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Transcriptional Regulation of Hematopoietic Differentiation

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Transcriptional Regulation of Hematopoietic Differentiation

By

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Abstract

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Gene expression is critical for the development, patterning, and homeostasis of the organism. Precise temporal and spatial regulation of gene expression at the level of transcription requires a large network of sequence-specific factors, general transcription factors, co-factors, and epigenetic regulators. Malignancies of specific tissues often arise from perturbation of various gene expression levels. Hematopoiesis is one of the most sensitive biological processes to mis-regulation of transcription. To generate all blood cell types from embryonic development throughout the lifetime of the organism, hematopoiesis requires an intricate balance between the maintenance of a permanent stem cell pool and differentiation of multi-potent stem cells into cell types with unique functions. To generate a terminally differentiated, functional immune cell, multiple lineage-restricting steps are involved, with each governed by a specific transcription program. Therefore, gene expression regulation in hematopoietic differentiation is particularly important for an organism to properly develop, maintain oxygen transport to all tissues, and fight against infections. Furthermore, because of detailed understanding of how to isolate cells at different stages and lineages of hematopoietic differentiation, it provides an important model to study the development and differentiation of other adult tissues.

Hematopoietic stem cells can be driven to differentiate along three main lineages: myeloid, erythroid, and lymphoid. Despite the discoveries of several transcription factors for specific lineages of hematopoietic differentiation, understanding the gene expression program that allow stem cells to make the decision to initiate lymphoid development still remains incomplete. For example, how is the preinititation complex of transcription (PIC) recruited to the gene promoters? Additionally, how are interactions, if any, coordinated among various sequence-specific factors that were identified via gene-by-gene knockout (KO) approaches?

To form the PIC at any gene promoter, transcription factor (TF) IIA, B, D, E, F, and H, and RNA polymerase II (Pol II) must coordinate their promoter-binding and enzymatic activities. TFIID, especially, is important for promoter recognition. As a multi-subunit complex containing TATA-box binding protein (TBP) and 13-14 TBP-associated factors (TAFs), TFIID binds to sequences in the proximal promoter and allows the recruitment of other TFs and Pol II. Previously thought to be invariant from one cell type to another, recently tissue-specific roles for certain TAFs have

been uncovered. TAF4B is one of the first TAFs found to have cell-specific expression, since it was identified in human B cells {Dikstein:1996wk}, though a role for its function in hematopoiesis has remained elusive. I used a *Taf4b* KO mouse line to study its function in both myeloid and lymphoid differentiation. I found that *Taf4b* KO mice were able to generate myeloid and lymphoid progenitors as well as their wild-type (WT) littermates. Furthermore, both of these types of progenitors from *Taf4b* KO mice can terminally differentiate into mature cells as well as those from WT mice. Finally, TAF4B-null cells are as competent as heterozygous cells (equivalent to WT in terms of *Taf4b* expression) to reconstitute the hematopoietic compartment of lethally irradiated mice in all cell lineages tested. In conclusion, TAF4B is dispensable in both myeloid and B cell differentiation. This could be due to TAF4B's high sequence homology with TAF4A. Alternatively, TAF4B can play a role in fine-tuning expression levels of certain B cell or myeloid-specific genes, together with another transcription factor, which cannot be uncovered in a KO mouse approach. I have made a TAF4B-specific polyclonal antibody that can be used to identify its transcriptional targets, as well as identify any potential interaction partners.

Though the basal machinery does not seem to play a role in hematopoietic lineage determination, sequence-specific factors have long been implicated in this process. A study using an inducible hematopoietic-specific KO mouse line found that myocyte enhancer factor 2c (MEF2C) is necessary for multi-potent progenitors to differentiate into the lymphoid lineage {StehlingSun:2009df}. Through a candidate approach, I have identified early B cell factor 1 (EBF1) to be a specific interacting partner of MEF2C. Together, they co-occupy and functionally co-activate many B cell specific genes. When MEF2C is depleted in mice, the animals had reduced B cell gene expression as well as increased myeloid gene expression, consistent with MEF2C's role as a lineage fate regulator. I have identified and confirmed several B cell-specific genes that are co-regulated by EBF1 and MEF2C through a genome-wide survey of their binding via chromatin immunoprecipitation followed by exonuclease treatment and deep-sequencing (ChIP-exo). Furthermore, I found that p38 MAPK is the pathway through which MEF2C is phosphorylated and activated to drive B cell differentiation. When phosphorylated, MEF2C prefers to bind its co-activator EBF1, and not its co-repressor HDAC7. Taken together, the results presented in this thesis elucidated the mechanism of activation, binding partners, and downstream targets by which MEF2C is able to regulate lymphoid-specific differentiation. This study contributes to understanding how transcriptional regulation of genes can drive progenitor cells to differentiate down a particular lineage, and provide a novel mechanism for a transcription repressor to switch to an activator during cellular differentiation.

This dissertation is dedicated to my parents

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For making me who I am and always believing in me

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Chapter 1

General Introduction

1.1 Initiation of eukaryotic transcription

Mammalian gene expression is one of the most crucial means of regulating the amount of each protein in a cell, which in turn is critical to the development, patterning, and homeostasis of the organism. Therefore, gene expression is modulated at several levels, including transcription initiation, post-transcriptional processing, and mRNA degradation. Precise temporal and spatial regulation of transcription requires several large multimeric protein complexes and many factors that were purified, identified, and characterized both biochemically and genetically. Three decades of research from the discovery of the first DNA-binding factor {Tjian:1978ul}-ERROR to the elucidation of many aspects of its initiation mechanisms (see references below), transcription modulation has remained the best-characterized process in gene expression control, and yet a continued source of surprising discoveries.

TFIID and promoter recognition

For transcription to initiate at a given locus, a preinitiation complex (PIC) has to assemble at the core promoter of the gene, which includes the general transcription factors (GTFs) TFIIA, B, D, E, F, and H, and RNA polymerase II (Pol II) (Figure 1.1.1). Promoter recognition is largely mediated by the TFIID complex, composed of the TATA-binding protein (TBP) and 13 to 14 Tbp-associated factors (TAFs). At TATA-containing promoters, TBP recognizes and binds the TATA-box upstream of the transcription start site (TSS) and allows the recruitment of other GTFs and Pol II. In addition to TBP binding, metazoan TAFs also recognize and bind conserved sequences in the promoters: TAF1 and TAF2 bind the Initiator (INR) {Verrijzer:1995wh}-ERROR {Smale:1989uv}-ERROR {Chalkley:1999gz}-ERROR, and TAF6 and TAF9 bind the downstream promoter elements (DPE) {Burke:1996uk}-ERROR (reviewed in {JuvenGershon:2010hg}-ERROR), which is thought to be especially important for TATA-less promoters to help focusing the site of transcription initiation by positioning the TFIID complex (reviewed in {Naar:2001dx}-ERROR {Roeder:1996um}-ERROR). Additionally, some TAFs possess enzymatic activities such as TAF1, which has histone acetyltransferase and kinase activities, the former function contributing to the formation of open chromatin and gene activation {Mizzen:1996wm}-ERROR {Dikstein:1996wk}-ERROR. Other TAFs help to integrate signals from sequence-specific transcription factors with the core promoter {Goodrich:1993wz}-ERROR (see section 1.2 below), such as Drosophila TafII40 and TafII60, which are able to bind p53 and drive p53-dependent transcription of cell proliferation genes (Tjian 1978; Thut et al. 1995).

Other GTFs and Pol II

In addition to TFIID, TFIIA, B, E, F, and H are also required to assemble the PIC along with Pol II (Figure 1.1.1), and these purified components are sufficient to activate transcription in *in vitro* transcription assays using naked DNA as a template. Works of many labs have

shown that TFIIA facilitates TFIID binding to the promoter, TFIIB bridges TFIID with Pol II, while a pre-bound factor with Pol II, TFIIF, modulates Pol II's promoter-specificity (reviewed in (Verrijzer et al. 1995; Roeder 1996)). TFIIH binds to the specific strand to be transcribed and uses its helicase activity for DNA melting at the promoter. TFIIE may also be involved in DNA melting and is essential for TFIIH to be able to unwind the promoter. This step signals for the complete assembly of the PIC and for Pol II to begin transcription. Furthermore, TFIIH contains kinase activity that is important in Pol II C-terminal domain (CTD) serine 5 phosphorylation for it to subsequently clear the promoter region and continue onto the elongation phase of transcription (reviewed in (Smale and Baltimore 1989; Svejstrup et al. 1996).

Beside recruitment and promoter clearance, the multi-subunit Pol II is also regulated by promoter-proximal pausing. Recent data have shown that pausing is accomplished through negative elongation factor (NELF) and DRB-sensitivity inducing factor (DSIF) complexes (DRB is 5,6-dichloro-1-β-D-ribofuranosylbenzimidazole, which inhibits RNA synthesis). This pausing needs to be alleviated by positive transcription elongation factor (P-TEFb) through its kinase activity on both DSIF and serine 2 of the Pol II CTD (Chalkley and Verrijzer 1999; Ping and Rana 2001). While transcribing, Pol II is further prevented from pausing by TFIIS and its associated factor TFIIF (Burke and Kadonaga 1996; Ishibashi et al. 2014). The CTD of Pol II is also involved in mRNA capping and splicing (reviewed in (Juven-Gershon and Kadonaga 2010; Kornblihtt et al. 2004)).

Mediator complex and co-activators

GTFs and Pol II are recruited to the promoter by sequence-specific transcription activators through adaptor proteins (co-activators), among which the most extensively characterized is the multi-protein complex, Mediator (MED). Originally discovered in the yeast in fraction that stimulate transcription assays (Näär et al. 2001; Kim et al. 1994), the MED complex contains SRB (suppressor of polymerase B) proteins and MED proteins (together termed SMCC), in addition to others. Though human SMCC cannot interact with Pol II CTD directly like the murine and yeast complexes, it still promotes CTD phosphorylation (reviewed in (Roeder 1996; Näär et al. 2001)). Other Mediator and Mediator-like co-activator complexes have since been identified that interact with diverse factors. For example a smaller co-activator complex CRSP is required for the activity of the sequence-specific transcription factor Sp1(Mizzen et al. 1996; Ryu and Tjian 1999) (Dikstein et al. 1996; Ryu et al. 1999), after which it was named. Other co-activator complexes were found to act at the level of the chromatin such as the ARC complex (Goodrich et al. 1993; Näär et al. 1999). Recently Mediator complex has been shown to interact with the Cohesin complex to reshape the chromatin landscape by inducing DNA looping and thus transcription activation (Kagey et al. 2010).

Epigenetic factors and nucleosome remodelers

To compact DNA in the nucleus, chromatin is formed by organizing genomic DNA around nucleosomes that are each an octamer of four core histone proteins. This tight compaction of DNA on the nucleosome poses a challenge for transcription factor binding. To allow access to the promoter, nucleosomes require repositioning, loosening or eviction, which is

often facilitated by covalent modifications of the histones and/or ATP-dependent chromatin remodeling factors. This forms another level of regulation for gene expression. Many eukaryotic proteins have been found to play important roles in remodeling and modifying histones, including ATPases such as the SWI/SNF remodeling complex and histone acetylation complexes such as CBP/p300, respectively.

SWI/SNF, originally identified genetically in yeast as required for active chromatin structure, uses ATP hydrolysis to disrupt the histone-DNA interactions and slide nucleosomes along the DNA molecule (reviewed in (Peterson 1996) (Sudarsanam and Winston 2000)). The other form of epigenetic regulation involves covalent modifications that range from methylation, acetylation, phosphorylation, to sumoylation of either the histone tail or its lateral surface. Histone acetylation has long been linked to gene activation with the identification of GCN5, a component of co-activator complex SAGA, which possesses histone acetylation activity (HAT) (reviewed in (Armstrong and Emerson 1998) (Smith and Shilatifard 2010)). Conversely, removal of acetyl moieties is associated with gene repression, facilitated by histone deacetylases (HDAC) such as Rpd3, the first to be purified (Taunton et al. 1996) (reviewed in (Hassig and Schreiber 1997)). Furthermore, HDACs and the associating co-repressors, SIN3A, have been implicated in gene repression in many developmental processes, such as hematopoiesis, where they are recruited by IKAROs to repress lineage-specific genes (Koipally et al. 1999). Histone methylation has been linked to either gene activation or repression depending on the specific tail residues where it occurs, which is then interpreted by the appropriate "reader", e.g. HP1 protein recognizes H3K9 methylation in promoting heterochromatin spreading and gene repression maintenance (Bannister et al. 2001) (Lachner et al. 2001) (reviewed in (Smith and Shilatifard 2010)). Whether histone modifications are drivers or simply cogs in transcription regulation has been the subject of much debate (Henikoff and Shilatifard 2011). Recently, data supporting the former notion started to emerge. For example, it has been shown that acetylation of a lateral residue, H3K64, actively facilitates the eviction of nucleosomes and results in gene activation (Di Cerbo et al. 2014).

Recently, a group of transcription factors (TF) termed pioneer factors have been discovered that can bind target sequences even if they are embedded in the chromatin and contribute to chromatin accessibility (reviewed in (Zaret and Carroll 2011)). For example, one such pioneer factor GATA2 is involved in androgen-responsive gene transcription in prostate cancers. Before androgen stimulation, GATA2 can already bind androgen-responsive gene enhancers. Then it can recruit p300 HAT to produce an open chromatin conformation, as well as maintain enhancer/promoter contact via binding with MED1 protein (Wu et al. 2014). Once DNA that needs to be accessed is exposed, other sequence-specific TFs are able to bind. One of the earliest identified eukaryotic transcription factors is SP1, which recognizes GC-rich sequences in the SV40 early promoter (Dynan and Tjian 1983). This discovery has since led to the identification of many more TFs either ubiquitous or playing tissue-specific and developmental stage-specific roles in the organism. These factors in turn, with the help of co-activators such as the Mediator complex, can bring TFIID and Pol II to the promoter, thereby initiating transcription.

1.2 Tissue-specific TAFs

TFIID was originally thought to play non-specific roles in transcription in facilitating the assembly of PIC at the promoter of all genes, thereby TAFs were believed to be ubiquitous factors. However, recent data have pointed to tissue- and gene-specific roles for these proteins in several developmental processes.

TAF4B

Purified from differentiated human B cell lines, TAF4B (previously termed TAFII105) was found to share a high sequence conservation with the C-terminal half of TAF4A (previously termed TAFII130) (Dikstein et al. 1996). Despite its involvement in B cell specific octamer-dependent transcription activation along with OCA-B protein (Wolstein et al. 2000), a role for TAF4B in B cell development and differentiation had been elusive (Freiman et al. 2002), presumably due to its high sequence similarity and thus possible functional redundancy with TAF4A. However, it was later shown that TAF4B plays a crucial role in germ cells, as older (3 months) *Taf4b* KO male mice become infertile due to the depletion of spermatogonial stem cells (Falender et al. 2005), and *Taf4b* KO female mice lack mature follicles and have impaired ovarian granulose cell proliferation that also result in infertility (Freiman et al. 2001) (Voronina et al. 2007) (reviewed in (Goodrich and Tjian 2011)).

TAF3

When it was first purified, TAF3 (previously TAFII 140) was found to contain a plant homeo domain (PHD) finger that marks it as a potential "reader" of H3K4me3 modification (Gangloff et al. 2001), which was later confirmed (Vermeulen et al. 2007). Together with TBP-related factor 3 (TRF3), TAF3 was found to be both important in muscle differentiation in mice to activate *Myogenin* expression in myotubes (Deato and Tjian 2007), and hematopoiesis in zebrafish, as it is required for *mespa* expression (Hart et al. 2009). More recently, TAF3 was discovered to play a crucial role in mouse embryonic stem cells, wherein it is necessary for endodermal lineage differentiation by interacting with CTCF and promoting DNA looping between distal cis-elements and promoters of key endodermal genes (Liu et al. 2011).

TAF7L

A paralog of TAF7, TAF7L has been shown to play a role in male germ cell development. *Taf7l* KO mice have sperms with folded tails and decreased motility (Cheng et al. 2007). More recently, Zhou et al. have shown that *Taf7l* KO mice have compromised adipocyte differentiation and specifically, less white fat tissue (WAT), because TAF7L cooperates with the key adipocyte transcription factor, PPARγ to activate adipocyte-specific genes (Zhou et al. 2013). Additionally, ectopic TAF7L can transdifferentiate myoblast into the adipocyte cell lineage, further supporting its function in fat tissue development.

Many other TAFs have been shown to play tissue-specific roles such as TAF10 in liver development (reviewed in (Goodrich and Tjian 2011)). Others have been shown to play roles in gene-specific activation, such as TAF3 in p53-dependent transcription regulation

through its interaction with H3K4me3 (Lauberth et al. 2013). The discovery of novel, specific roles for TAFs have debunked their previously held image of general transcription factors as a part of an invariant TFIID. With the advent of deep-sequencing, CRISPR (clustered regularly interspaced short palindromic repeats)/Cas9 or TALEN (transcription activator-like effector nuclease) gene targeting approaches, previously unobserved functions for these factors will start to emerge, where they could be key to fine-tune the exact levels of gene expression in the cell, thereby conferring it specific biological functions. Transcriptional control by either TAFs or sequence-specific TFs are important in all tissues, one of the best studied is the development of mammalian blood cells, or the process of hematopoiesis.

1.3 Mammalian hematopoiesis

Hematopoiesis is the process that generates all blood cell types throughout the lifetime of an animal. From oxygen transport to innate immunity, the enormous number of blood cells have many distinct functions, representing several different cell lineages (reviewed in (Rieger and Schroeder 2012)). Both embryonic and adult hematopoiesis require the proliferation and differentiation of multi-potent cells, the hematopoietic stem cells (HSCs).

Hematopoietic stem cells

HSCs were functionally defined in the 1960s in elegant experiments conducted by Till and McCulloch. They generated random chromosomal markers in bone marrow cells by irradiation. After introducing these cells intravenously into irradiated recipient mice, they found the clonal progeny of the donor cells proliferating in the spleen of the recipient (colony-forming unit-spleen, CFU-S), distinguishable by the very same chromosomal markers (TILL and McCULLOCH 1961). Since those experiments, decades of research have established HSCs as the best-characterized adult stem cells.

In the developing animal, mesodermal lineage-derived blood cells are not present until the embryo becomes too large for free diffusion of oxygen to sustain life. The first wave of transient blood cell production occurs in the yolk sac to generate primitive erythrocytes (embryonic day 7, or E7) and CFU-S (E8.5) (Moore and Metcalf 1970). These erythrocytes are distinct from their counterparts in adults as they retain their nuclei as well as express fetal hemoglobin (Rieger and Schroeder 2012). The second wave of definitive hematopoiesis occurs autonomously in the aorta-gonads-mesonephros (AGM) region surrounding the dorsal aorta to generate adult-like HSCs (E10) (Medvinsky et al. 1993). These intra-embryonically generated HSCs colonize the fetal liver by E11.5 to proliferate and expand, then migrate to other secondary blood tissues such as the spleen and the bone marrow around birth, where a permanent reservoir of HSCs is maintained in the adult animal (reviewed in (Rieger and Schroeder 2012) and (Durand and Dzierzak 2005)).

Adult HSCs are rare clonal progenitors that are stringently defined by three hallmarks: (1) able to differentiate into all blood cells, (2) have long-term proliferation and engraftment potential in an irradiated recipient, and (3) self-renew as shown by *in vivo* serial

transplantation, wherein the same engrafted cells can be transplanted to the next animal (Durand and Dzierzak 2005). Many labs have contributed to the molecular characterization of these cells. Notably, the discovery of cell surface markers coupled with the invention of fluorescence activated cell sorting (FACS) (Fulwyler 1965; Hulett et al. 1969) have made possible the isolation of HSCs, as well as progenitors and subsequent differentiated cell lineages. HSCs are devoid of lineage markers that are present on the cell surface of B cells, T cells, macrophages, granulocytes, natural killer (NK) cells, and erythrocytes. This first negative selection results in a pool of heterogeneous progenitors termed lineage negative (Lin-) cells. Mouse HSCs are further positive for Sca1 (Ly6A/E) and c-kit receptor tyrosine kinase. Only 30 of these Lin-/c-Kit+/Sca1+ (LKS) cells are sufficient to fully rescue the blood compartment in 50% of lethally irradiated mice (Spangrude et al. 1988) (Ikuta and Weissman 1992). In the LKS population, three subgroups of progenitor cells were further purified with the aid of SLAM family of markers (CD150, CD48, CD 229, and CD244) (Oguro et al. 2013): long-term (LT) HSCs that are largely quiescent—only 4% of these cells are in the cell cycle at any given time; short-term (ST) HSCs derived from LT-HSCs; and multipotent progenitors (MPPs) derived from ST-HSCs (Morrison et al. 1997). Human HSCs are not as well defined molecularly as their murine counterpart, due to more difficult experimentation. However, recent data have shown that CD34, CD90, and CD49f are all specific human HSC markers that could demarcate these cells from MPPs (Notta et al. 2011).

Hematopoietic differentiation and lineage specification

The differentiation of LT-HSCs to MPPs constitutes the first step to make mature blood cells. Downstream of MPPs, one of the first lineage-restricted progenitor discovered was the common lymphoid progenitor (CLP), which has upregulated expression of interleukin 7 receptor alpha (*IL7ra)* and can give rise to B cells, T cells, and NK cells in the lymphoid lineage (Kondo et al. 1997). Shortly thereafter, the counterpart to CLP, the common myeloid progenitor (CMP), was discovered, which can give rise to megakaryocytes/erythrocytes progenitors (MEPs) or granulocyte/macrophage progenitors (GMPs) (Akashi et al. 2000). For a long time, CLPs and CMPs were thought to be the earliest branching point between lymphoid and myeloid lineages. However, recent identification of a subpopulation of MPPs has redefined this simplistic model. The new population was found to have both macrophage/granulocyte and B/T cell lineage potential. It was subsequently termed lymphoid-primed multi-potent progenitors (LMPPs), which are Flt3-positive LKS cells (Adolfsson et al. 2005). Therefore, in this revised hierarchy of hematopoietic differentiation, MPPs can further be divided into two subpopulations that have distinct molecular signatures: (1) myelo-erythroid (functionally CMPs), and (2) LMPPs that include myelo-lymphoid (Arinobu et al. 2007) and early lymphoid progenitors (ELPs, committed to the lymphoid lineage but retaining minor GMP potential) (Igarashi et al. 2002). ELPs subsequently differentiate into functional CLPs, then pro-B, pro-T, and NK cells (see Figure 1.3.1).

From this differentiation model, B cell lineage specification may seem like a successive default restriction of non-B cell fates from HSCs, however several experiments have demonstrated that this requires active myeloid program repression. First, pro-B and pro-

T cells have some myeloid potential *in vitro* (Balciunaite et al. 2005). Notably, bi-potent B-macrophage progenitors can be isolated from the murine bone marrow (Montecino-Rodriguez et al. 2001). Furthermore, the finding that fish and frog B cells have phagocytosis ability, similar to macrophages, further supports that mammalian B cells evolved from an ancestral myeloid-like cell type (Jun Li et al. 2006) and that B-lineage commitment requires active suppression of myeloid genes. To generate antibody-producing mature B cells, progenitors (pre-pro-B cells) cease proliferation, undergo DNA rearrangements of their immunoglobulin heavy chain diversity (D) and joining (J) gene segments initiated by recombination activating gene (RAG) proteins, then differentiate into pro-B cells. While still receiving IL7 signaling from the stromal cell environment, pro-B cells add the recombined variable (V) segment to the (D)J regions. Following successful V(D)J recombination and expression of the mu heavy chain, this is joined at the cell surface with a surrogate light chain (SLC), comprised of λ5 and VpreB proteins, and two heterodimers of Igα and β proteins. The pre-B cell receptor (BCR) is now complete and can signal for expansion and survival of this pre-B cell (reviewed in (Clark et al. 2014) (Clark et al. 2005)). After a checkpoint to ensure a signaling-competent mu heavy chain, pre-B cell ceases proliferation and signals for the initiation of light chain rearrangement to replace the SLC. The resulting immature B cell now has a functional BCR and migrates to the spleen where it can further differentiate, through several transitional B cell stages, into two B cell types: marginal zone B (MZ) and follicular (FO) B cells (Clark et al. 2014). Whereas both types of naïve B cells, upon meeting specific foreign antigens, will mature into antibody producing mature plasma B cells or germinal center memory B cells (Louise J McHeyzer-Williams and Michael G McHeyzer-Williams 2005), they are two distinct lineages. MZ B cells are long-living and non-circulating, residing in the MZ of the spleen and participate early in an immune response as antigen presenting cells (Flavius Martin and Kearney 2002) (Pillai and Cariappa 2009). FO B cells are recirculating and reside in secondary and tertiary lymphoid organs, the spleen and the lymph node, respectively. They can interact with T cells residing in T cell zones and partake in T cell-dependent immune responses to protein antigens, or circulate in the bone marrow and respond, independent of T cells, to blood-borne pathogens (Cariappa et al. 2007). Regulating proliferation or differentiation for B cell development is crucial because double stranded DNA breaks generated by RAG during rearrangement in the S phase will result in chromosomal translocations, genomic instability, and oncogenic transformation (Li Zhang et al. 2011).

In addition to cell surface markers that help initially identify them, stem/progenitor cells and differentiated, lineage-restricted cells are described and functionally tested through their molecule signatures, which are largely dependent on the transcription program they employ.

Transcriptional regulation of hematopoietic differentiation

Differentiation along any of the three lineages—lymphoid, myeloid, erythroid—requires an intricate coordination of signal relay and transcriptional regulation. In their bone marrow niche, HSCs self-renewal is maintained by multiple signaling pathways such as WNT, c-Kit , NOTCH, and Sonic hedgehog (SHH), and a transcription factor network that

includes the bHLH factor SCL (stem cell leukemia, or TAL1), runt-related factor RUNX1, the homeo box protein MEIS1, the LIM-domain containing LMO2, a member of the Gata-family of zinc finger transcription factors-GATA2, a paralog of SCL—LYL1, and Ets-family of transcription factors (ERG, PU.1, and FLI-1) (reviewed in (Wilkinson and Göttgens 2013)). Many of these transcription factors were discovered and functionally tested through their abilities to expand HSCs *in vitro*, gene-by-gene knockout (KO) mice, and their binding to blood-specific target genes and motifs using HPC-like cell lines (HPC-7) and chromatin immunoprecipitation (Wilson et al. 2010; Wilkinson and Göttgens 2013). KO mouse approaches have been especially fruitful to understanding the molecular mechanisms of hematopoietic differentiation since KO often block the maturation of blood cells at a specific developmental stage, which can be collected by FACS. With the exception of red blood cells, depletion of many hematopoietic cells has no major effects on the mouse, thus making this a great model system to study adult stem cells and lineage determination.

Some of these key HSC factors are important in both definitive hematopoiesis and adult HSC maintenance. For example, SCL is required to generate all blood cell types in the embryo (Porcher et al. 1996), and it also regulates HSCs quiescence and protects their long-term reservoir by inhibiting cell cycle progression from G0 to G1 phase (Lacombe et al. 2010). Other transcription factors play important roles in lineage-specific differentiation of HSCs, such as E2A proteins and their inhibitors, Id proteins. While E47, an E2A isoform, maintains stem cell quiescence by targeting p21 cell cycle regulator (Yang et al. 2008), Id3 opposes E2A proteins to orchestrate T cell development (Miyazaki et al. 2011).

During lineage specification, the fate choice between lymphoid and myeloid is controlled by a set of transcription factors considered to be "master" regulators of specific fates. PU.1 and GATA1 are each responsible for the bifurcation of the lympho-myeloid (LMPPs) and myelo-erythroid (CMPs) lineages, respectively. Both are up-regulated at the LKS stage, as shown by GFP-tagged knock-in mouse lines (Arinobu et al. 2007). *Pu.1* KO mice cannot support HSCs self-renewal and fail to generate the earliest lymphoid and myeloid progenitors, also show reduced numbers of B/T cells, granulocytes, and macrophages (Iwasaki et al. 2005). *Gata1* KO mice have arrested development of embryonic erythrocyte precursors with no red blood cells in the animal (Fujiwara et al. 1996), while *Gata1* conditional KO in megakaryocytes results in mice with reduced platelets due to over-proliferation of their megakaryocyte precursors (Shivdasani et al. 1997). PU.1 and GATA1 are mutually inhibitory since they reciprocally repress each other's DNA binding ability and thus transcription activity (Nerlov et al. 2000) (Rekhtman et al. 1999; P Zhang et al. 2000).

IKAROS zinc-finger proteins, downstream of but indirectly regulated by PU.1, are important to specify lymphoid progenitors and early B-progenitors. *Ikaros* KO mice lack all stages of B cells due to loss of *Flt3* and *Il7ra* expression in LMPPs (J H Wang et al. 1996). In order for LMPPs to differentiate into CLPs, E2A proteins (E12 and E47) and early B cell factor (EBF1) are both required (Bain et al. 1997). EBF1 especially, is critical in B cell lineage specification since its ectopic expression alone in MPPs can drive B cell

development (Zheng Zhang et al. 2003). EBF1, also known as COE (Collier-Olf-Ebf), is a member of a family of transcription factors with a novel type of zinc finger DNA-binding domain (H-X3-C-X2-C-X5-C) and helix-loop-helix (HLH) dimerization domain (Siponen et al. 2010) (Hagman et al. 1995). EBF1 is downstream of E2A proteins and can rescue the differentiation but not the proliferation defects of *E2A* KO progenitor cells (Seet et al. 2004), presumably because EBF1 is also downstream of IL7R signaling which is absent in *E2A* KO cells (Kikuchi 2005) (and reviewed in (Nutt and Kee 2007)). EBF1 activates key B cell lineage genes such as *Igll1* and *VpreB* (encoding the surrogate light chain) (H Lin and Grosschedl 1995), *CD79a* (encoding Mb1, a transmembrane signaling subunit important in preB cells) (Sigvardsson et al. 2002), and importantly the gene that encodes the paired-domain factor PAX5. While the transcription factors mentioned above are required for lymphoid, and eventually B cell, specification, PAX5 is the crucial regulator that completes the commitment to this lineage. *Pax5* KO pro-B cells cannot differentiate into mature B cells, and regain multi-lineage potential that includes myeloid and T cells (Nutt et al. 1999) (Mikkola et al. 2002).

Different aspects of this stepwise and combinatorial transcription factor network in B cell specific hematopoietic differentiation are still being unraveled, as roles for new transcription factors or new roles for well-known transcription factors are uncovered. With advances in deep sequencing that allow for whole-genome survey of protein binding (ChIP) as well as transcript analyses of small number of cells, the RNA molecules present in the cell as well as proteins responsible for their expression can be discovered. In addition, mouse genetics are no longer limited to hematopoietic lineage-specific, promoter-driven Cre recombinases to delete/knock-in different genes; genome-editing based on CRISPR /Cas9 (Ran et al. 2013) and TALENs (Sung et al. 2013) provide new and efficient genetic manipulations of multiple organisms, which in turn allows elucidation of the molecular program responsible for hematopoietic differentiation.

Open questions

Our current understanding of hematopoietic differentiation and lineage specification is based on FACS sorting of specific populations of cells that may still be very heterogeneous. Single-cell tracking of individual HSC is really the key to understand when and where a given cell makes the decision to self-renew or differentiate. For example, when the LT-HSCs are differentiating into MPPs, they might need to lose contact with specific soluble or extracellular matrix-associated ligands in their stromal environment, since it is known that HSCs can no longer self-renew once taken out of the animal. Expression level of a particular molecular marker such as the c-Kit receptor might determine whether the cell differentiates. The expression could be stochastic wherein many LT-HSCs have transient up-regulation of c-Kit, but only a few have the right amount at the right time to differentiate. On the other hand, perhaps several molecules need to be co-expressed at a precise level, such as c-Kit and Sca1. Single-cell tracking by imaging either in culture or in the animal with tagged versions of cell surface markers, stromal environment proteins, and differentiation markers would address these questions.

Single-cell resolution can also help understanding the transcription program. For example, the transcription network described above for HSC maintenance may need to be

activated in a specific sequential order. Since most of our knowledge about transcriptional regulation came from studying mRNA levels and ChIP data in bulk number of cells, single-cell PCR of sorted progenitors based on differential expression of known surface markers can address the molecular content of an HSC either at cell cycle arrest or when it is poised to differentiate. This will also contribute to gaining a hierarchy and temporal sequence of protein expression that are required for differentiation. Furthermore, a recent report showed that certain cells fates are dependent on PU.1 expression level: high PU.1 leads to macrophages, and intermediate level leads to lymphoid cell fates (DeKoter 2000). These results are debated, and the exact mechanism by which PU.1 can accomplish this finely tuned control is not known. It is easy to imagine that mixed cell populations with different expression of PU.1 may confound the observation. With the maturation of CRISPR/Cas9 gene-editing technology, it will be easier to modulate gene expression levels in these cells. *Pu.1* enhancers and its core promoter are well-studied (Y Li et al. 2001) and could be targeted for differential levels of modulation endogenously (Maeder et al. 2013). The resulting cells could be monitored individually with tagged differentiation markers or cell surface markers to determine whether they prefer one cell fate versus another.

1.4 MEF2C in muscle and hematopoiesis

Summarized in the previous section, one of the earliest lineage decisions for multi-potent hematopoietic progenitor cells is to adopt the lymphoid or myeloid fate, which is regulated at the level of gene expression. Recently, the transcription factor myocyte enhancer factor 2c (MEF2C) has been shown to be required in lymphoid-specific differentiation in this decision (Stehling-Sun et al, 2009).

MEF2C is a member of MADS-box (MCM1, Agamous, Deficiens, Serum response factor) DNA binding domain-containing family of transcription factors (J F Martin et al. 1993). It was originally identified in skeletal and cardiac muscle development, where its expression begins in the precardiogenic mesoderm that gives rise to the primitive heart tube at E7.5 of mouse development, and later in the somatic skeletal muscle precursors at E9.5, and eventually in muscle fibers throughout the embryo (Edmondson et al. 1994). Accordingly, MEF2C is required for muscle differentiation and proper heart morphogenesis. In *Mef2c*-KO mice where the DNA binding and dimerization domains were targeted, heart tube looping was incomplete and the right ventricle failed to form, resulting in impaired circulation and death by E9.5 (Q Lin et al. 1997). MEF2C has since been shown to be important in vasculature development due to failure of smooth muscle cells to differentiate and endothelial cells to organize into the vasculature (Q Lin et al. 1998). In neuronal development, MEF2C expression is sufficient to induce neurogenesis of P19 murine embryonic carcinoma cells (Skerjanc and Wilton 2000), and in nestin-conditional *Mef2c* KO mice, neural stem cells had impaired differentiation, resulting in mice with behaviors similar to human Rett-syndrome and autism (Hao Li et al. 2008). In hematopoiesis, MEF2C is the only isoform in the MEF2 family with specific expression in B cells (Swanson et al. 1998). However, it was only recently that the role of MEF2C in B cells and other blood cell lineages has been examined in several conditional knockout (KO) mice with floxed-*Mef2c* exon 2 coding for the DNA-binding and dimerization domains (Vong et al. 2005).

Vav1-Cre (after fetal liver hematopoiesis) *Mef2c* KO showed slightly decreased numbers of peripheral blood B cells in younger mice and dramatically decreased bone marrow pre-pro-B populations in mice older than 1 year (Gekas et al. 2009). Deletion of *Mef2c* at early B cell development stage with Mb1-Cre also showed a delay in this process with expression of some key B cell genes down-regulated (Debnath et al. 2013). Mx1-Cre (inducible in all hematopoietic lineages) *Mef2c* KO line showed decreased numbers of common lymphoid progenitors (CLP) and very low numbers of B cells, but increased myeloid cell numbers in reconstitution of lethally irradiated mouse bone marrow (Stehling-Sun et al. 2009). In a similar Mx1-Cre *Mef2c* KO mouse line, its role in myeloid lineage choice was examined: although MEF2C-null mice had decreased monocytic and increased granulocytic differentiation due to decreased *c-Jun* expression as observed under stressed conditions (*Irf8* KO background or cytokine-induction), very moderate difference in monocyte percentage was observed *in vivo* between *Mef2c* KO and WT mice (Schüler et al. 2008). In addition, two studies using CD19-Cre (committed B cells) *Mef2c* KO mice both showed that these animals had defects in B cell proliferation upon B cell receptor (BCR) stimulation (Khiem et al. 2008; Wilker et al. 2008). Together, these studies present evidence that MEF2C is a lineage-restricting transcription factor that directs multi-potent hematopoietic progenitors to differentiate into the B cell lineage. However, the mechanism by which MEF2C transcriptionally regulates lymphoid differentiation and the identities of its downstream targets are not known. The two CD19-Cre *Mef2c* KO studies showed conflicting mechanism for MEF2C activation: either via p38 MAPK (Khiem et al. 2008) or the calcium-dependent calcineurin-calmodulin pathways (Wilker et al. 2008). The discrepancy could be partially explained by experiments in skeletal muscle where MEF2C was discovered to both exert transcriptional repression through class II HDACs (Lu et al. 2000) that could be regulated by calcium influx, and transcriptional activation after it is phosphorylated by p38 MAPK (Han et al. 1997).

1.5 Summary of this thesis

The work in my thesis utilized a combination of biochemistry, mouse genetics, FACS analysis, whole-genome mapping of protein binding, and transcriptome analyses to understand the molecular mechanisms involved in hematopoietic differentiation. My goals were three-fold: (1) to elucidate the role of TAF4B, a component of TFIID core transcription initiation complex, in myeloid and B cell specific hematopoietic differentiation, (2) to understand the mechanisms of bimodal transcription function of MEF2C in lymphoid fate commitment, and (3) to uncover targets regulated by MEF2C that form a transcription network in B cell differentiation. From quantitative PCR analyses, I was able to determine that *Taf4b* expression levels are the highest in common myeloid progenitors (CMPs) and B cells compared to its expression in hematopoietic stem cells (HSCs) and other differentiated cell types. Analysis of *Taf4b* KO progenitors cultured in myeloid-inducing cytokines revealed that there was no decrease in the self-renewal or differentiation ability of *Taf4b* KO cells compared to WT cells. FACS analyses of bone marrow and spleens of *Taf4b* KO mice also revealed no significant difference from their WT littermates, in all lymphoid progenitors, B cell progenitors, immature, and mature B cells populations examined. To further analyze whether TAF4B is dispensable in homeostatic hematopoietic cells but plays a crucial role in stressed cells, I examined the

competence of *Taf4b* KO cells to reconstitute the blood and bone marrow of irradiated recipient mice. No significant difference was observed between KO and *Taf4b* heterozygous cells (equivalent in *Taf4b* expression as WT cells), in their contribution to either the myeloid (measured by granulocyte and monocyte markers) or lymphoid (measured by B cell and T cell markers) compartments of the recipients. As a result, I concluded that TAF4B is dispensable for myeloid and lymphoid differentiation and specification of hematopoietic progenitors in both homeostasis and injury-induced reconstitution.

For the second part of my thesis, I focused on a more recently characterized hematopoietic transcription factor, MEF2C. To determine the mechanism by which MEF2C directs blood cell differentiation, I investigated the role phosphorylation plays in this process. To ascertain the need for MEF2C phosphorylation in its transcription activation of lymphoid specific differentiation program, I used MAPK inhibitors to treat progenitors in B cell *in vitro* differentiation assays. In addition to its well-studied function in stress-induced activation and myeloid differentiation, p38 MAPK was found to also play a role in directing progenitors down the B cell pathway at the expense of myeloid cells. Inhibition of other MAPK such as ERK1, 2, and 5 did not show similar defect in B cell differentiation as inhibition of p38 MAPK. This novel function of p38 is through its activation of MEF2C, as introducing a phosphomimetic mutant of MEF2C was able to reverse the phenotypes that resulted from inhibition of p38 MAPK. Furthermore, I found that MEF2C binds an important B cell transcription factor, EBF1 (described in section 1.3). This binding competes with MEF2C binding to HDAC7, a co-repressor of myeloid fate, only when MEF2C is phosphorylated. Due to a small number of hematopoietic progenitors present in the animal, it is difficult to determine at which cell differentiation stage MEF2C becomes phosphorylated and preferentially binds EBF1. However, these experiments suggest a novel mechanism by which MEF2C switches from a transcription repressor to an activator of lymphoid fate. MEF2C and EBF1 bind the regulatory regions of many B cell lineage genes, as shown by chromatin immunoprecipitation followed by exonuclease treatment and deep sequencing (ChIP-exo). I tested the functional relevance of binding using luciferase reporter assays at two representative B cell targets: *Il7ra* and *Ebf1.* Transcriptome analyses in LKS, CLP, pro-B and pre-B cells also revealed that mRNA levels of *Il7Ra*, *Ets1*, *Ebf1*, and genes encoding many other key B-cell factors are down-regulated in *Mef2c* KO mice compared to WT animals. Many down-regulated genes encode transcription factors such as ETS1, EBF1, MYB, and OCA-B/OBF1 (B-cell specific OCT-binding factor 1), which were confirmed by qRT-PCR. In addition, many myeloid genes were upregulated in *Mef2c* KO cells, such as *Cxcl9, Cfs2ra, and Csf1r*. These findings elucidated the mechanism, binding partners, and downstream targets by which MEF2C is able to regulate lymphoid-specific hematopoietic differentiation. It has been shown that PU.1 is a potential transcription regulator of *Mef2c* expression (Stehling-Sun et al. 2009), thus results presented in this thesis help connect the lymphoid specification role of PU.1 with the established B cell transcription network and provide a mechanism for MEF2C-dependent lymphoid differentiation; PU.1 activates the expression of *Mef2c*, encoding a key B cell transcription factor, that after phosphorylation, binds EBF1 to co-activate genes to promote B cell differentiation.

Figure 1.1.1: Eukaryotic transcription initiation

The assembly of transcription preinitiation complex (PIC) requires several large multi-subunit complexes at the promoter-proximal (PA) position relative to the transcription start site. To initiate transcription, co-regulators, chromatin remodelers, epigenetic factors, and sequence-specific factors need to integrate signals from the promoter-distal (DA) positions that can be kilobases away. TATA box (TATA), Initiator (INR), downstream promoter element (DPE), Pol II (RNA polymerase II), and TFIIA, B, D, E, F, and H (Adapted from Hochheimer and Tjian, 2003) (Hochheimer and Tjian 2003)

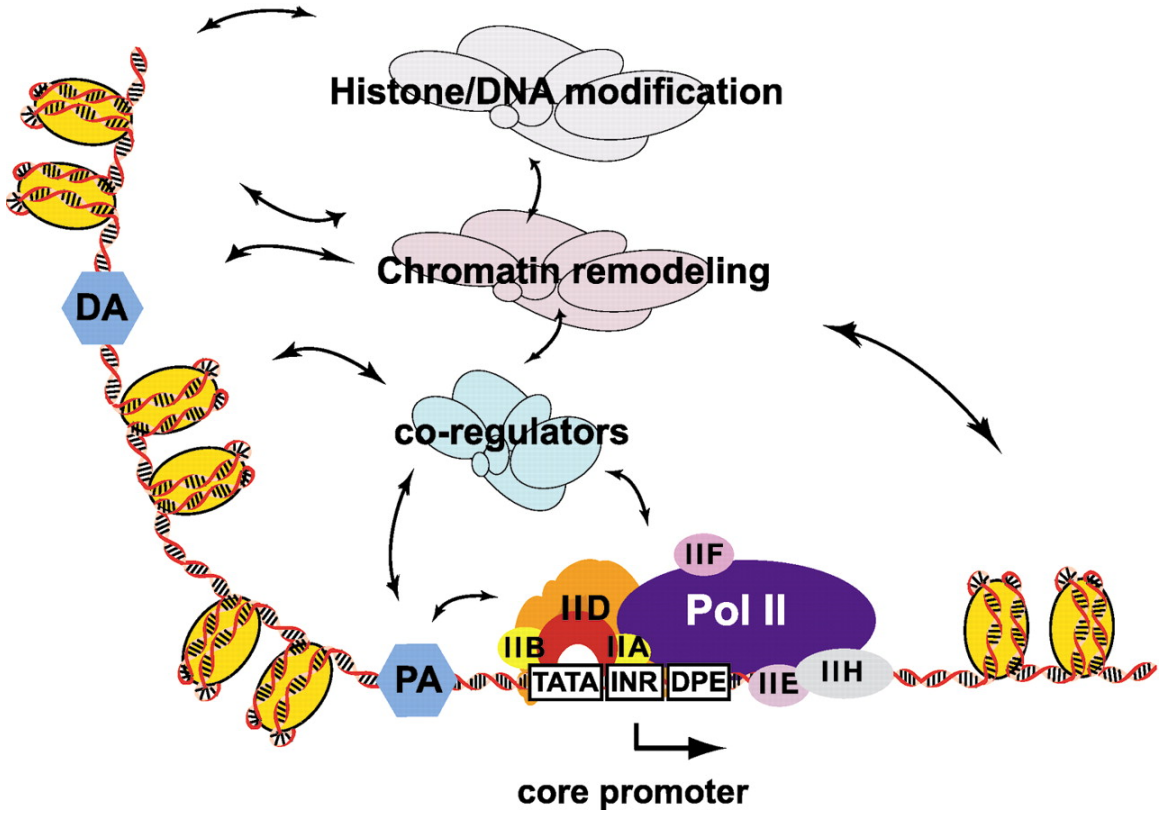
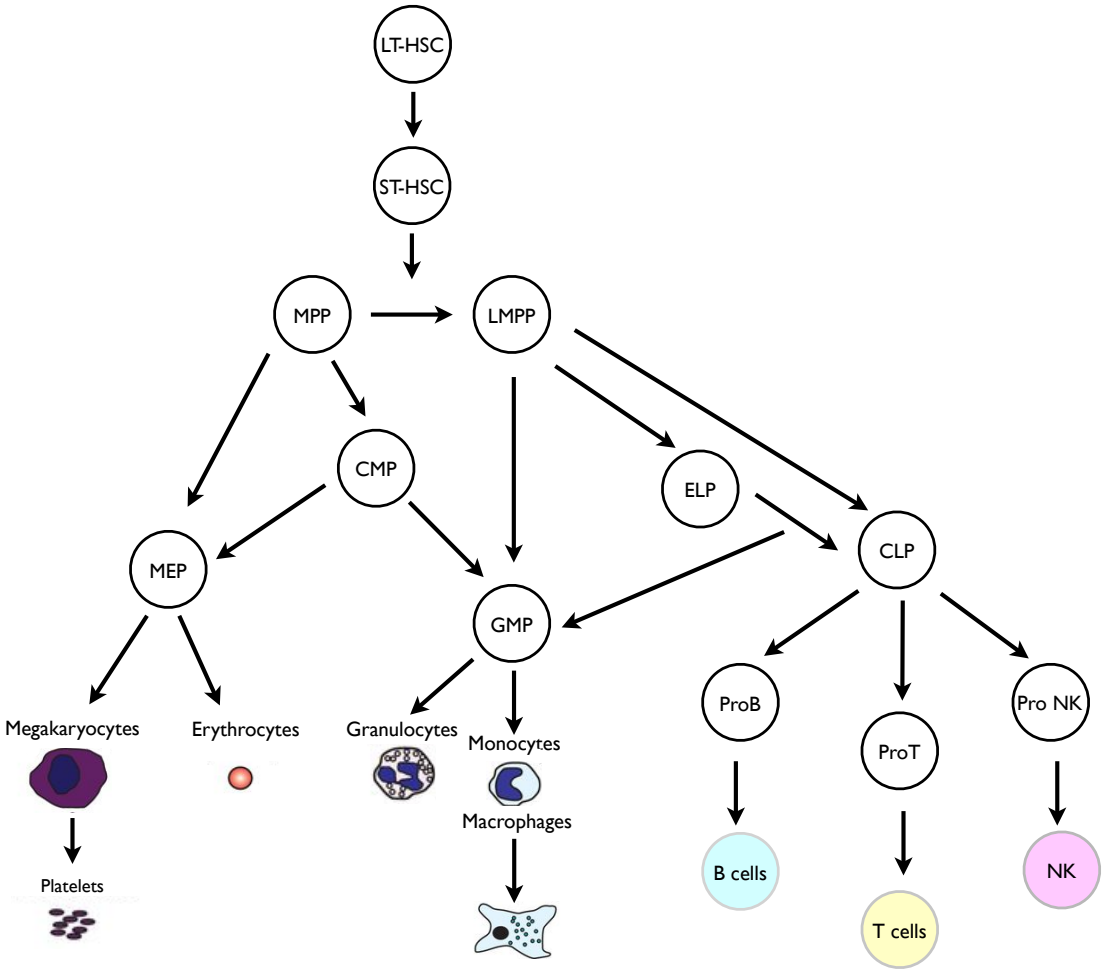


Figure 1.3.1: Hierarchy of hematopoietic differentiation and lineage specification in adult bone marrow
HSC, hematopoietic stem cell; MPP, multi-potent progenitor; LT-, long-term repopulating; ST-, short-term repopulating; LMPP, lymphoid-primed MPP; ELP, early lymphoid progenitor; CLP, common lymphoid progenitor; CMP, common myeloid progenitor; GMP, granulocyte–macrophage progenitor; MEP, megakaryocyte–erythrocyte progenitor; NK, natural killer cell. Adapted from Rieger M.A. and Schroeder T., Cold Spring Harbor Perspectives in Biology, 2012; 4 a008250 (Rieger and Schroeder 2012).



Chapter 2

Methods and Materials

Taf4b and *Mef2c* knockout (KO) mice

All mice were housed and treated according to UC Berkeley animal care and use committee (ACUC) guidelines and Tjian lab animal use protocol (AUP).

Taf4b KO mice were made by Richard Freiman (Freiman et al. 2001) and kept in mating with the help of Shuang Zheng. Lethal (9.5Gy) and sub-lethal (5Gy) doses of irradiation were performed in lucite chambers with a Cs-137 irradiator. Tail-vein injections of cells for competitive transplantation experiments were performed on mice under a mild heat lamp with 26 gauge needles.

Mef2c-floxed mice (129S) were a generous gift from John Schwarz's lab at Albany Medical College (Vong et al. 2005). Exon2 that encodes MEF2C DNA-binding and dimerization domains was flanked by loxP sites. Floxed mice were mated with Mx1-Cre black 6 mice (Jackson labs). The offspring were backcrossed for >4 generations to generate either *Mef2c*$^{flox/flox}$/Cre+ (KO), or *Mef2c*$^{flox/flox}$/Cre- (WT) littermates. Genotyping was performed from tailing, and in some cases to minimize pain, by ear tag piece according to standard protocols of proteinase K treatment in SDS-containing lysis buffer. Sex-matched littermate mice with the desired genotypes were injected intraperitoneally with 400ug of synthetic polyinosinic:polycytidylic acid (pIpC) to induce the activation of the Mx1 promoter and Cre expression, and subsequently *Mef2c* deletion. A total of four injections every other day were performed.

Bone marrow collection and magnetic cell separation

Six to 12-week old mice were euthanized according to ACUC guidelines and the Tjian lab AUP, and necropsied in a sterilized hood. Femurs, tibia, and fibula of mice were dissected out, bone marrow was flushed out with 1x PBS containing 2% FBS with a 25 gauge needle. Red blood cell lysis was performed on ice with Gey's balanced salt solution. Remaining lymphocytes were washed several times before proceeding to either staining for FACS or magnetic cell separation.

Mouse lineage cell depletion kit (130-090-858, Miltenyi Biotec) containing magnetic beads conjugated with antibodies was used to enrich for hematopoietic progenitors. All bead-binding, washing, and elution steps were performed according to manufacturer's instructions.

Fluorescence-activated cell sorting (FACS)/flow cytometry: sorting and analysis

Antibodies against various cell surface markers conjugated to various different were used for FACS staining (mainly APC, PE, PE-Cy7, Pacific Blue, and FITC). Cell sorting was performed at the core facility with the help of Hector Nolla, Alma Valeros, and Kartoosh Heydari, using the Influx sorter (BD Biosciences). All flow cytometry analyses were

performed on either an LSRII or LSRFortessa flow cytometers (BD Biosciences) and analyzed with FlowJo software. A list of FACS antibodies can be found in Appendix I.

Cell culture

All cells were cultured at 37°C with 5% CO_2. 293T cells were cultured in DMEM (Gibco) with 10% FBS (Gibco). Abelson Murine Leukemia Virus (AMulV)-transformed B cells (preB, generous gift from Mark Schlissel's lab) were cultured in RPMI with 5% FBS (Gemini) and beta-mercaptoethanol (2-ME, Gibco). Primary cell culturing and *in vitro* differentiation media are based on alpha-MEM (Gibco) with 10% FBS and 2-ME supplemented with various cytokines. Lhx2-HPC cells (generous gift from the Leif Carlsson's lab) were maintained in IMDM (Gibco) supplemented with 10% FBS, 2-ME, human IL3 (10ng/mL), and murine SCF (20ng/mL).

Lentiviral infection

One day prior to euthanizing the animals, 10cm plates of GP2-293T packaging cells (Clontech) at 70% confluency were transfected with 10ug each of MSCV-*Mef2c*-IRES-h*CD4* (WT or different mutant versions) and VSV-G envelope plasmids (gift from David Schaffer's lab).

Enriched lineage-negative cells derived from the mouse bone marrow were cultured in stimulating media (10ng/mL SCF, 10ng/mL FLT3L, and 2ng/mL TPO) overnight ($3x10^6$ cells/mL). 48 hours after viral plasmid transfection, media containing viruses were collected and filtered through a 45-micron syringe filter and the viral particles were collected with spinning at 90K RPM for 1.5 hours at 10°C. The viral particles were resuspended in culturing media containing various cytokines and polybrene (10ug/mL), and were added to stimulated lineage-negative cells from the previous day. The cells were spin-infected for 1.5 hours at room temperature (RT) at 650 RPM and returned to the 37°C incubators.

***In vitro* differentiation**

Progenitors obtained from murine bone marrow were cultured in either undifferentiating media (alpha-MEM, 100ng/mL FLT3L, 50ng/mL SCF, 2ng/mL TPO) or B cell differentiation media (alpha-MEM, 100ng/mL FLT3L, 50ng/mL SCF, 25ng/mL IL7). Fresh media were added 7 days after the start of culturing and after a portion of the cells were taken for FACS analysis. *In vitro* myeloid differentiation of LKS cells were performed in semi-solid media (MethoCult GF) supplemented with various recombinant myeloid cytokines and EPO.

Co-immunoprecipitation

10cm plates of 293T cells were transfected using FuGene6 (Roche) at 60-70% confluency with different combinations of 6ug of pCMV5a-FLAG-*Mef2c* (WT, EED, AAA), 2ug of pCAG-*Ebf1*-myc, and/or 8ug of pcDNA3.1-v5-HDAC7. 48 hours after transfection, cells were washed once with PBS and lysed with 1mL of lysis buffer (50mM HEPES, 140mM NaCl, 1mM EDTA, 0.5% Triton-X, 0.5% sodium deoxycholate) at 4°C for 15 minutes. The lysates

were passed through 25-gauge needle 10 times, then the supernatant was collected after spinning at 13K RPM for 30 minutes. After 20uL was saved for input, either anti-FLAG M2 affinity gel (Sigma) or anti-FLAG M2 antibody (Sigma) conjugated to protein A-sepharose beads was used to pull down the immunocomplex containing Mef2c. In either case, the beads were equilibrated three times with blocking buffer (0.5% BSA in 1x PBS). In the latter case, anti-FLAG M2 antibody was conjugated to protein A beads for over four hours at 4°C. Overnight rocking of beads with the cell lysates at 4°C facilitated antibody-protein complex binding. The following day, two 5-minute washes in the lysis buffer were performed—rocking at 4°C then centrifuge at 2000 RPM. A third wash was performed in lysis buffer with 500mM NaCl. Then the immunocomplex was boiled for 10 minutes in 2x SDS sample buffer.

Western blotting

For direct detection, cells were boiled and lysed in 2x SDS samples buffer for 15 minutes, then SDS-PAGE was performed, with anti-beta-actin as loading control. To detect proteins pulled down by MEF2C-FLAG-IP, input and immunocomplexes were run in SDS or Bis-Tris-PAGE. The gels were transferred onto nitrocellulose. After blocking in 10% nonfat milk in TBS buffer containing 1% Tween-20, primary antibodies were added to bind to the desired proteins. A complete list of antibodies can be found in Appendix II. HRP-conjugated secondary antibodies against goat, rabbit, and mouse were used for detection.

ChemiDoc and ImageLab software (BioRad) were used to detect and analyze the data, respectively.

RNA extraction from small-size samples

Trizol containing linear polyacrylamide (PLA, 5uL in 1mL of Trizol) was used to lyse the cells (up to 10,000 cells). After a 10-second vortex and 3-minute incubation at RT, 200uL of chloroform were added to extract the RNA, followed by a 30-second vortex and a 10-minute spin at 13K RPM at 4°C. The aqueous layer was transferred to a fresh tube with 0.7 volume of isopropanol added and mixed. After precipitation overnight at -20C, the RNA was collected by spinning at 13K RPM at 4°C, washed once with 70% ethanol, dried, and re-dissolved in RNase-free water.

Reverse transcription and real-time quantitative PCR (qPCR)

First-strand cDNA synthesis was performed either with iScript (BioRad) or SuperScriptIII (Life Technologies) reverse transcriptases according to manufacturer's instructions. qPCR amplifications were performed with either an Applied Biosystem real-time PCR instrument or CFX96 (BioRad) light cycler with melting curve analyses. Genes encoding Ribonucleoprotein (RNP) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) were used as internal controls. All qPCR primers were annealed at 60°C and are listed in Appendix III.

RNA-seq

Hematopoietic progenitor cells (LKS, lineage-negative/c-kit+/Sca1+), and common lymphoid progenitor cells (CLP, lineage-negative/c-kit^{lo}/Sca1^{lo}/Il7ra+) were sorted from either WT or KO littermate mice. RNA was extracted using the method described above. RNA-seq libraries were constructed according to manufacturer's instructions (Illumina). After Bioanalyzer quality control, samples were sequenced at UC Berkeley Vincent J. Coates Genomics Laboratory. Reads were mapped to the UCSC mouse genome MM10 and analyzed with the Tuxedo Suite comprising Bowtie, TopHat, and CuffLink to obtain differential mRNA transcript levels in WT and *Mef2c* KO cells.

Chromatin immunoprecipitation followed by exonuclease and deep-sequencing

1x10^8 cells were used per ChIP reaction. Pre-B cells or *Lhx2*-HPCs were crosslinked with 1% formaldehyde for 10 minutes at RT and quenched by the addition of 140mM glycine. After two 1x PBS washes, cell pellets were collected and stored in -80°C.

The night prior to ChIP, antibodies against MEF2C or EBF1 were bound with equilibrated protein G-sepharose beads in blocking buffer (0.5% BSA in 1x PBS) with rocking at 4°C. The next day, cell pellets were thawed and lysed in cell lysis buffer, the nuclear extracts were then obtained with nuclear lysis buffer. Fragmentation of DNA to 100-300bp was achieved with a water bath sonicator (Adaptive Focused Acoustics, Covaris S220) with tested conditions. Lysates were collected after 30-minute spin at 4°C. After 10% input was saved, lysates were incubated with antibody-bead complex overnight with rocking at 4°C.

Washes for ChIP-exo
The next day, while the immunocomplex was still immobilized on the beads, it was subjected to a series of enzymatic treatments and washes (Adapted from the Pugh lab and James Liu): End polishing with 4.5 units of T4 DNA polymerase, P2 adaptor ligation (5'OH-TGGAATTCTCGGGTGCC-OH 3'; 5'Phos-Phos-CCTTGGCACCCGAGAATTCCA-OH 3') with T4 DNA ligase; nick repair with 15 units of phi29 polymerase, 5' -> 3' DNA digest with Lambda exonuclease and RecJ$_f$ exonuclease. Between each step, washes with performed in sequential order at 4°C: 1x TE buffer, mixed micelle buffer (150mM NaCl, 20mM Tris-HCl pH 8, 5mM EDTA, 5.2% sucrose, 1% triton X-100, and 0.2% SDS), buffer-500 (250 mM NaCl, 5 mM Tris-HCl pH 8, 25 mM HEPES, 0.5% triton X-100, 0.05% sodium deoxycholate, and 0.5 mM EDTA), LiCl buffer (250mM LiCl, 0.5% NP-40, 10mM Tris-HCl pH 8, 0.5% sodium deoxycholate, and 10mM EDTA), and 10mM Tris-HCl (pH dependent on the subsequent enzymatic reaction).

After washing, the MEF2C or EBF1-immunocomplex was eluted at 65°C in elution buffer containing SDS for 15 minutes. After a 5-minute spin at 13K RPM at RT, the supernatant was collected. Crosslinking of both ChIP and input samples was reversed at 65°C overnight with shaking.

ChIP and input DNA were then treated with proteinase K (10ug/mL) and input with RNaseA (10ug/mL) for 2 hours each at 55°C and 37°C, respectively. Following phenol

chloroform extraction and ethanol/sodium acetate (pH 5.5) precipitation overnight at -20°C, DNA was washed with 70% ethanol, dried, and re-dissolved in water. Libraries from ChIP-exo DNA were constructed according to manufacturer's instructions (Illumina) and adaptor sequences from the small RNA-sample prep series. Bioanalyzer traces were used to quality control for the ChIP DNA before the samples were sequenced at UC Berkeley Vincent J. Coates Genomics Laboratory.

ChIP-exo data analysis

Single-end reads were mapped with Burrows-Wheeler Aligner (BWA) to the repeat-masked mouse MM10 genome (available from the UCSC Genome Browser). Following the removal of duplicated reads to reduce the impact of PCR duplication artifacts, peaks were called using MACS1.4 with input DNA as the control dataset. Different lineages—B, cells, T cells, myeloid— specific expression patterns of the targets were determined through the ImmGen database (Shay and Kang 2013).

Luciferase reporter assays

293T cells grown in 24-well plates were transfected with 0.1ug of pCMV5a-FLAG-*Mef2c* (WT and various mutants), 0.02ug of pCAG-*Ebf1*-Myc, 0.1ug of pGL4.23 containing the *Luc2* encoding the firefly luciferase and a minimal promoter (Promega), and 0.0025ug of pRL-TK vector containing *renilla luciferase* (Ren, Promega) for internal control. Regulatory regions for either *Il7ra* (WT or with mutated MEF2C-binding sites), *Nur77* (WT or with mutated MEF-binding sites), or *Ebf1* were cloned into pGL4.23 vectors. 48 hours after transfection, cell lysates were collected using 1x passive lysis buffer (Promega) according to manufacturer's instructions. The amount of luciferase activity was measured using Dual-Lucifease Reporter Assay kit (E1910, Promega) and either a GloMax 20/20 luminometer (Promega) or SpectraII Microplate Reader (Tecan). Ratio of *Luc2* and *Ren* luciferase reporter activities was used to determine the amount of activation by the tested transcription regulators.

TAF4B antibody generation

A 32-mer peptide in the N-terminal part of TAF4B that is very distinct from TAF4A in sequence, cys-SGAVTMAPVAALPVRVEGTPVALGPVTKAPVS, was made (David King, HHMI Mass Spec facility) and conjugated to maricuture keyhole limpet hemocyanin (mcKLH) according to manufacturer's instructions (Pierce Imject). In addition, DNA encoding the first 400aa of mouse TAF4B was cloned into the pGEX-4T-1 vector and transformed into BL21 bacteria. Overnight bacterial cultures were induced with isopropyl β-D-1-thiogalactopyranoside (IPTG, 0.2mM) for three hours at 37°C to produce glutathione S-transferase (GST) fusion TAF4B (GST-TAF4B-400). Cell pellets were collected by spinning at 5K RPM for 10 minutes at 4°C, washed with PBS, and resuspended with STE buffer (150mM NaCl, 10mM Tris pH 8, and 1mM EDTA with supplemented protease inhibitors and 1% triton-X). After 20-minute incubation on ice, the pellets were frozen and stored. Cells were lysed by thawing at RT and sonicated with a micro-tip (five times, 10 second intervals) at 4°C in STE buffer supplemented with NaCl (final concentration 0.8M), DTT

(5mM), and NP-40 (0.5%). The supernatant was collected after spinning at 13K for 30 minutes at 4°C.

Samples were thawed and added to STE-washed glutatione-sepharose beads (GS, 50% slurry). GST-TAF4B-400 and GS beads were allowed to bind with rocking at 4°C for 15 minutes. After washing, GST-TAF4B was eluted with glutathione (final 15mM).

The 32-mer TAF4B peptide conjugated to mcKLH and purified GST-TAF4B-400 were injected into separate rabbits (Covance, Inc). Bleeds were tested with 293T cell lysates overexpressing FLAG-tagged TAF4B (full length). After two additional boosting injections, the rabbits were euthanized and all of the sera collected.

Maltose binding protein (MBP)-fusion TAF4B 1-400aa (MBP-TAF4B-400) were used to purify the antibodies. The TAF4B fragment was cloned into the pMAL-c5X vectors and transformed into BL21 (DE3) expression plasmids. Overnight cultures (antibiotics and 0.2% dextrose) were grown at 37°C, and then induced with IPTG (0.1mM) for 3 hours at 30°C. Cell pellts were collected by spinning and resuspended in 0.5M NaCl/40mM HEPES pH 7.6/1mM EDTA/1mM DTT/10% glycerol supplemented with 1mL lysozyme (20mg/mL). The lysate was rocked for 20 minutes at 4°C, sonicated six times (20-second pulses) with a micro-tip sonicator, and then spun at 40K RPM for 30 minutes. The supernatant containing MBP-TAF4B-400 was batch bound to pre-equilibrated amylose resin overnight at 4°C, and eluted with maltose (10mM).

Finally, sera from the final bleeds of GST-TAF4B-400 immunized rabbits were purified with MBP-TAF4B-400 immobilized on a 1:1 mixture of Affi-gel 10 and 15 activated immunoaffinity supports (BioRad) according to manufacturer's instructions.

Chapter 3

Investigating the role of TAF4B in murine hematopoiesis

Introduction

Mammalian gene expression requires precise regulation of transcription initiation. Before RNA polymerase II (Pol II) begins transcribing, the TFIID complex and its core component TATA-binding protein (TBP) must first bind the promoter. TBP recognizes and binds the TATA box upstream of the transcription start site (TSS) in TATA-containing core promoters. TFIID is also composed of 13 to 14 TBP-associated factors (TAFs) that can help position TFIID through binding to the Initiator (INR) and downstream promoter element (DPE) at certain promoters (Verrijzer et al. 1995) (Smale and Baltimore 1989) (Chalkley and Verrijzer 1999). TAFs were originally thought to play non-specific roles in transcription to facilitate the assembly of preinitiation complex (PIC) of transcription at gene promoters. However, recent data have pointed to tissue- and gene-specific roles for these proteins in specific developmental processes.

TAF4B (previously termed TAFII105) was originally purified from differentiated IgG-producing human B-cells and is a component of TFIID specific to B cells compared to other cell types tested. It was found to share a high sequence conservation with the C-terminal half of TAF4A (previously termed TAFII130) (Dikstein et al. 1996). TAF4B plays a crucial role in spermatogenesis, as *Taf4b* KO male mice older than 3 months became infertile due to the depletion of spermatogonial stem cells (Falender et al. 2005), and *Taf4b* KO female mice lacked mature follicles and had impaired ovarian granulose cell proliferation that also resulted in infertility (Freiman et al. 2001) (Voronina et al. 2007) and reviewed in (Goodrich and Tjian 2011).

In B cells, TAF4B was found to bind OCA-B, a co-factor of B cell specific transcription factors OCT1 and 2, which bind and activate genes with octamer sequence-containing promoters and enhancers. This interaction with OCA-B enables TAF4B to activate transcription of a reporter gene with an octamer-containing promoter both *in vitro* and in luciferase reporter assays (Wolstein et al. 2000). Bacterial protein LPS (lipopolysaccharide) can induce TAF4B expression in B cells. But despite its specific expression in B cells and its ability to activate a key DNA motif associated with B cell functions, a role for TAF4B in B cell development and differentiation had been elusive. *Taf4b* KO mice have B cells with normal LPS-induced proliferation and can produce all antibody isotypes (Freiman et al. 2002). The lack of a B cell specific phenotype in *Taf4b* KO mice is presumably due to high sequence similarity with TAF4A and thus possible functional redundancy. However, though TAF4B seems dispensable for B cell development and function at homeostasis, its role in stressed B cells have not been examined. Furthermore, B cells and monocytes of the myeloid lineage share a common bi-potent progenitor in blood lineage specification (Montecino-Rodriguez et al. 2001) and TAF4B's function in myeloid cells have not been studied. Here, I tested TAF4B function in both B cell development and myeloid differentiation in stressed conditions using competitive transplantation assays and *in vitro* colony-forming unit assays, respectively. My assays revealed no significant differences in either lineages between *Taf4b* KO and

wild-type (WT) mice. Furthermore, I found no difference between the lymphoid and myeloid progenitor percentages when *Taf4b* is deleted in the animal. While these data suggest that TAF4B is dispensable for B cell development and function, there may still exist gene-specific and stress factor-specific roles for TAF4B that these assays were not sensitive enough to uncover. In addition, I have made and purified a TAF4B-specific polyclonal rabbit antibody, to make it feasibly to investigate binding partners of TAF4B in hematopoietic cells and its downstream targets. Finally, the results of these experiments contribute to the understanding of TAF4B's precise transcriptional function in blood cell differentiation.

Results

If there were cell type-specific roles for TAFs in the hematopoietic system, then I would expect to see specific expression patterns in different blood cells. Hematopoiesis is a multi-step developmental process wherein progenitor cells progressively lose their abilities to self-renew and differentiate into fate-restricted cells that comprise either the myeloid (granulocytes, macrophages, erythcoytes) or lymphoid (B/T cells, natural killer cells) lineages. To test whether TBP or any of the TFIID subunit TAFs have cell specific expression pattern within the hematopoietic system, I assayed their mRNA levels in various sorted hematopoietic cells by RT-qPCR. RNA was extracted from lineage-negative/c-Kit+/Sca1+ hematopoietic stem/progenitor cells (LKS), common myeloid progenitors (CMP), common lymphoid progenitors (CLP), megakaryocyte/erythrocyte progenitors (MEP), granulocyte-macrophage progenitors (GMP), granulocytes, macrophages, and B cells. The expression of *Tbp* was largely unchanged in most of the cell types examined (Figure 3.1A). However, *Taf4a* expression is upregulated in granulocytes (4.5 fold) and B cells (3 fold), and *Taf3* expression is similarly upregulated in B cells (4 fold), as compared to LKS cells. These are two very distinct cell types in the blood, but share a common ancestral progenitor in the LKS population, suggesting TAF4A and TAF3 may play roles in the differentiation capabilities of the stem/progenitor population in the blood. However, due to their integral roles in the core transcription machinery, TFIID, which is responsible of general transcription initiation, it may be difficult to study the effects of their loss-of-function in cells. Several other *Tafs* expression levels were also tested. Of note, *Taf4b*, encoding a substoichiometric TAF in the TFIID, showed the highest expression changes compared to *Taf7* and *Taf10* (Figure 3.1B). Specifically, *Taf4*b showed higher expression in CMP (>10 fold) and B cells (almost 5 fold) compared to LKS cells. The expression change of *Taf4b* is greater than that of *Taf3* and *Taf4* in both myeloid and B cell lineages, suggesting *Taf4b* may play an as-yet unidentified role in hematopoietic cell differentiation that may be independent from the rest of the TFIID subunits. The high expression level of *Taf4b* in CMP is especially interesting because these are the progenitor population that gives rise to all myeloid lineages. Transcription control is especially important in these cells compared to terminally differentiated cell types such as granulocytes where high expression of *Taf4a* and *Taf3* were found, because mis-reguation of key factors that drive cell fate determination in progenitors can result in imbalance of different cell types in the mouse bone marrow.

High expression level in myeloid cells suggests a functional role for TAF4B in these cells. I first wanted to confirm this observation in an *in vitro* culturing and differentiation system where cells are more easily obtained and manipulated than primary cells from the mice. To that end, a murine myeloid progenitor cell line, 32D, was used as a model for myeloid differentiation. 32D cells are immortalized myeloblast-like cells that can be kept from terminally differentiating when grown in the presence of interleukin 3 (IL3). In the presence of granulocyte-colony stimulating factor (G-CSF) however, 32D cells undergo terminal differentiation into granulocytes. Wright-Giemsa staining at Day 4 of differentiation showed that 32D cells started to exhibit segmented nuclei that are characteristic of granulocytes, comparing to the start of G-CSF induced differentiation (Day 0, Figure 3.1C). Meanwhile, expression analyses showed that two key myeloid transcription factors, *Pu.1* and *Cebpa*, had increased mRNA expression levels at Day 4 of differentiation compared to Day 0 (Figure 3.1D). Interestingly, *Pu.1* expression peaked at 16 fold on Day 2 of differentiation and then decreased to about 5 fold. This is consistent with PU.1's transcriptional role in commitment of the myeloid fate, and not terminal granulocyte differentiation. Conversely, *Cebpa*, a "master" regulator of the myeloid fate, showed gradually increased expression pattern, peaking at about 6 fold on Day 4 of differentiation compared to Day 0. Together, these results confirmed that indeed 32D cells were driven to terminal differentiate *in vitro.* However, *Taf4b*, similar to *Taf4a*, showed increased level of expression as 32D cells differentiated, in direct contrast to it expression changes in primary cells where its mRNA levels were the highest at the progenitor level and decreased in terminally differentiated cells (Figure 3.1E). Meanwhile, *Taf3* and *Tbp* expression remained largely unchanged (Figure 3.1E). The contrasting expression patterns for *Taf4b* in cell lines compared to primary cells suggests that 32D cells are not the most appropriate cell lines to model primary CMP differentiation *in vitro*, and thus not suitable for studying the role of TAF4B in myeloid differentiation.

Since these 32D differentiation results yielded unexpected expression patterns of *Taf4b* compared to primary cells, *Taf4b* KO mice were used to further analyze TAF4B's role, if any, in myeloid differentiation. To ascertain that the *Taf4b* KO mice truly lacked TAF4B proteins, two antigens were injected into rabbits to raise antibodies against TAF4B. The first is glutathione-S-transferase (GST)-fused TAF4B 1-400 amino acids (animal 4736 and 4737). The second is a 32-mer peptide in the N-terminal half of TAF4B distinguishing it from TAF4A that is conjugated to maricuture keyhole limpet hemocyanin (mcKLH) (animal 4752). Bleeds after injections were tested in western blots of 293T lysates from cells that were either transfected with empty vector or FLAG-tagged TAF4B, with FLAG-tagged OCT4 as a control for transfection (Figure 3.2A). Three different shRNA against *Taf4b* were also tested in the same experiments that showed no significant reduction of overexpressed TAF4B protein levels. Meanwhile, bleeds from all three rabbits injected with either GST-TAF4B-400 or 32mer-mcKLH antigens were tested with overexpressed TAF4B. The sera from all three animals contained antibodies that recognized FLAG-TAF4B (Figure 3.2A). After euthanizing animal #4737, antibodies from the sera were purified with maltose binding protein (MBP) fused-TAF4B (Figure 3.2B), wherein eluted fraction #4 contained the most anti-TAF4B antibodies (Figure 3.2C). Lysates prepared from either 293T cells overexpressing FLAG-TAF4B or spleens from *Taf4b* KO and WT mice were tested with the purified anti-TAF4B antibodies and showed the specificity of

the antibody. Ovary extracts from *Taf4b* KO mice and WT mice were also used to confirm the specificity of the antibody (data not shown). These results show that I have successfully made a polyclonal anti-TAF4B antibody that could be used in assays to either search for TAF4B binding partners or its downstream targets in a variety of tissues. In addition, *Taf4b* KO mice were confirmed to be truly lacking TAF4B protein.

To address the functional role of TAF4B in the myeloid lineage, I compared percentages of GMP, CMP, and MEP in either heterozygous (equivalent in *Taf4b* expression as WT) or *Taf4b* KO mouse bone marrow. I used known cell surface markers for these cell types and analyzed these populations by flow cytometry/fluorescence activated cell sorting (FACS). Analyses of myeloid populations of the *Taf4b* and WT mouse bone marrow showed no difference between littermates in any of the cell types examined (Figure 3.3A). This result suggests that TAF4B does not play a role in normal differentiation of hematopoietic stem/progenitor cells to generate myeloid progenitor cells. However, it remains possibly that TAF4B is required for differentiation or self-renewal of these cells, especially in stressed conditions. To functionally test whether the absence of TAF4B would affect the ability of progenitor cells to self-renew and differentiate in culture, LKS progenitors cells were isolated from WT or *Taf4b* KO mice and grown in semi-solid media supplemented with myeloid-differentiation cytokines. These cultures were then analyzed for differentiation into five different cell types. The resulting blast-forming unit-erythroid (BFU-E), colony-forming unit-granulocytes (CFU-G), CFU-granulocyte/monocyte (GM), CFU-monocyte (M), CFU-granulocyte/erythrocyte/monocyte/megakaryocyte (GEMM) were identified in bright-field microscopy by morphology and size and counted. This assay again revealed no significant difference in colony number or size between cultures that were differentiated from WT or KO progenitors (Figure 3.3B). The expression of the key myeloid transcription regulator *Pu.1* was, however, increased in B cells isolated from *Taf4b* KO mice compared to WT animals (Figure 3.3C), indicating that TAF4B may act as a protector and driver of B cell lineage. These results suggest that though its mRNA expression is very high in myeloid cells, TAF4B plays a dispensable role in myeloid differentiation. There may exist a CMP-specific role for TAF4B, thus it may be interesting to isolate CMPs from either *Taf4b* or WT mouse bone marrow, drive their differentiation toward granulocytes and macrophages *in vitro*, and examine any differentiation defects in TAF4B-null cells.

Previously, TAF4B's function in terminally differentiated B cells was found to be dispensable. In order to determine whether Taf4b has a functional role in lymphoid development at an earlier stage than previously examined (Freiman et al. 2002), bone marrow and spleens of WT and *Taf4b* KO mice were collected and the percentages of different lymphoid progenitor cells were analyzed by FACS. If TAF4B was important in lymphoid lineage-specification, then I would expect the percentages of lymphoid progenitors to be affected in *Taf4b* KO mice. However, *Taf4b* KO mice did not show any change in percentages of CLPs or lymphoid-primed multi-potent progenitors (LMPPs) compared to WT animals (Figure 3.4A). Further analyses of different immature and mature B cell populations also did not show significant differences between WT and *Taf4b* KO mice (Figure 3.4B, C). These results suggest that the absence of TAF4B did not affect the homeostasis of normal murine immune system. However, the key B cell gene,

recombination activating gene 1 (*Rag1*) expression was lower in cells deficient of TAF4B (0.1 fold compared to WT, Figure 3.3C).

It remained a possibility that the assays described above were not sensitive enough to uncover small changes in blood cells between KO and WT mice. Therefore, I used competitive transplantation assays to determine if a loss of TAF4B results in defects in hematopoiesis. This assay utilizes two functionally equivalent alleles of CD45 cell surface marker that is present in all blood cells: CD45.1 and CD45.2. CD45.1 mice were lethally irradiated to delete their hematopoietic system. Then a 1:1 mixture (1E6 cells total) of bone marrow cells from WT CD45.1/CD45.2 mice (competitor) and LKS cells from either *Taf4b* KO or heterozygous CD45.2 mice (experimental) were injected by tail-vein into irradiated recipient mice. Percentages of B cells (B220+) and macrophages (Mac1+) that were contributed from either competitors or experimental in the peripheral blood were analyzed from tail bleeds at week 2, 4, and 8 (representative week 4 data shown in Figure 3.5A, B). Examining cells injected with either heterozygous or *Taf4b* KO cells showed no significant differences in competitiveness of the KO cells to reconstitute the irradiated recipient's hematopoiesis compartments. Finally at week 16, the animals were euthanized and percentages of their bone marrow B cells, mature T cells (CD3ε+), macrophages, and granulocytes (Gr-1+) were analyzed by FACS (Figure 3.6A-E). No significant defects in reconstituting any of these lineages were observed in *Taf4b* KO cells compared to heterozygous cells. Together these results showed that *Taf4b* KO cells competed against WT cells just as well as heterozygous cells in reconstituting all cell lineages in both the bone marrow and peripheral blood of mice that were depleted of their hematopoietic systems.

Discussion

TAF4B was one of the first TAFs that were thought to have tissue-specific expression and activity. Although its functions in two key hematopoietic lineages, myeloid and lymphoid, were found to be dispensable, TAF4B may still have transcriptional activities that are gene-specific and cannot be detected in our assays. TAF4B may need a co-factor to exert any transcriptional function. The polyclonal antibody generated for this study can be used to identify binding partners in B or myeloid cells. In addition, TAF4B expression may be regulated at a very precise level, where complete loss of its expression leads to compensation from other factors such as its homolog, TAF4A. Transcription factors are needed to intricately regulate gene expression at the right time and place, thus their own expression patterns are tightly regulated. Recently, it was shown that graded level of PU.1 leads to different cell fates in hematopoiesis (DeKoter 2000). The authors used a hypomorphic allele of *Pu.1* to show that a moderate expression level of this transcription factor drives B cell development, whereas high expression level drives myeloid differentiation. Similarly, animals could be very sensitive to small changes in TAF4B expression. It may be of interest to overexpress *Taf4b* in mice to examine its function in hematopoietic cell proliferation and differentiation. Furthermore, differential levels of overexpression of *Taf4b* can be achieved using CRISPR/Cas9-mediated sequence-specific gene activation through directly targeting the core promoter of *Taf4b* with a transactivator such as VP16. Then I can determine whether graded levels TAF4B can lead

to a preference for differential cell fate determination. In summary, results presented in this chapter of my thesis suggest that TAF4B function is not essential in the commitment to both major lineages of hematopoietic differentiation, the myeloid and lymphoid cells. It may be due to TAF4B's functional redundancy with its homology, TAF4A, since *Taf4a* expression is also highly enriched in myeloid and B cells. This functional redundancy is important to maintain both homeostasis of the blood system and to protect it while the animal is under stress. However, since TAF4B is specifically expressed in myeloid progenitor cells where TAF4A is not present, it may be important to isolate its function in that particular cell type by using cell-specific promoters driving Cre recombinase. My experiments will inform future studies of TAFs where their integral roles in TFIID make them difficult to observe loss-of-function phenotypes in conventional knockout approaches.

Figure 3.1: Expression of *Taf*s in hematopoiesis and 32D cell differentiation
(A, B) Relative mRNA expression levels by RT-qPCR of *Tbp, Taf3, Taf4a, Taf4b, Taf7,* and *Taf10* in lineage-negative/c-Kit+/Sca1+ hematopoietic stem/progenitor cells (LKS), common myeloid progenitors (CMP), common lymphoid progenitors (CLP), megakaryocyte/erythrocyte progenitors (MEP), granulocyte-macrophage progenitors (GMP), granulocytes, macrophages, and B cells. (C) 32D myeloblast-like cell line at day 0 to day 4 of differentiation. Top panels (20x, bright-field)—left: undifferentiated in IL3; right: differentiated in G-CSF. Bottom panels (40x, bright-field after Wright-Giemsa stain): left-day 0, right-day 4 of differentiation, arrows show binucleated cells. (D) Relative mRNA expression levels of myeloid markers, *Pu.1* and *C/ebpa* at day 0-4 of 32D cell differentiation. (E) Relative mRNA expression levels of *Tbp, Taf3, Taf4a,* and *Taf4b* at day 0-4 of 32D cell differentiation.

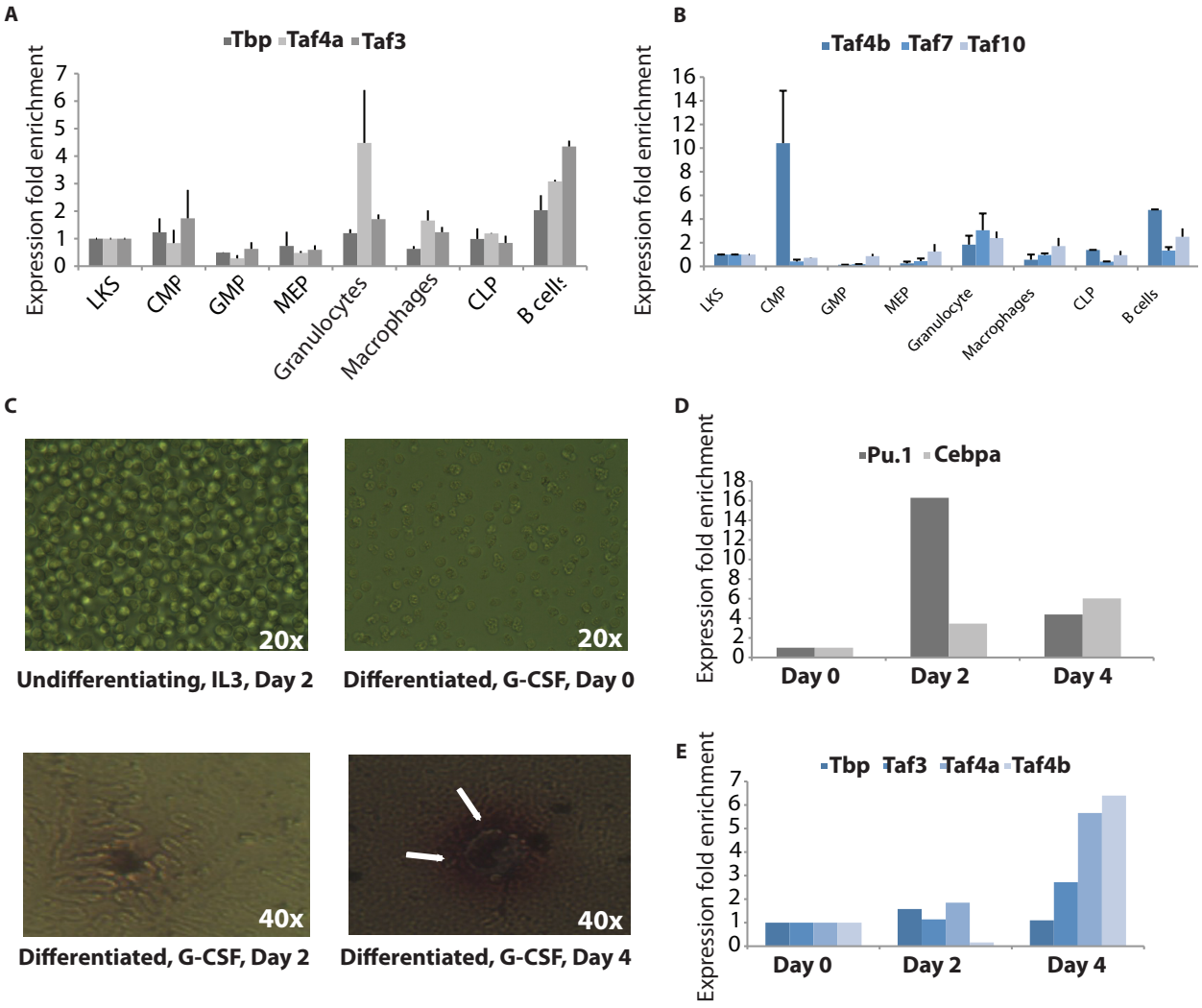

A
Tbp Taf4a Taf3
Expression fold enrichment
0 1 2 3 4 5 6 7
LKS CMP GMP MEP Granulocytes Macrophages CLP B cells
B
Taf4b Taf7 Taf10
Expression fold enrichment
0 2 4 6 8 10 12 14 16
LKS CMP GMP MEP Granulocyte Macrophages CLP B cells
C
20x
Undifferentiating, IL3, Day 2
20x
Differentiated, G-CSF, Day 0
40x
Differentiated, G-CSF, Day 2
40x
Differentiated, G-CSF, Day 4
D
Pu.1 Cebpa
Expression fold enrichment
0 2 4 6 8 10 12 14 16 18
Day 0 Day 2 Day 4
E
Tbp Taf3 Taf4a Taf4b
Expression fold enrichment
0 1 2 3 4 5 6 7
Day 0 Day 2 Day 4

Figure 3.2: TAF4B polyclonal antibody generation and testing
(A) Western-blot analysis showing 293T cells transfected with either empty vector (EV), FLAG-tagged TAF4B (TAF4B), FLAG-tagged OCT4 (OCT4), or a combination of FLAG-tagged TAF4B and three shRNA constructs against *Taf4b* (Sigma) (shRNA 1, 2, 3). Antibodies against FLAG (M2) or sera from animals injected with TAF4B antigens are indicated above each lane. (B) Purification of MBP-tagged TAF4B: UI-uninduced, IPTG-induced, M-marker, FT-flow through, E1/E2-eluted fractions 1 and 2, respectively. (C) Top: Purification of anti-TAF4B antibodies from sera of animal #4747 on Affi-Gel 10/15 matrix immobilized with MBP-TAF4B-400 from (B), collected in fractions 1-9 (only the first 6 fractions shown). Middle: western-blot analysis of 293T cells transfected with either empty vector (EV) or FLAG-tagged TAF4B, blotted with either anti-FLAG (M2) or purified fraction 4 from the top panel, as indicated above each lane. Bottom: western-blot analysis of spleen extracts from either *Taf4b* KO mice or WT (two animals each), blotted with purified fraction 4 from the top panel. Arrow indicates the band corresponding to TAF4B, asterisk denotes a non-specific band.

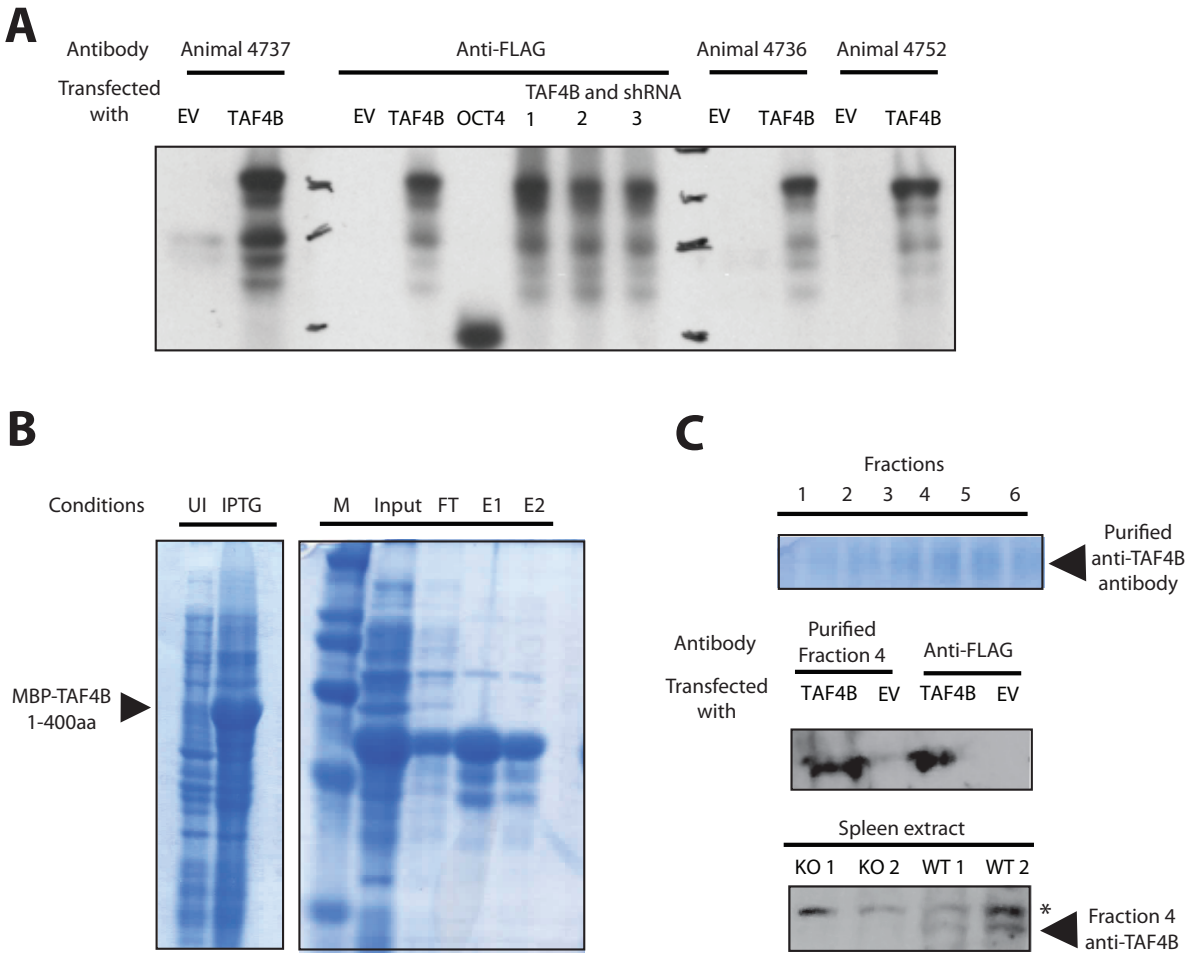

A
Antibody
Animal 4737
Anti-FLAG
Animal 4736
Animal 4752
Transfected with
EV
TAF4B
EV
TAF4B
OCT4
TAF4B and shRNA
1
2
3
EV
TAF4B
EV
TAF4B
B
Conditions
UI
IPTG
M
Input
FT
E1
E2
MBP-TAF4B
1-400aa
C
Fractions
1
2
3
4
5
6
Purified
anti-TAF4B
antibody
Antibody
Purified
Fraction 4
Anti-FLAG
Transfected with
TAF4B
EV
TAF4B
EV
Spleen extract
KO 1
KO 2
WT 1
WT 2
*
Fraction 4
anti-TAF4B

Figure 3.3: Role of TAF4B in myeloid progenitor cells
(A) Percentages of GMP, CMP, and MEP myeloid progenitors in two pairs of heterozygous (Het#1 and 2) or *Taf4b* KO (KO #1 and 2) mice. Bottom: quantification of FACS data. (B) *In vitro* culturing and differentiation of LKS cells from either WT or *Taf4b* KO mice grown in semisolid media (MethoCult GF). Colonies were counted at day 9 of culturing and categorized by morphology into blast forming unit-erythroid (BFU-E), colony forming unit-granuloycte/monocyte (CFU-GM), CFU-granulocytes (CFU-G), CFU-monocyte (CFU-M), and CFU-granulocyte/erythrocyte/megakaryocyte/ monocyte (CFU-GEMM). (C) Relative mRNA expression levels of *Taf4b, Pu.1*, and *Rag1* in LKS cells derived from WT or *Taf4b* KO mice.

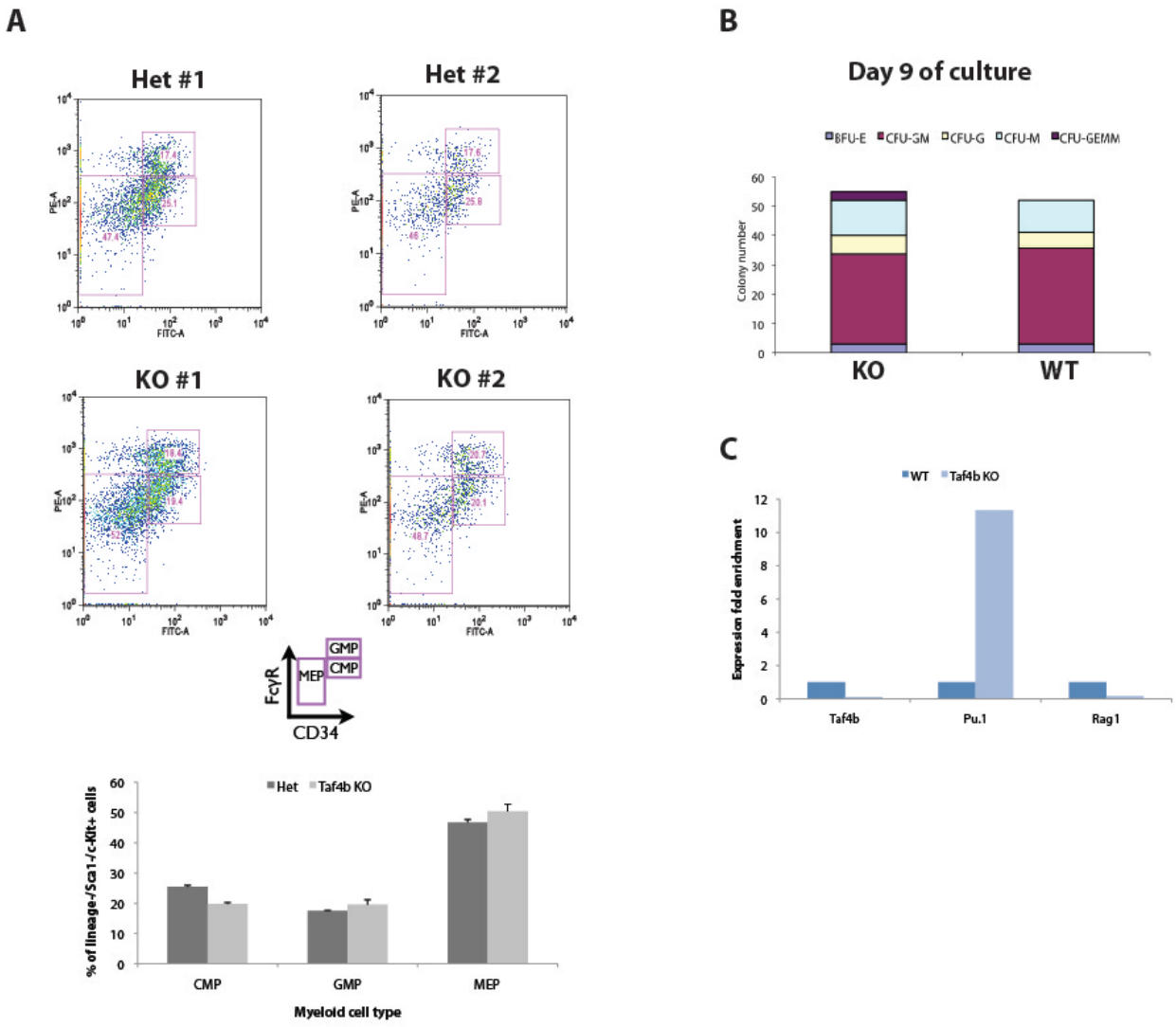

A
Het #1
Het #2
KO #1
KO #2
PE-A
FITC-A
FcγR
CD34
MEP
GMP
CMP
Het
Taf4b KO
% of lineage-/Sca1-/c-Kit+ cells
CMP
GMP
MEP
Myeloid cell type
B
Day 9 of culture
BFU-E
CFU-GM
CFU-G
CFU-M
CFU-GEMM
Colony number
KO
WT
C
WT
Taf4b KO
Expression fold enrichment
Taf4b
Pu.1
Rag1

Figure 3.4: Role of TAF4B in lymphoid progenitor cells
(A) Percentage of common lymphoid progenitors (CLP) in total lineage-negative cells from WT and *Taf4b* KO mice; percentage of lymphoid-primed multi-potent progenitors (LMPP) in lineage-negative/c-Kit+/Sca1+ cells from WT and *Taf4b* KO mice. (B) Percentages of various B progenitors in heterozygous (Het) and *Ta4b* KO mouse bone marrow. Top panels: percentages of pre/pro-B cells and immature B cells as outlined. Middle panels: percentages of pro-B and pre-B cells from pre-pro-B cell populations in the top panels. Bottom panel: quantification of top two panels. (C) Percentages of fraction E (splenic pre-B cells) and mature recirculating B cells in Het and *Taf4b* KO mouse spleens. Bottom panel: quantification of the top panels.

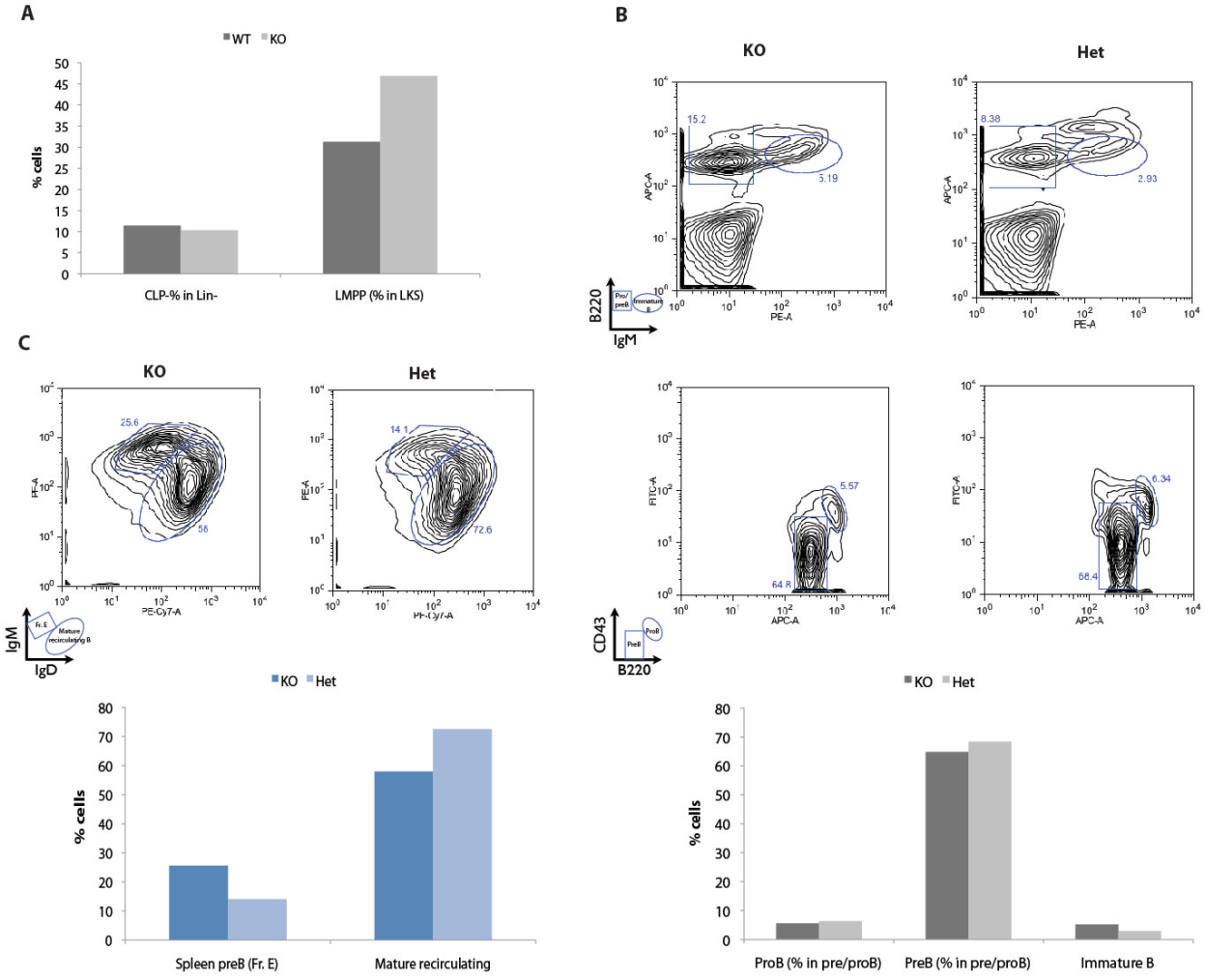

A
WT
KO
% cells
CLP-% in Lin-
LMPP (% in LKS)
B
KO
Het
15.2
5.19
8.38
2.93
APC-A
PE-A
B220
IgM
C
KO
Het
25.6
14.1
72.6
PE-A
PE-Cy7-A
IgM
IgD
Fr. E
Mature recirculating B
5.57
64.8
6.34
68.4
FITC-A
APC-A
CD43
B220
ProB
PreB
% cells
Spleen preB (Fr. E)
Mature recirculating
ProB (% in pre/proB)
PreB (% in pre/proB)
Immature B

Figure 3.5: Tail bleed analyses at week 4 of competitive transplantation
(A) Representative analyses of contribution of transplanted cells to the peripheral blood of recipient mice. After gating on either B cells (B220+, left panels) or macrophages (Mac1+, right panels), CD45.1+/CD45.2+ cells are WT competitors, CD45.2+ cells are either heterozygous (Het, top panels) or *Taf4b* KO (bottom panels) experimental cells. (B) Quantification of all eight recipient mice for four conditions: two pairs each of het and *Taf4b* KO.

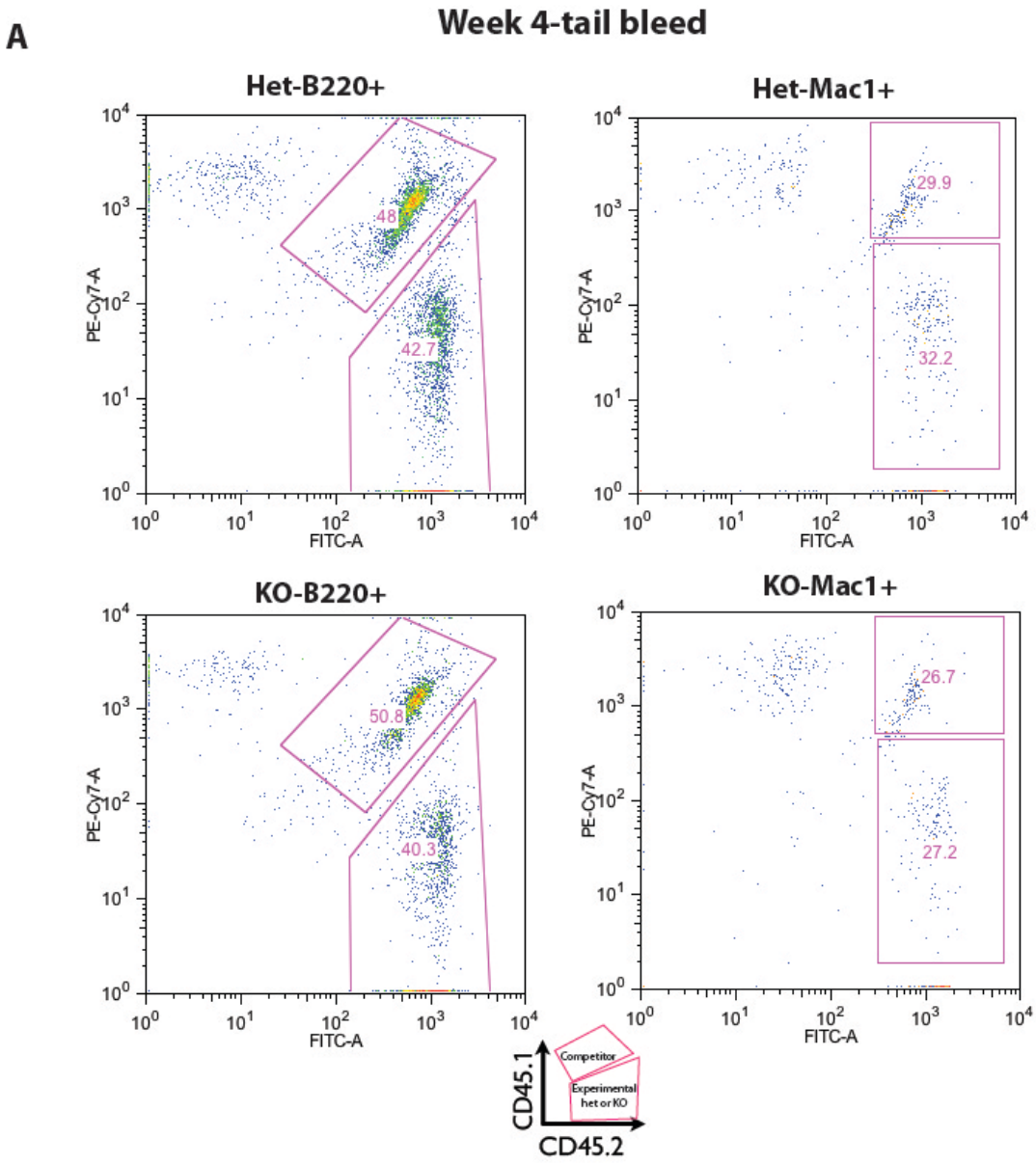
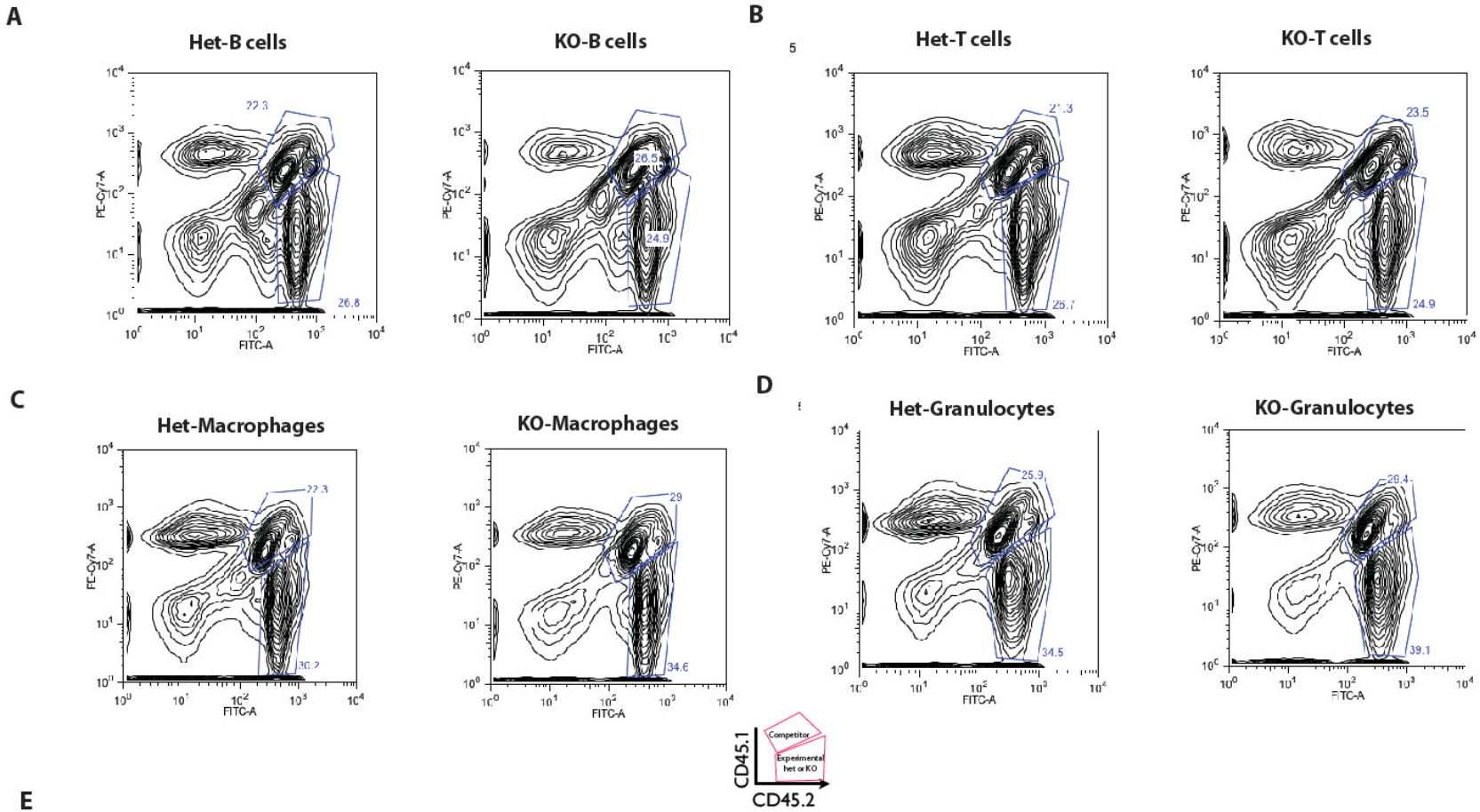

A
Week 4-tail bleed
Het-B220+
Het-Mac1+
KO-B220+
KO-Mac1+
PE-Cy7-A
FITC-A
48
42.7
29.9
32.2
50.8
40.3
26.7
27.2
Competitor
Experimental het or KO
CD45.1
CD45.2
B
Het
KO
% reconstitution in peripheral blood
60
50
40
30
20
10
0
B220+
Mac1+

Figure 3.6: Bone marrow analyses at week 16 of competitive transplantation
Representative analyses of B cell (A), T cell (B), macrophage (C), granulocyte (D) contributions of transplanted heterozygous (Het) or *Taf4b* KO cells to the bone marrow of recipient mice. CD45.1+/CD45.2+ cells are WT competitors, CD45.2+ cells are either Het or *Taf4b* KO experimental cells. (E) Quantification of all eight recipient mice for four conditions: two pairs each of het and *Taf4b* KO.


A
Het-B cells
KO-B cells
B
Het-T cells
KO-T cells
C
Het-Macrophages
KO-Macrophages
D
Het-Granulocytes
KO-Granulocytes
PE-Cy7-A
FITC-A
22.3
26.8
26.5
24.9
23.5
24.9
25.3
34.5
29.4
39.1
29
34.6
Competitor
Experimental het or KO
CD45.1
CD45.2
E
Het
KO
% reconstitution in BM
60
50
40
30
20
10
0
B cells
T cells
Macrophages
Granulocytes

Chapter 4

Mechanism of MEF2C-dependent transcription in lymphoid differentiation

Introduction

Hematopoiesis is the process that generates all blood cell types throughout the lifetime of an animal. Maintenance of homeostasis in blood cell differentiation is crucial for the immune system to fight against infections while also transporting oxygen throughout the body's tissues. The rapid turnover of blood cells requires the rare hematopoietic stem cells (HSC) to self-renew in their bone marrow niche, and differentiate when induced by a milieu of cytokines and signaling pathways (Rieger and Schroeder 2009). HSCs differentiate down three main pathways: myeloid, lymphoid, and erythroid (Rieger and Schroeder 2012). Differentiation along any of the three lineages requires an intricate coordination of signal relay and transcriptional regulation. One of the earliest lineage choices for differentiating HSCs is to adopt the lymphoid or myeloid fate. Several transcription factors involved in this choice have been identified. For example, CCAAT/enhancer binding protein alpha (C/EBPα) acts as the "master" myeloid regulator (Pu Zhang et al. 2002; Friedman 2007), and E2A proteins—E12 and E47 isoforms — function as key transcription factors for the lymphoid fates (Mandel and Grosschedl 2010). Finally, myocyte enhancer factor 2c (MEF2C) has recently been shown to be required in lymphoid-specific differentiation in this lineage decision (Stehling-Sun et al. 2009).

MEF2C is a member of MADS-box (MCM1, Agamous, Deficiens, Serum response factor) DNA binding domain-containing family of transcription factors (J F Martin et al. 1993). It was originally identified in skeletal and cardiac muscle development, wherein it is required for muscle differentiation and proper heart morphogenesis (Q Lin et al. 1997). Through conventional knockout (KO) mouse and cell line studies, MEF2C has also been shown to be required for proper vasculature development (Q Lin et al. 1998), neuronal differentiation (Skerjanc and Wilton 2000) (Hao Li et al. 2008), and chondrocyte hypertrophy during bone development (Arnold et al. 2007). In lymphocytes, however, MEF2C is the only isoform in the MEF2 family with specific expression in B cells (Swanson et al. 1998). Yet, only recently has the role for MEF2C in B cell development and function been investigated. Several conditional KO mice have been made with floxed-*Mef2c* exon 2 that codes for the MADS DNA-binding and dimerization domains (Vong et al. 2005). Vav-1 Cre *Mef2c* KO, where KO occurs after fetal liver hematopoiesis, showed slightly decreased numbers of peripheral blood B cells in younger mice and dramatically decreased bone marrow pre-pro-B populations in 1 year-old mice (Gekas et al. 2009). Furthermore, deletion of MEF2C at early B cell development with Mb1-Cre also showed a delay in this process with the expression of some key B cell genes decreased (Debnath et al. 2013). An Mx1-Cre (inducible in all hematopoietic lineages) *Mef2c* KO line showed decreased numbers of common lymphoid progenitors (CLP) and very low numbers of B cells but increased myeloid cell numbers in reconstitution of lethally irradiated mouse bone marrow (Stehling-Sun et al. 2009). In addition, two studies using CD19-Cre (committed B

cells) *Mef2c* KO mice showed that these animals had defects in B cell proliferation upon B cell receptor (BCR) stimulation (Khiem et al. 2008) (Wilker et al. 2008). Together, these studies present evidence that MEF2C is a lineage-restricting transcription factor that directs multi-potent hematopoietic progenitors to differentiate into the B cell lineage, as well as crucial for proper B cell function. However, how MEF2C transcriptionally regulates lymphoid differentiation and the identities of its downstream targets are not known.

The two CD19-Cre *Mef2c* KO studies showed conflicting mechanisms for MEF2C activation: either via p38 MAPK (Khiem et al. 2008) or the calcium-dependent calcineurin-calmodulin pathways (Wilker et al. 2008). The discrepancy can be partially explained by experiments in skeletal muscle where MEF2C was discovered to both exert transcriptional repression through class II HDACs (Lu et al. 2000) that could be regulated by calcium influx, and transcriptional activation via p38 MAPK-dependent phosphorylation (Han et al. 1997). Here, I address the bimodal regulation of MEF2C function. To that end, I identified p38 MAPK pathway as the activator of MEF2C in lymphoid versus myeloid fate decision, and the phosphorylation acts as a switch in MEF2C's preferential binding from a co-repressor, the B cell specific class II HDC7, for a key B cell transcription factor, early B cell factor (EBF1). This switch is important to turn on several B cell-specific MEF2C target genes that I identified here for the first time. My findings elucidated the mechanism, binding partners, and downstream targets by which MEF2C is able to drive lymphoid-specific hematopoietic differentiation.(Trompouki et al. 2011)

Results

MEF2C interacts with early B cell factor 1 (EBF1)

It has been shown in skeletal muscle cells that MEF2C can interact with basic helix-loop-helix (bHLH) transcription factors such as Myogenin when it forms a heterodimer with the E2A isoform, E12 protein (Molkentin et al. 1995). Therefore, it is likely that MEF2C binds known B cell transcription factors. To find MEF2C binding partners, I first took a candidate approach. Despite their wide range of expression patterns in various tissues, mice lacking E2A gene products, E12 and E47, have blocked B cell development (Bain et al. 1997). PAX5 was chosen due to its pivotal role as a B cell differentiation factor, without which pro-B cells still retain the ability to become macrophages and granulocytes. (Nutt et al. 1999). PU.1 is responsible for the bifurcation of the lympho-myeloid (LMPPs) from myelo-erythroid (CMPs) lineages. *Pu.1* KO mice fail to generate the earliest lymphoid and myeloid progenitors, thus show decreased numbers of B/T cells, granulocytes, and macrophages (Iwasaki et al. 2005). EBF1 is also a bHLH factor important in B cell lineage specification, specifically, in the regulation of differentiation and proliferation of B cells (Gyory et al. 2012) (Månsson et al. 2012). It contains an atypical zinc finger DNA binding domain and HLH dimerization domain (Siponen et al. 2010).

FLAG-tagged MEF2C was co-transfected with Myc-tagged E12, PAX5, PU.1, and EBF1. After FLAG pull-down, MEF2C was found to co-immunoprecipitate (co-IP) exclusively with EBF1 (Figure 4.1 A) and not with E12 (Figure 4.1B), PAX5 (Supplemental Figure

4.1A), or PU.1 (Supplemental Figure 4.1B). The reverse Myc pull-down confirmed EBF1 binding to FLAG-tagged MEF2C (Supplemental Figure 4.1D). Furthermore, the binding does not require DNA, because neither digestion of nucleic acids with benzonase treatment (Figure 4.1C) nor co-transfection of MEF2C with a DNA-binding mutant of EBF1 (H157A/C161S) (Fields et al. 2008) affected the interaction between the two factors (Supplemental Figure 4.1C). Despite a wealth of studies showing MEF2C phosphorylation is important for its transcriptional activity, the mechanism of this activation is still unknown. The phosphorylation sites were well characterized as T293, T300, and S387 in humans (Han et al. 1997) and T291, T298, and S378 in mice. These sites were mutated to either functional phosphomimetic (T291E, T298E, S387D, EED) or phospho-null (T291A, T298A, S287A, AAA). To test the role of MEF2C phosphorylation in binding to EBF1, FLAG-tagged MEF2C mutants were co-transfected into 293T cells with EBF1. Neither EED nor AAA mutants showed differential binding abilities to EBF1 compared to the WT MEF2C (Figure 4.1A and Supplemental Figure 4.1D). These results uncovered a novel binding partner of MEF2C, EBF1. However, this interaction is independent of DNA binding and the phosphorylation status of MEF2C.

MEF2C and EBF1 co-occupy potential enhancer elements genome-wide

If MEF2C and EBF1 binding is important for B cell fate determination, then they would be expected to bind common promoters and enhancers of B cell-specific genes. To test this hypothesis, targets of MEF2C and EBF1 co-regulation were obtained by chromatin immunoprecipitation followed by exonuclease treatment and deep sequencing (ChIP-exo) (Rhee and Pugh 2011). Since hematopoietic progenitors are rare in animals, we used an Lhx2 over-expressing hematopoietic progenitor cell line (HPC) (Pinto do O et al. 2002) and Abelson Murine Leukemia Virus (AMuLV)-transformed B cells (pre-B) (Muljo and Schlissel 2003) to represent their primary bone marrow counterparts. MEF2C ChIP-exo was performed with two different antibodies in both HPC and pre-B cells, while EBF1 ChIP-exo was performed with a goat polyclonal antibody only in pre-B cells since it is not expressed in HPCs. In pre-B cells, 16% of EBF1 peaks overlapped with MEF2C peaks, and 32.4% of MEF2C peaks overlapped with EBF1 peaks, resulting in a total of 8586 overlapped peaks (Figure 4.2A). This is consistent with the hypothesis that MEF2C and EBF1 bind each other and co-regulate downstream targets. Many of the MEF2C and EBF1 peaks mapped to inter-genic regions containing MEF2 or EBF1 consensus binding sequences, CTA(A/T)$_4$TAG and CCCNNGGG, respectively. Consistent with their roles in B cell development, many of the top 36% of targets bound by both MEF2C and EBF1 show B cell-specific expression patterns (Appendix IVa, bolded), some of the examples include: *IL7ra* (previously shown to be a MEF2C target (Stehling-Sun et al. 2009)), *Mef2c* and *Ebf1* themselves, *Ets*1, *Foxo1,* and *Myb* (representative gene tracks are shown in Figure 4.2 B-D). The finding that MEF2C regulates its own expression is not surprising since in skeletal muscle, a MEF2-reponsive cis-regulatory element in the *Mef2c* gene has been previously described (D Z Wang et al. 2001). Different lineage—B cells, T cells, myeloid— specific expression patterns of the targets were determined through the ImmGen database (Shay and Kang 2013).

MEF2C target genes in pre-B cells were also compared with MEF2C ChIP-exo data in HPCs. 12.3% of MEF2C peaks in HPCs overlapped with its peaks in pre-B cells, and 40% of pre-B peaks were found overlapping with HPC peaks, resulting in a total of 10580 overlapping peaks (Figure 4.2E). Interestingly, MEF2C targets unique in HPCs include many genes from other lineages, suggesting that MEF2C has B cell-independent functions in hematopoietic differentiation (Appendix IVb, myeloid genes are highlighted in red).

MEF2C and EBF1 can functionally co-activate transcription

To functionally verify that MEF2C and EBF1 can co-regulate their target genes, two B cell targets from the pre-B cell ChIP-exo datasets were selected for luciferase reporter activity assays: *Il7ra* and *Ebf1,* whose regulatory regions are highly conserved in humans and contain MEF2C and EBF1 binding sites. The regions around the MEF2C/EBF1 peaks were cloned into a vector containing the gene that encodes the firefly luciferase (*Luc2,* Promega) and co-transfected into 293T cells with Renilla luciferase reporter (Ren, Promega) as an internal control. FLAG-tagged MEF2C and Myc-tagged EBF1 were also co-transfected along with the luciferase reporters. The ratio of Luc2 over Ren luciferase reading represents the amount of Luc2 activation. *IL7ra* showed specific increase in luciferase activity when MEF2C and EBF1 were co-transfected, compared to either alone or the empty vector control (Figure 4.3A, black bars). Furthermore, when MEF2C and EBF1's DNA-binding activities were abolished by mutating the MEF2C binding site, *Il7ra*-Luc2 no longer showed MEF2C or EBF1-dependent luciferase activity (Figure 4.3A, white bars). This co-activation between MEF2C and a second transcription factor was specific to EBF1, since co-transfection of either E12 or E47 with MEF2C failed to activate *IL7ra* reporter (Figure 4.3B). This result was not due to differential expression of transfected proteins as all were expressed at similar levels (Figure 4.3C). EED mutant version of MEF2C did not show enhanced transcriptional activity alone or with EBF1 in *Il7ra* luciferase assays compared to WT MEF2C. However, the AAA MEF2C mutant did not have reduced luciferase activity when MEF2C binding site was mutated, suggesting that the activity from WT *Il7ra* reporter in the presence of AAA MEF2C is nonspecific. Therefore, phosphorylation is required, but not sufficient, to transactivate this MEF2C-dependent enhancer. The MEF2C/EBF1 binding sites near the *Ebf1* gene also showed specific activity that was the highest when both transcription factors were introduced into the cells (Supplemental Figure 4.2A). In this case, the relatively lower co-activation compared to either alone was due to less MEF2C WT and EED protein expression in cells that were co-transfected with EBF1 (Supplemental Figure 4.3B). Taken together, these results suggest that in hematopoietic differentiation, MEF2C binds a well-characterized B cell transcription factor, EBF1, and in turn the two together transcriptionally activate B lineage genes directly.

MEF2C target genes in B cells have reduced expression in Mef2c KO mice.

ChIP binding and luciferase assays suggest that MEF2C and EBF1 co-activate their B cell specific target genes. It reasons that if MEF2C functions to activate lymphoid-specific genes and repress myeloid genes, then MEF2C-null cells will have reduced lymphoid transcripts and higher myeloid gene expression. Therefore, I next tested if the expression levels of these targets were indeed down-regulated when cells are depleted of MEF2C

proteins. Mx1-Cre mice were mated with *Mef2c*-floxed mice (a generous gift from the Schwarz lab) and the offspring were injected with polyinosinic:polycytidylic acid (pIpC) to induce the efficient deletion of MEF2C protein. *Mef2c* KO mice have decreased level of common lymphoid progenitors (CLPs) that give rise to B, T, and natural killer (NK) cells, as well as decreased B cell differentiation potential when cultured *in vitro* (Stehling-Sun et al. 2009). To confirm this, I isolated bone marrow from either KO or WT littermates and checked for *Mef2c* deletion as well as CLP percentages. *Mef2c* transcript level was dramatically reduced in KO cells (Supplemental Figure 4.3A) and CLP percentage was decreased as previously reported (Supplemental Figure 4.3B). Additionally, B220+ cell percentage was decreased in *Mef2c* KO mice, consistent with its known function in B cell development (Supplemental Figure 4.3C). Interestingly, percentages of lineage negative/c-Kit+/Sca1+ (LKS) hematopoietic stem/progenitor cells were increased in KO mice, suggesting that in the absence of MEF2C, mice showed a blockage in differentiation, and specifically differentiation into the lymphoid lineage (Supplemental Figure 4.3D).

A survey of the transcriptome by RNA-seq of *Mef2c* KO and WT CLPs revealed that without MEF2C, many of the target genes found in ChIP-exo data have >2.5 fold down-regulated expression in *Mef2c* KO cells, especially those associated with the B lineage, such as *Il7ra, Ets1, Myb, Foxo1, and Ebf1.* Furthermore, many B cell markers or genes important for B cell functions were down-regulated in *Mef2c* KO CLPs: *Rag1*, *Rag2*, *Pax5, Il12a, Cd22,* sometimes more than 18 fold such as *Vpreb1* and *Igll* (Appendix Va, bolded). Consistent with MEF2C's role in lymphoid-specific development, many myeloid markers were up-regulated in MEF2C-null cells, such as *Csf2ra*, *Flt3l*, *Fcgr3, Stat1,* and *Stat2* (Appendix Vb, bolded). In addition, many T cell specific genes were down-regulated in *Mef2c* KO CLPs, such as *Tcf7, Cxcr3, Il6ra,* and *Gata3* (Appendix Va, red), suggesting that MEF2C may play a role in T cell development as well. Select targets from RNA-seq data were further confirmed in qRT-PCR analyses of various lineages in the blood (Figure 4.4A-C). The chosen B cell-specific genes—*Pou2af1, Myb, Rag1,* and *Il7ra*—were all down-regulated in *Mef2c* KO mice in all lymphoid lineages tested (Figure 4.4 A-C). Consistent with the phenotype that *Mef2c* KO mice have more myeloid cell differentiation at the expense of B lineage differentiation (Stehling-Sun et al. 2009), sorted lymphoid cells such as CLPs and B220+ B cells from *Mef2c* KO mice have high expression levels of myeloid genes in *Mef2c* KO mice (Figure 4.4A, B). Furthermore, this expression pattern was established earlier in LKS progenitor cells where MEF2C was first deleted in these mice (Figure 4.4D).

p38 MAPK activates MEF2C in B cell differentiation

While results above demonstrate MEF2C complexes with EBF1 to activate lymphoid genes, it is still unclear how MEF2C is activated. To determine the mechanism by which MEF2C drives progenitors to differentiate into B cells, I set up *in vitro* differentiation assay, wherein lineage negative progenitors were isolated from mouse bone marrow (Lin-) and grown either in stimulation/undifferentiation media or B cell differentiation media for two weeks (Figure 4.5A). I first tested the effect of MEF2C deletion on differentiation. *Mef2c*-floxed Lin- progenitor cells were either infected with a lentiviral vector encoding Cre recombinase and puromycin resistance (*Mef2c* KO) or in combination with a lentiviral

vector expressing WT MEF2 (*Mef2c* KO and WT *Mef2c* rescue). After puromycin selection for 2 days, these cells were plated in differentiation media. B cell differentiation potential was diminished in *Mef2c* KO cells as measured by CD19 and B220 cell surface markers. This defect was rescued in *Mef2c* KO cells with the ectopic expression of WT *Mef2c* (Figure 4.5B).

Small molecule inhibitors specific against either p38 MAPK (SB203580, or SB) or extracellular signal-induced kinases (Erk) (U0216) were used to treat the cells during differentiation. SB-treated cells mimicked the phenotype of *Mef2c*-KO cells, where B cell differentiation was severely impaired (Figure 4.5C), when compared to DMSO control-treated cells. In addition, SB-treated cells grown in B cell-inducing media exhibited slightly more myeloid surface markers, Gr-1, again consistent with the reported MEF2C-null phenotype (Stehling-Sun et al. 2009) where MEF2C is a potent lymphoid fate inducer (Figure 4.5D). Conversely, ERK inhibitor U0126-treated cells did not show a similar decrease of differentiated B cells in culture. In fact, U0126 treatment resulted in slightly more B cells than DMSO control-treated cultures (Figure 4.5C).

In skeletal muscle, upon an activating signal received by the differentiating muscle cells, MEF2C is phosphorylated through the p38 MAPK pathway at three specific residues in its transactivation domain, as described above. Lentiviral vectors containing WT, phosphomimetic (EED), or phospho-null (AAA) versions of MEF2C were constructed. These vectors contain IRES-hCD4 reporters so Lin- progenitors with ectopic *Mef2c* can be sorted by hCD4 expression. After sorting, cells were cultured in the same B cell differentiation condition and/or drug treatments as described above (Figure 4.5A). EED mutant-infected cells were able to partially overcome the B cell differentiation defect induced by p38 MAPK inhibitor SB, whereas WT or AAA mutant could not, compared to empty vector (EV) infected cells (Figure 4.6A, Supplemental Figure 4.4A-C, E). Furthermore, in skeletal muscle and chondrocyte differentiation, MEF2C was known to directly bind DNA and exert transcription repression through the recruitment of class II HDAC4 and 5. The repression can be reversed through calcium/calmodulin-dependent protein kinases (CaMK) that phosphorylate HDACs, resulting in their export out of the nucleus (Lu et al. 2000) (Mckinsey et al. 2000). To test whether relief of HDAC co-repression is important for MEF2C activation, I made a "super-activating" mutant of MEF2C, termed HBD-EED, wherein the HDAC binding domain in the EED MEF2C's MADS-box was mutated (VLL65-67/ASR). Lin- cells infected with this mutant could completely rescue the SB phenotype compared to DMSO control treated cells (Figure 4.6A, Supplemental Figure 4.4D). Analysis of the myeloid differentiation, as measured by Gr-1 cell surface marker, showed that by day 14, SB-treated EV, WT or AAA *Mef2c*-infected cells all had significant amount of myeloid differentiation though they were induced to become B cells, suggesting the importance of p38 MAPK in lymphoid lineage determination (Figure 4.6B). However, EED and HBD-EED *Mef2c*-infected cells maintained their potential to repress myeloid differentiation fate, bypassing the need for p38 MAPK (Figure 4.6B)

These results suggest that MEF2C is downstream of p38 MAPK pathway to drive B cell specific differentiation. The strong rescue results displayed by the HBD-EED mutant-

infected cells suggest that blocking MEF2C interaction with HDACs is also important in its activation.

MEF2C phosphorylation does not affect its subcellular localization

Since phosphorylation can affect the subcellular location of transcription factors such as NFAT in skeletal muscle growth (Hogan et al. 2003), I tested the effect of p38 MAPK inhibitor on MEF2C nuclear location in cells. A construct containing MEF2C fused to GFP was transfected into 293T cells before treatment with either DMSO-control or p38 MAPK inhibitor, SB. Fluorescence images taken with DAPI nuclear stain show that MEF2C nuclear location was not affected after SB treatment (Figure 4.7A). Cells that were transfected with phosphomimetic (EED) MEF2C also did not show a preference for nuclear or cytoplasmic localization with or without p38 MAPK inhibitor treatment (Figure 4.7B). Finally, phospho-null (AAA) mutant of MEF2C also showed exclusive nuclear staining (Figure 4.7C). These results demonstrate that phosphorylation at the three residues in MEF2C's transactivation domain does not affect its subcellular localization.

Phosphorylation of MEF2C regulates its preferential binding to co-activator or co-repressor

Transcriptome analyses of *Mef2c* KO and WT mice showed that several myeloid genes had up-regulated expression levels when MEF2C is depleted in the animal, such as *Csf2ra, Csf3r*, and *Cscl10* (Appendix Vb, bolded). Recently it has been shown that in a pre-B cell line that can be induced to transdifferentiate into myeloid cells, MEF2C binds a B cell specific class II HDAC, HDAC7. These experiments suggested that this interaction is required to deter transdifferentiation of B cells to myeloid cells by repressing myeloid genes such as *Cxcl10* (Barneda-Zahonero et al. 2013). However, since my ChIP-exo data did not show MEF2C binding to the myeloid genes that were down-regulated in *Mef2c* KO mice, it is unlikely that MEF2C is directly repressing myeloid genes with its co-repressor, HDAC7. In addition, some B cell genes important for B cell function had increased expression in MEF2C-null CLPs: *Il21r, Fcrl1,* and *Ciita* (Appendix Vb, red). ChIP-exo data in pre-B cells show strong MEF2C binding at these loci (Supplemental Figure 4.5 A-C), which are not activated until mature B cell stage. Taken together, these results suggest that MEF2C can repress as well as activate its downstream targets. Furthermore, B cell differentiation assays showed that phosphomimetic MEF2C with abolished HDAC binding ability, termed "super-activating", can overcome p38 MAPK inhibitor effect completely. This observation, along with the results that phosphomimetic alone can partially rescue p38 MAPK inhibition, suggests that the two mutations cooperate in activating MEF2C downstream of p38 MAPK. Therefore, I hypothesized that p38-dependent MEF2C phosphorylation acts as a switch for its binding from HDAC7 to EBF1, a co-activator of B cell development. In that case, phosphomimetic MEF2C will have preferential binding to EBF1 and/or less binding to HDAC7. To test this, I co-transfected EBF1, HDAC7, along with WT or EED mutant of MEF2C into 293T cells. Interestingly, when the EED mutant is present in the cells with EBF1 and HDAC7, MEF2C can no longer co-IP with HDAC7, compared to when WT MEF2C is present, suggesting the interaction between MEF2C and HDAC7 can be out-competed by its interaction with EBF1 when MEF2C is phosphorylated (Figure 4.8A, left panel, FLAG-IP, compare lanes 4 and 7). Varying the amount of EBF1 introduced into the cells also affected the binding between EED MEF2C and HDAC7; when

less EBF1 is expressed in the cells, EED MEF2C and HDAC7 interaction was increased, compared to WT MEF2C-transfected cells or cells with higher expression of EBF1 (Figure 4.8B, left panel, FLAG-IP, compare lanes 3, 6, and 7).

Together, these results suggest that p38 MAPK phosphorylation of MEF2C acts as a switch to skew its binding preference toward a co-activator of B cell function, EBF1, away from a co-repressor in order to prevent premature activation of lymphoid genes that are important in B cell functions.

Discussion

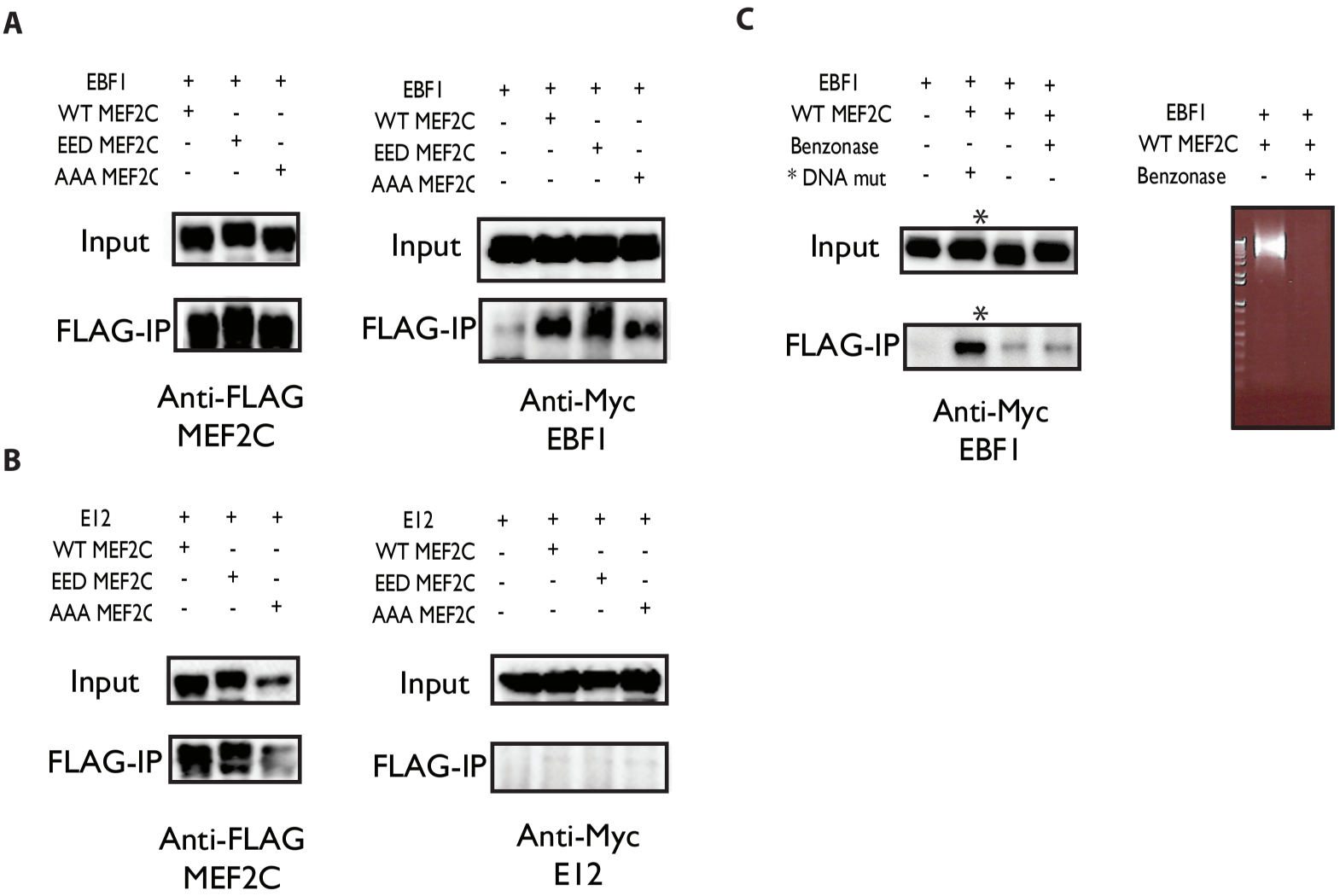
How MEF2C functions to activate lymphoid genes while repress the myeloid differentiation program has not been satisfactorily answered. I have shown in this study that p38 MAPK phosphorylation of MEF2C is important for its function to drive B cell differentiation. However, the mechanistic function of MEF2C phosphorylation remained elusive, since phosphorylation does not promote its interaction with EBF1 or affect its subcellular localization. I sought to elucidate the potential molecular function of these post-translational modifications. The experiments above suggest a mechanism where in the absence of activation by p38 MAPK, MEF2C complexes with HDAC7 at early precursor cell stages to repress genes that are responsible for B cell functions, thus preventing the premature activation of B cell genes before commitment to the B cell fate. Phosphorylation by p38 then alters MEF2C such that it complexes with a B cell-specific transcription factor, EBF1, to activate genes that are important for driving multi-potent progenitors toward the B cell fate.

My experiments showed that MEF2C and EBF1 co-regulate many B cell genes such as *Ets1* and *Myb.* Therefore, it will be of interest to analyze the effects of deleting both MEF2C and EBF1 in cells. To that end, *Ebf1* shRNA can be introduced via lentiviruses into *Mef2c* KO Lin- cells or CLP. Cells with successfully integrated shRNA can be differentiated toward the B cell lineage and/or their RNA can be extracted to test whether *Ets1* and *Myb* RNA levels were further decreased than loss-of-function for either MEF2C or EBF1 alone. A report that utilized a 4x MEF2C-responsive enhancer in luciferase reporter assays showed that the phospho-null mutant of MEF2C was unable to induce luciferase reporter activity (Khiem et al. 2008). However, my experiments did not show a large defect in transactivation when AAA mutant was used to induce WT *Il7ra* luciferase activity, compared to WT or phosphomimetic (EED) mutant of MEF2C. One explanation for this discrepancy could be due to the usage of native enhancers in my experiments, and the requirement for EBF1 to co-activate the particular genes that I tested. However, when MEF2C-binding site in the *Il7ra* regulatory region was mutated, WT and EEED MEF2C both had reduced levels of activation, and the AAA mutant did not. This suggests that the AAA mutant activity on the WT *Il7ra* reporter is non-specific. In addition, I have shown that phosphorylation of MEF2C acts as a switch for its binding preference from HDAC7 to EBF1. However, EED mutant alone was not as efficient in rescuing the p38 MAPK inhibition effects on B cell differentiation, compared to the "super-activating" EED mutant that also cannot bind HDAC7. This suggests that phosphorylation alone is not enough to transactivate MEF2C targets. Both phosphorylation and presence of EBF1 are needed to out-compete the co-repression exerted onto MEF2C by HDAC7.

Class II HDACs, particularly Class IIa HDAC 4, 5, 7, and 9, show tissue-specificity unlike their Class I counterparts. For example, KO mouse studies have shown that HDAC5 and 9 play important overlapping roles in heart development. Mice null for these genes lack the ability of the heart to respond to stress signals such as aortic constriction (Chang et al. 2004) (Chun Li Zhang et al. 2002). HDAC7 KO mice die early in embryogenesis due to the disruption of their endothelial cell-cell adhesion and thus rupture of blood vessels (Chang et al. 2006), similar to *Mef2c* conventional KO mice (Q Lin et al. 1998). Direct interactions between Class II HDACs and MEF2 proteins have been shown in muscle differentiation (Lu et al. 2000) and B cell lineage protection (Barneda-Zahonero et al. 2013), suggesting a general mechanism whereby Class IIa HDACs bind MEF2 family to co-repress MEF2-dependent genes. Class IIa HDACs are regulated by phosphorylation at conserved residues in their N-terminal domains by calcium/calmodulin-dependent protein kinases (CaMK). This phosphorylation leads to HDACs being shuttled out of the nucleus and anchored in the cytoplasm by 14-3-3 proteins, thus relieving their co-repression effect on MEF2C. Though several tissue developmental processes share this mechanism of regulating MEF2C target genes, CaMK role in directing lymphoid and B cell differentiation has not been elucidated. Though my results showed a novel mechanism of controlling HDAC-MEF2C binding—through p38 MAPK phosphorylation of MEF2C and its preferential binding to a co-activator—it cannot be ruled out that CaMKs can play a role in this developmental process. *Camk2d* encodes the most highly expressed CaMKll in hematopoiesis, especially at all stages of B cell development starting at the pro-B cells (ImmGen database (Shay and Kang 2013)). It will be of interest to treat Lin- progenitor cells with CaMKII inhibitors such as KN-93 before inducing B cell development, then check for any defects these cells might display in completing B cell differentiation. To verify the proposed mechanism here that EBF1 competes with HDAC7 for MEF2C binding when MEF2C is phosphorylated by p38 MAPK, the interaction domain between EBF1 and MEF2C will need to be mapped. Since HDAC binds MEF2C in its MADS box DNA binding and dimerization domains (Molkentin et al. 1996), the region between the N-terminal part of MEF2C and its transactivation domain should be examined.

These experiments identified a binding partner for MEF2C, EBF1, as well as a novel mechanism that phosphorylation by p38 MAPK pathway facilitates MEF2C switch from a transcription repressor to an activator of B cells specific genes. This study also identified numerous new direct targets of MEF2C, many of which are co-regulated by EBF1. These findings will contribute to the elucidation of a transcription network that is required to drive lymphoid and B cell-specific hematopoietic differentiation.

Figure 4.1: MEF2C binds early B cell factor, EBF1, and not other bHLH factors
FLAG-tagged WT, phosphomimetic (EED), or phospho-null (AAA) versions of MEF2C were co-transfected into 293T cells with Myc-tagged EBF1 (A) or E12 (B). After FLAG-IP, the immunocomplexes were blotted with anti-FLAG or anti-Myc antibodies, as indicated. (C) FLAG-tagged WT MEF2C was co-transfected into 293T cells with Myc-tagged EBF1. FLAG-IP was performed with or without benzonase and blotted with anti-Myc antibodies. Asterisk denotes a nonspecific band from an unrelated experiment. Right panel: ethidium bromide gel showing all nucleic acids were degraded following benzonase treatment (1 hour at 4°C).


A
EBF1 + + +
WT MEF2C + - -
EED MEF2C - + -
AAA MEF2C - - +
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FLAG-IP
Anti-FLAG
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FLAG-IP
Anti-Myc
EBF1
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EED MEF2C - + -
AAA MEF2C - - +
Input
FLAG-IP
Anti-FLAG
MEF2C
E12 + + + +
WT MEF2C - + - -
EED MEF2C - - + -
AAA MEF2C - - - +
Input
FLAG-IP
Anti-Myc
E12
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EBF1 + + + +
WT MEF2C - + + +
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EBF1 + +
WT MEF2C + +
Benzonase - +

Figure 4.2: MEF2C and EBF1 co-regulate many genes
(A) Venn diagram of MEF2C and EBF1 overlapping ChIP-exo peaks in pre-B cells. (B)-(D) Representative MEF2C and EBF1 binding profiles at *Myb, Il7r,* and *Mef2c* loci. Tracks 1-4: MEF2C binding with two different antibodies, Watson and Crick strands. Tracks 5 and 6: Pre-B cell input (from EBF1 ChIP-exo), Watson and Crick strands. Tracks 7 and 8: EBF1 binding, Crick and Watson strands. (E) Venn diagram of overlapping MEF2C ChIP-exo peaks between pre-B cells and HPCs.

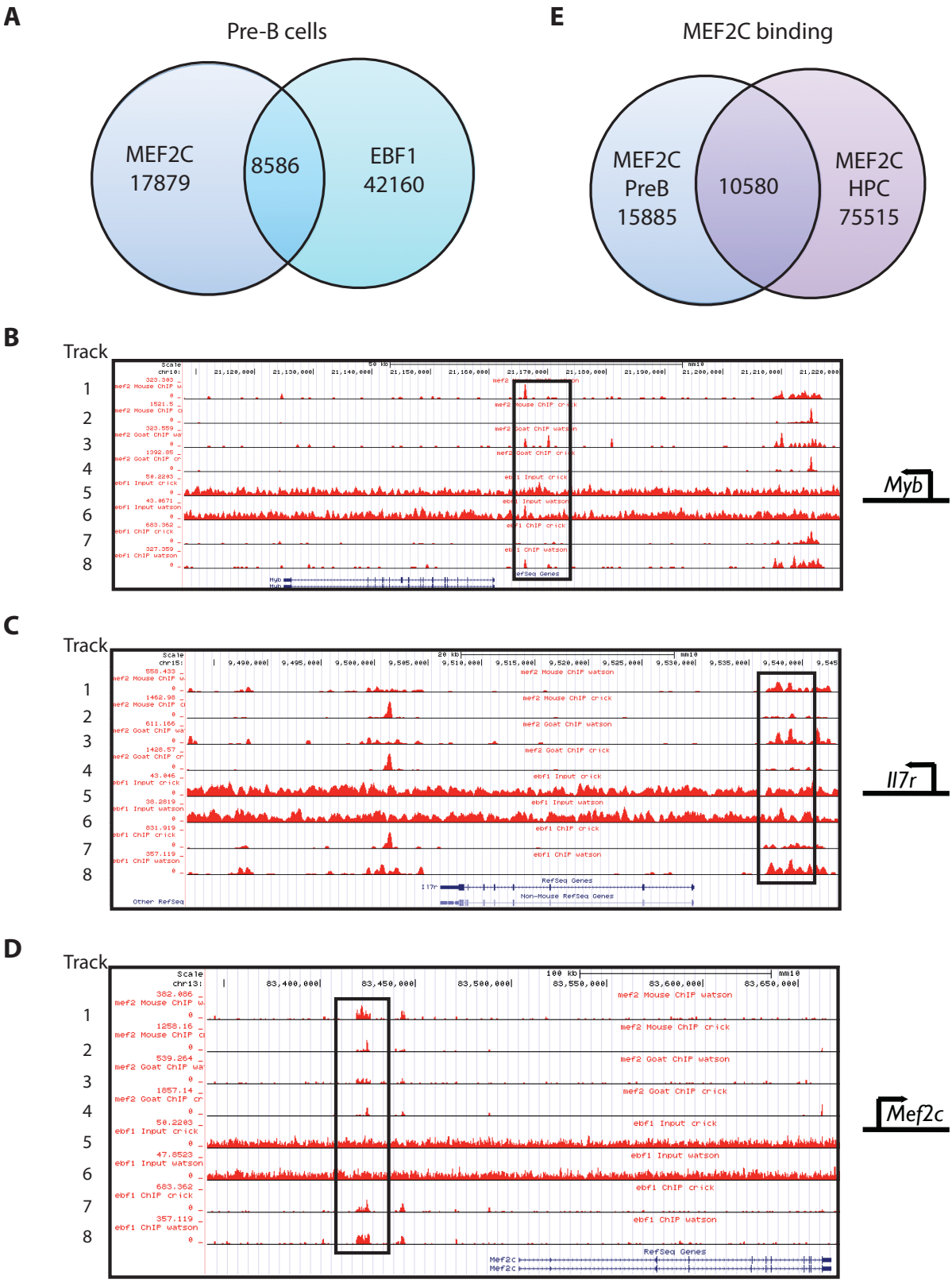

A
Pre-B cells
MEF2C
17879
8586
EBF1
42160
E
MEF2C binding
MEF2C
PreB
15885
10580
MEF2C
HPC
75515
B
Track
1
2
3
4
5
6
7
8
Myb
C
Track
1
2
3
4
5
6
7
8
Il7r
D
Track
1
2
3
4
5
6
7
8
Mef2c

Figure 4.3: Luciferase reporter assays show MEF2C and EBF1 can functionally co-activate their targets found in ChIP-exo
(A) Relative luciferase activity normalized to cell lysates with *Il7ra* alone. FLAG-tagged MEF2C WT, phosphomimetic (EED), or phospho-null (AAA) mutants were co-transfected with Myc-tagged EBF1, Renilla internal control vector, and either WT pGL4.23-*Il7ra* (black bars) or the luciferase reporter with mutated MEF2C binding site (white bars). (B) Relative luciferase activity from cell lysates co-transfected with FLAG-tagged MEF2C WT, phosphomimetic (EED), or phospho-null (AAA) mutants and Myc-tagged E12 or E47, Renilla internal control vector, and WT *Il7ra* reporter. (C) Protein expression of various transfected conditions, blotted either with anti-FLAG antibody for MEF2C, or anti-Myc antibody for EBF1, E12, or E47, as indicated.

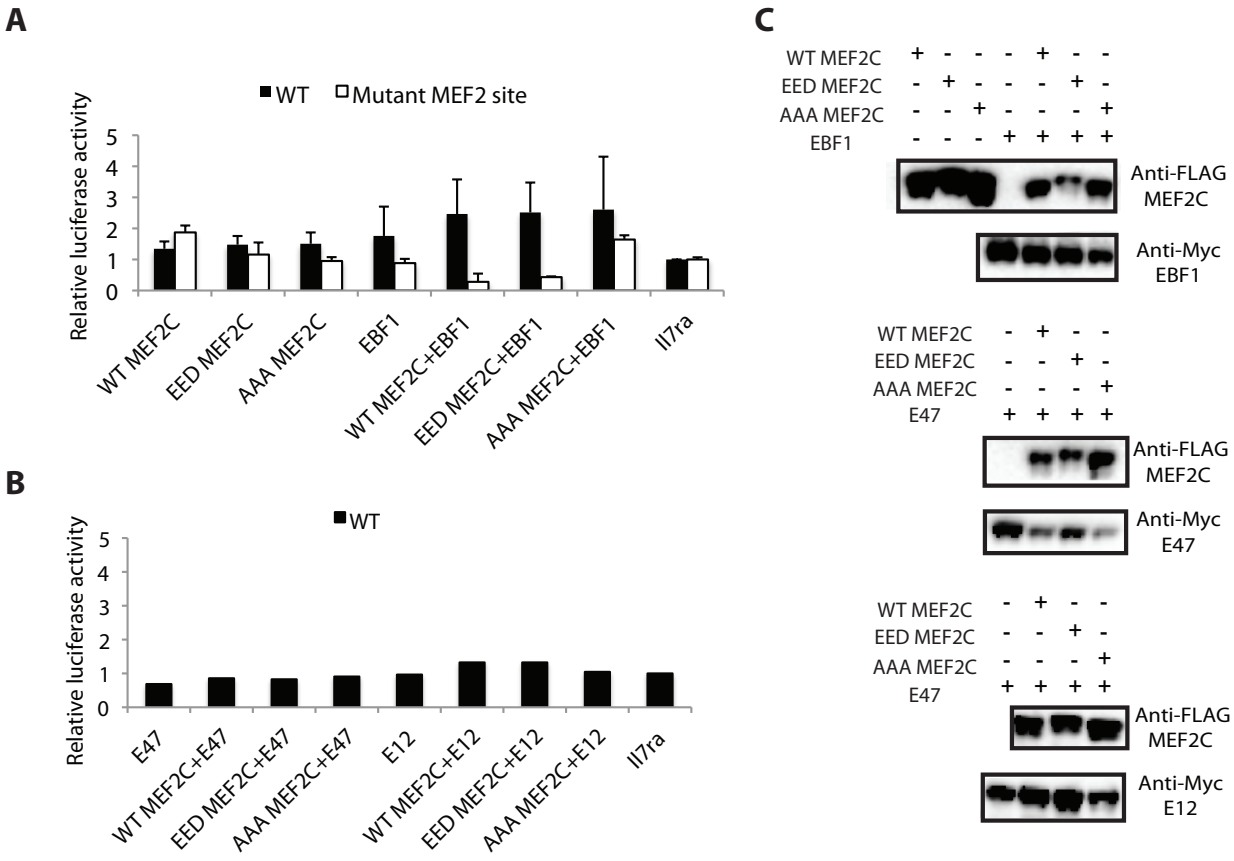
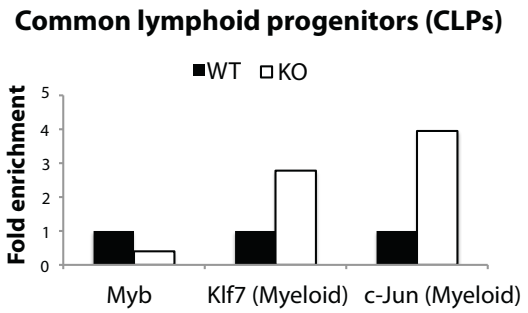
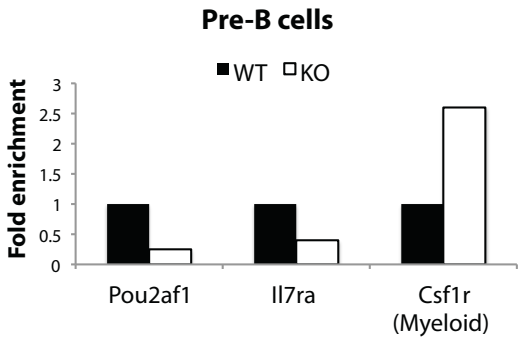

A
WT
Mutant MEF2 site
Relative luciferase activity
0
1
2
3
4
5
WT MEF2C
EED MEF2C
AAA MEF2C
EBF1
WT MEF2C+EBF1
EED MEF2C+EBF1
AAA MEF2C+EBF1
Il7ra
B
WT
Relative luciferase activity
0
1
2
3
4
5
E47
WT MEF2C+E47
EED MEF2C+E47
AAA MEF2C+E47
E12
WT MEF2C+E12
EED MEF2C+E12
AAA MEF2C+E12
Il7ra
C
WT MEF2C + - - - + - -
EED MEF2C - + - - - + -
AAA MEF2C - - + - - - +
EBF1 - - - + + + +
Anti-FLAG MEF2C
Anti-Myc EBF1
WT MEF2C - + - -
EED MEF2C - - + -
AAA MEF2C - - - +
E47 + + + +
Anti-FLAG MEF2C
Anti-Myc E47
WT MEF2C - + - -
EED MEF2C - - + -
AAA MEF2C - - - +
E47 + + + +
Anti-FLAG MEF2C
Anti-Myc E12

Figure 4.4: Relative expression levels of various B cell and myeloid genes in different hematopoietic lineages from *Mef2c* KO mice compared to WT littermates
(A) Relative expression of B cell gene *Myb* and myeloid genes *Klf7* and *c-Jun* in *Mef2c* KO CLPs compared to WT CLPs. (B) Relative expression of B cell genes *Pou2af1* and *Il7ra*, and myeloid gene *Csf1ra* in *Mef2c* KO pre-B cells compared to WT cells. (C) Relative expression of B cell genes *Il7ra*, *Rag1*, and *Myb* in *Mef2c* KO B220+ B cells compared to WT cells. (D) Relative expression of B cell genes *Il7ra* and *Myb*, and myeloid gene *Klf7* in *Mef2c* KO LKS (lineage negative/c-Kit+/Sca1+) progenitors compared to WT cells.

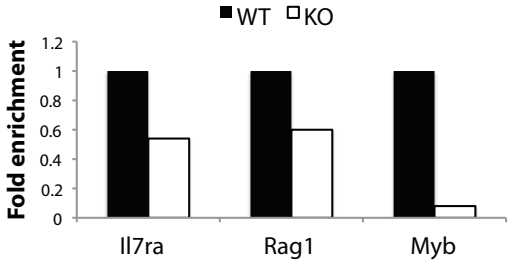
A


Common lymphoid progenitors (CLPs)
WT
KO
Fold enrichment
0
1
2
3
4
5
Myb
Klf7 (Myeloid)
c-Jun (Myeloid)

B


Pre-B cells
WT
KO
Fold enrichment
0
0.5
1
1.5
2
2.5
3
Pou2af1
Il7ra
Csf1r
(Myeloid)

C


B220+ cells
WT
KO
Fold enrichment
0
0.2
0.4
0.6
0.8
1
1.2
Il7ra
Rag1
Myb

D

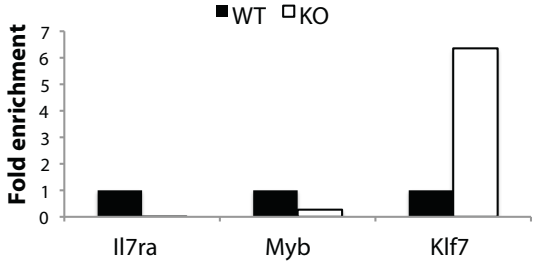

LKS stem/progenitor cells
WT
KO
Fold enrichment
0
1
2
3
4
5
6
7
Il7ra
Myb
Klf7

Figure 4.5: *In vitro* B cell differentiation of lineage negative progenitor cells (Lin-)
(A) Differentiation scheme. (B) FACS plots of B cell differentiation as measured by B220 and CD19 surface markers. Left: WT Lin- cells; middle: *Mef2c*$^{flox/flox}$ Lin- cells infected with Cre recombinase and selected with puromycin (*Mef2c* KO); right: *Mef2c* KO Lin- cells infected with Cre recombinase and WT *Mef2c* vector, then selected with puromycin. (C) and (D) FACS plots of B cell differentiation as measured by B220 and CD19 surface markers (C) or myeloid surface marker Gr-1 (D) in undifferentiated WT Lin- cells, DMSO control treated Lin- cells, p38 MAPK inhibitor (SB203580, SB-p38i) treated Lin- cells, or ERK inhibitor (U0126, ERKi) treated Lin- cells.

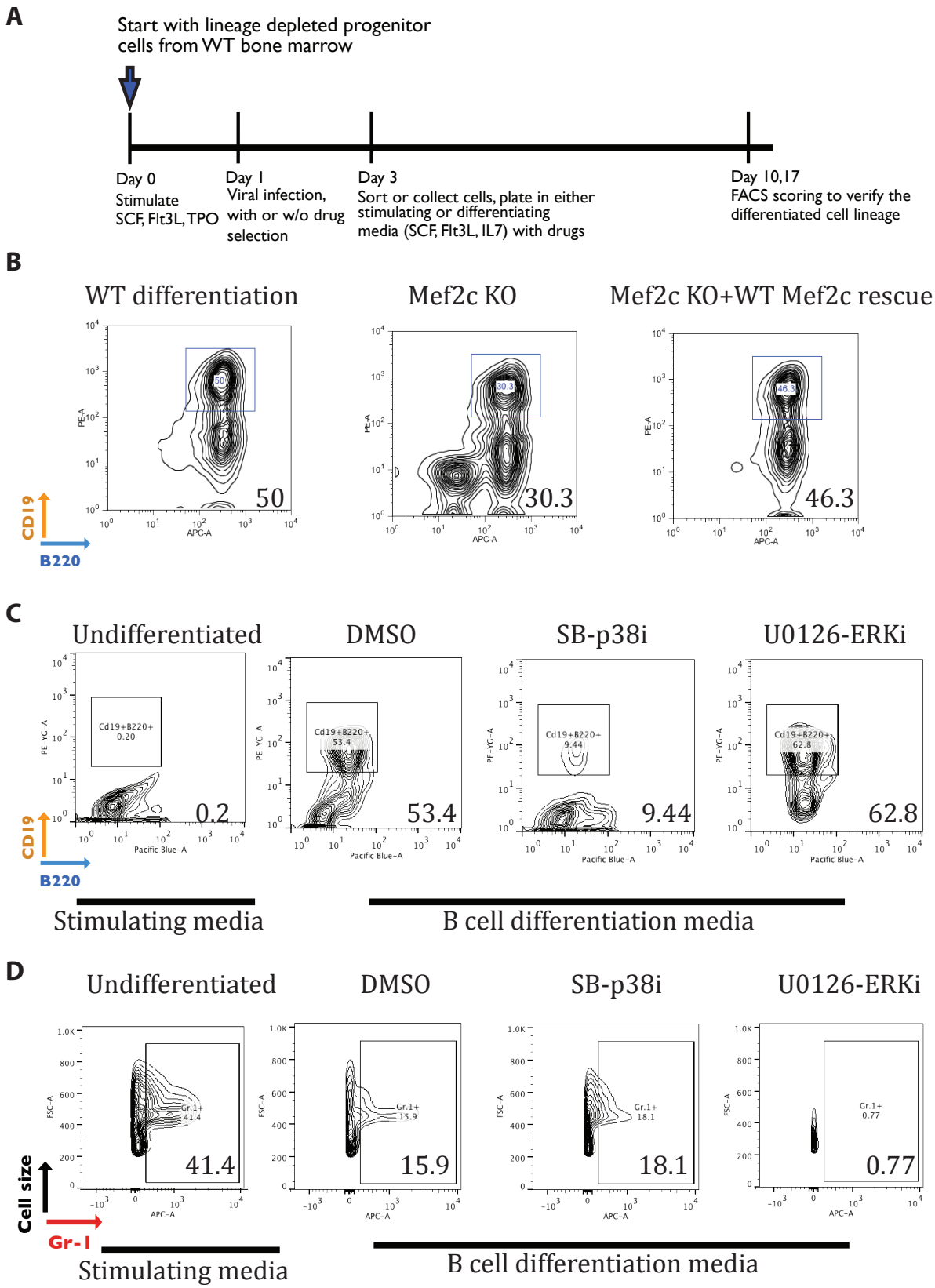
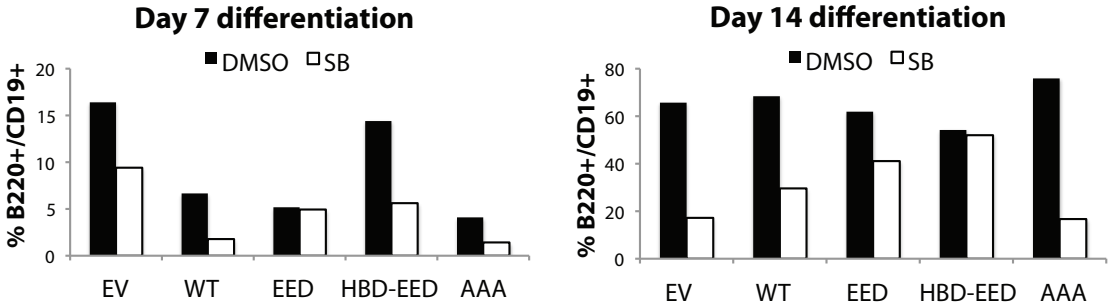

A
Start with lineage depleted progenitor cells from WT bone marrow
Day 0
Stimulate
SCF, Flt3L, TPO
Day 1
Viral infection, with or w/o drug selection
Day 3
Sort or collect cells, plate in either stimulating or differentiating media (SCF, Flt3L, IL7) with drugs
Day 10,17
FACS scoring to verify the differentiated cell lineage
B
WT differentiation
Mef2c KO
Mef2c KO+WT Mef2c rescue
50
30.3
46.3
CD19
B220
C
Undifferentiated
DMSO
SB-p38i
U0126-ERKi
Cd19+B220+
0.20
53.4
9.44
62.8
Stimulating media
B cell differentiation media
D
Undifferentiated
DMSO
SB-p38i
U0126-ERKi
Gr.1+
41.4
15.9
18.1
0.77
Cell size
Gr-1
Stimulating media
B cell differentiation media

Figure 4.6: p38 MAPK inhibitor-induced B cell differentiation defects can be rescued by MEF2C mutants

Percentages of B220 and CD19 positive cells (A) or Gr-1 positive cells (B) in culture after either 7 (left) or 14 (right) days of B cell differentiation. WT Lin- cells were infected with empty vector (EV), WT *Mef2c*, phosphomimetic *Mef2c* (EED), "super-activating" *Mef2c* with phosphomimetic and HDAC-binding mutations (HBD-EED), or phospho-null *Mef2c* (AAA). Cells were then sorted for hCD4 expression and cultured in B cell differentiation media with either DMSO (black bars) or p38 MAPK inhibitor SB203580 (white) treatments.

A


Day 7 differentiation
DMSO
SB
% B220+/CD19+
20
15
10
5
0
EV
WT
EED
HBD-EED
AAA
Day 14 differentiation
DMSO
SB
% B220+/CD19+
80
60
40
20
0
EV
WT
EED
HBD-EED
AAA

B

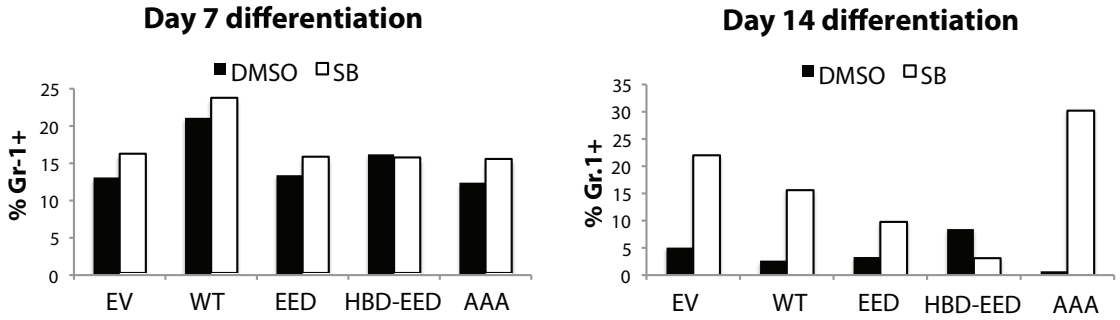
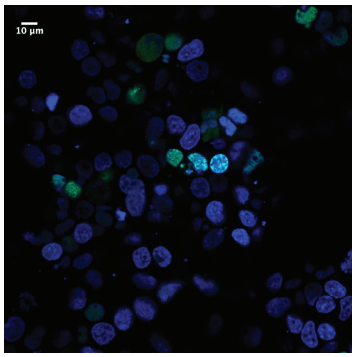

Day 7 differentiation
DMSO
SB
% Gr-1+
25
20
15
10
5
0
EV
WT
EED
HBD-EED
AAA
Day 14 differentiation
DMSO
SB
% Gr.1+
35
30
25
20
15
10
5
0
EV
WT
EED
HBD-EED
AAA

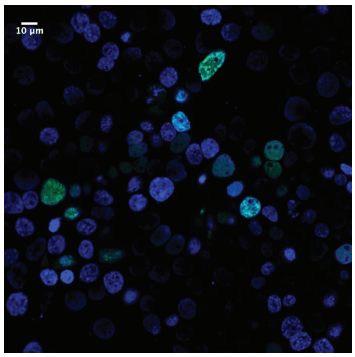
Figure 4.7: MEF2C shows exclusive nuclear localization, despite its phosphorylation status
293T cells transiently transfected with WT MEF2C-GFP (A), phosphomimetic (EED) MEF2C-GFP (B), or phospho-null (AAA) MEF2C-GFP (C). Cells were treated with either DMSO or p38 MAPK inhibitor SB203580 except for the AAA-transfected cells, and imaged with DAPI nuclear staining.

A

WT MEF2C
DMSO

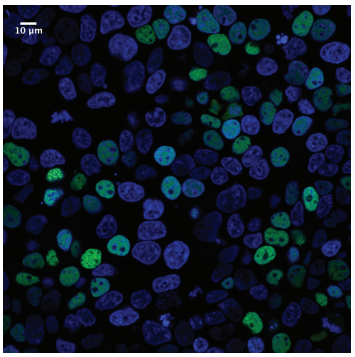


WT MEF2C
p38 MAPKi SB

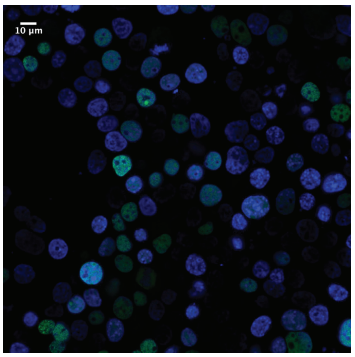


B

EED MEF2C
DMSO



EED MEF2C
p38 MAPKi SB



C

AAA MEF2C
DMSO

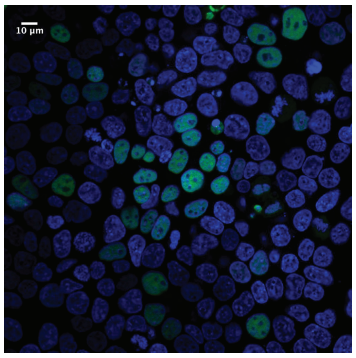
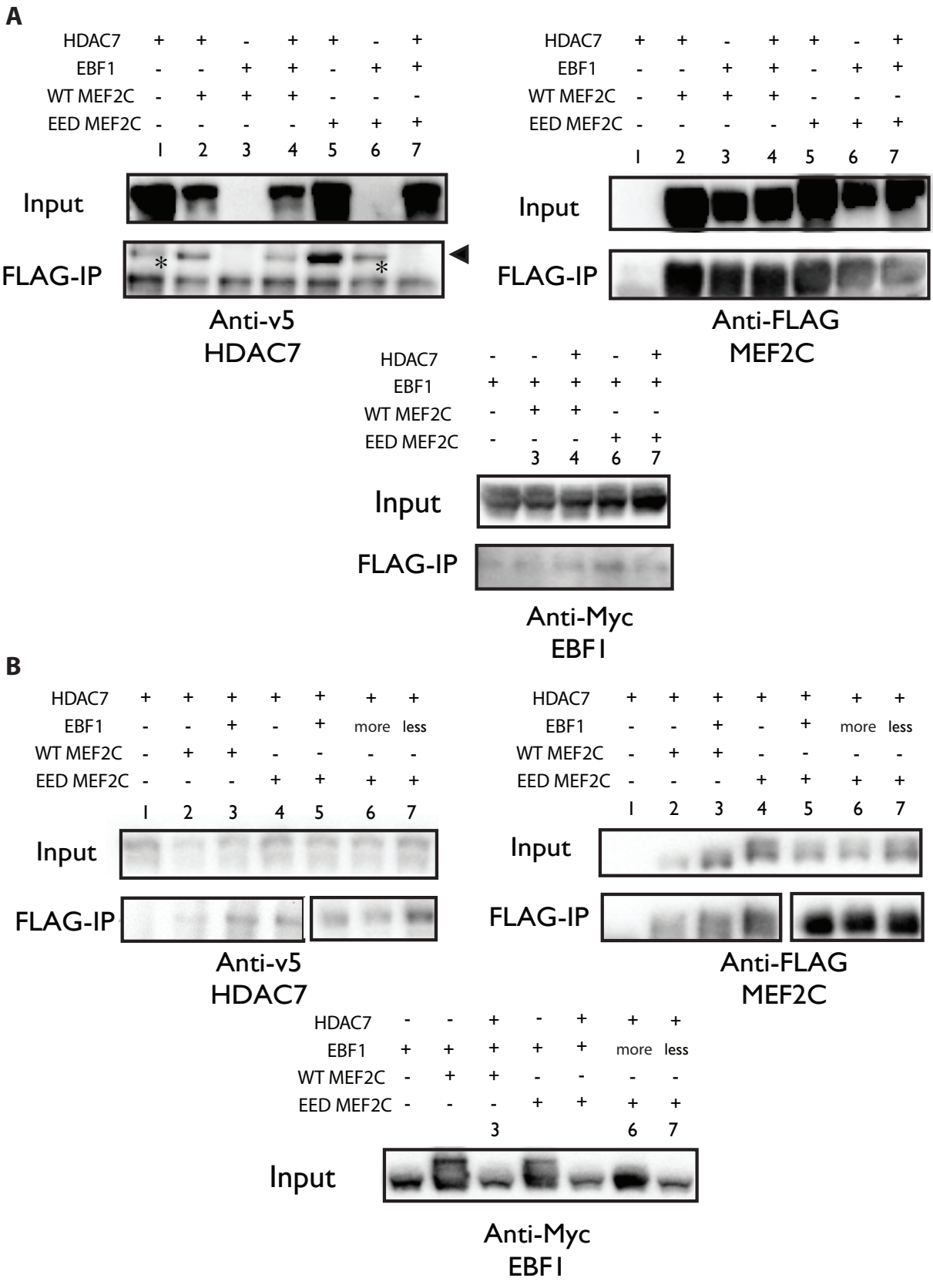
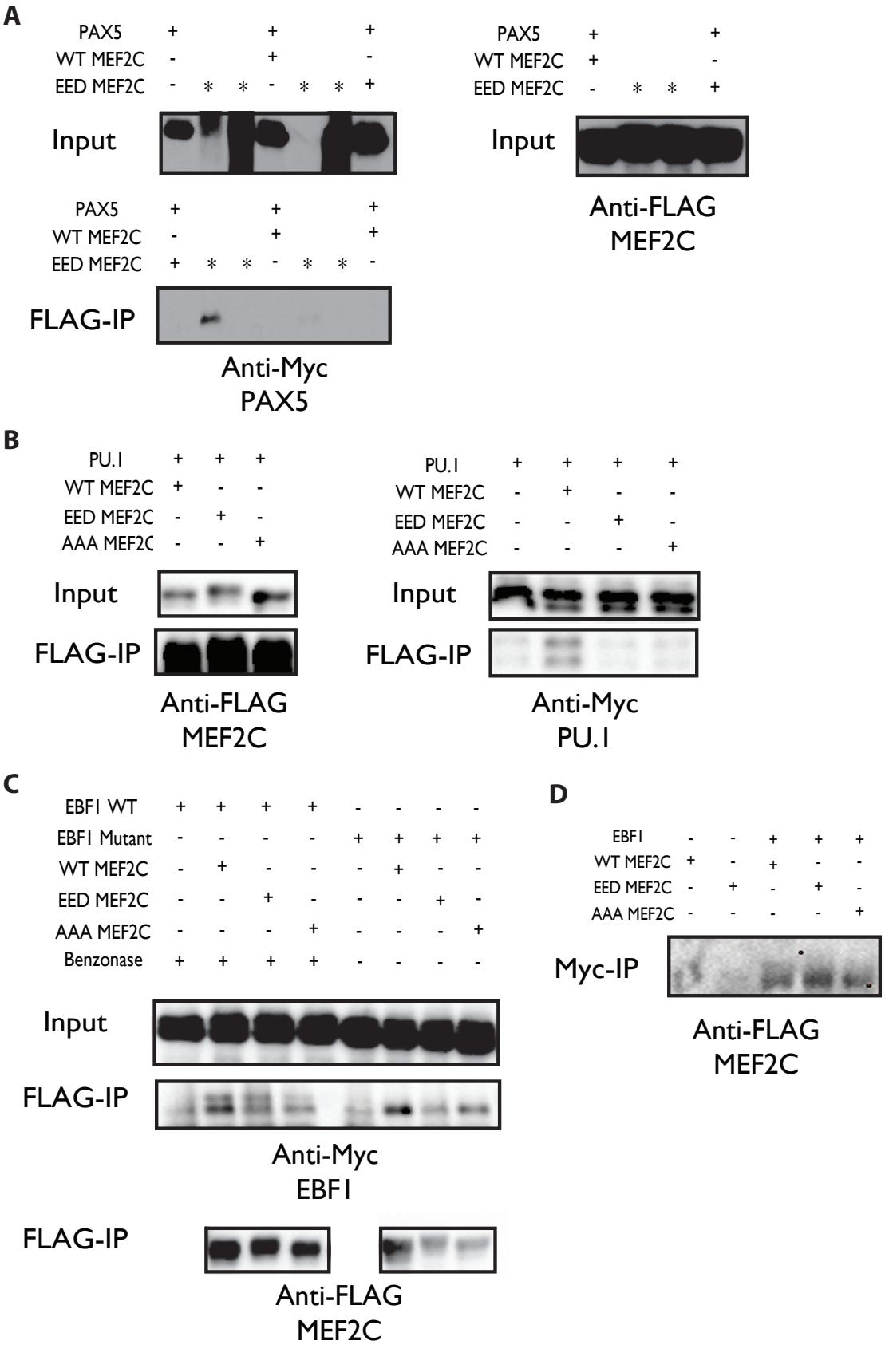


Figure 4.8: MEF2C phosphorylation switches its binding from a co-repressor, HDAC7, to a co-activator of transcription, EBF1
(A) FLAG-tagged WT or phosphomimetic (EED) MEF2C was co-transfected either alone with v5-tagged HDAC7 or Myc-tagged EBF1, or in combination with both. After FLAG-IP, the immunocomplexes were blotted with different antibodies, as indicated. Arrowhead indicates HDAC7; asterisks denote the two background bands from IP. (B) Same as above, except in lane 6 and 7 of both left and right panels, varying amount of Myc-tagged EBF1 was co-transfected with FLAG-tagged EED MEF2C and v5-tagged HDAC7.


A
HDAC7 + + - + + - +
EBF1 - - + + - + +
WT MEF2C - + + + - - -
EED MEF2C - - - - + + +
1 2 3 4 5 6 7
Input
FLAG-IP
*
*
Anti-v5
HDAC7
HDAC7 + + - + + - +
EBF1 - - + + - + +
WT MEF2C - + + + - - -
EED MEF2C - - - - + + +
1 2 3 4 5 6 7
Input
FLAG-IP
Anti-FLAG
MEF2C
HDAC7 - - + - +
EBF1 + + + + +
WT MEF2C - + + - -
EED MEF2C - - - + +
3 4 6 7
Input
FLAG-IP
Anti-Myc
EBF1
B
HDAC7 + + + + + + +
EBF1 - - + - + more less
WT MEF2C - + + - - - -
EED MEF2C - - - + + + +
1 2 3 4 5 6 7
Input
FLAG-IP
Anti-v5
HDAC7
HDAC7 + + + + + + +
EBF1 - - + - + more less
WT MEF2C - + + - - - -
EED MEF2C - - - + + + +
1 2 3 4 5 6 7
Input
FLAG-IP
Anti-FLAG
MEF2C
HDAC7 - - + - + + +
EBF1 + + + + + more less
WT MEF2C - + + - - - -
EED MEF2C - - - + + + +
3 6 7
Input
Anti-Myc
EBF1

Supplemental Figure 4.1: MEF2C does not interact with other tested B cell transcription factors

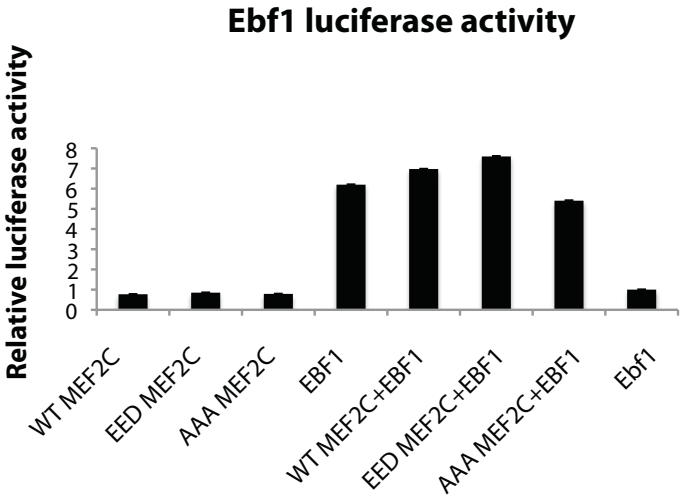
FLAG-tagged WT, phosphomimetic (EED), or phospho-null (AAA) versions of MEF2C were co-transfected into 293T cells with Myc-tagged PAX5 (A) or PU.1 (B). After FLAG-IP, the immunocomplexes were blotted with anti-FLAG or anti-Myc antibodies, as indicated. Asterisks denote unrelated bands from a separate experiment. (C) FLAG-tagged WT, EED, or AAA mutant MEF2C were co-transfected with either WT EBF1 or DNA-binding mutant of EBF1. After FLAG-IP with or without benzonase treatment, the immunocomplexes were blotted with Myc antibodies. (D) FLAG-tagged WT, EED, or AAA versions of MEF2C were co-transfected into 293T cells with Myc-tagged EBF1. After Myc-IP, the immunocomplex was blotted with anti-FLAG antibodies.


A
PAX5
WT MEF2C
EED MEF2C
Input
FLAG-IP
Anti-Myc
PAX5
Anti-FLAG
MEF2C
B
PU.1
WT MEF2C
EED MEF2C
AAA MEF2C
Input
FLAG-IP
Anti-FLAG
MEF2C
Anti-Myc
PU.1
C
EBF1 WT
EBF1 Mutant
WT MEF2C
EED MEF2C
AAA MEF2C
Benzonase
Input
FLAG-IP
Anti-Myc
EBF1
FLAG-IP
Anti-FLAG
MEF2C
D
EBF1
WT MEF2C
EED MEF2C
AAA MEF2C
Myc-IP
Anti-FLAG
MEF2C

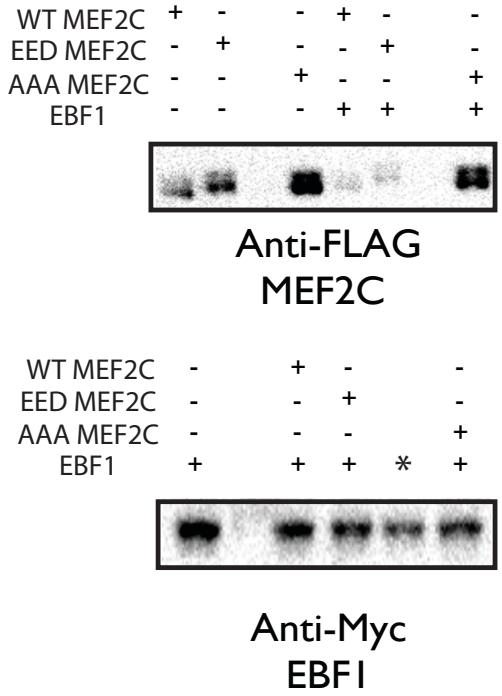
Supplemental Figure 4.2: Luciferase reporter assays show that MEF2C and EBF1 functionally co-activate *Ebf1*

(A) Relative luciferase activity normalized to cell lysates only containing the *Ebf1* luciferase reporter. 293T cells were co-transfected with FLAG-tagged WT, phosphomimetic (EED), or phospho-null (AAA) MEF2C, Myc-tagged EBF1, pGL4.23-*Ebf1*, and Renilla internal control luciferase. (B) Western blotting showing the relative protein expression, blotted with anti-FLAG for MEF2C, and anti-Myc for EBF1. Asterisk denotes a band from an unrelated experiment.

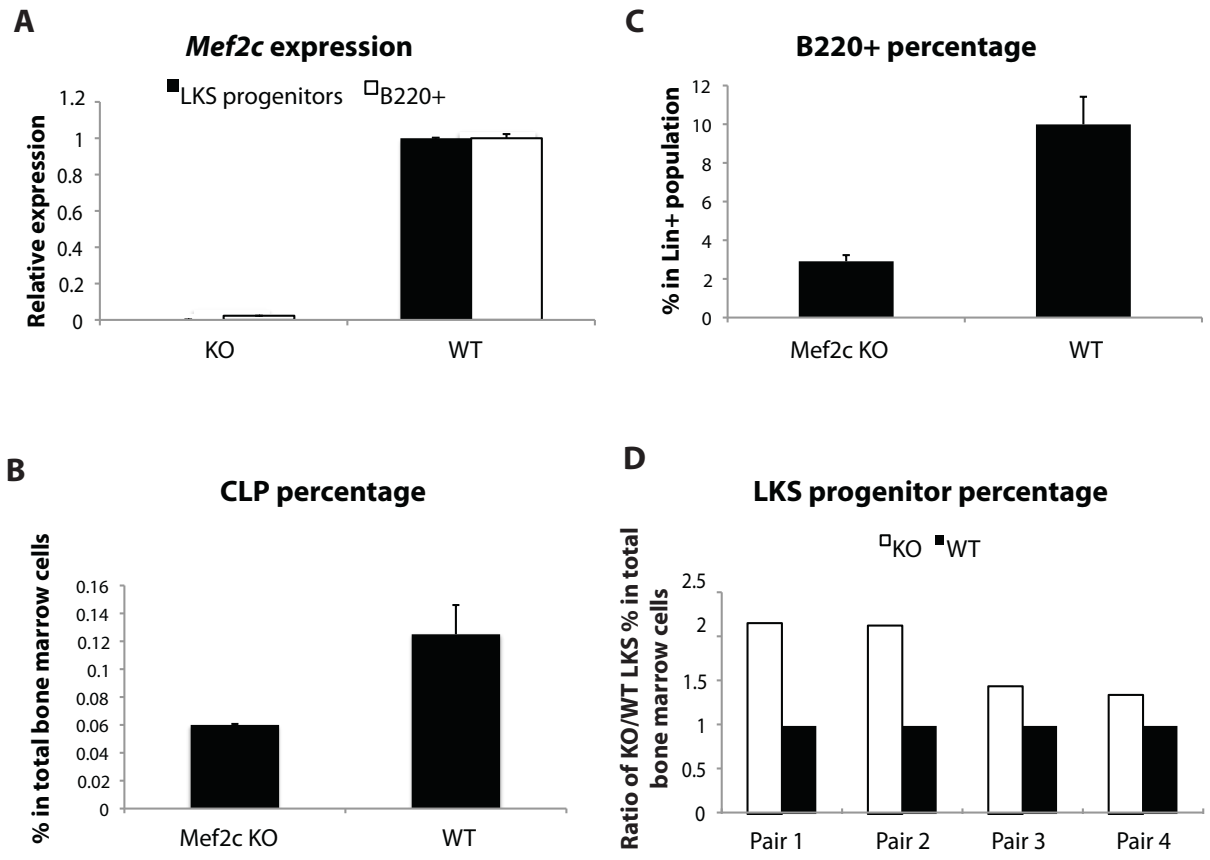
A


Ebf1 luciferase activity
Relative luciferase activity
0
1
2
3
4
5
6
7
8
WT MEF2C
EED MEF2C
AAA MEF2C
EBF1
WT MEF2C+EBF1
EED MEF2C+EBF1
AAA MEF2C+EBF1
Ebf1

B

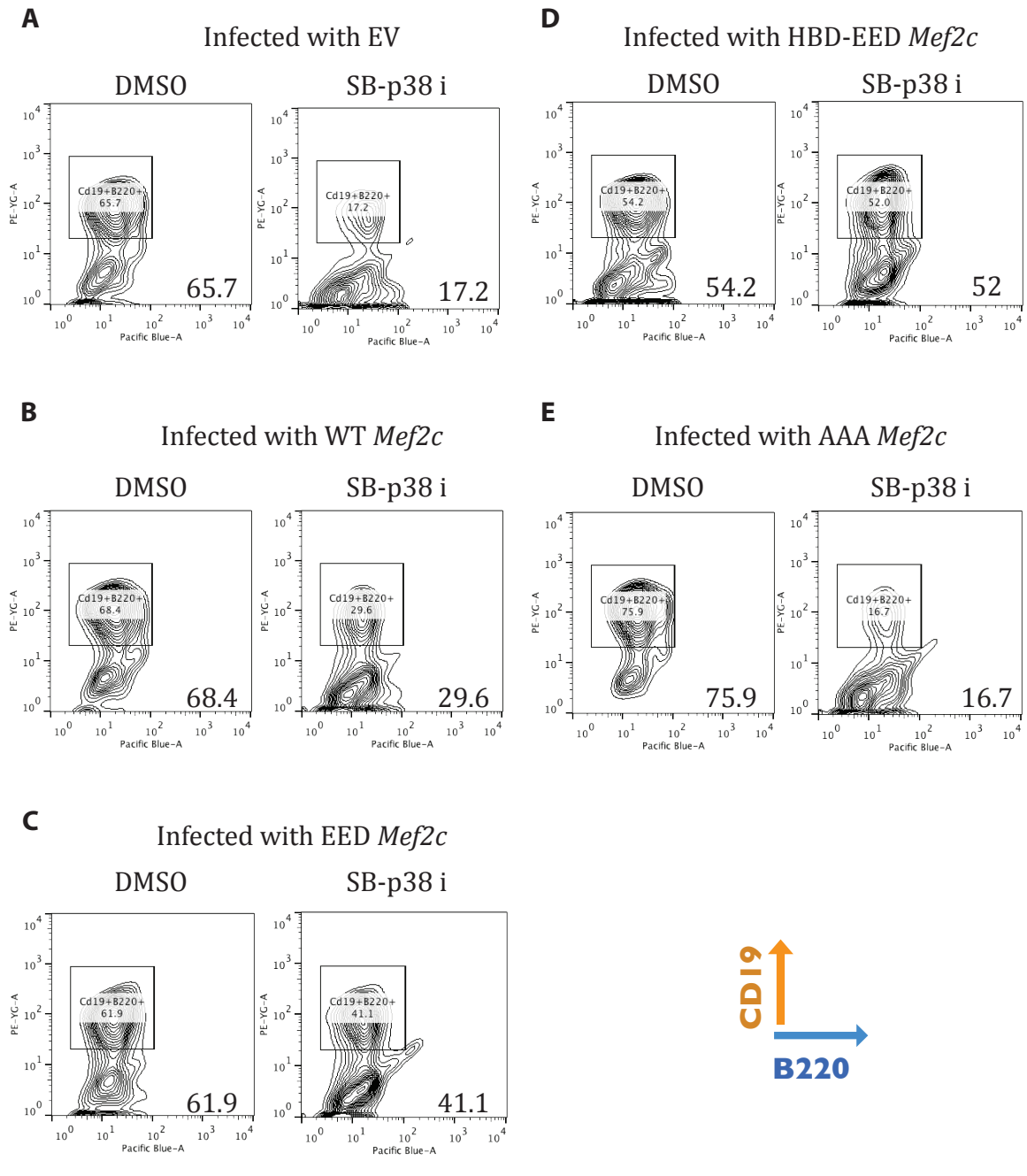

WT MEF2C + - - + - -
EED MEF2C - + - - + -
AAA MEF2C - - + - - +
EBF1 - - - + + +
Anti-FLAG
MEF2C
WT MEF2C - + - -
EED MEF2C - - + -
AAA MEF2C - - - +
EBF1 + + + * +
Anti-Myc
EBF1

Supplemental Figure 4.3: *Mef2c* KO mice characterization
(A) *Mef2c* transcript level is decreased in KO mouse LKS (lineage negative/c-Kit+/Sca1+) progenitors (black bars) and B220+ B cells (white bars) compared to their WT littermates. Percentages of common lymphoid progenitors (CLP) (B) and B cells (C) were decreased in *Mef2c* KO mice compared to their WT littermates. (D) LKS progenitors were consistently elevated in *Mef2c* KO mice compared to their WT littermates.


A
Mef2c expression
LKS progenitors
B220+
Relative expression
1.2
1
0.8
0.6
0.4
0.2
0
KO
WT
C
B220+ percentage
% in Lin+ population
12
10
8
6
4
2
0
Mef2c KO
WT
B
CLP percentage
% in total bone marrow cells
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
Mef2c KO
WT
D
LKS progenitor percentage
KO
WT
Ratio of KO/WT LKS % in total bone marrow cells
2.5
2
1.5
1
0.5
0
Pair 1
Pair 2
Pair 3
Pair 4

Supplemental Figure 4.4: p38 MAPK inhibitor-induced defects in B cell differentiation can be rescued by MEF2C mutants

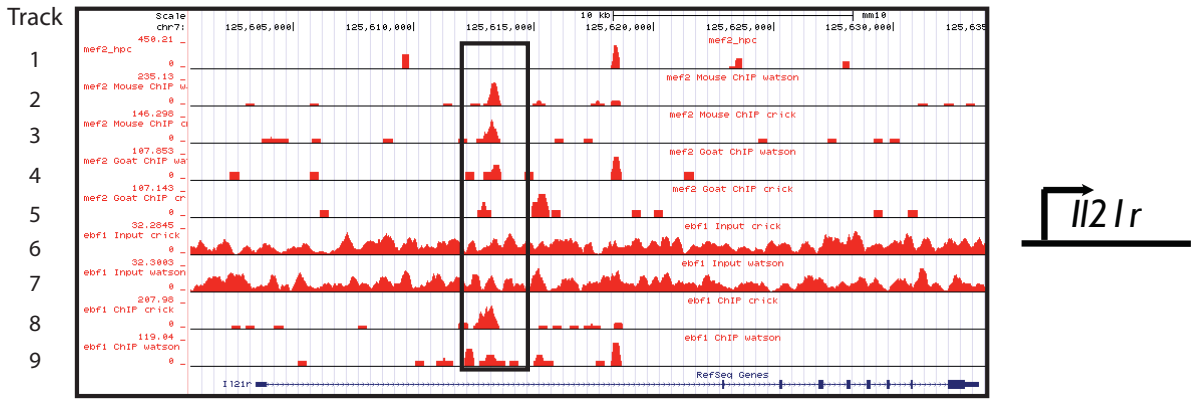
FACS plots measuring expression of B cell surface markers B220 and CD19 after 14 days in culture. Lin- cells were treated either with DMSO or p38 MAPK inhibitor SB203580 (p38 MAPK i). They were induced to differentiate into B cells after infection with empty vector (EV) (A), WT *Mef2c* (B), phosphomimetic (EED) *Mef2c* (C), "super-activating" *Mef2c* with phosphomimetic and HDAC-binding mutations (HBD-EED) (D), or phospho-null (AAA) *Mef2c* (E), then sorted by hCD4 expression before differentiation.


A
Infected with EV
DMSO
SB-p38 i
Cd19+B220+
65.7
17.2
PE-YG-A
Pacific Blue-A
D
Infected with HBD-EED Mef2c
DMSO
SB-p38 i
Cd19+B220+
54.2
52.0
54.2
52
B
Infected with WT Mef2c
DMSO
SB-p38 i
Cd19+B220+
68.4
29.6
68.4
29.6
E
Infected with AAA Mef2c
DMSO
SB-p38 i
Cd19+B220+
75.9
16.7
75.9
16.7
C
Infected with EED Mef2c
DMSO
SB-p38 i
Cd19+B220+
61.9
41.1
61.9
41.1
CD19
B220

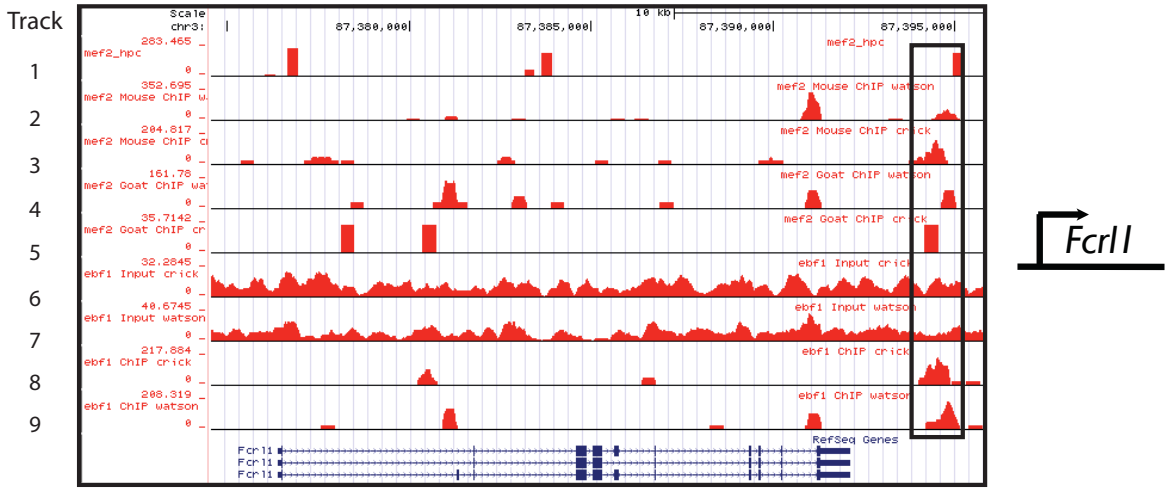
Supplemental Figure 4.5: MEF2C binds some B cell genes to repress their expression

Representative MEF2C and EBF1 binding profiles at *Il21r* (A), *Fcrl1* (B), and *Ciita* (C), which have up-regulated expression levels in *Mef2c* KO common lymphoid progenitors. Track 1: MEF2C binding in HPCs. Tracks 2-5: MEF2C binding with two different antibodies, Watson and Crick strands. Tracks 6 and 7: pre-B cell input (from EBF1 ChIP-exo). Tracks 8 and 9: EBF1 binding, Crick and Watson strands.

A


Track
1
2
3
4
5
6
7
8
9
Scale
chr7:
125,605,000
125,610,000
125,615,000
125,620,000
125,625,000
125,630,000
10 kb
mm10
mef2_hpc
mef2 Mouse ChIP watson
mef2 Mouse ChIP crick
mef2 Goat ChIP watson
mef2 Goat ChIP crick
ebf1 Input crick
ebf1 Input watson
ebf1 ChIP crick
ebf1 ChIP watson
RefSeq Genes
Il2 I r

B


Track
1
2
3
4
5
6
7
8
9
Scale
chr3:
87,380,000
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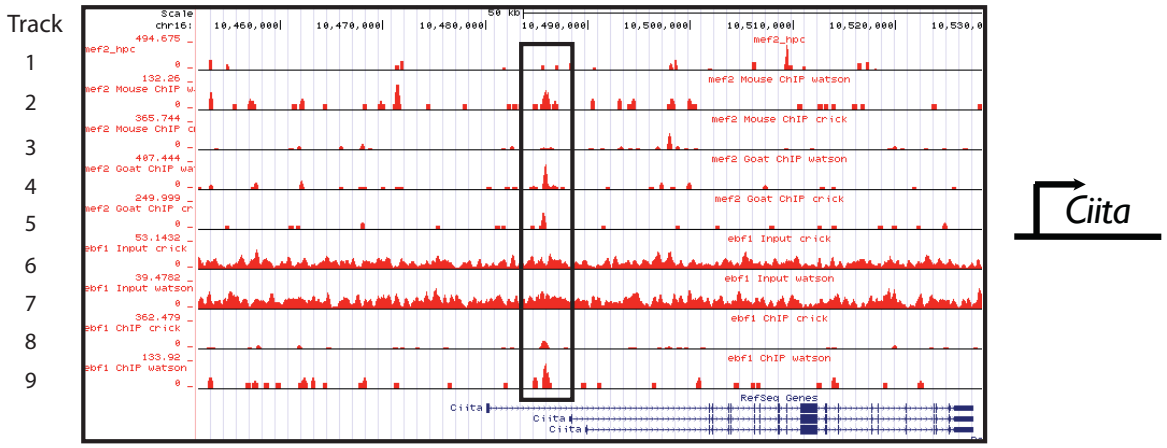
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Appendix I

List of FACS antibodies used in this work
All are anti-mouse unless denoted with *

Cell surface marker	Fluorochrome	Clone number	Company
Sca1/Ly-6A-E	Pacific blue	D7	Biolegend
Sca1/Ly-6A-E	FITC	D7	Biolegend
c-Kit/CD117	PE-Cy7	2B8	Biolegend
B220/CD45R	Pacific blue	RA3-6B2	Biolegend
B220/CD45R	APC	RA3-6B2	Biolegend
CD19	PE	6D5	Biolegend
CD43	PE or FITC	S7	BD Biosciences
IgM	PE	Il-41	Biolegend
IgM	PE-Cy7	Il-41	eBioscience
IgD	eFluor450	11-26c	eBioscience
Mac1/CD11b	APC	M1/70	Biolegend
Mac1/CD11b	FITC	M1/70	eBioscience
Gr-1/Ly-6G-C	APC	RB6-8C5	Biolegend
CD3ε	APC	145-2C11	Biolegend
TER-119	APC	TER-119	Biolegend
CD45.1	PE-Cy7	A20	eBioscience
CD45.2	FITC	104	eBioscience
IL-7ra	FITC	A7R34	Biolegend
Flt3/Flk2/CD135	PE	A2F10.1	BD Biosciences
*Human CD4	PE	RPA-T4	eBioscience
*Human CD2	PE	RPA2.10	eBioscience

Appendix II

List of antibodies used in this work

Antigen	Host species	Company	Description
MEF2C	Goat	Santa Cruz	E-17(x), ChIP, IP, IF, and western
MEF2C	Rabbit	Cell Signaling	D80C1, for western and ChIP
EBF1	Rabbit	Abcam	EPR4183, for western, IF
EBF1	Goat	Sigma	For ChIP, western
HDAC4/5/7	Rabbit	Santa Cruz	H-273, for western, IF
FLAG-tag	Mouse	Sigma	M2, western, IP
FLAG-agarose resin	Mouse	Sigma	M2, IP
Myc-tag	Rabbit	Abcam	Western
V5-tag	Mouse	Life Tech	Western
β-actin	Mouse	Sigma	AC-74, for western
Normal goat IgG	Goat	Santa Cruz	For ChIP

Appendix III

List of real time quantitative PCR primers
All were annealed at 60°C

Gene	Forward	Reverse
Mef2c-1	AAGAAACACGGGGACTATGG	ACAGCTTGTTGGTGCTGTTG
Mef2c-2	GTGCTGTGCGACTGTGAGAT	TTGAGGCCCTTCTTTCTCAA
Mef2c-3	CGAGGATAATGGATGAGCGTA	CATGTCAGTGCTGGCGTACT
Mef2c-4	AGGGAATGGATACGGCAAC	CTGCCAGGTGGGATAAGAAC
Ebf1-1	CCCTCCAACTGCAGTAGCTC	TTTCACATGGGAGGGACAAT
Ebf1-2	TGAAGGCCAAGACAAGAACC	AGGGAGTCTCATTTCGGTTG
Myb	TGTCCTCAAAGCCTTTACCG	CCGTCATCTGGTCCTCTGTC
Ets1	ATCCAGCTGTGGCAGTTTCT	CCACGGCTCAGTTTCTCATA
Flt3	GAACCCTTACCCTGGCATTC	TCAGGTTGGGGAAGGATG
Foxo1	TCCTGGGCCAAAATGTAATG	GGTTCATGGCAGATGTGTGA
Cxcl9	TTTTCCTCTTGGGCATCATC	TGTTGCAATTGGGGCTTG
Csf2ra	GACACGAGGATGAAGCACTG	GAACCTCCTGCACGTCACTC
Csf3r	GTAGCCTGAGCTCCTGGTTG	GGCTACCATTCCCAGAGCTT
Csf1r	CTGGGAGATCTTCTCGCTTG	TCTGTTGGAAGGTGGGTCTT
Rag1	TTTCACAAAACCTTGGCACA	CAGCCAGTGATGTTTCAGGA
Il7ra	GCCTAGTCTCCCCGATCATA	TCTCCAACTCCTCTGGCTGT
Sfpi1	GAGAAGCTGATGGCTTGGAG	GCTTGGACGAGAACTGGAAG
C/ebpa	GGGACCATTAGCCTTGTGTG	AGCATAGACGTGCACACTGC
Gata1	AGGCACCCAATGCACTAACT	TTCCTCGTCTGGATTCCATC
Gapdh	TGTGCAGTGCCAGCCTCGTC	TGAAGGGGTCGTTGATGGCAACA
RNP	TTGCAGGAAGAAGAGAGAGAGAGG	TGCCAAAGTCCAGGAGCTTCAG
Tbp	ACATCTCAGCAACCCACACA	CTGGTGTGGCAGGAGTGATA
Taf1	GAAAGGGGTGTGATCAATAGGA	TGGGAGGGAGATGAAGAGAA
Taf2	TTAATGCCCCAGCATTCATT	GCCTCCTTAGCAAACATGGA
Taf3	AGGAGAAGGAGGCTGGAAAG	TCTCGCTCTCTCCTCACGAT
Taf4	CAAGTGTTGGAAATGGTTGG	ACAAAGAAGGGGCTTTGCTC
Taf4b	AAAGTCCAGCATACTCCCACA	TCACAGAACCCAAATGCAAA
Taf5	TCTGGGATGTCCTCAATGGT	TCAAGCCGTGTCCAATATCC
Taf6	CTCCTCCTCAGCCTTCTCCT	GTGGAGACCAGCTTGACGAT
Taf7	GGTCCTTAGCCGTCTCATTG	GCGCATCGTCTTTGTTCTTA
Taf9	CTATCAGGCCAACAGGGAAA	TCCAATGTTGGCTATGTGGA
Taf10	CCCAGATGCAGTGACTGGT	AGAGGCTGTGCCCTTCATTT
Taf11	CATCACTGGCACCTCTGTGT	TGTGCTTTGAGTTGGGGATT
Taf12	TTTTGAAAATGGCTGCCTCT	AGGTTGATTAGCGCTGAAGG
Hdac4	CAGAGGCTGAATGTGAGCAA	GCCAAGTACTCAGCGTCTCC
Hdac5	GTGACACGGTGTGGAATGAG	AGCTGTGATGGCTACGGAGT
Bcl11b	GACTCAGGGTGAGGGTCAGA	AAGCCATGTGTGTTCTGTGC
Pou2af1	CCAGCCTGGCTTTGAACTTA	CGAGTCTGTAGTGCCTGCTG

Appendix IVa

Top 40% of MEF2C/EBF1 Overlapped Binding Peaks in Pre-B cells

Bold: B cell genes

Red: myeloid

Gene Name	Peak Score	Gene Name	Peak Score	Gene Name	Peak Score	Gene Name	Peak Score
Kctd16	176547	Gm10649	3311.75	Ccdc54	1957.73	Ttc37	1431.64
Prelid2	176547	Ddhd1	3305.28	Chmp2b	1955.57	Slc29a3	1431.64
Fbxo33	113621	Gm1821	3305.28	Vgll3	1955.57	Mir6408	1431.64
Gm20063	113621	Gm12887	3298.81	Mir6390	1955.57	BC030500	1427.33
Prl5a1	91359.8	9530002B09Rik	3298.81	Trim52	1955.57	Aadat	1427.33
2610307P16Rik	91359.8	1700001C19Rik	3288.03	Gtf2i	1953.41	Zfand5	1427.33
1700125H03Rik	59479.9	Taf8	3288.03	Clip2	1953.41	Gda	1427.33
Ints10	59479.9	Ndrg1	3257.84	Cetn3	1953.41	Scml2	1425.17
Olfr746	57313.1	1700012I11Rik	3257.84	**Mef2c**	**1953.41**	Nhs	1425.17
Olfr747	57313.1	Tmem233	3255.69	Ap3s1	1951.26	Rsrc1	1423.02
Mrgpra1	37004.9	B230112J18Rik	3255.69	Arl14epl	1951.26	Mlf1	1423.02
Mrgpra2b	37004.9	2310069B03Rik	3247.06	Pan2	1946.94	9430016H08Rik	1423.02
Zscan4f	35562.5	Sema4f	3247.06	Cs	1946.94	Spats2l	1423.02
Vmn1r72	35562.5	1700008P02Rik	3247.06	Tnc	1944.79	Itga2	1423.02
Usp9y	31207.2	Pkia	3247.06	Astn2	1944.79	Pelo	1423.02
Zfy2	31207.2	6030469F06Rik	3244.91	Vmn2r47	1942.63	4930563E22Rik	1423.02
Fam216b	28742.8	Lamb1	3244.91	Vmn2r46	1942.63	Slc13a5	1423.02

Mir1971	28742.8	Speer4f	3238.44	Deptor	1942.63	Hist4h4	1418.7
Olfr1349	28067.9	Cd36	3238.44	Mrpl13	1942.63	Wbp11	1418.7
Olfr1350	28067.9	Kdm6b	3236.28	Mir3473c	1940.48	Kcna4	1418.7
Zscan4f	24948.1	Efnb3	3236.28	Rcor3	1940.48	Mettl15	1418.7
Vmn1r72	24948.1	Pex13	3223.35	4930452A 19Rik	1938.32	Lhx1os	1418.7
Ctnna3	22908.4	Rel	3223.35	Qk	1938.32	1700109 G15Rik	1418.7
1700023F 02Rik	22908.4	Spz1	3216.88	Nrbf2	1938.32	Psmd11	1418.7
Dthd1	22755.3	Thbs4	3216.88	Egr2	1938.32	Cdk5r1	1418.7
Nwd2	22755.3	Gm12888	3206.1	Tgif2lx2	1936.16	Mir491	1416.55
Neurog2	19905	Gm12886	3206.1	Pabpc5	1936.16	Ptplad2	1416.55
Tifa	**19905**	5430437J10 Rik	3206.1	Casp12	1936.16	Snx7	1416.55
Mir6414	19881.3	Dab2	3206.1	Pdgfd	1936.16	Mir137	1416.55
Gm7854	19881.3	Klhl4	3175.91	Smpd3	1934.01	Nup133	1414.39
A830018 L16Rik	19316.4	Ube2dnl1	3175.91	Zfp90	1934.01	Taf5l	1414.39
Mir6341	19316.4	Kcnj6	3173.76	Glipr1	1934.01	Crbn	1414.39
Rgs18	18359.1	Kcnj15	3173.76	Glipr1l1	1934.01	Lrrn1	1414.39
Brinp3	18359.1	D3Ertd751e	3165.13	1700097N 02Rik	1931.85	Mir7681	1414.39
Mthfs	17485.8	2610316D01 Rik	3165.13	Glp1r	1931.85	Ccdc150	1414.39
AF52916 9	17485.8	AI606473	3162.98	Rasgef1c	1931.85	Prkar2a	1410.08
Reg3g	17462.1	Tyw3	3162.98	Rnf130	1931.85	Ip6k2	1410.08
Gm20362	17462.1	Tal2	3156.51	1700063A 18Rik	1927.54	Vapb	1410.08
Fbxo15	17168.9	Tmem38b	3156.51	4930533P 14Rik	1927.54	Stx16	1410.08
Neto1	17168.9	Zpld1	3156.51	Kcng1	1918.92	Gm3696	1407.92
Tmem177	17082.7	Nfkbiz	3156.51	Atp9a	1918.92	Gm5797	1407.92

Sctr	17082.7	D730050B12Rik	3145.73	Gm8883	1918.92	BC030870	1405.77
Ptchd1	16569.5	Irx4	3145.73	4933417E11Rik	1918.92	1-Mar	1405.77
4930503H13Rik	16569.5	Diap3	3143.57	Zdbf2	1918.92	Fam181b	1405.77
Nkain3	15400.9	Tdrd3	3143.57	Dytn	1918.92	Tenm4	1405.77
Prdm13	15400.9	4930545E07Rik	3139.26	Scp2	1916.76	Ablim2	1405.77
Slc4a4	15351.3	Dsc3	3139.26	Zyg11a	1916.76	Sorcs2	1405.77
Gc	15351.3	Olfr995	3137.1	Pou4f3	1916.76	Cobl	1405.77
Usp9y	15295.3	Olfr996	3137.1	Tcerg1	1916.76	1700046C09Rik	1405.77
Zfy2	15295.3	1500017E21Rik	3134.95	**Cd7**	**1912.45**	9130204L05Rik	1403.61
Gm20854	14808	Ppp1r3c	3134.95	Sectm1a	1912.45	Pglyrp3	1403.61
Gm20854	14808	Cybrd1	3132.79	Neil3	1910.29	Kynu	1403.61
Tbc1d2b	14618.3	Dync1i2	3132.79	Vegfc	1910.29	Arhgap15os	1403.61
Zic1	14618.3	Usp38	3124.17	Sipa1l3	1910.29	Tmem2	1403.61
Ccdc71l	14439.3	Inpp4b	3124.17	Catsperg2	1910.29	Trpm3	1403.61
Nampt	14439.3	Lrfn5	3124.17	Gm17821	1908.14	Scaf8	1403.61
Zscan4f	14322.9	Fscb	3124.17	Rps29	1908.14	Tiam2	1403.61
Vmn1r72	14322.9	D7Ertd443e	3115.54	Cxcr3	1905.98	Igsf11	1403.61
Nbas	13415.2	Dock1	3115.54	Rgag4	1905.98	Lsamp	1403.61
Fam84a	13415.2	Gm833	3111.23	Cdh20	1905.98	4930448F12Rik	1403.61
Eva1a	13408.7	Ajap1	3111.23	Rnf152	1905.98	Vps41	1403.61
Tacr1	13408.7	4921531P14Rik	3111.23	Kcng1	1903.82	Nars	1401.46
Zfp946	13354.8	Zadh2	3111.23	Nfatc2	1903.82	Nedd4l	1401.46
Vmn2r112	13354.8	Xrcc4	3104.76	Tex30	1897.35	Itgb3	1401.46
Nlrp1b	12606.6	Atp6ap1l	3104.76	Bivm	1897.35	Efcab3	1401.46

Wscd1	12606.6	Gm10790	3102.61	Mir466g	1895.2	Itih5	1397.14
Olfr746	12444.9	Hivep1	3102.61	Efna5	1895.2	Sfmbt2	1397.14
Olfr747	12444.9	Homer1	3100.45	Wwp1	1893.04	Sult1c1	1397.14
1700015 G11Rik	12358.7	Bhmt	3100.45	Atp6v0d2	1893.04	Slc5a7	1397.14
Mir6238	12358.7	Sel1l	3089.67	Zmynd11	1893.04	Nudt4	1397.14
Tmem177	12358.7	Mir8099-2	3089.67	Chrm3	1893.04	Eea1	1397.14
Sctr	12358.7	Gm5347	3083.2	AA545190	1886.57	Card11	1394.99
Rgs18	12175.4	Fat1	3083.2	Ndufa4	1886.57	Sdk1	1394.99
Brinp3	12175.4	5830454E08 Rik	3081.05	Wdr20rt	1886.57	Ahdc1	1394.99
Slc7a14	12041.7	1700020M2 1Rik	3081.05	Rpl10l	1886.57	Mir7017	1394.99
Kcnmb2	12041.7	Htr2c	3076.73	Fancb	1884.42	Mir205	1394.99
Vmn2r12 1	12026.6	Il13ra2	3076.73	Glra2	1884.42	4930503 O07Rik	1394.99
4932411 N23Rik	12026.6	Gm12070	3076.73	Spdl1	1884.42	4930548J 01Rik	1392.83
Fat3	11905.9	Ccdc85a	3076.73	Slit3	1884.42	Arid1b	1392.83
Chordc1	11905.9	Vmn2r47	3061.64	Cyp2b13	1882.26	4921504 A21Rik	1390.67
Fat3	11729.1	Vmn2r46	3061.64	Vmn1r184	1882.26	Phtf2	1390.67
Chordc1	11729.1	Trpc7	3057.33	Slc39a12	1882.26	1110019 D14Rik	1388.52
1700015 G11Rik	11545.8	Spock1	3057.33	Gm13315	1882.26	Ppp1r3a	1388.52
Mir6238	11545.8	Cyp4b1	3055.17	Sept7	1880.11	Dpysl3	1388.52
Med10	11429.4	Efcab14	3055.17	B3gat1	1880.11	Jakmip2	1388.52
1700084F 23Rik	11429.4	4930474H20 Rik	3053.02	Lta4h	1880.11	Myo10	1388.52
4930401 O12Rik	10965.8	4921530L21 Rik	3053.02	Hal	1880.11	Fam134b	1388.52
Foxq1	10965.8	Mocos	3050.86	4930412C 18Rik	1877.95	Gm11149	1386.36

Sh3bp4	10955.1	Tpgs2	3050.86	4930448K20Rik	1877.95	Plet1os	1386.36
C030007H22Rik	10955.1	1700015G11Rik	3042.24	Tac4	1877.95	Gpr149	1386.36
Grin3a	10920.6	Mir6238	3042.24	Kat7	1877.95	Mme	1386.36
Cylc2	10920.6	Gm53	3040.08	Atp1b1	1877.95	Klf13	1384.21
Mrgpra1	10894.7	Mir196a-1	3040.08	Dpt	1877.95	Trpm1	1384.21
Mrgpra2b	10894.7	Rgs18	3037.92	C1galt1c1	1873.64	D730050B12Rik	1384.21
Gm20871	10864.5	Brinp3	3037.92	Cypt15	1873.64	Irx4	1384.21
Gm20823	10864.5	Gm11762	3027.14	Ms4a13	1873.64	Hephl1	1382.05
Tmem177	10808.5	Rptor	3027.14	Ms4a1	1873.64	Vstm5	1382.05
Sctr	10808.5	Ankrd1	3024.99	Slc17a3	1871.48	Abhd17c	1382.05
Olfm4	10743.8	Pcgf5	3024.99	Slc17a4	1871.48	Gm2115	1382.05
Pcdh17	10743.8	Lama3	3020.68	Sec24b	1865.01	**Mbd2**	**1382.05**
1700125H03Rik	10698.5	Mir1948	3020.68	Etnppl	1865.01	Mex3c	1382.05
Ints10	10698.5	Sacs	3005.58	Ednra	1862.86	Gm3696	1382.05
Usp9y	10267.3	1700109G14Rik	3005.58	Pou4f2	1862.86	Gm5797	1382.05
Gm6026	10267.3	D3Ertd751e	3001.27	Ptpn12	1860.7	Rnf180	1382.05
Tbc1d2b	10008.5	2610316D01Rik	3001.27	Gsap	1860.7	Htr1a	1382.05
Zic1	10008.5	AW209491	2999.11	Taf1	1858.55	Mir7657	1379.89
Vwc2	9950.33	Gli3	2999.11	Cxcr3	1858.55	Pde5a	1379.89
4930415F15Rik	9950.33	D730050B12Rik	2992.65	Gys2	1854.23	Lekr1	1377.74
Vwc2	9933.08	Irx4	2992.65	Ldhb	1854.23	Ccnl1	1377.74
4930415F15Rik	9933.08	Gm21119	2988.33	Mroh5	1854.23	Foxr1	1375.58
F630028O10Rik	9833.9	Gm15319	2988.33	Mroh4	1854.23	Upk2	1375.58
Hsf3	9833.9	1700018A04Rik	2984.02	Agpat4	1852.08	**Pten**	**1375.58**

Esp15	9812.34	Foxf2	2984.02	Map3k4	1852.08	Rnls	1375.58
Esp38	9812.34	**Sox5**	**2975.4**	**Bcl6**	**1852.08**	Myo7b	1375.58
D630013 N20Rik	9723.94	Sox5os3	2975.4	1110054M 08Rik	1852.08	Proc	1375.58
Bicc1	9723.94	Igsf11	2964.62	Sox11	1845.61	D14Ertd6 70e	1375.58
1700015 G11Rik	9713.16	Lsamp	2964.62	Dcdc2c	1845.61	Saysd1	1375.58
Mir6238	9713.16	Wdr11	2962.46	Ube2u	1839.14	Rassf3	1375.58
Leprel1	9672.2	Gm4265	2962.46	Raver2	1839.14	Tbk1	1375.58
Cldn1	9672.2	Gm10033	2955.99	Rpl30	1839.14	4930525 M21Rik	1373.43
H2-M9	9579.49	Zfp868	2955.99	Hrsp12	1839.14	4930430 D24Rik	1373.43
H2-M1	9579.49	Cdh8	2955.99	Epha7	1836.98	Enpp6	1373.43
Ptchd1	9510.49	Cdh11	2955.99	4930556G 01Rik	1836.98	Trappc11	1373.43
4930503 H13Rik	9510.49	Klf15	2953.84	Osbpl1a	1836.98	Usp53	1373.43
Khdrbs2	9307.82	Aldh1l1	2953.84	Impact	1836.98	Synpo2	1373.43
Prim2	9307.82	Gm10584	2940.9	Far1	1834.83	Slc25a24	1373.43
Cdh8	9230.2	Oat	2940.9	Spon1	1834.83	Vav3	1373.43
Cdh11	9230.2	Gm12887	2938.74	Gm608	1834.83	Sfmbt2	1373.43
Ccdc37	8999.5	9530002B09 Rik	2938.74	Spice1	1834.83	Prkcq	1373.43
Klf15	8999.5	Reep5	2938.74	Klf12	1834.83	Ptger2	1373.43
Tssc1	8971.47	Fam13b	2938.74	Prr30	1834.83	Gpr137c	1373.43
Myt1l	8971.47	Srpx	2932.28	Ankrd34b	1832.67	Ralgps2	1373.43
4930548 K13Rik	8924.04	Rpgr	2932.28	Zfyve16	1832.67	Tex35	1373.43
Epha7	8924.04	Gm9731	2932.28	Prss52	1830.52	Mx2	1371.27
Klf13	8751.55	Tex24	2932.28	A930011O 12Rik	1830.52	Ripk4	1371.27
Mir211	8751.55	Lhx2	2930.12	1700100L	1830.52	Zmynd11	1371.27

				14Rik			
Fbxo33	8635.12	Psmb7	2930.12	Adamts16	1830.52	Zp4-ps	1371.27
Gm20063	8635.12	Dmrta2	2923.65	Asic2	1830.52	Clec3a	1369.11
Kif20b	8628.65	Elavl4	2923.65	Ccl2	1830.52	Maf	1369.11
Htr7	8628.65	Cyp4b1	2919.34	Nkain1	1828.36	Pdha1	1366.96
Slc25a40	8611.4	Efcab14	2919.34	Snord85	1828.36	Gpr64	1366.96
Abcb1a	8611.4	Artn	2915.03	Olfm4	1826.2	Trpm3	1364.8
Cntnap5a	8607.09	Kdm4a	2915.03	Pcdh17	1826.2	Klf9	1364.8
Tsn	8607.09	Thsd7a	2910.71	Gm10033	1824.05	Prdm9	1364.8
Rgs18	8553.19	Tmem106b	2910.71	Zfp868	1824.05	4933401 D09Rik	1364.8
Brinp3	8553.19	Tmem132b	2910.71	D330050G 23Rik	1824.05	Zmynd11	1364.8
Snord14d	8535.94	4933438B17 Rik	2910.71	Spred1	1824.05	Zp4-ps	1364.8
C130030 K03Rik	8535.94	Opcml	2906.4	Gm5084	1824.05	A830080 D01Rik	1362.65
Dok6	8456.17	Snx19	2906.4	Dapk1	1824.05	Map3k15	1362.65
Tmx3	8456.17	Ccser1	2899.93	Flrt3	1821.89	Mir2136	1362.65
1700063 A18Rik	8382.86	Atoh1	2899.93	Kif16b	1821.89	Mrpl3	1362.65
4930533 P14Rik	8382.86	Sall3	2889.15	**Myb**	**1819.74**	6820431 F20Rik	1362.65
Adck4	8326.8	Mir5127	2889.15	Hbs1l	1819.74	Gm15319	1362.65
Ltbp4	8326.8	Gm4850	2889.15	Mphosph6	1815.42	Ptbp2	1362.65
Nbas	8244.87	Khdrbs2	2889.15	Cdh13	1815.42	Rwdd3	1362.65
Fam84a	8244.87	Mir8099-1	2887	Cst10	1815.42	4930440 C22Rik	1362.65
6330415 B21Rik	8229.78	Flrt2	2887	Syndig1	1815.42	Fam174a	1362.65
Reg3b	8229.78	Nox4	2878.37	Npy	1813.27	Arhgap29	1360.49
Dbt	8169.41	Grm5	2878.37	Mpp6	1813.27	Gclm	1360.49
Lrrc39	8169.41	Shisa2	2878.37	4930545E	1811.11	Ythdc2	1360.49

				07Rik			
A330102I10Rik	8128.44	Nupl1	2878.37	Dsc3	1811.11	A330093E20Rik	1360.49
Cdkal1	8128.44	Prl5a1	2874.06	2700060E02Rik	1808.96	Jarid2	1360.49
Ptbp2	8100.41	2610307P16Rik	2874.06	D14Ertd670e	1808.96	Mylip	1360.49
Rwdd3	8100.41	Cd207	2871.91	Gm12250	1804.64	Creb5	1358.33
1700063A18Rik	8048.67	Vax2	2871.91	Igtp	1804.64	Tril	1358.33
4930533P14Rik	8048.67	Mir6769b	2869.75	Col18a1	1804.64	Ankrd13c	1358.33
Fbxo15	8046.51	Jak3	2869.75	Gm10941	1804.64	Srsf11	1358.33
Neto1	8046.51	Vmn2r47	2869.75	Arsj	1800.33	2500004C02Rik	1358.33
Vmn2r72	7990.45	Vmn2r46	2869.75	Ank2	1800.33	8430427H17Rik	1358.33
Vmn2r73	7990.45	Ccdc25	2865.44	Adra2a	1796.02	Rtp1	1358.33
Fat3	7983.98	Clu	2865.44	Gpam	1796.02	Masp1	1358.33
Chordc1	7983.98	Gm21119	2863.28	Mir6404	1793.86	1700009J07Rik	1358.33
1110059M19Rik	7977.51	Gm21944	2863.28	Cttn	1793.86	Trpm2	1358.33
Actrt1	7977.51	Wfdc15b	2863.28	Brms1l	1793.86	Auts2	1356.18
Dbt	7876.18	Svs3b	2863.28	Gm19990	1793.86	Gatsl2	1356.18
Lrrc39	7876.18	Slc5a8	2863.28	1700045H11Rik	1789.55	Mphosph9	1356.18
Gm7609	7753.28	Gas2l3	2863.28	Park7	1789.55	Cdk2ap1	1356.18
Sp110	7753.28	A530032D15Rik	2852.5	Gm10324	1789.55	Mecom	1356.18
4930548K13Rik	7513.96	Gm7609	2852.5	2410141K09Rik	1789.55	Actrt3	1356.18
Epha7	7513.96	Dopey1	2848.19	Vmn2r47	1787.39	Gm1653	1356.18
Rbmy	7475.15	Rwdd2a	2848.19	Vmn2r46	1787.39	Eltd1	1356.18
Gm20826	7475.15	Tmem45b	2846.03	Rnf145	1787.39	Gm20823	1354.02

H2-M9	7399.68	Barx2	2846.03	Gm12159	1787.39	Gm20871	1354.02
H2-M1	7399.68	Dtna	2846.03	Nup54	1785.24	LOC102633035	1354.02
Gm4710	7350.09	Mapre2	2846.03	Mir6415	1785.24	Mir7243	1354.02
Crim1	7350.09	Cxcr4	2843.88	Mrpl44	1785.24	Zbbx	1354.02
Neurog2	7313.44	Daf2	2843.88	Fam124b	1785.24	Serpini2	1354.02
Tifa	7313.44	Gm572	2837.41	Glt28d2	1783.08	Hnf4g	1354.02
Rap2b	7296.19	Pex14	2837.41	Lrba	1783.08	1110015O18Rik	1354.02
Arhgef26	7296.19	Nudt12	2835.25	Fbxl7	1783.08	1700029P11Rik	1354.02
BB019430	7272.47	Mir466g	2835.25	Ank	1783.08	Desi1	1354.02
Sept10	7272.47	Gm10745	2830.94	4930525M21Rik	1780.93	Dnah5	1354.02
A830018L16Rik	7263.85	4930539N22Rik	2830.94	4930430D24Rik	1780.93	Ctnnd2	1354.02
Mir6341	7263.85	Tmpo	2824.47	Defb7	1780.93	D730050B12Rik	1354.02
D630013N20Rik	7190.54	Mir135a-2	2824.47	4930467E23Rik	1780.93	Irx4	1354.02
Bicc1	7190.54	Mir466	2820.16	Tmem179	1780.93	Esrrb	1354.02
Fam216b	7175.45	4930524C18Rik	2820.16	Inf2	1780.93	Vash1	1354.02
Mir1971	7175.45	4930467E23Rik	2813.69	Lsm6	1778.77	Col18a1	1354.02
Kif20b	7162.51	6820431F20Rik	2813.69	1700011L22Rik	1778.77	Gm10941	1354.02
Htr7	7162.51	Edaradd	2809.38	Scml2	1776.61	4930453L07Rik	1351.87
Mrgpra1	7151.73	Gpr137b-ps	2809.38	Rai2	1776.61	Lig4	1351.87
Mrgpra2b	7151.73	Lrfn5	2809.38	Mcm4	1776.61	C030007H22Rik	1351.87
Cntnap5c	7117.24	Fscb	2809.38	Mzt2	1776.61	4933400F21Rik	1351.87
2610034	7117.24	Syt2	2809.38	1700063D	1772.3	Arl15	1351.87

M16Rik				05Rik			
Slc7a14	7007.28	Ppp1r12b	2809.38	3110039I08Rik	1772.3	Fst	1351.87
Kcnmb2	7007.28	Slc22a1	2807.22	Olfr986	1770.15	Bnc1	1349.71
6330415B21Rik	7000.81	Airn	2807.22	Scn3b	1770.15	Gm20744	1349.71
Reg3b	7000.81	Gm21119	2800.75	Raver1-fdx1l	1770.15	Nefm	1349.71
Ccdc104	6959.84	6820431F20Rik	2800.75	Cdc37	1770.15	Adam7	1349.71
Prorsd1	6959.84	Kdm2b	2798.6	Krt12	1770.15	Uchl3	1349.71
Map3k13	6942.59	A930024E05Rik	2798.6	Krt20	1770.15	Kctd12	1349.71
Liph	6942.59	Gm15319	2796.44	Mir669m-1	1767.99	Macrod2	1347.55
Ythdf3	6938.28	Gm21119	2796.44	Lphn3	1767.99	Flrt3	1347.55
2610100L16Rik	6938.28	Aox4	2787.82	BC048502	1767.99	Edn1	1347.55
Gm20172	6938.28	Bzw1	2787.82	Pde1b	1767.99	Phactr1	1347.55
4931408C20Rik	6938.28	Sec61b	2785.66	Barhl2	1757.21	Otor	1345.4
Klhl25	6908.1	Nr4a3	2785.66	Hfm1	1757.21	Pcsk2os1	1345.4
Ntrk3	6908.1	Gm20752	2777.04	Jag1	1757.21	11-Mar	1345.4
Cntnap5c	6880.07	Depdc1a	2777.04	Btbd3	1757.21	Ank	1345.4
2610034M16Rik	6880.07	Rps27a	2777.04	4930547E08Rik	1757.21	0610040B10Rik	1343.24
Gm5347	6873.6	Rtn4	2777.04	Lmo2	1757.21	Kdelr2	1343.24
Fat1	6873.6	Gm21119	2772.73	Atp10d	1755.05	Gpr180	1343.24
Shisa6	6830.48	Gm21944	2772.73	Nfxl1	1755.05	Sox21	1343.24
Gm12298	6830.48	Ptprj	2761.94	Pex10	1755.05	Cobl	1343.24
Tmem199	6821.85	Mir3110	2761.94	Morn1	1755.05	1700046C09Rik	1343.24
Tnfaip1	6821.85	Usp9y	2759.79	Rasd2	1752.9	Tbx15	1341.08
Gm20865	6804.6	Zfy2	2759.79	Gm10649	1752.9	Wdr3	1341.08

LOC100040786	6804.6	Prl2c5	2759.79	Npy4r	1752.9	Olfr1505	1341.08
Nkain3	6770.11	Gpr137b	2759.79	Syt15	1752.9	Rnu6	1341.08
Prdm13	6770.11	Gm21119	2755.48	Mtfr2	1752.9	Me2	1338.93
Mthfs	6759.33	Gm21944	2755.48	Ahi1	1752.9	Mapk4	1338.93
AF529169	6759.33	1110004F10Rik	2738.23	Scn2a1	1750.74	Clec14a	1338.93
Fam216b	6750.7	Rps13	2738.23	Galnt3	1750.74	Sec23a	1338.93
Mir1971	6750.7	Gm21119	2736.07	Dusp10	1750.74	Six2	1336.77
Dbt	6724.83	6820431F20Rik	2736.07	1700112H15Rik	1750.74	Srbd1	1336.77
Lrrc39	6724.83	Htr4	2736.07	Tnrc6b	1748.58	Ddx59	1336.77
Gm14851	6614.87	Spink10	2736.07	Sgsm3	1748.58	Kif14	1336.77
Gm15284	6614.87	Krt2	2736.07	Dux	1748.58	Clasp1	1336.77
Pop1	6595.46	Krt77	2736.07	Gm4981	1748.58	Gli2	1336.77
Nipal2	6595.46	Opcml	2733.92	2700081O15Rik	1744.27	Ptgfr	1334.62
Ugt2a3	6584.68	Ntm	2733.92	Snord118	1744.27	Dnajb4	1334.62
Ugt2b38	6584.68	Parva	2727.45	Npr1	1742.12	Lrfn5	1334.62
Olfr1271	6573.9	Rassf10	2727.45	Snapin	1742.12	Fscb	1334.62
Olfr1272	6573.9	Shfm1	2727.45	Ogdhl	1742.12	Slc7a6os	1330.3
Atp10a	6569.59	Dlx6os1	2727.45	Chat	1742.12	Smpd3	1330.3
Ube3a	6569.59	Tlr12	2727.45	Gpr68	1742.12	Scaf8	1330.3
Irx3	6558.81	A3galt2	2727.45	Mir1190	1742.12	Tiam2	1330.3
Crnde	6558.81	Rims1	2725.29	E2f8	1739.96	Zfp599	1328.15
Irx3	6530.78	4933415F23Rik	2725.29	Nav2	1739.96	Gm6607	1328.15
Crnde	6530.78	9130209A04Rik	2716.67	Mir466h	1739.96	Nfu1	1328.15
Cbln2	6414.35	G630055G22Rik	2716.67	Gm5860	1739.96	D6Ertd527e	1328.15
Socs6	6414.35	4930467E23Rik	2714.51	Adcyap1	1737.8	Gm1653	1328.15

Pou2af1	**6386.32**	6820431F20 Rik	2714.51	Mettl4	1737.8	Eltd1	1328.15
Gm684	6386.32	Kcnma1	2710.2	Gsc	1737.8	Hrh4	1328.15
Gm6164	6315.17	Mir7210	2710.2	Dicer1	1737.8	Zfp521	1328.15
Gm4498	6315.17	Acer2	2705.89	Cdk5r1	1737.8	Tbx22	1325.99
Olfr1271	6287.14	Mllt3	2705.89	Tmem98	1737.8	2610002 M06Rik	1325.99
Olfr1272	6287.14	Fank1	2701.57	Lrig3	1737.8	Slitrk6	1325.99
Depdc1a	6237.55	D7Ertd443e	2701.57	Xrcc6bp1	1737.8	Slitrk5	1325.99
Rpe65	6237.55	D3Ertd751e	2701.57	Cycs	1735.65	Galnt18	1323.84
1600019 K03Rik	6237.55	2610316D01 Rik	2701.57	Npvf	1735.65	Dkk3	1323.84
Dirc2	6237.55	Eltd1	2701.57	Spaca1	1735.65	Max	1323.84
Tmsb10	6215.99	Ifi44	2701.57	Akirin2	1735.65	Fut8	1323.84
Suclg1	6215.99	Rgs4	2697.26	Rps24	1735.65	Rgs7	1323.84
Rgs18	6211.68	1700084C01 Rik	2697.26	4930572O 13Rik	1735.65	Fh1	1323.84
Brinp3	6211.68	C130030K03 Rik	2697.26	Depdc1b	1735.65	Pja1	1321.68
Gm20752	6194.43	Ascc3	2697.26	Mir582	1735.65	Tmem28	1321.68
Depdc1a	6194.43	Mvb12b	2695.11	Rrbp1	1733.49	9530026 F06Rik	1321.68
Mir6414	6170.72	Pbx3	2695.11	Banf2	1733.49	Nrp2	1321.68
Gm7854	6170.72	Isoc1	2695.11	Ctla4	1729.18	Zfp503	1321.68
Astn2	6164.25	A730017C20 Rik	2695.11	Icos	1729.18	1700112 E06Rik	1321.68
Tlr4	6164.25	Rap2a	2686.48	Inhbc	1729.18	Rnmtl1	1321.68
Pard3	6149.15	Ipo5	2686.48	Stac3	1729.18	Timm22	1321.68
Mir21c	6149.15	Gm21119	2682.17	4921507L 20Rik	1727.02	Large	1319.52
Depdc1a	6118.97	Gm21944	2682.17	Hsd17b12	1727.02	Isx	1319.52
Rpe65	6118.97	2610034M1 6Rik	2682.17	Uggt2	1727.02	Jag1	1319.52

Atp10a	6114.66	Nudt12	2682.17	1700006F04Rik	1727.02	Btbd3	1319.52
Ube3a	6114.66	4930405A10Rik	2682.17	Sim1	1722.71	Cep192	1319.52
Gm5084	6114.66	Gm10248	2682.17	Gp49a	1722.71	Fam210a	1319.52
BC051665	6114.66	4930467E23Rik	2677.86	Snora30	1720.56	4921530L21Rik	1319.52
Fhl2	6073.69	6820431F20Rik	2677.86	Phkg2	1720.56	Klhl1	1319.52
Nck2	6073.69	Gm6756	2675.7	Iqsec1	1720.56	Olfr885	1317.37
A530072M11Rik	6060.75	Pcdha10	2675.7	Nup210	1720.56	Olfr887	1317.37
Mmp16	6060.75	Gm21119	2673.55	Mir122a	1720.56	Spata9	1317.37
Ctnna3	6021.95	6820431F20Rik	2673.55	Malt1	1720.56	Gpr150	1317.37
1700023F02Rik	6021.95	4921511I17Rik	2673.55	Asz1	1718.4	Hectd2	1315.21
1700008P02Rik	6015.48	Mycn	2673.55	Cttnbp2	1718.4	Ppp1r3c	1315.21
Pkia	6015.48	Ttc32	2667.08	Fyb	1718.4	Fam49b	1315.21
Zcchc13	5996.07	1700022H16Rik	2667.08	Osmr	1718.4	Adcy8	1315.21
Rlim	5996.07	Hipk2	2662.77	Rfk	1716.24	Acn9	1313.06
Sec24b	5989.6	1700025N23Rik	2662.77	Ostf1	1716.24	Tac1	1313.06
Etnppl	5989.6	Fam69a	2662.77	6720416L17Rik	1714.09	Fstl5	1310.9
Sorcs3	5983.14	Mtf2	2662.77	Mtx2	1714.09	Rapgef2	1310.9
Ins1	5983.14	Gm20871	2660.61	Dgkh	1714.09	Pdcd10	1310.9
Fbxo15	5976.67	Gm20823	2660.61	Vwa8	1714.09	2410007B07Rik	1310.9
Neto1	5976.67	Fli1	2660.61	Msl2	1711.93	3930402G23Rik	1308.74
Gm12887	5901.2	Ets1	2660.61	LOC102633035	1711.93	Irs2	1308.74
9530002	5901.2	Ppp1r3g	2658.45	St6galnac5	1711.93	Slc14a2	1308.74

B09Rik							
Med10	5866.71	Fars2	2658.45	4930482G09Rik	1711.93	Setbp1	1308.74
1700084F23Rik	5866.71	Gm4850	2656.3	Tenm3	1709.78	Trib2	1308.74
Reg3g	5849.46	Khdrbs2	2656.3	Gm2516	1709.78	Lpin1	1308.74
Gm20362	5849.46	Gm5766	2654.14	Mex3b	1709.78	Ctsc	1306.59
Gm20752	5810.65	Srl	2654.14	Tmc3	1709.78	Rab38	1306.59
Depdc1a	5810.65	Cox8c	2654.14	Sav1	1709.78	Cblb	1306.59
Gm10440	5786.93	Prima1	2654.14	Nin	1709.78	4930404A05Rik	1306.59
4932441J04Rik	5786.93	Gltpd1	2645.52	Xrra1	1707.62	Odf1	1306.59
Nkain3	5733.03	Pusl1	2645.52	Rnf169	1707.62	**Klf10**	**1306.59**
Prdm13	5733.03	Iqcj	2645.52	Tpk1	1707.62	Sox11	1306.59
Gm4850	5730.87	Schip1	2645.52	Cntnap2	1707.62	Dcdc2c	1306.59
Khdrbs2	5730.87	Ghitm	2643.36	Api5	1703.31	Atxn1	1304.43
1110001J03Rik	5709.31	Nrg3	2643.36	Lrrc4c	1703.31	Stmnd1	1304.43
Klrg2	5709.31	Tinag	2630.42	3100003L05Rik	1701.15	Gm5082	1304.43
H2-M9	5698.53	5730403I07Rik	2630.42	4933440M02Rik	1701.15	Adtrp	1304.43
H2-M1	5698.53	Csnk1d	2628.27	4930448I06Rik	1701.15	Itpk1	1304.43
D3Ertd751e	5689.91	Cd7	2628.27	Pou3f3os	1701.15	Moap1	1304.43
2610316D01Rik	5689.91	Chd6	2623.96	Cldn22	1698.99	2610005L07Rik	1302.28
4930486L24Rik	5640.32	Ptprtos	2623.96	Dctd	1698.99	Gm21119	1302.28
Ctla2b	5640.32	Gm10494	2621.8	Dapk2	1696.84	Gm16863	1302.28
Rprl1	5629.54	Cyp1b1	2621.8	Fbxl22	1696.84	2510009E07Rik	1302.28
Rpia	5629.54	Aifm3	2621.8	Isl2	1696.84	Cntn1	1302.28

Specc1	5623.07	Thap7	2621.8	Rfpl3s	1696.84	Gxylt1	1302.28
Adora2b	5623.07	Oprm1	2619.64	Slc45a1	1696.84	Cox7c	1302.28
6330415 B21Rik	5612.29	Ulbp1	2619.64	1700045H 11Rik	1696.84	Edil3	1302.28
Reg3b	5612.29	2810032G03 Rik	2608.86	B3galt1	1694.68	Mast4	1302.28
Toporsl	5590.73	1700101O22 Rik	2608.86	4933409G 03Rik	1694.68	Srek1	1302.28
4930552 N02Rik	5590.73	Mir509	2600.24	Igsf11	1694.68	Six4	1302.28
4930474 H20Rik	5571.32	Fmr1	2600.24	Gap43	1694.68	Trmt5	1302.28
Pcdh9	5571.32	Dock4	2587.3	Impg1	1692.53	Rnase13	1300.12
Tmsb10	5562.7	Immp2l	2587.3	Htr1b	1692.53	Zfp219	1300.12
Suclg1	5562.7	Col18a1	2587.3	Nfyc	1692.53	Mir2136	1297.96
Klhl25	5551.92	Gm10941	2587.3	Rims3	1692.53	Mrpl3	1297.96
Ntrk3	5551.92	Cypt12	2582.99	Lmx1a	1692.53	Gm1653	1297.96
Fat3	5538.98	Bhlhe22	2582.99	Mir6348	1692.53	Eltd1	1297.96
Chordc1	5538.98	As3mt	2576.52	Slc30a8	1690.37	Ankrd16	1297.96
Map4k4	5532.51	Nt5c2	2576.52	Med30	1690.37	Itga8	1297.96
Gm16894	5532.51	Lamc3	2574.37	Mgme1	1688.21	Trpm6	1297.96
Gm14851	5493.7	Nup214	2574.37	Pet117	1688.21	Anxa1	1297.96
Gm15284	5493.7	Tpx2	2574.37	Pam16	1688.21	Matr3	1297.96
Rprl1	5489.39	Mylk2	2574.37	Vasn	1688.21	Mzb1	1297.96
Rpia	5489.39	Mos	2565.74	Gpr101	1686.06	Oxgr1	1297.96
Peg12	5485.08	Plag1	2565.74	Zic3	1686.06	Mbnl2	1297.96
Chrna7	5485.08	Gm20752	2546.34	Slc10a2	1686.06	Gpr63	1295.81
Large	5480.77	Depdc1a	2546.34	Efnb2	1686.06	Ufl1	1295.81
Isx	5480.77	Tmem252	2544.18	Dicer1	1686.06	Oprk1	1295.81
Sh3bp4	5478.61	Foxd4	2544.18	Syne3	1686.06	Npbwr1	1295.81
C030007 H22Rik	5478.61	Sucla2	2544.18	Zfp369	1683.9	Gm20745	1293.65

4930401O12Rik	5472.14	Htr2a	2544.18	Gm10324	1683.9	4930502A04Rik	1293.65
Foxq1	5472.14	Actbl2	2544.18	Tex29	1681.75	Vmn1r29	1293.65
Kcnj2	5463.52	Gpbp1	2544.18	Gm5607	1681.75	Vmn1r30	1293.65
BC006965	5463.52	Scaf11	2542.02	Ypel2	1681.75	Cst3	1293.65
Fat3	5452.74	Slc38a2	2542.02	Smg8	1681.75	Cst10	1293.65
Chordc1	5452.74	Mir7025	2537.71	A830082N09Rik	1681.75	1700025F24Rik	1293.65
Ccdc104	5446.27	Kit	2537.71	Trappc3l	1681.75	Grip1os2	1293.65
Prorsd1	5446.27	Cldn14	2535.56	Gm815	1677.43	Sec23ip	1291.49
Myo5a	5433.33	Sim2	2535.56	Vldlr	1677.43	Ppapdc1a	1291.49
Gnb5	5433.33	1700101O22Rik	2531.24	4930548J01Rik	1677.43	Il7	1291.49
4930453L07Rik	5426.87	Apob	2531.24	Arid1b	1677.43	1700010I02Rik	1291.49
Lig4	5426.87	Prok2	2529.09	Gm16833	1673.12	Bmp2	1291.49
Col4a1	5426.87	Rybp	2529.09	Mir6237	1673.12	Hao1	1291.49
Rab20	5426.87	CK137956	2524.78	Magea10	1670.97	Pcdhb2	1289.34
Gm14461	5424.71	Csmd2os	2524.78	Mir767	1670.97	Pcdhb4	1289.34
Ube2e3	5424.71	Gm20268	2524.78	Krtap5-4	1670.97	Gypc	1287.18
Serpinb6e	5420.4	Cdh20	2524.78	Ifitm10	1670.97	4930455D15Rik	1287.18
Serpinb6a	5420.4	Eno1	2511.84	Ipo4	1670.97	4930558G05Rik	1285.03
1700036G14Rik	5388.06	Slc45a1	2511.84	Tssk4	1670.97	Pcdh19	1285.03
Fam160a1	5388.06	Pigu	2511.84	Maged2	1668.81	Gng10	1285.03
1110054M08Rik	5381.59	Ncoa6	2511.84	Gnl3l	1668.81	LOC101055769	1285.03
Lpp	5381.59	Fhl2	2511.84	Kcnt1	1668.81	Sorcs1	1285.03
Slc25a40	5366.5	Nck2	2511.84	Ubac1	1668.81	Ins1	1285.03
Abcb1a	5366.5	Pcdh17	2507.53	Nr1i2	1668.81	Olfr9	1285.03

Mir3102	5329.84	4930529K09 Rik	2507.53	Cox17	1668.81	Olfr765	1285.03
P2ry6	5329.84	Mt1	2494.59	Slc44a1	1666.65	Gm16833	1282.87
Lnx1	5321.22	Mir138-2	2494.59	Fsd1l	1666.65	Mir6237	1282.87
Gm6116	5321.22	Tm4sf20	2488.12	4930547E 14Rik	1664.5	A730082 K24Rik	1282.87
Pdgfra	5308.28	Agfg1	2488.12	Nsun3	1664.5	1700003 G18Rik	1282.87
Kit	5308.28	Grin3a	2483.81	Nrbf2	1664.5	Slmap	1282.87
Gm12887	5301.81	Cylc2	2483.81	Egr2	1664.5	Denndd6a	1282.87
9530002 B09Rik	5301.81	Pde4b	2483.81	Atf7ip	1662.34	Prpsap1	1282.87
Gm20854	5280.25	Sgip1	2483.81	Gucy2c	1662.34	Sphk1	1282.87
Gm20854	5280.25	Mir17hg	2479.5	Nalcn	1662.34	Lrrn1	1280.71
Plxna4os 1	5278.1	4930505G20 Rik	2479.5	Fgf14	1662.34	Setmar	1280.71
Chchd3	5278.1	5-Mar	2473.03	Flrt3	1660.19	Polr2b	1280.71
Lincrna-cox2	5271.63	4931408D14 Rik	2473.03	Kif16b	1660.19	Pea15b	1280.71
Pdc	5271.63	2700049A03 Rik	2473.03	Gm6756	1660.19	Snx10	1278.56
Astn2	5243.6	4930404H11 Rik	2473.03	Pcdha8	1660.19	Skap2	1278.56
Tlr4	5243.6	Vwc2	2470.87	Clip1	1658.03	5031426 D15Rik	1278.56
Edem1	5239.29	4930415F15 Rik	2470.87	Zcchc8	1658.03	1700061 F12Rik	1278.56
Grm7	5239.29	1700013G24 Rik	2460.09	St7l	1658.03	Gca	1278.56
Htr2c	5232.82	Hspg2	2460.09	Wnt2b	1658.03	Fign	1278.56
Il13ra2	5232.82	Mir3106	2455.78	Enoph1	1655.87	1810018 F18Rik	1278.56
Sorcs3	5224.19	Mcph1	2455.78	2310034O 05Rik	1655.87	Pnliprp2	1278.56
Ins1	5224.19	Gm6300	2445	Gm16998	1655.87	Pfkp	1278.56

Epha6	5217.73	Slc7a12	2445	Tbc1d32	1655.87	Wdr37	1278.56
Nsun3	5217.73	Runx1	2442.84	Ptchd1	1653.72	Mir1906-1	1276.4
4930474H20Rik	5209.1	1810053B23Rik	2442.84	4930503H13Rik	1653.72	Pet2	1276.4
Pcdh9	5209.1	Dok5	2440.69	Adcyap1r1	1653.72	Ercc5	1276.4
1110059M19Rik	5194.01	1700028P15Rik	2440.69	Neurod6	1653.72	Gulp1	1276.4
Actrt1	5194.01	Amot	2436.38	D3Ertd751e	1653.72	Btg1	1276.4
Gpr26	5150.89	Htr2c	2436.38	2610316D01Rik	1653.72	4930556N09Rik	1276.4
Cpxm2	5150.89	Gpc5	2436.38	S1pr3	1653.72	Vstm2b	1274.25
Tfcp2l1	5135.79	Gpc6	2436.38	Cks2	1653.72	4930433I11Rik	1274.25
Inhbb	5135.79	Fbxo32	2429.91	B130024G19Rik	1651.56	Sall3	1274.25
Vmn1r67	5092.67	Anxa13	2429.91	Mctp2	1651.56	Mir5127	1274.25
Zik1	5092.67	Rpl31	2427.75	Nhlh2	1647.25	Efcab1	1274.25
Pros1	5077.58	Cnot11	2427.75	Vangl1	1647.25	Ube2v2	1274.25
Epha3	5077.58	Zfp946	2425.6	1700016G22Rik	1647.25	Ednrb	1274.25
Fip1l1	5064.64	Vmn2r112	2425.6	Pitrm1	1647.25	4930432J09Rik	1274.25
Gm6116	5064.64	Usp15	2425.6	Zfp277	1647.25	Gm10324	1274.25
Prl5a1	5062.49	4930503E24Rik	2425.6	Immp2l	1647.25	2410141K09Rik	1274.25
2610307P16Rik	5062.49	Ccser1	2419.13	6030469F06Rik	1647.25	4930503O07Rik	1274.25
Mir5127	5040.93	Atoh1	2419.13	Dld	1647.25	Plxna2	1274.25
Galr1	5040.93	Egfem1	2391.1	Lingo2	1645.09	Brinp2	1274.25
Kcnh7	5025.83	Manr	2391.1	1700009N14Rik	1645.09	Mir488	1274.25
Fign	5025.83	Spaca3	2391.1	4930412D23Rik	1642.94	Lmo3	1272.09

Ptbp2	5008.59	1700071K01 Rik	2391.1	4930558G 05Rik	1642.94	Igbp1b	1272.09
Rwdd3	5008.59	Alox12e	2391.1	Sall3	1642.94	Atp12a	1272.09
Snord14d	5008.59	Pelp1	2391.1	Mir5127	1642.94	Cenpj	1272.09
C130030 K03Rik	5008.59	Tmem38b	2384.63	Mtnr1b	1638.62	Rnf145	1272.09
Zfp946	5002.12	Zfp462	2384.63	Chordc1	1638.62	**Ebf1**	**1272.09**
Vmn2r11 2	5002.12	Slco2b1	2382.47	Ccser1	1638.62	Pcdh11x	1269.93
Ppapdc1a	4991.34	Olfr520	2382.47	Atoh1	1638.62	Nap1l3	1269.93
Wdr11	4991.34	Pcif1	2382.47	Mir297c	1638.62	Nat3	1269.93
D3Ertd75 1e	4982.71	Mmp9	2382.47	Lyplal1	1638.62	Sh2d4a	1269.93
2610316 D01Rik	4982.71	Thumpd2	2382.47	Vmn2r47	1636.47	Spink7	1267.78
Edem1	4978.4	Gm19689	2382.47	Vmn2r46	1636.47	2700046 A07Rik	1267.78
Grm7	4978.4	Efnb1	2378.16	Tmem168	1634.31	Zfp28	1263.47
Ccdc37	4959	Gm14812	2378.16	Gpr85	1634.31	Olfr1344	1263.47
Klf15	4959	Dysf	2376.01	Epha5	1634.31	Galr1	1263.47
Abcc3	4950.37	Gm10445	2376.01	Cenpc1	1634.31	Mbp	1263.47
Spata20	4950.37	Oit1	2371.69	Plekho1	1634.31	Slc19a1	1263.47
D3Ertd75 1e	4946.06	4930455B14 Rik	2371.69	Mir1946b	1634.31	Gm10941	1263.47
2610316 D01Rik	4946.06	Tlr13	2360.91	Fstl5	1634.31	Penk	1261.31
Mir7224	4941.75	Pgk1	2360.91	Rapgef2	1634.31	Gm11780	1261.31
Mir6335	4941.75	Dcp2	2358.76	Spata31d1 c	1634.31	Atp6v1a	1261.31
Gm20268	4933.12	A930012L18 Rik	2358.76	Olfr466	1634.31	Gm608	1261.31
Cdh20	4933.12	Fabp3	2352.29	Pinx1	1632.16	Sall1	1259.15
Mettl11b	4907.25	Snrnp40	2352.29	Sox7	1632.16	Tox3	1259.15
Kifap3	4907.25	Dtna	2352.29	Sncaip	1630	Barhl2	1259.15

Vmn2r72	4896.47	Mapre2	2352.29	Snx2	1630	Zfp644	1259.15
Vmn2r73	4896.47	Gm14725	2350.13	AI593442	1627.84	Sp110	1259.15
A530072 M11Rik	4896.47	Mtm1	2350.13	Ddx10	1627.84	Sp100	1259.15
Mmp16	4896.47	Ccdc59	2347.98	Apbb2	1627.84	T	1259.15
Khdrbs2	4894.31	Acss3	2347.98	Uchl1os	1627.84	1700010I 14Rik	1259.15
Prim2	4894.31	Pcnx	2343.66	D030025E 07Rik	1627.84	Slc25a24	1257
Tbc1d2b	4887.84	Sipa1l1	2343.66	Pitx2	1627.84	Vav3	1257
Zic1	4887.84	Rnf8	2330.73	4930595M 18Rik	1625.69	4930402 F06Rik	1257
Map3k13	4885.69	Ccdc167	2330.73	Tsga8	1625.69	Gm13446	1257
Liph	4885.69	Wfdc16	2326.42	Card11	1623.53	Snhg11	1257
Gm20865	4825.32	Wfdc9	2326.42	Foxk1	1623.53	Adig	1257
LOC1000 40786	4825.32	Syt1	2324.26	Zfp369	1623.53	Zfp369	1257
Mir5127	4825.32	9230102K24 Rik	2324.26	Gm10324	1623.53	Gm10324	1257
Galr1	4825.32	4930467E23 Rik	2309.17	Rps15	1623.53	Slitrk4	1254.84
Gm7157	4805.91	6820431F20 Rik	2309.17	Apc2	1623.53	Ctag2	1254.84
Gpr143	4805.91	Grik3	2307.01	Hsd17b12	1621.38	Ppp1cb	1254.84
Adcy8	4782.2	2610028E06 Rik	2307.01	Mir129-2	1621.38	Yes1	1254.84
Efr3a	4782.2	Pex7	2307.01	Tmem27	1619.22	Gpr22	1254.84
5033403 H07Rik	4773.57	Map7	2307.01	Bmx	1619.22	Prkar2b	1254.84
Slc34a2	4773.57	4930486F22 Rik	2298.39	Commd6	1617.06	Mettl7b	1254.84
1700125 H03Rik	4760.64	1810014B01 Rik	2298.39	Uchl3	1617.06	Olfr763	1254.84
Ints10	4760.64	Etv1	2294.07	Gm17746	1617.06	Sphkap	1252.69
Grin3a	4760.64	Arl4a	2294.07	4930480M	1617.06	Pid1	1252.69

				12Rik			
Cylc2	4760.64	Api5	2287.61	Epha6	1612.75	Pfdn4	1250.53
4930453L07Rik	4749.86	Lrrc4c	2287.61	Nsun3	1612.75	4930470P17Rik	1250.53
Lig4	4749.86	Bub1	2287.61	7630403G23Rik	1610.6	Crtac1	1250.53
A830082K12Rik	4749.86	Bcl2l11	2287.61	St3gal4	1610.6	Loxl4	1250.53
Arrdc3	4749.86	Ppp1r2-ps7	2283.29	2610005L07Rik	1610.6	Hrh4	1250.53
1700125H03Rik	4745.54	Wdr44	2283.29	Gm21119	1610.6	Zfp521	1250.53
Ints10	4745.54	Med30	2283.29	Ncs1	1610.6	Dnah9	1250.53
Snord67	4728.29	Samd12	2283.29	Ass1	1610.6	Gm12298	1250.53
F2	4728.29	Nudt21	2278.98	Mapre3	1608.44	Lamc1	1250.53
Gm10033	4726.14	Bbs2	2278.98	Agbl5	1608.44	E330020D12Rik	1250.53
Zfp868	4726.14	Rell1	2276.83	Cdh6	1608.44	Acpp	1248.37
Grem1	4723.98	5830416I19Rik	2276.83	Cdh9	1608.44	Mir2136	1248.37
Arhgap11a	4723.98	4930426D05Rik	2276.83	Zfp369	1606.28	G630093K05Rik	1248.37
Olfr1349	4711.05	Asxl3	2276.83	Gm10324	1606.28	A330033J07Rik	1248.37
Olfr1350	4711.05	Gm12886	2274.67	Gm20098	1604.13	1700101O22Rik	1248.37
Gm20172	4708.89	Gm12887	2274.67	Kcnh8	1604.13	Apob	1248.37
4931408C20Rik	4708.89	Usp9y	2268.2	Gak	1601.97	Sfrp1	1246.22
Astn2	4702.42	Zfy2	2268.2	Idua	1601.97	Zmat4	1246.22
Tlr4	4702.42	Arx	2268.2	Gm5860	1601.97	A930018P22Rik	1246.22
Zfp946	4698.11	Pcyt1b	2268.2	Nfib	1601.97	Hipk3	1246.22
Vmn2r112	4698.11	Chl1	2268.2	Cybrd1	1599.82	Nova1	1246.22

1700125H03Rik	4695.95	Gm19757	2268.2	Slc25a12	1599.82	Mir5125	1246.22
Ints10	4695.95	Bmp2	2263.89	Usp25	1599.82	E2f7	1246.22
Slc14a2	4687.33	Hao1	2263.89	2810055G20Rik	1599.82	Csrp2	1246.22
Setbp1	4687.33	Depdc1b	2257.42	4933413L06Rik	1599.82	Fam122c	1244.06
4930474N09Rik	4683.02	Pde4d	2257.42	Mrps30	1599.82	Mospd1	1244.06
1700064M15Rik	4683.02	Rasip1	2255.26	Zfp873	1599.82	Nrxn1	1244.06
Kif26b	4678.7	Fut2	2255.26	AU041133	1599.82	Adcyap1	1244.06
Tfb2m	4678.7	Tgfbr2	2253.11	E230016M11Rik	1597.66	Spata31d1d	1244.06
Astn2	4672.24	Azi2	2253.11	Serbp1	1597.66	Isca1	1244.06
Tlr4	4672.24	Gm10375	2253.11	Arhgap24	1595.5	Gm4850	1244.06
Gm5935	4663.61	Ear1	2253.11	4930429D17Rik	1595.5	Gm9839	1244.06
Gm14819	4663.61	Nbea	2250.95	Gm6756	1595.5	Tmem132b	1241.91
4930448I18Rik	4648.52	Tm4sf1	2250.95	Pcdha4	1595.5	4933438B17Rik	1241.91
Mir6417	4648.52	Tyro3	2250.95	Ddx18	1595.5	Gm10857	1241.91
Ctdp1	4642.05	Mapkbp1	2250.95	Dpp10	1595.5	A230108P19Rik	1241.91
Gm2176	4642.05	Gbx2	2250.95	Pcdh11x	1593.35	Qtrtd1	1241.91
Cntnap5a	4637.74	Iqca	2250.95	Nap1l3	1593.35	Zdhhc23	1241.91
Tsn	4637.74	Appl2	2250.95	Hps1	1593.35	Gpatch2	1241.91
Lace1	4629.11	Nuak1	2250.95	Cnnm1	1593.35	Esrrg	1241.91
Snx3	4629.11	Map7d2	2244.48	Thumpd2	1593.35	Aldh1l1	1239.75
Pemt	4592.46	Sh3kbp1	2244.48	Slc8a1	1593.35	Slc41a3	1239.75
Rai1	4592.46	Acot10	2242.33	Neurog3	1593.35	Gm4710	1239.75
Med30	4557.96	Gm5803	2242.33	Mir7662	1593.35	Crim1	1239.75
Ext1	4557.96	Samd3	2238.02	Pnpla8	1591.19	Sohlh2	1237.59

Pcdh18	4547.18	L3mbtl3	2238.02	Stxbp6	1591.19	Dclk1	1237.59
Ccrn4l	4547.18	Nmnat2	2235.86	Gm21119	1589.03	Fndc3a	1237.59
Ss18	4545.03	Lamc1	2235.86	6820431F20Rik	1589.03	Gm9199	1237.59
Taf4b	**4545.03**	Robo1	2231.55	Gm6756	1589.03	Tmem263	1237.59
Adck1	4536.4	Robo2	2231.55	Pcdha8	1589.03	Cry1	1237.59
Mir466b-3	4536.4	Mir3063	2231.55	Stmn4	1586.88	Scn7a	1235.44
Rbmy	4532.09	Gip	2231.55	Adra1a	1586.88	Gm1322	1235.44
Gm20826	4532.09	Slc8a1	2229.39	Gm20063	1586.88	Slc6a14	1233.28
Gm19757	4525.62	Gm19689	2229.39	Fscb	1586.88	Ppp1r2-ps7	1233.28
Cntn4	4525.62	Snx16	2227.24	Gm10421	1586.88	Gm14015	1233.28
Ythdf3	4523.47	Gm10745	2227.24	Gm5441	1586.88	Mpped2	1233.28
2610100L16Rik	4523.47	2410141K09Rik	2227.24	Gm10280	1584.72	2700046G09Rik	1233.28
Gm20172	4495.44	Uqcrb	2227.24	4930571O06Rik	1584.72	Minpp1	1233.28
4931408C20Rik	4495.44	Mir466g	2220.77	Ghsr	1584.72	Inpp1	1233.28
Gm20823	4484.66	Efna5	2220.77	Mir3092	1584.72	Hibch	1233.28
Gm20823	4484.66	Cxcr4	2218.61	AW822252	1582.57	Map3k1	1233.28
Cdh8	4482.5	Daf2	2218.61	1700013H16Rik	1582.57	Ankrd55	1233.28
Cdh11	4482.5	Gm20752	2216.46	Tmtc4	1582.57	Pawr	1233.28
Kctd16	4480.34	Depdc1a	2216.46	AA536875	1582.57	Gm5136	1233.28
Prelid2	4480.34	4930545E07Rik	2216.46	Soat1	1582.57	Atp13a5	1231.12
Xpa	4476.03	Dsc3	2216.46	Tor3a	1582.57	Opa1	1231.12
Foxe1	4476.03	Nfasc	2216.46	Mir6368	1580.41	Olfr1242	1228.97
AW554918	4467.41	Lrrn2	2216.46	**Sox4**	**1580.41**	Olfr1243	1228.97

Celf4	4467.41	Gm561	2214.3	Nav3	1580.41	Upk1a	1226.81
Kcnip4	4448	Scp2d1	2214.3	9230102K 24Rik	1580.41	Cox6b1	1226.81
Gpr125	4448	Elf5	2214.3	Ccdc83	1578.25	Zfp462	1226.81
Klhl4	4428.6	Abtb2	2214.3	Sytl2	1578.25	Rad23b	1226.81
Ube2dnl1	4428.6	Pcdh11x	2212.14	Pax4	1576.1	Dock4	1226.81
Gm10220	4413.51	Nap1l3	2212.14	Lrrc4	1576.1	Lrrn3	1226.81
Gm7361	4413.51	Snrpg	2212.14	Gm2447	1576.1	Best3	1226.81
Smpdl3a	4413.51	Pcyox1	2212.14	Gm20750	1576.1	Lrrc10	1226.81
Dux	4413.51	Arsb	2209.99	Rxfp3	1576.1	Pde7b	1224.66
Fat3	4402.73	Lhfpl2	2209.99	Adamts12	1576.1	Ahi1	1224.66
Chordc1	4402.73	Becn2	2209.99	2210039B 01Rik	1576.1	Cybb	1222.5
1700008 P02Rik	4350.98	Cep170	2209.99	Prkch	1576.1	Gm5132	1222.5
Pkia	4350.98	Vwa2	2207.83	Slc1a4	1573.94	Sim2	1222.5
Klhl25	4342.36	Ablim1	2207.83	Sertad2	1573.94	Ripply3	1222.5
Ntrk3	4342.36	Gm10823	2205.68	Nol11	1573.94	Phf20l1	1222.5
Spdl1	4310.01	Fgf12	2205.68	Psmd12	1573.94	Wisp1	1222.5
Mir218-2	4310.01	Gzf1	2201.36	Mir138-2	1571.79	Gm6634	1220.34
Raly	4286.3	Cstl1	2201.36	Herpud1	1571.79	Sis	1220.34
a	4286.3	Gm5126	2197.05	Coq7	1571.79	1810007 C17Rik	1220.34
Smpdl3a	4279.83	Nap1l2	2197.05	Tmc5	1571.79	Prkd1	1220.34
Dux	4279.83	4930455J16 Rik	2197.05	Mc2r	1571.79	Rab10os	1220.34
Gm7361	4269.05	Agtpbp1	2197.05	Mir6356	1571.79	Kif3c	1220.34
4930584F 24Rik	4269.05	Piwil1	2194.89	5033404E 19Rik	1571.79	Gm17746	1220.34
Mthfs	4251.8	Stx2	2194.89	Mir297c	1571.79	4930480 M12Rik	1220.34
AF52916 9	4251.8	Cdc14a	2194.89	Lifr	1569.63	Sec16b	1220.34

Gm20854	4241.02	Rtca	2194.89	Gdnf	1569.63	Brinp2	1220.34
Gm20854	4241.02	Pax8	2194.89	AI429214	1567.47	Gm9871	1218.19
Impg1	4241.02	Cacna1b	2194.89	Sgcz	1567.47	Mir6373	1218.19
Htr1b	4241.02	Hnf4aos	2194.89	Fbxw4	1565.32	Tecrl	1218.19
4930486L 24Rik	4241.02	Ttpal	2194.89	4933429K 18Rik	1565.32	Epha5	1218.19
Ctla2b	4241.02	Mir7015	2192.74	Thap1	1561.01	4933421 O10Rik	1218.19
Lamp2	4230.24	Col9a2	2192.74	2310008N 11Rik	1561.01	Gabrr2	1218.19
Cul4b	4230.24	Epha3	2192.74	2610203C 20Rik	1558.85	Napg	1218.19
Ccdc71l	4228.08	Csnka2ip	2192.74	Sorl1	1558.85	Txnl1	1218.19
Nampt	4228.08	Igfbpl1	2190.58	Tmem261	1552.38	2810032 G03Rik	1218.19
Smpdl3a	4223.77	1300002K09 Rik	2190.58	Tyrp1	1552.38	1700101 O22Rik	1218.19
Dux	4223.77	Klf4	2181.96	Nlgn1	1552.38	Mei4	1216.03
Klhl4	4221.61	Actl7b	2181.96	Spata16	1552.38	Irak1bp1	1216.03
Ube2dnl1	4221.61	Tsc22d3	2179.8	1700010K 23Rik	1550.23	Scap	1216.03
Chsy1	4210.83	Tex13	2179.8	Speer2	1550.23	Ngp	1216.03
Mir7057	4210.83	0610039K10 Rik	2179.8	Sec16b	1550.23	Rfx3	1216.03
Tas2r108	4202.21	Pkig	2179.8	Brinp2	1550.23	D930032 P07Rik	1216.03
Prss37	4202.21	Gm6756	2177.65	4930459C 07Rik	1550.23	Gm5820	1216.03
Cyp4b1	4200.05	Pcdha3	2177.65	Btg1	1550.23	Nr3c1	1216.03
Efcab14	4200.05	Wdr20rt	2175.49	Gm19395	1550.23	Edn3	1213.88
Slc7a2	4193.59	Rpl10l	2175.49	Pln	1550.23	Gm14393	1213.88
Mtus1	4193.59	Tbr1	2173.33	Lrrc4	1548.07	Hspa9	1213.88
Zfp74	4161.24	Slc4a10	2173.33	Mir129-1	1548.07	Lrrtm2	1213.88
Zfp568	4161.24	Tsc22d3	2171.18	Klra4	1548.07	Gm5136	1211.72

Commd10	4146.15	Mid2	2171.18	Klra14-ps	1548.07	Nav3	1211.72
9130209 A04Rik	4146.15	Mir5127	2171.18	Rbbp7	1545.91	1700044 C05Rik	1209.56
Dcc	4120.28	Galr1	2171.18	Txlng	1545.91	Mir6391	1209.56
Mex3c	4120.28	5430437J10 Rik	2171.18	Nfe2l3	1545.91	Prss23	1207.41
Gm12887	4118.12	Dab2	2171.18	Cbx3	1545.91	Me3	1207.41
9530002 B09Rik	4118.12	Prl5a1	2171.18	Cnot4	1545.91	Tacr3	1207.41
Cyp4b1	4118.12	2610307P16 Rik	2171.18	Nup205	1545.91	Cenpe	1207.41
Efcab14	4118.12	4930448I06 Rik	2169.02	Cd200r4	1545.91	Mir6389	1205.25
Fat3	4115.97	Pou3f3os	2169.02	Cd200r2	1545.91	Atp10a	1205.25
Chordc1	4115.97	4930596I21 Rik	2169.02	Mocos	1543.76	4921531 C22Rik	1205.25
Bai3	4115.97	Crb1	2169.02	Tpgs2	1543.76	Lsm14b	1205.25
4931408 C20Rik	4115.97	Kcnj2	2169.02	4930440I1 9Rik	1541.6	1110034 G24Rik	1205.25
Thap4	4087.94	BC006965	2169.02	Gm14461	1541.6	Trmt6	1205.25
Dtymk	4087.94	Rft1	2166.87	Ccdc59	1541.6	Snx9	1205.25
Zfp428	4081.47	Tmem110	2166.87	Acss3	1541.6	Synj2	1205.25
Irgq	4081.47	Opalin	2162.55	Gm5382	1539.44	Cmss1	1205.25
Gm14461	4064.22	Tm9sf3	2162.55	Ppp1r2-ps9	1539.44	Dcbld2	1205.25
Ube2e3	4064.22	Mir669a-7	2162.55	Tlr3	1539.44	Rgs10	1203.1
Gm5460	4053.44	Gm20098	2162.55	Pdlim3	1539.44	Tial1	1203.1
Anxa8	4053.44	Mir7090	2160.4	Etl4	1537.29	Ptar1	1203.1
Fam53b	4044.82	Ulk4	2160.4	Gm13375	1537.29	Fam189a 2	1203.1
Mettl10	4044.82	Tpk1	2160.4	5031425F 14Rik	1537.29	Umodl1	1203.1
Ccnjl	4036.19	Cntnap2	2160.4	Mir6364	1537.29	Abcg1	1203.1
Fabp6	4036.19	Slc10a4	2158.24	Uggt2	1537.29	2410141	1203.1

						K09Rik	
Serpinb6e	4023.25	1700025M24Rik	2158.24	Hs6st3	1537.29	Uqcrb	1203.1
Serpinb6a	4023.25	Ube2dnl2	2153.93	Brcc3	1535.13	Rnf2	1203.1
Scrt1	4021.1	Cpxcr1	2153.93	Vbp1	1535.13	Edem3	1203.1
Fbxl6	4021.1	Sncaip	2147.46	Mrgprh	1535.13	Gm12887	1200.94
Hapln1	4018.94	Snx2	2147.46	Pnldc1	1535.13	9530002B09Rik	1200.94
Xrcc4	4018.94	Gm438	2145.3	C530044C16Rik	1532.98	Bfsp1	1200.94
Slc25a18	4003.85	Vps13d	2145.3	Mir148a	1532.98	Rrbp1	1200.94
Bcl2l13	4003.85	Lrrc4c	2143.15	BC052040	1532.98	Nudt12	1200.94
Thumpd2	3995.23	B230118H07Rik	2143.15	2810405F15Rik	1532.98	Mir466g	1200.94
Gm19689	3995.23	Tmem261	2130.21	Spdl1	1532.98	Gabrb2	1200.94
Klhl4	3993.07	Tyrp1	2130.21	Slit3	1532.98	Mir146	1200.94
Ube2dnl1	3993.07	Blcap	2130.21	Cypt1	1530.82	Mthfs	1198.78
Usp9y	3990.91	Vstm2l	2130.21	Maoa	1530.82	AF529169	1198.78
Zfy2	3990.91	Pou3f2	2128.06	Macrod2	1530.82	Zkscan2	1198.78
Ythdf3	3990.91	Mms22l	2128.06	Flrt3	1530.82	Hs3st4	1198.78
2610100L16Rik	3990.91	Abca13	2128.06	Klf14	1526.51	Sri	1198.78
Rbfox2	3982.29	Vwc2	2128.06	Mir29a	1526.51	Dbf4	1198.78
Apol7a	3982.29	Ska2	2125.9	Otol1	1524.35	Otud1	1198.78
Celf2	3967.2	Ppm1e	2125.9	Gm6634	1524.35	Arhgap21	1198.78
1700061F12Rik	3967.2	Vmn2r47	2121.59	1700015G11Rik	1522.2	Cd69	1196.63
Trak2	3967.2	Vmn2r46	2121.59	Mir6238	1522.2	4922502D21Rik	1196.63
Als2cr11	3967.2	Tnnt3	2121.59	Batf	1522.2	Cyp3a59	1196.63
Fam47c	3958.57	Mrpl23	2121.59	0610007P14Rik	1522.2	1700001J03Rik	1196.63

Gm8787	3958.57	Ccny	2117.28	1700017N19Rik	1522.2	Tmem132b	1196.63
Gm5347	3945.64	Cetn1	2117.28	Mgat4c	1522.2	4933438B17Rik	1196.63
AY512931	3945.64	Vmn2r-ps11	2115.12	Keap1	1520.04	Ptchd1	1194.47
Scrn1	3928.39	Kcnab1	2115.12	Atg4d	1520.04	4930503H13Rik	1194.47
Fkbp14	3928.39	Tab2	2115.12	Scp2d1	1520.04	Vamp3	1194.47
Irx3	3911.14	Ust	2115.12	Gm14092	1520.04	Camta1	1194.47
Crnde	3911.14	Edem1	2112.96	Peg13	1520.04	Dync1i2	1194.47
Gabre	3889.58	Grm7	2112.96	Chrac1	1520.04	Hat1	1194.47
Magea10	3889.58	Inhba	2110.81	Slain1	1520.04	Psg29	1192.32
Leprot	3887.42	Mplkip	2110.81	Ednrb	1520.04	Psg-ps1	1192.32
Lepr	3887.42	Mir216b	2106.5	Aktip	1517.88	Tmem38b	1192.32
Slc4a4	3876.64	Mir216a	2106.5	Fto	1517.88	Zfp462	1192.32
Gc	3876.64	Vmn2r72	2102.18	6330408A02Rik	1517.88	Gnas	1192.32
Ptchd1	3855.08	Vmn2r73	2102.18	Pla2g4c	1517.88	Nelfcd	1192.32
4930503H13Rik	3855.08	Gm19757	2102.18	Celf4	1517.88	Opalin	1192.32
Trib2	3855.08	**Il5ra**	**2102.18**	4930474G06Rik	1517.88	Tm9sf3	1192.32
Lpin1	3855.08	2610005L07Rik	2100.03	Ccdc14	1517.88	Dhrs2	1192.32
Ncs1	3835.68	Gm21119	2100.03	1700119H24Rik	1517.88	Dhrs4	1192.32
Fubp3	3835.68	Mir3106	2097.87	Ap5m1	1517.88	Epha7	1190.16
Cyth1	3814.11	Mcph1	2097.87	Naa30	1517.88	4930556G01Rik	1190.16
Usp36	3814.11	Gm10248	2097.87	2310002D06Rik	1517.88	Negr1	1190.16
Kif15	3794.71	Mir7210	2097.87	Erh	1517.88	Zranb2	1190.16
Tgm4	3794.71	Pcdh11x	2095.71	Mir6350	1515.73	Spg11	1190.16

Rragc	3792.55	Nap1l3	2095.71	Tmeff2	1515.73	Trim69	1190.16
1700057H15Rik	3792.55	Vamp3	2095.71	4930448I06Rik	1515.73	Irf4	1190.16
Setd6	3790.4	Camta1	2095.71	Pou3f3os	1515.73	Hus1b	1190.16
Mir7073	3790.4	Wnt3	2095.71	Lmf1	1513.57	Traf6	1188
Mast4	3790.4	Arf2	2095.71	Gng13	1513.57	Commd9	1188
Srek1	3790.4	Klra14-ps	2093.56	Znhit6	1509.26	Gpr111	1188
Lincrna-cox2	3770.99	Klra9	2093.56	Cyr61	1509.26	Tnfrsf21	1188
Pdc	3770.99	Mir466h	2093.56	Gm10790	1504.95	Oc90	1188
Gm20268	3764.52	Gm5860	2093.56	Hivep1	1504.95	Hhla1	1188
Cdh20	3764.52	Lrrc4c	2093.56	Prkag2	1502.79	Gm19784	1185.85
AA536875	3760.21	B230118H07Rik	2093.56	2900005J15Rik	1502.79	Chmp1b	1185.85
Itgbl1	3760.21	Pitx3	2084.93	Gm5095	1502.79	G630071F17Rik	1185.85
Gkn3	3758.06	Nfkb2	2084.93	Eno1b	1502.79	Rps14	1185.85
Arhgap25	3758.06	Cntnap5a	2082.78	Gm6377	1500.64	B4galt6	1185.85
Mocs2	3755.9	Tsn	2082.78	Gm7134	1500.64	Trappc8	1185.85
Itga1	3755.9	Vwc2	2080.62	Snord116l1	1498.48	Adcy8	1185.85
Mtnr1b	3753.74	4930415F15Rik	2080.62	D7Ertd715e	1498.48	Efr3a	1185.85
Chordc1	3753.74	Phyhip	2074.15	Cry1	1498.48	Cep112	1185.85
Celf2	3749.43	Sftpc	2074.15	Pwp1	1498.48	Axin2	1185.85
1700061F12Rik	3749.43	Ofcc1	2069.84	Gm3428	1496.32	Ubxn2a	1183.69
Tmem39a	3749.43	Tfap2a	2069.84	Gm5916	1496.32	Klhl29	1183.69
B4galt4	3749.43	Gm5148	2067.69	Hpca	1496.32	Psmd7	1181.53
Pros1	3745.12	Gm20755	2067.69	Fndc5	1496.32	Mir466g	1181.53
Epha3	3745.12	Nudt8	2065.53	1700023F02Rik	1496.32	St8sia2	1181.53
Ccl1	3734.34	Ndufv1	2065.53	LOC10263	1496.32	Sv2b	1181.53

				4101			
Tmem132e	3734.34	Ppp3r2	2063.37	1700034K08Rik	1494.17	Cbx3	1181.53
Fezf2	3723.56	Cylc2	2063.37	1190002N15Rik	1494.17	Snx10	1181.53
Gm5087	3723.56	Efcab2	2059.06	Hs3st1	1492.01	Tmem106b	1181.53
Nphp4	3717.09	Smyd3	2059.06	Rab28	1492.01	Vwde	1181.53
Gm833	3717.09	Xylt1	2056.91	Kctd16	1489.85	Grm3	1181.53
D830031N03Rik	3710.62	Rps15a	2056.91	Prelid2	1489.85	Gm6455	1181.53
Mir6398	3710.62	Vmn1r31	2052.59	Csmd3	1489.85	Gm6756	1181.53
Zfp946	3708.47	Abcg2	2052.59	Trps1	1489.85	Pcdhac2	1181.53
Vmn2r112	3708.47	Iqub	2052.59	Cstf3	1487.7	Tmem30c	1181.53
Nkain3	3671.81	Ndufa5	2052.59	Tcp11l1	1487.7	Filip1l	1181.53
Prdm13	3671.81	Rars	2052.59	Ddo	1487.7	Sox9	1181.53
Tmprss5	3669.66	Tenm2	2052.59	Cdc40	1487.7	2610035D17Rik	1181.53
Gm4894	3669.66	9530026F06Rik	2048.28	Lbx1	1485.54	Tbx18	1179.38
Adcyap1	3665.34	Nrp2	2048.28	Poll	1485.54	Nt5e	1179.38
Mettl4	3665.34	Dmrt2	2046.12	Adcyap1	1485.54	Gm5071	1177.22
Nkain3	3658.88	Smarca2	2046.12	Mettl4	1485.54	Mageb2	1177.22
Prdm13	3658.88	Csmd1	2043.97	Cntn1	1485.54	4930578E11Rik	1175.07
Gm19276	3648.1	Mcph1	2043.97	Gxylt1	1485.54	Pik3c3	1175.07
C1qtnf3	3648.1	Ccdc158	2041.81	Ufm1	1481.23	Snord71	1172.91
Pcdh11x	3643.78	Mir1961	2041.81	Postn	1481.23	Phlpp2	1172.91
Nap1l3	3643.78	Dapk1	2037.5	Gm7788	1481.23	Sema3d	1172.91
Gm4850	3643.78	Ctsll3	2037.5	Dtna	1481.23	Sema3a	1172.91
Khdrbs2	3643.78	Tmem126b	2033.19	Trat1	1481.23	Mb21d2	1172.91
2610206	3635.16	Dlg2	2033.19	Retnlb	1481.23	Atp13a5	1172.91

C17Rik							
Olfr291	3635.16	Ubl3	2033.19	Sv2c	1481.23	Il17rd	1172.91
4930548 K13Rik	3624.38	2210417A02 Rik	2033.19	Ankdd1b	1481.23	Arhgef3	1172.91
Epha7	3624.38	Edem1	2028.88	Tmem147	1476.92	Gdap1	1172.91
Atp10d	3611.44	1700054K19 Rik	2028.88	Sbsn	1476.92	Pi15	1172.91
Nfxl1	3611.44	Trim52	2028.88	Cbln2	1476.92	AI429214	1170.75
Gm10440	3611.44	1700128A07 Rik	2028.88	Socs6	1476.92	Mir383	1170.75
4932441J 04Rik	3611.44	Cftr	2026.72	3110043O 21Rik	1474.76	Snord116 l1	1170.75
Epha6	3596.35	Cttnbp2	2026.72	Mir876	1474.76	D7Ertd71 5e	1170.75
Nsun3	3596.35	Fxn	2026.72	Ppme1	1472.61	Tex38	1170.75
Cntnap5a	3594.19	Fam122a	2026.72	Ucp3	1472.61	Mob3c	1170.75
Tsn	3594.19	Ptplad2	2024.56	Ctsc	1470.45	Gm5544	1170.75
Gm5084	3587.73	Ifnb1	2024.56	Rab38	1470.45	Adam30	1170.75
Dapk1	3587.73	Ccdc112	2024.56	1700009N 14Rik	1470.45	9830132 P13Rik	1170.75
Olfr371	3585.57	Mospd4	2024.56	Aco1	1470.45	D030025 E07Rik	1170.75
Orc6	3585.57	Barx1	2024.56	Kif5c	1470.45	Zdhhc19	1170.75
Nbas	3579.1	Phf2	2024.56	Lypd6	1470.45	Tnk2	1170.75
Fam84a	3579.1	Vmn2r86	2024.56	Zfp217	1470.45	Zfp369	1170.75
Fbll1	3564.01	Vmn2r87	2024.56	Bcas1	1470.45	Gm10324	1170.75
Rars	3564.01	Pabpc4l	2022.41	Olfr1465	1470.45	Blzf1	1168.6
Spaca7	3559.7	Gm7977	2022.41	Olfr1466	1470.45	Atp1b1	1168.6
Gm15348	3559.7	Gm2176	2020.25	Kctd3	1470.45	Galnt4	1166.44
Large	3548.92	Nfatc1	2020.25	Cenpf	1470.45	Dusp6	1166.44
Isx	3548.92	Nr5a2	2020.25	1500012K 07Rik	1468.29	Dnajc24	1164.29
Gm10248	3542.45	Mir181a-1	2020.25	Klhl25	1468.29	Gm14015	1164.29

Mir7210	3542.45	4931412M21	2018.1	Flrt3	1468.29	Ado	1164.29
Cntnap5c	3540.29	7420701I03Rik	2018.1	Kif16b	1468.29	Zfp365	1164.29
2610034M16Rik	3540.29	Casp12	2015.94	Six2	1468.29	Kcnh7	1162.13
Mfap3l	3523.04	Pdgfd	2015.94	Srbd1	1468.29	Grb14	1162.13
2700029M09Rik	3523.04	Mir5127	2015.94	Gm8096	1466.14	Itsn1	1162.13
Palm2	3510.11	Galr1	2015.94	4933433F19Rik	1466.14	Atp5o	1162.13
Akap2	3510.11	1700064J06Rik	2015.94	Tmc1	1466.14	Gm5086	1162.13
Rprl1	3505.79	1700025F24Rik	2015.94	Zfand5	1466.14	Arhgef28	1162.13
Rpia	3505.79	Fgl1	2011.63	4930554C24Rik	1463.98	Snord116l2	1159.97
St8sia3os	3503.64	Asah1	2011.63	Fam46a	1463.98	Snord116	1159.97
Fech	3503.64	Frk	2011.63	Dmrt2	1463.98	1700019E08Rik	1159.97
Cyp2d26	3501.48	Hs3st5	2011.63	Smarca2	1463.98	Acvr2a	1159.97
Tbrg3	3501.48	5430434I15Rik	2009.47	Speer7-ps1	1461.83	Hdac4	1159.97
Prg4	3495.01	Ankrd50	2009.47	4930519H02Rik	1461.83	Ndufa10	1159.97
C730036E19Rik	3495.01	Arl5b	2007.32	Snord116l2	1459.67	Ccl1	1159.97
3100003L05Rik	3477.77	Plxdc2	2007.32	Snord116	1459.67	Tmem132e	1159.97
4933440M02Rik	3477.77	Fam86	2007.32	Slc30a9	1459.67	Usp38	1157.82
4930483O08Rik	3471.3	Rbfox1	2007.32	C330024D21Rik	1459.67	Inpp4b	1157.82
Tex36	3471.3	Arhgap15	2005.16	Has2	1459.67	Otud1	1157.82
Gm17019	3469.14	Arhgap15os	2005.16	Slc22a22	1459.67	Etl4	1157.82
Speer4d	3469.14	Gm17019	2003	Krt77	1459.67	Frk	1157.82

Edem1	3454.05	Speer4d	2003	Krt76	1459.67	Hs3st5	1157.82
Grm7	3454.05	Qtrt1	1998.69	Ociad2	1457.51	4930519 F24Rik	1155.66
Mir6414	3454.05	Mir199a-1	1998.69	Cwh43	1457.51	Il20rb	1155.66
Gm7854	3454.05	Cyp2b10	1998.69	Gpr115	1457.51	Ccdc144b	1155.66
Gm20823	3447.58	Cyp2b9	1998.69	**Cd2ap**	**1457.51**	D3Ertd25 4e	1155.66
Gm20823	3447.58	E130008D07 Rik	1998.69	Gap43	1457.51	Six1	1155.66
Klf4	3447.58	Gpr116	1998.69	4932412D 23Rik	1457.51	Mnat1	1155.66
Actl7b	3447.58	Lgals8	1996.53	Fads2	1455.36	Lmx1a	1155.66
Il15	3445.42	Edaradd	1996.53	Fads1	1455.36	Mir6348	1155.66
Zfp330	3445.42	Cnksr2	1994.38	Mir467a-10	1451.05	Kcnh7	1153.51
Med10	3443.27	Rps6ka3	1994.38	4930428E 07Rik	1451.05	Grb14	1153.51
1700084F 23Rik	3443.27	Dlx6os1	1994.38	Il15	1448.89	Mir6350	1153.51
Pla2g4e	3434.64	Acn9	1994.38	Zfp330	1448.89	Tmeff2	1153.51
Pla2g4f	3434.64	4930404A05 Rik	1992.22	Gm19303	1448.89	Ktn1	1153.51
1700092 K14Rik	3432.49	Zpld1	1992.22	Utp23	1448.89	4930447J 18Rik	1153.51
Mir466n	3432.49	1700029N11 Rik	1992.22	Ccdc25	1448.89	Gtpbp4	1153.51
Stmn4	3423.86	Jarid2	1992.22	Scara3	1448.89	Dip2c	1153.51
Adra1a	3423.86	Nt5dc1	1990.07	Olfr221	1448.89	Csmd1	1151.35
Gm20172	3423.86	Hs3st5	1990.07	Snord58b	1448.89	Mcph1	1151.35
4931408 C20Rik	3423.86	Ldlrad3	1987.91	Zfand1	1446.73	Cldn9	1151.35
Slc7a14	3421.71	Fjx1	1987.91	Snx16	1446.73	Pkmyt1	1151.35
Kcnmb2	3421.71	Ddx47	1983.6	Lemd2	1446.73	Sept9	1151.35
Peg12	3406.61	Gprc5a	1983.6	Mir7214	1446.73	2900041 M22Rik	1151.35

Chrna7	3406.61	Chd7	1981.44	Adamts5	1446.73	Cenpa	1149.19
C2cd3	3406.61	Asph	1981.44	N6amt1	1446.73	Mapre3	1149.19
Ucp2	3406.61	Ttll7	1979.29	Prkaa2	1444.58	Kcnj3	1149.19
Mir5127	3404.46	Lphn2	1979.29	Ppap2b	1444.58	Mir195b	1149.19
Galr1	3404.46	6330403K07 Rik	1977.13	Gtf2b	1444.58	Fut8	1149.19
4930518 P08Rik	3391.52	Nlrp1b	1977.13	A830019L 24Rik	1444.58	Gphn	1149.19
9430083 A17Rik	3391.52	Chd7	1974.97	Proc	1444.58	Gpr126	1149.19
Mir669m-1	3382.9	Clvs1	1974.97	Ercc3	1444.58	Vta1	1149.19
Lphn3	3382.9	Kcnh8	1974.97	Wdfy3	1442.42	Mgst2	1147.04
Fbxo15	3382.9	Efhb	1974.97	Arhgap24	1442.42	**Foxo1**	**1147.04**
Neto1	3382.9	Slc6a14	1970.66	Celrr	1442.42	1700019 E08Rik	1147.04
Olfr1271	3378.59	Ppp1r2-ps7	1970.66	Insig2	1442.42	Acvr2a	1147.04
Olfr1272	3378.59	4930431F12 Rik	1970.66	Acot11	1440.26	Adamts5	1147.04
Esp15	3352.71	Qdpr	1970.66	Mrpl37	1440.26	N6amt1	1147.04
Esp38	3352.71	Sall3	1970.66	4930547E 14Rik	1438.11	Deptor	1147.04
Plekhg1	3348.4	Mir5127	1970.66	Nsun3	1438.11	Mrpl13	1147.04
Akap12	3348.4	Mir7652	1970.66	Lrtm1	1438.11	Xiap	1144.88
Prkacb	3339.78	Ptgs2os	1970.66	Selk	1438.11	Sh2d1a	1144.88
Lphn2	3339.78	Slc25a39	1970.66	Tssc1	1438.11	Ces5a	1144.88
A2m	3326.84	Fam171a2	1970.66	Myt1l	1438.11	Gnao1	1144.88
Mug2	3326.84	Dis3l	1959.88	Smim23	1438.11	Stim2	1144.88
Apip	3326.84	Rab11a	1959.88	Npm1	1438.11	Gm10440	1144.88
Ehf	3326.84	Cmah	1959.88	9430014N 10Rik	1433.8	2410141 K09Rik	1144.88
Rasgrp1	3322.53	Gm11346	1959.88	D630010B 17Rik	1433.8	Uqcrb	1144.88

4930412 B13Rik	3322.53	4930405D11 Rik	1959.88	Zdhhc22	1433.8	Slc35d2	1142.73
Gm10516	3316.06	Kif2b	1959.88	Ngb	1433.8	Habp4	1142.73
Hhat	3316.06	Rprl2	1957.73	Zfp442	1431.64	Zfp42	1140.57
Rasd2	3311.75	Spata16	1957.73	Cst7	1431.64	Adam26b	1140.57

Appendix IVb

Top 32% of MEF2C Binding Peaks Overlapped in Pre-B cells and HPCs

Bold: B cell genes

Red: myeloid

Gene Name	Peak Score	Gene Name	Peak Score	Gene Name	Peak Score	Gene Name	Peak Score
Kctd16	703317	Galr1	2617.89	Six3os1	1906.44	Ednrb	1539.61
Prelid2	703317	Fbxo15	2612.33	Fam71a	1906.44	2210408I 21Rik	1539.61
Fbxo33	566886	Neto1	2612.33	Atf3	1906.44	Fam172a	1539.61
Gm20063	566886	Syn2	2606.77	Srrm4	1900.89	Stard3nl	1539.61
Prl5a1	338113	Pparg	2606.77	Suds3	1900.89	Epdr1	1539.61
2610307P1 6Rik	338113	Gm5084	2606.77	Gm5095	1900.89	Emb	1539.61
Eva1a	331744	BC05166 5	2606.77	Eno1b	1900.89	Hcn1	1539.61
Tacr1	331744	Trib2	2606.77	**Irf4**	**1900.89**	Prg4	1539.61
Olfr746	239184	Lpin1	2606.77	Hus1b	1900.89	C730036 E19Rik	1539.61
Olfr747	239184	Ppp1r2-ps7	2601.21	Slc6a14	1895.33	Atxn7l3b	1539.61
1700125H0 3Rik	188177	Wdr44	2601.21	Ppp1r2-ps7	1895.33	Mir669h	1539.61
Ints10	188177	Gm12887	2595.65	Il15	1895.33	Pax8	1534.05
Mrgpra1	130811	9530002 B09Rik	2595.65	Zfp330	1895.33	Cacna1b	1534.05
Mrgpra2b	130811	Tspan18	2590.1	Ufm1	1895.33	Gnas	1534.05
Zscan4f	123435	Gm13807	2590.1	Trpc4	1895.33	Nelfcd	1534.05
Vmn1r72	123435	Zpld1	2590.1	Rnf44	1895.33	A930018 P22Rik	1534.05
Fam216b	114231	Nfkbiz	2590.1	Cdhr2	1895.33	Hipk3	1534.05
Mir1971	114231	Pam16	2590.1	Lyve1	1889.77	4930474	1534.05

						H20Rik	
Adam3	85906.7	Vasn	2590.1	Gm16336	1889.77	4921530 L21Rik	1534.05
Adam32	85906.7	4933427 E13Rik	2584.54	Itgb3bp	1889.77	2810032 G03Rik	1534.05
Olfr1349	75829.8	Mir6372	2584.54	Pgm2	1889.77	1700101 O22Rik	1534.05
Olfr1350	75829.8	Eltd1	2578.98	Lrriq3	1889.77	Gm11762	1534.05
Ctnna3	73367.5	Ifi44	2578.98	9330178 D15Rik	1889.77	Chmp6	1534.05
1700023F0 2Rik	73367.5	Ogdhl	2578.98	4930405 L22Rik	1884.21	Mir1969	1528.49
Neurog2	70193.8	Chat	2578.98	Slit2	1884.21	1700026 F02Rik	1528.49
Tifa	70193.8	1700023 F02Rik	2578.98	Arsb	1884.21	Pea15b	1528.49
Klhl25	70138.2	LOC1026 34101	2578.98	Scamp1	1884.21	Lphn3	1528.49
Ntrk3	70138.2	Ttll7	2573.42	Rp1	1884.21	4930431 F12Rik	1528.49
Mir6414	67592.6	Lphn2	2573.42	Llgl2	1884.21	Qdpr	1528.49
Gm7854	67592.6	3930402 G23Rik	2567.86	Recql5	1884.21	Oscp1	1528.49
Reg3g	65625	Irs2	2567.86	Crbn	1878.65	Lsm10	1528.49
Gm20362	65625	Cyp4f37	2562.31	Lrrn1	1878.65	Nbea	1528.49
A830018L1 6Rik	56481.9	Cyp4f40	2562.31	Gm6634	1878.65	Tm4sf1	1528.49
Mir6341	56481.9	Scaf8	2562.31	Sis	1878.65	Pvt1	1528.49
Nkain3	54953.4	Tiam2	2562.31	Ncs1	1878.65	Gm20740	1528.49
Prdm13	54953.4	Epha6	2562.31	Fubp3	1878.65	Spz1	1528.49
Zfp946	53975.2	Nsun3	2562.31	Poteg	1873.1	Thbs4	1528.49
Vmn2r112	53975.2	Sema3d	2551.19	Gm8096	1873.1	Gm4850	1528.49
Ccdc71l	53408.2	Sema3a	2551.19	2310069 B03Rik	1873.1	Gm9839	1528.49
Nampt	53408.2	Gm16833	2545.63	Sema4f	1873.1	Gm4850	1528.49

Tmem177	49689.8	Mir6237	2545.63	2700089I 24Rik	1873.1	Khdrbs2	1528.49
Sctr	49689.8	Cox7c	2545.63	E330013 P04Rik	1873.1	Gm10230	1522.93
Mthfs	45393.4	Edil3	2545.63	Gm10549	1873.1	Il13ra1	1522.93
AF529169	45393.4	Prss23	2540.07	2410004 N09Rik	1873.1	Zfp28	1522.93
Cntnap5c	42725.5	Me3	2540.07	Xrcc4	1873.1	Olfr1344	1522.93
2610034M1 6Rik	42725.5	Klf4	2540.07	Atp6ap1l	1873.1	Tmem13 2b	1522.93
Gm20854	42342	Actl7b	2540.07	Gm1943	1867.54	4933438 B17Rik	1522.93
Gm20854	42342	Sec16b	2540.07	Dhx38	1867.54	3110043 O21Rik	1522.93
Sh3bp4	41335.9	Brinp2	2540.07	Dtwd1	1867.54	Mir876	1522.93
C030007H2 2Rik	41335.9	4930448I 06Rik	2534.51	Slc27a2	1867.54	4933438 K21Rik	1522.93
Olfm4	34766.2	Pou3f3os	2534.51	Gm10375	1867.54	Gm13152	1522.93
Pcdh17	34766.2	Gm10440	2528.96	Ear1	1867.54	Gm20755	1522.93
Ptchd1	32909.8	4932441J 04Rik	2528.96	1700101 O22Rik	1867.54	5430434I 15Rik	1522.93
4930503H1 3Rik	32909.8	Trat1	2528.96	Apob	1867.54	4921504 E06Rik	1522.93
Tbc1d2b	32515.2	Retnlb	2528.96	Cbll1	1867.54	Gm3230	1522.93
Zic1	32515.2	Mir7652	2528.96	Slc26a4	1867.54	Tfap2a	1522.93
493040101 2Rik	31903.8	Ptgs2os	2528.96	Slc5a8	1867.54	Gcnt2	1522.93
Foxq1	31903.8	Ythdf3	2523.4	Gas2l3	1867.54	**Ly86**	**1522.93**
Zscan4f	27568.4	2610100 L16Rik	2523.4	Pan2	1867.54	**Rreb1**	**1522.93**
Vmn1r72	27568.4	Hnf4g	2517.84	Cs	1867.54	Maml3	1517.37
Vmn2r121	26062.1	1110015 O18Rik	2517.84	Nkain3	1861.98	Gm2447	1517.37
4932411N2 3Rik	26062.1	Adck1	2517.84	Prdm13	1861.98	4933409 G03Rik	1517.37

1700003H04Rik	25917.6	Mir466b-3	2517.84	Pinx1	1861.98	4932414N04Rik	1517.37
Ndst4	25917.6	Mei4	2512.28	Sox7	1861.98	Vcan	1517.37
H2-M9	25734.2	Irak1bp1	2512.28	**Mast4**	**1861.98**	Tmem167	1517.37
H2-M1	25734.2	Wdr11	2512.28	Srek1	1861.98	2810032G03Rik	1517.37
Nbas	25406.3	Gm4265	2512.28	Tshz3	1856.42	1700101O22Rik	1517.37
Fam84a	25406.3	Sucla2	2512.28	Uri1	1856.42	Snord71	1511.82
Tssc1	24561.4	Htr2a	2512.28	Prl2c5	1856.42	Phlpp2	1511.82
Myt1l	24561.4	Tfcp2l1	2512.28	Gpr137b	1856.42	Tnc	1511.82
Slc7a14	22905.1	Inhbb	2512.28	1700064J06Rik	1856.42	Astn2	1511.82
Kcnmb2	22905.1	Gm8179	2506.72	1700025F24Rik	1856.42	Pdha2	1511.82
4930548K13Rik	21954.7	Gm3985	2506.72	Psg29	1850.86	Unc5c	1511.82
Epha7	21954.7	Rprl1	2506.72	Psg-ps1	1850.86	Kcnh7	1511.82
Leprel1	21660.1	Rpia	2506.72	Ccdc132	1850.86	Grb14	1511.82
Cldn1	21660.1	Plrg1	2506.72	Calcr	1850.86	2010106C02Rik	1511.82
Slc25a40	20492.9	1700028M03Rik	2506.72	Oit1	1850.86	Epas1	1511.82
Abcb1a	20492.9	D3Ertd751e	2506.72	4930455B14Rik	1850.86	Fbxl7	1511.82
Usp9y	20470.7	2610316D01Rik	2506.72	Mctp1	1850.86	Ank	1511.82
Gm6026	20470.7	Amot	2501.17	Ankrd32	1850.86	4930474H20Rik	1511.82
Irx3	20454	Htr2c	2501.17	1700092K14Rik	1850.86	Pcdh9	1511.82
Crnde	20454	Rbfox2	2501.17	Mir466n	1850.86	4930486F22Rik	1511.82
1700063A18Rik	20220.5	Apol7a	2501.17	4933411K20Rik	1845.3	1810014B01Rik	1511.82

4930533P14Rik	20220.5	Kbtbd12	2495.61	Helt	1845.3	Slc20a2	1506.26
Ccdc37	19798.1	Mgll	2495.61	Tnc	1845.3	Dkk4	1506.26
Klf15	19798.1	Ptpn12	2495.61	Pappa	1845.3	Arhgap29	1506.26
Ptbp2	19642.5	Gsap	2495.61	Rps3a1	1845.3	Gclm	1506.26
Rwdd3	19642.5	Lace1	2495.61	Lrba	1845.3	Opalin	1506.26
Usp9y	19581.3	Snx3	2495.61	Lrig2	1845.3	Tm9sf3	1506.26
Zfy2	19581.3	Dtna	2490.05	Fam19a3	1845.3	Proc	1506.26
Snord14d	19131.1	Mapre2	2490.05	Ap3s1	1845.3	Ercc3	1506.26
C130030K03Rik	19131.1	Mir6414	2484.49	Arl14epl	1845.3	Mir466g	1506.26
Zscan4f	18997.7	Gm7854	2484.49	Gm5766	1845.3	Fbxl17	1506.26
Vmn1r72	18997.7	Gm41	2478.93	Srl	1845.3	Gm20098	1506.26
1110059M19Rik	18981.1	Mir1906-1	2478.93	Tbx18	1839.75	Kcnh8	1506.26
Actrt1	18981.1	Speer4f	2478.93	Nt5e	1839.75	Agpat4	1506.26
A530072M11Rik	18947.7	Cd36	2478.93	Gm10220	1839.75	Map3k4	1506.26
Mmp16	18947.7	Htr4	2478.93	Gm7361	1839.75	Synj1	1506.26
Gm4710	18241.8	Spink10	2478.93	Lemd2	1839.75	Paxbp1	1506.26
Crim1	18241.8	Gm4850	2478.93	Mir7214	1839.75	4931429P17Rik	1506.26
Atp10a	18219.6	Khdrbs2	2478.93	Moxd1	1839.75	Id4	1506.26
Ube3a	18219.6	Siah1b	2473.38	Ctgf	1839.75	Lrfn5	1506.26
Rbmy	17963.9	Mir467a-10	2473.38	Mir6370	1834.19	Fscb	1506.26
Gm20826	17963.9	Prkaa2	2473.38	Kcnd2	1834.19	Gm12250	1506.26
1700008P02Rik	17836.1	Ppap2b	2473.38	Gm815	1834.19	Igtp	1506.26
Pkia	17836.1	Tyro3	2473.38	Vldlr	1834.19	Marcks	1506.26
Depdc1a	17708.3	Mapkbp1	2473.38	Cbln2	1834.19	Rfpl4b	1506.26
Rpe65	17708.3	Adcyap1	2473.38	Socs6	1834.19	Grip1os2	1506.26
Tmsb10	17524.8	Mettl4	2473.38	Cpne8	1834.19	Grip1	1506.26

Suclg1	17524.8	Mir5127	2467.82	Spn-ps	1834.19	Mid1ip1	1500.7
Fbxo15	17063.5	Galr1	2467.82	Ppp2r1b	1828.63	Gm14483	1500.7
Neto1	17063.5	Mir466g	2462.26	Layn	1828.63	Lipc	1500.7
Gm14851	16685.6	Efna5	2462.26	Large	1828.63	LOC102635087	1500.7
Gm15284	16685.6	Plxna4os1	2456.7	Isx	1828.63	2310008N11Rik	1500.7
Rprl1	16429.9	Chchd3	2456.7	1700045H11Rik	1828.63	Zfp703	1500.7
Rpia	16429.9	Xpa	2456.7	Park7	1828.63	Trim32	1500.7
Map3k13	16335.4	Foxe1	2456.7	Lmx1a	1828.63	Tlr4	1500.7
Liph	16335.4	Cetn3	2456.7	Pbx1	1828.63	Dcp2	1500.7
Dok6	15968.6	**Mef2c**	**2456.7**	Blzf1	1828.63	A930012L18Rik	1500.7
Tmx3	15968.6	Nrbf2	2456.7	Atp1b1	1828.63	Gm8883	1500.7
Olfr1271	15751.8	Egr2	2456.7	Xcr1	1823.07	4933417E11Rik	1500.7
Olfr1272	15751.8	Slc25a18	2451.14	Ccr1	1823.07	Rgs4	1500.7
Ptchd1	14451.2	Bcl2l13	2451.14	Sh3gl2	1823.07	1700084C01Rik	1500.7
4930503H13Rik	14451.2	Myo10	2451.14	Adamtsl1	1823.07	Limk2	1500.7
Sorcs3	14045.4	Fam134b	2451.14	4921507L20Rik	1823.07	8430429K09Rik	1500.7
Ins1	14045.4	Atp1b1	2451.14	Hsd17b12	1823.07	Dpf1	1495.14
Ythdf3	13367.3	Dpt	2451.14	4930474N09Rik	1823.07	Catsperg2	1495.14
2610100L16Rik	13367.3	Ube2u	2445.58	1700064M15Rik	1823.07	G6pd2	1495.14
Fbxo15	13295.1	Raver2	2445.58	Stxbp6	1823.07	Arap2	1495.14
Neto1	13295.1	A930019D19Rik	2445.58	Nova1	1823.07	Osbpl6	1495.14
Astn2	13284	4933406D12Rik	2445.58	Tmem199	1823.07	Prkra	1495.14

Tlr4	13284	Il22	2445.58	Tnfaip1	1823.07	Rxra	1495.14
4930486L24Rik	12933.8	Iltifb	2445.58	Cobl	1823.07	Fcnb	1495.14
Ctla2b	12933.8	Tsc22d3	2440.03	1700046C09Rik	1823.07	Speer2	1495.14
Med10	12350.2	Tex13	2440.03	Zfp873	1823.07	Gbe1	1495.14
1700084F23Rik	12350.2	Hmgcll1	2440.03	AU041133	1823.07	Dock9	1495.14
Gm8653	12161.2	Gfral	2440.03	Tbx22	1817.51	Gpr18	1495.14
Gm4498	12161.2	Tmem126b	2440.03	2610002M06Rik	1817.51	9230009I02Rik	1495.14
Tmem177	11788.8	Dlg2	2440.03	4930405L22Rik	1817.51	BC049762	1495.14
Sctr	11788.8	Gm5084	2440.03	Slit2	1817.51	Gm19757	1489.58
Slc4a4	11655.4	Dapk1	2440.03	Auts2	1817.51	**Il5ra**	**1489.58**
Gc	11655.4	Appl2	2440.03	Gatsl2	1817.51	Mir6414	1489.58
4930474H20Rik	11655.4	Nuak1	2440.03	Mir455	1817.51	Gm7854	1489.58
Pcdh9	11655.4	Sall3	2434.47	Orm1	1817.51	Apip	1489.58
Nlrp1b	11121.9	Mir5127	2434.47	D3Ertd751e	1817.51	Ehf	1489.58
Wscd1	11121.9	Depdc1a	2428.91	2610316D01Rik	1817.51	Tex30	1489.58
Vwc2	10454.9	Rpe65	2428.91	Gtsf1l	1817.51	Bivm	1489.58
4930415F15Rik	10454.9	2700049A03Rik	2428.91	Jph2	1817.51	Cybb	1484.03
Gm12887	10199.2	4930404H11Rik	2428.91	Gm16863	1817.51	Gm5132	1484.03
9530002B09Rik	10199.2	Lhfp	2423.35	Vps8	1817.51	Col1a2	1484.03
Eva1a	10154.7	Proser1	2423.35	Has2	1817.51	Casd1	1484.03
Tacr1	10154.7	Adcyap1	2423.35	Slc22a22	1817.51	Penk	1484.03
Fat3	10138.1	Mettl4	2423.35	St6galnac5	1811.96	Gm11780	1484.03
Chordc1	10138.1	Mir466g	2423.35	4930482	1811.96	Fstl5	1484.03

				G09Rik			
Rgs18	10049.1	Efna5	2423.35	BC048502	1811.96	Rapgef2	1484.03
Brinp3	10049.1	Rps12	2423.35	Pde1b	1811.96	Ttc30a1	1484.03
Slc7a14	9804.57	Vnn3	2423.35	Fhl2	1811.96	Cyct	1484.03
Kcnmb2	9804.57	Gm20752	2417.79	Nck2	1811.96	Csrp2bp	1484.03
Cdh8	9748.99	Depdc1a	2417.79	1700015G11Rik	1806.4	Zfp133-ps	1484.03
Cdh11	9748.99	Dusp6	2417.79	Mir6238	1806.4	1600019K03Rik	1484.03
Vwc2	9560.01	Gm20110	2417.79	Runx1t1	1806.4	Dirc2	1484.03
4930415F15Rik	9560.01	Tpk1	2412.24	Slc26a7	1806.4	Fezf2	1484.03
Serpinb6e	9548.9	Cntnap2	2412.24	D730050B12Rik	1806.4	Gm5087	1484.03
Serpinb6a	9548.9	4921511I17Rik	2412.24	Irx4	1806.4	Uggt2	1484.03
Gm20871	9393.27	Mycn	2412.24	Agbl3	1800.84	Hs6st3	1484.03
Gm20823	9393.27	Rbmy	2406.68	Tmem140	1800.84	Kif26b	1484.03
F630028O10Rik	9009.75	Gm20826	2406.68	Cftr	1800.84	Tfb2m	1484.03
Hsf3	9009.75	Mir5127	2406.68	Cttnbp2	1800.84	Zfp428	1478.47
Tbc1d2b	8987.52	Galr1	2406.68	Mir137	1800.84	Irgq	1478.47
Zic1	8987.52	AW554918	2406.68	Ptbp2	1800.84	Atf7ip	1478.47
1700015G11Rik	8893.03	Celf4	2406.68	1700016G22Rik	1800.84	Gucy2c	1478.47
Mir6238	8893.03	Zmynd11	2406.68	Pitrm1	1800.84	Gng10	1478.47
D630013N20Rik	8798.55	Chrm3	2406.68	Vstm2b	1795.28	LOC101055769	1478.47
Bicc1	8798.55	Maob	2401.12	4930433I11Rik	1795.28	Mmp16	1478.47
1700015G11Rik	8709.62	Efhc2	2401.12	Tpk1	1795.28	Cngb3	1478.47

Mir6238	8709.62	Minpp1	2401.12	Cntnap2	1795.28	**Pten**	**1478.47**
Khdrbs2	8670.71	Papss2	2401.12	8430423 G03Rik	1795.28	Rnls	1478.47
Prim2	8670.71	Slc22a1	2401.12	5930430 L01Rik	1795.28	Gp5	1478.47
Olfr746	8576.22	Airn	2401.12	Fat4	1795.28	Tmem44	1478.47
Olfr747	8576.22	Large	2395.56	1700017 G19Rik	1795.28	Stk3	1478.47
Fat3	8303.87	Isx	2395.56	Papss1	1795.28	BC048602	1478.47
Chordc1	8303.87	Celf2	2395.56	Dkk2	1795.28	4930474 H20Rik	1478.47
Vmn2r72	8298.31	1700061 F12Rik	2395.56	Alkbh3	1795.28	4921530 L21Rik	1478.47
Vmn2r73	8298.31	Flrt3	2395.56	Mir129-2	1795.28	Blzf1	1478.47
Usp9y	8270.52	Kif16b	2395.56	Mtbp	1795.28	Atp1b1	1478.47
Zfy2	8270.52	5430427 M07Rik	2395.56	Has2	1795.28	4930590 L20Rik	1478.47
Nbas	8259.41	Mir669c	2395.56	Mir3106	1789.72	Cdc73	1478.47
Fam84a	8259.41	Npr1	2390	Mcph1	1789.72	Vps26a	1478.47
Edem1	8098.22	Snapin	2390	Card11	1789.72	Srgn	1478.47
Grm7	8098.22	Sel1l	2390	Foxk1	1789.72	Gm4981	1478.47
Gm20752	8087.1	Mir8099-2	2390	Gm13582	1789.72	Gcc2	1478.47
Depdc1a	8087.1	Rims1	2390	Tank	1789.72	Srpx	1472.91
H2-M9	7903.68	4933415 F23Rik	2390	Otud1	1789.72	Rpgr	1472.91
H2-M1	7903.68	Rgs18	2390	Etl4	1789.72	Gys2	1472.91
Klhl4	7731.38	Brinp3	2390	Cadm2	1789.72	Ldhb	1472.91
Ube2dnl1	7731.38	Gm5071	2384.44	Speer2	1789.72	Nars	1472.91
A830018L16Rik	7703.59	Mageb2	2384.44	I730030J21Rik	1789.72	Nedd4l	1472.91
Mir6341	7703.59	Mfap3l	2378.89	Slc4a8	1789.72	Amer2	1472.91
1700125H0	7620.22	2700029	2378.89	9230009I	1789.72	C1qtnf9	1472.91

3Rik		M09Rik		02Rik			
Ints10	7620.22	5830416I19Rik	2378.89	5133400J02Rik	1789.72	Epm2a	1472.91
Tmem177	7603.54	Pgm1	2378.89	Fam184a	1789.72	Utrn	1472.91
Sctr	7603.54	Dopey1	2373.33	Man1a	1789.72	Zfp804b	1467.35
Slc7a14	7486.82	Rwdd2a	2373.33	Emp1	1784.16	Steap4	1467.35
Kcnmb2	7486.82	7630403G23Rik	2373.33	Gm8994	1784.16	1700063A18Rik	1467.35
Gm20871	7475.71	St3gal4	2373.33	Tmem252	1784.16	4930533P14Rik	1467.35
Gm20823	7475.71	Mir5127	2367.77	Foxd4	1784.16	Rn45s	1467.35
Bai3	7431.24	Galr1	2367.77	4931412M21	1784.16	Esp38	1467.35
4931408C20Rik	7431.24	1110054M08Rik	2367.77	7420701I03Rik	1784.16	Arsb	1467.35
Edem1	7370.1	Lpp	2367.77	4933411E08Rik	1784.16	Lhfpl2	1467.35
Grm7	7370.1	4930529K09Rik	2367.77	Il22	1784.16	Steap3	1467.35
Fat3	7220.03	Tdrd3	2367.77	Impg1	1778.61	Marco	1467.35
Chordc1	7220.03	Prkacb	2362.21	Htr1b	1778.61	Gm5635	1461.79
Cntnap5a	7081.08	Lphn2	2362.21	Slc35g2	1778.61	4930402K13Rik	1461.79
Tsn	7081.08	Gm10745	2362.21	Pccb	1778.61	Olfr948	1461.79
Zscan4f	7069.96	4930539N22Rik	2362.21	Galnt18	1778.61	Olfr951	1461.79
Vmn1r72	7069.96	Pfkp	2362.21	Dkk3	1778.61	Syt13	1461.79
Cbln2	7031.06	Wdr37	2362.21	1700008P02Rik	1778.61	4631405J19Rik	1461.79
Socs6	7031.06	Ccnjl	2362.21	Pkia	1778.61	Mir7224	1461.79
6330415B21Rik	6947.68	Fabp6	2362.21	A330050F15Rik	1778.61	Mir6335	1461.79
Reg3b	6947.68	Pdha1	2356.65	Tgif1	1778.61	Pcgf5	1461.79
Mir5127	6864.31	Gpr64	2356.65	Ap5m1	1778.61	1500017E21Rik	1461.79

Galr1	6864.31	2900079 G21Rik	2356.65	Naa30	1778.61	Cbln2	1461.79
Vwc2	6864.31	AU02376 2	2356.65	Tgfb2	1778.61	Socs6	1461.79
4930415F1 5Rik	6864.31	Cntn1	2356.65	Rrp15	1778.61	Fbxo32	1461.79
1700063A1 8Rik	6814.29	Gxylt1	2356.65	1700015 E13Rik	1778.61	Anxa13	1461.79
4930533P1 4Rik	6814.29	Neurog2	2351.1	Olfml2b	1778.61	Spata31d 1d	1461.79
Dbt	6608.64	**Tifa**	**2351.1**	Gm19395	1778.61	Isca1	1461.79
Lrrc39	6608.64	1700100 L14Rik	2351.1	Pln	1778.61	Ube2cbp	1456.23
Fbxo33	6436.33	Adamts1 6	2351.1	Sesn1	1778.61	Pgm3	1456.23
Gm20063	6436.33	Slc10a2	2345.54	Foxo3	1778.61	Gpr56	1456.23
Cntnap5a	6391.87	Efnb2	2345.54	Gm1720	1773.05	Ccdc135	1456.23
Tsn	6391.87	Snrpg	2345.54	Gm8817	1773.05	Cpxm2	1456.23
Smpdl3a	6341.84	Pcyox1	2345.54	Gm5347	1773.05	Chst15	1456.23
Dux	6341.84	Pdk4	2345.54	Fat1	1773.05	Wars2	1456.23
Gm20172	6275.15	Dync1i1	2345.54	Chsy1	1773.05	Spag17	1456.23
4931408C2 0Rik	6275.15	Grxcr1	2345.54	Mir7057	1773.05	Esp15	1456.23
Fbxo15	6252.91	Yipf7	2345.54	Tmem52 b	1773.05	Esp38	1456.23
Neto1	6252.91	4930467 E23Rik	2334.42	1700101I 11Rik	1773.05	Gm4850	1456.23
Gm20172	6152.87	6820431 F20Rik	2334.42	Usp53	1773.05	Khdrbs2	1456.23
4931408C2 0Rik	6152.87	Sumf1	2334.42	Synpo2	1773.05	1700031 P21Rik	1456.23
Smpdl3a	6036.15	Mir7661	2334.42	Pcmtd1	1773.05	Akap6	1456.23
Dux	6036.15	Gpr155	2328.86	Rrs1	1773.05	Mir205	1456.23
Cxcr4	6019.47	Wipf1	2328.86	Cenpf	1773.05	4930503 O07Rik	1456.23

Daf2	6019.47	Tmem39	2328.86	Ptpn14	1773.05	Tab2	1456.23
4930548K13Rik	5997.24	B4galt4	2328.86	Bod1	1773.05	Ust	1456.23
Epha7	5997.24	Mir3063	2328.86	D630024D03Rik	1773.05	Cd207	1450.68
Rgs18	5997.24	Gip	2328.86	Usp9y	1767.49	Vax2	1450.68
Brinp3	5997.24	Ubl3	2323.31	Zfy2	1767.49	Bpgm	1450.68
6330415B21Rik	5991.68	2210417A02Rik	2323.31	4933402E13Rik	1767.49	Cald1	1450.68
Reg3b	5991.68	Otud1	2323.31	1700019B21Rik	1767.49	Lekr1	1450.68
Smpdl3a	5919.43	Arhgap21	2323.31	Vmn1r31	1767.49	Ccnl1	1450.68
Dux	5919.43	Pfkp	2323.31	Abcg2	1767.49	Cdc42ep2	1450.68
Grem1	5880.52	Adarb2	2323.31	Gm12718	1767.49	Slc22a20	1450.68
Arhgap11a	5880.52	Lamc1	2323.31	Dab1	1767.49	Slc14a2	1450.68
Gm20172	5869.4	E330020D12Rik	2323.31	AW209491	1767.49	Setbp1	1450.68
4931408C20Rik	5869.4	Dpp10	2323.31	Gli3	1767.49	Sox17	1450.68
Depdc1a	5791.59	Actr3	2323.31	Mrgpra6	1761.93	Mrpl15	1450.68
Rpe65	5791.59	Swap70	2317.75	Mrgpra9	1761.93	Mir8099-1	1450.68
Cyp4b1	5758.24	Adm	2317.75	Sipa1l3	1761.93	Flrt2	1450.68
Efcab14	5758.24	Pax4	2317.75	Catsperg2	1761.93	1700112H15Rik	1450.68
Kif20b	5741.56	Lrrc4	2317.75	Gak	1761.93	4930488B22Rik	1450.68
Htr7	5741.56	4930547E14Rik	2317.75	Idua	1761.93	Vmn2r72	1445.12
Irx3	5652.63	Nsun3	2317.75	1500017E21Rik	1761.93	Vmn2r73	1445.12
Crnde	5652.63	0610007P14Rik	2317.75	Ppp1r3c	1761.93	1700015G11Rik	1445.12
Fam47c	5574.82	Tgfb3	2317.75	Ptar1	1761.93	Mir6238	1445.12
Gm8787	5574.82	Six1	2317.75	Apba1	1761.93	Mapk1ip	1445.12

						1	
Pop1	5541.47	Mnat1	2317.75	Olfr878	1756.37	Bnip3	1445.12
Nipal2	5541.47	Olfr325	2317.75	Olfr881	1756.37	Zfp316	1445.12
Klhl25	5480.33	2210407 C18Rik	2317.75	Cdh8	1756.37	E130309 D02Rik	1445.12
Ntrk3	5480.33	Tmem26 1	2312.19	Cdh11	1756.37	Wwtr1	1445.12
Rap2b	5413.63	Tyrp1	2312.19	C2cd3	1756.37	Commd2	1445.12
Arhgef26	5413.63	Slc25a24	2312.19	Ucp2	1756.37	Bmpr1b	1445.12
Kif20b	5385.84	Vav3	2312.19	Btg3	1756.37	Pdlim5	1445.12
Htr7	5385.84	Slc8a1	2312.19	D16Ertd4 72e	1756.37	Otor	1445.12
Nkain3	5258.01	Gm19689	2312.19	Hist1h2a a	1756.37	Pcsk2os1	1445.12
Prdm13	5258.01	6820431 F20Rik	2306.63	Lrrc16a	1756.37	Bmp2	1445.12
Gm14461	5252.45	Gm15319	2306.63	Gm4850	1756.37	Hao1	1445.12
Ube2e3	5252.45	D3Ertd75 1e	2306.63	Khdrbs2	1756.37	4930448I 06Rik	1445.12
Astn2	5202.42	2610316 D01Rik	2306.63	Gm5434	1756.37	Pou3f3os	1445.12
Tlr4	5202.42	Gabre	2301.07	Ankmy2	1756.37	Glipr1	1445.12
Gm20823	5163.52	Magea10	2301.07	Tmevpg1	1756.37	Glipr1l1	1445.12
Gm20823	5163.52	Gm5347	2301.07	Dyrk2	1756.37	4930558 G05Rik	1439.56
Atp10a	5124.61	AY51293 1	2301.07	1700125 H03Rik	1750.82	Pcdh19	1439.56
Ube3a	5124.61	Megf9	2301.07	Ints10	1750.82	Gtf2i	1439.56
Dbt	5035.68	Tle1	2301.07	Gm572	1750.82	Clip2	1439.56
Lrrc39	5035.68	Fbxo15	2301.07	Pex14	1750.82	Cldn14	1439.56
C030023E2 4Rik	5007.89	Neto1	2301.07	D830031 N03Rik	1750.82	Sim2	1439.56
Ldoc1	5007.89	D7Ertd44 3e	2295.51	Mir6398	1750.82	Rtp4	1439.56

Klhl25	5007.89	Dock1	2295.51	Lrba	1750.82	Sst	1439.56
Ntrk3	5007.89	Spry1	2295.51	Dclk2	1750.82	Fam49b	1439.56
Slc4a4	4996.77	Gm5148	2295.51	Fstl5	1750.82	Adcy8	1439.56
Gc	4996.77	Efna5	2295.51	Rapgef2	1750.82	Tnfrsf11b	1439.56
Gm10440	4996.77	Fert2	2295.51	Dtwd1	1750.82	Mal2	1439.56
4932441J04 Rik	4996.77	Syt2	2295.51	Atp8b4	1750.82	Dgkh	1439.56
Neurog2	4974.54	Ppp1r12b	2295.51	Lipo1	1750.82	Vwa8	1439.56
Tifa	4974.54	C1galt1c1	2289.96	Lipf	1750.82	Dhrs2	1439.56
Gm14851	4963.42	Cypt15	2289.96	Nppc	1750.82	Dhrs4	1439.56
Gm15284	4963.42	Glt28d2	2289.96	Alppl2	1750.82	Mir6390	1439.56
D630013N2 0Rik	4946.75	Prss48	2289.96	Ppap2b	1745.26	Trim52	1439.56
Bicc1	4946.75	D3Ertd75 1e	2289.96	Usp24	1745.26	Nova1	1439.56
Fat3	4935.63	2610316 D01Rik	2289.96	1700036 G14Rik	1745.26	Mir5125	1439.56
Chordc1	4935.63	Wdr20rt	2289.96	Fam160a 1	1745.26	Arpc5	1439.56
Rap2b	4913.4	Rpl10l	2289.96	Mir1945	1745.26	Smg7	1439.56
Arhgef26	4913.4	Spdl1	2289.96	Tnfrsf17	1745.26	Dsel	1439.56
Nkain3	4902.29	Slit3	2289.96	Rps24	1745.26	Tsn	1439.56
Prdm13	4902.29	Cypt12	2284.4	4930572 O13Rik	1745.26	Tex13a	1434
Mir6414	4896.73	Bhlhe22	2284.4	4930448I 06Rik	1745.26	Nrk	1434
Gm7854	4896.73	Nup35	2284.4	Pou3f3os	1745.26	Tcerg1l	1434
Cntnap5c	4874.49	Zfp804a	2284.4	Tmem16 7	1745.26	Mapk1ip 1	1434
2610034M1 6Rik	4874.49	Klf12	2284.4	Atp6ap1l	1745.26	Rxfp2	1434
Grin3a	4868.94	Prr30	2284.4	Insig2	1745.26	Fry	1434
Cylc2	4868.94	Cobl	2284.4	Ccdc93	1745.26	Gm6289	1434

Gm7361	4852.26	1700046C09Rik	2284.4	Palm2	1739.7	Clca6	1434
4930584F24Rik	4852.26	Gm20871	2278.84	Akap2	1739.7	Zfp937	1434
Peg12	4774.45	Gm20823	2278.84	Cd1d1	1739.7	3300002I08Rik	1434
Chrna7	4774.45	Ptchd1	2278.84	Kirrel	1739.7	Gm19784	1434
Sh3bp4	4774.45	4930503H13Rik	2278.84	Fbxo15	1739.7	Chmp1b	1434
C030007H22Rik	4774.45	Grsf1	2278.84	Neto1	1739.7	4930404A05Rik	1434
Lincrna-cox2	4713.31	Mob1b	2278.84	Sept9	1739.7	Zpld1	1434
Pdc	4713.31	E130008D07Rik	2278.84	2900041M22Rik	1739.7	4933402D24Rik	1434
Large	4691.08	Gpr116	2278.84	Zfp74	1734.14	Gm13749	1434
Isx	4691.08	Otud1	2273.28	Zfp568	1734.14	Homer1	1434
Gm12887	4663.28	Arhgap21	2273.28	Ociad2	1734.14	Bhmt	1434
9530002B09Rik	4663.28	Slc39a12	2273.28	Cwh43	1734.14	Srek1ip1	1434
Gm20865	4657.73	Gm13315	2273.28	Drc1	1734.14	Rgs7bp	1434
LOC100040786	4657.73	Mir5127	2273.28	1700001C02Rik	1734.14	4930503O07Rik	1434
Htr2c	4652.17	Galr1	2273.28	Gca	1734.14	Plxna2	1434
Il13ra2	4652.17	Sipa1l1	2273.28	Fign	1734.14	Gm14725	1428.44
Ctnna3	4652.17	1700085C21Rik	2273.28	Ldlrad3	1734.14	Mtm1	1428.44
1700023F02Rik	4652.17	Gm17821	2273.28	Fjx1	1734.14	Foxr1	1428.44
Esp15	4646.61	Rps29	2273.28	AA536875	1734.14	Upk2	1428.44
Esp38	4646.61	4930405D11Rik	2273.28	Itgbl1	1734.14	Slc44a1	1428.44
4930474H20Rik	4641.05	Kif2b	2273.28	Mis18bp1	1734.14	Fsd1l	1428.44
Pcdh9	4641.05	C030023	2267.72	Wdr20rt	1734.14	9430020	1428.44

		E24Rik				K01Rik	
Slc25a40	4635.49	Ldoc1	2267.72	Ddo	1734.14	Gm10556	1428.44
Abcb1a	4635.49	4933421 O10Rik	2267.72	Cdc40	1734.14	4930545 E07Rik	1428.44
493040101 2Rik	4635.49	Gabrr2	2267.72	Cbx3	1728.58	Dsc3	1428.44
Foxq1	4635.49	Chd6	2267.72	Skap2	1728.58	Defb41	1428.44
Sorcs3	4607.7	Ptprtos	2267.72	Nkain1	1728.58	Tfap2d	1428.44
Ins1	4607.7	Reep5	2267.72	Snord85	1728.58	Mpzl1	1428.44
Nkain3	4568.8	Fam13b	2267.72	Rif1	1728.58	Rcsd1	1428.44
Prdm13	4568.8	Epha6	2267.72	4930573 O16Rik	1728.58	Moxd1	1428.44
Tmsb10	4563.24	Nsun3	2267.72	Pitx3	1728.58	Ctgf	1428.44
Suclg1	4563.24	Mir3106	2262.17	Nfkb2	1728.58	Dhrs3	1422.89
1110059M1 9Rik	4557.68	Mcph1	2262.17	Diap2	1723.03	Tnfrsf1b	1422.89
Actrt1	4557.68	Shisa6	2262.17	Pcdh19	1723.03	Pvrl3	1422.89
Gm17019	4557.68	Gm12298	2262.17	Arglu1	1723.03	Dppa4	1422.89
Speer4d	4557.68	Mphosph 9	2256.61	4933430 N04Rik	1723.03	Hhip	1417.33
Med10	4552.12	Cdk2ap1	2256.61	Pds5b	1723.03	Gypa	1417.33
1700084F2 3Rik	4552.12	Gpx7	2256.61	Kl	1723.03	Cnot4	1417.33
Ccl1	4518.77	Prpf38a	2256.61	Msantd3	1723.03	Nup205	1417.33
Tmem132e	4518.77	Gm833	2251.05	Murc	1723.03	Arl5b	1417.33
Ugt2a3	4513.21	Ajap1	2251.05	Nbea	1723.03	4930515 L03Rik	1417.33
Ugt2b38	4513.21	Prkd1	2251.05	Tm4sf1	1723.03	Hspa9	1417.33
Serpinb6e	4485.42	G2e3	2251.05	Pabpc4l	1723.03	Lrrtm2	1417.33
Serpinb6a	4485.42	Adamtsl1	2245.49	Gm7977	1723.03	Dtnbp1	1417.33
Depdc1a	4468.75	Rraga	2245.49	Thumpd2	1723.03	Mylip	1417.33
Rpe65	4468.75	Tll1	2239.93	Gm19689	1723.03	Tle3	1411.77
Vwc2	4457.63	Mir710	2239.93	Ctsq	1723.03	Rplp1	1411.77

4930415F15Rik	4457.63	Tal2	2239.93	Ctsr	1723.03	Fam32a	1411.77
4930404A05Rik	4407.61	Tmem38b	2239.93	1700019M22Rik	1723.03	Klf2	1411.77
Zpld1	4407.61	Nphp4	2239.93	Galc	1723.03	1700125H03Rik	1411.77
Plxnc1	4407.61	Gm833	2239.93	Vstm2a	1723.03	Ints10	1411.77
2310039L15Rik	4407.61	Ints12	2239.93	Sec61g	1723.03	Mir466h	1411.77
Rbbp7	4402.05	Ppa2	2239.93	Hdx	1717.47	Gm5860	1411.77
Txlng	4402.05	Cnga3	2239.93	Tex16	1717.47	Elavl4	1411.77
Peg12	4368.7	Inpp4a	2239.93	Zic4	1717.47	Spata6	1411.77
Chrna7	4368.7	D430036J16Rik	2234.37	Plscr5	1717.47	Msln	1411.77
Epha6	4318.68	Mei4	2234.37	Esp34	1717.47	Haghl	1411.77
Nsun3	4318.68	Gm5086	2234.37	Esp31	1717.47	Abca12	1411.77
Gm12887	4285.33	Utp15	2234.37	Plekhg1	1717.47	Atic	1411.77
9530002B09Rik	4285.33	AW046200	2223.26	Akap12	1717.47	Sim2	1411.77
D3Ertd751e	4285.33	Gm15881	2223.26	Crlf2	1711.91	Ripply3	1411.77
2610316D01Rik	4285.33	Opalin	2223.26	Gm10416	1711.91	Gm5086	1411.77
Toporsl	4274.21	Tm9sf3	2223.26	Cdh17	1711.91	Utp15	1411.77
4930552N02Rik	4274.21	1700001C19Rik	2223.26	1700123M08Rik	1711.91	Lrrc16a	1411.77
Fat3	4235.31	Taf8	2223.26	Sncaip	1711.91	Cmah	1411.77
Chordc1	4235.31	Mb21d2	2223.26	Snx2	1711.91	Gpr22	1411.77
Esp15	4235.31	Atp13a5	2223.26	Esx1	1706.35	Prkar2b	1411.77
Esp38	4235.31	BC048602	2223.26	Tex13a	1706.35	Lyplal1	1411.77
Ppp3r2	4224.19	Mir599	2223.26	Ube2dnl2	1706.35	Tgfb2	1411.77
Cylc2	4224.19	Actbl2	2223.26	Cpxcr1	1706.35	1700034K08Rik	1406.21
6030469F0	4218.63	Gpbp1	2223.26	Gfral	1706.35	1190002	1406.21

6Rik						N15Rik	
Lamb1	4218.63	Tmem132b	2217.7	Fam83b	1706.35	4933405O20Rik	1406.21
Setd6	4207.52	4933438B17Rik	2217.7	1700042G15Rik	1706.35	Ano5	1406.21
Mir7073	4207.52	Zfp770	2217.7	Palm2	1706.35	Zfand4	1406.21
Adcyap1	4207.52	Dph6	2217.7	Pde4b	1706.35	Alox5	1406.21
Mettl4	4207.52	Gpr101	2206.58	Sgip1	1706.35	A430033K04Rik	1406.21
Prss38	4201.96	Zic3	2206.58	Elf5	1706.35	Fam20c	1406.21
Jmjd4	4201.96	Gm765	2206.58	Abtb2	1706.35	Gm12633	1406.21
Gm4850	4190.84	Foxp1	2206.58	Rcan1	1706.35	Elavl2	1406.21
Khdrbs2	4190.84	Epha6	2206.58	2410124H12Rik	1706.35	Smarca5-ps	1406.21
Cyth1	4185.28	Nsun3	2206.58	Rgs7	1706.35	Gm13212	1406.21
Usp36	4185.28	Clec14a	2206.58	Fh1	1706.35	Pgrmc2	1406.21
Ddhd1	4129.7	Sec23a	2206.58	Trove2	1706.35	C430002E04Rik	1406.21
Gm1821	4129.7	Dgkk	2201.03	Rgs2	1706.35	G630055G22Rik	1406.21
Fat3	4068.56	Akap4	2201.03	Kcnj2	1706.35	1700044K03Rik	1406.21
Chordc1	4068.56	Fip1l1	2201.03	BC006965	1706.35	D16Ertd472e	1406.21
Lincrna-cox2	4057.45	Gm6116	2201.03	B130024G19Rik	1700.79	Chodl	1406.21
Pdc	4057.45	Rragc	2201.03	Mctp2	1700.79	Prodh	1406.21
Olfr1349	4046.33	1700057H15Rik	2201.03	Kcnd2	1700.79	Rtn4r	1406.21
Olfr1350	4046.33	Mbd2	2201.03	Ing3	1700.79	Dnah5	1406.21
Gm20865	4029.66	Dcc	2201.03	Anxa3	1700.79	Ctnnd2	1406.21
LOC100040786	4029.66	Cyp2b10	2195.47	Bmp2k	1700.79	Cdh6	1406.21
Rbmy	4012.98	Cyp2b9	2195.47	Fshb	1700.79	Cdh9	1406.21

Gm20826	4012.98	Sncaip	2195.47	Kcna4	1700.79	4930448 F12Rik	1406.21
Edem1	4012.98	Snx2	2195.47	Ccdc112	1700.79	Vps41	1406.21
Grm7	4012.98	5033404 E19Rik	2195.47	Mospd4	1700.79	Colgalt2	1406.21
Zfp946	4012.98	Mir297c	2195.47	Tmem16 7	1700.79	Apobec4	1406.21
Vmn2r112	4012.98	Plcd3	2195.47	Atp6ap1l	1700.79	**Myb**	**1406.21**
Fat3	3985.19	Hexim1	2195.47	Rgs18	1700.79	Hbs1l	1406.21
Chordc1	3985.19	Ptprj	2189.91	Brinp3	1700.79	Cdkn2aip	1400.65
5-Mar	3974.07	Mir3110	2189.91	Mir509	1695.23	Cldn24	1400.65
4931408D1 4Rik	3974.07	4930448I 06Rik	2189.91	Fmr1	1695.23	Klf17	1400.65
Gm4850	3968.52	Pou3f3os	2189.91	Gldn	1695.23	Ccdc24	1400.65
Khdrbs2	3968.52	Gm20823	2184.35	Sh2d7	1695.23	Gm5547	1400.65
Phxr4	3907.38	Gm20823	2184.35	Tmem12 5	1695.23	Adora3	1400.65
Maml2	3907.38	Mir6238	2184.35	Ebna1bp 2	1695.23	Celf2	1400.65
Vwc2	3896.26	Siglech	2184.35	Krt2	1695.23	1700061 F12Rik	1400.65
4930415F1 5Rik	3896.26	Cyp4b1	2184.35	Krt77	1695.23	Kcnj3	1400.65
Gm21119	3885.14	Efcab14	2184.35	4930474 H20Rik	1695.23	Mir195b	1400.65
6820431F2 0Rik	3885.14	Kif15	2178.79	Pcdh9	1695.23	Arhgap15	1400.65
Gpr126	3885.14	Tgm4	2178.79	Fez1	1689.68	Gtdc1	1400.65
Vta1	3885.14	Il22	2178.79	Tmem21 8	1689.68	Kif20b	1400.65
Olfr1271	3874.03	Iltifb	2178.79	Tnnt3	1689.68	Htr7	1400.65
Olfr1272	3874.03	4930595 M18Rik	2173.24	Mrpl23	1689.68	Olfr1465	1400.65
Klhl4	3868.47	Tsga8	2173.24	Gpd2	1689.68	Olfr1466	1400.65
Ube2dnl1	3868.47	Trpm5	2173.24	Ermn	1689.68	Pdgfrb	1400.65

Cyp3a59	3829.56	Kcnq1ot1	2173.24	D330050 G23Rik	1689.68	Mir6983	1400.65
1700001J03 Rik	3829.56	Tmprss1 1f	2173.24	Spred1	1689.68	Slc8a1	1400.65
Gm20172	3812.89	Tmprss1 1bnl	2173.24	4921531 P14Rik	1689.68	Gm19689	1400.65
4931408C2 0Rik	3812.89	A530032 D15Rik	2173.24	Zadh2	1689.68	Cadm3	1400.65
Gm20854	3796.21	Gm7609	2173.24	Esp15	1689.68	Aim2	1400.65
Gm20854	3796.21	Fbxl7	2173.24	Esp38	1689.68	Prdm1	1400.65
Gm7157	3796.21	Mir7117	2173.24	Gm19276	1689.68	Prep	1400.65
Gpr143	3796.21	Cacna1d	2173.24	C1qtnf3	1689.68	Vmn2r86	1400.65
H2-M9	3785.1	Tkt	2173.24	Iars	1689.68	Vmn2r87	1400.65
H2-M1	3785.1	Ptchd1	2167.68	Gm906	1689.68	Fam122c	1395.09
Gm20268	3785.1	4930503 H13Rik	2167.68	Akap1	1689.68	Etd	1395.09
Cdh20	3785.1	Frmd4b	2167.68	Gm15698	1689.68	Tmem27	1395.09
Gm21119	3762.86	Mitf	2167.68	Rgs4	1689.68	Bmx	1395.09
Gm15319	3762.86	Edaradd	2167.68	1700084 C01Rik	1689.68	Mir1903	1395.09
Shisa2	3751.75	Gpr137b-ps	2167.68	Btg1	1689.68	Itgb1	1395.09
Nupl1	3751.75	Fam181b	2162.12	4930556 N09Rik	1689.68	4930519 H02Rik	1395.09
Tinag	3723.96	Tenm4	2162.12	Gclc	1684.12	Hgf	1395.09
5730403I07 Rik	3723.96	Mir7681	2162.12	Gcm1	1684.12	Tnc	1395.09
4930474H2 0Rik	3707.28	Ccdc150	2162.12	Gm8096	1684.12	Pappa	1395.09
Pcdh9	3707.28	Zfp277	2162.12	4933433 F19Rik	1684.12	Zfp608	1395.09
Gm20172	3690.61	Immp2l	2162.12	Plekha2	1684.12	Gramd3	1395.09
4931408C2 0Rik	3690.61	Spaca3	2162.12	Tacc1	1684.12	Adamts5	1395.09
D3Ertd751e	3685.05	1700071	2162.12	1600027J	1684.12	N6amt1	1395.09

		K01Rik		07Rik			
2610316D01Rik	3685.05	Sim1	2162.12	4933400L20Rik	1684.12	Brms1l	1395.09
Gm21119	3668.38	Gp49a	2162.12	Sec24b	1684.12	Gm19990	1395.09
Gm21944	3668.38	Pcdh17	2156.56	Etnppl	1684.12	Gm10516	1395.09
Kif20b	3668.38	4930529K09Rik	2156.56	Aqp4	1684.12	Hhat	1395.09
Htr7	3668.38	2410131K14Rik	2151	Cdh2	1684.12	Slc25a39	1395.09
Gm21119	3657.26	4930413E15Rik	2151	Gm4432	1684.12	Fam171a2	1395.09
Gm21944	3657.26	Arsj	2151	Akap8	1684.12	P2ry2	1389.54
Rell1	3657.26	Camk2d	2151	Nrg3os	1684.12	Atg16l2	1389.54
5830416I19Rik	3657.26	Peg12	2145.44	1700109I08Rik	1684.12	Far2	1389.54
Gm14461	3651.7	Chrna7	2145.44	Syt14	1684.12	4732416N19Rik	1389.54
Ube2e3	3651.7	Kcnip4	2145.44	Diexf	1684.12	Gm1653	1389.54
Actbl2	3629.47	Gpr125	2145.44	Cacng8	1678.56	Eltd1	1389.54
Gpbp1	3629.47	2210039B01Rik	2145.44	Cacng6	1678.56	Api5	1389.54
Htr2c	3618.35	Prkch	2145.44	Nkain3	1678.56	Lrrc4c	1389.54
Il13ra2	3618.35	C530044C16Rik	2139.89	Prdm13	1678.56	Ssfa2	1389.54
Gm15319	3618.35	Mir148a	2139.89	Dact2	1678.56	Ppp1r1c	1389.54
Gm21119	3618.35	Cxcr4	2139.89	Smoc2	1678.56	Kif18a	1389.54
Gm19757	3612.8	Daf2	2139.89	Zwint	1678.56	Bdnf	1389.54
Cntn4	3612.8	Csnk1d	2139.89	A330049N07Rik	1678.56	Gpr111	1389.54
Spaca7	3596.12	Cd7	2139.89	Myom2	1673	Tnfrsf21	1389.54
Gm15348	3596.12	Prl5a1	2134.33	Csmd1	1673	4930404A05Rik	1389.54
Scrt1	3579.45	2610307P16Rik	2134.33	Grik3	1673	Zpld1	1389.54

Fbxl6	3579.45	Ptplad2	2128.77	2610028 E06Rik	1673	4930448 F12Rik	1389.54
Cybrd1	3573.89	Ifnb1	2128.77	Spg11	1673	Vps41	1389.54
Dync1i2	3573.89	Gm3428	2123.21	Trim69	1673	Cfh	1389.54
170010102 2Rik	3573.89	Gm5916	2123.21	C030046 E11Rik	1673	Cdc73	1389.54
Apob	3573.89	A330050 F15Rik	2123.21	Mlana	1673	Nckap5	1389.54
Map3k13	3562.77	Dlgap1	2123.21	6330403 K07Rik	1673	Tmem16 3	1389.54
Liph	3562.77	4930505 G20Rik	2123.21	Nlrp1b	1673	Egfr	1389.54
Mir5127	3557.21	Gpc6	2123.21	D630024 D03Rik	1673	2810442I 21Rik	1389.54
Galr1	3557.21	Casp12	2117.65	4930524 B15Rik	1673	Ccdc53	1389.54
BB019430	3534.98	Pdgfd	2117.65	Edem1	1667.44	Gnptab	1389.54
Sept10	3534.98	Zfp42	2117.65	1700054 K19Rik	1667.44	6030498 E09Rik	1383.98
Gm5460	3529.42	Adam26b	2117.65	Gm10324	1667.44	Cypt15	1383.98
Anxa8	3529.42	Sumf1	2117.65	2410141 K09Rik	1667.44	E230019 M04Rik	1383.98
Ccdc104	3529.42	Mir7661	2117.65	Ofcc1	1667.44	Mir3475	1383.98
Prorsd1	3529.42	Elavl4	2117.65	Tfap2a	1667.44	2700038 G22Rik	1383.98
H2-M9	3523.86	Bend5	2117.65	Gm17821	1667.44	Fam126a	1383.98
H2-M1	3523.86	Nlgn1	2117.65	Rps29	1667.44	Lhx2	1383.98
Mir5127	3512.75	Spata16	2117.65	Myo5a	1661.89	Psmb7	1383.98
Galr1	3512.75	Samd3	2117.65	Gnb5	1661.89	Bfsp1	1383.98
Gm21119	3507.19	L3mbtl3	2117.65	Rasip1	1661.89	Rrbp1	1383.98
6820431F2 0Rik	3507.19	Olfr777	2117.65	Fut2	1661.89	Mir466g	1383.98
Pros1	3501.63	Olfr780	2117.65	Caln1	1661.89	Efna5	1383.98
Epha3	3501.63	Lsm6	2112.1	Auts2	1661.89	Depdc1b	1383.98

1700008P02Rik	3490.52	1700011L22Rik	2112.1	Eno1	1661.89	Mir582	1383.98
Pkia	3490.52	Zfp800	2112.1	Slc45a1	1661.89	Gsc	1383.98
Gm21119	3484.96	Gcc1	2112.1	Efcab1	1661.89	Dicer1	1383.98
Gm21944	3484.96	4930448I18Rik	2112.1	Ube2v2	1661.89	4933400L20Rik	1378.42
Gm12887	3479.4	Mir6417	2112.1	4930448I06Rik	1661.89	Cdh5	1378.42
9530002B09Rik	3479.4	Tdrd3	2112.1	Pou3f3os	1661.89	Evx1	1378.42
Alox12e	3473.84	Pcdh20	2112.1	D730050B12Rik	1661.89	1700094M24Rik	1378.42
Pelp1	3473.84	Etv6	2106.54	Irx4	1661.89	Gm3286	1378.42
Mthfs	3468.28	Lrp6	2106.54	Slc35d2	1661.89	BC061212	1378.42
AF529169	3468.28	Bub1	2106.54	Habp4	1661.89	Slc5a7	1378.42
Otor	3468.28	Bcl2l11	2106.54	Prox1	1661.89	St6gal2	1378.42
Pcsk2os1	3468.28	Runx1	2106.54	Rps6kc1	1661.89	Akr1e1	1378.42
Gm20268	3457.17	1810053B23Rik	2106.54	Cited2	1661.89	1700016G22Rik	1378.42
Cdh20	3457.17	Has2	2106.54	Txlnb	1661.89	1700085C21Rik	1378.42
Kcnj2	3451.61	Slc22a22	2106.54	Wwox	1656.33	Dpf3	1378.42
BC006965	3451.61	Mir6350	2106.54	Maf	1656.33	Tmem100	1378.42
Gm21119	3446.05	Tmeff2	2106.54	Mir1963	1656.33	Hlf	1378.42
Gm21944	3446.05	Dapk1	2106.54	Rasgrp4	1656.33	Frk	1378.42
Ptbp2	3446.05	Ctsll3	2106.54	Prok2	1656.33	Hs3st5	1378.42
Rwdd3	3446.05	Pex7	2106.54	Rybp	1656.33	Cdkl5	1372.86
Mbnl3	3429.38	Map7	2106.54	Dppa2	1656.33	Rai2	1372.86
Usp26	3429.38	Mir669a-9	2100.98	Gm5485	1656.33	Ttk	1372.86
Ythdf3	3423.82	Gm20098	2100.98	9430014N10Rik	1656.33	4930554C24Rik	1372.86

2610100L16Rik	3423.82	Klf7	2100.98	D630010B17Rik	1656.33	AB041803	1372.86
Chmp2b	3418.26	Creb1	2100.98	Rap2a	1656.33	Mkln1os	1372.86
Vgll3	3418.26	Mcm4	2100.98	Ipo5	1656.33	Gm9871	1372.86
Pou2af1	3396.03	Mzt2	2100.98	Tmem89	1650.77	Mir6373	1372.86
Gm684	3396.03	Fyb	2100.98	Uqcrc1	1650.77	Sh3gl2	1372.86
Cep85l	3396.03	Osmr	2100.98	Vmn1r29	1650.77	Adamtsl1	1372.86
Gm20597	3396.03	Foxf2	2100.98	Vmn1r30	1650.77	Vmn2r-ps11	1372.86
Adcy8	3384.91	Foxc1	2100.98	Frmd3	1650.77	Kcnab1	1372.86
Efr3a	3384.91	Wdr20rt	2100.98	Tmem261	1650.77	1700019E08Rik	1372.86
Tgif2lx2	3373.79	Rpl10l	2100.98	Arid1a	1650.77	Acvr2a	1372.86
Pabpc5	3373.79	**Ets1**	**2095.42**	Rps6ka1	1650.77	Pabpc2	1372.86
D3Ertd751e	3362.68	7630403G23Rik	2095.42	Kctd16	1650.77	Yipf5	1372.86
2610316D01Rik	3362.68	Slc13a1	2095.42	Prelid2	1650.77	1700010K23Rik	1372.86
Gm20172	3362.68	Iqub	2095.42	Itsn1	1650.77	Speer2	1372.86
4931408C20Rik	3362.68	4930470P17Rik	2095.42	Atp5o	1650.77	Cd209e	1367.3
Chl1	3357.12	1700028P15Rik	2095.42	Lrtm1	1650.77	Cd209d	1367.3
Gm19757	3357.12	Gnl3	2095.42	Selk	1650.77	Ccdc129	1367.3
A530072M11Rik	3357.12	Smim4	2095.42	Cast	1650.77	Ppp1r17	1367.3
Mmp16	3357.12	Gm10790	2095.42	Pcsk1	1650.77	Cntn6	1367.3
St7l	3346	Hivep1	2095.42	Fam81a	1645.21	Gm19757	1367.3
Wnt2b	3346	Cd180	2095.42	Myo1e	1645.21	C87414	1367.3
Slitrk4	3334.89	Srek1	2095.42	2010106C02Rik	1645.21	Gm7978	1367.3
Ctag2	3334.89	Gm16998	2095.42	Epas1	1645.21	Hnf4g	1367.3
Diap2	3334.89	Tbc1d32	2095.42	Mbnl3	1639.65	Atp13a5	1367.3

Pcdh19	3334.89	Gm16404	2089.86	Usp26	1639.65	Opa1	1367.3
Slc7a2	3334.89	3830403 N18Rik	2089.86	Tusc3	1639.65	Mir466	1367.3
Mtus1	3334.89	Gm20362	2089.86	Gm6213	1639.65	4930524 C18Rik	1367.3
Cdh8	3329.33	Gm20594	2089.86	4933430 H16Rik	1639.65	Vcan	1367.3
Cdh11	3329.33	1700019 E08Rik	2089.86	Tmc3	1639.65	Xrcc4	1367.3
Snord67	3329.33	Acvr2a	2089.86	Ppapdc1a	1639.65	Dock4	1367.3
F2	3329.33	D730050 B12Rik	2089.86	Wdr11	1639.65	Immp2l	1367.3
Ccdc37	3323.77	Irx4	2089.86	Pycard	1639.65	Rnf145	1367.3
Klf15	3323.77	1700029 N11Rik	2089.86	Trim72	1639.65	Gm12159	1367.3
Zfp946	3312.66	Jarid2	2089.86	0610040J 01Rik	1639.65	Dpp10	1367.3
Vmn2r112	3312.66	Tmem26 1	2084.3	5830416I 19Rik	1639.65	Actr3	1367.3
Trpm3	3307.1	Tyrp1	2084.3	4933402J 10Rik	1639.65	Mir669h	1367.3
Klf9	3307.1	Tpd52l2	2084.3	G6pd2	1639.65	Tph2	1367.3
Kctd16	3295.98	Uckl1	2084.3	Mir466h	1639.65	Pawr	1367.3
Prelid2	3295.98	Dsn1	2084.3	Gm5860	1639.65	Gm5136	1367.3
A830082K1 2Rik	3295.98	Tldc2	2084.3	Hrh4	1639.65	Defa-ps13	1361.75
Arrdc3	3295.98	Rnf180	2084.3	8430422 H06Rik	1639.65	Defb8	1361.75
Rps27a	3295.98	Htr1a	2084.3	1810013 L24Rik	1639.65	Olfr71	1361.75
Rtn4	3295.98	Pcolce2	2078.75	Grin2a	1639.65	Hrct1	1361.75
Kcnh7	3290.42	Pls1	2078.75	Brinp2	1639.65	Gltpd1	1361.75
Fign	3290.42	Scn5a	2078.75	Mir488	1639.65	Pusl1	1361.75
Samt2	3251.52	Scn10a	2078.75	4930596I 21Rik	1639.65	Pid1	1361.75

Gm16390	3251.52	Ccnd1	2078.75	Crb1	1639.65	Mir5126	1361.75
Sumo3	3240.4	1810010D01Rik	2078.75	BC030870	1634.09	Nrxn1	1361.75
Mir1930	3240.4	Polr2b	2078.75	1-Mar	1634.09	Adcyap1	1361.75
Lrrc4c	3229.28	Pea15b	2078.75	1700065L07Rik	1634.09	Arhgap28	1361.75
B230118H07Rik	3229.28	Rgs7bp	2078.75	Ctnna2	1634.09	Tmem200c	1361.75
Lrfn5	3229.28	Rnf180	2078.75	Gsx1	1634.09	Med30	1361.75
Fscb	3229.28	Pcnx	2078.75	Pdx1	1634.09	Ext1	1361.75
Snord14d	3223.72	Sipa1l1	2078.75	Fpgt	1634.09	Rev1	1361.75
C130030K03Rik	3223.72	1700063D05Rik	2073.19	9330178D15Rik	1634.09	Lonrf2	1361.75
Klhl25	3218.17	3110039I08Rik	2073.19	Tbr1	1634.09	4930448C13Rik	1361.75
Ntrk3	3218.17	Aqp11	2073.19	Slc4a10	1634.09	Trib2	1361.75
4930548K13Rik	3212.61	Pak1	2073.19	Rxfp3	1634.09	AW822252	1356.19
Epha7	3212.61	Pfkp	2073.19	Tars	1634.09	1700013H16Rik	1356.19
Il7	3212.61	Adarb2	2073.19	Mir669h	1634.09	Gm5347	1356.19
1700010I02Rik	3212.61	Wdr20rt	2073.19	Trhde	1634.09	Fat1	1356.19
Mocs2	3201.49	Rpl10l	2073.19	Emp1	1628.54	Pirb	1356.19
Itga1	3201.49	Vmn2r72	2067.63	Gm8994	1628.54	Pira2	1356.19
Slco2b1	3195.93	Vmn2r73	2067.63	Fbxw7	1628.54	Flrt3	1356.19
Olfr520	3195.93	Klf4	2067.63	1700036G14Rik	1628.54	Kif16b	1356.19
Stx19	3195.93	Actl7b	2067.63	Dmrt2	1628.54	Ctif	1356.19
Pros1	3195.93	A830082K12Rik	2067.63	Smarca2	1628.54	2900057B20Rik	1356.19
Vmn2r72	3184.82	Arrdc3	2067.63	Slc14a2	1628.54	Gm20740	1356.19
Vmn2r73	3184.82	Gm6377	2062.07	Setbp1	1628.54	Gsdmc	1356.19
Atp10d	3184.82	Gm7134	2062.07	4930474	1628.54	4933424	1356.19

				N09Rik		G06Rik	
Nfxl1	3184.82	Cyp4b1	2062.07	1700064 M15Rik	1628.54	Tmem13 1	1356.19
Astn2	3173.7	Efcab14	2062.07	2810032 G03Rik	1628.54	Trpc7	1356.19
Tlr4	3173.7	Zfp946	2062.07	1700101 O22Rik	1628.54	Spock1	1356.19
Kcnip4	3168.14	Vmn2r11 2	2062.07	Tmem12 6b	1622.98	4933425 L06Rik	1356.19
Gpr125	3168.14	Stxbp6	2062.07	Dlg2	1622.98	Htr1a	1356.19
Cyp4b1	3168.14	Nova1	2062.07	Ift74	1622.98	Brinp3	1356.19
Efcab14	3168.14	Folh1	2050.96	Tek	1622.98	Pla2g4a	1356.19
Gm5347	3162.59	Vmn2r78	2050.96	Zfp362	1622.98	Slitrk4	1350.63
Fat1	3162.59	Hnf4aos	2050.96	Trim62	1622.98	Ctag2	1350.63
Usp9y	3157.03	Ttpal	2050.96	Rfk	1622.98	Mir6769b	1350.63
Zfy2	3157.03	Lyzl1	2050.96	Ostf1	1622.98	Jak3	1350.63
Fxn	3157.03	Map3k8	2050.96	Gpr26	1617.42	Lcmt1	1350.63
Fam122a	3157.03	Ccser1	2045.4	Cpxm2	1617.42	Zkscan2	1350.63
Pard3	3151.47	Atoh1	2045.4	Tes	1617.42	1810018 F18Rik	1350.63
Mir21c	3151.47	Mir6380	2045.4	D830026I 12Rik	1617.42	Pnliprp2	1350.63
Tbc1d2b	3145.91	Gnb2l1	2045.4	Gap43	1617.42	Homer1	1350.63
Zic1	3145.91	Tapt1	2039.84	4932412 D23Rik	1617.42	Bhmt	1350.63
Klf13	3140.35	4930431 F12Rik	2039.84	Cmah	1617.42	Fgf10	1350.63
Mir211	3140.35	4930412 C18Rik	2039.84	Gm11346	1617.42	Nnt	1350.63
Celf2	3140.35	4930448 K20Rik	2039.84	Prkch	1617.42	Enox2	1345.07
1700061F1 2Rik	3140.35	Penk	2039.84	Snapc1	1617.42	Arhgap36	1345.07
Cntnap5c	3140.35	Gm11780	2039.84	Dpp10	1617.42	Mtnr1b	1345.07

2610034M16Rik	3140.35	Smndc1	2039.84	Actr3	1617.42	Chordc1	1345.07
Batf	3129.24	5830416P10Rik	2039.84	Scd2	1611.86	4930519F24Rik	1345.07
0610007P14Rik	3129.24	Slc14a2	2039.84	Scd4	1611.86	Il20rb	1345.07
Vmn2r47	3123.68	Setbp1	2039.84	Hlcs	1611.86	Aktip	1345.07
Vmn2r46	3123.68	1700123O21Rik	2039.84	Ripply3	1611.86	Fto	1345.07
Klra14-ps	3123.68	Cldn26	2039.84	Slitrk6	1611.86	Kcnj11	1345.07
Klra9	3123.68	Vmn2r95	2034.28	Slitrk5	1611.86	Abcc8	1345.07
Raly	3112.56	Vmn2r96	2034.28	2410141K09Rik	1611.86	Apbb2	1345.07
a	3112.56	Ptchd1	2028.72	Uqcrb	1611.86	Uchl1os	1345.07
Lrrc4c	3112.56	4930503H13Rik	2028.72	Tgfbi	1611.86	1700013G24Rik	1345.07
B230118H07Rik	3112.56	Mir669m-1	2028.72	Smad5	1611.86	Hspg2	1345.07
Magea10	3095.89	Lphn3	2028.72	Nrbf2	1611.86	AI606473	1345.07
Mir767	3095.89	Lamp5	2028.72	Egr2	1611.86	Tyw3	1345.07
Vmn2r47	3095.89	Ankef1	2028.72	Pcdh11x	1606.3	Palmd	1345.07
Vmn2r46	3095.89	St8sia3os	2028.72	Nap1l3	1606.3	1700061I17Rik	1345.07
4930404A05Rik	3090.33	Fech	2028.72	1700015G11Rik	1606.3	Commd10	1345.07
Zpld1	3090.33	Cblb	2028.72	Mir6238	1606.3	9130209A04Rik	1345.07
Nfasc	3084.77	4930404A05Rik	2028.72	Capza3	1606.3	Zfp952	1345.07
Lrrn2	3084.77	Rxfp3	2028.72	Aebp2	1606.3	4921501E09Rik	1345.07
4930405A10Rik	3079.21	Tars	2028.72	Lingo2	1606.3	Lmbrd1	1345.07
Gm10248	3079.21	1700092K14Rik	2028.72	1700009N14Rik	1606.3	Gm20172	1345.07
Slc7a15	3079.21	Mir466n	2028.72	4930564	1606.3	Pcdh11x	1339.51

				D02Rik			
Pum2	3079.21	Igsf1	2023.17	Kcnd3os	1606.3	Nap1l3	1339.51
Adam3	3062.54	Olfr1322	2023.17	Asxl3	1606.3	Wwc2	1339.51
Adam32	3062.54	Epha5	2023.17	Gm7788	1606.3	Dctd	1339.51
Khdrbs2	3062.54	Cenpc1	2023.17	Vmn1r235	1606.3	Gm15412	1339.51
Prim2	3062.54	Tram1l1	2023.17	Vmn1r237	1606.3	Gm15413	1339.51
Rgs18	3062.54	1700006A11Rik	2023.17	Fam83f	1606.3	Pira2	1339.51
Brinp3	3062.54	Bbx	2023.17	Mir5113	1606.3	Lilra6	1339.51
Iqcj	3056.98	Ccdc54	2023.17	4930455B14Rik	1606.3	Vmn1r173	1339.51
Schip1	3056.98	Tmem179	2023.17	Fhit	1606.3	Vmn1r174	1339.51
Irx3	3051.42	Inf2	2023.17	C130030K03Rik	1606.3	Gm10440	1339.51
Crnde	3051.42	A730082K24Rik	2017.61	Ascc3	1606.3	4932441J04Rik	1339.51
10-Mar	3051.42	1700003G18Rik	2017.61	1700017N19Rik	1606.3	Fstl5	1339.51
Cyb561	3051.42	Gm15328	2017.61	Mgat4c	1606.3	Rapgef2	1339.51
4930474H20Rik	3045.86	4921533I20Rik	2017.61	Mrpl1	1600.75	Gm5148	1339.51
Pcdh9	3045.86	4930542D17Rik	2017.61	Fras1	1600.75	Gm20755	1339.51
Tenm3	3034.75	5330426P16Rik	2017.61	Enoph1	1600.75	Arl5b	1339.51
Gm2516	3034.75	Tssc1	2017.61	2310034O05Rik	1600.75	Plxdc2	1339.51
Erich1	3034.75	Myt1l	2017.61	4930432M17Rik	1600.75	Zfp442	1339.51
Cln8	3034.75	1600027J07Rik	2012.05	F3	1600.75	Cst7	1339.51
Impg1	3023.63	4933400L20Rik	2012.05	Fads2	1600.75	Mir6393	1339.51

Htr1b	3023.63	Klf15	2012.05	Fads1	1600.75	B230214 G05Rik	1339.51
Mir669m-1	3023.63	Aldh1l1	2012.05	Ptprm	1600.75	Mir466	1339.51
Lphn3	3023.63	Npy	2012.05	Lrrc30	1600.75	4930524 C18Rik	1339.51
Igsf11	3023.63	Mpp6	2012.05	Keap1	1595.19	Gm20172	1339.51
Lsamp	3023.63	Sike1	2012.05	Atg4d	1595.19	4931408 C20Rik	1339.51
Mir17hg	3018.07	Nras	2012.05	Ces5a	1595.19	Etv1	1339.51
4930505G2 0Rik	3018.07	Gm5415	2012.05	Gnao1	1595.19	Arl4a	1339.51
Adck4	3012.52	Prim2	2012.05	Gm19757	1595.19	Zfp330	1333.96
Ltbp4	3012.52	Kdm6b	2012.05	Cntn4	1595.19	Tbc1d9	1333.96
Olfr161	3001.4	Efnb3	2012.05	Peg13	1595.19	Olfr694	1333.96
4930486L2 4Rik	3001.4	Col18a1	2012.05	Trappc9	1595.19	Olfr695	1333.96
Ctla2b	3001.4	Gm10941	2012.05	Edn1	1595.19	Artn	1333.96
Map4k4	2995.84	4933413 G19Rik	2006.49	Phactr1	1595.19	Kdm4a	1333.96
Gm16894	2995.84	Nrip2	2006.49	Snx13	1595.19	Gm1653	1333.96
4930467E2 3Rik	2990.28	Brinp1	2006.49	9130015 A21Rik	1595.19	Eltd1	1333.96
6820431F2 0Rik	2990.28	Cdk5rap2	2006.49	Rnf122	1589.63	Map4k3	1333.96
Mir7025	2984.72	Zmynd11	2006.49	Tti2	1589.63	Thumpd2	1333.96
Kit	2984.72	Zp4-ps	2006.49	Gm2447	1589.63	Epha6	1333.96
Trpc7	2979.17	Xlr	2000.93	Gm20750	1589.63	Nsun3	1333.96
Spock1	2979.17	Gm16430	2000.93	4930402 F06Rik	1589.63	D630010 B17Rik	1333.96
Gm21119	2973.61	Topbp1	2000.93	Gm13446	1589.63	Adamts2 0	1333.96
6820431F2 0Rik	2973.61	5830418 P13Rik	2000.93	Wdr33	1589.63	5430437J 10Rik	1333.96
D3Ertd751e	2956.93	Cdh6	2000.93	Sft2d3	1589.63	Dab2	1333.96

2610316D01Rik	2956.93	Cdh9	2000.93	Tm4sf20	1589.63	Plcxd3	1333.96
Arx	2951.38	Cdk5r1	2000.93	Agfg1	1589.63	C6	1333.96
Pcyt1b	2951.38	Tmem98	2000.93	Nudt12	1589.63	Ptger2	1333.96
Specc1	2951.38	Brinp2	2000.93	Mir466g	1589.63	Gpr137c	1333.96
Adora2b	2951.38	Mir488	2000.93	Tmx1	1589.63	Kcnma1	1333.96
Ccser1	2940.26	Cxcr3	1995.37	Frmd6	1589.63	Mir7210	1333.96
Atoh1	2940.26	Rgag4	1995.37	Pja1	1584.07	Prkch	1333.96
Gpr63	2940.26	Insr	1995.37	Tmem28	1584.07	Snapc1	1333.96
Ufl1	2940.26	1110019D14Rik	1995.37	Txn1	1584.07	Rgs7	1333.96
Gm5126	2934.7	Ppp1r3a	1995.37	Svep1	1584.07	Fh1	1333.96
Nap1l2	2934.7	Kap	1995.37	Gm14461	1584.07	Fmo2	1333.96
Vmn1r67	2929.14	Bcl2l14	1995.37	Ube2e3	1584.07	Fmo3	1333.96
Zik1	2929.14	Murc	1995.37	4930505G20Rik	1584.07	Rab1	1333.96
Pou3f2	2929.14	E130309F12Rik	1995.37	Gpc6	1584.07	Slc1a4	1333.96
Mms22l	2929.14	Snord14d	1995.37	Commd6	1584.07	Epha7	1328.4
Slc7a14	2929.14	C130030K03Rik	1995.37	Uchl3	1584.07	Map3k7	1328.4
Kcnmb2	2929.14	Wdr72	1989.82	Slc35b3	1584.07	Esp31	1328.4
Nudt12	2929.14	Gm16551	1989.82	Ofcc1	1584.07	Esp24	1328.4
Mir466g	2929.14	Mc5r	1989.82	BB019430	1584.07	Sntb1	1328.4
Hapln1	2923.58	Mc2r	1989.82	Sh3rf3	1584.07	Has2	1328.4
Xrcc4	2923.58	Krt80	1989.82	Fam19a2	1584.07	1700024P04Rik	1328.4
1110001J03Rik	2918.03	Krt7	1989.82	4930503E24Rik	1584.07	2310020H05Rik	1328.4
Klrg2	2918.03	2610203C20Rik	1984.26	Rab21	1584.07	4930563E22Rik	1328.4
H2-M9	2901.35	Sorl1	1984.26	Thap2	1584.07	Slc13a5	1328.4

H2-M1	2901.35	Aadat	1984.26	Zdhhc17	1584.07	Slc19a2	1328.4
Tdrd1	2895.79	2700029 M09Rik	1984.26	Bbs10	1584.07	Blzf1	1328.4
Afap1l2	2895.79	Trim32	1984.26	Tbx18	1578.51	Ado	1328.4
Rasgrp1	2890.24	Tlr4	1984.26	Nt5e	1578.51	Zfp365	1328.4
4930412B1 3Rik	2890.24	Tmem38 b	1984.26	Ccdc83	1578.51	Gpc4	1322.84
Pemt	2890.24	Zfp462	1984.26	Sytl2	1578.51	Mir6384	1322.84
Rai1	2890.24	Ahdc1	1984.26	Pax4	1578.51	Tox3	1322.84
Pdgfra	2879.12	Mir7017	1984.26	Lrrc4	1578.51	Rbl2	1322.84
Kit	2879.12	Flrt3	1984.26	Murc	1578.51	1700015 G11Rik	1322.84
Mir6414	2873.56	Kif16b	1984.26	E130309 F12Rik	1578.51	Mir6238	1322.84
Gm7854	2873.56	Kremen1	1984.26	Kynu	1578.51	Nfe2l3	1322.84
A830082N0 9Rik	2873.56	Xbp1	1984.26	Arhgap15 os	1578.51	Cbx3	1322.84
Trappc3l	2873.56	Defb7	1978.7	Macrod2	1578.51	Calr4	1322.84
6030469F0 6Rik	2868	4930467 E23Rik	1978.7	Flrt3	1578.51	Eps15	1322.84
Dld	2868	Sh3gl3	1978.7	Isoc1	1578.51	Zfp120	1322.84
4930467E2 3Rik	2862.45	Fam154b	1978.7	A730017 C20Rik	1578.51	Zfp937	1322.84
6820431F2 0Rik	2862.45	Shfm1	1978.7	Runx1	1578.51	Dnajb7	1322.84
Cdk14	2856.89	Dlx6os1	1978.7	1810053 B23Rik	1578.51	Rbx1	1322.84
1700015F1 7Rik	2856.89	Cftr	1978.7	Gm19782	1578.51	Snhg18	1322.84
Usp15	2856.89	Cttnbp2	1978.7	Fam135b	1578.51	Sdc2	1322.84
4930503E2 4Rik	2856.89	Gm14015	1978.7	Slc36a1	1578.51	Soat1	1322.84
Ipmk	2851.33	Mpped2	1978.7	Sparc	1578.51	Tor3a	1322.84
1700049L1 6Rik	2851.33	Prl5a1	1978.7	C1d	1578.51	Gabrb2	1322.84

Fbxw4	2845.77	2610307 P16Rik	1978.7	Etaa1	1578.51	Atp10b	1322.84
4933429K1 8Rik	2845.77	D430020J 02Rik	1978.7	Cdh20	1578.51	Sall1	1317.28
Vmn2r96	2840.21	Ptprn2	1978.7	Rnf152	1578.51	Tox3	1317.28
Vmn2r97	2840.21	4930525 M21Rik	1973.14	Tsc22d3	1572.96	Ctsc	1317.28
1700010K2 3Rik	2840.21	4930430 D24Rik	1973.14	Mid2	1572.96	Rab38	1317.28
Speer2	2840.21	H2afb3	1973.14	Col4a1	1572.96	Lmo4	1317.28
Gm20268	2840.21	Nap1l3	1973.14	Rab20	1572.96	Sept15	1317.28
Cdh20	2840.21	Stox2	1973.14	Vmn2r47	1572.96	Nup35	1317.28
Epha7	2829.1	Trappc11	1973.14	Vmn2r46	1572.96	Zc3h15	1317.28
4930556G0 1Rik	2829.1	Rnf32	1973.14	Glt1d1	1572.96	Chd6	1317.28
Rprl2	2829.1	Nom1	1973.14	5930412 G12Rik	1572.96	Ptprt	1317.28
Spata16	2829.1	Barhl2	1973.14	Tex38	1572.96	Lmf2	1317.28
Ptbp2	2823.54	Hfm1	1973.14	Mob3c	1572.96	Odf3b	1317.28
Rwdd3	2823.54	A930001 A20Rik	1973.14	0610039 K10Rik	1572.96	Itga1	1317.28
Bcl2a1d	2817.98	Gm9733	1973.14	Pkig	1572.96	Isl1	1317.28
Trim43c	2817.98	Gm10248	1973.14	Cdh6	1572.96	1810007 C17Rik	1317.28
Rprl1	2817.98	Mir7210	1973.14	Cdh9	1572.96	Prkd1	1317.28
Rpia	2817.98	Slitrk6	1967.58	Pole2	1572.96	Ikzf1	1317.28
Scn2a1	2817.98	Slitrk5	1967.58	Klhdc2	1572.96	Fignl1	1317.28
Galnt3	2817.98	Gm11944	1967.58	2810032 G03Rik	1572.96	Chm	1311.72
Ctla4	2812.42	Limk2	1967.58	1700101 O22Rik	1572.96	Klhl4	1311.72
Icos	2812.42	Tsc22d3	1962.03	Celrr	1572.96	4930433 N12Rik	1311.72
Gm20854	2801.31	Mid2	1962.03	Insig2	1572.96	Alkbh8	1311.72

Gm20854	2801.31	Nudt21	1962.03	D830032 E09Rik	1572.96	Aass	1311.72
Sacs	2801.31	Bbs2	1962.03	Cdh7	1572.96	Fezf1	1311.72
1700109G1 4Rik	2801.31	Gm20756	1962.03	Grik2	1572.96	Klra5	1311.72
Lrfn5	2801.31	Grm8	1962.03	Sim1	1572.96	Klra22	1311.72
Fscb	2801.31	Sec61b	1962.03	1810026 B05Rik	1567.4	Skint11	1311.72
Mir216b	2801.31	Nr4a3	1962.03	Gm4971	1567.4	Trabd2b	1311.72
Mir216a	2801.31	Nfyc	1962.03	Mir3095	1567.4	Pdcd10	1311.72
Rab10os	2795.75	Rims3	1962.03	Olfr267	1567.4	2410007 B07Rik	1311.72
Kif3c	2795.75	Fbll1	1962.03	Sema4a	1567.4	Cdh26	1311.72
Dux	2795.75	Rars	1962.03	Lmna	1567.4	4930591 A17Rik	1311.72
Gm4981	2795.75	C130030 K03Rik	1962.03	D030025 E07Rik	1567.4	Emilin3	1311.72
Vwc2	2784.63	Ascc3	1962.03	Pitx2	1567.4	Ptprt	1311.72
4930415F1 5Rik	2784.63	Slc16a7	1962.03	Wdr5	1567.4	Pik3c3	1311.72
Mos	2773.51	Lrig3	1962.03	Rxra	1567.4	Rit2	1311.72
Plag1	2773.51	Usp38	1956.47	Itpk1	1567.4	Ednrb	1311.72
Abcd3	2773.51	Inpp4b	1956.47	Moap1	1567.4	4930432J 09Rik	1311.72
Arhgap29	2773.51	2610005 L07Rik	1956.47	Smim23	1567.4	Fgfr4	1311.72
Tmtc4	2773.51	Gm21119	1956.47	Npm1	1567.4	Rab24	1311.72
AA536875	2773.51	Pla2g4e	1956.47	Vwc2	1567.4	Ptprk	1311.72
Ss18	2767.96	Pla2g4f	1956.47	4930415 F15Rik	1567.4	4930519 F09Rik	1311.72
Taf4b	**2767.96**	Myom2	1950.91	Fam181b	1561.84	A430089I 19Rik	1306.16
Slc10a7	2740.17	Csmd1	1950.91	Tenm4	1561.84	AA79289 2	1306.16
Lsm6	2740.17	Thsd7a	1950.91	4930483	1561.84	Mysm1	1306.16

				O08Rik			
Dctd	2740.17	Tmem106b	1950.91	Tex36	1561.84	Jun	1306.16
Gm2516	2740.17	Esp15	1950.91	**Tlr4**	**1561.84**	Has2	1306.16
Nox4	2740.17	Esp38	1950.91	Brinp1	1561.84	Zhx2	1306.16
Grm5	2740.17	Larp4b	1950.91	Snx16	1561.84	Csmd3	1306.16
Sox5	**2740.17**	Zmynd11	1950.91	Gm10745	1561.84	Trps1	1306.16
Sox5os3	2740.17	4931408C20Rik	1950.91	Ndrg1	1561.84	Mnd1-ps	1306.16
Gm20063	2740.17	Gm597	1950.91	1700012I11Rik	1561.84	Ptprg	1306.16
Fscb	2740.17	Cntnap5a	1950.91	Diap3	1561.84	4931429P17Rik	1306.16
Nefm	2734.61	Tsn	1950.91	Tdrd3	1561.84	Id4	1306.16
Adam7	2734.61	4930419G24Rik	1945.35	Trpc7	1561.84	Six4	1306.16
Tmem30c	2729.05	Ttc14	1945.35	Spock1	1561.84	Trmt5	1306.16
Filip1l	2729.05	Nmbr	1945.35	Akap6	1561.84	Ubxn2a	1306.16
4930579G18Rik	2729.05	Gm20125	1945.35	Egln3	1561.84	Klhl29	1306.16
1700123O20Rik	2729.05	4930525M21Rik	1939.79	1700020N15Rik	1556.28	Gpr68	1306.16
Mettl11b	2723.49	4930430D24Rik	1939.79	Ids	1556.28	Mir1190	1306.16
Kifap3	2723.49	Mtnr1b	1939.79	Cnksr2	1556.28	Spdl1	1306.16
Vmn2r47	2717.93	Chordc1	1939.79	Rps6ka3	1556.28	Slit3	1306.16
Vmn2r46	2717.93	Zfp770	1939.79	Clec3a	1556.28	Nol11	1306.16
Sh2d1a	2712.38	4930528P14Rik	1939.79	Maf	1556.28	Psmd12	1306.16
Gm362	2712.38	Usp25	1939.79	Spaca1	1556.28	Hccs	1300.61
Gm10280	2712.38	2810055G20Rik	1939.79	Akirin2	1556.28	Mid1	1300.61
4930571O06Rik	2712.38	Pitpnm3	1939.79	Fam188a	1556.28	Glra2	1300.61

Cox8c	2706.82	Txndc17	1939.79	Pter	1556.28	Gemin8	1300.61
Prima1	2706.82	Ralgps2	1939.79	Ankrd1	1556.28	Mir7090	1300.61
Xylt1	2695.7	Tex35	1939.79	Pcgf5	1556.28	Ulk4	1300.61
Rps15a	2695.7	Isl2	1934.23	Dcc	1556.28	LOC102633035	1300.61
Hist4h4	2695.7	Rfpl3s	1934.23	Mex3c	1556.28	Mir7243	1300.61
Wbp11	2695.7	Celf2	1934.23	Gm10494	1556.28	Tpk1	1300.61
Trak2	2695.7	1700061F12Rik	1934.23	Cyp1b1	1556.28	Cntnap2	1300.61
Als2cr11	2695.7	Slc35g1	1934.23	Fbxo33	1556.28	Cecr5	1300.61
Cyp2d26	2695.7	Noc3l	1934.23	Gm20063	1556.28	1700072O05Rik	1300.61
Tbrg3	2695.7	Tmpo	1934.23	Abcc3	1556.28	Grm3	1300.61
Trim52	2695.7	Mir135a-2	1934.23	Spata20	1556.28	Gm6455	1300.61
1700128A07Rik	2695.7	Olfr371	1928.68	Gm6150	1556.28	4930556G01Rik	1300.61
Dhrs7	2690.14	Orc6	1928.68	Stxbp5	1556.28	Map3k7	1300.61
4930447C04Rik	2690.14	Epha7	1928.68	Sgcz	1550.72	Hey1	1300.61
Gm20871	2684.58	4930556G01Rik	1928.68	Tusc3	1550.72	Mrps28	1300.61
Gm20823	2684.58	Gm12070	1928.68	Plxna4	1550.72	Lrrc40	1300.61
Tdrp	2684.58	Ccdc85a	1928.68	Exoc4	1550.72	Gm20752	1300.61
Erich1	2684.58	4930415L06Rik	1923.12	AU018829	1550.72	Dbt	1300.61
A830019L24Rik	2684.58	Gm44	1923.12	Gm3259	1550.72	Trmt13	1300.61
Lmo4	2684.58	Rgag1	1923.12	E130114P18Rik	1550.72	1700054A03Rik	1300.61
9430016H08Rik	2684.58	Pak3	1923.12	Tm2d1	1550.72	1700001K23Rik	1300.61
Spats2l	2684.58	**Frg1**	**1923.12**	Rpl34	1550.72	Gm10248	1300.61
1700022A21Rik	2679.03	2810404M03Rik	1923.12	**Lef1**	**1550.72**	Mir7210	1300.61

Nub1	2679.03	Gm13315	1923.12	Myoz2	1550.72	Htr1a	1300.61
Usp38	2673.47	Cacnb2	1923.12	Synpo2	1550.72	Ipo11	1300.61
Inpp4b	2673.47	4933406 G16Rik	1923.12	2700089I 24Rik	1550.72	Gm12159	1300.61
Ankrd13c	2662.35	Spred2	1923.12	Rab11fip 2	1550.72	F630206 G17Rik	1300.61
Srsf11	2662.35	Celf2	1917.56	9430020 K01Rik	1550.72	Wwc1	1300.61
Mtnr1b	2656.79	1700061 F12Rik	1917.56	Gm10556	1550.72	Gm12130	1300.61
Chordc1	2656.79	Cstf3	1917.56	1700113 H08Rik	1550.72	Tlr13	1295.05
Klra4	2656.79	Tcp11l1	1917.56	Ascl1	1550.72	Pgk1	1295.05
Klra14-ps	2656.79	1700108J 01Rik	1917.56	4930578 C19Rik	1545.16	Sntb2	1295.05
Scrn1	2645.68	Gm5089	1917.56	Mir221	1545.16	Vps4a	1295.05
Fkbp14	2645.68	Grxcr1	1912	Cask	1545.16	Dmrt2	1295.05
Tas2r108	2645.68	Kctd8	1912	Gm5382	1545.16	Smarca2	1295.05
Prss37	2645.68	Tmem13 0	1912	Otol1	1545.16	1700097 N02Rik	1295.05
Qtrtd1	2645.68	Smurf1	1912	Gm6634	1545.16	Glp1r	1295.05
Zdhhc23	2645.68	Lingo2	1912	Dcun1d1	1545.16	Fhl2	1295.05
Usp9y	2634.56	1700009 N14Rik	1912	Mccc1os	1545.16	Nck2	1295.05
Zfy2	2634.56	Gm7788	1912	Cst7	1545.16	Rnf145	1295.05
Mthfs	2634.56	Dtna	1912	Apmap	1545.16	**Ebf1**	**1295.05**
AF529169	2634.56	Nyap2	1912	4930548J 01Rik	1545.16	Rars	1295.05
Slc7a6os	2634.56	Mir6344	1912	Arid1b	1545.16	Tenm2	1295.05
Smpd3	2634.56	Epha4	1912	Cd200r1	1545.16	Msl2	1289.49
Ppm1d	2634.56	Sgpp2	1912	Cd200r4	1545.16	LOC1026 33035	1289.49
Bcas3os1	2634.56	Mir6342	1912	Gm10421	1545.16	Tenm3	1289.49
Prg4	2634.56	Phf3	1912	Gm5441	1545.16	Gm2516	1289.49

C730036E19Rik	2634.56	Fancb	1906.44	Ubr4	1539.61	Rprl2	1289.49
Ndnf	2629	Glra2	1906.44	Iffo2	1539.61	Nlgn1	1289.49
4930544G11Rik	2629	Thap4	1906.44	Pcdh18	1539.61	Api5	1289.49
Sohlh2	2617.89	Dtymk	1906.44	Ccrn4l	1539.61	Lrrc4c	1289.49
Dclk1	2617.89	Hdhd1a	1906.44	4930455B14Rik	1539.61	Cd200r4	1289.49
Mir5127	2617.89	Mir28	1906.44	Fhit	1539.61	Cd200r2	1289.49

Appendix Va

RNA-seq in common lymphoid progenitors (CLPs)
Most Down-regulated in *Mef2c* KO

Bold: B cell genes

Red: T cell genes

Gene name	WT/KO ratio	Gene name	WT/KO ratio	Gene name	WT/KO ratio	Gene name	WT/KO ratio
Vpreb1	**152.55**	Kdelc2	5.03	Ntn3	3.50	Zc3h6	2.84
Tcf7	45.94	**Rad1**	**5.03**	Emc9	3.50	Arhgef9	2.84
Ccr2	37.63	Slc35g1	5.03	Tmem170	3.50	Ide	2.84
Erg	**30.62**	Fdx1l	5.02	Apmap	3.50	Ldoc1l	2.84
Egln1	28.00	Apcdd1	5.01	Cwf19l1	3.50	Hsd17b10	2.84
S100a4	25.16	Zfp386	4.96	Slc9a9	3.50	Zfp593	2.84
Tbxa2r	22.46	Calcrl	4.96	Lrrn4	3.50	Ahcy	2.84
Epb4.1l4b	20.78	Hs2st1	4.92	Rdh14	3.50	Ddx31	2.84
Rcor2	19.69	**Bzw2**	**4.91**	P2ry10	3.50	Nmnat1	2.84
Pcgf6	19.69	Ttc27	4.91	Leprel4	3.50	Plk2	2.84
Prkch	19.25	Zbtb12	4.89	Slc25a23	3.50	Zcchc24	2.84
E130012A19 Rik	19.25	Cep128	4.89	Kif16b	3.50	Mex3c	2.84
Igll1	**18.81**	Mbnl3	4.88	Aig1	3.50	Tanc1	2.84
Emp1	18.81	Sap30	4.87	Slc11a1	3.50	Ccdc120	2.84
Hlf	18.37	Ccdc58	4.84	Lysmd2	3.50	Col9a3	2.84
Pcdhgb5	18.20	Slc45a3	4.81	Ranbp1	3.48	Pde4c	2.84
Aff3	18.16	Senp8	4.81	Klc2	3.46	Gzmm	2.84
Npas4	17.06	**Pax5**	**4.81**	Arpc5l	3.45	Nudt2	2.84
Prnp	16.19	Spryd7	4.81	Lamtor2	3.44	Sdc4	2.84
Lancl3	15.31	Tesk1	4.81	Tcof1	3.43	Nsun5	2.84
Ctnnbip1	14.89	Wrb	4.81	Kif20a	3.43	Aven	2.84
Prkg1	14.88	Ankrd24	4.81	Paqr7	3.40	Slc25a5	2.84

Dctd	14.87	Cth	4.81	Med30	3.40	**Fen1**	**2.83**
Sh3bp5	14.44	Matk	4.81	Msl3	3.40	Gspt1	2.83
Il6ra	14.44	Gm5607	4.81	Usp40	3.39	Cenpi	2.82
Traf4	14.44	Gemin2	4.81	**Npat**	**3.39**	Ddx51	2.82
Sorbs3	14.00	Fam102a	4.81	Cxcr6	3.39	Fbl	2.82
Ccdc8	14.00	Kcnk12	4.81	**Fbxo32**	**3.39**	Tmem205	2.82
Abcb1b	14.00	Gm5617	4.81	Ndufa5	3.39	Uri1	2.82
Itih5	14.00	Rom1	4.81	Noa1	3.39	Rbms1	2.81
Fam184b	14.00	**Klf9**	**4.81**	Rabl3	3.39	Zfp367	2.81
Jdp2	13.94	**Camk1d**	**4.81**	Crtam	3.39	Taf5l	2.81
Tanc2	13.78	Pdcd4	4.81	Kctd1	3.38	Bbip1	2.81
Tox	13.56	Fam136a	4.72	Atp8b2	3.38	Vps8	2.81
Vegfb	13.13	Fam3a	4.70	Gnpda2	3.37	Dctpp1	2.81
Tnks1bp1	13.13	Mpc2	4.70	Glrx3	3.36	Cisd1	2.80
Ryr1	12.91	Trmt44	4.70	Rbm4b	3.35	Arl2	2.80
Rogdi	12.69	Cd160	4.70	Nnt	3.34	Nr1d2	2.80
Nme6	12.25	Sqle	4.68	Fopnl	3.34	Gpn1	2.80
Tspan33	12.25	Ndufaf4	4.68	Fam92a	3.34	Rangrf	2.80
Coro2a	12.10	Lsm5	4.67	**Eef1d**	**3.33**	Trit1	2.80
Diras2	11.92	**Blnk**	**4.67**	Med29	3.32	Mrpl28	2.80
Gm13139	11.45	Dnph1	4.67	Mtfr1	3.31	Wbscr16	2.80
Arhgap22	11.38	Syce2	4.64	Gas2l3	3.31	Akr7a5	2.80
Rpp40	11.37	**Elmo1**	**4.62**	Exoc6b	3.31	Aldh6a1	2.80
Pyurf	11.37	Commd10	4.62	Gcat	3.31	Fam134b	2.80
Tmem108	11.37	Echs1	4.61	St3gal5	3.31	Rcsd1	2.79
Dach1	11.23	Slpi	4.59	Igsf8	3.31	Mrpl9	2.79
Plxnb2	10.79	Cryl1	4.59	Lsm3	3.30	Gm10052	2.79
Ndnf	10.79	Suox	4.59	Elac2	3.30	Ubald2	2.78
Dtna	10.79	Gpr65	4.59	Il1r1	3.28	Lig4	2.78

Spata24	10.67	Vwa8	4.58	Tnfrsf18	3.28	Pdss1	2.78
Phpt1	10.65	Emb	4.56	Slc25a15	3.28	Tsga14	2.78
Exoc3l4	10.65	Eny2	4.55	Bsn	3.28	Sgpp1	2.78
Triqk	10.51	Ttll5	4.55	Ift122	3.28	**Nup93**	**2.78**
Fbxw4	10.50	Usp10	4.53	Grwd1	3.28	Rpa2	2.78
Ccdc107	10.50	Wnk4	4.52	Trim34b	3.28	Shmt2	2.77
Nubpl	10.50	Pcbd2	4.52	Syde1	3.28	Sh3kbp1	2.77
Rxra	10.06	Serf1	4.52	Fitm2	3.28	Snx20	2.77
Icos	10.06	Selp	4.47	Fam108c	3.28	Snhg3	2.77
Pcdhgb7	9.91	Eefsec	4.46	Galnt11	3.28	Xkr6	2.77
Sdc1	9.84	Prlr	4.45	Klhl11	3.28	Rab30	2.77
Zfp771	9.77	Parl	4.45	6-Sep	3.28	H2-DMb1	2.77
Ttc8	9.64	Ikbkap	4.44	Serpinb1a	3.26	Fktn	2.77
Nme4	9.63	Impdh1	4.43	Ppapdc2	3.26	Fam110c	2.77
Pde7b	9.62	Chdh	4.42	**Banf1**	**3.26**	Nudt19	2.77
Mgll	9.46	Tgoln2	4.40	Hlx	3.25	N4bp2l1	2.77
BC017612	9.41	Atat1	4.38	Cox20	3.24	Tgm4	2.77
Slc25a13	9.41	Endou	4.38	Zfp524	3.24	Heatr1	2.77
Phgdh	9.30	Fgfr3	4.38	Slc26a2	3.24	Rab38	2.76
Acer2	9.26	Myo18b	4.38	Lias	3.23	Tuba1b	2.76
Ncr1	9.26	Camsap3	4.38	Oxct1	3.22	Dock9	2.76
Zfp251	9.19	Mfng	4.38	Grlf1	3.22	Pam	2.76
Pde3b	9.19	Efcab11	4.38	Nt5c3l	3.22	**Cad**	**2.76**
Cxcr3	9.19	Mrm1	4.38	Tubb2b	3.21	Ocel1	2.76
Als2cl	8.75	Zfp583	4.38	Hspbp1	3.21	Ap5m1	2.75
Oxld1	8.75	Hk2	4.37	Lrrc16a	3.21	Lmnb1	2.74
Stbd1	8.75	Xrcc2	4.37	Mcm8	3.21	Cdyl	2.74
Dtx4	8.75	Cdk5r1	4.37	Tst	3.21	Srm	2.74
Cep170b	8.75	Pard6g	4.37	**Rag2**	**3.21**	Cdc23	2.74

Opn3	8.75	Crebl2	4.37	Polr2h	3.21	Grsf1	2.73
Shroom4	8.75	Alkbh8	4.37	Pusl1	3.21	Pfas	2.73
Mettl13	8.53	Phf19	4.37	Mta1	3.20	Hmgxb4	2.73
Slc38a1	8.45	Slc22a21	4.37	Utp15	3.20	Uck2	2.73
Hmgn3	8.44	Cisd3	4.37	Serinc3	3.19	Sgcb	2.73
Glce	8.38	Mpnd	4.37	Lactb	3.19	Gfod1	2.73
Ptpn4	8.31	Eid2	4.37	**Nop16**	**3.18**	Mpp6	2.73
Klk8	8.31	Il1rl1	4.37	Ruvbl2	3.18	Lsm12	2.73
Gemin6	8.31	Gins1	4.37	Lrrn3	3.18	Fxyd5	2.73
Pygm	8.31	Sfxn3	4.34	Helq	3.17	Snhg12	2.72
Nedd4l	8.30	**Fkbp5**	**4.32**	Atg14	3.17	Ndufb4	2.72
Gng10	8.27	Apex1	4.31	Gstm5	3.17	**Rag1**	**2.72**
Gata3	8.09	Cep63	4.30	BC027231	3.17	Ifi30	2.72
Nbea	8.09	Ercc6l	4.30	Fam120c	3.17	Npm1	2.72
Rsph9	8.09	Tmc4	4.27	Cbfb	3.17	Hars2	2.71
Il12a	**8.06**	Ly86	4.27	Nde1	3.16	Clpx	2.70
Pcdhga10	8.04	Pdk1	4.27	Tpgs2	3.15	Anapc7	2.70
Pcdhga4	8.04	Cenpm	4.25	Nat2	3.15	Impdh2	2.70
Prokr1	7.98	Abcc4	4.24	Asf1a	3.15	**Ebf1**	**2.70**
Ggct	7.88	Id2	4.23	Grhpr	3.15	Smn1	2.69
Ammecr1	7.88	Rras2	4.23	Abhd8	3.15	Gtf2b	2.69
Slc27a1	7.87	Jakmip1	4.23	Mettl10	3.15	Zfp930	2.69
Ydjc	7.73	**Il18r1**	**4.22**	Rrp1b	3.14	Mad1l1	2.69
Rdh10	7.66	Il2rb	4.21	Ankrd32	3.14	Atp1b3	2.69
Yap1	7.55	Dis3	4.20	Klrb1f	3.14	Klf16	2.68
Asns	7.54	Pacs2	4.19	Tomm5	3.14	Actr1b	2.68
Lpar6	7.52	Gnl3	4.19	Vps9d1	3.14	Mrps14	2.68
Bean1	7.44	Hmgcs1	4.18	Dak	3.14	Nek2	2.68
Syne2	7.44	Ppp1r26	4.16	BC002163	3.14	Nop58	2.68

Oit3	7.44	Fam199x	4.16	Mpp7	3.13	Mif	2.67
Pnp2	7.44	Dse	4.16	Cdk4	3.13	Hells	2.67
Rabl2	7.44	Mtap7d3	4.16	Bola2	3.13	Suclg2	2.67
Mllt4	7.44	Ermap	4.16	Rara	3.13	Cep97	2.67
Gimap7	7.44	Dkkl1	4.16	Acyp1	3.13	Wdr43	2.66
Tnfaip2	7.44	Pxdc1	4.16	Hsd17b4	3.13	Bckdhb	2.66
Cd96	7.44	Ccdc102a	4.16	Rnf219	3.13	Zscan21	2.66
Txnrd3	7.33	Prodh	4.14	Mnd1	3.12	Racgap1	2.66
Gcsh	7.31	Dnajc19	4.13	Styx	3.12	Wdr18	2.66
Gbe1	7.22	Polr1b	4.13	Hmgb3	3.11	Polr3b	2.66
Lta	7.22	Katnb1	4.12	Emg1	3.11	Tmem176a	2.66
Lef1	**7.06**	Sphk1	4.11	Tk1	3.11	Ergic2	2.66
Nudcd1	7.00	Abcd3	4.11	Mcm4	3.11	Chek2	2.66
Cd22	**7.00**	Znrf2	4.09	Rbm12	3.11	Hmgb1	2.66
Sez6l2	7.00	Ddx28	4.08	Ergic1	3.10	Mad2l1	2.65
Tmem107	7.00	Ccdc135	4.08	Xrcc1	3.10	Fdps	2.65
Xlr	7.00	Cpne2	4.08	Rcbtb2	3.10	Glud1	2.65
Mtus2	7.00	Pmvk	4.06	Tmem201	3.10	Kcnj5	2.65
Fam84b	7.00	Dkc1	4.05	Tmem97	3.09	Ppp2r5e	2.65
Tbx21	7.00	Scd2	4.04	Eif2ak4	3.09	Elovl6	2.65
Exosc6	6.94	Wwc2	4.03	Nolc1	3.08	Myo5a	2.65
Bcl2	6.91	Mterfd1	4.03	BC052040	3.06	Pelp1	2.65
Mrpl47	6.89	Bcl7c	4.03	Homez	3.06	**Il7r**	**2.65**
Cbx6	6.89	Alpl	4.02	Pogk	3.06	Mrto4	2.64
Cd27	6.80	Rpap3	4.01	Snx16	3.06	Chst11	2.64
Rps6ka5	6.78	Lsm7	4.01	Slc14a2	3.06	Snrpf	2.64
Klhl7	6.77	Fam105b	4.00	Ldlrad3	3.06	Amigo1	2.63
Arhgap26	6.71	Slc29a1	4.00	Dcdc2c	3.06	Ak4	2.63
Dna2	6.62	Cox19	3.99	Nr2c1	3.06	Trmt1	2.63

Tifab	6.56	Ccdc86	3.99	Faah	3.06	Smoc1	2.63
Erlin1	6.56	Snrpg	3.97	Mthfs	3.06	Cacna1a	2.63
Gpr132	6.56	Acpp	3.94	Ghrl	3.06	Sema6b	2.63
Mex3a	6.56	Neo1	3.94	Lrfn4	3.06	Gnal	2.63
Dsel	6.56	Ska1	3.94	Gpr25	3.06	Morc4	2.63
Tcam1	6.56	Zfp839	3.94	Cpne5	3.06	Dgkh	2.63
Cyp26a1	6.56	Aldh7a1	3.94	Mccc1	3.06	Itfg3	2.63
Itm2a	6.56	Ppp1r9a	3.94	Lin52	3.06	Troap	2.63
Slc25a47	6.56	Nek6	3.94	Awat2	3.06	Rtkn	2.63
Cd28	6.56	Gm13212	3.94	Itpka	3.06	B3gnt9	2.63
Trpc6	6.54	Kremen1	3.94	Cog5	3.06	Trim45	2.63
Aprt	6.47	Fam129b	3.94	Rpl22l1	3.06	Alg14	2.63
Calhm2	6.42	Lats2	3.94	Agpat9	3.06	E030024N20Rik	2.63
Adcy5	6.42	Dbp	3.94	D19Ertd737e	3.06	Ccdc28a	2.63
Lrrc1	6.35	Dtl	3.94	Rbp1	3.06	Cntln	2.63
Ptrhd1	6.34	Rora	3.94	Plagl1	3.06	Agpat4	2.63
Sc5d	6.34	Acy3	3.94	Mrpl35	3.06	Haus1	2.63
Kif13b	6.34	Socs5	3.94	Gm3414	3.06	Gm9958	2.63
Taf4b	**6.34**	Slc16a2	3.94	Cd276	3.06	Ndufaf2	2.63
Trpc2	6.34	Tecpr1	3.94	Zfp28	3.06	Tmem245	2.63
Fmnl3	6.27	Vstm5	3.94	Sh3tc1	3.06	Prss36	2.63
Gemin8	6.20	Mrgpre	3.94	Zfp963	3.06	E2f3	2.63
Cnn3	6.19	Maged1	3.94	Msh3	3.06	Gria3	2.63
Serpine2	6.16	Neb	3.94	Fv1	3.06	Gja1	2.63
Mfge8	6.13	Trim62	3.94	Tmem27	3.06	Pecr	2.63
Adssl1	6.13	Hsd17b7	3.94	Zfp958	3.06	Ttc26	2.63
Aoah	6.13	Neil1	3.94	Aste1	3.06	Xcr1	2.63
Egln3	6.13	Sv2a	3.94	Chst15	3.06	Gm5506	2.63

Zfp772	6.13	Rarb	3.94	Dpep2	3.06	Zfp521	2.63
Ticam2	6.13	Ppm1f	3.94	Rcbtb1	3.06	H1f0	2.63
Shf	6.13	Pdp2	3.94	Gas2	3.06	Decr2	2.62
Zfp119b	6.13	Ceacam19	3.94	Trmu	3.06	Fndc3b	2.62
Gpc4	6.13	Slc26a1	3.94	Leng9	3.06	Afmid	2.62
Foxo1	**6.12**	Armc2	3.94	Zfp667	3.06	Heg1	2.62
Atp5s	6.12	Ccr6	3.93	Zfp689	3.06	Dph2	2.62
Fggy	6.12	Cplx2	3.91	Pabpc4	3.05	Zfp760	2.62
Sdc2	6.12	Rundc3a	3.91	Itgb5	3.04	Pigf	2.62
Tnfrsf19	6.02	Kcnk6	3.89	**Thy1**	**3.03**	Gpx8	2.62
Hddc2	5.98	Jrkl	3.89	Ltb	3.03	Evpl	2.62
Rcc1	5.96	Sap25	3.88	Csda	3.03	Tma16	2.62
Cep55	5.93	Smyd5	3.87	Chm	3.03	Adipoq	2.62
Atn1	5.91	Tsen15	3.86	Cenpn	3.02	Saysd1	2.62
Ttc32	5.91	Gtf2f2	3.84	Slamf6	3.02	Qtrt1	2.62
Zc2hc1a	5.91	Pdss2	3.84	Mmp19	3.02	S1pr4	2.62
Polr2d	5.90	Mmgt1	3.83	Entpd5	3.02	Mir703	2.62
Ctsc	5.88	Heatr3	3.82	Magoh	3.02	Plcl1	2.62
Arpp21	5.86	Tyw5	3.81	Mrpl11	3.02	Clec4a1	2.62
Thap3	5.83	Hyi	3.79	Pycrl	3.02	Pycr1	2.62
Mettl1	5.80	Zdhhc8	3.79	Ccnh	3.02	Spryd4	2.62
Trmt61a	5.78	Nabp1	3.79	**Nasp**	**3.02**	Trib3	2.62
Cdkl3	5.75	Polr3g	3.79	Ms4a4b	3.01	Gm13375	2.62
Trip13	5.74	Aim2	3.79	Sc4mol	3.01	Arhgef39	2.62
Rnf128	5.69	Fdft1	3.78	Nsun2	3.01	Col7a1	2.62
Zfp1	5.69	Klhl5	3.76	Satb1	3.01	Tipin	2.62
Rorc	5.69	Ecsit	3.76	Sgol2	3.00	Emr4	2.62
Prickle3	5.69	Endod1	3.76	**Bcl2l11**	**3.00**	Hmgn2	2.62
Psma8	5.69	Rala	3.76	Parp8	3.00	Rps2	2.61

Tmem37	5.69	Wdr61	3.75	Rps15a-ps6	3.00	Pno1	2.61
Hspa1l	5.69	**Mettl2**	**3.74**	Elp3	3.00	Sms	2.60
Gm13152	5.69	Zfp947	3.72	**Marcks**	**3.00**	**Park7**	**2.60**
Cradd	5.69	Tmem42	3.72	Cisd2	2.99	Slc16a1	2.60
Fuom	5.69	**Klf4**	**3.72**	Prdx1	2.99	Nup210	2.59
Med18	5.69	Gm14322	3.72	St8sia4	2.98	Pkd2l2	2.59
Fdxacb1	5.69	Ring1	3.72	Zfp935	2.98	Insr	2.59
Bag2	5.69	Cd1d1	3.72	Ckap2	2.98	Smad2	2.58
Man1c1	5.69	**Skp2**	**3.72**	**Ets1**	**2.98**	Zdhhc16	2.58
Gan	5.69	Rbm3	3.71	Upf3a	2.98	Ercc8	2.58
Sestd1	5.69	Gpr114	3.71	Mrpl54	2.97	Csrp2	2.58
Gar1	5.63	H2afy	3.70	Nufip1	2.97	Me2	2.58
Rpa3	5.60	**Scap**	**3.70**	Ncl	2.96	Ppat	2.58
Chchd10	5.59	Fam172a	3.69	Tsfm	2.96	Zc3h3	2.58
Lss	5.58	Ift57	3.69	B3gnt5	2.95	Gpatch4	2.57
Mlh3	5.54	Pcca	3.69	**Fxn**	**2.95**	Zfp706	2.57
Psd3	5.48	Gpsm2	3.69	Socs6	2.95	Coq3	2.57
Rhd	5.47	Cnih	3.69	Pemt	2.95	Tubb2a	2.57
Dhcr7	5.47	Asf1b	3.68	Ebpl	2.95	Gimap3	2.57
Tmem8	5.47	Ppp3cb	3.68	Qtrtd1	2.95	Fuca2	2.56
Ccdc57	5.47	Phtf2	3.68	Trmt10c	2.95	Klhl20	2.56
Lrp5	5.47	Nudt16l1	3.67	Ints10	2.95	Pex7	2.56
Acvr1b	5.47	E2f7	3.66	Haus4	2.95	Sssca1	2.56
D030028A08Rik	5.47	Pfdn4	3.66	Prmt6	2.95	Hspd1	2.56
Uevld	5.42	Tmem237	3.65	**Parp1**	**2.95**	Cluh	2.56
Tespa1	5.40	BC035044	3.65	Mical1	2.94	**Runx2**	**2.55**
Gfra2	5.40	Igsf3	3.65	Mrpl15	2.94	Mtx3	2.55
Acat2	5.40	Klhl12	3.63	Hsf2	2.94	**Chaf1b**	**2.55**

Tep1	5.40	Bmp2	3.63	**Nuf2**	**2.94**	Myg1	2.55
Eml4	5.38	**Nup37**	**3.62**	Hspa9	2.94	Klhl25	2.55
Hmgn1	5.30	Laptm4b	3.61	Adss	2.93	Cd79a	2.55
Plcb1	5.25	Siva1	3.60	**Eef1e1**	**2.93**	Ndufc2	2.55
Cep78	5.25	Rad51ap1	3.59	Slc7a6	2.93	Tbc1d10c	2.55
Immp2l	5.25	Timm8a1	3.59	Thoc7	2.92	Man1a	2.55
Bok	5.25	**Lat2**	**3.59**	Gnb1l	2.92	Dut	2.54
Cbx2	5.25	Crybg3	3.59	**Atf7**	**2.92**	Gtse1	2.54
Kbtbd11	5.25	Lancl2	3.59	Taf13	2.92	Isg20l2	2.54
Zfp462	5.25	Armc7	3.59	Ftsj3	2.92	Tbrg4	2.54
Gm129	5.25	Gmds	3.55	Ndst1	2.92	Tysnd1	2.54
Csad	5.25	Peo1	3.55	Cryz	2.92	Rps23	2.54
Zfp455	5.25	Aamdc	3.54	Xrcc6bp1	2.92	Mmd	2.54
Acot2	5.25	**Xpo4**	**3.54**	**Zeb1**	**2.92**	Gpr171	2.54
Trmt5	5.25	Prps1l3	3.54	Hspb11	2.92	Lrrc40	2.54
Gpr183	5.25	Slc4a7	3.54	Zfp870	2.92	Elp2	2.54
Card6	5.25	Timm21	3.54	Phldb1	2.92	Zfp395	2.54
Fra10ac1	5.25	Tmem48	3.53	Rwdd2b	2.92	Las1l	2.54
Habp4	5.25	Rarg	3.52	**Erh**	**2.91**	Alkbh4	2.54
Tmem191c	5.25	Mcoln2	3.50	**Prep**	**2.91**	Rpl22	2.54
Mrpl2	5.17	Enox1	3.50	Aga	2.91	Gm10069	2.53
Fabp5	5.16	Fchsd2	3.50	Prmt7	2.91	Gpam	2.53
Nav1	5.14	Gng2	3.50	Ext2	2.90	Rassf2	2.53
Ldlr	5.13	Lysmd4	3.50	Zfp362	2.90	Peg10	2.53
Txk	5.04	Tmem106c	3.50	Lactb2	2.90	Yipf5	2.52
Kank3	5.03	Thnsl1	3.50	Ly9	2.90	Pcp4l1	2.52

Appendix Vb

RNA-seq in common lymphoid progenitors (CLPs)
Most Up-regulated in *Mef2c* KO

Bold: myeloid genes

Red: B cell genes

Gene name	KO/WT ratio	Gene name	WT/KO ratio	Gene name	WT/KO ratio	Gene name	WT/KO ratio
Cxcl9	**98.29**	Ccrl2	7.10	Parp12	4.31	Ptplad2	3.11
Muc6	77.71	Prkab1	6.99	**Meis1**	**4.31**	Cd99l2	3.10
Ift172	77.71	Tbc1d8	6.99	Sp100	4.31	Ogfod2	3.09
Beta-s	73.90	Gbp5	6.96	Ccdc82	4.30	Setdb1	3.09
Rap1gap2	68.57	Tef	6.92	Serinc5	4.27	Fbxo2	3.09
Rps27	67.39	Trim2	6.87	Ppifos	4.27	Ticam1	3.09
Mx1	67.04	Csrp3	6.86	Srcrb4d	4.24	Slc25a19	3.08
Ear1	66.29	Enpp5	6.86	Ccng1	4.24	Gm4070	3.08
Hp	65.14	Lrrc27	6.86	Cited4	4.23	Frrs1	3.08
F630028 O10Rik	60.57	Slc46a3	6.86	Nhlrc2	4.22	Tax1bp3	3.08
Tmem106a	59.43	Zfp775	6.86	**Cd55**	**4.20**	Plxnc1	3.07
Lingo1	59.43	Il4ra	6.86	Colec12	4.19	Vash1	3.07
Il18bp	58.12	Gpr157	6.86	Dnase2a	4.19	Usp22	3.07
Ccdc130	57.14	Clock	6.86	Pydc3	4.19	Zscan29	3.07
Serpine1	56.69	Samd10	6.86	Atraid	4.19	Tdrd7	3.06
Gp49a	54.86	Slc28a2	6.86	Col4a1	4.19	Samd9l	3.05
Mtus1	53.74	Thap6	6.86	Rapsn	4.19	Ubr4	3.05
Syt13	50.69	Dnalc1	6.86	Enox2	4.17	Sulf2	3.05
Gm12185	50.29	Mier2	6.86	Khnyn	4.16	Phyhd1	3.05
Serpina3h	48.00	Ephb2	6.86	Hsdl2	4.16	Kcnn4	3.05
Batf2	46.86	C2	6.86	**Csf2ra**	**4.16**	Kif5a	3.05
Scn1b	45.26	Dpp7	6.86	Tle1	4.16	Zfp229	3.05

Ap5s1	43.42	Acad8	6.86	Ms4a6c	4.15	S100pbp	3.05
Hba-a1	42.57	Slc3a1	6.86	Spo11	4.11	**Scai**	**3.05**
Ddx60	39.51	Rhbdl3	6.86	Cped1	4.11	Ganc	3.05
Atp9a	38.86	Ccdc64	6.86	Tceanc2	4.11	Actr6	3.05
Lrg1	38.86	Lynx1	6.86	Gm13154	4.11	Sema4c	3.05
Pmp22	38.29	Mcmdc2	6.86	Clec4d	4.10	Fbxl15	3.05
Zbp1	37.07	Cd2	6.86	Bcas3	4.10	Ahr	3.05
Plk3	36.57	Map2k6	6.86	Stk10	4.10	Cd68	3.05
Hspb8	36.00	Pstpip2	6.86	Tcirg1	4.08	Cdkn2c	3.05
Xdh	35.05	Hist1h2bn	6.86	Pou2f2	4.06	Sdcbp2	3.05
Wdsub1	34.92	E030030I06 Rik	6.86	Ifnar1	4.06	Rnf167	3.05
Hbb-y	34.29	Zfp827	6.86	Cbfa2t2	4.06	D330023K1 8Rik	3.05
Hbq1b	32.00	Zfp346	6.86	Adamts3	4.06	Ifngr2	3.05
Csf3r	30.24	Herc3	6.86	Cdk5	4.06	Ccdc163	3.05
Errfi1	29.71	Aoc2	6.86	Crebbp	4.06	Ppm1h	3.05
Gm14047	29.71	Havcr2	6.86	Atg9a	4.06	Zfp780b	3.05
Col20a1	29.71	Maff	6.86	Tmem189	4.06	Cdc42bpg	3.05
Gprc5b	29.34	Xlr4c	6.86	H2-T23	4.05	Ghdc	3.05
Oas2	29.29	Gm8234	6.86	**Lima1**	4.05	Zfp952	3.05
Spta1	29.06	Smug1	6.86	Cd300a	4.05	Adam12	3.05
Clec4g	28.19	Mmp2	6.86	Nacc2	4.04	Slc36a1	3.05
Atg4c	27.89	Ly6g6f	6.84	Nkiras2	4.04	Styk1	3.05
Igsf6	27.43	Nlrp1b	6.83	Sp2	4.04	Malt1	3.05
Bloc1s4	27.43	Smox	6.82	Rgs14	4.03	Zfp874a	3.05
Ddb2	27.43	Col1a2	6.81	Hps4	4.03	Eya2	3.05
Camkk1	27.43	Trex1	6.70	Itga2b	4.02	Skil	3.03
Tlr3	27.43	Fcer1a	6.65	Atp6v0c	4.02	Bin1	3.03
Gm9895	27.43	Flt3l	6.56	Dnajb2	4.02	Klf2	3.02

Rab44	27.43	Cyba	6.53	Ccnyl1	4.00	Ninj1	3.02
Tg	27.41	Fcgr3	6.53	**Zfp7**	**4.00**	Cpne3	3.02
Irf7	26.73	Ift27	6.53	Igflr1	4.00	Gvin1	3.01
Ifit3	26.70	Ccl6	6.53	Myo1e	4.00	Ppfia1	3.01
Serpinb2	26.66	Ankrd16	6.53	Kntc1	4.00	Traf3	3.00
Col18a1	26.41	Nmnat3	6.51	Gm7609	4.00	Ppp1r9b	3.00
Ifi202b	25.17	Slc22a3	6.48	Prdm15	4.00	F2r	2.99
Ddhd1	25.16	Tgm2	6.48	Large	4.00	Bcl9	2.99
Tubb3	25.14	Ythdc2	6.48	Hps6	4.00	Gab1	2.99
Ly6c2	25.14	Ube2l6	6.45	Lrrc32	4.00	Ap4e1	2.99
Trim30d	24.88	Rnf180	6.44	Csf2rb	3.98	Pigyl	2.99
Mlkl	24.16	Mpo	6.40	Pycard	3.97	Tbcd	2.99
Gbp9	24.10	Reep6	6.40	Stoml1	3.97	Alg11	2.99
Zbtb6	23.62	Zmynd8	6.37	Psmf1	3.95	Ubap1	2.99
Hist1h2ac	23.53	Irgm1	6.36	Wdr67	3.95	Wdr59	2.97
Gbp3	23.38	Tnfsf12	6.36	Zfp275	3.95	Mtmr4	2.97
Prtn3	23.23	Vps37a	6.32	Usp37	3.95	Med13l	2.96
Grina	23.12	Slc24a6	6.29	Akap10	3.95	Lztr1	2.96
Qpctl	22.86	Zswim7	6.29	Tcp11l1	3.94	Clca1	2.96
Tctn1	22.86	Eif5a2	6.29	Carhsp1	3.94	Trim14	2.96
Mctp2	22.86	Ndst2	6.29	Zfp51	3.94	Tnrc6c	2.96
Iigp1	22.40	Adam19	6.29	Gypc	3.94	Itga2	2.95
H2-T22	22.24	Il17rb	6.29	Evi5l	3.92	Ormdl3	2.95
Agrn	20.80	Parp14	6.22	Snx18	3.92	Agtpbp1	2.94
Adam8	20.57	Bzrap1	6.20	Plekhg2	3.92	Ilk	2.94
Zfp810	20.57	Plvap	6.17	Trim34a	3.92	Gm10336	2.94
Serpina3n	20.57	Fbxw17	6.15	Lrp12	3.92	Abcd4	2.94
Adam22	20.57	Sardh	6.13	Slc18a2	3.91	Gm12839	2.94
Matn1	20.57	Tnfsf10	6.11	Wdr91	3.90	Dcaf6	2.94

BC051226	20.57	Ifit1	6.10	Zc3h12a	3.90	Sgsm3	2.94
B3galt6	20.57	Pld1	6.10	Kdm6b	3.90	Pms2	2.94
Fam198b	20.57	Azi1	6.10	Ifi47	3.89	Slfn9	2.94
Themis2	20.57	Fam46c	6.10	Flad1	3.89	Kcng2	2.94
Oas3	20.27	Psd	6.10	Cog7	3.89	Scarb2	2.93
Irgm2	19.74	Loxl3	6.10	Ssh2	3.89	Snx9	2.93
Gypa	19.57	Tsga10	6.10	Ascc3	3.88	Ubc	2.93
Kif3b	19.43	H2-K2	6.10	Afap1l1	3.87	**Fbxo9**	**2.92**
Cst7	19.31	Zfp677	6.10	Zfp513	3.87	**Mxd1**	**2.92**
Isg15	18.49	Wdr25	6.10	Zfp773	3.87	Rhbdf1	2.92
Ddah2	18.29	Tapbp	6.06	Itgb2	3.87	Dctn4	2.92
Mettl15	18.29	Bace1	6.05	Gm14446	3.86	Tapbpl	2.91
B230378P21Rik	18.29	Zfp518a	6.03	Tnfsf14	3.86	Anxa3	2.91
Ms4a4d	18.29	Dopey1	6.03	Ddit3	3.86	Vcpip1	2.91
Rbks	18.29	Osbpl7	6.03	**Il21r**	3.84	**Flot1**	**2.91**
Hdc	17.96	Flcn	6.01	Olfr56	3.84	Tbk1	2.90
Slfn1	17.83	Samhd1	6.00	Mdm2	3.84	Slx4ip	2.90
Tmem86a	17.83	Optn	5.97	St3gal4	3.83	Git1	2.90
Il1a	**17.48**	Mcf2l	5.91	F11r	3.82	Ube3b	2.90
Hpn	17.31	Igtp	5.87	Hk3	3.82	**Cd97**	**2.89**
Apbb2	17.14	Herc6	5.86	Pgs1	3.82	Gnb4	2.89
Ltbp2	17.14	Hace1	5.85	**Trim30a**	**3.81**	Ftl1	2.89
Gm11201	17.14	Ell2	5.84	Cd163	3.81	Fam117a	2.89
Ckap4	17.14	Lgals3bp	5.84	Pdlim2	3.81	Ifrd1	2.88
Ext1	16.91	Gadd45g	5.83	Cyb561d1	3.81	Cttn	2.88
Dmwd	16.76	Uba7	5.75	Gm16515	3.81	Clec9a	2.88
Mx2	16.57	Zfp14	5.72	Ccng2	3.81	Gm166	2.88
Bmp8a	16.01	Pilra	5.71	Grap	3.81	Adcy7	2.88
Tmem181c-ps	16.00	Chtf18	5.71	Rnf31	3.81	Zfc3h1	2.87

ps							
Katnal1	16.00	Zbtb49	5.71	Mex3d	3.81	Ninl	2.87
Zfp563	16.00	Acvr2a	5.71	Zdhhc15	3.81	**Tug1**	**2.87**
Plek2	16.00	Il1f9	5.71	Ptrh1	3.81	Stx5a	2.86
Tctn2	16.00	Fas	5.71	Fbxo36	3.81	Pigo	2.86
Tmprss7	16.00	Tmem143	5.71	Chst14	3.81	Rasd1	2.86
Gm20605	15.97	Mxra7	5.71	Gadd45b	3.81	Zfp27	2.86
Hist3h2a	15.91	Dpy19l4	5.71	Zfp90	3.81	**Braf**	**2.86**
Ear7	15.77	LOC100504703	5.71	Phf13	3.81	Akap8l	2.86
Elane	15.42	Col5a1	5.71	Zcchc4	3.81	Ly6f	2.86
Ifit2	14.98	Pyroxd2	5.71	Agt	3.81	Sdccag8	2.86
Il1rn	14.86	Plbd1	5.71	**Hoxa9**	**3.81**	Hemk1	2.86
Gm5595	14.86	Gtf2ird2	5.71	Appl2	3.81	St6galnac2	2.86
Pik3r2	14.86	Zfp30	5.71	Gabbr1	3.81	Ebi3	2.86
Gbp4	14.82	Cd300lb	5.71	Dgkq	3.81	Stab1	2.86
Gsdmd	14.55	Trpm4	5.71	Nmrk1	3.81	Taf1a	2.86
Rsad2	14.53	Tmem63b	5.71	Gm17745	3.81	St14	2.86
Rgag4	14.47	Nfil3	5.71	Galnt10	3.81	Arhgef11	2.86
Gbp6	14.22	Afap1	5.71	Zfp426	3.80	**Epor**	**2.85**
Vangl1	13.85	Ctns	5.71	Kdm5b	3.78	Ftsjd2	2.85
Acy1	13.73	Napepld	5.71	Xaf1	3.78	Trim12c	2.85
Sfmbt2	13.73	Abtb2	5.71	Mll3	3.78	Glipr2	2.85
Lpin1	13.72	Tango6	5.71	Snx30	3.77	Rab36	2.84
Cep95	13.72	Stat1	5.68	Pik3cb	3.77	Golga4	2.84
Gstm4	13.72	Sorbs1	5.68	Zfp507	3.77	Tspan32	2.84
Amot	13.71	Pnkp	5.65	Cebpa	3.77	Fam193b	2.83
Ercc5	13.71	Slc43a3	5.65	Parp10	3.76	Fam109b	2.83
Dleu2	13.71	Ptgir	5.64	Tssc1	3.76	Spns3	2.83
Padi4	13.71	Ttll1	5.62	H2-T9	3.76	Rev3l	2.83

Asic4	13.71	Hspa2	5.61	G6b	3.76	Nxpe2	2.83
Pabpc1l	13.71	Map1a	5.55	Acox3	3.76	Myo10	2.83
Gm10509	13.71	Cecr2	5.55	**Arf2**	3.75	Ifi203	2.83
Siah1b	13.71	Rab13	5.55	Plekhm1	3.75	Herc2	2.83
Rilp	13.71	Bgn	5.55	Fam220a	3.74	Htt	2.82
Rab3ip	13.71	Zfp276	5.52	Phc3	3.74	Smg9	2.82
Rhobtb2	13.71	Rras	5.52	Zfp120	3.74	Med22	2.82
D430020J02Rik	13.71	Mob3c	5.49	Fam122a	3.74	Tpst1	2.82
Gm4636	13.71	Synrg	5.49	Zfp710	3.73	Zbtb43	2.81
Fnip2	13.71	Tmem151b	5.49	Aftph	3.72	Mb21d1	2.81
Msantd2	13.71	Abcb9	5.49	Fam217b	3.71	Pomt2	2.81
Sapcd1	13.69	Mir5130	5.47	Adamtsl5	3.70	Slfn8	2.81
Gbp2	13.36	Dusp14	5.46	**Fcrl1**	**3.70**	Gpr160	2.81
Pot1b	13.33	Adrbk2	5.43	Phlda1	3.70	**Gfi1**	**2.80**
Egr1	13.24	Mll2	5.42	Snca	3.69	Stxbp3a	2.80
D030025P21Rik	13.14	Pdzk1ip1	5.42	Dennd4b	3.69	B2m	2.80
Lilrb4	13.14	Slc25a14	5.41	Gtpbp6	3.69	Stx16	2.80
Serpinb9	13.06	Adra2a	5.37	Fam65c	3.69	Zcchc6	2.80
Socs3	12.98	Depdc7	5.33	Gp6	3.68	Myef2	2.80
Ublcp1	12.95	Coil	5.33	Parp6	3.67	Gpm6b	2.80
Naglu	12.73	Hyal2	5.33	Mvp	3.67	Zfand2a	2.79
Fam46a	12.68	Ccl4	5.33	Tap1	3.67	Hist1h2be	2.79
Tulp4	12.57	Phf11b	5.33	Gas6	3.66	Flt1	2.79
Siglece	12.57	Zfp953	5.33	Gm17644	3.66	Polr3a	2.79
Nrxn2	12.46	Gnpda1	5.33	Sec14l2	3.66	Prpf4	2.79
Rab11fip3	12.20	Ltb4r1	5.33	Ppp1r16a	3.66	Tmem104	2.79
Efemp2	12.19	F830016B08Rik	5.33	Tmem161a	3.66	**Baz2a**	**2.79**
Mtfp1	12.19	Pcbp3	5.33	Zfp160	3.66	Nfkbie	2.78

Ctsh	12.19	Dst	5.33	**Relb**	**3.66**	Phactr4	2.78
Tuft1	12.00	Eno3	5.32	Lnpep	3.64	Zkscan14	2.78
Oas1g	11.92	Sparc	5.29	Plekha7	3.63	D11Wsu47e	2.78
Ptpn13	11.81	Zfp385c	5.29	Mfsd8	3.62	Kat6a	2.78
Tgtp2	11.78	Pafah1b3	5.27	Shkbp1	3.61	H2-Q4	2.77
Oasl1	11.77	Ccdc6	5.25	Ifi35	3.61	**Bcl2l1**	**2.77**
Mtss1l	11.46	Zfand4	5.24	Hba-a2	3.60	Prcp	2.77
Clec5a	11.44	Pnpla7	5.22	Sp110	3.59	Lgalsl	2.77
Apol9a	11.43	Them6	5.21	Zfp318	3.59	Vav3	2.77
Zfp688	11.43	Gm7120	5.20	S1pr3	3.59	**Xist**	**2.77**
Dusp18	11.43	Mlxip	5.19	Gpatch2	3.59	Furin	2.77
Slc12a9	11.43	Daxx	5.19	Brpf1	3.58	Vmn1r58	2.77
Mthfd2l	11.43	Cdc42ep2	5.18	Ctsg	3.58	Peli1	2.77
Otud3	11.43	Zfp672	5.18	Rffl	3.57	Zbed6	2.77
P2rx3	11.43	Thsd4	5.14	Siae	3.57	Asb7	2.77
Hgf	11.43	Ggt5	5.14	Lgals9	3.56	Slamf1	2.77
Ltc4s	11.43	Atp8b5	5.14	Otub2	3.56	Cep120	2.76
Adamts5	11.43	Kitl	5.14	Phf1	3.56	Acss1	2.76
Arl5b	11.43	Vcam1	5.14	B330016D10Rik	3.56	Tap2	2.76
Slc31a2	11.43	Cyp11a1	5.14	**Stx6**	**3.54**	Syvn1	2.75
Tlr2	11.43	Zbtb14	5.14	Morc3	3.54	Treml1	2.75
Cc2d2a	11.43	Tmem218	5.14	Letmd1	3.53	Fn1	2.75
Rapgef2	11.43	Itfg2	5.14	Ccdc30	3.53	Alox12	2.74
Tbc1d30	11.43	Ptp4a1	5.14	**Fcgr2b**	3.53	H2-Q7	2.74
Trem3	11.43	Rab11fip2	5.13	Rnf114	3.52	Bbs9	2.74
Gm16576	11.43	Capn1	5.12	Lysmd1	3.52	Pcgf2	2.74
Tcn2	11.40	Nlrc5	5.11	Klc4	3.52	Dyrk3	2.74
Serpina3f	11.30	Prss34	5.11	Sdc3	3.52	Dnahc11	2.74

Spp1	11.21	Dlg4	5.10	St3gal2	3.51	Zfp943	2.74
Stat2	11.18	Dolpp1	5.10	Crim1	3.50	Tefm	2.74
Oasl2	11.04	Gm8979	5.10	Egfl7	3.50	Msl3l2	2.74
Cysltr2	10.86	Igf2r	5.08	Zscan22	3.50	Tigd2	2.74
Ifitm1	10.86	Ms4a2	5.08	2-Mar	3.50	Zfp933	2.74
Dnmbp	10.86	Slc8a1	5.03	Gpr107	3.50	Dgat1	2.74
Isg20	10.78	Fam109a	5.03	**Ly6e**	**3.50**	Naip6	2.74
Fam73b	10.78	Gm6034	5.03	Pim1	3.49	Pacsin1	2.74
Gm9199	10.67	Atp1b2	5.03	Blvrb	3.49	Mknk1	2.74
Cp	10.61	Pramef8	5.03	Ttc39b	3.49	Med13	2.74
Atp6v0a1	10.43	Nat6	5.03	Tmem9	3.48	Ap1b1	2.73
Mib2	10.29	Fam160b2	5.03	Kdm6a	3.48	Apaf1	2.73
Popdc2	10.29	Parp3	5.03	Fam110b	3.48	Casp8	2.73
Irak2	10.15	Hexa	5.02	Wdfy3	3.47	Man2b1	2.73
Ifi44l	10.11	**Irs2**	**5.01**	Cish	3.47	Wdr11	2.72
Gm4951	10.06	Lrrc8a	5.00	Esam	3.46	Fam129c	2.72
Apbb1	10.06	Cass4	4.99	Slc9a1	3.46	Gbx2	2.72
Pak6	10.05	Gpr146	4.99	Slc25a24	3.46	Ctsd	2.72
Prom1	10.04	Rab11fip1	4.96	Plac8	3.46	Hmgxb3	2.71
Gem	10.02	Dusp19	4.95	Pitpnc1	3.45	Mark4	2.71
Ddc	9.91	Tonsl	4.95	Cdc42ep5	3.45	Zfp605	2.71
Mgst1	9.90	Nudt13	4.95	Ano10	3.44	**Map2k1**	**2.71**
Trmt10b	9.90	Ppp1r12b	4.95	Ifih1	3.44	Zfp654	2.71
Syn3	9.90	**Tspo**	**4.94**	Fam221a	3.43	Arhgap23	2.71
Iffo2	9.82	Hsh2d	4.92	Ank1	3.43	Smg7	2.70
Ttbk2	9.72	Oas1b	4.92	Pydc4	3.43	Eml2	2.70
Zranb3	9.70	Oraov1	4.90	**Fcrla**	**3.43**	Hpse	2.70
Gstt1	9.66	Agtrap	4.89	Tspan8	3.43	Draxin	2.70
Pglyrp1	9.65	Dync1li2	4.89	Cdc14b	3.43	Abhd12	2.70

Vps13c	9.52	Slc24a5	4.86	Dmpk	3.43	Ric8b	2.70
Sult4a1	9.42	Polk	4.86	Zdhhc12	3.43	Synj1	2.69
Ddx58	9.36	Polm	4.83	Tmem161b	3.43	Szt2	2.69
Pnpla6	9.25	Tnnt1	4.83	Tbc1d25	3.43	Plscr1	2.69
Grn	9.23	**Cxcr2**	**4.82**	Rhou	3.43	Chd6	2.69
Kif1a	9.15	Plod1	4.80	**Pbx3**	**3.43**	**Il1b**	**2.68**
Itgam	9.15	Parp11	4.78	**Notch2**	**3.43**	Atf6	2.68
Btbd6	9.15	Trem1	4.76	Gipc2	3.43	Klhl24	2.68
Fastkd5	9.14	Sirt3	4.76	Ucn2	3.43	Aagab	2.68
Zfp790	9.14	Mcpt8	4.75	Ptprv	3.43	Ctsz	2.68
Selenbp1	9.14	**Mlx**	**4.73**	Dnahc8	3.43	H2-Q9	2.67
Tas1r3	9.14	Nupr1	4.72	Spata1	3.43	Abhd14b	2.67
Fbxl22	9.14	**Fosb**	**4.72**	Plag1	3.43	Gfpt1	2.67
Rsph3b	9.14	Slfn2	4.71	Efcab5	3.43	Taf1c	2.67
Zbtb38	9.14	Fam78a	4.70	Ephx4	3.43	Gstm2	2.67
Nbeal1	9.14	Oas1a	4.69	Kctd7	3.43	Grtp1	2.67
Epb4.2	9.14	Daglb	4.69	Rnase6	3.43	Gm8773	2.67
Erich1	9.14	H2-Q5	4.67	Snord89	3.43	Psmc3ip	2.67
Tpcn2	9.14	**Galns**	**4.66**	Lyrm7	3.43	Atp8b4	2.67
Pik3c2b	9.14	**Ncor2**	**4.63**	Dcp1b	3.43	Thra	2.67
Angptl4	9.14	Tnfaip3	4.62	Gjc3	3.43	Alpk1	2.67
Avil	9.14	Pfkfb2	4.61	**Igf1r**	**3.43**	Rft1	2.67
Fam101b	9.14	**Trafd1**	**4.60**	Rin1	3.43	Ttll3	2.66
Trpm2	9.14	Dhx58	4.59	Cyp4x1	3.43	**Mll1**	**2.66**
Snora81	9.14	Serac1	4.58	Tcp11l2	3.43	Gm5643	2.64
Pde1b	9.14	Nrap	4.57	Atxn7l2	3.43	Rnf19b	2.64
Bcl6	9.14	Arhgef10	4.57	Lenep	3.43	Jmjd8	2.64
Spa17	9.14	Emc1	4.57	Hsd17b14	3.43	Tle6	2.64
Il7	9.14	Gm1976	4.57	Gm6313	3.43	Aldh1a1	2.64

Cdh17	9.14	**Ciita**	**4.57**	Zbtb10	3.43	Adal	2.64
Cnbd2	9.14	E230016K23 Rik	4.57	Plxnb3	3.43	Steap4	2.64
Trim21	9.09	Pvrl4	4.57	Abca5	3.43	Ube4a	2.63
Gm12250	9.09	Sall2	4.57	Tnfsf9	3.43	Dennd2d	2.63
Usp18	9.07	B3galt5	4.57	Foxj2	3.43	P2ry14	2.63
Bst2	8.96	Chpf	4.57	Zfp316	3.43	Slc25a43	2.63
Gm14005	8.94	Dcn	4.57	Cachd1	3.43	R3hdm1	2.63
Cpeb4	8.90	Fgfrl1	4.57	Suco	3.43	S100a11	2.63
Lypd1	8.86	Rhbdd1	4.57	B3galt4	3.43	Rufy1	2.62
Lrrk1	8.86	Snx11	4.57	Zfp867	3.43	Dnpep	2.62
Csf2rb2	8.82	Ppp1r3f	4.57	Shpk	3.43	Gramd1a	2.62
Cdkn1a	8.77	Ttn	4.57	Rsph3a	3.43	Dmtf1	2.62
Sfi1	8.74	Rabgef1	4.57	**Elk4**	**3.43**	Smpd1	2.62
Pcdh7	8.74	Zbtb24	4.57	Olfr613	3.43	Rasl10a	2.62
Ifi44	8.71	Mir3064	4.57	Aqp3	3.43	Atp6v0a2	2.62
Ptger2	8.57	Zfp169	4.57	Dkk3	3.43	Pram1	2.61
Mpp2	8.57	Phf11a	4.57	B4galt6	3.43	Mier1	2.61
Csf1	8.53	Tmem86b	4.57	Micall2	3.43	Rps4y2	2.61
Dtx3l	8.52	Pard6b	4.57	Apex2	3.43	**Tns4**	**2.61**
Dusp28	8.49	Dennd1c	4.57	Veph1	3.43	Hist2h2be	2.61
Phf11d	8.48	Trim56	4.57	Hspa1b	3.43	Ccdc14	2.61
Ms4a3	8.46	**Megf9**	**4.57**	Tnip2	3.43	Bcl2l12	2.61
Gm20594	8.41	Zfp286	4.57	Milr1	3.42	Nt5dc3	2.61
Htr2a	8.38	Pp2d1	4.57	Smim5	3.40	Gm4285	2.61
Cmpk2	8.38	**Lix1l**	**4.57**	Shisa5	3.39	Kif14	2.61
Bend4	8.23	Icam1	4.57	Lbh	3.39	Fbxl18	2.61
Rhoh	8.19	Tesk2	4.57	Acsf2	3.38	Rttn	2.61
Ly6g6c	8.16	Pex11c	4.57	Aldh3a2	3.38	**Tlr4**	**2.61**
Pias4	8.16	Zfp300	4.57	Cit	3.38	Slc35e4	2.61

Slco4a1	8.16	Ccdc171	4.57	Lepre1	3.38	Fam193a	2.61
Capn5	8.10	Zfp407	4.57	Spty2d1	3.37	Lpcat2	2.61
Hist1h1c	8.04	Cds1	4.57	Cdkn2d	3.37	Tyr	2.61
Rab17	8.03	Zmat1	4.57	Zfp646	3.37	Samd14	2.60
Ralgds	8.01	Sfxn4	4.57	Ceacam1	3.35	Sh3bgrl2	2.60
Irf1	8.00	Cenpv	4.57	Ppp1r3b	3.35	Asap2	2.60
Eva1b	8.00	Ccdc141	4.57	Nf1	3.35	Ctdnep1	2.60
Ttc38	8.00	Gpatch3	4.57	Zkscan3	3.35	Cacfd1	2.59
Pdpr	8.00	Nlrp3	4.57	Gna13	3.35	Ankzf1	2.59
Elmo3	8.00	Ldhb	4.57	Akap13	3.35	Pdk2	2.59
Rpgrip1l	8.00	Brip1	4.57	Ctla2a	3.35	Spred2	2.59
Ssh3	8.00	Nucb2	4.57	Fam21	3.35	Apeh	2.59
Hck	8.00	Btnl9	4.57	Scly	3.34	Slc38a10	2.59
Zfp691	8.00	Acacb	4.57	Ap3m2	3.34	Rint1	2.59
Helz2	7.91	Zfp3	4.57	Zfyve1	3.34	Frmd4a	2.59
Mtf1	7.87	Rtn4r	4.57	Layn	3.34	Pikfyve	2.58
Hist1h4i	7.84	**Il12rb2**	**4.57**	Parp9	3.33	Kcnk5	2.58
Tmem140	7.84	Gm20257	4.57	Tusc2	3.32	Ppp1r15a	2.58
Dusp10	7.81	Mylk4	4.57	Cpne8	3.32	Pi4k2b	2.58
Cxcl14	7.77	E130311K13 Rik	4.57	Plk1s1	3.32	Ecm1	2.57
Kat2b	7.67	Gstt3	4.57	Ap4b1	3.32	Acbd4	2.57
Dvl3	7.62	Tigd3	4.57	Lyz2	3.31	Ern1	2.57
Bsdc1	7.62	Gsta2	4.57	Fam188a	3.31	Gpbp1l1	2.57
Cdh11	7.62	Zfp784	4.57	Zbtb40	3.30	Gm19757	2.57
B430306N0 3Rik	7.62	Tmem150a	4.57	Wdr20a	3.29	Slc38a5	2.57
Igfbp5	7.62	**Cd38**	**4.57**	Tmc1	3.27	Tagap1	2.57
Adora2a	7.58	Zfp87	4.57	Zfp758	3.27	Tmf1	2.57
Pigw	7.56	Tbc1d10a	4.57	Atg4d	3.27	Tbc1d2	2.57

Bcorl1	7.51	Rps6ka2	4.57	Pus7l	3.27	Atxn7l1	2.57
Lime1	7.51	Snx32	4.57	Dnajc18	3.27	Npc1	2.57
Ksr1	7.50	St8sia1	4.57	Phf20	3.27	Kalrn	2.57
Nfkbid	7.43	Pla2g10	4.57	Tmem38b	3.25	Usp24	2.57
Apold1	7.43	Fam118a	4.57	Fchsd1	3.25	Spib	2.56
Gca	7.43	Fndc3a	4.57	Casp4	3.25	Polg2	2.56
Intu	7.43	Smim8	4.57	L3mbtl3	3.25	Acad11	2.55
Plp1	7.39	Ddr2	4.57	Gp9	3.25	**Ets2**	**2.55**
Gbp1	7.35	Cep152	4.57	Thbs1	3.24	Kif21b	2.55
Serpina3g	7.34	Arl11	4.57	Dock5	3.24	Tmem87b	2.55
Emilin2	7.34	Rad51c	4.57	Galt	3.24	Lepr	2.54
Tmcc2	7.34	Zcchc14	4.57	Spg11	3.24	Acaa1a	2.54
Slfn5	7.33	Cx3cl1	4.57	**Il2ra**	**3.24**	Entpd7	2.54
Znfx1	7.32	Abcg1	4.57	Msl1	3.24	**Bcl3**	**2.54**
Slc2a6	7.32	D330041H03Rik	4.57	H2-T24	3.23	Mylpf	2.54
Ptprn	7.16	Zdhhc1	4.57	Spns2	3.23	Pak4	2.54
Rusc2	7.16	Tnfrsf13c	4.57	Adnp2	3.23	Anxa1	2.54