein 236
ZNF627	1.56	FLJ90365	NM_145295	zinc finger protein 627
GBGT1	1.56	FS; A3GALNT; UNQ2513; MGC44848; RP11-326L24.6	NM_021996	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1
ZNF24	1.56	KOX17; RSG-A; ZNF191; ZSCAN3; Zfp191	NM_006965	zinc finger protein 24
RBM15B	1.56	OTT3; HUMAGCGB	NM_013286	RNA binding motif protein 15B
LOC400509	1.559	ETV2	NM_001012391	RUN domain containing 2B
SLC16A3	1.558	MCT3; MCT4; MGC138472; MGC138474	NM_004207	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)
PLXNA3	1.555	6.3; SEX; PLXN3; PLXN4; XAP-6; HSSEXGENE; PLEXIN-A3	NM_017514	plexin A3
NOTUM	1.555	HMGA1	NM_178493	notum pectinacetylesterase homolog (Drosophila)
CRAMP1L	1.555	TCE4	NM_020825	Crm, cramped-like (Drosophila)
PPP1R14A	1.551	CPI-17; PPP1INL	NM_033256	protein phosphatase 1, regulatory (inhibitor) subunit 14A
KIAA0999	1.551	KIAA0999; L19; FLJ12240	NM_025164	KIAA0999 protein
ZNF438	1.551	FLJ32761; MGC126671; bA330O11.1; RP11-330O11.1	NM_182755	zinc finger protein 438
SRF	1.55	SRF	NM_003131	serum response factor (c-fos serum response element-binding transcription factor)
DKFZP727G131	1.55	FLJ36794; DKFZp727G131	NM_145111	chromosome 7 open reading frame 38
MAGI3	1.548	MAGI-3; dJ730K3.2; RP4-730K3.1	NM_020965	membrane associated guanylate kinase, WW and PDZ domain

				containing 3
MCART1	1.548	CG7943; MGC14836	NM_033412	mitochondrial carrier triple repeat 1
S100A8	1.546	P8; MIF; NIF; CAGA; CFAG; CGLA; L1Ag; MRP8; CP-10; MA387; 60B8AG	NM_002964	S100 calcium binding protein A8
MTA2	1.546	PID; MTA1L1; DKFZp686F2281	NM_004739	metastasis associated 1 family, member 2
ANXA2	1.545	P36; ANX2; LIP2; LPC2; CAL1H; LPC2D; ANX2L4; PAP-IV	NM_001002857	annexin A2
NKIRAS2	1.543	KBRAS2; MGC74742; kappaB-Ras2; DKFZP434N1526	NM_017595	NFKB inhibitor interacting Ras-like 2
NTN4	1.543	PRO3091; FLJ23180	NM_021229	netrin 4
C17ORF68	1.543	FLJ22170; MGC133331	NM_025099	chromosome 17 open reading frame 68
DDX31	1.539	FLJ13633; FLJ14578; FLJ23349; helicain A; helicain B; helicain C	NM_022779	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31
PCNT2	1.539	KEN; PCN; PCNT2; PCNTB; PCTN2	NM_006031	pericentrin (kendrin)
SLC6A9	1.536	GLYT1; DKFZp547A1118	NM_006934	solute carrier family 6 (neurotransmitter transporter, glycine), member 9
SMG7	1.535	EST1C; SMG-7; SGA56M; C1orf16; FLJ23717; KIAA0250	NM_014837	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)
C1ORF131	1.534	DKFZp547B1713	NM_152379	chromosome 1 open reading frame 131
LOC158160	1.533		NM_001031744	
ALPP	1.532	ALP; PLAP	NM_001632	alkaline phosphatase, placental (Regan isozyme)
B3GNT4	1.531	B3GN-T4; beta3Gn-T4	NM_030765	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
ELAVL1	1.53	HUR; Hua; MelG; ELAV1	NM_001419	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
NIPA1	1.529	FSP3; SPG6; MGC35570; MGC102724	NM_144599	non imprinted in Prader-Willi/Angelman syndrome 1
MAFG	1.529	MGC13090; MGC20149	NM_002359	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)
CNN2	1.528	WDR18	NM_201277	calponin 2
ZNF703	1.528	ZNF503L; FLJ14299	NM_025069	zinc finger protein 703
PPP1R10	1.526	FB19; CAT53; PNUTS	NM_002714	protein phosphatase 1, regulatory subunit 10
ZNF499	1.525	FLJ14486; DKFZp547H249	NM_032792	zinc finger protein 499
GYS1	1.524	GSY; GYS	NM_002103	glycogen synthase 1 (muscle)
ELMO3	1.523	CED12; CED-12; ELMO-3; FLJ13824	NM_024712	engulfment and cell motility 3
UNQ467	1.522	UNQ467	NM_207392	KIPV467
SSTR2	1.522	SSTR2	NM_001050	somatostatin receptor 2
PPP1R16A	1.52	MYPT3; MGC14333	NM_032902	protein phosphatase 1, regulatory (inhibitor) subunit 16A
TULP4	1.518	TUSP; KIAA1397; RP3-442A17.1	NM_020245	tubby like protein 4
HRASLS5	1.518	HRLP5	NM_054108	HRAS-like suppressor family, member 5
LSR	1.517	LISCH7; MGC10659; MGC48312; MGC48503	NM_015925	lipolysis stimulated lipoprotein receptor
LDLRAD3	1.517	SLC41A1	NM_174902	low density lipoprotein receptor class A domain containing 3
PRSS8	1.516	CAP1; PROSTASIN	NM_002773	protease, serine, 8 (prostasin)
KCNH3	1.515	BEC1; ELK2; Kv12.2; KIAA1282	NM_012284	potassium voltage-gated channel, subfamily H (eag-related), member 3
GGTL3	1.514		NM_178025	
C6ORF84	1.513	QN1; C6orf84; FLJ13551	NM_014895	KIAA1009
PLXNB1	1.512	SEP; PLXN5; KIAA0407; PLEXIN-B1	NM_002673	plexin B1
PHF23	1.511	MGC2941; FLJ16355; FLJ22884; hJUNE-1b	NM_024297	PHD finger protein 23
MGC70863	1.51	MGC70863	NM_203477	similar to RPL23AP7 protein
MGC10992	1.51	MGC10992; MGC13119	NM_033212	coiled-coil domain containing 102A
FAM103A1	1.51	MGC2560; C15orf18; HsT19360; MGC102778	NM_031452	family with sequence similarity 103, member A1
ZNF200	1.509	MGC45293	NM_198088	zinc finger protein 200
MMP23A	1.508		NM_004659	
LOC339344	1.507	LOC339344	NM_001012643	hypothetical protein LOC339344
C12ORF36	1.506	FLJ33810; MGC120140	NM_182558	chromosome 12 open reading frame 36
WDFY3	1.506	ALFY; ZFYVE25; KIAA0993; MGC16461	NM_178583	WD repeat and FYVE domain containing 3
ZNF264	1.505	KIF1B	NM_003417	zinc finger protein 264
FLJ14213	1.505	FLJ14213; MGC16218	NM_024841	hypothetical protein FLJ14213
PDZRN4	1.502	LNX4; SAMCAP3L	NM_013377	PDZ domain containing RING finger 4
SLC2A8	1.502	GLUT8; GLUTX1	NM_014580	solute carrier family 2, (facilitated glucose transporter) member 8
CRKL	1.502	CRKL	NM_005207	v-crk sarcoma virus CT10 oncogene homolog (avian)-like
HYOU1	1.501	ORP150; DKFZp686N08236	NM_006389	hypoxia up-regulated 1
APOLD1	1.498	FLJ25138; DKFZP434F0318	NM_030817	apolipoprotein L domain containing 1
RAB3IL1	1.497	GRAB	NM_013401	RAB3A interacting protein (rabin3)-like 1
ZFAND2B	1.494	CHFR	NM_138802	zinc finger, AN1-type domain 2B
OSBPL6	1.494	ORP6; FLJ36583; MGC59642	NM_145739	oxysterol binding protein-like 6
C1ORF102	1.494	NOR1; OSCP1; MGC26685	NM_206837	chromosome 1 open reading frame 102
HRAS	1.493	HRAS1; K-ras; N-ras; RASH1; c-bas/has	NM_176795	v-Ha-ras Harvey rat sarcoma viral oncogene homolog
RPH3AL	1.493	NOC2	NM_006987	rabphilin 3A-like (without C2 domains)
ODF2	1.493	ODF84; ODF2/1; ODF2/2; MGC9034; FLJ44866; MGC111096	NM_153437	outer dense fiber of sperm tails 2
BTBD4	1.49	RINZF; ZNF340; FLJ13502; dJ583P15.7; dJ583P15.8	NM_025224	BTB (POZ) domain containing 4

KIAA1706	1.49	KIAA1706	NM_030636	KIAA1706 protein
ALS2CR13	1.488	FAM117B; FLJ38771; DKFZp686H01244	NM_173511	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13
ZNF189	1.488	PRKCBP1	NM_003452	zinc finger protein 189
FLJ22531	1.486	FLJ22531	NM_024650	hypothetical protein FLJ22531
SIDT2	1.486		NM_015996	
ASB18	1.486	ASB-18	NM_212556	ankyrin repeat and SOCS box-containing 18
ALS2	1.484	ALSJ; PLSJ; IAHSP; ALS2CR6; FLJ31851; KIAA1563; MGC87187	NM_020919	amyotrophic lateral sclerosis 2 (juvenile)
ZNF93	1.483	TF34; HPF34; HTF34; ZNF505	NM_001004126	zinc finger protein 93
PRPH	1.483	NEF4	NM_006262	Peripherin
NR3C1	1.483	GR; GCR; GRL; GCCR	NM_001020825	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
FLJ12571	1.481	dyf-13; FLJ12571	NM_024926	tetratricopeptide repeat domain 26
FES	1.48	FPS	NM_002005	feline sarcoma oncogene
TBC1D13	1.479	FLJ10743; RP11-545E17.5	NM_018201	TBC1 domain family, member 13
C1ORF102	1.478	NOR1; OSCP1; MGC26685	NM_206837	chromosome 1 open reading frame 102
HES6	1.478	HES6	NM_018645	hairy and enhancer of split 6 (Drosophila)
AGPAT3	1.478	MGC4604; LPAAT-GAMMA1	NM_020132	1-acylglycerol-3-phosphate O-acyltransferase 3
NUTF2	1.477	NTF2; PP15	NM_005796	nuclear transport factor 2
TP53INP1	1.477	SIP; Teap; FLJ22139; p53DINP1; TP53DINP1; TP53INP1A; TP53INP1B; DKFZp434M1317	NM_033285	tumor protein p53 inducible nuclear protein 1
FGA	1.477	Fib2; MGC119422; MGC119423; MGC119425	NM_021871	fibrinogen alpha chain
WDR20	1.477	DMR; FLJ33659; MGC33177; MGC33183	NM_181308	WD repeat domain 20
PLEKHJ1	1.477	GNRPX; FLJ10297	NM_018049	pleckstrin homology domain containing, family J member 1
FBXW4	1.476	DAC; FBW4; FBWD4; SHFM3; SHSF3	NM_022039	F-box and WD-40 domain protein 4
PGAP1	1.476	PGAP1; FLJ42774; ISPD3024	NM_024989	GPI deacylase
ZNF214	1.475	BAZ1	NM_013249	zinc finger protein 214
TMEM20	1.475	C10orf60; FLJ33990	NM_153226	transmembrane protein 20
PSKH2	1.474	PSKH2	NM_033126	protein serine kinase H2
ADD3	1.474	ADDL	NM_016824	adducin 3 (gamma)
SNX26	1.473	TCGAP; FLJ39019	NM_052948	sorting nexin 26
ET	1.473	ET	NM_024311	hypothetical protein ET
SAP30BP	1.472	HTRG; HTRP; HCNGP; DKFZp586L2022	NM_013260	SAP30 binding protein
MRPL28	1.472	p15; MAAT1; MGC8499	NM_006428	mitochondrial ribosomal protein L28
MMP11	1.472	ST3; SL-3; STMY3	NM_005940	matrix metallopeptidase 11 (stromelysin 3)
MEST	1.471	PEG1; MGC8703; MGC111102; DKFZp686L18234	NM_177524	mesoderm specific transcript homolog (mouse)
HS3ST1	1.469	3OST; 3OST1	NM_005114	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
CCDC47	1.469	GK001; MSTP041	NM_020198	coiled-coil domain containing 47
WDR60	1.467	FLJ10300; FLJ23575	NM_018051	WD repeat domain 60
RABL5	1.467	FLJ13225; FLJ14117; DKFZp761N0823	NM_022777	RAB, member RAS oncogene family-like 5
COL18A1	1.467	KNO; FLJ27325; MGC74745	NM_030582	collagen, type XVIII, alpha 1
SLC2A4RG	1.467	GEF; HDBP1; Si-1-2; Si-1-2-19	NM_020062	SLC2A4 regulator
GDPD1	1.467	GDE4; UGPQ; FLJ27503; FLJ37451; MGC35046	NM_182569	glycerophosphodiester phosphodiesterase domain containing 1
ZNF205	1.466	ZNF205	NM_001031686	synonym: ZNF210; zinc finger protein 210; Homo sapiens zinc finger protein 205 (ZNF205), transcript variant 1, mRNA.
TP53INP2	1.465	PINH; FLJ21759; FLJ23500; C20orf110; dJ1181N3.1; DKFZp434B2411; DKFZp434O0827	NM_021202	tumor protein p53 inducible nuclear protein 2
CBS	1.465	HIP4	NM_000071	cystathionine-beta-synthase
KIAA1285	1.464	KIAA1285	NM_015694	zinc finger protein 777
EDARADD	1.463	Sep-09	NM_145861	EDAR-associated death domain
DKFZP666G057	1.461	DKFZp666G057	NM_001008226	hypothetical protein DKFZp666G057
SETD8	1.461	SET8; SET07; PR-Set7	NM_020382	SET domain containing (lysine methyltransferase) 8
MGAT4A	1.46	GNT-IV; GNT-IVA	NM_012214	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A
C21ORF55	1.459	C21orf78	NM_017833	chromosome 21 open reading frame 55
PODXL	1.458	PCLP; Gp200; MGC138240	NM_005397	podocalyxin-like
ASB7	1.456	FLJ22551	NM_024708	ankyrin repeat and SOCS box-containing 7
ATN1	1.456	B37; NOD; DRPLA; D12S755E	NM_001007026	atrophin 1
CLSTN2	1.455	CS2; CSTN2; FLJ39113; FLJ39499; MGC119560; alcagamma	NM_022131	calsyntenin 2
TMEM16H	1.455	KIAA1623	NM_020959	transmembrane protein 16H
C11ORF17	1.454	BCA3; AKIP1	NM_182901	chromosome 11 open reading frame 17
RUFY1	1.454	RABIP4; ZFYVE12; FLJ22251	NM_025158	RUN and FYVE domain containing 1
C1ORF26	1.453	FLJ20121; FLJ35944	NM_017673	chromosome 1 open reading frame 26
ST8SIA6	1.452	SIAT8F; ST8SIA-VI; ST8Sia VI	NM_001004470	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6
FLJ20294	1.451	FLJ20294; KIAA1736; MGC33725	NM_017749	hypothetical protein FLJ20294
CD163	1.451	M130; MM130	NM_203416	CD163 molecule
RARA	1.45	RAR; NR1B1	NM_001024809	retinoic acid receptor, alpha
CTBP1	1.449	BARS; MGC104684	NM_001012614	C-terminal binding protein 1
NDRG4	1.449	SMAP-8; FLJ30586; FLJ42011; KIAA1180;	NM_020465	NDRG family member 4

		MGC19632; DKFZp686I1615		
CPSF1	1.449	CPSF160; P/cl.18; HSU37012	NM_013291	cleavage and polyadenylation specific factor 1, 160kDa
GLTSCR1	1.448	GLTSCR1	NM_015711	glioma tumor suppressor candidate region gene 1
C9ORF98	1.447	DDX31; FLJ32704; RP11-143F18.1	NM_152572	chromosome 9 open reading frame 98
CPS1	1.446	CPS1	NM_001875	carbamoyl-phosphate synthetase 1, mitochondrial
SLC22A17	1.446	BOCT; BOIT; hBOIT	NM_016609	solute carrier family 22 (organic cation transporter), member 17
ZNF618	1.446	ZNF618	NM_133374	zinc finger protein 618
SPRED1	1.446	FLJ33903	NM_152594	sprouty-related, EVH1 domain containing 1
FAM65A	1.445	FLJ13725; KIAA1930	NM_024519	family with sequence similarity 65, member A
PTPN14	1.444	PEZ; PTP36; MGC126803	NM_005401	protein tyrosine phosphatase, non-receptor type 14
ITPR1	1.443	IP3R; IP3R1; Insp3r1	NM_002222	inositol 1,4,5-triphosphate receptor, type 1
C20ORF46	1.442	FLJ11190	NM_018354	chromosome 20 open reading frame 46
NFRKB	1.441	DKFZp547B2013	NM_006165	nuclear factor related to kappaB binding protein
MAT2B	1.441	TGR; MAT-II; MGC12237; MATIIbeta; Nbla02999	NM_013283	methionine adenosyltransferase II, beta
SEPP1	1.44	SeP; SELP	NM_005410	selenoprotein P, plasma, 1
HLA-DRB3	1.439	HLA-DR3B; MGC117330	NM_022555	major histocompatibility complex, class II, DR beta 3
CYP3A43	1.439	MGC119315; MGC119316	NM_057096	cytochrome P450, family 3, subfamily A, polypeptide 43
FOXJ1	1.438	HFH4; HFH-4; FKHL13; MGC35202	NM_001454	forkhead box J1
ZNF671	1.437	FLJ23506	NM_024833	zinc finger protein 671
ASRGL1	1.437	ALP; ALP1; FLJ22316	NM_025080	asparaginase like 1
IGSF4D	1.436	NECL3; Necl-3; synCAM2; MGC104534; MGC138341; MGC138343	NM_153184	immunoglobulin superfamily, member 4D
KIAA1202	1.435	KIAA1202	NM_020717	shroom family member 4
TAOK2	1.434	PSK; PSK1; TAO1; TAO2; MAP3K17; KIAA0881	NM_016151	TAO kinase 2
EPHB6	1.434	HEP; MGC129910; MGC129911	NM_004445	EPH receptor B6
ANKRD30B	1.433	NY-BR-1.1	NM_001029862	ankyrin repeat domain 30B
PCTK1	1.433	PCTAIRE; FLJ16665; PCTAIRE1; PCTGAIRE	NM_033018	PCTAIRE protein kinase 1
ZNF161	1.433	DB1; ZNF161	NM_007146	vascular endothelial zinc finger 1
HYI	1.43	HT036; MGC20767; RP11-506B15.5	NM_031207	hydroxypyruvate isomerase homolog (E. coli)
CNTN4	1.43	AXCAM; BIG-2; CNTN4A; MGC33615	NM_175613	contactin 4
GYPA	1.43	MN; GPA; MNS; GPSAT; CD235a; GPErik; HGpMiV; HGpMiX; GpMiIII; HGpMiXI; HGpMiIII; HGpSta(C)	NM_002099	glycophorin A (MNS blood group)
FADS2	1.43	D6D; DES6; TU13; FADSD6; LLCDL2; SLL0262	NM_004265	fatty acid desaturase 2
VTN	1.43	VN; V75; VNT	NM_000638	vitronectin
FOXN4	1.427	FLJ35967	NM_213596	forkhead box N4
KIAA0350	1.427	MGC111457	NM_015226	KIAA0350
FLJ21742	1.427	FLJ21742	NM_032207	chromosome 19 open reading frame 44
RASSF6	1.426	DKFZp686K23225	NM_177532	Ras association (RalGDS/AF-6) domain family 6
SLC44A2	1.426	CTL2; PP1292; FLJ44586; DKFZp666A071	NM_020428	solute carrier family 44, member 2
KIAA0649	1.425	RP11-426A6.6	NM_014811	KIAA0649
GALNT4	1.425	GalNAcT4; GALNAC-T4	NM_003774	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)
SLC29A4	1.424	ENT4; PMAT; FLJ34923	NM_153247	solute carrier family 29 (nucleoside transporters), member 4
LOC552891	1.424	LOC552891	NM_004125	hypothetical protein LOC552891
LOC90693	1.424	FLJ23031; MGC104248	NM_138771	coiled-coil domain containing 126
ENPP4	1.424	NPP4; KIAA0879	NM_014936	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)
PRSS16	1.423	TSSP; FLJ40714	NM_005865	protease, serine, 16 (thymus)
MGC39900	1.422	MGC39900	NM_194324	hypothetical protein MGC39900
MGC33692	1.421	MGC33692	NM_001001794	family with sequence similarity 116, member B
CLIC3	1.42	CLIC3	NM_004669	chloride intracellular channel 3
CXORF44	1.42	CXorf44; FLJ20434	NM_138362	family with sequence similarity 104, member B
C12ORF61	1.419	FLJ25590	NM_175895	chromosome 12 open reading frame 61
FOXH1	1.419	FAST1; FAST-1	NM_003923	forkhead box H1
MTHFR	1.418	MTHFR	NM_005957	5,10-methylenetetrahydrofolate reductase (NADPH)
STRA6	1.418	PP14296; FLJ12541	NM_022369	stimulated by retinoic acid gene 6 homolog (mouse)
ACSS2	1.417	ACS; ACSA; ACAS2; AceCS; MYH7B; dJ1161H23.1; DKFZp762G026	NM_139274	acyl-CoA synthetase short-chain family member 2
CADPS	1.415	CAPS; CAPS1; KIAA1121	NM_183394	Ca2+-dependent secretion activator
PHF2	1.414	GRC5; KIAA0662	NM_024517	PHD finger protein 2
FUK	1.414	FLJ39408; 1110046B12Rik	NM_145059	fucokinase
APOB	1.414	FLDB	NM_000384	apolipoprotein B (including Ag(x) antigen)
NUAK2	1.413	SNARK; FLJ90349; DKFZP434J037; DKFZp686F01113	NM_030952	NUAK family, SNF1-like kinase, 2
HHAT	1.411	Skn; ski; GUP2; SKI1; MART2; MART-2; FLJ10724; FLJ34867	NM_018194	hedgehog acyltransferase
BANP	1.41	SMAR1; SMARBP1; FLJ10177; FLJ20538; DKFZp761H172	NM_079837	BTG3 associated nuclear protein
ALDH6A1	1.41	MMSDH; MMSADHA; MGC40271	NM_005589	aldehyde dehydrogenase 6 family, member A1
C1ORF60	1.409	INT3; C1orf60; FLJ21919; DKFZp686E1950; DKFZp781I1253; RP11-216N14.2;	NM_023015	integrator complex subunit 3

		DKFZp686O20115		
JAK2	1.408	JAK2	NM_004972	Janus kinase 2 (a protein tyrosine kinase)
TCF2	1.407	FJHN; HNF2; LFB3; HNF1B; MODY5; VHNF1; HNF1beta	NM_006481	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor
ZSCAN5	1.406	ZNF495; MGC4161	NM_024303	zinc finger and SCAN domain containing 5
MGC16385	1.406	MGC16385; FLJ23771; FLJ31569; MGC13198	NM_145039	hypothetical protein MGC16385
PHYHIPL	1.405	KIAA1796	NM_032439	phytanoyl-CoA 2-hydroxylase interacting protein-like
RORA	1.405	ROR1; ROR2; ROR3; RZRA; NR1F1; MGC119326; MGC119329	NM_134262	RAR-related orphan receptor A
SLC30A4	1.404	ZNT4	NM_013309	solute carrier family 30 (zinc transporter), member 4
CCBP2	1.403	D6; hD6; CCR9; CCR10; CMKBR9; MGC126678; MGC138250	NM_001296	chemokine binding protein 2
INADL	1.402	Cipp; PATJ; FLJ26982	NM_176878	InaD-like (Drosophila)
DCHS1	1.402	FIB1; CDH25; PCDH16; FLJ11790; KIAA1773	NM_003737	dachsous 1 (Drosophila)
FNDC5	1.402	FRCP2	NM_153756	fibronectin type III domain containing 5
ZNF354A	1.402	EZNF; HKL1; KID1; KID-1; TCF17	NM_005649	zinc finger protein 354A
FIGNL1	1.401	FIGNL1	NM_022116	fidgetin-like 1
C14ORF80	1.4	MGC16771	NM_173608	chromosome 14 open reading frame 80
VPS37C	1.399	FLJ20847	NM_017966	vacuolar protein sorting 37 homolog C (S. cerevisiae)
DMWD	1.399	DMRN9; DMR-N9; gene59; D19S593E	NM_004943	dystrophia myotonica-containing WD repeat motif
ARHGAP24	1.398	p73; FLJ33877; RC-GAP72; p73RhoGAP; DKFZP564B1162	NM_031305	Rho GTPase activating protein 24
VASP	1.398	PTH	NM_001008736	vasodilator-stimulated phosphoprotein
C22ORF19	1.397	Fmip; PK1.3; C22orf19	NM_001002878	THO complex 5
OAS1	1.397	OIAS; IFI-4; OIASI	NM_002534	2',5'-oligoadenylate synthetase 1, 40/46kDa
HCN3	1.397	KIAA1535	NM_020897	hyperpolarization activated cyclic nucleotide-gated potassium channel 3
CPLX2	1.397	CPX2; 921-L; CPX-2; MGC138492	NM_006650	complexin 2
MGC4399	1.396	BMSC-MCP; MGC4399	NM_032315	PNC1 protein
FLJ367779	1.396	FLJ36779	NM_152571	chromosome 9 open reading frame 163
KBTBD2	1.395	BKLHD1	NM_015483	kelch repeat and BTB (POZ) domain containing 2
HOXD1	1.395	HOX4; HOX4G; Hox-4.7	NM_024501	homeobox D1
AGL	1.395	GDE	NM_000028	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)
PCSK4	1.394	PC4; SPC5; MGC34749; DKFZp434B217	NM_017573	proprotein convertase subtilisin/kexin type 4
BCL6B	1.394	BAZF; ZNF62; ZBTB28	NM_181844	B-cell CLL/lymphoma 6, member B (zinc finger protein)
TTYH3	1.394	KIAA1691	NM_025250	tweety homolog 3 (Drosophila)
PLEKHG3	1.393	KIAA0599	NM_015549	pleckstrin homology domain containing, family G (with RhoGef domain) member 3
TOP3B	1.393	TOP3B	NM_003935	topoisomerase (DNA) III beta
GALNT3	1.393	HHS; HFTC; MGC61909; GalNAc-T3; DKFZp686C10199	NM_004482	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)
GYG2	1.392	GN2; GN-2	NM_003918	glycogenin 2
KIAA0323	1.389	KIAA0323	NM_015299	KIAA0323
ZNF322A	1.388	ZNF322; ZNF388; ZNF489; FLJ23393; bA457M11.3	NM_024639	zinc finger protein 322A
TCF2	1.388	FJHN; HNF2; LFB3; HNF1B; MODY5; VHNF1; HNF1beta	NM_000458	transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor
PTPLAD2	1.388	DKFZp686F01145; DKFZp686G24132	NM_001010915	protein tyrosine phosphatase-like A domain containing 2
SLC25A36	1.387	FLJ10618	NM_018155	solute carrier family 25, member 36
RBMS2	1.386	SCR3	NM_002898	RNA binding motif, single stranded interacting protein 2
FAM13C1	1.386	MGC33233	NM_198215	family with sequence similarity 13, member C1
MLL5	1.385	FLJ10078; FLJ14026; HDCMC04P; MGC70452	NM_018682	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)
RAP1GA1	1.384	RAP1GA1; KIAA0474; rap1GAPII	NM_002885	RAP1 GTPase activating protein
COL27A1	1.383	FLJ11895; KIAA1870; MGC11337; RP11-82I1.1	NM_032888	collagen, type XXVII, alpha 1
UMODL1	1.383	DICER1	NM_173568	uromodulin-like 1
LOC317671	1.382	LOC317671	NM_173362	Rieske (Fe-S) domain containing
CBX2	1.382	M33; CDCA6; MGC10561	NM_005189	chromobox homolog 2 (Pc class homolog, Drosophila)
PEX13	1.382	ZWS; NALD	NM_002618	peroxisome biogenesis factor 13
ZNF606	1.381	ZNF328; FLJ14260; KIAA1852	NM_025027	zinc finger protein 606
GGA1	1.38	GGA1	NM_001001561	golgi associated, gamma adaptin ear containing, ARF binding protein 1
IL18	1.38	IGIF; IL-18; IL-1g; IL1F4; MGC12320	NM_001562	interleukin 18 (interferon-gamma-inducing factor)
ZNF566	1.38	FLJ14779; MGC12515	NM_032838	zinc finger protein 566
APOA4	1.38	MGC142154; MGC142156	NM_000482	apolipoprotein A-IV
ARPC4	1.379	ARC20; p20-Arc; MGC13544	NM_005718	actin related protein 2/3 complex, subunit 4, 20kDa
PRMT1	1.378	ANM1; HCP1; IR1B4; HRMT1L2	NM_198319	protein arginine methyltransferase 1
FLJ10996	1.378	FLJ10996; FLJ25197; MGC13033	NM_019044	coiled-coil domain containing 93
SEC10L1	1.378	SEC10; HSEC10; SEC10P; PRO1912; SEC10L1; DKFZp666H126	NM_006544	exocyst complex component 5
GCN5L2	1.378	GCN5; hGCN5; MGC102791	NM_021078	GCN5 general control of amino-acid synthesis 5-like 2 (yeast)
KIAA0961	1.376	ZNF745; KIAA0961	NM_014898	zinc finger protein 30 homolog (mouse)
JPH3	1.376	JP3; HDL2; JP-3; TNRC22; CAGL237; FLJ44707	NM_020655	junctophilin 3
ZNF503	1.375	NOLZ-1; MGC2555; FLJ45745	NM_032772	zinc finger protein 503

LSM14B	1.375	FT005; LSM13; FAM61B; C20orf40; FLJ25473; bA11M20.3	NM_144703	LSM14 homolog B (SCD6, S. cerevisiae)
KIAA1906	1.375	KIAA1786; KIAA1906	NM_052907	transmembrane protein 132B
EPM2AIP1	1.373	FLJ11207; KIAA0766	NM_014805	EPM2A (laforin) interacting protein 1
TRIM41	1.372	MGC1127; MGC31991	NM_201627	tripartite motif-containing 41
DHX8	1.371	DDX8; HRH1; PRP22; PRPF22	NM_004941	DEAH (Asp-Glu-Ala-His) box polypeptide 8
KHDRBS2	1.371	SLM1; SLM-1; MGC26664; bA535F17.1	NM_152688	KH domain containing, RNA binding, signal transduction associated 2
MAFB	1.371	KRML; MGC43127	NM_005461	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
NAPRT1	1.371	PP3856	NM_145201	nicotinate phosphoribosyltransferase domain containing 1
C14ORF135	1.369	FBP2; FLJ12799; FLJ38170	NM_022495	chromosome 14 open reading frame 135
CNTFR	1.368	MGC1774	NM_147164	ciliary neurotrophic factor receptor
RAB24	1.367	RAB24	NM_130781	RAB24, member RAS oncogene family
MAP1LC3A	1.366	MAP1ALC3; MAP1BLC3	NM_181509	microtubule-associated protein 1 light chain 3 alpha
TMPO	1.366	TP; LAP2; CMD1T; PRO0868; MGC61508	NM_003276	thymopoietin
ZNF297B	1.366	ZNF-X; ZBTB22B; ZNF297B	NM_014007	zinc finger and BTB domain containing 43
RTN4R	1.366	NGR; NOGOR	NM_023004	reticulon 4 receptor
SIRT4	1.366	SIR2L4; MGC57437; MGC130046; MGC130047; sirtuin 4	NM_012240	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)
LMLN	1.366	Msp; Gp63	NM_033029	leishmanolysin-like (metallopeptidase M8 family)
ZNF136	1.365	pHZ-20	NM_003437	zinc finger protein 136
HBG1	1.365	HBGA; HBGR; HSGGL1; PRO2979	NM_000559	hemoglobin, gamma A
FLCN	1.364	BHD; FLCL; MGC17998; MGC23445	NM_144606	folliculin
ZNF429	1.364	ZNF429	NM_001001415	zinc finger protein 429
FLVCR	1.364	FLVCR; FLVCR1	NM_014053	feline leukemia virus subgroup C cellular receptor
PIM3	1.363	pim-3	NM_001001852	pim-3 oncogene
CD300A	1.362	IRC1; IRC2; IRp60; IGSF12; CMRF35H; CMRF-35H; CMRF35H9; CMRF-35-H9	NM_007261	CD300a molecule
MGC34713	1.362	MGC34713	NM_173665	hypothetical protein MGC34713
HLRC1	1.361	HLRC1; MGC4293	NM_031304	deoxyhypusine hydroxylase/monooxygenase
FLJ457177	1.361	FLJ45717	NM_207401	FLJ45717 protein
CLASP1	1.361	MAST1; FLJ33821; KIAA0622; MGC131895; DKFZp686D1968; DKFZp686H2039	NM_015282	cytoplasmic linker associated protein 1
ZBTB8OS	1.361	ARCH; ARCH2; MGC62007	NM_178547	zinc finger and BTB domain containing 8 opposite strand
CDCA7	1.361	JPO1; FLJ14722; FLJ14736; MGC34109	NM_031942	cell division cycle associated 7
VASP	1.359	PTH	NM_003370	vasodilator-stimulated phosphoprotein
MLL3	1.358	HALR; FLJ12625; FLJ38309; KIAA1506; DKFZp686C08112	NM_170606	myeloid/lymphoid or mixed-lineage leukemia 3
OVCH2	1.358	OVTN	NM_198185	ovochymase 2
AGRN	1.358	AGRN; FLJ45064	NM_198576	agrin
CCRK	1.357	p42; CDCH	NM_178432	cell cycle related kinase
MGC4093	1.355	MGC4093	NM_030578	hypothetical protein MGC4093
PB1	1.355	PB1; BAF180	NM_181042	polybromo 1
LOC197336	1.355	FLJ36483; FLJ44660; KIAA1924	NM_145294	WD repeat domain 90
PTCD1	1.354	KIAA0632	NM_015545	pentatricopeptide repeat domain 1
AGL	1.354	GDE	NM_000642	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)
PIK3C2A	1.353	CPK; MGC142218; PI3-K-C2A; DKFZp686L193; PI3-K-C2(ALPHA)	NM_002645	phosphoinositide-3-kinase, class 2, alpha polypeptide
CTNNA2	1.353	CAPR; CTNR; CAP-R; DKFZp686H02198	NM_004389	catenin (cadherin-associated protein), alpha 2
C9ORF58	1.351	IBA2; FLJ12783; MGC29466; RP11-544A12.2	NM_031426	chromosome 9 open reading frame 58
C15ORF38	1.351	MGC61550	NM_182616	chromosome 15 open reading frame 38
ZNF707	1.35	ZNF707	NM_173831	zinc finger protein 707
YWHAE	1.35	MDS; MDCR; KCIP-1; 14-3-3E; FLJ45465	NM_006761	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
TRAF4	1.348	CART1; MLN62; RNF83	NM_004295	TNF receptor-associated factor 4
FLJ10404	1.347	FLJ10404; KIAA1931; DKFZp313I142	NM_019057	hypothetical protein FLJ10404
LOC124751	1.347	LOC124751	NM_213597	KRAB-A domain containing 2
KLHL9	1.347	RP11-380P16.6	NM_018847	kelch-like 9 (Drosophila)
C10ORF119	1.346	FLJ13081; FLJ36756	NM_024834	chromosome 10 open reading frame 119
Sep-05	1.346	H5; CDCREL; PNUTL1; CDCREL1; CDCREL-1	NM_002688	septin 5
SORBS3	1.346	SH3D4; SCAM-1; vinexin	NM_005775	sorbin and SH3 domain containing 3
RPRC1	1.345	PARCC1; FLJ10350; MGC117315	NM_018067	arginine/proline rich coiled-coil 1
BRWD3	1.344	BRODL; FLJ38568	NM_153252	bromodomain and WD repeat domain containing 3
EVI1	1.343	EVI-1; PRDM3; MDS1-EVI1; AML1-EVI-1	NM_005241	ecotropic viral integration site 1
ADPN	1.343	ADPN; C22orf20; iPLA(2)epsilon	NM_025225	patatin-like phospholipase domain containing 3
CKM	1.342	CKMM; M-CK	NM_001824	creatine kinase, muscle
BTBD2	1.341	BTBD2	NM_017797	BTB (POZ) domain containing 2
IL28RA	1.339	IFNLR; LICR2; IFNLR1; CRF2/12	NM_170743	interleukin 28 receptor, alpha (interferon, lambda receptor)
GAS8	1.339	GAS11; MGC138326	NM_001481	growth arrest-specific 8
JMJD4	1.339	FLJ12517; MGC129896	NM_023007	jumonji domain containing 4
FGF12	1.339	FHF1; FGF12B	NM_021032	fibroblast growth factor 12
HEXDC	1.338	FLJ23825	NM_173620	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing
CDC2L5	1.337	CHED; CDC2L; FLJ35215; KIAA1791	NM_003718	cell division cycle 2-like 5 (cholinesterase-related cell division controller)

KIAA0423	1.336	DKFZp686D12126	NM_015091	KIAA0423
ACRC	1.336	NAAR1	NM_052957	acidic repeat containing
CNOT7	1.335	CAF1; hCAF-1	NM_054026	CCR4-NOT transcription complex, subunit 7
RGS5	1.334	MST092; MST106; MST129; MSTP032; MSTP092; MSTP106; MSTP129	NM_003617	regulator of G-protein signalling 5
COLEC11	1.334	MGC3279; DKFZp686N1868	NM_024027	collectin sub-family member 11
CMTM3	1.333	BNAS2; CKLFSF3; FLJ31762; MGC51956	NM_181553	CKLF-like MARVEL transmembrane domain containing 3
MMAB	1.333	ATR; MGC20496	NM_052845	methylmalonic aciduria (cobalamin deficiency) cblB type
NAPB	1.332	MGC26066; MGC48335; SNAP-BETA	NM_022080	N-ethylmaleimide-sensitive factor attachment protein, beta
DNASE1L2	1.332	DNAS1L2	NM_001374	deoxyribonuclease I-like 2
PLA2G12B	1.331	FKSG71; PLA2G13; MGC138151; GXIIIsPLA2	NM_032562	phospholipase A2, group XIIB
MBD3	1.331	MBD3	NM_003926	methyl-CpG binding domain protein 3
NNAT	1.33	Peg5; MGC1439	NM_005386	neuronatin
NPB	1.33	PPL7; PPNPB	NM_148896	neuropeptide B
TRRAP	1.33	Tra1; TR-AP; PAF400; STAF40; FLJ10671; PAF350/400	NM_003496	transformation/transcription domain-associated protein
C20ORF177	1.329	dJ551D2.5	NM_022106	chromosome 20 open reading frame 177
CMTM4	1.329	CKLFSF4	NM_178818	CKLF-like MARVEL transmembrane domain containing 4
PARD6B	1.327	PAR6B	NM_032521	par-6 partitioning defective 6 homolog beta (C. elegans)
CEP164	1.327	KIAA1052	NM_014956	centrosomal protein 164kDa
GATAD1	1.326	ODAG; FLJ22489; RG083M05.2	NM_021167	GATA zinc finger domain containing 1
RAB11FIP3	1.325	KIAA0665; Rab11-FIP3	NM_014700	RAB11 family interacting protein 3 (class II)
THAP8	1.324	FLJ32891	NM_152658	THAP domain containing 8
FLJ23861	1.324	FLJ23861	NM_152519	hypothetical protein FLJ23861
ABCB6	1.322	ABC; PRP; umat; ABC14; MTABC3; EST45597; FLJ22414	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6
GDPD3	1.322	MGC4171; FLJ22603	NM_001031718	glycerophosphodiester phosphodiesterase domain containing 3
BBS1	1.321	BBS2L2; FLJ23590; MGC51114; MGC126183; MGC126184	NM_024649	Bardet-Biedl syndrome 1
PDE9A	1.321	HSPDE9A2	NM_001001573	phosphodiesterase 9A
LOC147808	1.319	MGC75238	NM_203374	zinc finger protein 784
ZNF573	1.319	FLJ30921	NM_152360	zinc finger protein 573
HLX1	1.318	HB24	NM_021958	H2.0-like homeobox 1 (Drosophila)
HEMK1	1.318	HEMK; MTQ1; FLJ22320	NM_016173	HemK methyltransferase family member 1
KIAA0446	1.317	KIAA0446; RP11-54H19.3	NM_014655	KIAA0446 gene product
LOC388323	1.317	LOC388323	NM_001014985	hypothetical LOC388323
C13ORF7	1.317	FLJ13449; FLJ25774; DKFZp686A01276; DKFZp686N15250; DKFZp686O03173	NM_024546	chromosome 13 open reading frame 7
RCBTB1	1.316	GLP; CLLD7; CLLL7; MGC33184; RP11-185C18.1	NM_018191	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1
FBXO11	1.313	VIT1; FBX11; PRMT9; FLJ12673; MGC44383; UG063H01	NM_012167	F-box protein 11
UBTF	1.312	UBF; NOR-90	NM_014233	upstream binding transcription factor, RNA polymerase I
TCF7L1	1.312	TCF3; TCF-3	NM_031283	transcription factor 7-like 1 (T-cell specific, HMG-box)
KIAA0040	1.312	MGC133301	NM_014656	KIAA0040
PCYOX1	1.311	PCL1; KIAA0908	NM_016297	prenylcysteine oxidase 1
XYLB	1.31	FLJ10343; FLJ12539; FLJ22075	NM_005108	xylulokinase homolog (H. influenzae)
CXORF39	1.307	C10orf18	NM_207318	chromosome X open reading frame 39
HM13	1.307	H13; SPP; IMP1; PSL3; IMPAS; PSENL3; MSTP086; dJ324O17.1	NM_178582	histocompatibility (minor) 13
SEMA3D	1.307	coll-2; Sema-Z2; MGC39708	NM_152754	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D
FLJ31568	1.307	FLJ31568; MGC126046; MGC126047	NM_152509	FLJ31568 protein
DIO1	1.305	5DI; TXDI1; MGC130050; MGC130051	NM_000792	deiodinase, iodothyronine, type I
SLCO1A2	1.303	OATP; OATP-A; OATP1A2; SLC21A3	NM_005075	solute carrier organic anion transporter family, member 1A2
ACE2	1.303	ACEH; DKFZP434A014	NM_021804	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
NUP98	1.302	ADIR2; NUP196	NM_139131	nucleoporin 98kDa
DOCK7	1.301	ZIR2; KIAA1771	NM_033407	dedicator of cytokinesis 7
LOC375449	1.301	LOC375449	NM_198828	similar to microtubule associated testis specific serine/threonine protein kinase
C4ORF8	1.301	RES4-22	NM_003704	chromosome 4 open reading frame 8
C20ORF195	1.3	MGC5356	NM_024059	chromosome 20 open reading frame 195
NPAL1	1.3	DKFZp686A06115	NM_207330	NIPA-like domain containing 1
TPM2	1.3	DA1; TMSB; AMCD1	NM_003289	tropomyosin 2 (beta)
HRK	1.3	DP5; HARAKIRI	NM_003806	harakiri, BCL2 interacting protein (contains only BH3 domain)
DIAPH3	1.299	DRF3; diap3; FLJ34705; DKFZP434C0931; DKFZp686A13178	NM_030932	diaphanous homolog 3 (Drosophila)
JAKMIP1	1.299	JAMIP1; MARLIN1; FLJ31564; Gababrbp	NM_144720	janus kinase and microtubule interacting protein 1
SLC27A6	1.298	FATP6; ACSVL2; FACVL2; VLCS-H1; DKFZp779M0564	NM_001017372	solute carrier family 27 (fatty acid transporter), member 6
NFIB	1.298	NFIB2; NFIB3; NFI-RED	NM_005596	nuclear factor I/B
CACNA2D2	1.297	CACNA2D; gene 26; KIAA0558; LUAC11.1	NM_001005505	calcium channel, voltage-dependent, alpha 2/delta subunit 2
C9ORF93	1.296	FLJ39267; FLJ46740; MGC50805; bA536D16.1; bA778P13.1	NM_173550	chromosome 9 open reading frame 93

HEXIM 1	1.296	CLP1; EDG1; HIS1; MAQ1	NM_006460	hexamethylene bis-acetamide inducible 1
CLCN6	1.294	CLC-6; KIAA0046	NM_021737	chloride channel 6
MAP1B	1.294	MAP5; FUTSCH; FLJ38954; DKFZp686E1099; DKFZp686F1345	NM_005909	microtubule-associated protein 1B
PGEA1	1.293	CBY; arb1; C22orf2; PIGEA14; PIGEA-14; HS508I15A	NM_001002 880	PKD2 interactor, golgi and endoplasmic reticulum associated 1
ULK1	1.293	ATG1; UNC51; Unc51.1; FLJ38455	NM_003565	unc-51-like kinase 1 (C. elegans)
RGS12	1.293	DKFZp761K1617; DKFZp761K1817	NM_002926	regulator of G-protein signalling 12
SLC25A 24	1.293	APC1; SCAMC-1; DKFZp586G0123	NM_013386	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24
CD37	1.292	GP52-40; TSPAN26; MGC120234	NM_001774	CD37 molecule
PDE4D	1.292	DPDE3; STRK1; HSPDE4D; PDE4DN2	NM_006203	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)
SPAG1	1.291	SP75; TPIS; HSD-3.8; FLJ32920	NM_172218	sperm associated antigen 1
SLC44A 1	1.291	CTL1; CDW92; CHTL1; RP11-287A8.1	NM_022109	solute carrier family 44, member 1
PHF20L 1	1.29	CGI-72; MGC64923	NM_016018	PHD finger protein 20-like 1
ZNF689	1.29	TIPUH1; FLJ90415; DKFZp762C173	NM_138447	zinc finger protein 689
CYP2R1	1.29	MGC4663	NM_024514	cytochrome P450, family 2, subfamily R, polypeptide 1
HPX	1.29	HBA2	NM_000613	hemopexin
IRF6	1.29	LPS; PIT; PPS; VWS; OFC6	NM_006147	interferon regulatory factor 6
SOSTD C1	1.289	USAG1; CDA019; ECTODIN; DKFZp564D206	NM_015464	sclerostin domain containing 1
ZNF543	1.289	DKFZp434H055	NM_213598	zinc finger protein 543
GSDML	1.285	PP4052; PRO2521	NM_018530	gasdermin-like
DOK6	1.285	DOK5L; HsT3226; MGC20785	NM_152721	docking protein 6
ZNF549	1.285	FLJ34917	NM_153263	zinc finger protein 549
C21ORF 29	1.284	TSPEAR; MGC11251	NM_144991	chromosome 21 open reading frame 29
NPEPPS	1.284	PSA; MP100	NM_006310	aminopeptidase puromycin sensitive
SLC38A 5	1.284	SN2; JM24; pp7194	NM_033518	solute carrier family 38, member 5
RGS6	1.284	GAP; MGC142132	NM_004296	regulator of G-protein signalling 6
PMF1	1.284	IL8RA	NM_007221	polyamine-modulated factor 1
PDK1	1.284	PTPRF	NM_002610	pyruvate dehydrogenase kinase, isozyme 1
C1ORF1 04	1.283		NM_173639	
PSEN1	1.283		NM_007319	
MRPL43	1.283	bMRP36a; MGC17989; MGC48892	NM_176794	mitochondrial ribosomal protein L43
SCTR	1.282	SR	NM_002980	secretin receptor
SLC2A6	1.282	GLUT6; GLUT9; HSA011372	NM_017585	solute carrier family 2 (facilitated glucose transporter), member 6
STAU	1.282	STAU; FLJ25010	NM_017453	staufen, RNA binding protein, homolog 1 (Drosophila)
GGA1	1.282	GGA1	NM_001001 561	golgi associated, gamma adaptin ear containing, ARF binding protein 1
SRC	1.281	ASV; SRC1; c-SRC; p60-Src	NM_198291	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
ZDHHC 12	1.281	ZNF400; FLJ14524; MGC13153; MGC54050	NM_032799	zinc finger, DHHC-type containing 12
SPINK5	1.28	NS; NETS; LEKTI; LETKI; VAKTI; FLJ21544	NM_006846	serine peptidase inhibitor, Kazal type 5
DMGD H	1.279	DMGDHD; ME2GLYDH	NM_013391	dimethylglycine dehydrogenase
CCDC7	1.279	FLJ32762; DKFZp686N0559; RP11-479G22.1	NM_145023	coiled-coil domain containing 7
BAZ1A	1.279	ACF1; WALp1; hACF1; WCRF180; FLJ14383; DKFZP586E0518	NM_182648	bromodomain adjacent to zinc finger domain, 1A
CAPN10	1.278	CAPN10	NM_021251	calpain 10
FLJ4113 1	1.278	FLJ41131; MGC103014	NM_198476	chromosome 19 open reading frame 54
NANP	1.278	HDHD4; MGC26833; C20orf147; dJ694B14.3	NM_152667	N-acetylneuraminic acid phosphatase
FGF13	1.277	FGF2; FHF2	NM_004114	fibroblast growth factor 13
FKBP2	1.277	PPIase; FKBP-13	NM_057092	FK506 binding protein 2, 13kDa
UBXD8	1.277	ETEA; KIAA0887	NM_014613	UBX domain containing 8
NCOA1	1.276	SRC1; NCoA-1; RIP160; F-SRC-1; MGC129719; MGC129720	NM_147223	nuclear receptor coactivator 1
FLJ1008 1	1.276	FLJ10081; FLJ23799; KIAA1310	NM_017991	hypothetical protein FLJ10081
REPS2	1.275	POB1	NM_004726	RALBP1 associated Eps domain containing 2
ONECU T1	1.274	HNF6; HNF-6; HNF6A	NM_004498	one cut domain, family member 1
SAMD1 4	1.274	FLJ36890	NM_174920	sterile alpha motif domain containing 14
CIC	1.274	KIAA0306	NM_015125	capicua homolog (Drosophila)
NOXA1	1.273	p51NOX; FLJ25475; NY-CO-31; SDCCAG31; MGC131800	NM_006647	NADPH oxidase activator 1
KRTAP 17-1	1.273	KAP17.1; KRTAP16.1; KRTAP17.1	NM_031964	keratin associated protein 17-1
PLAGL2	1.273	FLJ23283	NM_002657	pleiomorphic adenoma gene-like 2
TAF6L	1.273	PAF65A; MGC4288; FLJ11136	NM_006473	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa
FZR1	1.272	FZR; CDH1; FZR2; HCDH; HCDH1; CDC20C; KIAA1242	NM_016263	fizzy/cell division cycle 20 related 1 (Drosophila)
TMEPAI	1.272	STAG1; PMEPA1	NM_199171	transmembrane, prostate androgen induced RNA
IFT81	1.271	CDV1; CDV-1; CDV1R; CDV-1R; MGC4027; MGC102777	NM_031473	intraflagellar transport 81 homolog (Chlamydomonas)
MGC52 423	1.271	MGC52423	NM_182517	chromosome 1 open reading frame 210
KLC4	1.27	KNSL8; MGC111777; bA387M24.3	NM_138343	kinesin light chain 4
TTC25	1.27	DKFZP434H0115	NM_031421	tetratricopeptide repeat domain 25
ITK	1.269	EMT; LYK; PSCTK2; MGC126257; MGC126258	NM_005546	IL2-inducible T-cell kinase
ZNF334	1.269	CDCA8	NM_018102	zinc finger protein 334
TSSC4	1.269	TSSC4	NM_005706	tumor suppressing subtransferable candidate 4
GMPPB	1.269	KIAA1851	NM_013334	GDP-mannose pyrophosphorylase B
ZNF440 L	1.269	ZNF; ZNF440L	NM_001012 753	zinc finger protein 763
CHMP6	1.269	VPS20; FLJ11749	NM_024591	chromatin modifying protein 6

BRCC2	1.268	BRCC2	NM_001001786	BRCC2
FBXL11	1.268	FBL7; CXXC8; FBL11; JHDM1A; LILINA; FLJ00115; FLJ46431; KIAA1004; DKFZP434M1735	NM_012308	F-box and leucine-rich repeat protein 11
LMO1	1.266	TTG1; RBTN1; RHOM1; MGC116692	NM_002315	LIM domain only 1 (rhombotin 1)
BCAM	1.265	AU; LU; CD239; MSK19	NM_001013257	basal cell adhesion molecule (Lutheran blood group)
MYO9A	1.264	FLJ11061; FLJ13244; MGC71859	NM_006901	myosin IXA
C1ORF201	1.264	FLJ33340	NM_178122	chromosome 1 open reading frame 201
PAK4	1.264	CRMP1	NM_001014832	p21(CDKN1A)-activated kinase 4
C3ORF19	1.264	FLJ33839	NM_016474	chromosome 3 open reading frame 19
C10ORF85	1.263	FLJ37402; MGC131689	NM_001012711	chromosome 10 open reading frame 85
ZFAND3	1.263	TEX27; FLJ13222	NM_021943	zinc finger, AN1-type domain 3
GAB1	1.262	GAB1	NM_207123	GRB2-associated binding protein 1
PCDH17	1.262		NM_014459	
SMARCA4	1.261	BRG1; BAF190; SNF2L4; SNF2LB; hSNF2b; SNF2-BETA	NM_003072	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
OATL1	1.261	MGC126866; MGC126868	NM_001006113	ornithine aminotransferase-like 1
AKT2	1.261	PRKBB; PKBBETA; RAC-BETA	NM_001626	v-akt murine thymoma viral oncogene homolog 2
PSMA7	1.26		NM_152255	
CPNE8	1.259	MGC129645; MGC129646	NM_153634	copine VIII
UBE3B	1.259		NM_183414	
RNF32	1.259	HSD15; FKSG33	NM_030936	ring finger protein 32
PAOX	1.259	PAO; MGC45464; DKFZp434J245; RP11-122K13.11	NM_152911	polyamine oxidase (exo-N4-amino)
TMLHE	1.259	TMLH; BBOX2; XAP130; FLJ10727	NM_018196	trimethyllysine hydroxylase, epsilon
CLMN	1.258	FLJ12383; KIAA1188	NM_024734	calmin (calponin-like, transmembrane)
RNF24	1.258	G1L	NM_007219	ring finger protein 24
SLC4A1AP	1.257	HLC3; FLJ10624; MGC120646; MGC120648	NM_018158	solute carrier family 4 (anion exchanger), member 1, adaptor protein
UBE2D2	1.257	UBC4; PUBC1; UBC4/5; UBCH5B; E2(17)KB2	NM_181838	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
ARG99	1.257		NM_031920	
CDKL4	1.255	IL20	NM_001009565	cyclin-dependent kinase-like 4
RCOR1	1.255	RCOR; COREST; KIAA0071	NM_015156	REST corepressor 1
C19ORF23	1.254	MGC39338	NM_152480	chromosome 19 open reading frame 23
IER5	1.254	SBBI48; MGC102760	NM_016545	immediate early response 5
C6ORF48	1.254		NM_016947	
OR2T8	1.254	OR2T8P	NM_001005522	olfactory receptor, family 2, subfamily T, member 8
SIX5	1.254	DMAHP	NM_175875	sine oculis homeobox homolog 5 (Drosophila)
ATF5	1.253	ATFX; FLJ34666; HMFN0395	NM_012068	activating transcription factor 5
VEGFB	1.253	VRF; VEGFL	NM_003377	vascular endothelial growth factor B
FLNA	1.252	FLN; FMD; MNS; OPD; ABPX; FLN1; NHBP; OPD1; OPD2; ABP-280; filamin A; DKFZp434P031	NM_001456	filamin A, alpha (actin binding protein 280)
THRAP5	1.252	MED16; DRIP92; TRAP95	NM_005481	thyroid hormone receptor associated protein 5
CLK4	1.252	DKFZp686A20267	NM_020666	CDC-like kinase 4
LRRC35	1.252	El; FLJ14177; MGC10233	NM_152715	leucine rich repeat containing 35
B3GALT3	1.251	P; P1; GLOB; GLCT3; galT3; Gb4Cer; B3GALT3; beta3Gal-T3	NM_033169	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
ZFP95	1.251	FLJ39233; KIAA1015; MGC33710	NM_014569	zinc finger protein 95 homolog (mouse)
PCDH1	1.25	PC42; PCDH42; MGC45991	NM_032420	protocadherin 1 (cadherin-like 1)
TTMB	1.25	TTMB; MGC90489; MGC102864	NM_001003682	TTMB protein
GGPS1	1.25	GGPPS; GGPPS1	NM_004837	geranylgeranyl diphosphate synthase 1
FLJ38159	1.249	FLJ38159	NM_152723	coiled-coil domain containing 89
MTRR	1.249	MSR; MGC129643	NM_024010	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
CD163	1.249	M130; MM130	NM_004244	CD163 molecule
ZMYND10	1.247	BLU; FLU	NM_015896	zinc finger, MYND-type containing 10
ABC1	1.246	ABC1; FLJ22087; MGC148096; DKFZp686D22141	NM_022070	amplified in breast cancer 1
NALP9	1.246	NOD6	NM_176820	NACHT, leucine rich repeat and PYD containing 9
RFFL	1.246	RNF189; RNF34L	NM_001017368	ring finger and FYVE-like domain containing 1
L3MBTL	1.246	L3MBTL1; KIAA0681; H-L(3)MBT; dJ138B7.3; DKFZp586P1522	NM_032107	l(3)mbt-like (Drosophila)
SSX7	1.245	SSX2	NM_173358	synovial sarcoma, X breakpoint 7
ALK	1.245	CD246	NM_004304	anaplastic lymphoma kinase (Ki-1)
MKL2	1.245	MRTF-B; NPD001; FLJ31823; DKFZp686J1745	NM_014048	MKL/myocardin-like 2
HCK	1.245	JTK9	NM_002110	hemopoietic cell kinase
ITIH5	1.245	pp14776; MGC10848; DKFZp686F0145	NM_032817	inter-alpha (globulin) inhibitor H5
LOC94431	1.244		NM_145237	
DDN	1.243	KIAA0749	NM_015086	dendrin
TREML2	1.242	TLT2; C6orf76; FLJ13693; dJ238O23.1	NM_024807	triggering receptor expressed on myeloid cells-like 2
RAXL1	1.242	QRX; MGC15631	NM_032753	retina and anterior neural fold homeobox like 1
LOC401286	1.242	LOC401286	NM_001023565	hypothetical gene supported by AK127120
CNNM4	1.242	ACDP4; KIAA1592	NM_020184	cyclin M4
FLJ38288	1.242	FLJ38288; DKFZp781G1213; DKFZp686K10134	NM_173632	zinc finger protein 776

FAM73B	1.241	C9orf54; FLJ00199; FLJ14596	NM_032809	family with sequence similarity 73, member B
REPS2	1.24	POB1	NM_004726	RALBP1 associated Eps domain containing 2
BAT3	1.24	G3; D6S52E	NM_080703	HLA-B associated transcript 3
TMTC2	1.238	DKFZp762A217	NM_152588	transmembrane and tetratricopeptide repeat containing 2
PXMP2	1.238	PMP22	NM_018663	peroxisomal membrane protein 2, 22kDa
AHDC1	1.236	CL23945; DJ159A19.3; RP1-159A19.1	NM_001029882	AT hook, DNA binding motif, containing 1
LONRF3	1.236	RNF127; FLJ22612; MGC119463; MGC119465	NM_024778	LON peptidase N-terminal domain and ring finger 3
NOS3	1.236	eNOS; ECNOS; NOS III	NM_000603	nitric oxide synthase 3 (endothelial cell)
CRLF3	1.236	FRWS; CREME9; CYTOR4; MGC20661	NM_015986	cytokine receptor-like factor 3
SSX8	1.236	SSX8	NM_174961	synovial sarcoma, X breakpoint 8
PDGFB	1.234	SIS; SSV; PDGF2; c-sis; FLJ12858	NM_033016	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)
MORF4L1	1.234	Eaf3; MRG15; FWP006; S863-6; HsT17725; MGC10631; MORFRG15	NM_206839	mortality factor 4 like 1
FLG	1.232	FLG	NM_002016	filaggrin
PLCXD2	1.232	FLJ31579	NM_153268	phosphatidylinositol-specific phospholipase C, X domain containing 2
KIF5B	1.232	KNS; KINH; KNS1; UKHC; U-KHC	NM_004521	kinesin family member 5B
ZNF136	1.231	pHZ-20	NM_003437	zinc finger protein 136
OTOA	1.23	DFNB22; FLJ32773; MGC39813	NM_144672	otoancorin
FLJ43692	1.23	FLJ43692	NM_001003702	ARHGEF5-like
ZP1	1.23	MGC87693	NM_207341	zona pellucida glycoprotein 1 (sperm receptor)
ZNF268	1.229	HZF3; MGC126498	NM_152943	zinc finger protein 268
RGPD5	1.228	RGP5; BS-63; DKFZp686I1842	NM_032260	RANBP2-like and GRIP domain containing 5
KRTAP10-12	1.228	KAP10.12; KRTAP18-12; KRTAP18.12	NM_198699	keratin associated protein 10-12
TMEM104	1.228	FLJ00021; FLJ20255	NM_017728	transmembrane protein 104
LOC401622	1.226		NM_001013689	
C2ORF21	1.226	FLJ33496	NM_182587	chromosome 2 open reading frame 21
PPEF1	1.226	PP7; PPEF; PPP7C	NM_006240	protein phosphatase, EF-hand calcium binding domain 1
TRIAD3	1.226		NM_019011	
DAB1	1.225	EIF4G1	NM_021080	disabled homolog 1 (Drosophila)
ARL4C	1.225	LAK; ARL7	NM_005737	ADP-ribosylation factor-like 4C
ADPRHL1	1.225	ARH2	NM_199162	ADP-ribosylhydrolase like 1
TSNAXIP1	1.225	TXI1; MGC111443	NM_018430	translin-associated factor X interacting protein 1
PHCA	1.224	APHC; FLJ11238	NM_018367	phytoceramidase, alkaline
C10ORF61	1.222	TECT3; DKFZp564D116	NM_015631	chromosome 10 open reading frame 61
CTNND1	1.222	CAS; p120; CTNND; P120CAS; P120CTN; KIAA0384	NM_001331	catenin (cadherin-associated protein), delta 1
PPHLN1	1.222	HSPC206; HSPC232; MGC48786	NM_016488	periphilin 1
RGS9BP	1.222	RGS9BP; FLJ45744	NM_207391	RGS9 anchor protein
MXI1	1.221	MXI; MAD2; MXD2; MGC43220	NM_001008541	MAX interactor 1
CDH20	1.22	Cdh7; CDH7L3; FLJ37047	NM_031891	cadherin 20, type 2
DAPK3	1.219	ZIP; ZIPK; FLJ36473	NM_001348	death-associated protein kinase 3
TROAP	1.219	TASTIN	NM_005480	trophinin associated protein (tastin)
FLAD1	1.218	FAD1; PP591; MGC31803; MGC40255; RP11-307C12.7	NM_025207	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)
CPT1B	1.217	CPT1-M; M-CPT1; KIAA1670	NM_152247	carnitine palmitoyltransferase 1B (muscle)
ADPRH	1.217	ARH1	NM_001125	ADP-ribosylarginine hydrolase
KCNK10	1.216	TREK2; TREK-2	NM_138318	potassium channel, subfamily K, member 10
ESRRG	1.216	ERR3; NR3B3; FLJ16023; KIAA0832; DKFZp781L1617	NM_206594	estrogen-related receptor gamma
POLE	1.216	POLE1; FLJ21434; DKFZp434F222	NM_006231	polymerase (DNA directed), epsilon
SMAD9	1.215	MADH6; MADH9; SMAD8A; SMAD8B	NM_005905	SMAD, mothers against DPP homolog 9 (Drosophila)
CRYBA2	1.215	C6orf25	NM_057093	crystallin, beta A2
STRN4	1.215	ZIN; zinedin; FLJ35594	NM_013403	striatin, calmodulin binding protein 4
MGC42105	1.214	MGC42105	NM_153361	hypothetical protein MGC42105
PKHD1L1	1.213	PKHDL1; DKFZp586C1021	NM_177531	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1
TBX6	1.213	TBX6	NM_080758	T-box 6
ALDH8A1	1.213	ALDH12; MGC138650; DJ352A20.2; DKFZp779D2315	NM_022568	aldehyde dehydrogenase 8 family, member A1
SNAPC4	1.213	SNAP190; FLJ13451; PTFalpha	NM_003086	small nuclear RNA activating complex, polypeptide 4, 190kDa
SLC22A3	1.213	EMT; EMTH; OCT3	NM_021977	solute carrier family 22 (extraneuronal monoamine transporter), member 3
ANKFY1	1.212	ANKHZN; ZFYVE14; KIAA1255; DKFZp686M19106	NM_020740	ankyrin repeat and FYVE domain containing 1
GPR123	1.211	GPR123	NM_032422	G protein-coupled receptor 123
C6ORF68	1.211	MGC7199; MGC:7199; MGC117249	NM_138459	chromosome 6 open reading frame 68
SF1	1.211	ZFM1; ZNF162; D11S636	NM_201997	splicing factor 1
BRF1	1.21	BRF; hBRF; GTF3B; TAF3C; TAF3B2; TF3B90; FLJ42674; TAFIII90; TFIIIB90; MGC105048	NM_145696	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)
KCTD11	1.21	REN; C17orf36; MGC129844; REN/KCTD11	NM_001002914	potassium channel tetramerisation domain containing 11
SLCO1A2	1.209	OATP; OATP-A; OATP1A2; SLC21A3	NM_134431	solute carrier organic anion transporter family, member 1A2
MGC4728	1.209	ZNF773; MGC4728	NM_198542	zinc finger protein 419B
ZFYVE1	1.209	DFCP1; TAFF1; ZNFN2A1; KIAA1589	NM_021260	zinc finger, FYVE domain containing 1
PTPN9	1.209	MEG2	NM_002833	protein tyrosine phosphatase, non-receptor type 9
EYA4	1.209		NM_172104	

SLC25A35	1.208	FLJ40217; MGC120446; MGC120448	NM_201520	solute carrier family 25, member 35
EHD1	1.208	PAST; PAST1; H-PAST; HPAST1; FLJ42622; FLJ44618	NM_006795	EH-domain containing 1
DRD1	1.207	DADR; DRD1A	NM_000794	dopamine receptor D1
KRTAP20-2	1.207	KAP20.2; MGC133104	NM_181616	keratin associated protein 20-2
ZNF418	1.206	FLJ31551; KIAA1956; MGC138449	NM_133460	zinc finger protein 418
PBX4	1.205	PBX4	NM_025245	pre-B-cell leukemia transcription factor 4
ZCWPW1	1.205	ZCW1; FLJ10057; DKFZp434N0510	NM_017984	zinc finger, CW type with PWWP domain 1
DCUN1D2	1.204	C13orf17; FLJ10704; FLJ20092	NM_018185	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)
DGCR13	1.204	DGS-H	NM_001024733	DiGeorge syndrome critical region gene 13
LOC91689	1.203	dJ186O1.1	NM_033318	chromosome 22 open reading frame 32
KIAA1271	1.203	VISA; MAVS; Ips-1; FLJ27482; FLJ41962; KIAA1271; DKFZp666M015	NM_020746	virus-induced signaling adapter
CSPP1	1.203	CSPP; FLJ22490; FLJ38886	NM_024790	centrosome and spindle pole associated protein 1
FLJ25476	1.202	FLJ25476; MGC138318; RP11-415J8.1	NM_152493	FLJ25476 protein
RBP3	1.201	IRBP; RBPI; D10S64; D10S65; D10S66	NM_002900	retinol binding protein 3, interstitial
FLJ37562	1.201	FLJ37562	NM_152409	chromosome 5 open reading frame 24
PDE4C	1.2	DPDE1; MGC126222; PDE4C-791	NM_000923	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)
VGLL2	1.199	VGL2; VITO1	NM_153453	vestigial like 2 (Drosophila)
LYZL2	1.199	ZNF294	NM_183058	lysozyme-like 2
JPH2	1.199	JP2; JP-2; FLJ40969	NM_020433	junctophilin 2
NOTCH3	1.199	CASIL; CADASIL	NM_000435	Notch homolog 3 (Drosophila)
SLC29A3	1.199	ENT3; FLJ11160	NM_018344	solute carrier family 29 (nucleoside transporters), member 3
C1ORF110	1.198	FLJ41579; MGC48998; RP11-331H2.2	NM_178550	chromosome 1 open reading frame 110
LOC283219	1.198	LCMT1	NM_001029859	potassium channel tetramerisation domain containing 21
CRYGS	1.198	CRYG8	NM_017541	crystallin, gamma S
MTA1	1.198	MTA1	NM_004689	metastasis associated 1
STX16	1.197	SYN16; hsyn16; MGC90328	NM_001001433	syntaxin 16
ZNF605	1.196	FLJ14967	NM_183238	zinc finger protein 605
C2ORF10	1.195	C2orf10	NM_194250	chromosome 2 open reading frame 10
TRIM67	1.195	TNL; FLJ44831	NM_001004342	tripartite motif-containing 67
TRPC5	1.195	TRP5	NM_012471	transient receptor potential cation channel, subfamily C, member 5
ZNF473	1.195	ZN473; HZFP100	NM_015428	zinc finger protein 473
BMF	1.195	FLJ00065	NM_033503	Bcl2 modifying factor
TRPM7	1.195	CHAK; CHAK1; LTRPC7; FLJ20117; FLJ25718; TRP-PLIK	NM_017672	transient receptor potential cation channel, subfamily M, member 7
POLR3H	1.194	RPC8; KIAA1665; MGC29654; MGC111097	NM_138338	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)
A2BP1	1.193	A2BP1; FOX1; HRNBP1	NM_018723	ataxin 2-binding protein 1
ZNF623	1.193	MGC103965; MGC104128	NM_014789	zinc finger protein 623
COBL	1.192	KIAA0633; DKFZp686G13227	NM_015198	cordon-bleu homolog (mouse)
BCL2L14	1.191	BCLG	NM_138723	BCL2-like 14 (apoptosis facilitator)
LYCAT	1.191	ALCAT1; UNQ1849; FLJ37965	NM_182551	lysocardiolipin acyltransferase
OSGEP	1.191	KAE1; GCPL1; OSGEP1; PRSMG1; FLJ20411	NM_017807	O-sialoglycoprotein endopeptidase
PPP1R15B	1.19	FLJ14744	NM_032833	protein phosphatase 1, regulatory (inhibitor) subunit 15B
MECP2	1.19	RTS; RTT; PPMX; MRX16; MRX79; AUTSX3; DKFZp686A24160	NM_004992	methyl CpG binding protein 2 (Rett syndrome)
IL2RA	1.19	CD25; IL2R; TCGFR; IDDM10	NM_000417	interleukin 2 receptor, alpha
AK3L1	1.19	AK3; AK4	NM_001005353	adenylate kinase 3-like 1
TMOD2	1.19	NTMOD; MGC39481	NM_014548	tropomodulin 2 (neuronal)
OPN1SW	1.189	BCP; BOP; CBT	NM_001708	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)
LOC284361	1.188	LOC284361; INM02; MGC33203	NM_175063	hematopoietic signal peptide-containing
RGR	1.187	RGR	NM_001012722	retinal G protein coupled receptor
SLC5A10	1.186	SGLT5; FLJ25217	NM_152351	solute carrier family 5 (sodium/glucose cotransporter), member 10
NBPF14	1.186	NBPF; FLJ35032; RP3-328E19.1; DJ328E19.C1.1	NM_015383	neuroblastoma breakpoint family, member 14
HIF3A	1.186	IPAS; MOP7; PASD7; HIF-3A; HIF-3A4	NM_022462	hypoxia inducible factor 3, alpha subunit
FLJ369980	1.186		NM_182598	
TMEM70	1.186	FLJ20533	NM_017866	transmembrane protein 70
RHOT2	1.184	RASL; ARHT2; MIRO-2; C16orf39	NM_138769	ras homolog gene family, member T2
LOC148898	1.184	FLJ90508	NM_001008896	chromosome 1 open reading frame 213
ZNF384	1.184	NP; CIZ; NMP4; CAGH1; ERDA2; TNRC1; CAGH1A	NM_133476	zinc finger protein 384
DGKZ	1.184	DAGK5; DAGK6; DGK-ZETA; hDGKzeta	NM_003646	diacylglycerol kinase, zeta 104kDa
ARHGEF1	1.182	GEF1; LBCL2; SUB1.5; P115-RHOGEF	NM_199002	Rho guanine nucleotide exchange factor (GEF) 1
SIPA1L1	1.181	E6TP1; KIAA0440; DKFZp686G1344	NM_015556	signal-induced proliferation-associated 1 like 1
AP1G2	1.181	G2AD	NM_080545	adaptor-related protein complex 1, gamma 2 subunit
LRRN6	1.18	LERN3; LINGO2; FLJ31810	NM_152570	leucine rich repeat neuronal 6C

C				
FLJ32130	1.179	FLJ32130	NM_152458	zinc finger protein 785
AIFL	1.179	AIFL; FLJ30473	NM_144704	apoptosis-inducing factor like
P2RY2	1.179	P2U; HP2U; P2U1; P2UR; P2Y2; P2RU1; P2Y2R; MGC20088; MGC40010	NM_176071	purinergic receptor P2Y, G-protein coupled, 2
SYVN1	1.179	HRD1; KIAA1810; MGC40372	NM_032431	synovial apoptosis inhibitor 1, synoviolin
DDC	1.179	AADC	NM_000790	dopa decarboxylase (aromatic L-amino acid decarboxylase)
TMEM16B	1.178	C12orf3; DKFZp434P102	NM_020373	transmembrane protein 16B
TNRC6B	1.178	KIAA1093	NM_015088	trinucleotide repeat containing 6B
FLJ90757	1.178		NM_001004336	
C11ORF9	1.175	KIAA0954; MGC10781	NM_013279	chromosome 11 open reading frame 9
ZNF624	1.175	KIAA1349; MGC119602; MGC119603; MGC119605	NM_020787	zinc finger protein 624
USP11	1.175	UHX1	NM_004651	ubiquitin specific peptidase 11
KIAA0789	1.174	KIAA0789; MGC117165	NM_014653	KIAA0789 gene product
OR4C12	1.174	OR11-259	NM_001005270	olfactory receptor, family 4, subfamily C, member 12
NDST4	1.173	VCX3A	NM_022569	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
SRCAP	1.173	SRCAP; KIAA0309	NM_006662	Snf2-related CBP activator protein
TCF7L2	1.173	TCF4; TCF-4	NM_030756	transcription factor 7-like 2 (T-cell specific, HMG-box)
C19ORF25	1.173	FLJ36666	NM_152482	chromosome 19 open reading frame 25
AKAP4	1.172	HI; p82; FSC1; AKAP82; hAKAP82	NM_139289	A kinase (PRKA) anchor protein 4
C10ORF99	1.171	UNQ1833; FLJ21763	NM_207373	chromosome 10 open reading frame 99
VPS16	1.171	hVPS16	NM_022575	vacuolar protein sorting 16 (yeast)
PLEKHB2	1.171	EVT2; FLJ20783	NM_017958	pleckstrin homology domain containing, family B (evectins) member 2
IGF1R	1.171	CD221; IGFIR; JTK13; MGC142170; MGC142172	NM_000875	insulin-like growth factor 1 receptor
SHE	1.171	RP11-350G8.8; DKFZp451D1511; DKFZp686E14106	NM_001010846	Src homology 2 domain containing E
MAGEB3	1.17	MAGEB3	NM_002365	melanoma antigen family B, 3
CYSLTR1	1.17	HG55; CYSLT1; CYSLTR; CYSLT1R; HMTMF81; MGC46139	NM_006639	cysteinyl leukotriene receptor 1
GCNT3	1.17	GnT-M; C2GnT2; C2/4GnT; C2GnT-M	NM_004751	glucosaminyl (N-acetyl) transferase 3, mucin type
CDK3	1.169	CDK3	NM_001258	cyclin-dependent kinase 3
C20ORF116	1.169	MGC2592; dJ1187M17.3	NM_023935	chromosome 20 open reading frame 116
SCAND2	1.168	SCAND2	NM_033633	SCAN domain containing 2
PIP5K3	1.168	CFD; PIP5K; PIKfyve; KIAA0981; MGC40423	NM_152671	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III
NR2E1	1.168	TLL; TLX; XTLL	NM_003269	nuclear receptor subfamily 2, group E, member 1
VSIG2	1.168	CTH; CTXL; 2210413P10Rik	NM_014312	V-set and immunoglobulin domain containing 2
ANKRD19	1.167	FLJ36178; bA526D8.2	NM_001010925	ankyrin repeat domain 19
KIAA0265	1.167	KIAA0265	NM_014997	KIAA0265 protein
CHRM2	1.166	HM2; FLJ43243; MGC120006; MGC120007	NM_001006626	cholinergic receptor, muscarinic 2
PLXNA1	1.166	NOV; NOVP; PLXN1; PLEXIN-A1	NM_032242	plexin A1
DYSFIP1	1.166	MGC138299	NM_001007533	dysferlin interacting protein 1 (toonin)
CP110	1.166	CP110; KIAA0419; DKFZp781G1416	NM_014711	CP110 protein
FLJ27505	1.166	FLJ27505	NM_207408	FLJ27505 protein
LRRC37B	1.165	LRRC37B	NM_052888	leucine rich repeat containing 37B
AMAC1L2	1.163	AMAC	NM_054028	acyl-malonyl condensing enzyme 1-like 2
FDX1	1.163	ADX; FDX; LOH11CR1D	NM_004109	ferredoxin 1
GLYCTK	1.163	GLYCTK; HBeAgBP4A	NM_145262	glycerate kinase
B3GAT2	1.162	GLCATS; GlcAT-S; KIAA1963; MGC138535	NM_080742	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)
ZNF10	1.162	KOX1	NM_015394	zinc finger protein 10
TNK1	1.162	MGC46193	NM_003985	tyrosine kinase, non-receptor, 1
C17ORF81	1.161	DERP6; MST071; HSPC002; MSTP071	NM_203414	chromosome 17 open reading frame 81
MPPED1	1.161	239AB; FAM1A; C22orf1; MGC88045	NM_001585	metallophosphoesterase domain containing 1
FLJ25067	1.16	FLJ25067; RP4-784N16.1	NM_152504	chromosome 20 open reading frame 196
POLR2A	1.16	RPB1; RPO2; POLR2; POLRA; RPBh1; RPOL2; RpIILS; hsRPB1; hRPB220; MGC75453	NM_000937	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa
BAP1	1.159	hucep-6; FLJ35406; FLJ37180; HUCEP-13; KIAA0272; DKFZp686N04275	NM_004656	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)
IFNB1	1.159	IFB; IFF; IFNB; MGC96956	NM_002176	interferon, beta 1, fibroblast
C1ORF88	1.158	FLJ23853; MGC126550; RP5-1125M8.4	NM_181643	chromosome 1 open reading frame 88
DGKQ	1.158	DAGK; DAGK4; DAGK7	NM_001347	diacylglycerol kinase, theta 110kDa
HEXIM2	1.158	L3; FLJ32384	NM_144608	hexamthylene bis-acetamide inducible 2
RPS6KA6	1.158	RSK4	NM_014496	ribosomal protein S6 kinase, 90kDa, polypeptide 6
LNX1	1.157	LNX; MPDZ; PDZRN2	NM_032622	ligand of numb-protein X 1
FIGLA	1.156	DOCK8	NM_001004311	folliculogenesis specific basic helix-loop-helix

PRDM15	1.156	PFM15; ZNF298; C21orf83	NM_022115	PR domain containing 15
HNRPF	1.156	HNRNPF; mcs94-1; MGC110997	NM_004966	heterogeneous nuclear ribonucleoprotein F
HSPG2	1.156	PLC; SJA; SJS; SJS1	NM_005529	heparan sulfate proteoglycan 2 (perlecan)
RAD54B	1.155	FSBP	NM_012415	RAD54 homolog B (S. cerevisiae)
TXNRD2	1.155		NM_145748	
OR2A2	1.155	OR2A2P; OR7-11; OST008; OR2A17P	NM_001005480	olfactory receptor, family 2, subfamily A, member 2
CYFIP1	1.155	SHYC; FLJ45151; P140SRA-1	NM_014608	cytoplasmic FMR1 interacting protein 1
AMDHD1	1.154	HMFT1272; MGC35366	NM_152435	amidohydrolase domain containing 1
KCNH7	1.154	ERG3; HERG3; Kv11.3; MGC45986	NM_173162	potassium voltage-gated channel, subfamily H (eag-related), member 7
R7BP	1.154	R7BP	NM_001029875	R7 binding protein
AQP12A	1.153	AQP12	NM_198998	aquaporin 12A
EMP2	1.153	XMP; MGC9056	NM_001424	epithelial membrane protein 2
OR9Q2	1.153	OR9Q2P	NM_001005283	olfactory receptor, family 9, subfamily Q, member 2
MCOLN1	1.152	ML4; MLIV; MST080; TRPML1; MSTP080; TRP-ML1	NM_020533	mucolipin 1
GOLGA7	1.152	GCP16; HSPC041; MGC4876; MGC21096; GOLGA3AP1	NM_016099	golgi autoantigen, golgin subfamily a, 7
C6ORF152	1.152	C6orf152	NM_181714	chromosome 6 open reading frame 152
ZNF167	1.151	ZFP; ZNF64; FLJ12738	NM_025169	zinc finger protein 167
FRS2	1.151	SNT; SNT1; FRS2A; SNT-1; FRS2alpha	NM_006654	fibroblast growth factor receptor substrate 2
ELK4	1.151	SAP1	NM_001973	ELK4, ETS-domain protein (SRF accessory protein 1)
FKBPL	1.151	NG7; DIR1; WISP39	NM_022110	FK506 binding protein like
ZNF491	1.151	FLJ34791; MGC126639; MGC126641	NM_152356	zinc finger protein 491
C20ORF118	1.151	dJ132F21.2	NM_080628	chromosome 20 open reading frame 118
ARMCX4	1.15	FLJ43051; MGC40053; DKFZp781M0415	NM_152583	armadillo repeat containing, X-linked 4
GHSR	1.15	GHSR	NM_198407	growth hormone secretagogue receptor
TGFBR1	1.15	SKR4; ALK-5; TGFR-1; ACVRLK4	NM_004612	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
WDR81	1.149	FLJ23776; FLJ33817	NM_152348	WD repeat domain 81
GREB1	1.149	GREB1; KIAA0575	NM_148903	GREB1 protein
ACTN2	1.149	ACTN2	NM_001103	actinin, alpha 2
DMPK	1.149	DM; DM1; DMK; DM1PK	NM_004409	dystrophia myotonica-protein kinase
HIST1H4B	1.149	H4/I; H4FI	NM_003544	histone 1, H4b
S100A9	1.148	MIF; NIF; P14; CAGB; CFAG; CGLB; L1AG; LIAG; MRP14; 60B8AG; MAC387	NM_002965	S100 calcium binding protein A9
C14ORF119	1.148	FLJ20671; MGC74723	NM_017924	chromosome 14 open reading frame 119
LRRC4C	1.148	NGL1; NGL-1; KIAA1580	NM_020929	leucine rich repeat containing 4C
RSN	1.148	CLIP; CLIP1; CYLN1; CLIP170; CLIP-170; MGC131604	NM_002956	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)
OS9	1.148	OS9	NM_001017956	amplified in osteosarcoma
PPARBP	1.148	PBP; MED1; CRSP1; RB18A; TRIP2; CRSP200; DRIP205; DRIP230; PPARGBP; TRAP220; MGC71488	NM_004774	PPAR binding protein
ZNF354B	1.147	KID2; FLJ25008; MGC138316	NM_058230	zinc finger protein 354B
ING4	1.147		NM_198287	
IHPK1	1.147	PiUS; IP6K1; MGC9925	NM_153273	inositol hexaphosphate kinase 1
CASKIN2	1.147	ANKS5B; FLJ21609; KIAA1139	NM_020753	CASK interacting protein 2
PRKRIP1	1.146	C114; FLJ13902	NM_024653	PRKR interacting protein 1 (IL11 inducible)
CASP8	1.145		NM_033357	
DEFB32	1.145	DEFB32; UNQ827	NM_207469	defensin, beta 32 (UNQ827) (DEFB32)
GCC2	1.145	GCC185; KIAA0336	NM_181453	GRIP and coiled-coil domain containing 2
ATF3	1.144	ATF3	NM_004024	activating transcription factor 3
DGKD	1.144	dgkd-2; DGKdelta; KIAA0145	NM_152879	diacylglycerol kinase, delta 130kDa
C5ORF3	1.144	133K02	NM_018691	chromosome 5 open reading frame 3
GIF	1.143	IF; INF; IFMH; TCN3	NM_005142	gastric intrinsic factor (vitamin B synthesis)
KRTAP21-1	1.143	KAP21.1	NM_181619	keratin associated protein 21-1
NTRK1	1.141	MTC; TRK; TRK1; TRKA; p140-TrkA; DKFZp781I14186	NM_001007792	neurotrophic tyrosine kinase, receptor, type 1
CATSPER1	1.141	CATSPER; MGC33335; MGC33368	NM_053054	cation channel, sperm associated 1
MAGEA12	1.141	MAGE12	NM_005367	melanoma antigen family A, 12
EMCN	1.14	EMCN2; MUC14	NM_016242	endomucin
SUMO4	1.14	IDDM5; SMT3H4; SUMO-4; dJ281H8.4	NM_001002255	SMT3 suppressor of mif two 3 homolog 4 (S. cerevisiae)
TICAM1	1.139	TRIF; PRVTIRB; TICAM-1; MGC35334	NM_014261	toll-like receptor adaptor molecule 1
ZNF574	1.139	FP972; FLJ22059	NM_022752	zinc finger protein 574
ZNF563	1.139	FLJ34797	NM_145276	zinc finger protein 563
NEK7	1.138	JMJD1B	NM_133494	NIMA (never in mitosis gene a)-related kinase 7
FASTK	1.138	FAST	NM_006712	Fas-activated serine/threonine kinase
DDA1	1.138	DDA1; PCIA1; MGC2594	NM_024050	chromosome 19 open reading frame 58
KRT20	1.136	K20; CK20; KRT21; MGC35423	NM_019010	keratin 20
DHX57	1.136		NM_144995	
WISP1	1.136	CCN4; WISP1c; WISP1i; WISP1tc	NM_080838	WNT1 inducible signaling pathway protein 1
ZNF654	1.136	FLJ10997; FLJ21142	NM_018293	zinc finger protein 654
LOC402176	1.136	LOC402176	NM_001011538	similar to 60S ribosomal protein L21

YTHDC1	1.136	YT521; YT521-B; KIAA1966	NM_001031732	YTH domain containing 1
RNF146	1.135	dJ351K20.1; RP3-351K20.1; DKFZP434O1427	NM_030963	ring finger protein 146
LOC51233	1.134	LOC51233; MGC33025; MGC75009	NM_016449	hypothetical protein LOC51233
FLJ33790	1.133		NM_173583	
KRTAP12-4	1.133	KRTAP12.4	NM_198698	keratin associated protein 12-4
OXGR1	1.133	GPR80; GPR99; P2Y15; P2RY15; MGC119206; MGC119207; MGC119208	NM_080818	oxoglutarate (alpha-ketoglutarate) receptor 1
BTBD12	1.133	KIAA1784; KIAA1987	NM_032444	BTB (POZ) domain containing 12
CS	1.133	CS	NM_198324	citrate synthase
TSGA10	1.131	CEP4L	NM_025244	testis specific, 10
MSH5	1.131	G7; NG23; MutSH5; MGC2939; DKFZp434C1615	NM_025259	mutS homolog 5 (E. coli)
MRM1	1.13	FLJ22578	NM_024864	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)
LRRCC1	1.129	SAP2; KIAA1764	NM_033402	leucine rich repeat and coiled-coil domain containing 1
GOLGB1	1.129	GCP; GCP372; GIANTIN	NM_004487	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1
OR10A5	1.128	JCG6; OR10A1; OR11-403	NM_178168	olfactory receptor, family 10, subfamily A, member 5
MSR1	1.128	SR-A; CD204; phSR1; phSR2; SCARA1	NM_138715	macrophage scavenger receptor 1
REXO1	1.127	REX1; ELOABP1; EloA-BP1; KIAA1138; TCEB3BP1	NM_020695	REX1, RNA exonuclease 1 homolog (S. cerevisiae)
FAIM	1.127	FAIM1	NM_018147	Fas apoptotic inhibitory molecule
FLJ14397	1.127	FLJ14397	NM_032779	hypothetical protein FLJ14397
C17ORF57	1.127	FLJ40342	NM_152347	chromosome 17 open reading frame 57
HTR2A	1.127	HTR2; 5-HT2A	NM_000621	5-hydroxytryptamine (serotonin) receptor 2A
SERINC3	1.126	TDE; TDE1; AIGP1; TMS-1; DIFF33; SBBI99	NM_198941	serine incorporator 3
COL11A2	1.126	HKE5; PARP; STL3; DFNA13; DFNB53	NM_080680	collagen, type XI, alpha 2
PCDHB15	1.124	PCDH-BETA15	NM_018935	protocadherin beta 15
MC5R	1.124	MC5R	NM_005913	melanocortin 5 receptor
POU4F2	1.124	BRN3B; BRN3.2; Brn-3b	NM_004575	POU domain, class 4, transcription factor 2
LOC400924	1.123	LOC400924	NM_001013676	hypothetical gene supported by AK056895
GLIS1	1.123	FLJ36155	NM_147193	GLIS family zinc finger 1
TXNDC11	1.123	EFP1	NM_015914	thioredoxin domain containing 11
SVOP	1.122	DKFZp761H039	NM_018711	SV2 related protein homolog (rat)
IFNA16	1.122	IFNA21	NM_002173	interferon, alpha 16
FBXL22	1.122	Fbl22; FLJ39626; MGC75496	NM_203373	F-box and leucine-rich repeat protein 22
DCT	1.122	TYRP2	NM_001922	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)
LILRB1	1.122	CD85; ILT2; LIR1; MIR7; CD85J; LIR-1; MIR-7	NM_006669	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1
SUPT6H	1.121	SPT6; SPT6H; emb-5; KIAA0162; MGC87943	NM_003170	suppressor of Ty 6 homolog (S. cerevisiae)
KIAA0963	1.121	FLJ00173	NM_014963	KIAA0963
TIAM2	1.12	STEF; FLJ41865	NM_012454	T-cell lymphoma invasion and metastasis 2
TRIM7	1.119	GNIP; RNF90	NM_203297	tripartite motif-containing 7
DUX4C	1.119	DUX4C	NM_001023569	double homeobox 4c
SLC35E2	1.119	KIAA0447; MGC104754; MGC117254; MGC126715; MGC138494; DKFZp686M0869	NM_182838	solute carrier family 35, member E2
HGF	1.118	SF; HGFB; HPTA; F-TCF	NM_001010934	hepatocyte growth factor (hepapoietin A; scatter factor)
ZNF682	1.118	FLJ90362; BC39498_3	NM_033196	zinc finger protein 682
GARNL4	1.118	RAP1GA3; KIAA1039; DKFZp686O238	NM_015085	GTPase activating Rap/RanGAP domain-like 4
FAM69A	1.117	FLJ23493	NM_001006605	family with sequence similarity 69, member A
LASS2	1.117	L3; SP260; TMSG1; MGC987; FLJ10243	NM_013384	LAG1 longevity assurance homolog 2 (S. cerevisiae)
CNR2	1.117	CB2; CX5	NM_001841	cannabinoid receptor 2 (macrophage)
INVS	1.117	INV; NPH2; NPHP2; KIAA0573; MGC133080; MGC133081	NM_183245	inversin
KRT16	1.116	K16; CK16; K1CP; NEPPK; KRT16A	NM_005557	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
LRRC39	1.116	MGC14816; DKFZp313O1122	NM_144620	leucine rich repeat containing 39
CCDC27	1.115	FLJ32825; MGC138313; MGC138317; RP1-286D6.1	NM_152492	coiled-coil domain containing 27
RBKS	1.114	RBSK; DKFZp686G13268	NM_022128	ribokinase
DPM2	1.114		NM_152690	
ZNF625	1.113	LOC136263	NM_145233	zinc finger protein 625
RNF148	1.113	MGC35222	NM_198085	ring finger protein 148
F2	1.113	PT	NM_000506	coagulation factor II (thrombin)
RHOBTB2	1.111	DBC2; KIAA0717	NM_015178	Rho-related BTB domain containing 2
ZNF595	1.111	FLJ31740	NM_182524	zinc finger protein 595
ZNF567	1.11	MGC45586	NM_152603	zinc finger protein 567
CCDC62	1.11	aaa; TSP-NY; FLJ40344	NM_032573	coiled-coil domain containing 62
SCN8A	1.109	MED; Nav1.6	NM_014191	sodium channel, voltage gated, type VIII, alpha
ZNF642	1.109	Zfp69; FLJ16030; RP11-656D10.2	NM_198494	zinc finger protein 642
OR1D2	1.109	OLFR1; OR17-4; MGC119942; MGC119943	NM_002548	olfactory receptor, family 1, subfamily D, member 2
P2RX7	1.109	P2X7; MGC20089	NM_002562	purinergic receptor P2X, ligand-gated ion channel, 7
LOC400891	1.108	LOC400891	NM_001013675	similar to chromosome 14 open reading frame 166B
SMR3B	1.108	P-B; PRL3; PROL3; MGC104379	NM_006685	submaxillary gland androgen regulated protein 3 homolog B (mouse)
CLEC4D	1.108	MCL; MPCL; CLEC6; CLEC-6; CLECSF8; MGC40078	NM_080387	C-type lectin domain family 4, member D
TAOK3	1.108	DPK; JIK; MAP3K18; FLJ31808;	NM_016281	TAO kinase 3

		DKFZp666H245		
FLJ41046	1.108	FLJ41046	NM_207479	FLJ41046 protein
ZNF471	1.107	ERP1; Z1971; KIAA1396	NM_020813	zinc finger protein 471
MGC39715	1.106	MGC39715	NM_152628	hypothetical protein MGC39715
L3MBTL3	1.106	MBT1; MBT-1; RP11-73O6.1	NM_032438	l(3)mbt-like 3 (Drosophila)
ANKH	1.105	ANK; CMDJ; HANK; MANK; CCAL2; CPPDD; FLJ27166	NM_054027	ankylosis, progressive homolog (mouse)
PPM1B	1.105	PP2CB; MGC21657; PP2CBETA; PPC2BETAX; PP2C-beta-X	NM_001033556	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
CACNA1S	1.105	MHS5; HOKPP; hypoPP; CCHL1A3; CACNL1A3	NM_000069	calcium channel, voltage-dependent, L type, alpha 1S subunit
ZNF132	1.105	pHZ-12; MGC126390; MGC126391	NM_003433	zinc finger protein 132
GABRB3	1.104	MGC9051	NM_021912	gamma-aminobutyric acid (GABA) A receptor, beta 3
C21ORF124	1.103	PRED79; FLJ31940; MGC15873	NM_032920	chromosome 21 open reading frame 124
TSC1	1.103	LAM; TSC; KIAA0243; MGC86987	NM_001008567	tuberous sclerosis 1
OR4K14	1.102	OR14-18; OR14-22	NM_001004712	olfactory receptor, family 4, subfamily K, member 14
TIGD4	1.102	MGC43837	NM_145720	tigger transposable element derived 4
U1SNRNPBP	1.102	U1SNRNPBP; HM-1; MGC138160	NM_180699	U11/U12 snRNP 35K
GPR133	1.101	PGR25; FLJ16770; MGC138512; MGC138514; DKFZp434B1272	NM_198827	G protein-coupled receptor 133
NKX2-8	1.101	NKX2H; NKX2.8; Nkx2-9	NM_014360	NK2 transcription factor related, locus 8 (Drosophila)
PRKCBP1	1.101	RACK7; ZMYND8; PRO2893; MGC31836	NM_183047	protein kinase C binding protein 1
RFX3	1.1	MGC87155; bA32F11.1	NM_134428	regulatory factor X, 3 (influences HLA class II expression)
OR5AT1	1.099	OR5W2	NM_001001966	olfactory receptor, family 5, subfamily AT, member 1
ZDHHC5	1.098	ZNF375; KIAA1748; DKFZP586K0524	NM_015457	zinc finger, DHHC-type containing 5
LOC51057	1.098	LOC51057; DKFZp686C12204	NM_015910	hypothetical protein LOC51057
CBWD5	1.097	RPL9	NM_001024916	COBW domain containing 5
LRMP	1.097	JAW1	NM_006152	lymphoid-restricted membrane protein
FUT6	1.096	FT1A; FLJ40754	NM_000150	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)
THAP3	1.095	MGC33488	NM_138350	THAP domain containing, apoptosis associated protein 3
WNT16	1.095	PRKCBP1	NM_057168	wingless-type MMTV integration site family, member 16
IRF4	1.095	MUM1; LSIRF	NM_002460	interferon regulatory factor 4
LIG3	1.094	LIG3	NM_002311	ligase III, DNA, ATP-dependent
OR4F4	1.094	OR4F18; OLA-7501	NM_001004195	olfactory receptor, family 4, subfamily F, member 4
CNIH2	1.094	Cnil; MGC50896	NM_182553	cornichon homolog 2 (Drosophila)
FLJ35740	1.094	FLJ35740; ANKRD18A; FLJ40632	NM_147195	FLJ35740 protein
LOC613266	1.093	LOC613266; FLJ43606	NM_001033516	hypothetical LOC613266
FLJ21159	1.092		NM_024826	
C6ORF15	1.092	STG	NM_014070	chromosome 6 open reading frame 15
KRTAP9-3	1.091	KAP9.3; KRTAP9.3	NM_031962	keratin associated protein 9-3
AMELX	1.09	AMG; AIH1; ALGN; AMGL; AMGX	NM_001142	amelogenin (amelogenesis imperfecta 1, X-linked)
USP21	1.09	USP16; USP23; MGC3394	NM_012475	ubiquitin specific peptidase 21
ZNF406	1.09	KIAA1485; MGC126815; MGC126817	NM_020863	zinc finger protein 406
GNG13	1.089	h2-35; G(gamma)13	NM_016541	guanine nucleotide binding protein (G protein), gamma 13
BTNL3	1.089	BTNLR	NM_197975	butyrophilin-like 3
CD33	1.088	p67; SIGLEC3; FLJ00391; SIGLEC-3	NM_001772	CD33 molecule
POLR1A	1.087	RPA1; RPO1-4; FLJ21915; MGC87965; DKFZP586M0122	NM_015425	polymerase (RNA) I polypeptide A, 194kDa
COL17A1	1.087	BP180; BPAG2; LAD-1; KIAA0204; BA16H23.2	NM_000494	collagen, type XVII, alpha 1
C18ORF1	1.087	C18orf1	NM_181481	chromosome 18 open reading frame 1
MARK2	1.085	EMK1; PAR-1; MGC99619	NM_017490	MAP/microtubule affinity-regulating kinase 2
MYEF2	1.084	MEF-2; MST156; MSTP156; FLJ11213; HsT18564; KIAA1341; MGC87325	NM_016132	myelin expression factor 2
FBXW12	1.084	Fbw12; FBXO35; MGC120385; MGC120386; MGC120387	NM_207102	F-box and WD-40 domain protein 12
RBM35B	1.084	FLJ21918; FLJ22248	NM_024939	RNA binding motif protein 35B
CDSN	1.083	S; HTSS; D6S586E	NM_001264	corneodesmosin
C9ORF50	1.083	FLJ35803	NM_199350	chromosome 9 open reading frame 50
KIAA0556	1.083	KIAA0556	NM_015202	KIAA0556
OR2M7	1.083	OR1-58	NM_001004691	olfactory receptor, family 2, subfamily M, member 7
CMIP	1.081	CMIP; KIAA1694	NM_030629	c-Maf-inducing protein
NEIL1	1.08	NEI1; hFPG1; FLJ22402	NM_024608	nei endonuclease VIII-like 1 (E. coli)
RAB33B	1.079	MGC138182; DKFZP434G099	NM_031296	RAB33B, member RAS oncogene family
GNRH1	1.079	GRH; GNRH; LHRH; LNRH	NM_000825	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)
PDZD7	1.079	PDZK7	NM_024895	PDZ domain containing 7
PRH1	1.079	Pa	NM_006250	proline-rich protein HaeIII subfamily 1
TIAF1	1.078	MAJN; MYO18A; MYSPDZ; SPR210	NM_004740	TGFB1-induced anti-apoptotic factor 1
TAOK2	1.078	PSK; PSK1; TAO1; TAO2; MAP3K17; KIAA0881	NM_004783	TAO kinase 2
XKR3	1.077	XRG3; XTES; MGC57211	NM_175878	XK, Kell blood group complex subunit-related family, member 3

KIF3A	1.075	KIF21A	NM_007054	kinesin family member 3A
FLJ45422	1.075	FLJ45422	NM_001004349	FLJ45422 protein
USP16	1.073	UBP-M	NM_001032410	ubiquitin specific peptidase 16
ARPP-21	1.073	ARPP-21	NM_198399	cyclic AMP-regulated phosphoprotein, 21 kD
ABCG1	1.072	ABC8; WHITE1; MGC34313	NM_004915	ATP-binding cassette, sub-family G (WHITE), member 1
AIM2	1.071	PYHIN4	NM_004833	absent in melanoma 2
CDH7	1.071	CDH7L1	NM_033646	cadherin 7, type 2
LOC442444	1.07	FLJ44005	NM_001013736	family with sequence similarity 47, member C
BIRC8	1.07	ILP2; ILP-2; hILP2	NM_033341	baculoviral IAP repeat-containing 8
C5ORF4	1.07	FLJ13758	NM_032385	chromosome 5 open reading frame 4
TRIM54	1.069	MURF; RNF30; MURF-3	NM_187841	tripartite motif-containing 54
RXRG	1.069	RXRC; NR2B3	NM_001009598	retinoid X receptor, gamma
IFNA10	1.068	MGC119878; MGC119879	NM_002171	interferon, alpha 10
AICDA	1.068	AID; ARP2; CDA2; HIGM2	NM_020661	activation-induced cytidine deaminase
ZYG11A	1.068		NM_001004339	
CYP4A22	1.066	BCAS4	NM_001010969	cytochrome P450, family 4, subfamily A, polypeptide 22
SEC24B	1.066	SEC24; MGC48822	NM_006323	SEC24 related gene family, member B (S. cerevisiae)
CCNB3	1.066	CCNB3	NM_033031	cyclin B3
NTN1	1.065	NTN1L	NM_004822	netrin 1
FLJ383377	1.065	FLJ38377	NM_152698	hypothetical protein FLJ38377
CABP2	1.064	CABP2	NM_031204	calcium binding protein 2
KIAA0703	1.059	KIAA0703; SPCA2; ATP2C2; DKFZp686H22230	NM_014861	KIAA0703 gene product
TRPM2	1.058	KNP3; EREG1; TRPC7; LTRPC2; NUDT9H; NUDT9L1; MGC133383	NM_001001188	transient receptor potential cation channel, subfamily M, member 2
DLGAP1	1.058	GKAP; DAP-1; hGKAP; SAPAP1; MGC88156; DAP-1-BETA; DAP-1-ALPHA	NM_001003809	discs, large (Drosophila) homolog-associated protein 1
OR4F5	1.057	OR2T3	NM_001005484	olfactory receptor, family 4, subfamily F, member 5
CCDC67	1.055	FLJ25393	NM_181645	coiled-coil domain containing 67
NDUFC2	1.055	B14.5b; NADHDH2	NM_004549	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
POU2F1	1.054	OCT1; OTF1	NM_002697	POU domain, class 2, transcription factor 1
KCTD2	1.049	KIAA0176	NM_015353	potassium channel tetramerisation domain containing 2
KIAA1754L	1.049	KIAA1754L	NM_178495	KIAA1754-like
COL14A1	1.048	UND	NM_021110	collagen, type XIV, alpha 1 (undulin)
C3ORF35	1.039		NM_178343	
AAK1	1.035	KIAA1048; MGC138170	NM_014911	AP2 associated kinase 1
HCN4	1.033	HCN4	NM_005477	hyperpolarization activated cyclic nucleotide-gated potassium channel 4
APBB1	1.032	RIR; FE65; MGC:9072	NM_001164	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)
LCE1D	1.032	LEP4	NM_178352	late cornified envelope 1D
IL17C	1.025	CX2; IL-21; IL-17C; MGC126884; MGC138401	NM_013278	interleukin 17C
TCEAL4	1.008	NPD017; FLJ21174; DKFZp686M0279	NM_024863	transcription elongation factor A (SII)-like 4
TBC1D10C	0.97	FLJ00332; MGC46488	NM_198517	TBC1 domain family, member 10C
BPESC1	0.968		NM_021812	
TMEM130	0.967	FLJ42643; DKFZp761L1417	NM_152913	transmembrane protein 130
WNT2B	0.964	WNT13; XWNT2	NM_004185	wingless-type MMTV integration site family, member 2B
FLJ90575	0.96	FLJ90575; MGC138479	NM_153376	coiled-coil domain containing 96
KLK9	0.954	KLK8; KLKL3; KLK-L3	NM_012315	kallikrein 9
HRB2	0.948	HRB2; RIP-1	NM_007043	KRR1, small subunit (SSU) processome component, homolog (yeast)
CDIPT	0.947	PIS; PIS1; MGC1328	NM_006319	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
SYT12	0.942	SRG1; SYT11	NM_177963	synaptotagmin XII
SENP3	0.942	SSP3; SMT3IP1; DKFZp762A152; DKFZP586K0919	NM_015670	SUMO1/sentrin/SMT3 specific peptidase 3
ZNF667	0.94	FLJ14011; DKFZp686O111	NM_022103	zinc finger protein 667
IPO7	0.939	RANBP7; MGC138673	NM_006391	importin 7
MADCAM1	0.938	MACAM1	NM_130760	mucosal vascular addressin cell adhesion molecule 1
KIAA1900	0.938	BKLHD5; MGC51280; MGC87753; dJ21F7.1; UG0030H05; RP1-39B17.1	NM_052904	KIAA1900
C6ORF81	0.933	FLJ25390	NM_145028	chromosome 6 open reading frame 81
ACYP1	0.932	ACYPE	NM_203488	acylphosphatase 1, erythrocyte (common) type
GMCL1	0.931	GCL; GCL1; BTBD13	NM_178439	germ cell-less homolog 1 (Drosophila)
TDRKH	0.931	TDRD2	NM_006862	tudor and KH domain containing
TRPC6	0.928	TRP6; FSGS2; FLJ11098; FLJ14863	NM_004621	transient receptor potential cation channel, subfamily C, member 6
NR2C1	0.928	TR2; TR2-11	NM_001032287	nuclear receptor subfamily 2, group C, member 1
RETNLB	0.927	XCP2; FIZZ1; FIZZ2; HXCP2; RELMb; RELMbeta; RELM-beta	NM_032579	resistin like beta
PON3	0.927	PON3	NM_000940	paraoxonase 3
CDON	0.925	CDO; ORCAM; MGC111524	NM_016952	Cdon homolog (mouse)
KCNH2	0.922	ERG1; HERG; LQT2; SQT1; HERG1; Kv11.1	NM_172057	potassium voltage-gated channel, subfamily H (eag-related), member 2
PARVB	0.922	CGI-56	NM_013327	parvin, beta
TGM1	0.919	LI; KTG; LI1; TGK; ICR2; TGASE	NM_000359	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)

GIMAP8	0.917	IANT; hIAN6; MGC129545; DKFZp667I133	NM_175571	GTPase, IMAP family member 8
MCOLN 3	0.913	TRPML3; FLJ11006; MGC71509	NM_018298	mucolipin 3
CLYBL	0.912	CLB; bA134O15.1	NM_138280	citrate lyase beta like
C1S	0.911	MSR1	NM_201442	complement component 1, s subcomponent
PRDM1 0	0.909	PFM7; KIAA1231; MGC131802	NM_020228	PR domain containing 10
MATN4	0.909	FLJ14417; HE6WCR54	NM_030590	matrilin 4
ZNF347	0.905	ZNF1111	NM_032584	zinc finger protein 347
ATXN3	0.904	AT3; JOS; MJD; ATX3; MJD1; SCA3	NM_030660	ataxin 3
TPM4	0.903	TPM4	NM_003290	tropomyosin 4
C1ORF1 60	0.902	MGC111002; DKFZP564D0478; RP11-4K3__A.4	NM_032125	chromosome 1 open reading frame 160
SLC1A6	0.902	EAAT4; MGC33092; MGC43671	NM_005071	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
AGTRA P	0.902	ATRAP; MGC29646	NM_020350	angiotensin II receptor-associated protein
ABCA3	0.902	ABC3; ABC-C; LBM180; MGC72201; EST111653	NM_001089	ATP-binding cassette, sub-family A (ABC1), member 3
CACNG 5	0.902	MGC126656; MGC126682	NM_014404	calcium channel, voltage-dependent, gamma subunit 5
CCDC74 A	0.901	FLJ40345	NM_138770	coiled-coil domain containing 74A
CABP7	0.901	MGC57793	NM_182527	calcium binding protein 7
DRD4	0.899	D4DR	NM_000797	dopamine receptor D4
GRHL1	0.899	MGR; LBP32; LBP-32; TFCP2L2	NM_198182	grainyhead-like 1 (Drosophila)
BCCIP	0.898	TOK-1	NM_078469	BRCA2 and CDKN1A interacting protein
Sep-06	0.897	SEP2; KIAA0128; MGC16619; MGC20339; RP5-876A24.2	NM_145802	septin 6
CALCR L	0.897	CRLR; CGRPR	NM_005795	calcitonin receptor-like
HSP90A B6P	0.895		NM_001014 441	
TRAK1	0.894	OIP106	NM_014965	trafficking protein, kinesin binding 1
BCL2L1 1	0.892		NM_138625	
ADAM1 2	0.887	MCMP; MLTN; MLTNA; MCMPMltna	NM_003474	ADAM metallopeptidase domain 12 (meltrin alpha)
IQCD	0.886	4933433C09Rik	NM_138451	IQ motif containing D
DGCR1 4	0.886	ES2; DGSI; DGS-I; Ese2el	NM_022719	DiGeorge syndrome critical region gene 14
KCNK4	0.883	TRAAK; TRAAK1	NM_033310	potassium channel, subfamily K, member 4
PSCD3	0.882	GRP1; ARNO3	NM_004227	pleckstrin homology, Sec7 and coiled-coil domains 3
CARD4	0.88	NOD1	NM_006092	caspase recruitment domain family, member 4
LOC116 236	0.88	LOC116236	NM_198147	hypothetical protein LOC116236
GDF11	0.879	BMP11; BMP-11	NM_005811	growth differentiation factor 11
PPWD1	0.878	KIAA0073	NM_015342	peptidylprolyl isomerase domain and WD repeat containing 1
TAC1	0.874	NK2; NKNA; TAC2; Hs.2563	NM_013998	tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neuropeptide K, neuropeptide gamma)
SAMD1 3	0.873	RP11-376N17.1	NM_001010 971	sterile alpha motif domain containing 13
TBC1D1	0.873	TBC; TBC1; KIAA1108	NM_015173	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1
TCF19	0.873	SC1; SC1-1	NM_007109	transcription factor 19 (SC1)
FAHD2 A	0.873	CGI-105; MGC131995	NM_016044	fumarylacetoacetate hydrolase domain containing 2A
SULT1C 1	0.871	ST1C1; ST1C2; SULT1C#1; humSULTC2	NM_001056	sulfotransferase family, cytosolic, 1C, member 1
ZYX	0.871	ESP-2; HED-2	NM_003461	zyxin
SYCP1	0.871	SCP1; MGC104417; HOM-TES-14	NM_003176	synaptonemal complex protein 1
SYNE2	0.87	NUA; NUANCE; SYNE-2; FLJ11014; FLJ43727; FLJ45710; FLJ46790; KIAA1011; Nesprin-2; DKFZP434H2235; DKFZp686H1931	NM_015180	spectrin repeat containing, nuclear envelope 2
MME	0.87	NEP; CD10; CALLA; MGC126681; MGC126707; DKFZp686O16152	NM_007287	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
LOC285 382	0.87	LOC285382	NM_001025 266	hypothetical gene supported by AK091454
SNTG2	0.869	SYN5; G2SYN	NM_018968	syntrophin, gamma 2
FLJ3977 9	0.869	FLJ39779	NM_207442	FLJ39779 protein
CEP68	0.869	KIAA0582	NM_015147	centrosomal protein 68kDa
MTMR9	0.868	MTMR8; C8orf9; LIP-STYX; MGC126672; DKFZp434K171	NM_015458	myotubularin related protein 9
CASP3	0.868	CPP32; SCA-1; CPP32B	NM_004346	caspase 3, apoptosis-related cysteine peptidase
SCAP2	0.867	PRAP; RA70; SAPS; SKAP55R; MGC10411; MGC33304; SKAP-HOM	NM_003930	src family associated phosphoprotein 2
MC1R	0.867	MSH-R; MGC14337	NM_002386	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
EVA1	0.866	EVA; MPZL2	NM_144765	epithelial V-like antigen 1
TTLL5	0.866	KIAA0998; MGC117189	NM_015072	tubulin tyrosine ligase-like family, member 5
KLHL18	0.866	FLJ13703; KIAA0795	NM_025010	kelch-like 18 (Drosophila)
SMARC A3	0.865	HLTF; ZBU1; HLTF1; RNF80; HIP116; SNF2L3; HIP116A	NM_003071	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3
VMD2	0.864	BMD; BEST; TU15B	NM_004183	vitelliform macular dystrophy 2 (Best disease, bestrophin)
CNFN	0.864	PLAC8L2	NM_032488	cornifelin
CBFA2T 3	0.863	ETO2; MTG16; MTGR2; ZMYND4	NM_005187	core-binding factor, runt domain, alpha subunit 2; translocated to, 3
CDC91L 1	0.863	PIGU; MGC40420	NM_080476	CDC91 cell division cycle 91-like 1 (S. cerevisiae)
FSIP1	0.862	HSD10; FLJ35989	NM_152597	fibrous sheath interacting protein 1
CSTF2T	0.862	CstF-64T; KIAA0689; DKFZp434C1013	NM_015235	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant
KIAA18 38	0.86	PGCC1; KIAA0183; KIAA1838; dJ894D12.1	NM_032448	family with sequence similarity 120B
MRPS23	0.86	CGI-138; HSPC329; MRP-S23	NM_016070	mitochondrial ribosomal protein S23

NUBP2	0.859	CFD1; NUBP1	NM_012225	nucleotide binding protein 2 (MinD homolog, E. coli)
A2ML1	0.858	CPAMD9; FLJ16045; FLJ25179; FLJ39129; FLJ41597; FLJ41598; FLJ41607; DKFZp686C1729; DKFZp686D2011; DKFZp686G1812; DKFZp686L1821; DKFZp686O1010	NM_144670	alpha-2-macroglobulin-like 1
PAQR4	0.857	FLJ30002	NM_152341	progestin and adipoQ receptor family member IV
WAS	0.857	THC; IMD2; WASP	NM_000377	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
POLM	0.856	Tdt-N	NM_013284	polymerase (DNA directed), mu
NKX3-1	0.854	NKX3A; NKX3.1	NM_006167	NK3 transcription factor related, locus 1 (Drosophila)
SMARCD1	0.853	Rsc6p; BAF60A; CRACD1	NM_003076	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
VPS53	0.853	hVps53L; pp13624; FLJ10979; MGC39512	NM_018289	vacuolar protein sorting 53 (S. cerevisiae)
TES	0.852	TESS; TESS-2; TESTIN; MGC1146; DKFZP586B2022	NM_015641	testis derived transcript (3 LIM domains)
DOK5	0.851	MGC16926; C20orf180	NM_018431	docking protein 5
SPTBN1	0.851	ELF; SPTB2; betaSpII	NM_003128	spectrin, beta, non-erythrocytic 1
RND1	0.85	ARHS; RHO6; FLJ42294	NM_014470	Rho family GTPase 1
WDR45	0.849	JM5; WDRX1; WIPI4; WIPI-4	NM_001029896	WD repeat domain 45
PLOD2	0.849	LH2; TLH	NM_182943	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2
GRIK5	0.849	KA2; EAA2; GRIK2	NM_002088	glutamate receptor, ionotropic, kainate 5
SDCCAG33	0.849	TSH1; NY-CO-33; SDCCAG33	NM_005786	teashirt family zinc finger 1
IQSEC1	0.846	KIAA0763	NM_014869	IQ motif and Sec7 domain 1
GIMAP4	0.846	IAN1; IMAP4; hIAN1; HIMAP4; MSTP062; FLJ11110	NM_018326	GTPase, IMAP family member 4
ATF7IP2	0.845	MCAF2; FLJ12668	NM_024997	activating transcription factor 7 interacting protein 2
CYP19A1	0.844	ARO; ARO1; CPV1; CYAR; CYP19; MGC104309; P-450AROM	NM_031226	cytochrome P450, family 19, subfamily A, polypeptide 1
TMEM62	0.844	FLJ23375	NM_024956	transmembrane protein 62
C10ORF96	0.844	MGC35062	NM_198515	chromosome 10 open reading frame 96
CPNE4	0.843	CPN4; COPN4; MGC15604	NM_130808	copine IV
ADAM22	0.842	MDC2	NM_004194	ADAM metallopeptidase domain 22
TGFB2	0.842	MGC116892; TGF-beta2	NM_003238	transforming growth factor, beta 2
YIF1B	0.841	FinGER8	NM_033557	Yip1 interacting factor homolog B (S. cerevisiae)
SMCY	0.841	HY; HYA; JARID1D; KIAA0234	NM_004653	Smcy homolog, Y-linked (mouse)
CLTCL1	0.84	CLTD; CHC22; CLH22; CLTCL	NM_007098	clathrin, heavy polypeptide-like 1
C1ORF109	0.84	FLJ20508	NM_017850	chromosome 1 open reading frame 109
IMPACT	0.839	MGC33718	NM_018439	Impact homolog (mouse)
ZNF569	0.839	ZNF; ZAP1; FLJ32053	NM_152484	zinc finger protein 569
FLT1	0.839	FLT; VEGFR1	NM_002019	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
GPR63	0.838	PSP24B; PSP24(beta)	NM_030784	G protein-coupled receptor 63
PAK2	0.838	PAK65; PAKgamma	NM_002577	p21 (CDKN1A)-activated kinase 2
ULBP1	0.837	RAET1I	NM_025218	UL16 binding protein 1
MGC19604	0.837	MGC19604; MGC74760	NM_001031734	similar to RIKEN cDNA B230118G17 gene
NPM3	0.835	PORMIN; TMEM123	NM_006993	nucleophosmin/nucleoplasmin, 3
PRKCE	0.835	PKCE; MGC125656; MGC125657; nPKC-epsilon	NM_005400	protein kinase C, epsilon
NOL6	0.835	NRAP; UTP22; FLJ21959; MGC14896; MGC14921; MGC20838; bA311H10.1	NM_022917	nucleolar protein family 6 (RNA-associated)
SPARCL1	0.835	SC1; PIG33	NM_004684	SPARC-like 1 (mast9, hevin)
KIAA1333	0.834	FLJ20333	NM_017769	KIAA1333
NBEA	0.832	BCL8B; LYST2	NM_015678	neurobeachin
HOXC8	0.83	HOX3; HOX3A	NM_022658	homeobox C8
HNMT	0.83	HMT; HNMT-S1; HNMT-S2	NM_001024074	histamine N-methyltransferase
CPLX1	0.83	CPX1; CPX-I	NM_006651	complexin 1
NGEF	0.83	EPHEXIN	NM_019850	neuronal guanine nucleotide exchange factor
GMIP	0.829	GMIP	NM_016573	GEM interacting protein
CA11	0.829	CARP2; CA-RP XI	NM_001217	carbonic anhydrase XI
HMGN2	0.828	HMG17; MGC5629; MGC88718	NM_005517	high-mobility group nucleosomal binding domain 2
CXORF23	0.828	IGL@	NM_198279	chromosome X open reading frame 23
FLJ13611	0.828	FLJ13611; MGC48585	NM_024941	hypothetical protein FLJ13611
MAP3K6	0.827	ASK2; MAPKKK6; MGC20114; MGC125653	NM_004672	mitogen-activated protein kinase kinase kinase 6
JPH4	0.826	JPHL1; hJP-4; KIAA1831	NM_032452	junctophilin 4
CXXC4	0.826	IDAX; MGC149872	NM_025212	CXXC finger 4
THAP9	0.825	FLJ23320; FLJ34093	NM_024672	THAP domain containing 9
BSN	0.825	ZNF231	NM_003458	bassoon (presynaptic cytomatrix protein)
B3GAT1	0.825	CD57; LEU7; NK-1; HNK-1; GLCATP; GlcAT-P; GlcUAT-P	NM_054025	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)
USP13	0.824	ISOT3; IsoT-3	NM_003940	ubiquitin specific peptidase 13 (isopeptidase T-3)
TMEM106B	0.824	FLJ11273; MGC33727	NM_018374	transmembrane protein 106B
COPG2	0.824	2-COP; FLJ11781	NM_012133	coatomer protein complex, subunit gamma 2
VPS13D	0.824	FLJ23066	NM_015378	vacuolar protein sorting 13 homolog D (S. cerevisiae)
CNTNAP3	0.823	CASPR3; CNTNAP3A; RP11-290L7.1; RP11-138L21.1	NM_033655	contactin associated protein-like 3
SALL3	0.823	ZNF796	NM_171999	sal-like 3 (Drosophila)
SCARA3	0.822	CSR; APC7; CSR1; MSLR1; MSRL1	NM_182826	scavenger receptor class A, member 3
TSN	0.821	TRSLN; BCLF-1; REHF-1	NM_004622	translin
FAM20C	0.821	FAM20C	NM_020223	family with sequence similarity 20, member C

NANOS1	0.821	HMGB4	NM_199461	nanos homolog 1 (Drosophila)
LRRN3	0.821	NLRR3; NLRR-3; FLJ11129	NM_018334	leucine rich repeat neuronal 3
EZH2	0.821	EZH1; ENX-1; MGC9169	NM_152998	enhancer of zeste homolog 2 (Drosophila)
LSAMP	0.82	LAMP	NM_002338	limbic system-associated membrane protein
PIAS3	0.82	FLJ14651	NM_006099	protein inhibitor of activated STAT, 3
TNRC6A	0.82	GW182; TNRC6; CAGH26; FLJ22043; KIAA1460; MGC75384; DKFZp666E117	NM_014494	trinucleotide repeat containing 6A
MED25	0.82	P78; ACID1; ARC92; MGC70671; TCBAP0758; DKFZp434K0512	NM_030973	mediator of RNA polymerase II transcription, subunit 25 homolog (S. cerevisiae)
C10ORF59	0.819	FLJ11218	NM_001031709	chromosome 10 open reading frame 59
MAST1	0.818	SAST; SAST170; KIAA0973	NM_014975	microtubule associated serine/threonine kinase 1
DNAJA5	0.818	DNAJA5	NM_194283	DnaJ homology subfamily A member 5
TAF15	0.817	Npl3; RBP56; TAF2N; TAFII68; hTAFII68	NM_003487	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
SPINK2	0.816	HUSI-II	NM_021114	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)
TRIM5	0.815	RNF88; TRIM5alpha	NM_033092	tripartite motif-containing 5
ZMYND12	0.815	DKFZp434N2435	NM_032257	zinc finger, MYND-type containing 12
RFC2	0.814	A1; RFC40; MGC3665	NM_002914	replication factor C (activator 1) 2, 40kDa
SH3GL1	0.813	EEN; CNSA1; SH3P8; SH3D2B; MGC111371	NM_003025	SH3-domain GRB2-like 1
SLC35A5	0.813	FLJ11130; FLJ20730; FLJ25973; DKFZp434E102	NM_017945	solute carrier family 35, member A5
TMF1	0.813	ARA160	NM_007114	TATA element modulatory factor 1
C6ORF203	0.813	PRED31; HSPC230; RP11-59I9.1	NM_016487	chromosome 6 open reading frame 203
SLC32A1	0.812	VGAT; VIAAT	NM_080552	solute carrier family 32 (GABA vesicular transporter), member 1
LRRC8E	0.811	FLJ23420	NM_025061	leucine rich repeat containing 8 family, member E
C16ORF30	0.808	CLP24; FLJ20898; MGC111564	NM_024600	chromosome 16 open reading frame 30
PET112L	0.808	PET112; HSPC199	NM_004564	PET112-like (yeast)
PROM2	0.808	PROM-2; MGC138714	NM_144707	prominin 2
CYP2U1	0.805	P450TEC	NM_183075	cytochrome P450, family 2, subfamily U, polypeptide 1
SULT1A4	0.804	SULT1A4	NM_001017389	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4
POLR3A	0.804	RPC1; RPC155; hRPC155	NM_007055	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa
TSPAN7	0.804	A15; MXS1; CD231; MRX58; CCG-B7; TM4SF2; TALLA-1; TM4SF2b; DXS1692E	NM_004615	tetraspanin 7
HECA	0.804	HDC; HDCL; HHDC; dJ225E12.1	NM_016217	headcase homolog (Drosophila)
KIAA1018	0.804	DKFZp451H236; DKFZp686K16147	NM_014967	KIAA1018
CCK	0.803	MGC117187	NM_000729	cholecystokinin
WDR69	0.802	FLJ25955	NM_178821	WD repeat domain 69
CD8A	0.801	CD8; MAL; p32; Leu2	NM_001768	CD8a molecule
C9ORF24	0.801	CBE1; MGC32921; MGC33614; NYD-SP22; bA573M23.4	NM_147168	chromosome 9 open reading frame 24
ABHD9	0.799	FLJ22408; MGC131519	NM_024794	abhydrolase domain containing 9
TRAIP	0.798	TRIP; RNF206	NM_005879	TRAF interacting protein
GALNT2	0.798	GalNAc-T2	NM_004481	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)
FLJ14437	0.798	MYOP	NM_032578	myopalladin
TNPO3	0.797	IPO12; TRNSR; MTR10A; TRN-SR; TRN-SR2	NM_012470	transportin 3
MTUS1	0.797	ATIP; MP44; MTSG1; FLJ14295; KIAA1288; DKFZp586D1519; DKFZp686F20243	NM_020749	mitochondrial tumor suppressor 1
FRMD5	0.797	FRMD5	NM_001031729	synonyms: FLJ41022, MGC14161; isoform 2 is encoded by transcript variant 2; Homo sapiens FERM domain containing 5 (FRMD5), transcript variant 2, mRNA.
RUSC2	0.797	KIAA0375	NM_014806	RUN and SH3 domain containing 2
PCP4	0.796	PEP-19	NM_006198	Purkinje cell protein 4
BAALC	0.795	FLJ12015	NM_024812	brain and acute leukemia, cytoplasmic
MRE11A	0.793	ATLD; HNGS1; MRE11; MRE11B	NM_005590	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
F2R	0.793	TR; HTR; CF2R; PAR1	NM_001992	coagulation factor II (thrombin) receptor
KEAP1	0.793	INrf2; KLHL19; MGC1114; MGC4407; MGC9454; KIAA0132; MGC10630; MGC20887	NM_012289	kelch-like ECH-associated protein 1
FLJ10847	0.793	FLJ10847; MATE1; MATE2; MGC64822	NM_018242	hypothetical protein FLJ10847
FBXO4	0.793	FBX4; FLJ10141; DKFZp547N213	NM_012176	F-box protein 4
E2F4	0.793	E2F-4	NM_001950	E2F transcription factor 4, p107/p130-binding
LCE2B	0.793	XP5; LEP10; SPRL1B	NM_014357	late cornified envelope 2B
KIRREL2	0.793	NLG1; NEPH3; FILTRIN; MGC15718; DKFZP564A1164	NM_199180	kin of IRRE like 2 (Drosophila)
TNPO1	0.792	MIP; TRN; IPO2; MIP1; KPNB2	NM_153188	transportin 1
AP1M1	0.792	AP47; CLTNM; MU-1A; CLAPM2	NM_032493	adaptor-related protein complex 1, mu 1 subunit
RARRES1	0.791	TIG1	NM_002888	retinoic acid receptor responder (tazarotene induced) 1
BCL2A1	0.791	GRS; BFL1; ACC-1; ACC-2; HBPA1; BCL2L5	NM_004049	BCL2-related protein A1
SLC25A17	0.79	PMP34	NM_006358	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17
RNPEP	0.79	DKFZP547H084	NM_020216	arginyl aminopeptidase (aminopeptidase B)
FBXO18	0.79	FBH1; Fbx18; FLJ14590; MGC131916; MGC141935; MGC141937	NM_032807	F-box protein, helicase, 18
RSC1A1	0.789	RS1	NM_006511	regulatory solute carrier protein, family 1, member 1
SGCD	0.789	SGD; DAGD; 35DAG; CMD1L; SGCDP; MGC22567; SG-delta	NM_172244	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
CEPT1	0.789	MGC45223; DKFZp313G0615	NM_006090	choline/ethanolamine phosphotransferase 1
ZRANB3	0.789	MGC75012; MGC105033	NM_032143	zinc finger, RAN-binding domain containing 3
GNB5	0.789	GB5; FLJ37457	NM_006578	guanine nucleotide binding protein (G protein), beta 5
DKFZP5	0.788	DKFZP564J102; MST119; MSTP119	NM_015398	DKFZP564J102 protein

64J102				
EFHC2	0.787	FLJ22601; FLJ22843; dJ1158H2.1; DKFZp686G08235	NM_025184	EF-hand domain (C-terminal) containing 2
CDON	0.787	CDO; ORCAM; MGC111524	NM_016952	Cdon homolog (mouse)
ZNF215	0.787	BAZ2	NM_013250	zinc finger protein 215
ZBTB24	0.786	BIF1; ZNF450	NM_014797	zinc finger and BTB domain containing 24
NAALAD2	0.786	MGC26353; MGC116996; NAADALASE2; NAALADASE2	NM_005467	N-acetylated alpha-linked acidic dipeptidase 2
TCERG1L	0.786	MGC126584	NM_174937	transcription elongation regulator 1-like
LETM1	0.786	LETM1	NM_012318	leucine zipper-EF-hand containing transmembrane protein 1
HCN1	0.785	BCNG1; HAC-2; BCNG-1	NM_021072	hyperpolarization activated cyclic nucleotide-gated potassium channel 1
POLD1	0.785	POLD	NM_002691	polymerase (DNA directed), delta 1, catalytic subunit 125kDa
CHD5	0.785	KIAA0444; DKFZp434N231	NM_015557	chromodomain helicase DNA binding protein 5
PLAC1	0.784	RPL41	NM_021796	placenta-specific 1
A2M	0.784	CPAMD5; FWP007; S863-7; alpha 2M; DKFZp779B086	NM_000014	alpha-2-macroglobulin
SRP72	0.783	SRP72	NM_006947	signal recognition particle 72kDa
PSMD5	0.783	S5B; KIAA0072; MGC23145	NM_005047	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5
LOC388799	0.782	LOC388799; C20orf107; MGC104273	NM_001013646	similar to dJ1153D9.4 (novel protein)
AMPD3	0.781	DUT	NM_001025389	adenosine monophosphate deaminase (isoform E)
SOX13	0.781	ICA12; Sox-13; MGC117216; SRY-box 13	NM_005686	SRY (sex determining region Y)-box 13
NOVA2	0.781	ANOVA; NOVA3	NM_002516	neuro-oncological ventral antigen 2
CEP63	0.781	FLJ13386; MGC78416	NM_025180	centrosomal protein 63kDa
WDR62	0.781	C19orf14; FLJ33298; DKFZP434J046; DKFZp686G1024	NM_173636	WD repeat domain 62
ZHX3	0.781	TIX1; KIAA0395	NM_015035	zinc fingers and homeoboxes 3
SYNJ2	0.781	INPP5H; KIAA0348; MGC44422	NM_003898	synaptojanin 2
PLCL3	0.781	PLCL3; PLCeta1; MGC117152; DKFZp434C1372	NM_014996	phospholipase C, eta 1
GALK2	0.78	GK2; MGC1745	NM_002044	galactokinase 2
ATP6V0A1	0.78	a1; Stv1; VPP1; Vph1; ATP6N1; ATP6N1A; DKFZp781J1951	NM_005177	ATPase, H+ transporting, lysosomal V0 subunit a1
STK17B	0.78	DRAK2	NM_004226	serine/threonine kinase 17b (apoptosis-inducing)
TOR1AIP2	0.779	LULL1; MGC126581; MGC138430; RP11-12M5.5	NM_145034	torsin A interacting protein 2
2'-PDE	0.779	2'-PDE	NM_177966	2'-phosphodiesterase
CCDC76	0.779	FLJ10287; FLJ11219	NM_019083	coiled-coil domain containing 76
FLJ22688	0.778	FY; FLJ22688	NM_025129	fuzzy homolog (Drosophila)
WNT10B	0.778	WNT-12	NM_003394	wingless-type MMTV integration site family, member 10B
SLC35E3	0.778	BLOV1	NM_018656	solute carrier family 35, member E3
ABCA4	0.778	FFM; RMP; ABCR; RP19; STGD; ABC10; CORD3; STGD1; DKFZp781N1972	NM_000350	ATP-binding cassette, sub-family A (ABC1), member 4
FAM26A	0.777	bA225H22.7	NM_182494	family with sequence similarity 26, member A
CREB5	0.777	CRE-BPA	NM_001011666	cAMP responsive element binding protein 5
FLJ10661	0.777	FLJ10661; FLJ27199; MGC45068	NM_152563	family with sequence similarity 86, member C
GART	0.777	AIRS; GARS; PAIS; PGFT; PRGS; GARTF; MGC47764	NM_175085	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
PLAA	0.777	PLAP; PLA2P; FLJ11281; FLJ12699	NM_001031689	phospholipase A2-activating protein
ZNF651	0.777	KIAA1190; DKFZp434N0615	NM_145166	zinc finger protein 651
DAAM2	0.776	KIAA0381; MGC90515; dJ90A20A.1; RP1-278E11.1	NM_015345	dishevelled associated activator of morphogenesis 2
MYCBP2	0.776	PAM; FLJ10106; FLJ13826; FLJ21597; FLJ21646; KIAA0916; DKFZp686M08244	NM_015057	MYC binding protein 2
PRKACB	0.775	PKACB; MGC9320; MGC41879; DKFZp781I2452	NM_207578	protein kinase, cAMP-dependent, catalytic, beta
RP1-32F7.2	0.775	RP1-32F7.2	NM_173698	hypothetical protein FLJ37659
SRGAP1	0.774	ARHGAP13; FLJ22166; KIAA1304	NM_020762	SLIT-ROBO Rho GTPase activating protein 1
ZNF691	0.773	Zfp691; RP11-342M1.5	NM_015911	zinc finger protein 691
RAB3GAP1	0.772	P130; WARBM1; RAB3GAP; KIAA0066; RAB3GAP130; DKFZp434A012	NM_012233	RAB3 GTPase activating protein subunit 1 (catalytic)
PRKDC	0.772	HYRC; p350; DNAPK; DNPK1; HYRC1; XRCC7	NM_006904	protein kinase, DNA-activated, catalytic polypeptide
PIK4CB	0.772	PI4Kbeta; PI4K-BETA; PI4KIIIbeta	NM_002651	phosphatidylinositol 4-kinase, catalytic, beta polypeptide
CASC4	0.772	H63; MGC74708; DKFZp459F1927	NM_138423	cancer susceptibility candidate 4
NFKBIL2	0.772	IKBR	NM_013432	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2
BAIAP2	0.772	BAP2; IRSP53	NM_006340	BAI1-associated protein 2
NPR3	0.772	NPRC; ANPRC	NM_000908	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
CHRM3	0.772	HM3	NM_000740	cholinergic receptor, muscarinic 3
CDC26	0.771	C9orf17	NM_139286	cell division cycle 26
FLJ22028	0.771	FLJ22028	NM_024854	hypothetical protein FLJ22028
FDPS	0.771	FPS	NM_002004	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)
C3ORF63	0.77	RAP140; se89-1; KIAA1105; DKFZp686C2456	NM_015224	chromosome 3 open reading frame 63
HELB	0.769	HELB	NM_033647	helicase (DNA) B
CSDE1	0.769	UNR; D1S155E; FLJ26882; DKFZp779B0247; DKFZp779J1455; RP5-1000E10.3	NM_001007553	cold shock domain containing E1, RNA-binding
CCNB1IP1	0.769	HEI10; C14orf18	NM_182852	cyclin B1 interacting protein 1
THAP4	0.768	CGI-36	NM_015963	THAP domain containing 4
SHQ1	0.768	FLJ10539; DKFZp686H07226	NM_018130	SHQ1 homolog (S. cerevisiae)
PIB5PA	0.768	PIPP; INPP5; MGC129984	NM_014422	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A

PLEK2	0.768	FMNL2	NM_016445	pleckstrin 2
LYPLA3	0.767	ACS; LLPL; LPLA2; DKFZp564A0122	NM_012320	lysophospholipase 3 (lysosomal phospholipase A2)
CALD1	0.767	CDM; H-CAD; L-CAD; NAG22; MGC21352	NM_033138	caldesmon 1
ABHD2	0.767	HS1-2; LABH2; PHPS1-2; MGC26249; MGC111112	NM_007011	abhydrolase domain containing 2
SLC27A2	0.767	VLCS; FATP2; VLACS; ACSVL1; FACVL1; hFACVL1; HsT17226	NM_003645	solute carrier family 27 (fatty acid transporter), member 2
KCNJ8	0.766	KIR6.1; uKATP-1	NM_004982	potassium inwardly-rectifying channel, subfamily J, member 8
GALNAC4S-6ST	0.765	GALNAC4S-6ST; BRAG; KIAA0598; MGC34346; RP11-47G11.1; DKFZp781H1369	NM_015892	B cell RAG associated protein
FKBP3	0.765	PPIase; FKBP-25	NM_002013	FK506 binding protein 3, 25kDa
IFT80	0.765	WDR56; KIAA1374; MGC126543	NM_020800	intraflagellar transport 80 homolog (Chlamydomonas)
RELB	0.764	I-REL	NM_006509	v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian)
AKAP12	0.764	AKAP250; DKFZp686M0430; DKFZp686O0331	NM_005100	A kinase (PRKA) anchor protein (gravin) 12
ZNF451	0.764	COASTER; FLJ90693; KIAA0576; MGC26701; dJ417I1.1	NM_001031623	zinc finger protein 451
LOC400566	0.764	LOC400566	NM_001013672	hypothetical gene supported by AK128660
LOC441168	0.764	LOC441168	NM_001010919	hypothetical protein LOC441168
CDCP1	0.763	CD318; TRASK; SIMA135	NM_178181	CUB domain containing protein 1
MDM2	0.763	hdm2; MGC71221	NM_002392	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)
PRAC	0.762	PRAC; MGC32520	NM_032391	small nuclear protein PRAC
TMEM68	0.762	FLJ32370; MGC87778	NM_152417	transmembrane protein 68
RAD1	0.762	REC1; HRAD1	NM_133377	RAD1 homolog (S. pombe)
LGP1	0.761	LGP1; D11LGP1	NM_032484	GH3 domain containing
FBXO27	0.761	FBG5; Fbx27	NM_178820	F-box protein 27
DENND1A	0.761	FAM31A; FLJ38464; KIAA1608; RP11-230L22.3	NM_024820	DENN/MADD domain containing 1A
SH3KBP1	0.761	CIN85; GIG10; MIG18	NM_031892	SH3-domain kinase binding protein 1
PDCD11	0.758	NFBP; ALG-4; KIAA0185	NM_014976	programmed cell death 11
MON1A	0.758	SAND1; MGC13272	NM_032355	MON1 homolog A (yeast)
SDCCAG1	0.758	NY-CO-1; FLJ10051	NM_004713	serologically defined colon cancer antigen 1
FGD1	0.758	AAS; FGDY; ZFYVE3	NM_004463	FYVE, RhoGEF and PH domain containing 1 (faciogenital dysplasia)
TSPAN18	0.757	TSPAN	NM_130783	tetraspanin 18
C21ORF51	0.757	C21orf51	NM_058182	chromosome 21 open reading frame 51
ARHGAP18	0.756	MacGAP; FLJ25728; MGC126757; MGC138145; bA307O14.2	NM_033515	Rho GTPase activating protein 18
ATP5S	0.756	ATPW; HSU79253	NM_015684	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)
FAM105A	0.755	FLJ11127	NM_019018	family with sequence similarity 105, member A
SLC13A4	0.755	SUT1; SUT-1	NM_012450	solute carrier family 13 (sodium/sulfate symporters), member 4
LOC387921	0.755	LOC387921; DKFZp313M1221; DKFZp686E1140	NM_001012754	similar to RIKEN cDNA 8030451K01
CD79B	0.755	B29; IGB	NM_000626	CD79b molecule, immunoglobulin-associated beta
WDR77	0.754	MEP50; MGC2722; HKMT1069; Nbla10071; RP11-552M11.3	NM_024102	WD repeat domain 77
NFX1	0.754	NFX2; MGC20369	NM_147134	nuclear transcription factor, X-box binding 1
DZIP3	0.753	DZIP3; UURF2; FLJ13327; KIAA0675	NM_014648	zinc finger DAZ interacting protein 3
RPL34	0.753	MGC111005	NM_000995	ribosomal protein L34
RALBP1	0.752	RIP; RIP1; RLIP76	NM_006788	ralA binding protein 1
BAG4	0.752	SODD; BAG-4	NM_004874	BCL2-associated athanogene 4
NAT9	0.752	EBSP; DKFZP564C103	NM_015654	N-acetyltransferase 9
RNF10	0.752	RIE2; KIAA0262; MGC126758; MGC126764	NM_014868	ring finger protein 10
SLC16A4	0.752	MCT4; MCT5	NM_004696	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)
DDX25	0.751	GRTH	NM_013264	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25
KIAA1794	0.751	FLJ10719	NM_018193	KIAA1794
FAM107A	0.75	DRR1; TU3A; FLJ45473	NM_007177	family with sequence similarity 107, member A
TBC1D16	0.75	FLJ20748; MGC25062	NM_019020	TBC1 domain family, member 16
SLC27A5	0.749	ACSB; FATP5; ACSVL6; FACVL3; VLACSR; VLCSH2; VLCS-H2; FLJ22987	NM_012254	solute carrier family 27 (fatty acid transporter), member 5
DONSON	0.749	B17; C21orf60; DKFZP434M035	NM_017613	downstream neighbor of SON
HS6ST2	0.749	MGC130022; MGC130023	NM_147175	heparan sulfate 6-O-sulfotransferase 2
NR4A1	0.749	HMR; N10; TR3; NP10; GFRP1; NAK-1; NGFIB; NUR77; MGC9485	NM_173158	nuclear receptor subfamily 4, group A, member 1
CHCHD1	0.748	C2360; C10orf34; FLJ25854	NM_203298	coiled-coil-helix-coiled-coil-helix domain containing 1
ST3GAL4	0.747	STZ; SAT3; CGS23; SIAT4; NANTA3; SIAT4C; FLJ11867; ST3GalIV; ST3Gal IV	NM_006278	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
LSG1	0.747	FLJ11301	NM_018385	large subunit GTPase 1 homolog (S. cerevisiae)
PCDHAC2	0.747	MGC71598; PCDH-ALPHA-C2	NM_031883	protocadherin alpha subfamily C, 2
NDUFS2	0.747	DCTN2	NM_004550	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)
ABI1	0.747	E3B1; ABI-1; NAP1BP; SSH3BP; SSH3BP1	NM_001012752	abl-interactor 1
DCX	0.746	DC; DBCN; LISX; SCLH; XLIS	NM_178151	doublecortex; lissencephaly, X-linked (doublecortin)
ANK3	0.746	FLJ45464; ANKYRIN-G	NM_001149	ankyrin 3, node of Ranvier (ankyrin G)
HIRIP3	0.746	CYP2U1	NM_003609	HIRA interacting protein 3
SUMF1	0.746	FGE; MGC131853	NM_182760	sulfatase modifying factor 1

FAM86B1	0.745	MGC16279; MGC104828	NM_032916	family with sequence similarity 86, member B1
ZFP36L1	0.745	BRF1; ERF1; cMG1; ERF-1; Berg36; TIS11B; RNF162B	NM_004926	zinc finger protein 36, C3H type-like 1
CDC42BPA	0.744	MRCK; MRCKA; PK428; FLJ23347; KIAA0451; DKFZp686L1738; DKFZp686P1738	NM_014826	CDC42 binding protein kinase alpha (DMPK-like)
PSMD13	0.744	p40.5; HSPC027	NM_002817	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
FTSJ3	0.744	EPCS3; FLJ20062	NM_017647	FtsJ homolog 3 (E. coli)
NEF3	0.744	NFM; NEFM; NF-M	NM_005382	neurofilament 3 (150kDa medium)
BOC	0.744	BOC	NM_033254	Boc homolog (mouse)
NFIC	0.744	CTF; NFI; CTF5; NF-I; MGC20153	NM_205843	nuclear factor I/C (CCAAT-binding transcription factor)
C8ORF53	0.744	MGC14595	NM_032334	chromosome 8 open reading frame 53
ABCA2	0.742	ABC2	NM_001606	ATP-binding cassette, sub-family A (ABC1), member 2
UHRF1	0.742	Np95; ICBP90; RNF106; huNp95; FLJ21925; MGC138707	NM_013282	ubiquitin-like, containing PHD and RING finger domains, 1
BAT4	0.742	G5; D6S54E	NM_033177	HLA-B associated transcript 4
LOC126295	0.742	ZNF424	NM_173480	zinc finger protein 57
CENPF	0.741	CENF; PRO1779	NM_016343	centromere protein F, 350/400ka (mitosin)
GFRA2	0.741	NTNRA; RETL2; TRNR2; GDNFRB; NRTNR-ALPHA	NM_001495	GDNF family receptor alpha 2
TRIAP1	0.74	WF-1; P53CSV; HSPC132	NM_016399	TP53 regulated inhibitor of apoptosis 1
CPEB1	0.74	CPEB; FLJ13203	NM_030594	cytoplasmic polyadenylation element binding protein 1
KIAA1727	0.739	KIAA1727	NM_033393	KIAA1727 protein
RHBDL1	0.739	RRP; RHBDL	NM_003961	rhomboid, veinlet-like 1 (Drosophila)
ZMYM1	0.739	MYM; FLJ23151; FLJ43753; RP11-181E22.4	NM_024772	zinc finger, MYM-type 1
MRPL19	0.739	RLX1; RPML15; MRP-L15; KIAA0104; MGC20675	NM_014763	mitochondrial ribosomal protein L19
FAM29A	0.738	MGC102696; MGC138798; MGC138799; RP11-296P7.3	NM_017645	family with sequence similarity 29, member A
TPARL	0.738	TPARL; TMPT27	NM_018475	transmembrane protein 165
PRKG2	0.738	cGKII; PRKGR2	NM_006259	protein kinase, cGMP-dependent, type II
FSD1	0.737	MIR1; GLFND; MGC3213	NM_024333	fibronectin type III and SPRY domain containing 1
YPEL4	0.737	FLJ30213; MGC102723; MGC138324	NM_145008	yippee-like 4 (Drosophila)
MINA	0.737	MDIG; NO52; MINA53; FLJ14393; DKFZp762O1912	NM_032778	MYC induced nuclear antigen
DNMT3B	0.737	ICF; M.HsaIIIB	NM_006892	DNA (cytosine-5-)-methyltransferase 3 beta
GRHL2	0.736	BOM; DFNA28; TFCP2L3; FLJ11172; FLJ13782	NM_024915	grainyhead-like 2 (Drosophila)
NSMAF	0.736	FAN	NM_003580	neutral sphingomyelinase (N-SMase) activation associated factor
TAF9	0.735	AK6; CIP; CINAP; TAF2G; AD-004; CGI-137; MGC1603; MGC3647; MGC5067; TAFII31; TAFII32; MGC:1603; MGC:3647; MGC:5067; TAFIID32	NM_016283	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
PTCD2	0.735	FLJ12598	NM_024754	pentatricopeptide repeat domain 2
FLJ43855	0.735		NM_198857	
PDZK3	0.735	AIPC; PIN1; PAPIN; PDZK3; KIAA0300	NM_178140	PDZ domain containing 2
ZBTB20	0.734	HOF; DPZF; ODA-8S; ZNF288; DKFZp566F123	NM_015642	zinc finger and BTB domain containing 20
URG4	0.733	URG4; DKFZp666G166; DKFZp686O0457	NM_017920	up-regulated gene 4
TESK2	0.733	TESK2	NM_007170	testis-specific kinase 2
PTPN4	0.732	PTPMEG; PTPMEG1	NM_002830	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)
SLC35F1	0.731	C6orf169; FLJ13018; dJ230I3.1	NM_001029858	solute carrier family 35, member F1
MYOZ1	0.731	CS-2; FATZ; MYOZ	NM_021245	myozenin 1
KIF22	0.73	KID; OBP; KNSL4; OBP-1; OBP-2	NM_007317	kinesin family member 22
RNF123	0.73	KPC1; FP1477; FLJ12565; DKFZp686C2222	NM_022064	ring finger protein 123
SLC4A4	0.73	KNBC; NBC1; NBC2; pNBC; HNBC1; hhNMC; SLC4A5; DKFZp781H1314	NM_003759	solute carrier family 4, sodium bicarbonate cotransporter, member 4
INSM1	0.73	IA1; IA-1	NM_002196	insulinoma-associated 1
POLQ	0.729	POLH; PRO0327; DKFZp781A0112	NM_199420	polymerase (DNA directed), theta
MXRA8	0.728	MGC3047; DKFZp586E2023	NM_032348	matrix-remodelling associated 8
SMPDL3B	0.728	ASML3B	NM_001009568	sphingomyelin phosphodiesterase, acid-like 3B
MSH2	0.728	FCC1; COCA1; HNPCC; HNPCC1	NM_000251	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
DPP7	0.728	QPP; DPP2; DPPII	NM_013379	dipeptidyl-peptidase 7
TCF21	0.727	POD1	NM_003206	transcription factor 21
ABCB7	0.727	ABC7; ASAT; Atm1p; EST140535	NM_004299	ATP-binding cassette, sub-family B (MDR/TAP), member 7
JAM2	0.727	JAMB; CD322; JAM-B; VEJAM; PRO245; VE-JAM; C21orf43	NM_021219	junctional adhesion molecule 2
HMX2	0.726	H6L; Nkx5-2	NM_005519	homeobox (H6 family) 2
EIF2AK4	0.726	GCN2; KIAA1338	NM_001013703	eukaryotic translation initiation factor 2 alpha kinase 4
SULT1C1	0.725	ST1C1; ST1C2; SULT1C#1; humSULTC2	NM_001056	sulfotransferase family, cytosolic, 1C, member 1
UNQ9433	0.724	UNQ9433	NM_207413	RPLK9433
ADAMTS2	0.724	NPI; PCINP; PCPNI; hPCPNI; ADAM-TS2; ADAMTS-3	NM_014244	ADAM metallopeptidase with thrombospondin type 1 motif, 2
PLK1	0.724	PLK; STPK13	NM_005030	polo-like kinase 1 (Drosophila)
LOC96610	0.723	LOC96610	NM_080926	hypothetical protein similar to KIAA0187 gene product
PGF	0.723	PLGF; PlGF-2	NM_002632	placental growth factor, vascular endothelial growth factor-related protein
LYK5	0.723	LYK5; STRAD; FLJ90524	NM_001003786	protein kinase LYK5
SCMH1	0.723	Scml3	NM_001031694	sex comb on midleg homolog 1 (Drosophila)
ZNF294	0.723	RNF160; C21orf10; C21orf98; FLJ11053; KIAA0714	NM_015565	zinc finger protein 294
LOC150223	0.723	LOC150223; MGC133160	NM_001017964	hypothetical protein LOC150223

NARG1L	0.723	MGC40612; RP11-396A22.1	NM_018527	NMDA receptor regulated 1-like
PAP2	0.722	PAP2D; PAP2	NM_001010861	phosphatidic acid phosphatase type 2
GOT1	0.722	GIG18	NM_002079	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
HBQ1	0.72	HBG1	NM_005331	hemoglobin, theta 1
NAGLU	0.72	NAG; MPS3B; UFHSD; MPS IIIB	NM_000263	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)
C1ORF198	0.719	FLJ14525; FLJ16283; FLJ38847; MGC10710; DKFZp667D152	NM_032800	chromosome 1 open reading frame 198
AMBP	0.719	HCP; ITI; UTI; ITIL	NM_001633	alpha-1-microglobulin/bikunin precursor
CRYBB1	0.719	CRYBB1	NM_001887	crystallin, beta B1
EIF3S10	0.718	EIF3; P167; p180; p185; EIF3A; KIAA0139; eIF3-p170; eIF3-theta	NM_003750	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
SHMT1	0.718	SHMT; CSHMT; MGC15229; MGC24556	NM_148918	serine hydroxymethyltransferase 1 (soluble)
MAP2K3	0.717	MEK3; MKK3; MAPKK3; PRKMK3	NM_145110	mitogen-activated protein kinase kinase 3
BFSP1	0.717	CP94; CP115; LIFL-H; FILENSIN	NM_001195	beaded filament structural protein 1, filensin
CD109	0.717	CPAMD7; FLJ38569; FLJ41966; RP11-525G3.1; DKFZp762L1111	NM_133493	CD109 molecule
KIAA0404	0.717	KIAA0404; MGC117153	NM_015104	hypothetical protein LOC23130
MYOZ3	0.716	CS3; CS-3; FRP3	NM_133371	myozenin 3
C13ORF23	0.716	FLJ12661; FLJ23780; bA50D16.2; RP11-50D16.2	NM_025138	chromosome 13 open reading frame 23
BAIAP2L1	0.716	IRTKS	NM_018842	BAI1-associated protein 2-like 1
C20ORF59	0.715	FLJ23412	NM_022082	chromosome 20 open reading frame 59
SYT11	0.715	SYT12; KIAA0080; MGC10881; MGC17226; DKFZp781D015	NM_152280	synaptotagmin XI
B4GALT6	0.714	B4Gal-T6; beta4Gal-T6	NM_004775	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6
DHFRL1	0.714	DHFRP4; FLJ16119	NM_176815	dihydrofolate reductase-like 1
ESM1	0.714	endocan	NM_007036	endothelial cell-specific molecule 1
OPRS1	0.714		NM_147160	
NOVA1	0.714	Nova-1	NM_006491	neuro-oncological ventral antigen 1
ETHE1	0.714	HSCO; YF13H12	NM_014297	ethylmalonic encephalopathy 1
MDS028	0.713	MDS028	NM_018463	integrin alpha FG-GAP repeat containing 2
SORCS2	0.713	WFDC2	NM_020777	sortilin-related VPS10 domain containing receptor 2
ADH5	0.713	FDH; ADHX; ADH-3	NM_000671	alcohol dehydrogenase 5 (class III), chi polypeptide
ACTN1	0.713	FLJ40884	NM_001102	actinin, alpha 1
GNL3L	0.713	FLJ10613; RP11-353K22.1	NM_019067	guanine nucleotide binding protein-like 3 (nucleolar)-like
KIAA0863	0.713	KIAA0863	NM_014913	zinc finger protein 508
RLN2	0.712	H2; RLXH2; bA12D24.1.1; bA12D24.1.2	NM_005059	relaxin 2
IRAK1BP1	0.712	AIP70; SIMPL; MGC138458; MGC138460	NM_001010844	interleukin-1 receptor-associated kinase 1 binding protein 1
DNAPTP6	0.712	DNAPTP6; DKFZp564A2416	NM_015535	DNA polymerase-transactivated protein 6
MSH3	0.712	DUP; MRP1	NM_002439	mutS homolog 3 (E. coli)
ARL4	0.711	ARL4	NM_212460	ADP-ribosylation factor-like 4A
KCNAB1	0.711	hKvb3; AKR6A3; KCNA1B; Kvb1.3; hKvBeta3; KV-BETA-1	NM_172159	potassium voltage-gated channel, shaker-related subfamily, beta member 1
PAGE5	0.711	GAGEE1; PAGE-5	NM_130467	P antigen family, member 5 (prostate associated)
DCLRE1A	0.711	PSO2; SNM1; KIAA0086	NM_014881	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)
VTI1B	0.71	VTI1; VTI2; VTI1L	NM_006370	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)
PNMA2	0.71	MA2; MM2; RGAG2; KIAA0883	NM_007257	paraneoplastic antigen MA2
SARS2	0.71	SYS; SARS; SERS; SARSM; SerRSmt; mtSerRS; FLJ20450	NM_017827	seryl-tRNA synthetase 2
PES1	0.709	PES	NM_014303	pescadillo homolog 1, containing BRCT domain (zebrafish)
FJX1	0.709	FLJ22416	NM_014344	four jointed box 1 (Drosophila)
WDR4	0.709	TRM82	NM_033661	WD repeat domain 4
C3ORF14	0.709	HT021	NM_020685	chromosome 3 open reading frame 14
IPO4	0.708	Imp4; FLJ23338; MGC131665	NM_024658	importin 4
SC65	0.708	SC65; NOL55	NM_006455	synaptonemal complex protein SC65
WDR53	0.708	MGC64882	NM_182627	WD repeat domain 53
RAMP2	0.707	TSPO	NM_005854	receptor (calcitonin) activity modifying protein 2
FAIM3	0.707	TOSO	NM_005449	Fas apoptotic inhibitory molecule 3
BMS1L	0.707	KIAA0187	NM_014753	BMS1-like, ribosome assembly protein (yeast)
TNFSF11	0.707	ODF; OPGL; sOdf; CD254; RANKL; TRANCE; hRANKL2	NM_003701	tumor necrosis factor (ligand) superfamily, member 11
TGOLN2	0.707	TGN38; TGN46; TGN48; TGN51; TTGN2; MGC14722	NM_006464	trans-golgi network protein 2
PPARGC1B	0.707	PERC; PGC1B; PGC-1(beta)	NM_133263	peroxisome proliferative activated receptor, gamma, coactivator 1, beta
ROBO1	0.707	SAX3; DUTT1; FLJ21882; MGC131599; MGC133277	NM_133631	roundabout, axon guidance receptor, homolog 1 (Drosophila)
RFC1	0.706	A1; RFC; PO-GA; RECC1; MHCBFB; RFC140; MGC51786	NM_002913	replication factor C (activator 1) 1, 145kDa
PCDH19	0.706	KIAA1313; DKFZp686P1843	NM_020766	protocadherin 19
FXYD5	0.706	RIC; IWU1; KCT1; OIT2; IWU-1; dysad; HSPC113; PRO6241	NM_144779	FXYD domain containing ion transport regulator 5
FLJ20628	0.705	FLJ20628; DKFZp564I2178	NM_017910	hypothetical protein FLJ20628
ABHD8	0.705	MGC2512; FLJ11743; MGC14280	NM_024527	abhydrolase domain containing 8
RPL7	0.705	humL7-1	NM_000971	ribosomal protein L7
BMP6	0.705	VGR; VGR1	NM_001718	bone morphogenetic protein 6
ARHGEF12	0.705	LARG; PRO2792; KIAA0382; DKFZp686O2372	NM_015313	Rho guanine nucleotide exchange factor (GEF) 12
NIN	0.704	KIAA1565	NM_016350	ninein (GSK3B interacting protein)

SSBP2	0.704	HSPC116; DKFZp686F03273	NM_012446	single-stranded DNA binding protein 2
TMEM87A	0.702	DKFZP564G2022	NM_015497	transmembrane protein 87A
KIAA0859	0.702	CGI-01; FLJ10310; 5630401D24Rik	NM_015935	KIAA0859
BCL11A	0.702	EVI9; CTIP1; BCL11A-L; BCL11A-S; FLJ10173; FLJ34997; KIAA1809; BCL11A-XL	NM_138559	B-cell CLL/lymphoma 11A (zinc finger protein)
GPATC4	0.702	RPIA	NM_182679	G patch domain containing 4
OGFRL1	0.701	FLJ21079; MGC102783; dJ331H24.1	NM_024576	opioid growth factor receptor-like 1
NUDT22	0.7	MGC13045	NM_032344	nudix (nucleoside diphosphate linked moiety X)-type motif 22
LRRC34	0.699	FLJ27346; MGC27085	NM_153353	leucine rich repeat containing 34
HARS2	0.699	DUEB; C20orf88; MGC41905; MGC119131; bA379J5.3; bA555E18.1	NM_080820	histidyl-tRNA synthetase 2
MKKS	0.699	KMS; MKS; BBS6; HMCS	NM_018848	McKusick-Kaufman syndrome
SRI	0.699	SCN; FLJ26259	NM_003130	sorcin
SLC9A1	0.698	APNH; NHE1; FLJ42224	NM_003047	solute carrier family 9 (sodium/hydrogen exchanger), member 1 (antiporter, Na+/H+, amiloride sensitive)
SLC13A3	0.698	NADC3; SDCT2	NM_001011554	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
EIF5A2	0.698	EIF-5A2; eIF5AII	NM_020390	eukaryotic translation initiation factor 5A2
KISS1	0.698	KiSS-1; MGC39258	NM_002256	KiSS-1 metastasis-suppressor
SLC35D3	0.697	FRCL1; MGC102873; bA55K22.3	NM_001008783	solute carrier family 35, member D3
BPNT1	0.697	PIP	NM_006085	3'(2'), 5'-bisphosphate nucleotidase 1
LOC90624	0.697	FLJ20796; MGC24679	NM_181705	chromosome 5 open reading frame 31
ATRN	0.697	MGCA; DPPT-L; KIAA0548; MGC126754	NM_139322	attractin
HHLA1	0.697	UTS2	NM_005712	Urotensin 2
CCRL1	0.696	PPR1; CCBP2; CCR10; CCR11; VSHK1; CKR-11; CCX-CKR; CC-CKR-11	NM_178445	chemokine (C-C motif) receptor-like 1
MSTO1	0.696	MST; LST005; FLJ10504; RP11-29H23.3; DKFZp686B1757; DKFZp686I01261	NM_018116	misato homolog 1 (Drosophila)
FLJ41841	0.696	FLJ41841	NM_207499	FLJ41841 protein
C9ORF140	0.696	C9orf140	NM_178448	chromosome 9 open reading frame 140
FKBP9	0.696	FKBP60; FKBP63; PPIase; MGC126772; MGC138258; DKFZp586B1723	NM_007270	FK506 binding protein 9, 63 kDa
DPEP3	0.696	MBD3	NM_022357	dipeptidase 3
PLEKHA9	0.696	FLJ14156	NM_015899	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 9
WDFY1	0.695	WDF1; FENS-1; ZFYVE17	NM_020830	WD repeat and FYVE domain containing 1
HHLA3	0.694	ARL4A	NM_001031693	HERV-H LTR-associating 3
TSEN2	0.694	SEN2; SEN2L; MGC2776; MGC4440	NM_025265	tRNA splicing endonuclease 2 homolog (S. cerevisiae)
EIF3S8	0.694	eIF3-p110	NM_003752	eukaryotic translation initiation factor 3, subunit 8, 110kDa
C20ORF11	0.694	TWA1	NM_017896	chromosome 20 open reading frame 11
HAPLN3	0.694	EXLD1; HsT19883	NM_178232	hyaluronan and proteoglycan link protein 3
ARHGEF19	0.694	WGEF; FLJ33962; RP4-733M16.1	NM_153213	Rho guanine nucleotide exchange factor (GEF) 19
KLF10	0.694	EGRA; TIEG; TIEG1	NM_005655	Kruppel-like factor 10
MTCP1	0.693	C6.1B	NM_001018025	mature T-cell proliferation 1
C5ORF16	0.693	FLJ90583	NM_173828	chromosome 5 open reading frame 16
KIAA0672	0.693	KIAA0672	NM_014859	KIAA0672 gene product
ARHGAP1	0.693	RHOGAP; RHOGAP1; CDC42GAP; p50rhoGAP	NM_004308	Rho GTPase activating protein 1
KIAA1524	0.692	FLJ12850	NM_020890	KIAA1524
MID1	0.692	OS; FXY; OSX; OGS1; XPRF; BBBG1; GBBB1; RNF59; ZNFXY; TRIM18	NM_000381	midline 1 (Opitz/BBB syndrome)
TREX1	0.691	AGS1; DRN3; ATRIP; FLJ12343; DKFZp434J0310	NM_032166	three prime repair exonuclease 1
FBXL15	0.691	PSD; Fbl15; FBXO37; FLJ16137; MGC11279	NM_024326	F-box and leucine-rich repeat protein 15
SLC4A11	0.691	BTR1; CHED2; NABC1; MGC126418; MGC126419; dJ794I6.2	NM_032034	solute carrier family 4, sodium bicarbonate transporter-like, member 11
ACACB	0.69	ACC2; ACCB; HACC275	NM_001093	acetyl-Coenzyme A carboxylase beta
KLHL7	0.689	KLHL6; SBBI26	NM_001031710	kelch-like 7 (Drosophila)
NFIA	0.689	NFI-L; KIAA1439; DKFZp434L0422	NM_005595	nuclear factor I/A
KIAA1212	0.689	APE; GIV; GRDN; HkRP1; DKFZp686D0630	NM_018084	KIAA1212
C9ORF37	0.689	C9orf37	NM_032937	chromosome 9 open reading frame 37
ACAD8	0.689	ACAD-8; FLJ22590	NM_014384	acyl-Coenzyme A dehydrogenase family, member 8
HSD17B6	0.689	HSE; RODH	NM_003725	hydroxysteroid (17-beta) dehydrogenase 6
MKLN1	0.688	FLJ11162	NM_013255	muskelin 1, intracellular mediator containing kelch motifs
CCL11	0.688	SCYA11; MGC22554	NM_002986	chemokine (C-C motif) ligand 11
CCDC21	0.688	FLJ13976; FLJ22000; DKFZp434P232; DKFZP434L0117	NM_022778	coiled-coil domain containing 21
FYN	0.688	SLK; SYN; MGC45350	NM_153047	FYN oncogene related to SRC, FGR, YES
SIX6	0.688	Six9; OPTX2; MCOPCT2	NM_007374	sine oculis homeobox homolog 6 (Drosophila)
CYB5D2	0.688	MGC32124	NM_144611	cytochrome b5 domain containing 2
SIVA	0.688	SIVA; CD27BP	NM_006427	CD27-binding (Siva) protein
CSTF1	0.687	CstF-50; CstFp50	NM_001033521	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa
SLC25A	0.687	SAMC; DKFZp434E079	NM_173471	solute carrier family 25, member 26

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C10ORF78	0.687	FLJ41960; bA373N18.1; RP11-373N18.1	NM_145247	chromosome 10 open reading frame 78
ZC3H12A	0.687	MCPIP; FLJ23231; dJ423B22.1; RP3-423B22.1	NM_025079	zinc finger CCCH-type containing 12A
PSMD2	0.687	S2; P97; TRAP2; MGC14274	NM_002808	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
QPCTL	0.687	FLJ20084	NM_017659	glutaminyl-peptide cyclotransferase-like
CXORF45	0.686		NM_024810	
CHST10	0.686	HNK1ST; HNK-1ST; MGC17148	NM_004854	carbohydrate sulfotransferase 10
RPUSD2	0.686	C18B11; C15orf19; FLJ31409	NM_152260	RNA pseudouridylate synthase domain containing 2
ATM	0.686	AT1; ATA; ATC; ATD; ATE; ATDC; TEL1; MGC74674; DKFZp781A0353	NM_000051	ataxia telangiectasia mutated (includes complementation groups A, C and D)
LHX6	0.686	LHX6.1; MGC119542; MGC119544; MGC119545	NM_199160	LIM homeobox 6
JSRP1	0.686	JP-45; FLJ32416	NM_144616	junctional sarcoplasmic reticulum protein 1
CDC25A	0.686	CDC25A2	NM_001789	cell division cycle 25A
C8A	0.686	C8A	NM_000562	complement component 8, alpha polypeptide
C1ORF31	0.685	RPL10A	NM_001012985	chromosome 1 open reading frame 31
MFSD2	0.685	FP1147; PP10484; FLJ14490; FLJ35904; HMFN0656; RP3-342P20.1	NM_032793	major facilitator superfamily domain containing 2
NAG6	0.685	NAG6; MGC129657; DKFZP434G156	NM_022742	hypothetical protein DKFZp434G156
POR	0.684	CPR; CYPOR; P450R; FLJ26468; DKFZp686G04235	NM_000941	P450 (cytochrome) oxidoreductase
TRUB2	0.684	CLONE24922; RP11-339B21.1	NM_015679	TruB pseudouridine (psi) synthase homolog 2 (E. coli)
YPEL3	0.684	MGC10500	NM_031477	yippee-like 3 (Drosophila)
ARSG	0.683	KIAA1001	NM_014960	arylsulfatase G
DNASE2	0.683	DNL; DNL2; DNASE2A	NM_001375	deoxyribonuclease II, lysosomal
ACAA1	0.683	ACAA; THIO; PTHIO	NM_001607	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
HSPC171	0.683	HSPC171	NM_014187	HSPC171 protein
ECHDC3	0.683	FLJ20909	NM_024693	enoyl Coenzyme A hydratase domain containing 3
ATAD3A	0.682	FLJ10709	NM_018188	ATPase family, AAA domain containing 3A
LPHN3	0.682	LEC3; CIRL3	NM_015236	latrophilin 3
MRPL47	0.682	NCM1; CGI-204; MGC45403	NM_020409	mitochondrial ribosomal protein L47
WDR3	0.681	FLJ12796	NM_006784	WD repeat domain 3
CHST6	0.681	MCDC1	NM_021615	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6
FAM72A	0.68	GCUD2; MGC57827; RP11-312O7.1	NM_207418	family with sequence similarity 72, member A
C12ORF31	0.68	MGC14817; MGC104302	NM_032338	chromosome 12 open reading frame 31
R3HDM1	0.68	R3HDM; FLJ23334; KIAA0029	NM_015361	R3H domain containing 1
APTX	0.68	AOA; AOA1; AXA1; EAOH; EOAHA; FHA-HIT; MGC1072; FLJ20157	NM_175073	aprataxin
NUDCD1	0.68	CML66; FLJ14991	NM_032869	NudC domain containing 1
CSPG5	0.68	NGC; MGC44034	NM_006574	chondroitin sulfate proteoglycan 5 (neuroglycan C)
HAS3	0.679	HAS3	NM_005329	hyaluronan synthase 3
FLJ32363	0.679	FLJ32363; MGC46448	NM_198566	FLJ32363 protein
SLC25A28	0.679	MRS4L; MRS3/4; NPD016; DKFZp547C109	NM_031212	solute carrier family 25, member 28
C12ORF30	0.678	FLJ13089; DKFZp667K2112	NM_024953	chromosome 12 open reading frame 30
SNX8	0.678	SNX8	NM_013321	sorting nexin 8
BTN3A3	0.678	BTF3	NM_006994	butyrophilin, subfamily 3, member A3
CDC45L	0.677	CDC45; CDC45L2; PORC-PI-1	NM_003504	CDC45 cell division cycle 45-like (S. cerevisiae)
AIM1	0.676	ST4	NM_001624	absent in melanoma 1
KCTD17	0.676	FLJ12242	NM_024681	potassium channel tetramerisation domain containing 17
PPIAL4	0.675	COAS2	NM_178230	peptidylprolyl isomerase A (cyclophilin A)-like 4
TRIM9	0.675	RNF91; SPRING; KIAA0282	NM_015163	tripartite motif-containing 9
ACTR3B	0.675	ARP11; ARP3BETA; DKFZp686O24114	NM_020445	ARP3 actin-related protein 3 homolog B (yeast)
ADAMTSL1	0.675	ADAMTSR1; MGC40193	NM_052866	ADAMTS-like 1
PHLPPL	0.675	KIAA0931	NM_015020	PH domain and leucine rich repeat protein phosphatase-like
TSC22D1	0.675	TSC22; TGFB1I4; MGC17597; RP11-269C23.2; DKFZp686O19206	NM_183422	TSC22 domain family, member 1
MAN2B2	0.674	KIAA0935	NM_015274	mannosidase, alpha, class 2B, member 2
KIAA0564	0.674	KIAA0564; FLJ21779	NM_001009814	KIAA0564 protein
APOM	0.674	G3a; NG20; HSPC336; MGC22400	NM_019101	apolipoprotein M
VDAC1	0.673	PORIN; MGC111064; PORIN-31-HL	NM_003374	voltage-dependent anion channel 1
NARG1L	0.673	MGC40612; RP11-396A22.1	NM_024561	NMDA receptor regulated 1-like
VKORC1L1	0.672	DKFZp762H0113	NM_173517	vitamin K epoxide reductase complex, subunit 1-like 1
RTP1	0.672	MGC35450	NM_153708	receptor transporter protein 1
BCL2L12	0.672	MGC120313; MGC120314; MGC120315	NM_138639	BCL2-like 12 (proline rich)
UBL7	0.672	TCBA1; BMSC-UbP; MGC14421	NM_201265	ubiquitin-like 7 (bone marrow stromal cell-derived)
OLFM1	0.671	AMY; NOE1; OlfA; NOELIN; NOELIN1; NOELIN1_V1; NOELIN1_V2; NOELIN1_V4; NOELIN1_V5	NM_006334	olfactomedin 1
VWCE	0.671	VWC1; URG11; FLJ32009	NM_152718	von Willebrand factor C and EGF domains
POLR3G	0.671	RPC7; RPC32	NM_006467	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
LRRC47	0.671	KIAA1185; RP1-286D6.3	NM_020710	leucine rich repeat containing 47

GNLY	0.671	519; LAG2; NKG5; LAG-2; D2S69E; TLA519; lymphokine	NM_006433	granulysin
G6PD	0.67	G6PD1	NM_000402	glucose-6-phosphate dehydrogenase
FBP1	0.67	FBP	NM_000507	fructose-1,6-bisphosphatase 1
CAPN11	0.669	calpain11	NM_007058	calpain 11
BNC1	0.669	BNC; BSN1; HsT19447	NM_001717	basonuclin 1
NUP35	0.668	MP44; NP44	NM_138285	nucleoporin 35kDa
C14ORF130	0.668	MGC9518; FLJ10483	NM_018108	chromosome 14 open reading frame 130
PABPC3	0.668	PABP3; PABPL3	NM_030979	poly(A) binding protein, cytoplasmic 3
DUT	0.667	dUTPase; FLJ20622	NM_001025248	dUTP pyrophosphatase
C15ORF42	0.667	FLJ41618; MGC45866	NM_152259	chromosome 15 open reading frame 42
FVT1	0.667	FVT1	NM_002035	follicular lymphoma variant translocation 1
GLRX2	0.666	GRX2; bA101E13.1	NM_197962	glutaredoxin 2
HLA-G	0.666	MHC-G	NM_002127	HLA-G histocompatibility antigen, class I, G
FAM46A	0.666	XTP11; C6orf37; FLJ20037; FLJ31495	NM_017633	family with sequence similarity 46, member A
OACT5	0.666	C3F; OACT5; nessy	NM_005768	membrane bound O-acyltransferase domain containing 5
C1ORF135	0.666	MGC2603; FLJ14264	NM_024037	chromosome 1 open reading frame 135
C12ORF32	0.665	HKMT1188; MGC13204	NM_031465	chromosome 12 open reading frame 32
FAM98C	0.665	FLJ44669	NM_174905	family with sequence similarity 98, member C
IFIH1	0.665	Hlcd; MDA5; MDA-5; IDDM19; MGC133047	NM_022168	interferon induced with helicase C domain 1
KIAA1904	0.664	KIAA1904; dJ63G5.3	NM_052906	KIAA1904 protein
MPP2	0.664	DLG2; DKFZp686J2189; DKFZp761D0712; DKFZp686A06252	NM_005374	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
CCNA2	0.664	CCN1; CCNA	NM_001237	cyclin A2
GCN1L1	0.664	GCN1; GCN1L; KIAA0219	NM_006836	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)
TPX2	0.664	DIL2; p100; DIL-2; HCTP4; FLS353; HCA519; REPP86; C20orf1; C20orf2; GD:C20orf1	NM_012112	TPX2, microtubule-associated, homolog (Xenopus laevis)
MBNL2	0.663	MBLL; MBLL39; PRO2032; MGC120625; MGC120626; MGC120628; DKFZp781H1296; RP11-128N14.1	NM_144778	muscleblind-like 2 (Drosophila)
SART2	0.663	SART2	NM_013352	squamous cell carcinoma antigen recognized by T cells 2
RIMS3	0.663	NIM3; RIM3; KIAA0237	NM_014747	regulating synaptic membrane exocytosis 3
OLIG2	0.662	BHLHB1; OLIGO2; RACK17; PRKCBP2	NM_005806	oligodendrocyte lineage transcription factor 2
ZNF226	0.662	ZNF226	NM_001032374	zinc finger protein 226
BTN2A2	0.662	BTF2; BT2.2	NM_181531	butyrophilin, subfamily 2, member A2
MIR16	0.662	MIR16; GDE1; 363E6.2	NM_016641	membrane interacting protein of RGS16
WDR67	0.661	Gm85; MGC21654; MGC104222; MGC126773; MGC138159	NM_145647	WD repeat domain 67
ABI3BP	0.661	TARSH; NESHBP; FLJ41743; FLJ41754	NM_015429	ABI gene family, member 3 (NESH) binding protein
PDXK	0.66	PKH; PNK; C21orf97	NM_003681	pyridoxal (pyridoxine, vitamin B6) kinase
CCDC25	0.66	CCDC25	NM_001031708	synonym: FLJ10853; Homo sapiens coiled-coil domain containing 25 (CCDC25), mRNA.
C1ORF112	0.66	FLJ10706; FLJ13470; MGC130018; MGC130019; RP1-97P20.1	NM_018186	chromosome 1 open reading frame 112
OSTALPHA	0.66	OSTalpha; MGC39807	NM_152672	organic solute transporter alpha
PRIM2A	0.66	p58; PRIM2; MGC75142	NM_000947	primase, polypeptide 2A, 58kDa
LAMB3	0.659	LAMNB1	NM_000228	laminin, beta 3
AURKC	0.659	AIE2; AIK3; AurC; STK13; aurora-C	NM_001015878	aurora kinase C
ELL3	0.659	FLJ22637	NM_025165	elongation factor RNA polymerase II-like 3
TDP1	0.658	FLJ11090; MGC104252	NM_018319	tyrosyl-DNA phosphodiesterase 1
HRIHFB2122	0.658	TARA; DFNB28; KIAA1662; dJ37E16.4; HRIHFB2122	NM_138632	TRIO and F-actin binding protein
CARD10	0.658	BIMP1; CARMA3; MGC142219	NM_014550	caspase recruitment domain family, member 10
LRRC49	0.658	FLJ20156	NM_017691	leucine rich repeat containing 49
DTYMK	0.658	CDC8; TMPK; TYMK	NM_012145	deoxythymidylate kinase (thymidylate kinase)
OVOL2	0.658	ZNF339; EUROIMAGE566589	NM_021220	ovo-like 2 (Drosophila)
HIBCH	0.658	HIBYL-COA-H	NM_014362	3-hydroxyisobutyryl-Coenzyme A hydrolase
EDG2	0.657	LPA1; LPAR1; edg-2; vzg-1; Gpcr26; Mrec1.3; rec.1.3	NM_057159	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
DDEF1	0.657	PAP; PAG2; AMAP1; ASAP1; ZG14P; KIAA1249	NM_018482	development and differentiation enhancing factor 1
LANCL1	0.657	p40; GPR69A	NM_006055	LanC lantibiotic synthetase component C-like 1 (bacterial)
SACS	0.657	ARSACS; DKFZp686B15167	NM_014363	spastic ataxia of Charlevoix-Saguenay (sacsin)
DNAJA3	0.656	TID1; hTid-1	NM_005147	DnaJ (Hsp40) homolog, subfamily A, member 3
RAD54B	0.656	FSBP	NM_012415	RAD54 homolog B (S. cerevisiae)
UNQ1940	0.656	UNQ1940	NM_205855	HWKM1940
ZWILCH	0.655	KNTC1AP; hZwilch; FLJ10036; FLJ16343; MGC111034	NM_017975	Zwilch, kinetochore associated, homolog (Drosophila)
WDR51A	0.655	MGC131902; DKFZP434C245	NM_015426	WD repeat domain 51A
SNTB2	0.655	SNT3; SNTL; SNT2B2; EST25263; D16S2531E	NM_006750	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)
ABL1	0.655	ABL; JTK7; p150; c-ABL; v-abl	NM_007313	v-abl Abelson murine leukemia viral oncogene homolog 1
IRX4	0.654	MGC131996	NM_016358	iroquois homeobox protein 4
ZSCAN2	0.654	ZFP29; FLJ20595	NM_001007072	zinc finger and SCAN domain containing 2
CRIM1	0.654	S52; MGC138194	NM_016441	cysteine rich transmembrane BMP regulator 1 (chordin-like)
DNMT1	0.654	DNMT; MCMT; CXXC9; FLJ16293; MGC104992	NM_001379	DNA (cytosine-5-)-methyltransferase 1
SDAD1	0.654	FLJ10498; DKFZp686E22207	NM_018115	SDA1 domain containing 1

C9ORF77	0.654	CGI-67; RP11-409O11.2	NM_001025780	chromosome 9 open reading frame 77
CD83	0.653	BL11; HB15	NM_004233	CD83 molecule
ATG4C	0.653	APG4C; AUTL1; AUTL3; APG4-C; FLJ14867	NM_032852	ATG4 autophagy related 4 homolog C (S. cerevisiae)
DUSP23	0.653	VHZ; LDP-3; DUSP25; FLJ20442; RP11-190A12.1	NM_017823	dual specificity phosphatase 23
ANKRD28	0.653	PITK; KIAA0379	NM_015199	ankyrin repeat domain 28
RAC1	0.653	MIG5; TC-25; p21-Rac1; MGC111543	NM_018890	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
CTH	0.653	MGC9471	NM_153742	cystathionase (cystathionine gamma-lyase)
SPON1	0.652	KIAA0762; MGC10724; f-spondin	NM_006108	spondin 1, extracellular matrix protein
TPP1	0.652	CLN2; GIG1; LINCL; TPP I; TPP-I	NM_000391	tripeptidyl peptidase I
EIF2S1	0.652	EIF2; EIF-2; EIF2A; EIF-2A; EIF-2alpha	NM_004094	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
SORT1	0.651	NT3; Gp95	NM_002959	sortilin 1
HADHA	0.651	GBP; HADH; MTPA; LCHAD; MGC1728; TP-ALPHA	NM_000182	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
GALK2	0.651	GK2; MGC1745	NM_001001556	galactokinase 2
TSPAN4	0.651	NAG2; NAG-2; TM4SF7; TSPAN-4; TETRASPAN	NM_001025235	tetraspanin 4
ASAH1	0.65	AC; PHP; ASAH; PHP32; FLJ21558; FLJ22079	NM_177924	N-acylsphingosine amidohydrolase (acid ceramidase) 1
PVRL1	0.65	ED4; PRR; HIgR; HVEC; OFC7; PRR1; PVRR; CD111; PVRR1; SK-12; CLPED1; MGC16207; nectin-1; MGC142031	NM_203286	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
BTN3A1	0.65	BTF5; BT3.1; CD277	NM_007048	butyrophilin, subfamily 3, member A1
AP3B1	0.65	PE; HPS; HPS2; ADTB3; ADTB3A	NM_003664	adaptor-related protein complex 3, beta 1 subunit
SCARA3	0.649	CSR; APC7; CSR1; MSLR1; MSRL1	NM_182826	scavenger receptor class A, member 3
SYDE1	0.649	7h3; FLJ13511	NM_033025	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)
JPH1	0.649	JP1; JP-1; DKFZp762L0313	NM_020647	junctophilin 1
CD164	0.649	MGC-24; MUC-24; endolyn	NM_006016	CD164 molecule, sialomucin
ALDH1A1	0.649	ALDC; ALDH1; PUMB1; ALDH11; RALDH1; ALDH-E1; MGC2318	NM_000689	aldehyde dehydrogenase 1 family, member A1
PLK4	0.648	SAK; STK18	NM_014264	polo-like kinase 4 (Drosophila)
PVRL1	0.648	ED4; PRR; HIgR; HVEC; OFC7; PRR1; PVRR; CD111; PVRR1; SK-12; CLPED1; MGC16207; nectin-1; MGC142031	NM_203285	poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
ANKRD29	0.647	FLJ25053	NM_173505	ankyrin repeat domain 29
SNAPC5	0.647	SNAP19	NM_006049	small nuclear RNA activating complex, polypeptide 5, 19kDa
FOXRED1	0.646	H17; FP634	NM_017547	FAD-dependent oxidoreductase domain containing 1
HERC6	0.645	FLJ20637	NM_001013005	hect domain and RLD 6
KLF10	0.645	EGRA; TIEG; TIEG1	NM_005655	Kruppel-like factor 10
FLJ11286	0.645	FLJ11286; FLJ40743	NM_018381	hypothetical protein FLJ11286
MCM6	0.644	Mis5; P105MCM; MCG40308	NM_005915	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)
TRMT1	0.644	FLJ20244	NM_017722	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)
PLA2G3	0.644	GIII-SPLA2	NM_015715	phospholipase A2, group III
MANSC1	0.644	FLJ10298; LOH12CR3; 9130403P13Rik	NM_018050	MANSC domain containing 1
UNC5D	0.644	Unc5h4; FLJ16019; KIAA1777; PRO34692	NM_080872	unc-5 homolog D (C. elegans)
LRRC15	0.644	LIB	NM_130830	leucine rich repeat containing 15
PUS1	0.643	MLASA; MGC11268	NM_025215	pseudouridylate synthase 1
PXN	0.643	FLJ16691	NM_002859	paxillin
C18ORF54	0.642	MGC33382	NM_173529	chromosome 18 open reading frame 54
BCOR	0.642	MAA2; ANOP2; MCOPS2; FLJ20285; FLJ38041; KIAA1575; MGC71031; MGC131961	NM_017745	BCL6 co-repressor
OSAP	0.642	OSAP; MGC125827; MGC125828	NM_032623	ovary-specific acidic protein
KIAA0971	0.642	KIAA0971	NM_014929	FAST kinase domains 2
ETV5	0.641	ERM	NM_004454	ets variant gene 5 (ets-related molecule)
RIN1	0.641	RIN1	NM_004292	Ras and Rab interactor 1
CCNE1	0.641	CCNE	NM_001238	cyclin E1
SYNGR1	0.641	MGC:1939	NM_145738	synaptogyrin 1
SLC41A1	0.641	MgtE	NM_173854	solute carrier family 41, member 1
PPM1G	0.64	PP2CG; PPP2CG; MGC1675; MGC2870; PP2CGAMMA	NM_002707	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
FBL	0.64	FIB; FLRN; RNU3IP1	NM_001436	fibrillarin
GPR23	0.64	P2Y9; LPAR4; P2RY9; P2Y5-LIKE	NM_005296	G protein-coupled receptor 23
LIAS	0.64	LAS; LIP1; HUSSY-01; MGC23245	NM_006859	lipoic acid synthetase
HLA-DMB	0.639	RING7; D6S221E	NM_002118	major histocompatibility complex, class II, DM beta
SNX5	0.639	FLJ10931	NM_014426	sorting nexin 5
DNAJC12	0.639	JDP1; RP11-57G10.2	NM_021800	DnaJ (Hsp40) homolog, subfamily C, member 12
SLITL2	0.638	SLITL2	NM_138440	vasorin
STK4	0.638	KRS2; MST1; YSK3; DKFZp686A2068	NM_006282	serine/threonine kinase 4
NOP5/NOP58	0.638	NOP5/NOP58; HSPC120	NM_015934	nucleolar protein NOP5/NOP58
PLAC9	0.638	MGC104710	NM_001012973	placenta-specific 9
LARS	0.638	LRS; LEUS; LARS1; LEURS; PIG44; RNTLS; HSPC192; hr025Cl; FLJ10595; FLJ21788	NM_020117	leucyl-tRNA synthetase
MMP25	0.638	MMP20; MT-MMP6; MT6-MMP	NM_022718	matrix metallopeptidase 25
IGSF21	0.638	MGC15730; RP11-121A23.1	NM_032880	immunoglobin superfamily, member 21
SRP46	0.637	SRP46	NM_032102	splicing factor, arginine/serine-rich 2B
C16ORF58	0.637	FLJ13868	NM_022744	chromosome 16 open reading frame 58

DENND 2A	0.636	FAM31D; KIAA1277	NM_015689	DENN/MADD domain containing 2A
RHEBL 1	0.636	RHEBL1c; FLJ25797; MGC34869	NM_144593	Ras homolog enriched in brain like 1
SPIB	0.635	SPI-B	NM_003121	Spi-B transcription factor (Spi-1/PU.1 related)
RNF175	0.635	FLJ34190	NM_173662	ring finger protein 175
TNS3	0.634	TEM6; TENS1; FLJ13732; FLJ35545; MGC88434; H_NH049I23.2; DKFZp686M1045	NM_022748	tensin 3
PIGS	0.634	FLJ45226; DKFZp686K20216	NM_033198	phosphatidylinositol glycan anchor biosynthesis, class S
GFOD1	0.634	C6orf114	NM_018988	glucose-fructose oxidoreductase domain containing 1
FXYD1	0.633	PLM; MGC44983	NM_005031	FXYD domain containing ion transport regulator 1 (phospholemman)
C21ORF 25	0.633	TMEM24L; MGC71445; C21orf258; DKFZp686O198; DKFZP586F0422	NM_199050	chromosome 21 open reading frame 25
UQCRH	0.633	MGC111572	NM_006004	ubiquinol-cytochrome c reductase hinge protein
PPRC1	0.632	PRC; KIAA0595; MGC74642; RP11-302K17.6	NM_015062	peroxisome proliferative activated receptor, gamma, coactivator-related 1
PPIL1	0.632	CYPL1; hCyPX; MGC678; PPIase; CGI-124	NM_016059	peptidylprolyl isomerase (cyclophilin)-like 1
AGA	0.632	GA; AGU; ASRG	NM_000027	aspartylglucosaminidase
KIAA05 86	0.632	Talpid3	NM_014749	KIAA0586
CCT4	0.632	SRB; Cctd; MGC126164; MGC126165	NM_006430	chaperonin containing TCP1, subunit 4 (delta)
PSMF1	0.631	PI31	NM_178578	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)
PELP1	0.631	HMX3; MNAR; P160	NM_014389	proline, glutamic acid and leucine rich protein 1
ANKRA 2	0.631	ANKRA	NM_023039	ankyrin repeat, family A (RFXANK-like), 2
SLC27A 1	0.631	FATP; FATP1; ACSVL5; FLJ00336; MGC71751	NM_198580	solute carrier family 27 (fatty acid transporter), member 1
E2F2	0.63	E2F-2	NM_004091	E2F transcription factor 2
KIF15	0.63	HKLP2; KNSL7; FLJ25667; NY-BR-62	NM_020242	kinesin family member 15
EIF5B	0.63	IF2; FLJ10524; KIAA0741; DKFZp434I036	NM_015904	eukaryotic translation initiation factor 5B
METAP 1	0.63	KIAA0094; DKFZp781C0419	NM_015143	methionyl aminopeptidase 1
LRRC17	0.63	P37NB	NM_001031 692	leucine rich repeat containing 17
VARS	0.63	G7A; VARS2	NM_006295	valyl-tRNA synthetase
C6ORF1 68	0.629	MGC2817; dJ273F20	NM_032511	chromosome 6 open reading frame 168
FLJ1171 2	0.629	AGS2; DLEU8; FLJ11712	NM_024570	ribonuclease H2, subunit B
METTL 3	0.629	M6A; Spo8; MT-A70; MGC4336	NM_019852	methyltransferase like 3
ITGB1B P1	0.629	ICAP1; ICAP1A; ICAP1B; ICAP-1A; ICAP-1B; DKFZp686K08158	NM_022334	integrin beta 1 binding protein 1
KIAA12 74	0.628	PALD	NM_014431	KIAA1274
PRKCH	0.628	PKCL; PKC-L; PRKCL; MGC5363; MGC26269; nPKC-eta	NM_006255	protein kinase C, eta
TATDN 1	0.628	CDA11	NM_032026	TatD DNase domain containing 1
ARMCX 2	0.628	ALEX2; MGC8742; KIAA0512; MGC13343	NM_177949	armadillo repeat containing, X-linked 2
C12ORF 52	0.627	FLJ14827	NM_032848	chromosome 12 open reading frame 52
TCEAL1	0.627	p21; SIIR; pp21	NM_004780	transcription elongation factor A (SII)-like 1
CACNA 1F	0.627	JM8; JMC8; CSNB2; CSNBX2	NM_005183	calcium channel, voltage-dependent, alpha 1F subunit
LOC342 897	0.627	LOC342897	NM_001001 414	similar to F-box only protein 2
UNG	0.626	DGU; UDG; UNG1; HIGM4; UNG15; DKFZp781L1143	NM_080911	uracil-DNA glycosylase
TMEM9 B	0.624	C11orf15	NM_020644	TMEM9 domain family, member B
TRIM47	0.624	GOA; RNF100	NM_033452	tripartite motif-containing 47
MGC13 114	0.624	MGC13114; JFP2	NM_032366	hypothetical protein MGC13114
FLJ4298 6	0.624		NM_207403	
COQ2	0.623	CL640; FLJ26072	NM_015697	coenzyme Q2 homolog, prenyltransferase (yeast)
NCOR2	0.623	SMRT; CTG26; SMRTE; TRAC1; TNRC14; TRAC-1; SMRTE-tau	NM_006312	nuclear receptor co-repressor 2
PPIL5	0.623	LRR-1; 4-1BBLRR; MGC20689	NM_152329	peptidylprolyl isomerase (cyclophilin)-like 5
LOC571 46	0.623	TMEM159	NM_020422	transmembrane protein 159
MFNG	0.622	MFNG	NM_002405	manic fringe homolog (Drosophila)
DNAJC1 2	0.622	JDP1; RP11-57G10.2	NM_201262	DnaJ (Hsp40) homolog, subfamily C, member 12
CEBPA	0.622	CEBP; C/EBP-alpha	NM_004364	CCAAT/enhancer binding protein (C/EBP), alpha
FUT4	0.622	CD15; ELFT; FCT3A; FUC-TIV	NM_002033	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
PDCD2	0.621	RP8; ZMYND7; MGC12347	NM_144781	programmed cell death 2
RAB38	0.621	rrGTPbp; NY-MEL-1	NM_022337	RAB38, member RAS oncogene family
CDX4	0.62	CDX4	NM_005193	caudal type homeobox transcription factor 4
MYLIP	0.62	MIR	NM_013262	myosin regulatory light chain interacting protein
ENPP2	0.619	ATX; NPP2; ATX-X; PDNP2; LysoPLD; FLJ26803; PD-IALPHA	NM_006209	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)
C14ORF 4	0.619	IRF2BPL; KIAA1865	NM_024496	chromosome 14 open reading frame 4
EPB41L 4B	0.619	CG1; EHM2; FLJ21596; DKFZp761N1814	NM_018424	erythrocyte membrane protein band 4.1 like 4B
SOD2	0.619	IPO-B; MNSOD; Mn-SOD	NM_000636	superoxide dismutase 2, mitochondrial
C1ORF7 1	0.617	FLJ32001; MGC18089; RP11-452J6.1	NM_152609	chromosome 1 open reading frame 71
SNAP23	0.617	SNAP23A; SNAP23B; HsT17016	NM_003825	synaptosomal-associated protein, 23kDa
CCDC77	0.617	MGC13183	NM_032358	coiled-coil domain containing 77
MST150	0.617	MST150; NID67; MGC117221; MGC126887;	NM_032947	MSTP150

		MGC126889		
PINK1	0.616	BRPK; PARK6; FLJ27236	NM_032409	PTEN induced putative kinase 1
ZNF323	0.616	ZNF310P; FLJ23407; ZNF20-Lp; dJ874C20.2	NM_145909	zinc finger protein 323
LAMC2	0.616	B2T; EBR2; BM600; EBR2A; LAMB2T; LAMNB2; MGC138491; MGC141938	NM_018891	laminin, gamma 2
FLJ21945	0.616	PP384; FLJ21945	NM_025203	chromosome 2 open reading frame 44
C10ORF77	0.616	FLJ22529; bA18I14.8; RP11-18I14.8	NM_024789	chromosome 10 open reading frame 77
PCDH11X	0.615	PCDHX; PCDHY; PCDH-X; PCDH11	NM_032967	protocadherin 11 X-linked
PODXL2	0.615	PODLX2	NM_015720	podocalyxin-like 2
ATP6V1E2	0.614	VMA4; ATP6E1; ATP6EL2; MGC9341; ATP6V1EL2	NM_080653	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2
CCNH	0.613	CAK; p34; p37	NM_001239	cyclin H
EXT2	0.613	SOTV	NM_000401	exostoses (multiple) 2
OCRL	0.613	LOCR; NPHL2; OCRL1; INPP5F	NM_000276	oculocerebrorenal syndrome of Lowe
SURF6	0.613	FLJ30322	NM_006753	surfeit 6
ELP3	0.612	FLJ10422	NM_018091	elongation protein 3 homolog (S. cerevisiae)
ANGEL1	0.612	KIAA0759	NM_015305	angel homolog 1 (Drosophila)
SLC25A21	0.612	ODC; ODC1; MGC126570	NM_030631	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
DIXDC1	0.611	CCD1; KIAA1735	NM_033425	DIX domain containing 1
STC2	0.611	STC-2; STCRP	NM_003714	stanniocalcin 2
ADCY9	0.611	HLA-DRB1	NM_001116	adenylate cyclase 9
PIGB	0.61	MGC21236	NM_004855	phosphatidylinositol glycan anchor biosynthesis, class B
ST8SIA5	0.61	SIAT8E; ST8Sia V; MGC119670; MGC119671	NM_013305	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5
LOC221955	0.61	DAGLBETA; KCCR13L	NM_139179	diacylglycerol lipase beta
MRPL4	0.61	L4mt; CGI-28; MGC2681; MGC16367	NM_015956	mitochondrial ribosomal protein L4
TXLNA	0.609	TXLN; MGC118870; MGC118871; RP4-622L5.4; DKFZp451J0118	NM_175852	taxilin alpha
DEF6	0.609	IBP	NM_022047	differentially expressed in FDCP 6 homolog (mouse)
FAM43B	0.609	FLJ44952	NM_207334	family with sequence similarity 43, member B
CENTD3	0.609	ARAP3; DRAG1; FLJ21065	NM_022481	centaurin, delta 3
LARGE	0.609	MDC1D; KIAA0609	NM_004737	like-glycosyltransferase
C1ORF187	0.609	UNQ3119; AGPA3119; FLJ34999; MGC117222	NM_198545	chromosome 1 open reading frame 187
SVIL	0.609	DKFZp686A17191	NM_003174	supervillin
CHAC1	0.608	MGC4504	NM_024111	ChaC, cation transport regulator-like 1 (E. coli)
SFRS10	0.608	TRA2B; SRFS10; TRA2-BETA; Htra2-beta; DKFZp686F18120	NM_004593	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
TFF3	0.608	ITF; TFI; HITF; hP1.B	NM_003226	trefoil factor 3 (intestinal)
ARHGAP11A	0.608	KIAA0013; MGC70740; GAP (1-12)	NM_199357	Rho GTPase activating protein 11A
FLJ13984	0.608	TIP; FLJ13984; FLJ42098	NM_024770	methyltransferase like 8
MPDZ	0.608	MUPP1; FLJ25909; FLJ34626; FLJ90240; DKFZp781P216	NM_003829	multiple PDZ domain protein
IMP3	0.608	BRMS2; MRPS4; C15orf12; FLJ10968; DKFZp586L0118	NM_018285	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)
USP9X	0.608		NM_004652	
RRM1	0.607	R1; RR1; RIR1	NM_001033	ribonucleotide reductase M1 polypeptide
C12ORF62	0.607	MGC14288	NM_032901	chromosome 12 open reading frame 62
LSM6	0.607	YDR378C	NM_007080	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)
M6PR	0.607	SMPR; MPR46; CD-MPR	NM_002355	mannose-6-phosphate receptor (cation dependent)
WRN	0.606	RECQ3; RECQL2; RECQL3; DKFZp686C2056	NM_000553	Werner syndrome
AURKAIP1	0.606	AIP; AKIP; FLJ20608	NM_017900	aurora kinase A interacting protein 1
CCDC34	0.606	L15; RAMA3; NY-REN-41	NM_030771	coiled-coil domain containing 34
NXT2	0.606	P15-2	NM_018698	nuclear transport factor 2-like export factor 2
ULBP2	0.606	N2DL2; RAET1H	NM_025217	UL16 binding protein 2
DLST	0.606	DLTS	NM_001933	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
RIC8B	0.605	RIC8; hSyn; FLJ10620; MGC39476	NM_018157	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)
CYB5A	0.605	CYB5; MCB5	NM_148923	cytochrome b5 type A (microsomal)
NRK	0.604	NESK; FLJ16788; MGC131849; DKFZp686A17109	NM_198465	Nik related kinase
NUP155	0.604	N155; KIAA0791	NM_004298	nucleoporin 155kDa
ARL1	0.603	ARFL1	NM_001177	ADP-ribosylation factor-like 1
NGLY1	0.602	PNG1; FLJ11005; FLJ12409	NM_018297	N-glycanase 1
IGSF1	0.601	IGCD1; IGDC1; INHBP; PGSF2; KIAA0364; MGC75490	NM_205833	immunoglobulin superfamily, member 1
ACAD10	0.601	MGC5601	NM_025247	acyl-Coenzyme A dehydrogenase family, member 10
UAP1	0.601	AgX; AGX1; SPAG2	NM_003115	UDP-N-acteylglucosamine pyrophosphorylase 1
IGSF1	0.601	IGCD1; IGDC1; INHBP; PGSF2; KIAA0364; MGC75490	NM_001555	immunoglobulin superfamily, member 1
C14ORF29	0.6	c14_5314; MGC129926; MGC129927	NM_181533	chromosome 14 open reading frame 29
TBC1D8	0.6	AD3; VRP; HBLP1	NM_007063	TBC1 domain family, member 8 (with GRAM domain)
WDR35	0.6	KIAA1336; MGC33196	NM_001006657	WD repeat domain 35
CRYBA4	0.6	KLK4	NM_001886	crystallin, beta A4
PCSK1N	0.6	SAAS; PROSAAS	NM_013271	proprotein convertase subtilisin/kexin type 1 inhibitor
RAB3C	0.6	RAB3C	NM_138453	RAB3C, member RAS oncogene family
KCNJ2	0.599	IRK1; LQT7; SQT3; HHIRK1; KIR2.1; HHBIRK1	NM_000891	potassium inwardly-rectifying channel, subfamily J, member 2
PDPR	0.599	PDPR; FLJ10079; DKFZp686A088;	NM_017990	pyruvate dehydrogenase phosphatase regulatory subunit

		DKFZp686D16130		
ACBD6	0.598	MGC2404	NM_032360	acyl-Coenzyme A binding domain containing 6
DPH2	0.597	DPH2L2	NM_001384	DPH2 homolog (S. cerevisiae)
PCMTD1	0.597	FLJ10883	NM_052937	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1
GFM1	0.597	EFG; GFM; EFG1; EFGM; EGF1; hEFG1; FLJ12662; FLJ13632; FLJ20773	NM_024996	G elongation factor, mitochondrial 1
TOR1B	0.597	DQ1; MGC4386	NM_014506	torsin family 1, member B (torsin B)
GCNT2	0.596	II; IGNT; ULG3; GCNT5; GCNT2C; NACGT1; NAGCT1; bA421M1.1; bA360O19.2	NM_001491	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
SPATA18	0.595	FLJ32906	NM_145263	spermatogenesis associated 18 homolog (rat)
NIP7	0.595	KD93; CGI-37; HSPC031; FLJ10296	NM_016101	nuclear import 7 homolog (S. cerevisiae)
KIAA0406	0.595	ABHD2	NM_014657	KIAA0406
SIAE	0.595	LSE; YSG2; CSE-C; MGC87009	NM_170601	sialic acid acetylesterase
KDELC1	0.595	EP58; KDEL1; MGC5302	NM_024089	KDEL (Lys-Asp-Glu-Leu) containing 1
POPDC3	0.594	POP3; MGC22671; bA355M14.1	NM_022361	popeye domain containing 3
IKIP	0.593	IKIP; FLJ31051	NM_201612	IKK interacting protein
ETV5	0.593	ERM	NM_004454	ets variant gene 5 (ets-related molecule)
TBPL1	0.593	TLF; TLP; STUD; TRF2; MGC:8389; MGC:9620	NM_004865	TBP-like 1
CDCA5	0.592	MGC16386	NM_080668	cell division cycle associated 5
PTP4A1	0.592	HH72; PRL1; PRL-1; PTPCAAX1; PTP(CAAX1); DKFZp779M0721	NM_003463	protein tyrosine phosphatase type IVA, member 1
EDG7	0.592	GPCR; LPA3; Edg-7; LP-A3; LPAR3; HOFNH30; RP4-678I3	NM_012152	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
STAT1	0.592	ISGF-3; STAT91; DKFZp686B04100	NM_007315	signal transducer and activator of transcription 1, 91kDa
FAM54A	0.592	DUFD1	NM_138419	family with sequence similarity 54, member A
PEMT	0.592	PNMT; PEAMT; PEMPT; PEMT2; MGC2483	NM_148173	phosphatidylethanolamine N-methyltransferase
HSPC196	0.591	HSPC196	NM_016464	transmembrane protein 138
CRYGD	0.591	CACA; CCA3; CRYG4; cry-g-D	NM_006891	crystallin, gamma D
PTRH1	0.591	PTH1; C9orf115; MGC51999	NM_001002913	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)
EBI2	0.59	SGCE	NM_004951	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
RPL13	0.59	BBC1; D16S444E; FLJ27453; FLJ27454; MGC71373; MGC117342	NM_033251	ribosomal protein L13
AIF1	0.59	IBA1; AIF-1; IRT-1	NM_001623	allograft inflammatory factor 1
WDR42A	0.59	H326; FLJ35857; MGC99640; MGC117276; MGC118891; DKFZp781G1096	NM_015726	WD repeat domain 42A
TNKS1BP1	0.59	TAB182; FLJ45975; KIAA1741	NM_033396	tankyrase 1 binding protein 1, 182kDa
MARVELD3	0.589	MARVD3; MRVLDC3; FLJ32280	NM_052858	MARVEL domain containing 3
RFWD3	0.588	RNF201; FLJ10520	NM_018124	ring finger and WD repeat domain 3
TTLL12	0.588	FLJ41795; KIAA0153; dJ526I14.2	NM_015140	tubulin tyrosine ligase-like family, member 12
MLKL	0.588	FLJ34389	NM_152649	mixed lineage kinase domain-like
CTSL	0.588	MEP; CATL; FLJ31037	NM_001912	cathepsin L
ASS	0.588	ASS; CTLN1	NM_054012	argininosuccinate synthetase 1
FRAG1	0.588	FRAG1; PGAP2; MGC799	NM_014489	FGF receptor activating protein 1
TCP1	0.588	CCT1; CCTa; D6S230E; CCT-alpha; TCP-1-alpha	NM_030752	t-complex 1
C6ORF72	0.587	dJ12G14.2	NM_138785	chromosome 6 open reading frame 72
RASAL2	0.587	nGAP; MGC129919	NM_170692	RAS protein activator like 2
IRF1	0.587	MAR; IRF-1	NM_002198	interferon regulatory factor 1
NPAS1	0.586	MOP5; PASD5	NM_002517	neuronal PAS domain protein 1
C20ORF103	0.585	C20orf103	NM_012261	chromosome 20 open reading frame 103
RNF150	0.585	MGC125502	NM_020724	ring finger protein 150
SCRL	0.585	SCRL; MGC33947; PLAL6978; PRO21961	NM_152358	chromosome 19 open reading frame 41
PPAP2C	0.584	LPP2; PAP-2c; PAP2-g	NM_177543	phosphatidic acid phosphatase type 2C
LGP2	0.584	LGP2; D11lgp2e	NM_024119	likely ortholog of mouse D11lgp2
PDCD1LG2	0.584	B7DC; Btdc; PDL2; CD273; PD-L2; PDCD1L2; MGC142238; MGC142240; bA574F11.2	NM_025239	programmed cell death 1 ligand 2
NOMO2	0.584	PM5; Nomo	NM_173614	NODAL modulator 2
FAM8A1	0.584	AHCP; FLJ23721	NM_016255	family with sequence similarity 8, member A1
C19ORF19	0.583	FLJ40059; MGC129962; MGC129963	NM_182577	chromosome 19 open reading frame 19
MARVELD3	0.583	MARVD3; MRVLDC3; FLJ32280	NM_001017967	MARVEL domain containing 3
TNFRSF10D	0.583	DCR2; CD264; TRUNDD; TRAILR4	NM_003840	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
IFI30	0.583	GILT; IP30; IFI-30; MGC32056	NM_006332	interferon, gamma-inducible protein 30
C14ORF94	0.582	FLJ20424	NM_017815	chromosome 14 open reading frame 94
THBD	0.582	TM; THRM; CD141	NM_000361	thrombomodulin
LRP16	0.582	LRP16	NM_014067	LRP16 protein
PPA1	0.581	PP; PP1; IOPPP; MGC111556; SID6-8061	NM_021129	pyrophosphatase (inorganic) 1
AP3M2	0.581	P47B; AP47B; CLA20	NM_006803	adaptor-related protein complex 3, mu 2 subunit
MGC17624	0.581	MGC17624	NM_206967	chromosome 16 open reading frame 74
WDR36	0.581	GLC1G; UTP21; TAWDRP; TA-WDRP; DKFZp686I1650	NM_139281	WD repeat domain 36
ENPP5	0.58	KIAA0879	NM_021572	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)
EYA3	0.58		NM_172098	
C9ORF45	0.58		NM_030814	
LRRFIP2	0.58	HUFI-2; FLJ20248; FLJ22683; DKFZp434H2035	NM_017724	leucine rich repeat (in FLII) interacting protein 2
BACE2	0.579	ASP1; BAE2; DRAP; AEPLC; ALP56; ASP21;	NM_012105	beta-site APP-cleaving enzyme 2

		CDA13; CEAP1		
TAP2	0.578	APT2; PSF2; ABC18; ABCB3; RING11; D6S217E	NM_018833	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
C14ORF93	0.578	FLJ12154	NM_021944	chromosome 14 open reading frame 93
C21ORF63	0.578	B18; SUE21; PRED34	NM_058187	chromosome 21 open reading frame 63
TNFRSF12A	0.577	FN14; CD266; TWEAKR	NM_016639	tumor necrosis factor receptor superfamily, member 12A
ATP6V0E2L	0.577	C7orf32	NM_145230	ATPase, H+ transporting V0 subunit E2-like (rat)
CSPG2	0.577	VERSICAN; DKFZp686K06110	NM_004385	chondroitin sulfate proteoglycan 2 (versican)
CHRNA5	0.577	CHRNA5	NM_000745	cholinergic receptor, nicotinic, alpha 5
EXOSC7	0.576	p8; EAP1; RRP42; Rrp42p; hRrp42p; FLJ26543; KIAA0116	NM_015004	exosome component 7
MULK	0.576	AGK; FLJ10842	NM_018238	multiple substrate lipid kinase
VAV1	0.576	VAV	NM_005428	vav 1 oncogene
APP	0.576	AAA; AD1; PN2; ABPP; APPI; CVAP; ABETA; CTFgamma	NM_000484	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)
RRS1	0.576	KIAA0112	NM_015169	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
MRPL3	0.575	MRL3; RPML3	NM_007208	mitochondrial ribosomal protein L3
DKC1	0.575	DKC; NAP57; NOLA4; XAP101; dyskerin	NM_001363	dyskeratosis congenita 1, dyskerin
LOC112937	0.574		NM_138416	
TTF2	0.573	HuF2	NM_003594	transcription termination factor, RNA polymerase II
TACC2	0.573	AZU-1; ECTACC	NM_006997	transforming, acidic coiled-coil containing protein 2
KCNQ2	0.573	EBN; BFNC; EBN1; ENB1; HNSPC; KV7.2; KCNA11; KVEBN1	NM_172109	potassium voltage-gated channel, KQT-like subfamily, member 2
BCL11A	0.573	EVI9; CTIP1; BCL11A-L; BCL11A-S; FLJ10173; FLJ34997; KIAA1809; BCL11A-XL	NM_022893	B-cell CLL/lymphoma 11A (zinc finger protein)
GCDH	0.573	GCD; ACAD5	NM_013976	glutaryl-Coenzyme A dehydrogenase
KIAA1804	0.573	KIAA1804; MLK4; dJ862P8.3; RP5-862P8.2	NM_032435	mixed lineage kinase 4
FUCA1	0.573	G6PD	NM_000147	fucosidase, alpha-L- 1, tissue
KATNB1	0.571	KAT	NM_005886	katanin p80 (WD repeat containing) subunit B 1
CLIC4	0.571	H1; huH1; p64H1; CLIC4L; FLJ38640; DKFZP566G223	NM_013943	chloride intracellular channel 4
FAT	0.571	ME5; FAT1; CDHF7; hFat1	NM_005245	FAT tumor suppressor homolog 1 (Drosophila)
MRPS35	0.571	MDS023; MRPS28; MRP-S28; HDCMD11P; MGC104278; DKFZp762P093	NM_021821	mitochondrial ribosomal protein S35
HNRPDL	0.571	HNRNP; JKTBP; JKTBP2; laAUF1	NM_031372	heterogeneous nuclear ribonucleoprotein D-like
CLN5	0.571	NCL; FLJ90628	NM_006493	ceroid-lipofuscinosis, neuronal 5
PSD3	0.571	EFA6R; HCA67; DKFZp761K1423	NM_206909	pleckstrin and Sec7 domain containing 3
COQ3	0.571	bA9819.1; UG0215E05	NM_017421	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)
PARP14	0.571	BAL2; KIAA1268	NM_017554	poly (ADP-ribose) polymerase family, member 14
MLLT7	0.571	AFX; AFX1; FOXO4; MGC120490	NM_005938	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7
SDF4	0.571	Cab45; RP5-902P8.6	NM_016547	stromal cell derived factor 4
FLJ10986	0.571	FLJ10986; RP11-242B9.1	NM_018291	hypothetical protein FLJ10986
HADHSC	0.57	HAD; HHF4; HADH1; SCHAD; HADHSC; M/SCHAD; MGC8392	NM_005327	hydroxyacyl-Coenzyme A dehydrogenase
FLJ45909	0.57	FLJ45909; FLJ44131	NM_198445	FLJ45909 protein
BUB3	0.569	BUB3L; hBUB3	NM_004725	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)
MGC3207	0.568	MGC3207	NM_032285	hypothetical protein MGC3207
COQ9	0.568	C16orf49; DKFZP434K046	NM_020312	coenzyme Q9 homolog (S. cerevisiae)
SEMA4B	0.568	SemC; SEMAC; KIAA1745; MGC131831	NM_020210	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B
OXCT2	0.568	FKSG25; SCOT-T; FLJ00030	NM_022120	3-oxoacid CoA transferase 2
MGC3265	0.567	MGC3265	NM_024028	prenylcysteine oxidase 1 like
HIST1H2BE	0.567	H2B.h; H2B/h; H2BFH; H2BFN; dJ221C16.8	NM_003523	histone 1, H2be
NEFH	0.567	NFH	NM_021076	neurofilament, heavy polypeptide 200kDa
EXOSC2	0.566	p7; RRP4; Rrp4p; hRrp4p	NM_014285	exosome component 2
AGPAT5	0.566	LPAAT-e; 1-AGPAT5; LPAAT-epsilon	NM_018361	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)
MRPL12	0.566	5c5-2; L12mt; MRPL7; RPML12; MGC8610; MRPL7/L12; MRP-L31/34	NM_002949	mitochondrial ribosomal protein L12
CDT1	0.566	DUP; RIS2	NM_030928	chromatin licensing and DNA replication factor 1
BLM	0.565	BS; RECQ2; RECQL2; RECQL3; MGC126616; MGC131618; MGC131620	NM_000057	Bloom syndrome
ITPR2	0.565	IP3R2	NM_002223	inositol 1,4,5-triphosphate receptor, type 2
OGDHL	0.565	IARS	NM_018245	oxoglutarate dehydrogenase-like
GAL3ST3	0.565	GAL3ST2; MGC142112; MGC142114	NM_033036	galactose-3-O-sulfotransferase 3
CSDA	0.565	DBPA; CSDA1; ZONAB	NM_003651	cold shock domain protein A
MTHFD2	0.564	NMDMC	NM_006636	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
MRS2L	0.564	HPT; MRS2; MGC78523	NM_020662	MRS2-like, magnesium homeostasis factor (S. cerevisiae)
PRP2	0.564	PRP2	NM_173490	transmembrane protein 171
ZCCHC7	0.564	AIR1; HSPC086; FLJ22611; RP11-397D12.1	NM_032226	zinc finger, CCHC domain containing 7
SUV420H1	0.564	CGI-85; MGC703; MGC21161; MGC118906; MGC118909	NM_016028	suppressor of variegation 4-20 homolog 1 (Drosophila)
GNS	0.564	G6S; MGC21274	NM_002076	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)
MET	0.563	HGFR; RCCP2	NM_000245	met proto-oncogene (hepatocyte growth factor receptor)
WBSCR27	0.563	MGC40131	NM_152559	Williams Beuren syndrome chromosome region 27
MYBBP	0.563	P160; PAP2; FLJ37886	NM_014520	MYB binding protein (P160) 1a

1A				
NARG1	0.561	Ga19; NAT1; NATH; TBDN100	NM_057175	NMDA receptor regulated 1
DEPDC 1B	0.561	XTP1; FLJ11252	NM_018369	DEP domain containing 1B
SERTA D4	0.561	DJ667H12.2	NM_019605	SERTA domain containing 4
LTBP1	0.56	LTBP1	NM_000627	latent transforming growth factor beta binding protein 1
H2BFS	0.559	H2BFS	NM_017445	H2B histone family, member S
CHAF1 B	0.559	CAF1; MPP7; CAF-1; CAF1A; CAF1P60; CAF-IP60; MPHOSPH7	NM_005441	chromatin assembly factor 1, subunit B (p60)
PPM1B	0.559	PP2CB; MGC21657; PP2CBETA; PPC2BETAX; PP2C-beta-X	NM_001033 556	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
ADCK1	0.559	FLJ39600	NM_020421	aarF domain containing kinase 1
RFC5	0.558	RFC36; MGC1155	NM_007370	replication factor C (activator 1) 5, 36.5kDa
MRPL16	0.558	L16mt; FLJ20484; PNAS-111	NM_017840	mitochondrial ribosomal protein L16
UBE1	0.558	A1S9; A1ST; GXP1; A1S9T; UBE1X; MGC4781	NM_153280	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)
PPP1R1 4C	0.558	KEPI; NY-BR-81; CPI17-like	NM_030949	protein phosphatase 1, regulatory (inhibitor) subunit 14C
AKAP12	0.558	AKAP250; DKFZp686M0430; DKFZp686O0331	NM_005100	A kinase (PRKA) anchor protein (gravin) 12
TJP2	0.558	ZO2; X104; ZO-2; MGC26306	NM_201629	tight junction protein 2 (zona occludens 2)
PAQR8	0.558	MPRB; LMPB1; C6orf33; FLJ32521; FLJ46206	NM_133367	progestin and adipoQ receptor family member VIII
TUBB4	0.557	TUBB5; beta-5	NM_006087	tubulin, beta 4
MLF1IP	0.557	CENPU; KLIP1; CENP-U; CENP-50; FLJ23468; CENP-U(50)	NM_024629	MLF1 interacting protein
ARHGE F10	0.556	GEF10; MGC131664; DKFZp686H0726	NM_014629	Rho guanine nucleotide exchange factor (GEF) 10
MCM10	0.556	CNA43; PRO2249; MGC126776	NM_018518	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)
KIAA05 23	0.556	KIAA0523	NM_015253	KIAA0523 protein
AYTL2	0.556	lpcat; LPCAT1; PFAAP3; FLJ12443	NM_024830	acyltransferase like 2
KLRG1	0.556	2F1; MAFA; MAFA-L; MAFA-2F1; MGC13600	NM_005810	killer cell lectin-like receptor subfamily G, member 1
HOOK1	0.556	HK1; MGC10642	NM_015888	hook homolog 1 (Drosophila)
BAIAP2 L2	0.555	FLJ22582	NM_025045	BAI1-associated protein 2-like 2
KIAA19 70	0.555	MSE1; KIAA1970	NM_133451	glutamyl-tRNA synthetase 2 (mitochondrial)(putative)
NDUFV 2	0.555	NDUFV2	NM_021074	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
IMP4	0.555	BXDC4; MGC19606	NM_033416	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
FYN	0.554	SLK; SYN; MGC45350	NM_002037	FYN oncogene related to SRC, FGR, YES
PENK	0.554	MYLK	NM_006211	proenkephalin
FAM86 A	0.554	SB153; MGC19636	NM_201400	family with sequence similarity 86, member A
PRO185 3	0.554	PRO1853	NM_144736	hypothetical protein PRO1853
SNX5	0.553	FLJ10931	NM_152227	sorting nexin 5
CCDC25	0.553	FLJ10853	NM_018246	coiled-coil domain containing 25
LRCH4	0.553	LRN; LRRN1; LRRN4; SAP25; PP14183; FLJ40101; FLJ46315	NM_002319	leucine-rich repeats and calponin homology (CH) domain containing 4
FLJ3254 9	0.552	FLJ32549	NM_152440	hypothetical protein FLJ32549
VAMP1	0.552	SYB1; VAMP-1; DKFZp686H12131	NM_016830	vesicle-associated membrane protein 1 (synaptobrevin 1)
RASD1	0.552	AGS1; DEXRAS1; MGC:26290	NM_016084	RAS, dexamethasone-induced 1
CIRH1A	0.552	NAIC; CIRHIN; TEX292; FLJ14728; KIAA1988	NM_032830	cirrhosis, autosomal recessive 1A (cirhin)
PRMT3	0.551	HRMT1L3	NM_005788	protein arginine methyltransferase 3
CSPG4	0.55	NG2; MCSP; MCSPG; MSK16; MEL-CSPG	NM_001897	chondroitin sulfate proteoglycan 4 (melanoma-associated)
TTK	0.55	ESK; PYT; MPS1L1; FLJ38280	NM_003318	TTK protein kinase
LOC816 91	0.55	LOC81691; DKFZp434J0315	NM_030941	exonuclease NEF-sp
PNPLA2	0.55	ATGL; FP17548; TTS-2.2; DKFZp667M109; 1110001C14Rik	NM_020376	patatin-like phospholipase domain containing 2
HERC4	0.549	KIAA1593; DKFZP564G092	NM_015601	hect domain and RLD 4
IMPDH1	0.549	IMPD; RP10; IMPD1; sWSS2608; DKFZp781N0678	NM_000883	IMP (inosine monophosphate) dehydrogenase 1
CLYBL	0.549	CLB; bA134O15.1	NM_206808	citrate lyase beta like
CBR1	0.548	CBR; hCBR1	NM_001757	carbonyl reductase 1
MICAL2	0.548	KIAA0750; MICAL2PV1; MICAL2PV2; DKFZp686H2469; DKFZp686H03148	NM_014632	microtubule associated monoxygenase, calponin and LIM domain containing 2
Sep-02	0.548	DIFF6; NEDD5; hNedd5; KIAA0158	NM_001008 491	septin 2
TGFBR3	0.548	TGFBR3	NM_003243	transforming growth factor, beta receptor III (betaglycan, 300kDa)
ARG2	0.547	ARG2	NM_001172	arginase, type II
HNRPA 1	0.547	HNRNPA1; MGC102835	NM_002136	heterogeneous nuclear ribonucleoprotein A1
KIAA09 22	0.547	FLJ10592; TMEM131L; DKFZp586H1322	NM_015196	KIAA0922
C6ORF8 5	0.547	FLJ22174; DKFZP434F011	NM_021945	chromosome 6 open reading frame 85
C1ORF1 81	0.547	FLJ20729; FLJ20760; NY-BR-75; MGC131963	NM_017953	chromosome 1 open reading frame 181
CDC42E P2	0.547	CEP2; BORG1	NM_006779	CDC42 effector protein (Rho GTPase binding) 2
EVA1	0.547	EVA; MPZL2	NM_005797	epithelial V-like antigen 1
ANKRD 25	0.546	SIP; MXRA3; FLJ20004; KIAA1518; MGC119707; DKFZp434N161	NM_015493	ankyrin repeat domain 25
RHOU	0.546	ARHU; WRCH1; hG28K; CDC42L1; FLJ10616; DJ646B12.2; fJ646B12.2	NM_021205	ras homolog gene family, member U
CD19	0.545	B4; MGC12802	NM_001770	CD19 molecule
LEPRE1	0.544	P3H1; GROS1; MGC117314	NM_022356	leucine proline-enriched proteoglycan (leprecan) 1
ACACA	0.544		NM_000664	
LRRFIP 2	0.543	HUFI-2; FLJ20248; FLJ22683; DKFZp434H2035	NM_006309	leucine rich repeat (in FLII) interacting protein 2
EHBP1	0.543	NACSIN; KIAA0903	NM_015252	EH domain binding protein 1

CDO1	0.542	CDO1	NM_001801	cysteine dioxygenase, type I
C18ORF56	0.542	FLJ36208	NM_001012716	chromosome 18 open reading frame 56
TCP1	0.542	CCT1; CCTa; D6S230E; CCT-alpha; TCP-1-alpha	NM_030752	t-complex 1
WDHD1	0.542	AND-1	NM_001008396	WD repeat and HMG-box DNA binding protein 1
RAB3B	0.541	RAB3B	NM_002867	RAB3B, member RAS oncogene family
PIK3CD	0.541	p110D	NM_005026	phosphoinositide-3-kinase, catalytic, delta polypeptide
CPT1C	0.541	CATL1; CPTIC; FLJ23809	NM_152359	carnitine palmitoyltransferase 1C
SEMA3A	0.54	SemD; SEMA1; SEMAD; SEMAL; coll-1; Hsema-I; SEMAIII; sema III; Hsema-III	NM_006080	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
ZNF323	0.539	ZNF310P; FLJ23407; ZNF20-Lp; dJ874C20.2	NM_030899	zinc finger protein 323
ICA1	0.538		NM_022308	
USP28	0.538	KIAA1515	NM_020886	ubiquitin specific peptidase 28
EREG	0.537	ER	NM_001432	epiregulin
HEATR1	0.537	BAP28; FLJ10359; MGC72083; RP11-385F5.3	NM_018072	HEAT repeat containing 1
MRPS12	0.537	RPS12; RPMS12; RPSM12; MPR-S12; MT-RPS12	NM_033363	mitochondrial ribosomal protein S12
RFC3	0.537	RFC38; MGC5276	NM_002915	replication factor C (activator 1) 3, 38kDa
IL27RA	0.536	CRL1; TCCR; WSX1; IL27R; zcytor1	NM_004843	interleukin 27 receptor, alpha
C20ORF27	0.536		NM_017874	
SAC3D1	0.536	SHD1; HSU79266	NM_013299	SAC3 domain containing 1
TFPI	0.536	EPI; TFI; LACI	NM_001032281	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
PELI2	0.535	PELI2	NM_021255	pellino homolog 2 (Drosophila)
KRTCAP3	0.535	KCP3; MRV222; PRO9898; MGC126736; MGC126738	NM_173853	keratinocyte associated protein 3
CACNG6	0.535	CACNG7	NM_031897	calcium channel, voltage-dependent, gamma subunit 6
FAM111A	0.534	FLJ22794; KIAA1895; DKFZp686A06175	NM_022074	family with sequence similarity 111, member A
STOX2	0.534	DKFZp762K222	NM_020225	storkhead box 2
STOM	0.534	BND7; EPB7; EPB72	NM_004099	stomatin
PHF19	0.534	PCL3; MGC23929; MGC131698	NM_015651	PHD finger protein 19
SLC43A1	0.534	LAT3; PB39; POV1; R00504	NM_003627	solute carrier family 43, member 1
RNASET2	0.533	RNASE6PL; bA514O12.3; RP11-514O12.3	NM_003730	ribonuclease T2
TRIM8	0.533	GERP; RNF27	NM_030912	tripartite motif-containing 8
SEC24D	0.532	FLJ43974; KIAA0755	NM_014822	SEC24 related gene family, member D (S. cerevisiae)
SERBP1	0.532	CGI-55; CHD3IP; HABP4L; PAIRBP1; FLJ90489; PAI-RBP1; DKFZp564M2423	NM_001018068	SERPINE1 mRNA binding protein 1
GEMIN6	0.532	FLJ23459	NM_024775	gem (nuclear organelle) associated protein 6
MAN1C1	0.532	HMIC; MAN1C; MAN1A3; pp6318	NM_020379	mannosidase, alpha, class 1C, member 1
ST7	0.532	HELG; RAY1; SEN4; TSG7; ETS7q; FAM4A1; DKFZp762O2113	NM_018412	suppression of tumorigenicity 7
TSPAN9	0.531	NET-5; PP1057	NM_006675	tetraspanin 9
ZSCAN2	0.531	ZFP29; FLJ20595	NM_181877	zinc finger and SCAN domain containing 2
LARP6	0.531	FLJ11196	NM_197958	La ribonucleoprotein domain family, member 6
C19ORF4	0.531	BSMAP	NM_012109	chromosome 19 open reading frame 4
SHC1	0.529	SHC; p66; SHCA; p52SHC; p66SHC; FLJ26504	NM_003029	SHC (Src homology 2 domain containing) transforming protein 1
RPP40	0.529	RNASEP1; bA428J1.3	NM_006638	ribonuclease P 40kDa subunit
IMPA2	0.529	CDK6	NM_014214	inositol(myo)-1(or 4)-monophosphatase 2
ZSCAN2	0.528	ZFP29; FLJ20595	NM_001007072	zinc finger and SCAN domain containing 2
SLC16A9	0.527	MCT9; C10orf36; FLJ43803	NM_194298	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)
LHPP	0.526	LHPP; MGC117251; MGC142189; MGC142191	NM_022126	phospholysine phosphohistidine inorganic pyrophosphate phosphatase
C20ORF160	0.526	FLJ43600; dJ310O13.5	NM_080625	chromosome 20 open reading frame 160
CABLES1	0.526	HsT2563; FLJ35924	NM_138375	Cdk5 and Abl enzyme substrate 1
PYCARD	0.526	ASC; TMS1; CARD5; MGC10332	NM_145183	PYD and CARD domain containing
CD82	0.526	R2; 4F9; C33; IA4; ST6; GR15; KAI1; SAR2; TSPAN27	NM_002231	CD82 molecule
TCEA1	0.526	SII; TCEA; TF2S; GTF2S; TFIIS	NM_006756	transcription elongation factor A (SII), 1
PPP3CA	0.526	CALN; CCN1; CNA1; CALNA; PPP2B; CALNA1	NM_000944	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)
FLJ20674	0.525	FLJ20674	NM_019086	hypothetical protein FLJ20674
FZD9	0.524	FZD3	NM_003508	frizzled homolog 9 (Drosophila)
TCF4	0.524	E2-2; ITF2; SEF2; SEF2-1; SEF2-1A; SEF2-1B	NM_003199	transcription factor 4
ERCC5	0.524	XPG; UVDR; XPGC; ERCM2	NM_000123	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
CHPT1	0.524	CPT; CPT1	NM_020244	choline phosphotransferase 1
PSME3	0.524	Ki; PA28G; REG-GAMMA; PA28-gamma	NM_005789	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
NAT5	0.524	ARD1; NAT3; dJ1002M8.1	NM_181528	N-acetyltransferase 5
PAK1IP1	0.523	PIP1; MAK11; WDR84; hPIP1; FLJ20624; bA421M1.5; RP11-421M1.5	NM_017906	PAK1 interacting protein 1
TMEM108	0.523	MGC3040	NM_023943	transmembrane protein 108
ANAPC1	0.523	APC1; MCPR; TSG24	NM_022662	anaphase promoting complex subunit 1
SAR1B	0.523	CMRD; GTBPB; SARA2	NM_016103	SAR1 gene homolog B (S. cerevisiae)
ASMTL	0.521	ASTML; ASMTLX; ASMTLY	NM_004192	acetylserotonin O-methyltransferase-like
TUFM	0.521	EFTU; EF-TuMT	NM_003321	Tu translation elongation factor, mitochondrial

AZIN1	0.52	OAZI; OAZIN; ODC1L; MGC691; MGC3832	NM_015878	antizyme inhibitor 1
PKIA	0.52	PRKACN1	NM_006823	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
MAN2A1	0.52	MANA2; MANII	NM_002372	mannosidase, alpha, class 2A, member 1
CHAC2	0.519	LMBRD2	NM_001008708	ChaC, cation transport regulator-like 2 (E. coli)
ETV6	0.518	TEL	NM_001987	ets variant gene 6 (TEL oncogene)
MGC33926	0.518	MGC33926	NM_152390	hypothetical protein MGC33926
ACP5	0.516	TRAP; MGC117378	NM_001611	acid phosphatase 5, tartrate resistant
LFNG	0.516		NM_002304	
IL10RB	0.516	CRFB4; CRF2-4; D21S58; D21S66; CDW210B; IL-10R2	NM_000628	interleukin 10 receptor, beta
HLA-DMA	0.515	DMA; HLADM; RING6; D6S222E	NM_006120	major histocompatibility complex, class II, DM alpha
ZNF589	0.515	SZF1	NM_016089	zinc finger protein 589
SMTN	0.515	FLJ35365; FLJ38597	NM_006932	smoothelin
DET1	0.515	FLJ10103; MGC126156; MGC126157	NM_017996	de-etiolated homolog 1 (Arabidopsis)
PHLDB1	0.515	LL5A; FLJ00141; FLJ90266; KIAA0638; MGC111531; DKFZp686H039; DKFZp686O24210	NM_015157	pleckstrin homology-like domain, family B, member 1
TRIP13	0.515	16E1BP	NM_004237	thyroid hormone receptor interactor 13
QTRT1	0.514	TGT; FP3235	NM_031209	queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase)
CDC14B	0.514	CDC14B3; Cdc14B1; Cdc14B2; hCDC14B	NM_003671	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
ELOVL4	0.514	ADMD; STGD2; STGD3	NM_022726	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
RPL41	0.513	RPL41	NM_021104	ribosomal protein L41
MPP4	0.513	DLG6; ALS2CR5	NM_033066	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
TIMP2	0.512	CSC-21K	NM_003255	TIMP metallopeptidase inhibitor 2
AKR1A1	0.511	ALR; ALDR1; MGC1380; MGC12529	NM_006066	aldo-keto reductase family 1, member A1 (aldehyde reductase)
MPHOSPH1	0.511	MPP1; KRMP1; MPP-1; DKFZp434B0435; DKFZp434P0810	NM_016195	M-phase phosphoprotein 1
HOXC6	0.51	CP25; HOX3; HOX3C; HHO.C8	NM_153693	homeobox C6
RBPSUH	0.51	csl; CBF1; KBF2; RBP-J; RBPJK; IGKJRB; IGKJRB1; MGC61669	NM_203284	recombining binding protein suppressor of hairless (Drosophila)
SLC19A3	0.51	SLC19A3	NM_025243	solute carrier family 19, member 3
RBPSUH	0.51	csl; CBF1; KBF2; RBP-J; RBPJK; IGKJRB; IGKJRB1; MGC61669	NM_203284	recombining binding protein suppressor of hairless (Drosophila)
MGC2408	0.51	MGC2408	NM_032331	hypothetical protein MGC2408
GMNN	0.509	Gem; RP3-369A17.3	NM_015895	geminin, DNA replication inhibitor
TXNDC	0.508	TMX; TXNDC1; DKFZP564E1962	NM_030755	thioredoxin domain containing
PSRC1	0.508	DDA3; FP3214; MGC1780; RP11-297O4.2	NM_001005290	proline/serine-rich coiled-coil 1
CMTM7	0.507	CKLFSF7; FLJ30992	NM_138410	CKLF-like MARVEL transmembrane domain containing 7
UNG	0.507	DGU; UDG; UNG1; HIGM4; UNG15; DKFZp781L1143	NM_080911	uracil-DNA glycosylase
KIF2C	0.507	MCAK; KNSL6	NM_006845	kinesin family member 2C
KIAA0528	0.506	DKFZp779N2044	NM_014802	KIAA0528
RSU1	0.506	RSP-1; FLJ31034	NM_152724	Ras suppressor protein 1
SKP2	0.505	FBL1; FLB1; FBXL1; MGC1366	NM_032637	S-phase kinase-associated protein 2 (p45)
IVD	0.505	ACAD2	NM_002225	isovaleryl Coenzyme A dehydrogenase
FAM113B	0.505	MGC16044	NM_138371	family with sequence similarity 113, member B
METRNL	0.505	MGC99788	NM_001004431	meteorin, glial cell differentiation regulator-like
PLA2G4C	0.505	CPLA2-gamma; DKFZp586C0423	NM_003706	phospholipase A2, group IVC (cytosolic, calcium-independent)
CENTB1	0.505	ACAP1; KIAA0050	NM_014716	centaurin, beta 1
RBPMS	0.504	HERMES	NM_001008712	RNA binding protein with multiple splicing
NDE1	0.504	NUDE; NUDE1; FLJ20101; HOM-TES-87	NM_017668	nudE nuclear distribution gene E homolog 1 (A. nidulans)
LIAS	0.503	LAS; LIP1; HUSSY-01; MGC23245	NM_006859	lipoic acid synthetase
PRIM1	0.503	p49; MGC12308	NM_000946	primase, polypeptide 1, 49kDa
RPL29	0.502	HIP; HUMRPL29; MGC88589	NM_000992	ribosomal protein L29
KPNA2	0.502	QIP2; RCH1; IPOA1; SRP1alpha	NM_002266	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
SCG2	0.502	SN; CHGC; SgII	NM_003469	secretogranin II (chromogranin C)
DCC1	0.502	DCC1; MGC5528	NM_024094	defective in sister chromatid cohesion homolog 1 (S. cerevisiae)
GOLPH2	0.502	GP73; PSEC0257	NM_016548	golgi phosphoprotein 2
RPUSD3	0.502	FLJ34707; MGC29784	NM_173659	RNA pseudouridylate synthase domain containing 3
TFB2M	0.501	Hkp1; FLJ22661; FLJ23182	NM_022366	transcription factor B2, mitochondrial
CENPH	0.501	C12orf52	NM_022909	centromere protein H
EIF2S2	0.5	EIF2; EIF2B; MGC8508; EIF2beta; DKFZp686L18198	NM_003908	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
SLCO4A1	0.5	POAT; OATP1; OATP-E; OATP4A1; OATPRP1; SLC21A12	NM_016354	solute carrier organic anion transporter family, member 4A1
RHOQ	0.5	ARHQ; TC10; TC10A; RASL7A	NM_012249	ras homolog gene family, member Q
CD55	0.499	CR; TC; DAF	NM_000574	CD55 molecule, decay accelerating factor for complement (Cromer blood group)
PDE4B	0.499	DPDE4; PDEIVB; MGC126529; DKFZp686F2182	NM_002600	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
COPS7A	0.499	MGC110877	NM_016319	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)
TYSND1	0.498	MGC34695; MGC131934	NM_173555	trypsin domain containing 1
C20ORF72	0.498	FLJ14597; bA504H3.4	NM_052865	chromosome 20 open reading frame 72
LYPLA1	0.498	LPL1; APT-1; LYSOPLA	NM_006330	lysophospholipase I
CD24	0.498	CD24A	NM_013230	CD24 molecule

TMEM30B	0.498	CDC50B; MGC126775	NM_001017970	transmembrane protein 30B
LAP3	0.498	LAP; PEPS; LAPEP	NM_015907	leucine aminopeptidase 3
PHYH2	0.498	HPCL; HPCL2; PHYH2; 2-HPCL	NM_012260	2-hydroxyacyl-CoA lyase 1
PAPSS2	0.497	SK2; ATPSK2	NM_001015880	3'-phosphoadenosine 5'-phosphosulfate synthase 2
CUL1	0.497	CDK6	NM_003592	cullin 1
PHF17	0.497	JADE1; FLJ22479; KIAA1807	NM_024900	PHD finger protein 17
KCNG3	0.496	KV6.3; KV10.1	NM_172344	potassium voltage-gated channel, subfamily G, member 3
SNCA	0.496	PD1; NACP; PARK1; PARK4; MGC110988	NM_007308	synuclein, alpha (non A4 component of amyloid precursor)
KLHL3	0.496	KIAA1129; MGC44594	NM_017415	kelch-like 3 (Drosophila)
AKNA	0.496	KIAA1968; RP11-82I1.4	NM_030767	AT-hook transcription factor
SRI	0.496	SCN; FLJ26259	NM_003130	sorcin
PACSIN1	0.494	SDPI; KIAA1379	NM_020804	protein kinase C and casein kinase substrate in neurons 1
NFKB1	0.494	KBF1; EBP-1; MGC54151; NFKB-p50; NFKB-p105; NF-kappa-B; DKFZp686C01211	NM_003998	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
GMDS	0.493	GMD	NM_001500	GDP-mannose 4,6-dehydratase
LOC57149	0.492	A211C6.1	NM_020424	LYR motif containing 1
CBLC	0.492	CBL-3; RNF57; CBL-SL	NM_012116	Cas-Br-M (murine) ecotropic retroviral transforming sequence c
LTBP3	0.492	LTBP2; LTBP-3; pp6425; FLJ33431; FLJ39893; DKFZP586M2123	NM_021070	latent transforming growth factor beta binding protein 3
PIAS2	0.492	miz; MIZ1; SIZ2; MGC102682; PIASX-BETA; PIASX-ALPHA	NM_173206	protein inhibitor of activated STAT, 2
LEPREL2	0.49	GRCB; P3H3; HSU47926	NM_014262	leprecan-like 2
SPRYD3	0.49	FLJ14800	NM_032840	SPRY domain containing 3
RASIP1	0.49	RAIN; FLJ20401	NM_017805	Ras interacting protein 1
MTHFD1	0.49	MTHFC; MTHFD	NM_005956	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
LOC139886	0.49	LOC139886; MGC133224	NM_001012968	hypothetical protein LOC139886
C9ORF10	0.489	C9orf10; DNAPTP1; DNAPTP5; MGC111527; MGC133257	NM_014612	family with sequence similarity 120A
HSPA4L	0.489	APG-1; Osp94	NM_014278	heat shock 70kDa protein 4-like
ALG3	0.489		NM_001006940	
ALDH9A1	0.488	E3; ALDH4; ALDH7; ALDH9; TMABADH	NM_000696	aldehyde dehydrogenase 9 family, member A1
RGMB	0.488	DRAGON; FLJ90406; MGC86970	NM_001012761	RGM domain family, member B
CYTL1	0.488	C17	NM_018659	cytokine-like 1
EPDR1	0.487	UCC1; MERP1; MERP-1	NM_017549	ependymin related protein 1 (zebrafish)
MCM7	0.487	MCM2; CDC47; P85MCM; P1CDC47; PNAS-146; CDABP0042; P1.1-MCM3	NM_182776	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)
FLJ25416	0.487	FLJ25416; FLJ13936	NM_145018	hypothetical protein FLJ25416
TM7SF3	0.486	TM7SF3	NM_016551	transmembrane 7 superfamily member 3
STXBP6	0.486	amisyn; HSPC156; FLJ39638	NM_014178	syntaxin binding protein 6 (amisyn)
MGC45840	0.485	MGC45840; MGC88858	NM_173584	EF-hand calcium binding domain 4A
HSPC111	0.485	HSPC111; HSPC185	NM_016391	hypothetical protein HSPC111
UST	0.485	2OST	NM_005715	uronyl-2-sulfotransferase
EBNA1BP2	0.484	P40; EBP2; NOBP	NM_006824	EBNA1 binding protein 2
WDR12	0.484	YTM1; FLJ10881; FLJ12719; FLJ12720	NM_018256	WD repeat domain 12
PCDH18	0.483	PCDH68L; KIAA1562; DKFZP434B0923	NM_019035	protocadherin 18
NCLN	0.483	SCARB1	NM_020170	nicalin homolog (zebrafish)
EDNRB	0.483	ETB; ETRB; HSCR; ABCDS; HSCR2	NM_003991	endothelin receptor type B
VKORC1	0.482	VKOR; MST134; MST576; VKCFD2; EDTP308; MGC2694; FLJ00289; IMAGE3455200	NM_024006	vitamin K epoxide reductase complex, subunit 1
MGST1	0.482	MGST; GST12; MGST-I; MGC14525	NM_020300	microsomal glutathione S-transferase 1
C1GALT1C1	0.481	COSMC; C1GALT2; HSPC067; C1Gal-T2; MGC19947; c38h2-l1	NM_001011551	C1GALT1-specific chaperone 1
SSPN	0.481	KRAG; SPN1; SPN2	NM_005086	sarcospan (Kras oncogene-associated gene)
SDHA	0.481	FP; SDH2; SDHF	NM_004168	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
SERPINB8	0.481	PI8; CAP2	NM_001031848	serpin peptidase inhibitor, clade B (ovalbumin), member 8
NLN	0.48	AGTBP; KIAA1226; DKFZp564F123	NM_020726	neurolysin (metallopeptidase M3 family)
SORBS1	0.479	CAP; FLAF2; R85FL; SH3D5; SORB1; SH3P12; FLJ12406; KIAA1296; DKFZp451C066; DKFZp586P1422	NM_015385	sorbin and SH3 domain containing 1
ARHGEF6	0.479	PIXA; COOL2; MRX46; Cool-2; KIAA0006; alphaPIX; alpha-PIX	NM_004840	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
CHAF1A	0.477	CAF1; P150; CAF-1; CAF1B; CAF1P150; MGC71229	NM_005483	chromatin assembly factor 1, subunit A (p150)
EIF4E3	0.476	MGC39820; MGC86971	NM_173359	eukaryotic translation initiation factor 4E member 3
HMMR	0.476	CD168; IHABP; RHAMM; MGC119494; MGC119495	NM_012485	hyaluronan-mediated motility receptor (RHAMM)
KIAA1914	0.476	XB130; FLJ14564	NM_001001936	KIAA1914
EXOSC5	0.476	p12B; RRP46; RRP41B; Rrp46p; hRrp46p; MGC12901; MGC111224	NM_020158	exosome component 5
UGT3A2	0.476	MGC119426; MGC119429	NM_174914	UDP glycosyltransferase 3 family, polypeptide A2
CDR2	0.475	Yo; CDR62	NM_001802	cerebellar degeneration-related protein 2, 62kDa
DYNLT3	0.475	RP3; TCTE1L; TCTEX1L	NM_006520	dynein, light chain, Tctex-type 3
AP1S1	0.474	AP19; CLAPS1; SIGMA1A	NM_057089	adaptor-related protein complex 1, sigma 1 subunit
MGST1	0.474	MGST; GST12; MGST-I; MGC14525	NM_020300	microsomal glutathione S-transferase 1
TNNC2	0.473	TNNC2	NM_003279	troponin C type 2 (fast)
BID	0.473	MGC15319; MGC42355	NM_001196	BH3 interacting domain death agonist
THYN1	0.473	MY105; THY28; MDS012; HSPC144;	NM_199298	thymocyte nuclear protein 1

		THY28KD; MGC12187		
TPST2	0.473	TPST2	NM_001008566	tyrosylprotein sulfotransferase 2
PBK	0.471	SPK; TOPK; Nori-3; FLJ14385	NM_018492	PDZ binding kinase
GAJ	0.47	GAJ	NM_032117	meiotic nuclear divisions 1 homolog (S. cerevisiae)
GRAMD3	0.47	NS3TP2; FLJ21313	NM_023927	GRAM domain containing 3
IRS1	0.47	HIRS-1	NM_005544	insulin receptor substrate 1
RASL11B	0.47	MGC2827; MGC4499	NM_023940	RAS-like, family 11, member B
TYK2	0.469	JTK1	NM_003331	tyrosine kinase 2
HEXB	0.469	ENC-1AS	NM_000521	hexosaminidase B (beta polypeptide)
SRPK1	0.469	SFRSK1	NM_003137	SFRS protein kinase 1
TEAD4	0.468	RTEF1; TEF-3; EFTR-2; RTEF-1; TEFR-1; MGC9014; TCF13L1; hRTEF-1B	NM_201441	TEA domain family member 4
HSD17B8	0.468	KE6; FABG; HKE6; FABGL; RING2; H2-KE6; D6S2245E; dJ1033B10.9	NM_014234	hydroxysteroid (17-beta) dehydrogenase 8
SLC6A15	0.467	V7-3; NTT73; hv7-3; FLJ10316; MGC87066; DKFZp761I0921	NM_182767	solute carrier family 6, member 15
GMPS	0.467	CFB	NM_003875	guanine monphosphate synthetase
ZNF483	0.466	ZNF483	NM_001007169	zinc finger protein 483
PSAT1	0.465	PSA; MGC1460	NM_021154	phosphoserine aminotransferase 1
ST7	0.465	HELG; RAY1; SEN4; TSG7; ETS7q; FAM4A1; DKFZp762O2113	NM_018412	suppression of tumorigenicity 7
BXDC1	0.465	RPF2; FLJ21087; bA397G5.4	NM_032194	brix domain containing 1
ALDH4A1	0.465	P5CD; ALDH4; P5CDh; P5CDhL; P5CDhS	NM_170726	aldehyde dehydrogenase 4 family, member A1
MCM7	0.464	MCM2; CDC47; P85MCM; P1CDC47; PNAS-146; CDABP0042; P1.1-MCM3	NM_005916	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)
FRAT2	0.464	MGC10562	NM_012083	frequently rearranged in advanced T-cell lymphomas 2
INPP5D	0.464	SHIP; SHIP1; hp51CN; SIP-145; MGC104855; MGC142140; MGC142142	NM_001017915	inositol polyphosphate-5-phosphatase, 145kDa
ACYP1	0.464	ACYPE	NM_203488	acylphosphatase 1, erythrocyte (common) type
KATNAL2	0.462	MGC33211; DKFZP667C165	NM_031303	katanin p60 subunit A-like 2
PARP9	0.462	BAL; BAL1; FLJ26637; MGC:7868; DKFZp666B0810; DKFZp686M15238	NM_031458	poly (ADP-ribose) polymerase family, member 9
XPC	0.461	XP3; XPCC	NM_004628	xeroderma pigmentosum, complementation group C
CXORF12	0.461	ITBA1; DXS9878E	NM_003492	chromosome X open reading frame 12
MCCC2	0.461	MCCB	NM_022132	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
DKK3	0.461	REIC	NM_013253	dickkopf homolog 3 (Xenopus laevis)
STRBP	0.46	SPNR; MGC3405; FLJ11307; FLJ14223; FLJ14984; MGC21529; DKFZp434N214	NM_018387	spermatid perinuclear RNA binding protein
LMO4	0.46	LMO4	NM_006769	LIM domain only 4
MFSD1	0.459	FLJ14153; UG0581B09	NM_022736	major facilitator superfamily domain containing 1
NME1	0.457	AWD; GAAD; NM23; NDPKA; NM23-H1	NM_198175	non-metastatic cells 1, protein (NM23A) expressed in
ABLIM1	0.457	ABLIM; LIMAB1; LIMATIN; MGC1224; FLJ14564; KIAA0059; DKFZp781D0148	NM_006720	actin binding LIM protein 1
PHB	0.457	PHB	NM_002634	prohibitin
POLE2	0.456	DPE2	NM_002692	polymerase (DNA directed), epsilon 2 (p59 subunit)
SATB2	0.456	FLJ21474; FLJ32076; KIAA1034; MGC119474; MGC119477	NM_015265	SATB family member 2
EPB41L4B	0.455	CG1; EHM2; FLJ21596; DKFZp761N1814	NM_018424	erythrocyte membrane protein band 4.1 like 4B
PARP1	0.454	PARP; PPOL; ADPRT; ADPRT1; PARP-1; pADPRT-1	NM_001618	poly (ADP-ribose) polymerase family, member 1
TRAF3IP2	0.453	ACT1; CIKS; C6orf4; C6orf5; C6orf6; MGC3581; DKFZP586G0522	NM_147200	TRAF3 interacting protein 2
DAZAP1	0.452	MGC19907	NM_018959	DAZ associated protein 1
TMEM5	0.452	HP10481	NM_014254	transmembrane protein 5
CD74	0.452	DHLAG; HLADG; Ia-GAMMA; protein 41	NM_001025158	CD74 molecule, major histocompatibility complex, class II invariant chain
CSRP2	0.451	CRP2; LMO5; SmLIM	NM_001321	cysteine and glycine-rich protein 2
GPR160	0.449	GPCR1; GPCR150	NM_014373	G protein-coupled receptor 160
TRAP1	0.449	HSP75; HSP90L	NM_016292	TNF receptor-associated protein 1
NPFFR2	0.447	GPR74; NPFF2; NPGPR	NM_053036	neuropeptide FF receptor 2
ACAT1	0.447	T2; MAT; ACAT; THIL	NM_000019	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)
TXNDC12	0.446	ERP18; ERP19; TLP19	NM_015913	thioredoxin domain containing 12 (endoplasmic reticulum)
NOL6	0.446	NRAP; UTP22; FLJ21959; MGC14896; MGC14921; MGC20838; bA311H10.1	NM_022917	nucleolar protein family 6 (RNA-associated)
VRK1	0.446	MGC117401; MGC138280; MGC142070	NM_003384	vaccinia related kinase 1
REEP5	0.446	DP1; TB2; D5S346; C5orf18; MGC70440	NM_005669	receptor accessory protein 5
WDSOF1	0.446	Gm83; HSPC064; MGC126859; MGC138247; DKFZP564O0463	NM_015420	WD repeats and SOF1 domain containing
SYT1	0.445	P65; SYT; SVP65; DKFZp781D2042	NM_005639	synaptotagmin I
NOX4	0.442	KOX; KOX-1; RENOX	NM_016931	NADPH oxidase 4
PHGDH	0.44	PDG; PGD; PGAD; PGDH; SERA; 3PGDH; 3-PGDH; MGC3017	NM_006623	phosphoglycerate dehydrogenase
STAT1	0.44	ISGF-3; STAT91; DKFZp686B04100	NM_139266	signal transducer and activator of transcription 1, 91kDa
PYGL	0.438	RB1	NM_002863	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)
SLC7A1	0.436	ERR; ATRC1; CAT-1; HCAT1; REC1L	NM_003045	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
F12	0.435	HAF	NM_000505	coagulation factor XII (Hageman factor)
LYAR	0.434	LYAR; FLJ20425	NM_017816	hypothetical protein FLJ20425
CEBPD	0.433	CELF; CRP3; C/EBP-delta; NF-IL6-beta	NM_005195	CCAAT/enhancer binding protein (C/EBP), delta
CHGA	0.432	CGA	NM_001275	chromogranin A (parathyroid secretory protein 1)
PTN	0.432	HARP; HBNF; HBGF8; NEGF1	NM_002825	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)
TIMM8A	0.431	DDP; MTS; DDP1; DFN1; MGC12262	NM_004085	translocase of inner mitochondrial membrane 8 homolog A (yeast)

SF3A3	0.431	PRP9; PRPF9; SAP61; SF3a60	NM_006802	splicing factor 3a, subunit 3, 60kDa
EFNB2	0.431	HTKL; EPLG5; Htk-L; LERK5; MGC126226; MGC126227; MGC126228	NM_004093	ephrin-B2
HHLA2	0.431	CERK	NM_007072	HERV-H LTR-associating 2
NES	0.43	FLJ21841; Nbla00170	NM_006617	nestin
ITGA2B	0.43	GTA; CD41; GP2B; HPA3; CD41B; GPIIb	NM_000419	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)
C18ORF26	0.43	FLJ39106	NM_173629	chromosome 18 open reading frame 26
LAD1	0.43	LadA; MGC10355	NM_005558	ladinin 1
DPYSL2	0.43	DRP2; CRMP2; DRP-2; DHPRP2	NM_001386	dihydropyrimidinase-like 2
WIPI1	0.428	Atg18; WIPI49; FLJ10055	NM_017983	WD repeat domain, phosphoinositide interacting 1
OLFM1	0.427	AMY; NOE1; OlfA; NOELIN; NOELIN1; NOELIN1_V1; NOELIN1_V2; NOELIN1_V4; NOELIN1_V5	NM_014279	olfactomedin 1
CORO2B	0.426	CLIPINC; KIAA0925	NM_006091	coronin, actin binding protein, 2B
FBXO22	0.426	FBX22; FLJ13986	NM_012170	F-box protein 22
MCM5	0.426	CDC46; MGC5315; P1-CDC46	NM_006739	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)
ISOC2	0.425	TMEM101	NM_024710	isochorismatase domain containing 2
NAP1L3	0.425	MB20; NPL3; MGC26312	NM_004538	nucleosome assembly protein 1-like 3
SEMA4D	0.425	CD100; SEMAJ; coll-4; M-sema G; M-sema-G	NM_006378	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D
BUB1B	0.424	SSK1; BUBR1; Bub1A; MAD3L; hBUBR1; BUB1beta	NM_001211	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
HSD11B1	0.424	HDL; 11-DH; HSD11; HSD11B; HSD11L; MGC13539; 11-beta-HSD1	NM_181755	hydroxysteroid (11-beta) dehydrogenase 1
AP1S1	0.424	AP19; CLAPS1; SIGMA1A	NM_001283	adaptor-related protein complex 1, sigma 1 subunit
C12ORF24	0.424	HSU79274	NM_013300	chromosome 12 open reading frame 24
RPS7	0.423	RPS7	NM_001011	ribosomal protein S7
FLJ31204	0.423	FLJ31204; RP11-479E16.1	NM_174912	amidase domain containing
RAI14	0.422	RAI13; NORPEG; KIAA1334; DKFZp564G013	NM_015577	retinoic acid induced 14
F2RL1	0.422	PAR2; GPR11	NM_005242	coagulation factor II (thrombin) receptor-like 1
VAMP4	0.422	VAMP24	NM_003762	vesicle-associated membrane protein 4
SLC24A6	0.421	NCLX; NCKX6; FLJ22233	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6
ATP5G1	0.421	ATP5A; ATP5G	NM_001002027	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)
PANX1	0.421	MRS1; UNQ2529; MGC21309	NM_015368	pannexin 1
EXTL3	0.419	REG; RPR; REGR; botv; EXTR1; KIAA0519; DKFZp686C2342	NM_001440	exostoses (multiple)-like 3
MRPL24	0.419	MGC9831; MRP-L18; FLJ20917; MGC22737	NM_024540	mitochondrial ribosomal protein L24
ASPH	0.419	BAH; HAAH; JCTN; junctin; CASQ2BP1	NM_020164	aspartate beta-hydroxylase
ACO1	0.419	IRP1; IREB1; IREBP	NM_002197	aconitase 1, soluble
RIN2	0.419	RASSF4	NM_018993	Ras and Rab interactor 2
HBA1	0.419	CD31; MGC126895; MGC126897	NM_000558	hemoglobin, alpha 1
DBC1	0.419	FAM5A; DBCCR1	NM_014618	deleted in bladder cancer 1
ZNF206	0.418	ZSCAN10; FLJ14549	NM_032805	zinc finger protein 206
LYN	0.418	JTK8; FLJ26625	NM_002350	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
ARIH2	0.417	ARI2; TRIAD1; FLJ10938; FLJ33921	NM_006321	ariadne homolog 2 (Drosophila)
ASCC3	0.416	RNAH; HELIC1; ASC1p200; MGC26074; DJ467N11.1; dJ121G13.4	NM_006828	activating signal cointegrator 1 complex subunit 3
MICB	0.416	PERB11.2	NM_005931	MHC class I polypeptide-related sequence B
GLTP	0.415	GLTP	NM_016433	glycolipid transfer protein
ASPHD1	0.414	ASPHD1	NM_181718	aspartate beta-hydroxylase domain containing 1
GART	0.414	AIRS; GARS; PAIS; PGFT; PRGS; GARTF; MGC47764	NM_000819	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
DNAJB6	0.413	MRJ; HSJ2; HHDJ1; HSJ-2; MSJ-1; MGC1152; FLJ42837; MGC117297; DKFZp566D0824	NM_005494	DnaJ (Hsp40) homolog, subfamily B, member 6
RAB7L1	0.413	RAB7L; DKFZp686P1051	NM_003929	RAB7, member RAS oncogene family-like 1
SMS	0.412	SRS; SpS; MRSR; SPMSY	NM_004595	spermine synthase
NQO1	0.412	DTD; QR1; DHQU; DIA4; NMOR1; NMORI	NM_000903	NAD(P)H dehydrogenase, quinone 1
LOXL3	0.412	LOXL	NM_032603	lysyl oxidase-like 3
ISG20L1	0.412	AEN; pp12744; FLJ12484; FLJ12562	NM_022767	interferon stimulated exonuclease gene 20kDa-like 1
HK1	0.412	HKI; HXK1; HK1-ta; HK1-tb	NM_033500	hexokinase 1
LCK	0.411	YT16; p56lck; pp58lck	NM_005356	lymphocyte-specific protein tyrosine kinase
BCAS4	0.41	FLJ20495	NM_017843	breast carcinoma amplified sequence 4
CMTM8	0.41	CKLFSF8	NM_178868	CKLF-like MARVEL transmembrane domain containing 8
RARRES2	0.41	TIG2; HP10433	NM_002889	retinoic acid receptor responder (tazarotene induced) 2
FLJ90231	0.41		NM_173581	
MGC26856	0.409	PRO7434; ALKN2972; MGC26856	NM_152779	GLI pathogenesis-related 1 like 1
MGC4172	0.409	MGC4172; ARPG836; FLJ39232	NM_024308	short-chain dehydrogenase/reductase
CYP2S1	0.408	CYP2S1	NM_030622	cytochrome P450, family 2, subfamily S, polypeptide 1
FKBP11	0.406	FKBP19; MGC54182	NM_016594	FK506 binding protein 11, 19 kDa
C3ORF26	0.406	MGC4308	NM_032359	chromosome 3 open reading frame 26
PDGFRB	0.406	JTK12; PDGFR; CD140B; PDGFR1; PDGF-R-beta	NM_002609	platelet-derived growth factor receptor, beta polypeptide
ANK3	0.406	FLJ45464; ANKYRIN-G	NM_001149	ankyrin 3, node of Ranvier (ankyrin G)
RPL8	0.406	RPL8	NM_033301	ribosomal protein L8
CCRN4L	0.405	NOC; CCR4L; MGC78549; MGC142054; MGC142060; MGC4120817	NM_012118	CCR4 carbon catabolite repression 4-like (S. cerevisiae)
RAB31	0.403	Rab22B	NM_006868	RAB31, member RAS oncogene family
PFS2	0.403	PSF2; Pfs2; HSPC037	NM_016095	GINS complex subunit 2 (Psf2 homolog)
TPM2	0.402	DA1; TMSB; AMCD1	NM_213674	tropomyosin 2 (beta)
GNG4	0.402	VPS13B	NM_004485	guanine nucleotide binding protein (G protein), gamma 4
NSBP1	0.4	NSBP1	NM_030763	nucleosomal binding protein 1

LAMC1	0.4	LAMB2; MGC87297	NM_002293	laminin, gamma 1 (formerly LAMB2)
RNMTL1	0.399	HC90; FLJ10581	NM_018146	RNA methyltransferase like 1
ORC1L	0.398	ORC1; PARC1; HSORC1	NM_004153	origin recognition complex, subunit 1-like (yeast)
SULF1	0.398	SULF-1; HSULF-1; FLJ38022; FLJ41750; KIAA1077	NM_015170	sulfatase 1
TFPI	0.397	EPI; TFI; LACI	NM_006287	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
SESN1	0.395	PA26; SEST1; MGC138241; MGC142129; RP11-787I22.1	NM_014454	sestrin 1
MAD2L2	0.394	REV7; MAD2B	NM_006341	MAD2 mitotic arrest deficient-like 2 (yeast)
DTL	0.393	RAMP; L2DTL	NM_016448	denticleless homolog (Drosophila)
TNC	0.392	TN; HXB	NM_002160	tenascin C (hexabrachion)
SLC17A5	0.392	SD; AST; NSD; SLD; ISSD; SIASD; SIALIN; FLJ22227; FLJ23268	NM_012434	solute carrier family 17 (anion/sugar transporter), member 5
GRM4	0.391	mGlu4; GPRC1D; MGLUR4	NM_000841	glutamate receptor, metabotropic 4
RPS15	0.391	RIG; MGC111130	NM_001018	ribosomal protein S15
FLJ20701	0.391	FLJ20701; HMFN2073	NM_017933	hypothetical protein FLJ20701
REXO2	0.39	RFN; SFN; CGI-114; MGC111570; DKFZP566E144	NM_015523	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
GULP1	0.39	CED6; GULP; CED-6; FLJ31156	NM_016315	GULP, engulfment adaptor PTB domain containing 1
IDH3A	0.39	PXDN	NM_005530	isocitrate dehydrogenase 3 (NAD+) alpha
SIX4	0.39	AREC3; MGC119450; MGC119452; MGC119453	NM_017420	sine oculis homeobox homolog 4 (Drosophila)
FKBP4	0.389	HBI; p52; Hsp56; FKBP52; FKBP59; PPIase	NM_002014	FK506 binding protein 4, 59kDa
CALD1	0.388	CDM; H-CAD; L-CAD; NAG22; MGC21352	NM_004342	caldesmon 1
MCEE	0.388	RPL12	NM_032601	methylmalonyl CoA epimerase
AP1S1	0.387	AP19; CLAPS1; SIGMA1A	NM_001283	adaptor-related protein complex 1, sigma 1 subunit
PCNXL2	0.387	FLJ11383; KIAA0435	NM_024938	pecanex-like 2 (Drosophila)
C3ORF54	0.387	MGC20416	NM_203370	chromosome 3 open reading frame 54
SLC7A8	0.386	LAT2; LPI-PC1	NM_012244	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
BRP44	0.385	MGC125752; MGC125753; DKFZP564B167	NM_015415	brain protein 44
HNT	0.384	HNT; NTM; MGC60329	NM_016522	neurotrimin
CDCP1	0.382	CD318; TRASK; SIMA135	NM_178181	CUB domain containing protein 1
WWC1	0.382	KIBRA; FLJ10865; FLJ23369; KIAA0869	NM_015238	WW, C2 and coiled-coil domain containing 1
TRAM2	0.382	KIAA0057	NM_012288	translocation associated membrane protein 2
TNFRSF8	0.381	CD30; KI-1; D1S166E	NM_001243	tumor necrosis factor receptor superfamily, member 8
MAPRE2	0.379	EB1; EB2; RP1	NM_014268	microtubule-associated protein, RP/EB family, member 2
JARID2	0.378	JMJ	NM_004973	Jumonji, AT rich interactive domain 2
FAM98A	0.378	DKFZP564F0522; DKFZp686O03192	NM_015475	family with sequence similarity 98, member A
SLC25A19	0.376	DNC; MUP1; MCPHA	NM_021734	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19
LRRC8D	0.376	LRRC5; FLJ10470; FLJ20403	NM_018103	leucine rich repeat containing 8 family, member D
PRPS1	0.375	PRSI; PRS I; KIAA0967	NM_002764	phosphoribosyl pyrophosphate synthetase 1
SLC6A15	0.375	V7-3; NTT73; hv7-3; FLJ10316; MGC87066; DKFZp761I0921	NM_018057	solute carrier family 6, member 15
ADCY3	0.375	AC3; KIAA0511	NM_004036	adenylate cyclase 3
LNK	0.372	LNK	NM_005475	SH2B adaptor protein 3
H2AFJ	0.37	MGC921; FLJ10903	NM_177925	H2A histone family, member J
IGSF1	0.368	IGCD1; IGDC1; INHBP; PGSF2; KIAA0364; MGC75490	NM_205833	immunoglobulin superfamily, member 1
FXYD5	0.368	RIC; IWU1; KCT1; OIT2; IWU-1; dysad; HSPC113; PRO6241	NM_014164	FXYD domain containing ion transport regulator 5
BTBD11	0.367	FLJ33957; FLJ42845	NM_152322	BTB (POZ) domain containing 11
LRP11	0.367	MANSC3; FLJ14735; MGC39092; bA350J20.3	NM_032832	low density lipoprotein receptor-related protein 11
TIMP2	0.366	CSC-21K	NM_003255	TIMP metallopeptidase inhibitor 2
CIT	0.366	CRIK; STK21; KIAA0949	NM_007174	citron (rho-interacting, serine/threonine kinase 21)
TSPAN5	0.366	NET-4; TM4SF9; TSPAN-5	NM_005723	tetraspanin 5
HRASLS3	0.366	HREV107; HREV107-3; MGC118754; H-REV107-1	NM_007069	HRAS-like suppressor 3
LOC134147	0.366	FLJ23617	NM_138809	carboxymethylenebutenolidase-like (Pseudomonas)
MCM4	0.364	CDC21; CDC54; hCdc21; MGC33310; P1-CDC21	NM_005914	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)
LOC387882	0.363	LOC387882	NM_207376	hypothetical protein
HPRT1	0.363	HPRT; HGPRT	NM_000194	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
FOS	0.362	c-fos	NM_005252	v-fos FBJ murine osteosarcoma viral oncogene homolog
L2HGDH	0.362	FLJ12618; C14orf160	NM_024884	L-2-hydroxyglutarate dehydrogenase
SYT6	0.36	SYT6	NM_205848	synaptotagmin VI
CEBPZ	0.359	CBF2; HSP-CBF	NM_005760	CCAAT/enhancer binding protein zeta
MIMITIN	0.357	MMTN; B17.2L; mimitin	NM_174889	NDUFA12-like
FHL2	0.357	DRAL; AAG11; SLIM3	NM_001450	four and a half LIM domains 2
PLEKHF1	0.355	APPD; MGC4090; PHAFIN1; ZFYVE15	NM_024310	pleckstrin homology domain containing, family F (with FYVE domain) member 1
PARD6A	0.352	PAR6; PAR6C; TAX40; PAR-6A; TIP-40; PAR6alpha	NM_016948	par-6 partitioning defective 6 homolog alpha (C.elegans)
C13ORF3	0.352	RAMA1; MGC4832	NM_145061	chromosome 13 open reading frame 3
SLC39A10	0.35	LZT-Hs2; MGC126565; MGC138428; DKFZp781L10106	NM_020342	solute carrier family 39 (zinc transporter), member 10
PROK2	0.35	BV8; PK2; MIT1	NM_021935	prokineticin 2
NASP	0.349	FLB7527; MGC2297; PRO1999; FLJ31599; FLJ35510; MGC19722; MGC20372; DKFZp547F162	NM_002482	nuclear autoantigenic sperm protein (histone-binding)
PECI	0.346	DRS1; ACBD2; HCA88; dJ1013A10.3	NM_006117	peroxisomal D3,D2-enoyl-CoA isomerase

LYSMD2	0.346	MGC35274; DKFZp686I2243	NM_153374	LysM, putative peptidoglycan-binding, domain containing 2
LRRN6A	0.345	LERN1; LINGO1; UNQ201; FLJ14594; MGC17422	NM_032808	leucine rich repeat neuronal 6A
P2RY5	0.344	P2Y5; MGC120358	NM_005767	purinergic receptor P2Y, G-protein coupled, 5
CASP3	0.343	CPP32; SCA-1; CPP32B	NM_032991	caspase 3, apoptosis-related cysteine peptidase
TCEAL2	0.342	my048; MY0876G05	NM_080390	transcription elongation factor A (SII)-like 2
PUNC	0.341	HsT18880	NM_004884	putative neuronal cell adhesion molecule
FDXR	0.34	ADXR	NM_024417	ferredoxin reductase
SASH1	0.34	KIAA0790; dJ323M4.1; RP3-323M4.1	NM_015278	SAM and SH3 domain containing 1
SCG3	0.339	SGIII; FLJ90833	NM_013243	secretogranin III
FZD10	0.338	FzE7; FZ-10; hFz10	NM_007197	frizzled homolog 10 (Drosophila)
INHBE	0.336	MGC4638	NM_031479	inhibin, beta E
TIMP4	0.334	TIMP4	NM_003256	TIMP metallopeptidase inhibitor 4
UBE2L6	0.332	RIG-B; UBCH8; MGC40331	NM_004223	ubiquitin-conjugating enzyme E2L 6
PCOLCE	0.332	PCPE	NM_002593	procollagen C-endopeptidase enhancer
PFTK1	0.331	KIAA0834; PFTAIRE1	NM_012395	PFTAIRE protein kinase 1
TM4SF18	0.331	L6D	NM_138786	transmembrane 4 L six family member 18
DPPA5	0.331	Esg1	NM_001025290	developmental pluripotency associated 5
KCNN2	0.33	SK2; hSK2; SKCA2; KCa2.2	NM_170775	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2
TMBIM4	0.327	S1R; ZPRO; CGI-119	NM_016056	transmembrane BAX inhibitor motif containing 4
FGF19	0.325	FGF19	NM_005117	fibroblast growth factor 19
MGC24665	0.325	MGC24665	NM_152308	chromosome 16 open reading frame 75
STOM	0.324	BND7; EPB7; EPB72	NM_004099	stomatin
SOX8	0.324	MGC24837	NM_014587	SRY (sex determining region Y)-box 8
PHC1	0.323	EDR1; HPH1; RAE28	NM_004426	polyhomeotic-like 1 (Drosophila)
STEAP1	0.323	STEAP; PRSS24; MGC19484	NM_012449	six transmembrane epithelial antigen of the prostate 1
DCAMKL1	0.323	DCLK; KIAA0369	NM_004734	doublecortin and CaM kinase-like 1
HEY2	0.321	GRL; CHF1; HRT2; HERP1; HESR2; MGC10720	NM_012259	hairy/enhancer-of-split related with YRPW motif 2
DUT	0.321	dUTPase; FLJ20622	NM_001025248	dUTP pyrophosphatase
ALG9	0.319	DIBD1; FLJ21845; DKFZp586M2420	NM_024740	asparagine-linked glycosylation 9 homolog (S. cerevisiae, alpha-1,2-mannosyltransferase)
PPP2R2B	0.319	SCA12; MGC24888; PR55-BETA; PP2A-PR55B; PR2AB-BETA; PR2AB55-BETA; PR2APR55-BETA	NM_181676	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform
SEPHS1	0.315	SPS; SELD; SPS1; MGC4980	NM_012247	selenophosphate synthetase 1
FLJ25801	0.314	FLJ25801; MGC138164; MGC138166	NM_173553	hypothetical protein FLJ25801
PSMB8	0.314	LMP7; D6S216; RING10; D6S216E; MGC1491	NM_148919	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
CABC1	0.312	COQ8; ADCK3; MGC4849	NM_020247	chaperone, ABC1 activity of bc1 complex like (S. pombe)
OCIAD2	0.312	MGC45416; DKFZp686C03164	NM_001014446	OCIA domain containing 2
KCND2	0.309	RK5; KV4.2; KIAA1044; MGC119702; MGC119703	NM_012281	potassium voltage-gated channel, Shal-related subfamily, member 2
FLJ22662	0.309	FLJ22662	NM_024829	hypothetical protein FLJ22662
GFPT2	0.306	GFAT2; FLJ10380	NM_005110	glutamine-fructose-6-phosphate transaminase 2
FGD5	0.306	ZFYVE23	NM_152536	FYVE, RhoGEF and PH domain containing 5
PAK1	0.305	PAKalpha; MGC130000; MGC130001	NM_002576	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
ITGB1BP3	0.304	MIBP; NRK2; MGC126624	NM_170678	integrin beta 1 binding protein 3
OAZ2	0.303	OAZ2	NM_002537	ornithine decarboxylase antizyme 2
AKAP7	0.3	AKAP18	NM_016377	A kinase (PRKA) anchor protein 7
APCDD1	0.296	B7323; DRAPC1; FP7019	NM_153000	adenomatosis polyposis coli down-regulated 1
CTGF	0.294	CCN2; NOV2; HCS24; IGFBP8; MGC102839	NM_001901	connective tissue growth factor
PRDM14	0.292	PFM11; MGC59730	NM_024504	PR domain containing 14
C7ORF24	0.29	MGC3077; FLJ11717	NM_024051	chromosome 7 open reading frame 24
NELL2	0.289	NRP2	NM_006159	NEL-like 2 (chicken)
SMPDL3B	0.289	ASML3B	NM_014474	sphingomyelin phosphodiesterase, acid-like 3B
HSPA2	0.289	HSPA2	NM_021979	heat shock 70kDa protein 2
SCGB3A2	0.288	LU103; PNSP1; UGRP1	NM_054023	secretoglobin, family 3A, member 2
ICAM3	0.286	CD50; CDW50; ICAM-R	NM_002162	intercellular adhesion molecule 3
UGP2	0.284	UDPG; UGPP2; UDPGP2; pHC379	NM_006759	UDP-glucose pyrophosphorylase 2
CHST7	0.281	C6ST-2	NM_019886	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7
OCIAD2	0.277	MGC45416; DKFZp686C03164	NM_152398	OCIA domain containing 2
CXCL12	0.275	PBSF; SDF1; SDF1A; SDF1B; TPAR1; SCYB12; SDF-1a; SDF-1b; TLSF-a; TLSF-b	NM_001033886	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
FAM57B	0.269	FP1188; DKFZP434I2117	NM_031478	family with sequence similarity 57, member B
SMPDL3B	0.268	ASML3B	NM_014474	sphingomyelin phosphodiesterase, acid-like 3B
SEMA6A	0.265	VIA; SEMA; HT018; SEMAQ; SEMA6A1; KIAA1368; sema VIa	NM_020796	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
FABP5	0.264	EFABP; E-FABP; PAFABP; PA-FABP	NM_001444	fatty acid binding protein 5 (psoriasis-associated)
RTN4IP1	0.264	NIMP; MGC12934	NM_032730	reticulon 4 interacting protein 1
KIAA0746	0.264	KIAA0746; FLJ21629; DKFZp781J1697	NM_015187	KIAA0746 protein
MT1A	0.261	MT1; MTC; MT1S; MGC32848	NM_005946	metallothionein 1A (functional)
DIAPH2	0.26	DIA; POF; DIA2; POF2; FLJ11167	NM_007309	diaphanous homolog 2 (Drosophila)
CCND1	0.259	BCL1; PRAD1; U21B31; D11S287E	NM_053056	cyclin D1
DNMT3	0.256	ICF; M.HsaIIIB	NM_006892	DNA (cytosine-5-)-methyltransferase 3 beta

B				
NANOG	0.255	FGA	NM_024865	Nanog homeobox
IQGAP2	0.25	ARIH2	NM_006633	IQ motif containing GTPase activating protein 2
CYP2S1	0.249	CYP2S1	NM_030622	cytochrome P450, family 2, subfamily S, polypeptide 1
NFE2L3	0.243	NRF3	NM_004289	nuclear factor (erythroid-derived 2)-like 3
ADAM15	0.241	MDC15	NM_207195	ADAM metallopeptidase domain 15 (metargidin)
MT1X	0.241	MT1; MT-1l	NM_005952	metallothionein 1X
DPPA2	0.237	PESCRG1	NM_138815	developmental pluripotency associated 2
DPPA4	0.234	FLJ10713; 2410091M23Rik	NM_018189	developmental pluripotency associated 4
ITGB1BP3	0.23	MIBP; NRK2; MGC126624	NM_014446	integrin beta 1 binding protein 3
MMP9	0.228	GELB; CLG4B	NM_004994	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)
HPCAL1	0.227	BDR1; HLP2; VILIP-3	NM_002149	hippocalcin-like 1
GLDC	0.226	GCE; NKH; GCSP; HYGN1; MGC138198; MGC138200	NM_000170	glycine dehydrogenase (decarboxylating)
CKMT1B	0.225	CKMT; CKMT1; UMTCK	NM_020990	creatine kinase, mitochondrial 1B
TERF1	0.223	TRF; PIN2; TRF1; TRBF1; t-TRF1; hTRF1-AS	NM_017489	telomeric repeat binding factor (NIMA-interacting) 1
CDCA7L	0.223	R1; RAM2; DKFZp762L0311	NM_018719	cell division cycle associated 7-like
AASS	0.22	LKRSDH; LORSDH; LKR/SDH	NM_005763	aminoadipate-semialdehyde synthase
DACT1	0.217	DPR1; FRODO; HDPR1; DAPPER; THYEX3; DAPPER1	NM_016651	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
SILV	0.21	SI; SIL; ME20; gp100; PMEL17; D12S53E	NM_006928	silver homolog (mouse)
UBE2L6	0.204	RIG-B; UBCH8; MGC40331	NM_004223	ubiquitin-conjugating enzyme E2L 6
PDPN	0.204	T1A; GP36; GP40; Gp38; OTS8; T1A-2; HT1A-1; PA2.26	NM_001006625	podoplanin
CH25H	0.204	C25H	NM_003956	cholesterol 25-hydroxylase
SCNN1A	0.201	ENaCa; SCNEA; SCNN1; FLJ21883; ENaCalpha	NM_001038	sodium channel, nonvoltage-gated 1 alpha
FLJ12505	0.199	FLJ12505; RP11-275G3.1	NM_024749	vasohibin 2
FAH	0.191	FAH	NM_000137	fumarylacetoacetate hydrolase (fumarylacetoacetase)
POU5F1	0.187	OCT3; OTF3; OTF4; Oct4; MGC22487	NM_203289	POU domain, class 5, transcription factor 1
PTPRZ1	0.175	PTPZ; HPTPZ; PTP18; PTPRZ; RPTPB; HPTPzeta; RPTPbeta	NM_002851	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
FAM46B	0.175	MGC16491; MGC20845; RP11-344H11.8	NM_052943	family with sequence similarity 46, member B
HAS3	0.164	HAS3	NM_005329	hyaluronan synthase 3
USP44	0.158	FLJ14528; DKFZP434D0127	NM_032147	ubiquitin specific peptidase 44
POU5F1	0.147	OCT3; OTF3; OTF4; Oct4; MGC22487	NM_002701	POU domain, class 5, transcription factor 1
VSNL1	0.146	HLP3; VILIP; HPCAL3; HUVISL1; VILIP-1	NM_003385	visinin-like 1
CKMT1A	0.139	CKMT1; UMTCK	NM_001015001	creatine kinase, mitochondrial 1A
SFRP2	0.136	FRP-2; SARP1; SDF-5	NM_003013	secreted frizzled-related protein 2

d4AA only

Gene Name	Fold Change	Common	Genbank	Description
CD1D	2.844	R3; CD1A; MGC34622	NM_001766	CD1d molecule
C2ORF34	2.622	FLJ23451	NM_024766	chromosome 2 open reading frame 34
PPP2R2C	2.4	PR52; IMYPNO; IMYPNO1; MGC33570	NM_181876	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform
VANGL1	2.349	LPP2; STB2; MGC5338	NM_138959	vang-like 1 (van gogh, Drosophila)
IFRD1	2.203	PC4; TIS7	NM_001550	interferon-related developmental regulator 1
HES1	2.14	HHL; HRY; HES-1; FLJ20408	NM_005524	hairy and enhancer of split 1, (Drosophila)
SLC2A1	2.088	GLUT; GLUT1; MGC141895; MGC141896	NM_006516	solute carrier family 2 (facilitated glucose transporter), member 1
TMEPAI	2.024	STAG1; PMEPA1	NM_020182	transmembrane, prostate androgen induced RNA
NTS	2.005	NN; NT; NT/N; NTS1; NMN-125	NM_006183	neurotensin
IL17RD	1.974	SEF; IL-17RD; IL17RLM; FLJ35755; MGC133309; DKFZp434N1928	NM_017563	interleukin 17 receptor D
GPR64	1.974	HE6; TM7LN2; FLJ00282; MGC104454; MGC138738; MGC138739	NM_005756	G protein-coupled receptor 64
PPT2	1.917	G14; NG3; C6orf8; DKFZp564P1516	NM_138717	palmitoyl-protein thioesterase 2
KAL1	1.902	HHA; KAL; KMS; ADMLX; KALIG-1	NM_000216	Kallmann syndrome 1 sequence
ADAMTS18	1.9	ADAMTS21	NM_199355	ADAM metallopeptidase with thrombospondin type 1 motif, 18
SLC36A2	1.875	PAT2; TRAMD1; FLJ16051; MGC119658; MGC119660	NM_181776	solute carrier family 36 (proton/amino acid symporter), member 2
SHB	1.873	bA3J10.2; RP11-3J10.8	NM_003028	Src homology 2 domain containing adaptor protein B
SON	1.866		NM_138926	
ZNF278	1.861	ZSG; MAZR; PATZ; RIAZ; ZBTB19; dJ400N23	NM_032051	zinc finger protein 278
ANGPT1	1.854	AGP1; AGPT; ANG1	NM_001146	angiopoietin 1
KLF5	1.84	CKLF; IKLF; BTEB2	NM_001730	Kruppel-like factor 5 (intestinal)
GDF3	1.786	GDF3	NM_020634	growth differentiation factor 3
CHRD	1.751		NM_177978	
C17ORF39	1.738	MGC3048	NM_024052	chromosome 17 open reading frame 39
CROP	1.725	CROP; LUC7A; OA48-18	NM_016424	cisplatin resistance-associated overexpressed protein
KIAA1944	1.704	MOLT; KIAA1944; MGC138770; MGC138771	NM_133448	transmembrane protein 132D
NEBL	1.701	LNEBL; bA56H7.1; MGC119746; MGC119747	NM_006393	nebulette
JOSD3	1.697	MGC5306	NM_024116	Josephin domain containing 3
RNF44	1.692	KIAA1100	NM_014901	ring finger protein 44
GAD1	1.68	GAD	NM_000817	glutamate decarboxylase 1 (brain, 67kDa)
CLK2	1.673	hCLK2; MGC61500	NM_001291	CDC-like kinase 2
SS18L1	1.66	CREST; LP2261; KIAA0693; MGC26711; MGC78386	NM_015558	synovial sarcoma translocation gene on chromosome 18-like 1
MATR3	1.628	MGC9105; KIAA0723; DKFZp686K0542; DKFZp686K23100	NM_018834	matrin 3
RBM35A	1.615	FLJ20171	NM_017697	RNA binding motif protein 35A
BCOR	1.612	MAA2; ANOP2; MCOPS2; FLJ20285; FLJ38041; KIAA1575; MGC71031; MGC131961	NM_020926	BCL6 co-repressor
C10ORF47	1.609	MGC35403	NM_153256	chromosome 10 open reading frame 47
C9ORF77	1.607	CGI-67; RP11-409O11.2	NM_016014	chromosome 9 open reading frame 77
CCNG2	1.606	SCOTIN	NM_004354	cyclin G2
ZNF202	1.605	ZNF202	NM_003455	zinc finger protein 202
BTBD6	1.604	BDPL	NM_033271	BTB (POZ) domain containing 6
ZNF498	1.603	ZNF498	NM_145115	zinc finger protein 498
ANK2	1.601	LQT4; FLJ38277; DKFZp686P0948; DKFZp686M09125	NM_020977	ankyrin 2, neuronal
EGLN1	1.591	PHD2; SM20; ECYT3; SM-20; HIFPH2; ZMYND6; C1orf12; DKFZp761F179	NM_022051	egl nine homolog 1 (C. elegans)
NRIP1	1.582	RIP140	NM_003489	nuclear receptor interacting protein 1
NPY5R	1.568	NPYR5	NM_006174	neuropeptide Y receptor Y5
PPARGC1A	1.56	LEM6; PGC1; PGC1A; PGC-1v; PPARGC1; PGC-1(alpha)	NM_013261	peroxisome proliferative activated receptor, gamma, coactivator 1, alpha
TNMD	1.553	TEM; CHM1L; BRICD4; tendin; myodulin; CHM1-LIKE	NM_022144	tenomodulin
NUDT10	1.541	DIPP3a; hDIPP3alpha	NM_153183	nudix (nucleoside diphosphate linked moiety X)-type motif 10
ZNF435	1.54	ZNF392; ZSCAN16; FLJ22191; dJ265C24.3	NM_025231	zinc finger protein 435
ANP32C	1.505	PP32R1	NM_012403	acidic (leucine-rich) nuclear phosphoprotein 32 family, member C
GABBR1	1.492	hGB1a; GPRC3A; GABABR1; GABBR1-3; GABAB(1e);	NM_021905	gamma-aminobutyric acid (GABA) B receptor, 1

		dJ271M21.1.1; dJ271M21.1.2		
KIAA1468	1.491	HsT885; HsT3308; FLJ33841	NM_020854	KIAA1468
ATF4	1.487	CREB2; TXREB; CREB-2; TAXREB67	NM_001675	activating transcription factor 4 (tax-responsive enhancer element B67)
DOCK1	1.48	ced5; DOCK180	NM_001380	dedicator of cytokinesis 1
RYR2	1.478	ARVC2; ARVD2; VTSIP	NM_001035	ryanodine receptor 2 (cardiac)
ZSWIM3	1.472	C20orf164	NM_080752	zinc finger, SWIM-type containing 3
TP53RK	1.472	PRPK; Nori-2; Nori-2p; C20orf64	NM_033550	TP53 regulating kinase
ZNF350	1.466	ZFQR; ZBRK1	NM_021632	zinc finger protein 350
C20ORF10	1.465	CLG01; TP53TG5	NM_014477	chromosome 20 open reading frame 10
FUT11	1.462	MGC33202; MGC119338; MGC119339	NM_173540	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)
ATP7B	1.454	WD; PWD; WC1; WND	NM_000053	ATPase, Cu++ transporting, beta polypeptide
SIAH1	1.454	Siah-1; hSIAH1; HUMSIAH; Siah-1a	NM_001006610	seven in absentia homolog 1 (Drosophila)
NR2C1	1.443	TR2; TR2-11	NM_001032287	nuclear receptor subfamily 2, group C, member 1
ANKHD1	1.43	MASK	NM_017747	ankyrin repeat and KH domain containing 1
SNTB1	1.427	A1B; SNT2; BSYN2; 59-DAP; DAPA1B; SNT2B1; TIP-43; FLJ22442; MGC111389	NM_021021	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
FGF12	1.427	FHF1; FGF12B	NM_004113	fibroblast growth factor 12
C1ORF84	1.42	FLJ34502; RP11-506B15.1	NM_001012960	chromosome 1 open reading frame 84
ZBED4	1.42	GON4L	NM_014838	zinc finger, BED-type containing 4
SCAND2	1.417	SCAND2	NM_033640	SCAN domain containing 2
CRY1	1.415	PHLL1	NM_004075	cryptochrome 1 (photolyase-like)
FLJ22639	1.401		NM_024796	
WDR19	1.399	ORF26; PWDMP; FLJ23127; KIAA1638	NM_025132	WD repeat domain 19
COL4A4	1.396	CA44	NM_000092	collagen, type IV, alpha 4
KIAA1434	1.394	KIAA1434; FLJ11085; MGC26147; RP5-1022P6.2	NM_019593	hypothetical protein KIAA1434
EDNRA	1.388	ETA; ETRA	NM_001957	endothelin receptor type A
JRK	1.387	JH8; FLJ45729; DKFZp686C24207	NM_003724	jerky homolog (mouse)
PHF16	1.386	JADE3; KIAA0215; MGC138748; MGC138749	NM_014735	PHD finger protein 16
RCE1	1.386	FACE2; RCE1A; RCE1B	NM_001032279	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)
CSAG2	1.382	TRAG3; MGC149851; MGC149852	NM_004909	CSAG family, member 2
PCF11	1.379	KIAA0824	NM_015885	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)
GMEB1	1.373	PIF96; P96PIF	NM_006582	glucocorticoid modulatory element binding protein 1
FLJ14768	1.365	ZNF798; FLJ14768	NM_032836	FLT3-interacting zinc finger 1
MARS2	1.365	MetRS; mtMetRS	NM_138395	methionine-tRNA synthetase 2 (mitochondrial)
MAN1A2	1.359	MAN1B	NM_006699	mannosidase, alpha, class 1A, member 2
THAP1	1.343	FLJ10477; MGC33014	NM_199003	THAP domain containing, apoptosis associated protein 1
HDHD3	1.34	C9orf158; MGC12904; 2810435D12Rik	NM_031219	haloacid dehalogenase-like hydrolase domain containing 3
ALDH1A3	1.338	ALDH6; RALDH3; ALDH1A6	NM_000693	aldehyde dehydrogenase 1 family, member A3
CEP27	1.337	C15orf25; FLJ10460; HsT17025	NM_018097	centrosomal protein 27kDa
BRSK2	1.332	SAD1; STK29; PEN11B; C11orf7	NM_003957	BR serine/threonine kinase 2
CTDSP1	1.331	SCP1; NLIIF	NM_182642	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
MRPL27	1.331	L27mt; MGC23716	NM_148571	mitochondrial ribosomal protein L27
INPP5F	1.323	SAC2; hSAC2; MSTP007; MSTPO47; FLJ13081; KIAA0966; MGC59773; MGC131851	NM_198330	inositol polyphosphate-5-phosphatase F
RET	1.319	PTC; MTC1; HSCR1; MEN2A; MEN2B; RET51; CDHF12; RET-ELE1	NM_020630	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)
ZNF16	1.314	KOX9	NM_001029976	zinc finger protein 16
ATF2	1.309	HB16; CREB2; TREB7; CRE-BP1; MGC111558	NM_001880	activating transcription factor 2
ZNF93	1.307	TF34; HPF34; HTF34; ZNF505	NM_001004126	zinc finger protein 93
RNF170	1.304	FLJ38306; DKFZP564A022	NM_030954	ring finger protein 170
ZNF233	1.304	FLJ38032	NM_181756	zinc finger protein 233
WWOX	1.302	FOR; WOX1; FRA16D; HHCMA56; PRO0128; WWOX v8; D16S432E	NM_130844	WW domain containing oxidoreductase
BTRC	1.302	FWD1; FBW1A; bTrCP; FBXW1A; bTrCP1; MGC4643; betaTrCP; BETA-TRCP	NM_003939	beta-transducin repeat containing
MESDC1	1.301	MGC99595	NM_022566	mesoderm development candidate 1
NR2C2	1.298	TR4; TAK1; TR2R1; hTAK1	NM_003298	nuclear receptor subfamily 2, group C, member 2
HLA-DQB1	1.298	IDDM1; CELIAC1; HLA-DQB; HLA DQB1	NM_002123	major histocompatibility complex, class II, DQ beta 1
ZNFN1A5	1.297	PEGASUS; ZNFN1A5; FLJ22973; DKFZp781B0249	NM_022466	IKAROS family zinc finger 5 (Pegasus)
HNRPK	1.296	CSBP; TUNP; HNRNPK	NM_031263	heterogeneous nuclear ribonucleoprotein K
IFRD1	1.293	PC4; TIS7	NM_001007245	interferon-related developmental regulator 1
YWHAZ	1.292	KCIP-1; MGC111427; MGC126532; MGC138156	NM_003406	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
ZNF71	1.29	EZFIT	NM_021216	zinc finger protein 71
MAML3	1.288	GDN; MAM2; CAGH3; ERDA3; MAM-2; TNRC3	NM_018717	mastermind-like 3 (Drosophila)
ARL5B	1.287	ARL8	NM_178815	ADP-ribosylation factor-like 5B
GLCCI1	1.287	GIG18; FAM117C	NM_138426	glucocorticoid induced transcript 1

CDK10	1.286	PISSLRE	NM_052988	cyclin-dependent kinase (CDC2-like) 10
ING3	1.284	Eaf4; ING2; p47ING3; FLJ20089	NM_198267	inhibitor of growth family, member 3
FAM24B	1.281	MGC45962; DKFZp667I0323	NM_152644	family with sequence similarity 24, member B
NOL9	1.274	FLJ23323; MGC131821; MGC138483	NM_024654	nucleolar protein 9
ZNF586	1.274	FLJ20070	NM_017652	zinc finger protein 586
KCNG1	1.274	K13; kH2; KCNG; KV6.1; MGC12878	NM_172318	potassium voltage-gated channel, subfamily G, member 1
PITX2	1.271	RS; RGS; ARP1; Brx1; IDG2; IGDS; IHG2; PTX2; RIEG; IGDS2; IRID2; Otlx2; RIEG1; MGC20144; MGC111022	NM_000325	paired-like homeodomain transcription factor 2
KLHL4	1.266	KHL4; DKELCHL; KIAA1687	NM_057162	kelch-like 4 (Drosophila)
IL23A	1.265	P19; SGRF; IL-23; IL-23A; IL23P19; MGC79388	NM_016584	interleukin 23, alpha subunit p19
SOCS6	1.263	CIS4; SSI4; SOCS4; STAI4; STAT4; STATI4; HSPC060	NM_004232	suppressor of cytokine signaling 6
SMURF1	1.26	KIAA1625	NM_181349	SMAD specific E3 ubiquitin protein ligase 1
KCR1	1.257	KCR1; ALG10	NM_001013620	asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)
COX11	1.252	COX11P	NM_004375	COX11 homolog, cytochrome c oxidase assembly protein (yeast)
GTF2I	1.252	DIWS; SPIN; IB291; BAP135; BTKAP1; TFII-I; WBSCR6; BAP-135	NM_033001	general transcription factor II, i
BTNL2	1.248	BTL-II; HSBLMHC1	NM_019602	butyrophilin-like 2 (MHC class II associated)
ACHE	1.246	YT; ARACHE; N-ACHE	NM_015831	acetylcholinesterase (Yt blood group)
GOLPH3L	1.245	GPP34R; FLJ10687	NM_018178	golgi phosphoprotein 3-like
ZNF607	1.245	FLJ14802; MGC13071	NM_032689	zinc finger protein 607
GABRE	1.241	GABRE	NM_021990	gamma-aminobutyric acid (GABA) A receptor, epsilon
FLJ11171	1.24	FLJ11171	NM_018348	hypothetical protein FLJ11171
ZNF675	1.237	TIZ; TBZF; FLJ36350	NM_138330	zinc finger protein 675
SLC40A1	1.233	FPN1; HFE4; MTP1; IREG1; MST079; MSTP079; SLC11A3	NM_014585	solute carrier family 40 (iron-regulated transporter), member 1
OR2A7	1.231	OR2A21; HSDJ0798C17	NM_001005328	olfactory receptor, family 2, subfamily A, member 7
TMEM16J	1.22	PIG5; TP53I5	NM_001012302	transmembrane protein 16J
LOC112869	1.219	FLJ32446	NM_138414	coiled-coil domain containing 101
DSCR1L1	1.217	CSP2; RCN2; MCIP2; hRCN2; ZAKI-4	NM_005822	Down syndrome critical region gene 1-like 1
ZNF419	1.211	ZNF419; FLJ23233	NM_024691	zinc finger protein 419A
ZNF197	1.211	P18; VHLaK; ZNF20; ZNF166; D3S1363E	NM_001024855	zinc finger protein 197
PLA2G6	1.211	GVI; PLA2; INAD1; iPLA2; PNPLA9; CaI-PLA2	NM_003560	phospholipase A2, group VI (cytosolic, calcium-independent)
RANBP2L1	1.21	RGP5; BS-63; DKFZp686I1842	NM_005054	RANBP2-like and GRIP domain containing 5
KIAA1414	1.207	KIAA1414	NM_019024	KIAA1414 protein
IFIT1L	1.205	bA149I23.6; DKFZp781M1841	NM_001010987	interferon-induced protein with tetratricopeptide repeats 1-like
F7	1.202	F7	NM_000131	coagulation factor VII (serum prothrombin conversion accelerator)
FTSJ2	1.201		NM_177442	
AGPAT4	1.194	1-AGPAT4; dJ473J16.2; LPAAT-delta; RP3-473J16.2	NM_001012733	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)
NUP43	1.194		NM_024647	
GSTZ1	1.193	MAI; MAAI; GSTZ1-1; MGC2029	NM_001513	glutathione transferase zeta 1 (maleylacetoacetate isomerase)
EPB41L5	1.192	BE37; FLJ12957; KIAA1548	NM_020909	erythrocyte membrane protein band 4.1 like 5
MXD1	1.191	MAD; MAD1; MGC104659	NM_002357	MAX dimerization protein 1
ZSWIM3	1.19	C20orf164	NM_080752	zinc finger, SWIM-type containing 3
HIP2	1.189	LIG; HYPG; UBE2K	NM_005339	huntingtin interacting protein 2
PCGF6	1.187	MBLR; RNF134; MGC15678; MGC17541	NM_032154	polycomb group ring finger 6
GLUL	1.182	GS; GLNS; PIG43	NM_001033044	glutamate-ammonia ligase (glutamine synthetase)
FBXO9	1.176	FBX9; VCIA1; KIAA0936; NY-REN-57; dJ341E18.2; DKFZp434C0118	NM_033481	F-box protein 9
EIF5	1.175	EIF-5A	NM_183004	eukaryotic translation initiation factor 5
LOC399900	1.174	LOC399900	NM_001013667	hypothetical gene supported by AK093779
TMPRSS3	1.169	DFNB8; DFNB10; ECHOS1; TADG12	NM_032401	transmembrane protease, serine 3
ATG16L1	1.168	WDR30; APG16L; ATG16L; FLJ00045; FLJ10035; FLJ10828; FLJ22677	NM_030803	ATG16 autophagy related 16-like 1 (S. cerevisiae)
MLL4	1.167	MLL4; HRX2; MLL2; TRX2; KIAA0304	NM_014727	myeloid/lymphoid or mixed-lineage leukemia 4
C11ORF35	1.167	MGC35138	NM_173573	chromosome 11 open reading frame 35
ZDHHC18	1.164	DKFZp667O2416	NM_032283	zinc finger, DHHC-type containing 18
WASF1	1.164	WAVE; SCAR1; WAVE1; FLJ31482; KIAA0269	NM_003931	WAS protein family, member 1
LRP2	1.164	gp330	NM_004525	low density lipoprotein-related protein 2
STARD4	1.164	STARD4	NM_139164	START domain containing 4, sterol regulated
MAPK14	1.163	RK; p38; EXIP; Mxi2; CSBP1; CSBP2; CSPB1; PRKM14; PRKM15; SAPK2A; p38ALPHA	NM_139013	mitogen-activated protein kinase 14
ARHGAP29	1.16	PARG1; RP11-255E17.1	NM_004815	Rho GTPase activating protein 29
ST14	1.159	HAI; MTSP1; SNC19; MT-SP1; MTSP-1; PRSS14; TADG-15	NM_021978	suppression of tumorigenicity 14 (colon carcinoma)
KIF19	1.159	KIF19A; FLJ37300	NM_153209	kinesin family member 19
IFITM5	1.158	IFITM5	NM_001025295	interferon induced transmembrane protein 5
FLRT2	1.156	KIAA0405	NM_013231	fibronectin leucine rich transmembrane protein 2
NCOA2	1.151	TIF2; GRIP1; NCoA-2;	NM_006540	nuclear receptor coactivator 2

		MGC138808		
EPS8L1	1.15	DRC3; EPS8R1; MGC4642; PP10566; FLJ20258; MGC23164	NM_133180	EPS8-like 1
SLA/LP	1.149	SLA/LP	NM_016955	soluble liver antigen/liver pancreas antigen
GGA3	1.147	KIAA0154	NM_138619	golgi associated, gamma adaptin ear containing, ARF binding protein 3
DKFZP686I15217	1.146	DKFZp686I15217	NM_207495	hypothetical protein DKFZp686I15217
LPIN3	1.145	SMP2; LIPN3L; dJ450M14.2; dJ450M14.3; dJ620E11.2	NM_022896	lipin 3
FANCC	1.141	FA3; FAC; FACC; FLJ14675	NM_000136	Fanconi anemia, complementation group C
RET	1.14	PTC; MTC1; HSCR1; MEN2A; MEN2B; RET51; CDHF12; RET-ELE1	NM_020975	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)
C13ORF6	1.139	C13orf6; FLJ14906; MGC27058; bA153I24.2; RP11-153I24.2	NM_032859	abhydrolase domain containing 13
RFX4	1.138	NYD-SP10	NM_213594	regulatory factor X, 4 (influences HLA class II expression)
SUV39H2	1.133	FLJ23414	NM_024670	suppressor of variegation 3-9 homolog 2 (Drosophila)
GPR12	1.132	GPCR12; GPCR21; MGC138349; MGC138351	NM_005288	G protein-coupled receptor 12
LOC389118	1.131	LOC389118; PRO34300	NM_001007540	VLLR9392
ST6GALNAC1	1.131	SIAT7A; HSY11339; ST6GalNAcI	NM_018414	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
PSD	1.13	TYL; KIAA2011	NM_002779	pleckstrin and Sec7 domain containing
HTN3	1.126	HIS2; HTN2; HTN5	NM_000200	histatin 3
RNPEPL1	1.122	FLJ10806; FLJ26675; MGC99544	NM_018226	arginyl aminopeptidase (aminopeptidase B)-like 1
TREML1	1.122	TLT1; TLT-1; PRO3438; GLTL1825; MGC119173; dJ238O23.3	NM_178174	triggering receptor expressed on myeloid cells-like 1
LGALS2	1.121	HL14; MGC75071	NM_006498	lectin, galactoside-binding, soluble, 2 (galectin 2)
HAAO	1.119	HAO; 3-HAO	NM_012205	3-hydroxyanthranilate 3,4-dioxygenase
WBSCR23	1.118		NM_025042	
ARTN	1.118	EVN; NBN	NM_057160	artemin
PSCDBP	1.116	HE; B3-1; CASP; CYBR; CYTIP	NM_004288	pleckstrin homology, Sec7 and coiled-coil domains, binding protein
FAM91A1	1.115	FLJ23790; DKFZp666B104	NM_144963	family with sequence similarity 91, member A1
PCDHA11	1.114	CNR7; CNRN7; CNRS7; CRNR7; PCDH-ALPHA11	NM_031861	protocadherin alpha 11
MYH3	1.107	HEMHC; SMHCE; MYHSE1; MYHC-EMB	NM_002470	myosin, heavy polypeptide 3, skeletal muscle, embryonic
C8ORF37	1.105	FLJ30600	NM_177965	chromosome 8 open reading frame 37
SPTB	1.104	HSpTB1	NM_001024858	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)
TSHB	1.103	TSH-BETA	NM_000549	thyroid stimulating hormone, beta
RFNG	1.102	RFNG	NM_002917	radical fringe homolog (Drosophila)
LOC390667	1.095	LOC390667	NM_001013658	similar to Neuronal pentraxin II precursor (NP-II) (NP2)
KA21	1.094	KA21; MGC45562	NM_152349	keratin 222 pseudogene
TAS2R4	1.093	T2R4	NM_016944	taste receptor, type 2, member 4
MMP28	1.091	MM28; MMP25	NM_001032278	matrix metallopeptidase 28
C1ORF157	1.09	FLJ40343; MGC120329; MGC120330; MGC120332	NM_182579	chromosome 1 open reading frame 157
CRYM	1.09	THBP; DFNA40	NM_001014444	crystallin, mu
CLUL1	1.088	RA337M	NM_199167	clusterin-like 1 (retinal)
LTBP1	1.084	LTBP1	NM_206943	latent transforming growth factor beta binding protein 1
NUP155	1.083	N155; KIAA0791	NM_153485	nucleoporin 155kDa
CMIP	1.081	CMIP; KIAA1694	NM_198390	c-Maf-inducing protein
PLEC1	1.081	HD1; PCN; EBS1; EBSO; PLTN; PLEC1b	NM_201380	plectin 1, intermediate filament binding protein 500kDa
FLJ36492	1.08	FLJ36492; MGC126634	NM_182568	hypothetical protein FLJ36492
GHRHR	1.078	GRFR; GHRFR; GHRHRpsv	NM_001009824	growth hormone releasing hormone receptor
ARHGAP11A	1.078	KIAA0013; MGC70740; GAP (1-12)	NM_014783	Rho GTPase activating protein 11A
PRKCABP	1.074	PRKCABP; MGC15204	NM_012407	protein interacting with PRKCA 1
FYTTD1	1.069	DKFZp761B1514	NM_001011537	forty-two-three domain containing 1
HIST1H2BI	1.066	H2B/k; H2BFK	NM_003525	histone 1, H2bi
OR52A4	1.064	OR52A4	NM_001005222	olfactory receptor, family 52, subfamily A, member 4
TIGD1	1.059	EEYORE	NM_145702	tigger transposable element derived 1
LOC400986	1.058	LOC400986	NM_001010914	synonym: HEM1; Homo sapiens protein immuno-reactive with anti-PTH polyclonal antibodies (LOC400986), mRNA.
SPG7	1.057	CAR; PGN; CMAR; MGC126331; MGC126332	NM_199367	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
SUCNR1	1.044	GPR91	NM_033050	succinate receptor 1
ELA2A	1.04	ELA2A; ELA1; PE-1	NM_033440	elastase 2A
MAP4	1.035	MGC8617; DKFZp779A1753	NM_030884	microtubule-associated protein 4
DLX3	1.034	TDO	NM_005220	distal-less homeobox 3
KIAA0513	1.033	KIAA0513	NM_014732	KIAA0513
GLYAT	0.972	CAT; GAT; ACGNAT	NM_005838	glycine-N-acyltransferase
KRTAP10-10	0.97	KAP10.10; KAP18.10; KRTAP18-10; KRTAP18.10	NM_181688	keratin associated protein 10-10
UNQ9217	0.964	UNQ9217	NM_205548	AASA9217
KRTAP1-1	0.961	HB2A; KAP1.1; KAP1.6; KAP1.7; KAP1.1A; KAP1.1B; KRTAP1A; hKAP1.7; KRTAP1.1	NM_030967	keratin associated protein 1-1
TSKS	0.944	TSKS; TSKS1	NM_021733	testis-specific kinase substrate
CC2D1A	0.941	MRT3; FREUD-1; FLJ20241; FLJ41160	NM_017721	coiled-coil and C2 domain containing 1A
SHOX	0.94	SS; GCFX; PHOG; SHOXY	NM_000451	short stature homeobox

STAG3	0.936	STAG3	NM_012447	stromal antigen 3
TNPO1	0.936	MIP; TRN; IPO2; MIP1; KPNB2	NM_002270	transportin 1
GUCY1A2	0.935	GC-SA2; GUC1A2	NM_000855	guanylate cyclase 1, soluble, alpha 2
MLL2	0.928	ALR; AAD10	NM_003482	myeloid/lymphoid or mixed-lineage leukemia 2
F11	0.92	FXI	NM_000128	coagulation factor XI (plasma thromboplastin antecedent)
PPP1R14D	0.92	GBPI-1; FLJ20251; MGC119014; MGC119016; CPI17-like	NM_017726	protein phosphatase 1, regulatory (inhibitor) subunit 14D
UACA	0.919	NUCLING; FLJ10128; KIAA1561; MGC141967; MGC141969	NM_018003	uveal autoantigen with coiled-coil domains and ankyrin repeats
CIB3	0.919	KIP3; MGC96922; MGC138405; MGC142151	NM_054113	calcium and integrin binding family member 3
ST8SIA4	0.919	PST; PST1; SIAT8D; MGC34450; MGC61459; ST8SIA-IV	NM_175052	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
ZDHHC9	0.918	DHHC9; CGI-89; ZNF379	NM_016032	zinc finger, DHHC-type containing 9
LZTFL1	0.917	RAPH1	NM_020347	leucine zipper transcription factor-like 1
C20ORF135	0.914	MGC42974; dJ591C20.1	NM_080622	chromosome 20 open reading frame 135
FLJ42393	0.913	FLJ42393	NM_207488	FLJ42393 protein
RDH8	0.912	PRRDH	NM_015725	retinol dehydrogenase 8 (all-trans)
FLJ23447	0.91	SLRR5B; FLJ23447	NM_024825	podocan-like 1
CUBN	0.907	IFCR; MGA1; gp280; FLJ90055; FLJ90747	NM_001081	cubilin (intrinsic factor-cobalamin receptor)
EEFSEC	0.902	SELB; EFSEC	NM_021937	eukaryotic elongation factor, selenocysteine-tRNA-specific
Sep-06	0.901	SEP2; KIAA0128; MGC16619; MGC20339; RP5-876A24.2	NM_145799	septin 6
TCP11	0.9	D6S230E; KIAA0229; MGC111103	NM_018679	t-complex 11 (mouse)
OSR2	0.9	FLJ90037	NM_053001	odd-skipped related 2 (Drosophila)
PPFIA1	0.894	LIP1; LIP.1; LIPRIN; MGC26800	NM_177423	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
CATSPER2	0.893	MGC33346	NM_172097	cation channel, sperm associated 2
ASCC3	0.891	RNAH; HELIC1; ASC1p200; MGC26074; DJ467N11.1; dJ121G13.4	NM_022091	activating signal cointegrator 1 complex subunit 3
FLJ42102	0.888	FLJ42102	NM_001001680	FLJ42102 protein
ZNF658	0.886	FLJ32813; MGC35232; DKFZp572C163	NM_033160	zinc finger protein 658
PROP1	0.884	PROP1	NM_006261	prophet of Pit1, paired-like homeodomain transcription factor
ATR	0.882	FRP1; MEC1; SCKL; SCKL1	NM_001184	ataxia telangiectasia and Rad3 related
BICD1	0.88	BICD	NM_001714	bicaudal D homolog 1 (Drosophila)
POMZP3	0.877	POM121; MGC8359; POM-ZP3	NM_012230	POM (POM121 homolog, rat) and ZP3 fusion
KLHL4	0.876	KHL4; DKELCHL; KIAA1687	NM_019117	kelch-like 4 (Drosophila)
BHMT	0.875	BHMT	NM_001713	betaine-homocysteine methyltransferase
MAP4K3	0.874	GLK; MAPKKKK3; RAB8IPL1	NM_003618	mitogen-activated protein kinase kinase kinase kinase 3
LOC51315	0.87	FLJ22333	NM_016618	lysine-rich coiled-coil 1
MAWBP	0.868	MAWBP; FLJ35507	NM_001033083	MAWD binding protein
SSH1	0.866	SSH-1; FLJ38102; KIAA1298	NM_018984	slingshot homolog 1 (Drosophila)
IGSF4B	0.865	BIgR; NECL1; TSLL1; Necl-1; synCAM3; FLJ10698	NM_021189	immunoglobulin superfamily, member 4B
PRKCB1	0.865	PKCB; PRKCB; PRKCB2; MGC41878; PKC-beta	NM_212535	protein kinase C, beta 1
MAGI1	0.862	AIP3; BAP1; WWP3; BAIAP1; MAGI-1; TNRC19	NM_001033057	membrane associated guanylate kinase, WW and PDZ domain containing 1
NPAS2	0.861	MOP4; PASD4; FLJ23138; MGC71151	NM_002518	neuronal PAS domain protein 2
IQCG	0.853	FLJ11667; FLJ23571; DKFZp434B227	NM_032263	IQ motif containing G
CCBE1	0.851	FLJ30681; MGC50861	NM_133459	collagen and calcium binding EGF domains 1
UXT	0.849	ART-27	NM_153477	ubiquitously-expressed transcript
RSHL2	0.847	RSP3; dJ111C20.1	NM_031924	radial spokehead-like 2
NAT2	0.846	AAC2	NM_000015	N-acetyltransferase 2 (arylamine N-acetyltransferase)
INSIG1	0.845	CL-6; MGC1405	NM_198336	insulin induced gene 1
PRKAA1	0.844	AMPK; AMPKa1; MGC33776; MGC57364	NM_206907	protein kinase, AMP-activated, alpha 1 catalytic subunit
ABCB4	0.843	MDR3; PGY3; ABC21; MDR2/3; PFIC-3	NM_000443	ATP-binding cassette, sub-family B (MDR/TAP), member 4
BLOC1S2	0.84	BLOS2; FLJ30135; MGC10120; RP11-316M21.4	NM_001001342	biogenesis of lysosome-related organelles complex-1, subunit 2
GABRD	0.839	MGC45284	NM_000815	gamma-aminobutyric acid (GABA) A receptor, delta
ASTN2	0.837	KIAA0634; bA67K19.1	NM_198188	astrotactin 2
RBL2	0.832	Rb2; P130; FLJ26459	NM_005611	retinoblastoma-like 2 (p130)
DNM1	0.831	DNM	NM_004408	dynamin 1
FA2H	0.83	FAAH; FAXDC1; FLJ25287	NM_024306	fatty acid 2-hydroxylase
HOXA11	0.829	HOX1; HOX1I	NM_005523	homeobox A11
CPZ	0.826	MGC99682	NM_001014447	carboxypeptidase Z
NDUFB4	0.826	B15; CI-B15; MGC5105	NM_004547	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
MSRB3	0.821	FLJ36866; DKFZp686C1178	NM_001031679	methionine sulfoxide reductase B3
KCNH2	0.819	ERG1; HERG; LQT2; SQT1; HERG1; Kv11.1	NM_172056	potassium voltage-gated channel, subfamily H (eag-related), member 2
MOCS1	0.818	MIG11; MOCOD; MOCS1A; MOCS1B; KIAA0381	NM_138928	molybdenum cofactor synthesis 1
PEX11A	0.816	MGC138534; PEX11-ALPHA	NM_003847	peroxisomal biogenesis factor 11A
UNQ2541	0.815	UNQ2541	NM_203347	MSFL2541
C6ORF167	0.814	FLJ46180; KIAA1900; dJ39B17.2; DKFZp781C2113; DKFZp686C20164	NM_198468	chromosome 6 open reading frame 167
MCAM	0.814	CD146; MUC18	NM_006500	melanoma cell adhesion molecule

FAM112B	0.814	FLJ32942	NM_144594	family with sequence similarity 112, member B
PLEKHQ1	0.813	PP1628; pp9099; FLJ38884; DKFZp761K2312	NM_025201	pleckstrin homology domain containing, family Q member 1
PPIL6	0.813	MGC41939; bA425D10.6; dJ919F19.1	NM_173672	peptidylprolyl isomerase (cyclophilin)-like 6
GATA2	0.807	NFE1B; MGC2306	NM_032638	GATA binding protein 2
EBF	0.806	COE1; EBF1; OLF1; O/E-1	NM_024007	early B-cell factor
KLK7	0.806	SCCE; PRSS6	NM_139277	kallikrein 7 (chymotryptic, stratum corneum)
NOX5	0.806	NOX5A; NOX5B	NM_024505	NADPH oxidase, EF-hand calcium binding domain 5
COL13A1	0.805	COL13A1	NM_080805	collagen, type XIII, alpha 1
KARS	0.802	KARS2; KIAA0070	NM_005548	lysyl-tRNA synthetase
USP48	0.802	USP31; RAP1GA1; MGC14879; MGC132556; DKFZp762M1713	NM_001032730	ubiquitin specific peptidase 48
DNTTIP2	0.8	ERBP; TdIF2; HSU15552; LPTS-RP2; RP4-561L24.1	NM_014597	deoxynucleotidyltransferase, terminal, interacting protein 2
SEZ6	0.8	ZC3HC1	NM_178860	seizure related 6 homolog (mouse)
BTN3A3	0.799	BTF3	NM_006994	butyrophilin, subfamily 3, member A3
PTPRE	0.798	PTPE; HPTPE; DKFZp313F1310; R-PTP-EPSILON	NM_006504	protein tyrosine phosphatase, receptor type, E
FLJ45121	0.797	FLJ45121	NM_207451	FLJ45121 protein
C9ORF132	0.795	EEIG1; C9orf132; MGC50853; bA203J24.7	NM_203305	family with sequence similarity 102, member A
WDR63	0.793	FLJ30067; NYD-SP29; RP11-507C22.2	NM_145172	WD repeat domain 63
DOK4	0.793	FLJ10488	NM_018110	docking protein 4
SELO	0.792	SELO; MGC131879	NM_031454	selenoprotein O
SEZ6L2	0.785	PSK-1; FLJ90517	NM_201575	seizure related 6 homolog (mouse)-like 2
HIST1H2BJ	0.784	H2B/r; H2BFR	NM_021058	histone 1, H2bj
C3ORF34	0.782	MGC14126	NM_032898	chromosome 3 open reading frame 34
RWDD2	0.781	MGC13523; MGC138208; dJ747H23.2	NM_033411	RWD domain containing 2
SLC35A2	0.78	UGT; UGAT; UGT1; UGT2; UGTL; UGALT	NM_005660	solute carrier family 35 (UDP-galactose transporter), member A2
PPFIA3	0.777	LPNA3; KIAA0654; MGC126567; MGC126569	NM_003660	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3
C14ORF28	0.774	DRIP1; c14_5270	NM_001017923	chromosome 14 open reading frame 28
CARS	0.773	CYSRS; MGC:11246	NM_001751	cysteinyl-tRNA synthetase
ACADS	0.772	SCAD; ACAD3	NM_000017	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain
GRHL3	0.771	SOM; TFCP2L4; MGC46624	NM_021180	grainyhead-like 3 (Drosophila)
PPM1F	0.771	FEM-2; POPX2; hFEM-2; CaMKPase; KIAA0015	NM_014634	protein phosphatase 1F (PP2C domain containing)
CYP51A1	0.768	LDM; CP51; CYP51; CYPL1; P450L1; P450-14DM	NM_000786	cytochrome P450, family 51, subfamily A, polypeptide 1
KRT17	0.768	PC; K17; PC2; PCHC1	NM_000422	keratin 17
KCTD13	0.767	PDIP1; FKSG86; POLDIP1	NM_178863	potassium channel tetramerisation domain containing 13
LOC196463	0.766	LOC196463	NM_173542	hypothetical protein LOC196463
SLC25A20	0.766	CAC; CACT	NM_000387	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
C1ORF33	0.766	dJ657E11.4	NM_016183	chromosome 1 open reading frame 33
ADC	0.765	ODC-p; ODC1L; KIAA1945	NM_052998	arginine decarboxylase
EGFL6	0.762	W80; MAEG; DKFZp564P2063	NM_015507	EGF-like-domain, multiple 6
CRI1	0.761	EID1; EID-1; RBP21; PTD014; C15orf3; PNAS-22; IRO45620; MGC138883; MGC138884	NM_014335	CREBBP/EP300 inhibitor 1
WDR23	0.759	GL014; PRO2389; DKFZp779A1629	NM_025230	WD repeat domain 23
ZDHHC24	0.759	ZDHHC24	NM_207340	zinc finger, DHHC-type containing 24
PNKD	0.755	MR1; PDC; DYT8; FPD1; MR-1; BRP17; FKSG19; TAHCCP2; KIAA1184; KIPP1184; MGC31943; DKFZp564N1362	NM_022572	paroxysmal nonkinesiogenic dyskinesia
CPA4	0.755	CPA3	NM_016352	carboxypeptidase A4
C1ORF24	0.755	C1orf24	NM_022083	synonyms: NIBAN, FLJ38228; isoform 2 is encoded by transcript variant 2; cell growth inhibiting protein 39; Homo sapiens chromosome 1 open reading frame 24 (C1orf24), transcript variant 2, mRNA.
POU2F3	0.754	OCT11; PLA-1; Epoc-1; Skn-1a; FLJ40063; MGC126698	NM_014352	POU domain, class 2, transcription factor 3
RRAD	0.751	RAD; RAD1; REM3	NM_004165	Ras-related associated with diabetes
KIAA1324	0.75	RP11-352P4.1	NM_020775	KIAA1324
BICD2	0.748	KIAA0699; bA526D8.1	NM_001003800	bicaudal D homolog 2 (Drosophila)
HTR3A	0.747	HTR3; 5HT3R; 5-HT-3; 5-HT3A; 5-HT3R	NM_000869	5-hydroxytryptamine (serotonin) receptor 3A
ABCA8	0.747	KIAA0822	NM_007168	ATP-binding cassette, sub-family A (ABC1), member 8
C1ORF83	0.742	FLJ32112; FLJ39169; RP4-758J24.3	NM_153035	chromosome 1 open reading frame 83
UPF3B	0.735	UPF3X; HUPF3B; RENT3B	NM_080632	UPF3 regulator of nonsense transcripts homolog B (yeast)
PRKCB1	0.73	PKCB; PRKCB; PRKCB2; MGC41878; PKC-beta	NM_212535	protein kinase C, beta 1
RIPK5	0.723	RIP5; DustyPK; HDCMD38P; KIAA0472	NM_015375	receptor interacting protein kinase 5
KLHL13	0.721	BKLHD2; FLJ10262; KIAA1309; MGC74791	NM_033495	kelch-like 13 (Drosophila)
GDF6	0.719	CDMP2	NM_001001557	growth differentiation factor 6
HSD17B2	0.714	HSD17; EDH17B2	NM_002153	hydroxysteroid (17-beta) dehydrogenase 2
ARL3	0.711	ARFL3	NM_004311	ADP-ribosylation factor-like 3
GSTM5	0.711	GTM5; GSTM5-5	NM_000851	glutathione S-transferase M5

NOXO1	0.709	P41NOX; P41NOXA; P41NOXB; P41NOXC; SH3PXD5; MGC20258	NM_144603	NADPH oxidase organizer 1
NUDT6	0.707	gfg; bFGF; FGF-2; gfg-1; ASFGF2; FGF-AS; FGF2AS	NM_198041	nudix (nucleoside diphosphate linked moiety X)-type motif 6
RAB11FIP4	0.707	FLJ00131; KIAA1821; MGC11316; MGC126566; RAB11-FIP4	NM_032932	RAB11 family interacting protein 4 (class II)
CD36	0.702	FAT; GP4; GP3B; GPIV; PASIV; SCARB3	NM_001001548	CD36 molecule (thrombospondin receptor)
APS	0.702	APS	NM_020979	SH2B adaptor protein 2
PTGER1	0.7	EP1	NM_000955	prostaglandin E receptor 1 (subtype EP1), 42kDa
CRH	0.7	CRF	NM_000756	corticotropin releasing hormone
AHNAK	0.699	AHNAKRS; MGC5395	NM_024060	AHNAK nucleoprotein (desmoyokin)
STARD8	0.698	KIAA0189; DKFZp686H1668	NM_014725	START domain containing 8
FLJ10260	0.692	SLFN3; FLJ10260	NM_018042	schlafen family member 12
APBB1IP	0.69	RIAM; INAG1; PREL1; RARP1	NM_019043	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein
MGC31967	0.689	MGC31967; RP11-331F9.6	NM_174923	coiled-coil domain containing 107
SERPING1	0.688	C1IN; C1NH; HAE1; HAE2; C1INH	NM_000062	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)
RARRES3	0.687	RIG1; TIG3; HRASLS4; MGC8906	NM_004585	retinoic acid receptor responder (tazarotene induced) 3
C4ORF18	0.685	AD021; AD036; FLJ38155; DKFZp434L142	NM_016613	chromosome 4 open reading frame 18
TGFB1I1	0.684	HIC5; ARA55; HIC-5; TSC-5	NM_015927	transforming growth factor beta 1 induced transcript 1
ETV1	0.684	ER81; MGC104699; MGC120533; MGC120534; DKFZp781L0674	NM_004956	ets variant gene 1
ATG4A	0.679	APG4A; AUTL2	NM_052936	ATG4 autophagy related 4 homolog A (S. cerevisiae)
IL11RA	0.677	MGC2146	NM_004512	interleukin 11 receptor, alpha
C1ORF116	0.677	SARG; MGC2742; MGC4309; FLJ36507; DKFZp666H2010	NM_023938	chromosome 1 open reading frame 116
CNN1	0.674	SMCC; Sm-Calp	NM_001299	calponin 1, basic, smooth muscle
SYAP1	0.666	PRO3113; FLJ14495; FLJ44185; DKFZp686K221	NM_032796	synapse associated protein 1, SAP47 homolog (Drosophila)
DOC1	0.664	DOC1; GIP90	NM_182909	downregulated in ovarian cancer 1
MYL9	0.663	LC20; MLC2; MRLC1; MYRL2; MGC3505	NM_006097	myosin, light polypeptide 9, regulatory
MEIS2	0.659	MRG1; MGC2820; HsT18361	NM_020149	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)
C20ORF18	0.654	XAP4; RBCK2; RNF54; ZRANB4; C20orf18; UBCE7IP3	NM_006462	RanBP-type and C3HC4-type zinc finger containing 1
TNFRSF10A	0.652	DR4; APO2; CD261; MGC9365; TRAILR1; TRAILR-1	NM_003844	tumor necrosis factor receptor superfamily, member 10a
GSTM3	0.652	GST5; GSTB; GTM3; GSTM3-3; MGC3310; MGC3704	NM_000849	glutathione S-transferase M3 (brain)
F2RL2	0.652	PAR3	NM_004101	coagulation factor II (thrombin) receptor-like 2
FBXO32	0.645	Fbx32; MAFbx; ATROGIN1; FLJ32424; MGC33610	NM_148177	F-box protein 32
DKFZP686A01247	0.643	DKFZP686A01247; MGC72127; DKFZp434I0312; DKFZp686B2470; DKFZp686G2094; DKFZp781C1754; DKFZp781I1455; DKFZp686A01247; DKFZp686G18243	NM_014988	hypothetical protein
PTGDS	0.638	PDS; PGD2; PGDS; PGDS2	NM_000954	prostaglandin D2 synthase 21kDa (brain)
FLI1	0.637	EWSR2; SIC-1	NM_002017	Friend leukemia virus integration 1
AMPD3	0.633	DUT	NM_001025389	adenosine monophosphate deaminase (isoform E)
CDKN1A	0.629	P21; CIP1; SDI1; WAF1; CAP20; CDKN1; MDA-6; p21CIP1	NM_078467	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GNA15	0.628	GNA16	NM_002068	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
HEXA	0.626	TSD; MGC99608	NM_000520	hexosaminidase A (alpha polypeptide)
ACPP	0.626	PAP; ACP3; ACP-3	NM_001099	acid phosphatase, prostate
CFH	0.616	FH; HF; HF1; HF2; HUS; FHL1; CFHL3; MGC88246	NM_001014975	complement factor H
BHMT2	0.615	FLJ20001	NM_017614	betaine-homocysteine methyltransferase 2
AK5	0.612	AK6; MGC33326	NM_174858	adenylate kinase 5
ATP1B2	0.609	AMOG	NM_001678	ATPase, Na+/K+ transporting, beta 2 polypeptide
IDS	0.607	MPS2; SIDS	NM_000202	iduronate 2-sulfatase (Hunter syndrome)
HOXA10	0.605	PL; HOX1; HOX1H; HOX1.8; MGC12859	NM_153715	homeobox A10
ELLS1	0.604	Ells1; FLJ25903	NM_152793	chromosome 7 open reading frame 41
PTMA	0.602	TMSA; MGC104802	NM_002823	prothymosin, alpha (gene sequence 28)
DOC1	0.601	DOC1; GIP90	NM_014890	downregulated in ovarian cancer 1
AHNAK	0.598	AHNAKRS; MGC5395	NM_024060	AHNAK nucleoprotein (desmoyokin)
MYEOV	0.597	OCIM	NM_138768	myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas)
LRP10	0.597	LRP9; MST087; MGC8675; MSTP087; MGC142274; MGC142276; DKFZP564C1940	NM_014045	low density lipoprotein receptor-related protein 10
COL11A1	0.595	STL2; COLL6; CO11A1	NM_080629	collagen, type XI, alpha 1
A4GALT	0.592	P1; PK; A14GALT; A4GALT1	NM_017436	alpha 1,4-galactosyltransferase (globotriaosylceramide synthase)
IL6ST	0.592	CD130; GP130; CDw130; IL6R-beta; GP130-RAPS	NM_002184	interleukin 6 signal transducer (gp130, oncostatin M receptor)
C9ORF89	0.589	BinCARD; MGC11115;	NM_032310	chromosome 9 open reading frame 89

		MGC110898; bA370F5.1		
TGM2	0.578	TG2; TGC	NM_198951	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
TRPM4	0.578	TRPM4B; FLJ20041	NM_017636	transient receptor potential cation channel, subfamily M, member 4
BMP1	0.577	PCP; TLD; PCOLC; FLJ44432	NM_006129	bone morphogenetic protein 1
ABCC3	0.574		NM_020037	
PTPRN	0.566	IA2; IA-2; ICA512; R-PTP-N; FLJ16131; IA-2/PTP	NM_002846	protein tyrosine phosphatase, receptor type, N
NRG1	0.557	GGF; HGL; HRG; NDF; ARIA; GGF2; HRG1; HRGA; SMDF	NM_013960	neuregulin 1
H2AFY	0.542	H2A.y; H2A/y; H2AFJ; mH2A1; H2AF12M; MACROH2A1.1; macroH2A1.2	NM_138609	H2A histone family, member Y
ATP2B4	0.537	MXRA1; PMCA4; ATP2B2; DKFZp686M088; DKFZp686G08106	NM_001684	ATPase, Ca++ transporting, plasma membrane 4
SGCE	0.526	ESG; DYT11	NM_003919	sarcoglycan, epsilon
MYO1D	0.518	myr4; KIAA0727	NM_015194	myosin ID
ALCAM	0.517	MEMD; CD166; FLJ38514; MGC71733	NM_001627	activated leukocyte cell adhesion molecule
TICAM1	0.515	TRIF; PRVTIRB; TICAM-1; MGC35334	NM_182919	toll-like receptor adaptor molecule 1
IL1A	0.513	IL1; IL-1A; IL1F1; IL1-ALPHA	NM_000575	interleukin 1, alpha
STAT1	0.495	ISGF-3; STAT91; DKFZp686B04100	NM_139266	signal transducer and activator of transcription 1, 91kDa
FLJ90166	0.493	FLJ90166; MGC126807; MGC126809; RP4-685L9.2	NM_153360	adenomatosis polyposis coli down-regulated 1-like
CEECAM1	0.474	CerCAM; GLT25D3; MGC149620; MGC149621	NM_016174	cerebral endothelial cell adhesion molecule 1
IL24	0.471	C49A; FISP; MDA7; ST16; IL-24; IL10B; Mob-5; mda-7	NM_006850	interleukin 24
DHRS3	0.461	SDR1; RDH17; Rsdr1; retSDR1	NM_004753	dehydrogenase/reductase (SDR family) member 3
JAK1	0.46	JAK1A; JAK1B	NM_002227	Janus kinase 1 (a protein tyrosine kinase)
DEGS1	0.457	MLD; DEGS; DES1; Des-1; FADS7; MIG15; MGC5079	NM_003676	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)
NRP1	0.447	NRP; CD304; VEGF165R; DKFZp781F1414; DKFZp686A03134	NM_001024629	neuropilin 1
HSDL2	0.426	C9orf99; FLJ25855; MGC10940	NM_032303	hydroxysteroid dehydrogenase like 2
COMT	0.417	COMT	NM_000754	catechol-O-methyltransferase
DFNA5	0.407	ICERE-1	NM_004403	deafness, autosomal dominant 5
THRA	0.404	AR7; EAR7; ERBA; ERBA1; NR1A1; THRA1; THRA2; THRA3; EAR-7.1; EAR-7.2; ERB-T-1; MGC43240; c-ERBA-1; MGC000261; ERBA-ALPHA; TR-ALPHA-1; c-ERBA-ALPHA-2	NM_003250	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)
GPR177	0.401	MRP; WLS; C1orf139; FLJ23091; MGC14878; MGC131760	NM_024911	G protein-coupled receptor 177
LIMA1	0.395	EPLIN; SREBP3; MGC131726	NM_016357	LIM domain and actin binding 1
LOC388610	0.381	LOC388610	NM_001013642	hypothetical LOC388610
ECM1	0.368	ECM1	NM_004425	extracellular matrix protein 1
S100A4	0.359	42A; 18A2; CAPL; MTS1; P9KA; PEL98	NM_002961	S100 calcium binding protein A4
S100A4	0.358	42A; 18A2; CAPL; MTS1; P9KA; PEL98	NM_002961	S100 calcium binding protein A4
FAP	0.351	FAPA; DPPIV; SEPRASE; DKFZp686G13158	NM_004460	fibroblast activation protein, alpha
EDG2	0.346	LPA1; LPAR1; edg-2; vzg-1; Gpcr26; Mrec1.3; rec.1.3	NM_001401	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
CCL20	0.333	CKb4; LARC; ST38; MIP3A; MIP-3a; SCYA20	NM_004591	chemokine (C-C motif) ligand 20
SPARC	0.333	ON	NM_003118	secreted protein, acidic, cysteine-rich (osteonectin)
TGM2	0.313	TG2; TGC	NM_004613	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
HS3ST3A1	0.29	30ST3A1; 3OST3A1	NM_006042	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1
CASP4	0.228	TX; ICH-2; Mih1/TX; ICEREL-II; ICE(rel)II	NM_033306	caspase 4, apoptosis-related cysteine peptidase