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Molecular Landscape of Induced Reprogramming: A Dissertation

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MOLECULAR LANDSCAPE OF INDUCED REPROGRAMMING

A Dissertation Presented

By

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DEDICATION

In Memory of My Mother, Hsiu-Mei.

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ABSTRACT

Recent breakthroughs in creating induced pluripotent stem cells (iPS cells) provide alternative means to obtain embryonic stem (ES) cell-like cells without destroying embryos by introducing four reprogramming factors (*Oct3/4*, *Sox2*, and *Klf4*/*c-Myc or Nanog/Lin28*) into somatic cells. However, the molecular basis of reprogramming is largely unknown. To address this question, we employed microRNAs, small molecules, and conducted genome-wide RNAi screen, to investigate the regulatory mechanisms of reprogramming.

First we showed that depleting miR-21 and miR-29a enhances reprogramming in mouse embryonic fibroblasts (MEFs). We also showed that p53 and ERK1/2 pathways are regulated by miR-21 and miR-29a and function in reprogramming.

Second, we showed that computational chemical biology combined with genomic analysis can be used to identify small molecules regulating reprogramming. We discovered that the NSAID Nabumetone and the anti-cancer drug OHTM could replace Sox2 during reprogramming. Nabumetone could also replace c-Myc or Sox2 without

compromising self-renewal and pluripotency of derived iPS cells.

To identify the cell-fate determinants during reprogramming, we integrated a genome-wide RNAi screen with transcriptome analysis to dissect the molecular requirements in reprogramming. We found that extensive interactions of embryonic stem cell core circuitry regulators are established in mature iPS cells, including *Utf1, Nr6a1, Tdgf1, Gsc, Fgf10, T, Chrd, Dppa3, Fgf17, Eomes, Foxa2*. Remarkably, genes with non-differential change play the most critical roles in the transitions of reprogramming. Functional validation showed that some genes act as essential or barrier roles to reprogramming. We also identified several genes required for maintaining ES cell properties. Altogether, our results demonstrate the significance of miRNA function in regulating multiple signaling networks involved in reprogramming. And our work further advanced the reprogramming field by identifying several new key modulators.

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LIST OF ABBREVIATION

Induced pluripotent stem cell (iPS cell)

Somatic cell nuclear transfer (SCNT)

Oct4, Sox2, Klf4, c-Myc (OSKM)

MicroRNA (miRNA)

Small interfering RNA (siRNA)

miRNA inhibitor (antagomir)

RNA-induced silencing complex (RISC)

Embryonic stem cell (ESC)

Mouse embryonic fibroblast (MEF)

Mouse embryonic stem cell (MESC)

Human embryonic stem cell (hESC)

Non-steroidal anti-inflammatory drug (NSAID)

Histone lysine methylase/methyltransferase (HKMT)

Polycomb repressive complex (PRC)

PREFACE

This thesis comprises the following published and unpublished work.

Learning the molecular mechanisms of the reprogramming factors: let's start from microRNAs.

Yang CS, Rana TM. Mol Biosyst. 2013 Jan 27;9(1):10-7. doi: 10.1039/c2mb25088h. Epub 2012 Oct 5. Review.

Discovery of non-steroidal anti-inflammatory drug and anticancer drug enhancing reprogramming and induced pluripotent stem cell generation.

Yang CS, Lopez CG, Rana TM. Stem Cells. 2011 Oct;29(10):1528-36. doi: 10.1002/stem.717.

microRNAs modulate iPS cell generation.

Yang CS, Li Z, Rana TM. RNA. 2011 Aug;17(8):1451-60. doi: 10.1261/rna.2664111. Epub 2011 Jun 21.

Illuminating the cell-fate determinants of induced reprogramming by a genome-wide RNAi Screen

Yang CS, Chang KY, and Rana TM. Cell Report. 2014 (under revision).

CHAPTER I

Introduction

Mouse embryonic stem cells (MESCs) were first derived from normal mouse embryos (Evans and Kaufman, 1981), and the first established mammalian cell type with the capacities to differentiate into cells from the three major germ layers. More than a decade later, human embryonic stem cells (hESCs) were successfully cultured in the lab (Thomson *et al.*, 1998). This provided a resource to create desired cell types and tissues for regenerative therapy. However, the ethical concerns regarding human embryo acquisition and applications of human embryos are always under debate in society. Recently, a technique breakthrough provides an alternative method to obtain pluripotent cells. Yamanaka's group induced pluripotency in somatic cells (Takahashi and Yamanaka, 2006) by simply introducing four transcription factors: Oct4, Sox2, c-Myc, and Klf4 (OSKM). This technology not only provided an unlimited resource to regenerative medicine, but also opened the possibility of "customized" therapy.

Historic View of Reversing the Differentiation Process

For several decades, scientists have investigated how and what decides cell-fate changes during development. Since the late 19^{th} century, it was a general belief that differentiation is an irreversible process. This central dogma was first challenged by John Gurdon in 1958; he successfully grew adult frogs from tadpole nuclei transferred into enucleated oocytes by somatic cell nuclear transfer (SCNT) (Gurdon *et al.*, 1958). Differentiated cells re-gaining multi-potentiality were later found again in embryonal carcinoma cells (Kleinsmith and Pierce, 1964). Thirty years later, the Campbell's group (Wilmut *et al.*, 1997) created a vertebrate clone, known as Dolly the sheep. Different groups also created mouse clones (Hochedlinger and Jaenisch, 2002; Wakayama *et al.*, 1998). These seminal experiments showed that somatic cells carry all the genetic information to restore the pluripotency. Several years later, Yamanaka's breakthrough led us into a new era where nuclear reprogramming can be achieved by simply transducing four transgenes (OSKM) into somatic cells (Takahashi and Yamanaka, 2006). This surprising finding prompted numerous researchers worldwide to investigate this direct reprogramming phenomenon.

Acquiring ESC-like Identities by Direct Reprogramming of Somatic Cells

Several methods have been developed to reprogram somatic cells, including nuclear transfer, cell fusion, and direct reprogramming by transcription factors. Among these techniques, direct reprogramming by transcription factors is a more feasible and robust method, which has been achieved in many different cell types, such as fibroblasts, keratinocytes, stomach cells, melanocytes, platelets, astrocytes, liver cells neural cells, lymphocytes, B cells, amniotic cells, cord blood cells, pancreatic β cells, and adipose tissues (Rajasingh, 2012).

Initially mouse induced pluripotent stem cells (iPS cells) were first generated by using pseudo retroviruses as vehicles to deliver OSKM into somatic cells (Takahashi and Yamanaka, 2006). Shortly after that, human iPS cells were created with similar approaches (Takahashi *et al.*, 2007). Thomson's group developed another recipe for reprogramming using Oct4, Sox2, Lin28, and Nanog, and lentiviral transduction, instead of a retroviral system (Yu *et al.*, 2007). Those induced pluripotent stem cells (iPS cells) gain embryonic stem cell identity in about 2 weeks (mouse cells) or 6 weeks (human cells) post viral transductions. Reprogrammed cells were transformed into small compact cell colonies, resembling ESC colonies. Reprogrammed cells also express pluripotent markers, such as SSEA1 (mouse), SSEA3/4 (human), alkaline phosphatase activity (AP), and endogenous Oct4 re-activation. The transcriptome profiling of iPS cells is highly similar, if not identical, to that of ESCs. Reprogrammed cells can be cultured indefinitely, in theory, and still remain genomic integrity (normal karyotypes). The pluripotency of iPS cells has also been vigorously tested to show their ability to differentiate into various cell types derived from the three major germ layers: mesoderm, ectoderm, and endoderm. Therefore, direct reprogramming technology provides an alternative to human ESCs with no ethical concerns, and paves the road to "customized" regenerative medicine in the future, since they can be created with one's own somatic cells. This direct reprogramming technique has also worked successfully in various species (Stadtfeld and Hochedlinger, 2010), providing other possibilities to preserve extinct or endangered animals.

Advances in Methodology to directly induce reprogramming in somatic cells

Although the direct reprogramming technique is simple, there are few major roadblocks to apply this technology for therapeutic purposes. First, the reported reprogramming efficiency is low: ~0.1% in mouse cells and ~0.01% in human cells. This low efficiency is not a concern in the laboratory setting, but a higher rate might be required to create "customized" iPS cells from precious patient samples. Second, the random viral-integrations introduce the changes to the genome. Finally, the usage of oncogenes, c-Myc and Klf4 that may lead the reprogrammed cells into tumorigenesis. Therefore, a great effort has been made by numerous labs to find different methods to enhance the reprogramming efficiency or reduce/replace any transgenes.

The major advantage of using a retrovirus-based delivery system (Takahashi and Yamanaka, 2006) is that transgenes can be delivered into cells with high efficiency. This high transduction efficiency is essential, because high expression of OSKM in recipient cells is needed to drive rare reprogramming events. When reprogrammed cells restore ESC identities, endogenous regulatory networks (LSD1/KDM1A and ZFP809) will repress transgenic OSKM by silencing retroviral long terminal regions (LTRs) (Macfarlan *et al.*, 2011; Wolf and Goff, 2009). This is beneficial for the goals of differentiating pluripotent cells without the interference of reprogramming factors. A lentivirus-based system has also been used to generate iPS cells (Yu *et al.*, 2007), showing broader recipient cell types for reprogramming. But lentiviral-transduced cells fail to suppress transgenes in iPS cells at higher rate, which may interfere or block the differentiation abilities of transformed cells. Although both retro- and lenti-virus based delivery systems provide high transduction efficiency, transgene integration and the use of oncogenes (Klf4 and c-Myc) are the major concerns to potential therapeutic applications of iPS cells. Therefore, non-integration delivery system have been introduced by several labs to minimize the transgene integrations.

Non-integration delivery methods, such as adenovirus or plasmids only, have been shown to successfully generate iPS cells without transgene integrations (Okita *et al.*, 2008; Stadtfeld *et al.*, 2008b). Those successful attempts are promising to generate iPS cells without insertional mutagenesis. However, the frequency of successful iPS cell generation (~0.001 to 0.0001%) is substantially lower than that obtained with viral-integration methods (~0.1 to 0.01%). While none of iPS cells derived with retro- or lenti-viruses developed into tetraploid karyotypes, significant abnormal karyotypes were induced with adenovirus-derived iPS cells (~23% of iPS cell clones). For plasmid-only delivery approaches, the possibility of transgene integrations still cannot be ruled out, unless whole-genome sequencing is performed for each iPS cell clone. Transfecting modified mRNAs (cytidine replaced by 5-methylcytidine) expressing OSKM into recipient cells might serve as another solution for non-integrative delivery system, which shows no induction of innate immune responses and generates iPS cells in much higher efficiency (~36-fold increase) (Warren *et al.*, 2010). But all those techniques require repetitive administration of non-integrative viruses, plasmids, or mRNAs to sustain the effective transgene dosages for reprogramming; which is at least once every other day during the reprogramming process (from 7 days to several weeks). This high demanding labor is another drawback of those non-integration delivery systems.

To minimize the oncogenic integrations, Yamanaka's group further showed that iPS cells can be created by using only three factors OSK, without employing the most potent oncogene c-Myc (Nakagawa *et al.*, 2008), although with about ~10-fold lower reprogramming efficiency compared with OSKM. One alternative approach is using microRNAs as the substitutive genes to boost the reprogramming efficiency.

Diverse Regulatory Functions of miRNAs Might Be a Two-Edged Sword for Investigating Reprogramming Mechanisms

MicroRNAs (miRNAs) are ~22 nucleotide small non-coding RNAs that are highly conserved among species (Ambros, 2004; Bartel, 2004; Cao *et al.*, 2008; Kim *et al.*, 2009b; Rana, 2007a). They contain short sequences in the 5′ end (“seed” regions) that direct target gene recognition of miRNA-loaded processing complexes, RISCs (RNA-induced Silencing Complexes). In mammals, miRNAs act as post-transcriptional regulators to reduce translation of target genes by either destabilizing mRNAs or blocking their translation. miRNAs have been shown to play critical roles in various physiological processes, including embryogenesis (Ambros, 2011; Subramanyam and Blelloch, 2011; Tiscornia and Izpisua Belmonte, 2010) and tumorigenesis (Esteller, 2011;

Farazi *et al.*, 2011; Kasinski and Slack, 2010; Kim *et al.*, 2011a; van Kouwenhove *et al.*, 2011). Mouse ESC-enriched miRNAs, miR-290 clusters, were first shown to boost reprogramming efficiency (Judson *et al.*, 2009b), while let-7 family exert opposing roles to reprogramming progress (Melton *et al.*, 2010). Several miRNAs of miR-290 clusters, including miR-291a-3p, miR-291b-3p, miR-295, and miR302 family (Wang *et al.*, 2008), have been shown to associate with ES cell-specific cell cycle regulation (ESCC). These findings indicate that ESCC miRNAs may play significant roles in induced reprogramming, through regulating cell cycles (Judson *et al.*, 2009b). The advantage of using miRNAs to induce reprogramming is that miRNAs can be introduced easily by transfection and that no genomic modification is made. But the number of miRNAs' target genes can be hundreds and the effects at the molecular level can be hard to define. This could be challenging to investigate the regulatory mechanisms of reprogramming or design other molecules for more specific targeting.

Small Molecules Provide a Safe Way to Generate Induced Pluripotent Stem Cells

Several reports have shown that chemical molecules greatly increase iPS cell formation during reprogramming. Rho-associated kinase (ROCK) inhibitor increases the clonal and reprogramming efficiency in human fibroblast reprogramming (Park *et al.*, 2008a). Reprogramming efficiency can be boosted by ~4- to 10-fold by adding DNA methyltransferase inhibitor 5-aza-cytidine (AZA) during reprogramming (Huangfu *et al.*, 2008; Mikkelsen *et al.*, 2008). Many histone deacetylase (HDAC) inhibitors have been shown to improve reprogramming efficiency (Huangfu *et al.*, 2008). Among those inhibitors, valproic acid (VPA) can even increase reprogramming efficiency by ~100-fold with OSKM (Huangfu *et al.*, 2008). Few small molecules even show an ability to replace certain reprogramming factors, such as Sox2 replaced by BIX-01294 (Shi *et al.*, 2008b), and Klf4 replaced by kenpaullone (Lyssiotis *et al.*, 2009). Highly selective small molecules can also be used to reveal the important gene regulations or pathways during reprogramming. For example, PD0325901 and CHIR99021 (MEK and GSK3 pathway inhibitors respectively) have the ability to replace Sox2 and Klf4 during reprogramming and to promote the ground state of pluripotency in iPS cells (Silva *et al.*, 2008a). TGF−β signaling pathway also has been shown to modulate Nanog re-activation in partial iPS cells by using the inhibitor SB431542 (Ichida *et al.*, 2009; Maherali and Hochedlinger, 2009b). Therefore, it is promising to employ chemical molecules to develop more efficient and non-transgenic induced reprogramming methods.

Mechanistic understanding of induced reprogramming

An increasing body of evidence shows that induced reprogramming process occurs in a generally stochastic manner (Hanna *et al.*, 2009; MacArthur *et al.*, 2008; Yamanaka, 2009a) but that the transformed cells are able to achieve step-wise transitions at later stages of reprogramming (Brambrink *et al.*, 2008; Sridharan *et al.*, 2009; Stadtfeld *et al.*, 2008a; Yamanaka, 2009a). The OSKM reprogramming factors bind their targets in a coordinated fashion (Sridharan *et al.*, 2009) to initiate the first step of reprogramming: the transcriptional and epigenetic changes (Koche *et al.*, 2011; Sridharan *et al.*, 2009). Furthermore, it has been suggested that OSKM may assemble an inhibitory circuit against somatic identities prior to building up the transcriptional network of pluripotency in the later stages of the transition (Koche *et al.*, 2011; Sridharan *et al.*, 2009). This observation is supported by other reports showing that a number of barriers need to be overcome to reach the next steps in the transition (Ho *et al.*, 2011; Plath and Lowry, 2011).

It has been shown that only a few markers, including Thy1, alkaline phosphatase (AP), and SSEA1, activated in sequential stages, can be used to identify cells that transform through the process of induced reprogramming, while embryonic stem cell-specific genes (*Nanog, Oct4, Tert*) are activated only at later stages (Brambrink *et al.*, 2008; Stadtfeld *et al.*, 2008a). More recent research suggests that induced reprogramming is a step-wise event, comprising initial, mature, and stabilization stages (Samavarchi-Tehrani *et al.*, 2010). Several key cellular events have been observed during reprogramming, such as mesenchymal-to-epithelial transition (Li *et al.*, 2010; Samavarchi-Tehrani *et al.*, 2010) and cell-cycle modulation (Banito *et al.*, 2009a; Hong *et al.*, 2009; Kawamura *et al.*, 2009b; Li *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009). Furthermore, the epigenome is reset upon induced reprogramming (Koche *et al.*, 2011; Maherali *et al.*, 2007), and several epigenetic regulators play important roles in the reprogramming process (Onder *et al.*, 2012). The cooperation of OSKM has also been considered as a critical factor to efficient reprogramming (Carey *et al.*, 2011; Soufi *et al.*, 2012; Sridharan *et al.*, 2009).

Remaining Questions and Challenges

One of the primary obstacles to the successful application of iPS cells for medical purposes is their low reprogramming efficiency. Significant effort has been devoted to enhancing induced reprogramming efficiency as described above, including approaches focusing on the use of mRNA (Warren *et al.*, 2010); small molecules (Ichida *et al.*, 2009; Li and Rana, 2012; Maherali and Hochedlinger, 2009b; Nichols *et al.*, 2009; Silva *et al.*, 2008a; Yang *et al.*, 2011b; Ying *et al.*, 2008; Zhu *et al.*, 2011); and miRNAs (Choi *et al.*, 2011; Judson *et al.*, 2009b; Kim *et al.*, 2011b; Li and He, 2012; Li *et al.*, 2011; Liao *et al.*, 2011; Lipchina *et al.*, 2011; Melton *et al.*, 2010; Pfaff *et al.*, 2011; Subramanyam *et al.*, 2011; Yang and Rana, 2013; Yang *et al.*, 2011a). However, none of these studies have been able to sufficiently describe the molecular mechanisms of induced cellular reprogramming. The complexity of cell types in reprogramming is major hurdle to dissect the mechanisms during the cell-fate transitions. To address those major challenges, we sought the answers by utilizing miRNAs and small molecules as tools to possibly increase the reprogramming frequency, as well as to replace oncogenes. These approaches may also shed light about specific gene targets or pathways modulating iPS cell induction. To elucidate comprehensive molecular mechanisms and to determine the functional requirements of genes during the reprogramming process, we ambitiously applied genome-wide RNAi screen and cell sorting to dissect the molecular landscape of induced reprogramming in a step-wise manner.

Since microRNAs (miRNAs) modulate target genes tissue-specifically, we reasoned that distinct mouse embryonic fibroblast (MEF)-enriched miRNAs post-transcriptionally modulate proteins that function as reprogramming barriers. Inhibiting these miRNAs should influence cell signaling to lower those barriers. Therefore, we hypothesized that somatic cell-enriched miRNAs, such miR-21 and miR29, might play inhibiting roles in the reprogramming process. Here we show that depleting miR-21 and miR-29a enhances reprogramming efficiency in MEFs. We also show that p53 and ERK1/2 pathways are regulated by miR-21 and miR-29a and function in reprogramming. We further provide the first evidence that c-Myc enhances reprogramming partly by repressing MEF-enriched miRNAs, such as miR-21 and miR-29a. Our results demonstrate the significance of miRNA function in regulating multiple signaling networks involved in iPS cell reprogramming.

In addition, we describe a strategy to analyze genomic datasets of mouse embryonic fibroblasts (MEFs) and embryonic stem (ES) cells to identify genes that constitute barriers to reprogramming. We further show that computational chemical biology combined with genomics analysis can be used to identify small molecules regulating reprogramming. Specific down-regulation by siRNAs of several key MEF-specific genes encoding proteins with catalytic or regulatory functions, including *Wisp1, Prrx1, Hmga2, Nfix, Prkg2, Cox2,* and *Tgf*-β3, greatly increased reprogramming efficiency. Based on this rationale, we screened only 17 small molecules in reprogramming assays and discovered that Nabumetone and the anti-cancer drug OHTM can replace Sox2 during reprogramming. Nabumetone was also able to replace c-Myc or Sox2 in reprogramming without compromising the self-renewal and pluripotency of derived iPS cells. In summary, we report a new concept of combining genomics and computational chemical biology to identify new drugs useful for iPS cell generation. This hypothesis-driven approach provides an alternative to shot-gun screening and accelerates understanding of molecular mechanisms underlying iPS cell induction.

Moreover, we attempted to dissect the molecular mechanism in step-wise manner by applying FACS to separate distinct populations, representing four critical steps from initiation to maturation of induced reprogramming. We discovered five categories of the transcriptome that change dramatically along reprogramming. Numerous genes are shown to be key players in each transitional stage from mouse embryonic fibroblast to induced pluripotent stem cells. Our data suggest that attaining SSEA1+ stages is the rate-limiting step during reprogramming. *Nanog, Sall4, Esrrb, Dppa4, Dppa5a, Dnmt3b and Dnmt3l* are activated in $SSEA1^+$ cells, while more extensive interactions of embryonic stem cell core circuitry (ESCCC) regulators are established in mature iPS cells, including *Utf1, Nr6a1, Tdgf1, Gsc, Fgf10, T, Chrd, Dppa3, Fgf17, Eomes, Foxa2*. Remarkably, we found that genes with non-differential change play the most critical roles in the transitions of reprogramming, while analysis of differential transcriptome might not comprehensively reveal the key regulators. Functional validation showed that genes, such as *Dmbx1, Gsc, Med21, Hnf4g, Mef2c, Psmd9, Tfdp1, Nfe2, Foxn3, Erf, Cdkn2aip, Msx3, Ssbp3, Dbx1, Hoxd4, Lzts1, Arx, Hoxd12, Gtf2i, Nkx6-2, Ankrd22*, and *Hoxc10*, have essential or barrier roles to reprogramming.

To further understand the mechanism of regulatory networks during reprogramming, we performed a genome wide RNAi screen and purified cellular populations during four key steps of reprogramming: We integrated genome-wide RNAi screen with step-wise transcriptome analysis to analyze the molecular requirements in induced reprogramming. We found that genes associated with cell signaling pathways (e.g., *Itpr1*, *Itpr2*, *Pdia3*, *Camk4*) constitute the major regulatory networks before cells acquire pluripotency. Activation of a specific gene set (e.g., *Utf1, Nr6a1, Tdgf1, Gsc*) is important to become mature iPS cells. Strikingly, a major proportion of identified RNAi targets (~53% to 70%) are non-induced or changed genes (defined as *NINCHA* group) during reprogramming, suggesting that these genes are important for reprogramming transitions. Among *NINCHA* genes, *Dmbx1, Hnf4g*, *Nobox* and *Asb4*, are essentials for reprogramming, while *Nfe2, Cdkn2aip, Msx3, Dbx1, Lzts1, Arx, Gtf2i,* and *Ankrd22* act as roadblocks to reprogramming. We also confirmed several genes required for maintaining ES cell properties, such as *Srsf2, Hcfc1, Ruvbl2, Asb4, Dmbx1, Gbx2, Gsc, Hnf4g, Klf5, L3mbtl2, Med21, Mef2c, Nobox, Pcgf6, Phox2a, Tcf15, Oct4/Pou5f1, Nanog*, and *Trim28*. Altogether, our work advances the field by identifying several new key modulations, by combining genome-wide shRNA library screening with transcriptome analysis.

CHAPTER II

MicroRNAs modulate iPS cell generation

Summary

Although induced pluripotent stem cells (iPS cells) hold great promise for customized regenerative medicine, the molecular basis of reprogramming is largely unknown. Overcoming barriers that maintain cell identities is a critical step in the reprogramming of differentiated cells. Since microRNAs (miRNAs) modulate target genes tissue-specifically, we reasoned that distinct mouse embryonic fibroblast (MEF)–enriched miRNAs post-transcriptionally modulate proteins that function as reprogramming barriers. Inhibiting these miRNAs should influence cell signaling to lower those barriers. Here we show that depleting miR-21 and miR-29a enhances reprogramming efficiency in MEFs. We also show that the p53 and ERK1/2 pathways are regulated by miR-21 and miR-29a and function in reprogramming. In addition, we provide the first evidence that c-Myc enhances reprogramming partly by repressing

MEF-enriched miRNAs, such as miR-21 and miR-29a. Our results demonstrate the significance of miRNA function in regulating multiple signaling networks involved in iPS cell generation. These studies should facilitate development of clinically applicable reprogramming strategies.

Introduction

Embryonic stem (ES) cells can proliferate indefinitely and differentiate into all cells that form an individual. Therefore, ES cells are versatile tools for the study of early developmental processes and provide a promising source of tissues or cells useful for regenerative therapies. However, the derivation of human ES cells from embryos has been an ethical concern in the field. Recent breakthroughs in creating induced pluripotent stem (iPS) cells provide an alternative way to obtain ES-like cells without destroying embryos. iPS cells were first established by introducing four reprogramming factors (*Oct3/4*, *Sox2*, *Klf4*, and *c-Myc*) into mouse embryonic fibroblasts (MEFs) (Takahashi and Yamanaka, 2006) or human fibroblasts (Takahashi *et al*., 2007). iPS cells have also been created following expression of *Oct3/4*, *Sox2*, *Nanog*, and *Lin28* (Yu *et al*., 2007).

Overall, iPS cells exhibit morphology, transcriptome, and pluripotency similar to that of ES cells (Okita *et al.*, 2007; Yu *et al.*, 2007). However, retrovirus-mediated transgene expression and extremely low efficiency remain obstacles for their therapeutic application (Geoghegan and Byrnes, 2008; Seifinejad *et al.*, 2010; Yoshida and Yamanaka, 2010). Moreover, although the combinatorial functions (Geoghegan and Byrnes, 2008) and regulatory activity (Boyer *et al.*, 2005; Chen *et al.*, 2008; Kim *et al.*, 2008; Sridharan *et al.*, 2009) of reprogramming factors have been established, the basic molecular mechanisms of each factor during the reprogramming process remain unknown.

c-Myc, one of the four reprogramming factors (4F: Oct3/4, Sox2, Klf4, and c-Myc), plays crucial roles in cell proliferation and tumor development (Pelengaris *et al.*, 2002). c-Myc is a key regulator of cytostasis and apoptosis through repression of the cyclin-dependent kinase (CDK) inhibitor $p21^{Cip1}$ (Seoane *et al.*, 2002). By abrogating Miz-1 function and suppressing $p15^{INK4b}$, c-Myc plays a critical role in the immortalization of primary cells (Seoane *et al.*, 2001). Many transcriptional functions of c-Myc require cooperation with Max or Miz-1 (Wanzel *et al.*, 2003a). As a proto-oncogene c-Myc greatly enhances reprogramming efficiency, although it is dispensable for reprogramming (Nakagawa *et al.*, 2008; Sridharan *et al.*, 2009). Therefore, defining molecular pathways downstream of c-Myc during reprogramming could enhance therapeutic application of iPS cells, without compromising reprogramming efficiency.

c-Myc reportedly acts to maintain ES cell renewal in part by regulating microRNA (miRNA) expression (Li *et al.*, 2009a; Smith *et al.*, 2010). MicroRNAs are 22-nucleotide non-coding small RNAs, which are loaded into RNA-induced silencing complex (RISC) to exert a global gene-silencing function (Chu and Rana, 2007). Expression of miR-141, miR-200, and miR-429 is induced by c-Myc in ES cells to antagonize differentiation (Lin *et al.*, 2009a). c-Myc also promotes tumorigenesis by upregulating the miR-17-92 microRNA cluster (Dews *et al.*, 2006) or by repressing known tumor suppressors, such as the let-7 family, miR-15a/16–1, the miR-29 family, and miR-34a (Chang *et al.*, 2008b; Chang *et al.*, 2009a). Nonetheless, how c-Myc functions to initiate reprogramming is still unclear.

Overcoming barriers securing somatic cell identity and mediated by factors such as Ink4-Arf, p53, and p21 is a rate-limiting step in reprogramming (Banito *et al.*, 2009b; Hong *et al.*, 2009; Judson *et al.*, 2009a; Kawamura *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009). Since miRNAs modulate target genes tissue-specifically (Farh *et al.*, 2005; Rana, 2007b), we reasoned that distinct MEF miRNAs (Mayr and Bartel, 2009) post-transcriptionally modulate proteins that function as reprogramming regulators. Inhibiting these miRNAs should influence cell signaling to lower those barriers.

Here, we show that depleting the abundant miRNAs miR-21 and miR-29a in MEFs enhances reprogramming efficiency by ~2.4- to 3-fold. We also report that c-Myc represses miRNAs miR-21 and miR-29a to enhance reprogramming of MEFs. Finally we report that miR-21 and miR-29a regulate p53 and ERK1/2 pathways by indirectly down-regulating p53 levels and ERK1/2 phosphorylation during the reprogramming process.

Results

Inhibition of miR-21 or miR-29a enhances reprogramming efficiency

To determine whether inhibiting MEF-specific miRNAs lowers reprogramming barriers, we first analyzed MEF-enriched miRNAs and compared their levels with those seen in mouse ES cells. As shown in Fig 1A, let-7a, miR-21, and miR-29a were highly expressed in MEFs compared with ES cells. By contrast, miR-291 was highly abundant in ES cells but absent in MEFs (Figure 2.1A). Next, we introduced miRNA inhibitors against let-7a, miR-21, and miR-29a into Oct4-EGFP MEFs (MEFs harboring Oct4-EGFP reporter) together with retroviruses expressing Oct3/4, Sox2, Klf4, and c-Myc (OSKM). At day 14 post-transduction, cells treated with miR-21 inhibitors showed a ~2.4-fold increase in reprogramming efficiency compared with a non-targeting (NT) control (Figure 2.1B). Similarly, reprogramming efficiency increased significantly by ~3-fold following inhibition of miR-29a (Figure 2.1B). Under similar miRNA-inhibitor treatments as used for miR-29a or -21 inhibition, we observed a minor effect on OSKM-reprogramming following let-7a inhibition (Figure 2.1B).

Figure 2.1

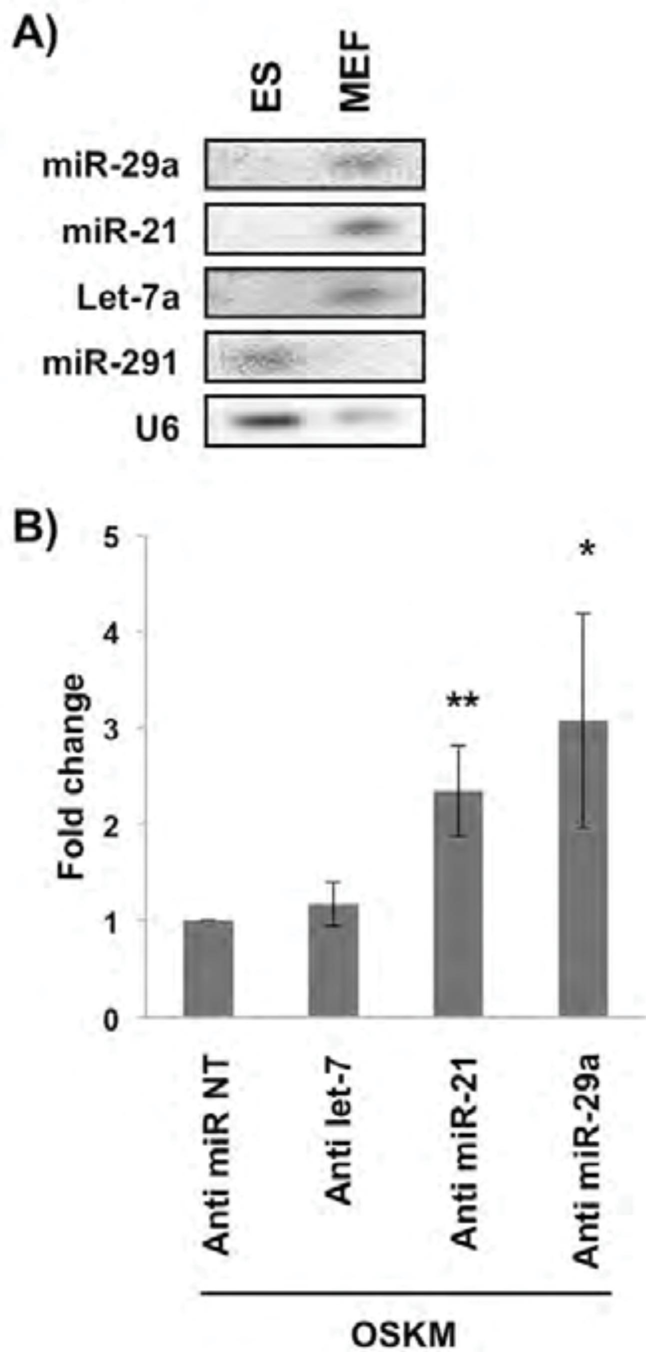

A)
ES
MEF
miR-29a
miR-21
Let-7a
miR-291
U6
B)
Fold change
5
4
3
2
1
0
**
*
Anti miR NT
Anti let-7
Anti miR-21
Anti miR-29a
OSKM

Figure 2.1.

Inhibition of MEF-enriched microRNAs, miR-21 and miR-29a, enhances reprogramming efficiency.

(A) miR-29a, miR-21, and let7a are highly expressed in MEFs. Total RNAs were isolated from Oct4-EGFP MEFs and mouse ES cells and resolved by gel electrophoresis. Specific radioactive-labeled probes against the indicated miRNAs were used to detect expression. U6 snRNA served as a loading control.

(B) miRNA inhibition enhances reprogramming efficiency. Oct4-EGFP MEFs were transduced with OSKM as described in the Materials and Methods. GFP-positive colonies were identified and counted by fluorescence microscopy at day 14 after transduction. GFP+ colony number was normalized to the number of anti-miR nontargeting control treatment and is reported as fold-change. Error bars, SD of three independent experiments. **P*-value <0.05; ***P*-value <0.005.

To further test whether miRNA inhibition enhances reprogramming with three factors in the absence of c-Myc, cells were transduced with the miRNA inhibitor together with OSK, which reprograms cells at much lower efficiency than OSKM (Nakagawa *et al.*, 2008). The number of OSK-reprogrammed iPS cell colonies increased in the presence of the miR-21 inhibitor relative to treatment with OSK alone (Figure 2.2). These results demonstrate that the depletion of the MEF-enriched miRNAs miR-21 and miR-29 enhances 4F-reprogramming significantly and that blocking miR-21 moderately increases the efficiency of OSK reprogramming.

c-Myc represses expression of miRNAs let-7a, miR-16, miR-21, miR-29a, and miR-143 during reprogramming

Recent work indicates that the OSKM factors alter cell identity through both epigenetic and transcriptional mechanisms (Sridharan *et al.*, 2009). Therefore, we hypothesized that OSKM reprogramming factors could down-regulate MEF-enriched miRNAs. To evaluate the potential effect of each reprogramming factor on miRNA expression, MEFs were transduced with various combinations of the OSKM factors and

Figure 2.2

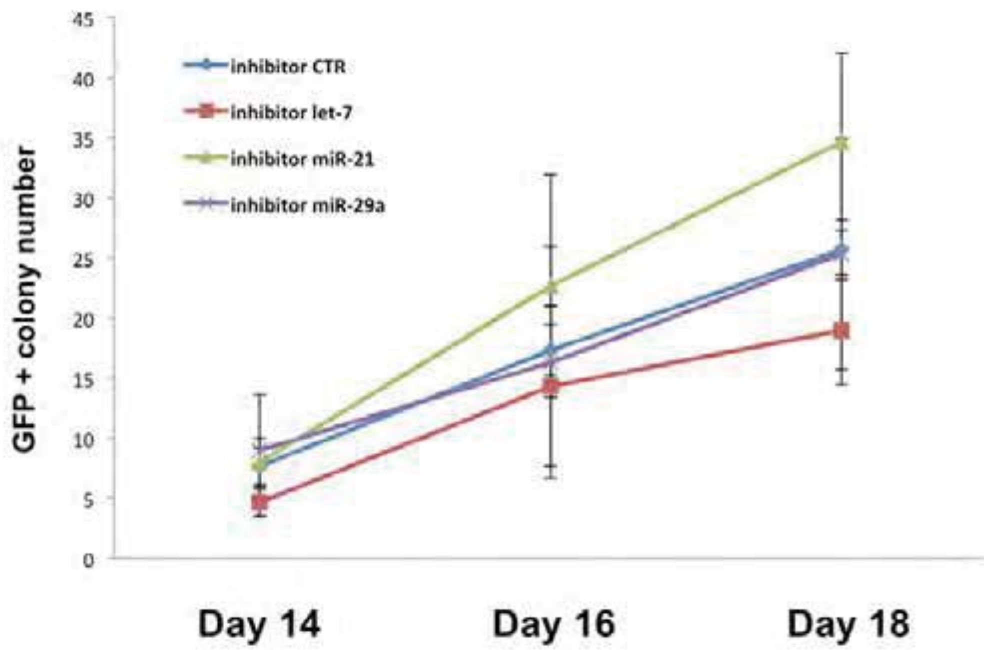

45
40
35
30
25
20
15
10
5
0
GFP + colony number
inhibitor CTR
inhibitor let-7
inhibitor miR-21
inhibitor miR-29a
Day 14
Day 16
Day 18

Figure 2.2

Inhibition of miR-21 enhances iPS cell reprogramming by OSK.

Inhibitors of miRNAs were introduced into Oct4-MEFs during reprogramming with OSK. GFP-positive colonies were counted at various time points post-transduction. Error bars represent standard deviation of two independent experiments.

subjected to Northern blot analysis (Figure 2.3A). Interestingly, Sox2 alone induced expression level of miR-21, miR-29a, and let-7a by more than two folds, compared with MEF control (Figure 2.3B, left). Klf4 also induced miR-29a and let-7a by ~1.5 and 1.8 folds, respectively (Figure 2.3B, left). With Oct3/4 overexpression only, miRNAs did not change expression level (Figure 2.3B, left). In contrast to Oct4, Sox2, and Klf4, the single factor c-Myc down-regulated expression of miR-21 and miR-29a, the most abundant miRNAs in MEFs, by ~70% of MEF control (Figures 2.3A & 2.3B, left panels). Furthermore, among various combinations of two factors (2F) shown in Figure 2.3B (middle), inclusion of c-Myc enhanced decreases in all three miRNAs, including miR-21, miR-29a, and let-7a, by ~25-80% (Figure 2.3B, middle). Similar to single-factor effect on miRNA expression, Sox2 and Oct4 together increased miR-21 and miR-29a by 1.5 fold and 2.3 fold of MEF control respectively, while OK and SK had no obvious effects on miRNA expression (Figure 2.3B, middle). Moreover, among various three-factor (3F) combinations, the expression of miRNA-21 decreased by ~70 and 78% in SKM and OKM cells, respectively, relative to expression seen in MEFs (Figure 2.3B, right).

Figure 2.3

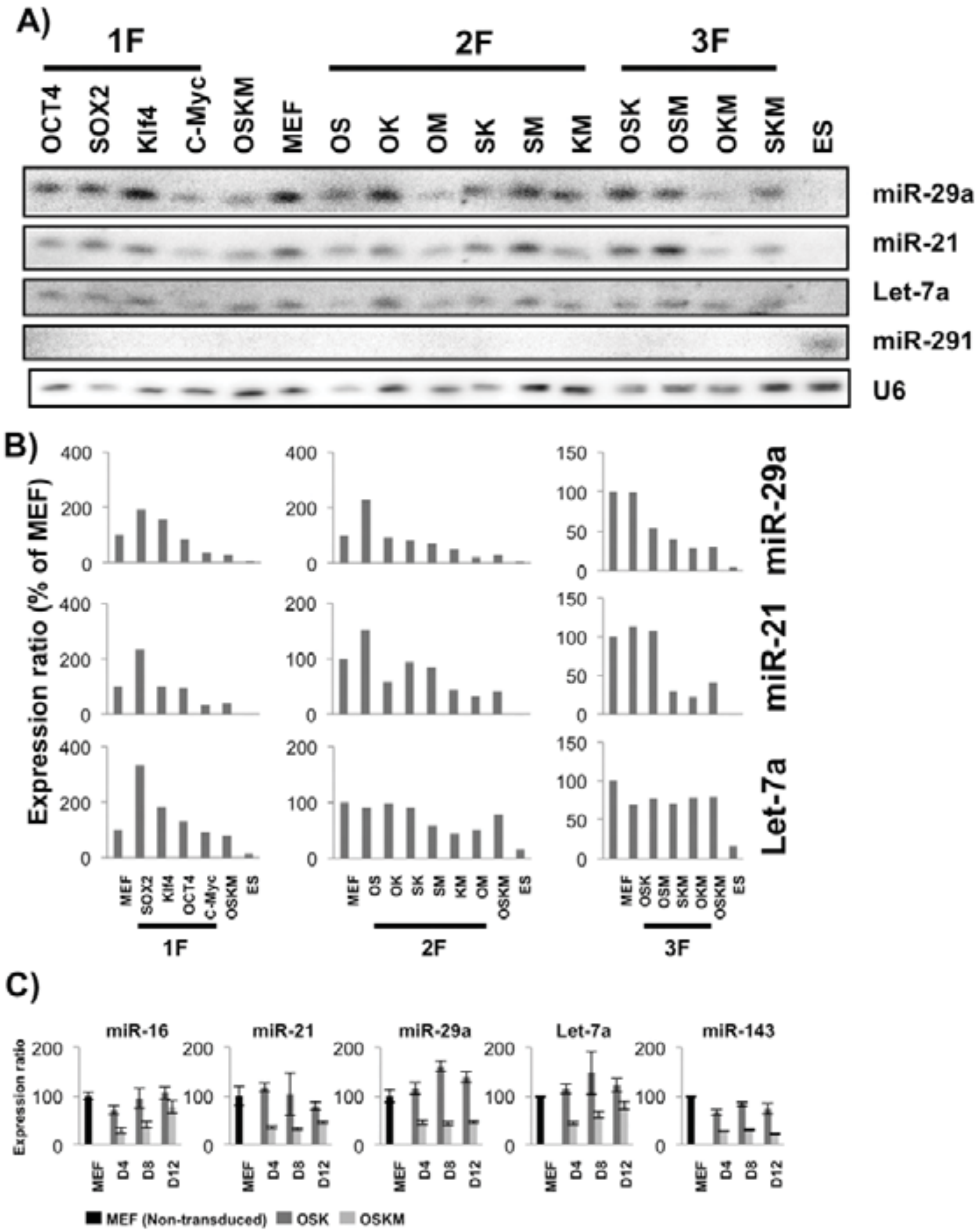

A)
1F
2F
3F
OCT4
SOX2
Klf4
C-Myc
OSKM
MEF
OS
OK
OM
SK
SM
KM
OSK
OSM
OKM
SKM
ES
miR-29a
miR-21
Let-7a
miR-291
U6
B)
Expression ratio (% of MEF)
miR-29a
miR-21
Let-7a
MEF
SOX2
Klf4
OCT4
C-Myc
OSKM
ES
1F
2F
3F
C)
miR-16
miR-21
miR-29a
Let-7a
miR-143
Expression ratio
MEF
D4
D8
D12
MEF (Non-transduced)
OSK
OSKM

Figure 2.3

c-Myc is the primary repressor of MEF-enriched miRNAs during reprogramming.

(A) Northern analysis of selected miRNAs at day 5 after reprogramming. Oct4-EGFP MEFs were transduced with a single factor or various combinations of reprogramming factors, as indicated. 1F indicates one factor; 2F, two factors; 3F, three factors. OSKM indicates Oct3/4, Sox2, Klf4, and c-Myc. U6 is used as a loading control RNA. Total RNA from embryonic stem (ES) cells serve as negative control to MEF and transduced cells. Various probes were used to detect specific miRNAs as indicated on the *right* side. miR-291 blotting is a positive control for ES RNA.

(B) Quantitative representation of miRNA expression in the presence of various reprogramming factors. Signal intensity was normalized to intensity of U6 snRNA. The expression ratio is calculated as the percentage of expression of each miRNA relative to expression in MEFs, which was arbitrarily set to 100%. Various miRNAs were quantified (from panel *A*) and indicated on the *right* side.

Figure 2.3 (continuation)

(C) Real-time RT-PCR analysis of selected miRNAs in Oct4-EGFP MEFs at various time points following OSK- or OSKM-reprogramming. RNA was isolated at the indicated day after transduction for real time RT-PCR analysis. Signals were normalized to U6 and are shown as a percentage of miRNAs expressed in MEFs, which was arbitrarily set to 100. Error bars, SD of two independent experiments.

Similarly, miR-29a expression decreased by ~48-70% in 3F combinations containing c-Myc (Figure 2.3B, right). Inclusion of c-Myc in 3F combinations also slightly decreased let-7a levels (Figure 2.3B, right). OSK without c-Myc had little effect on miRNA expression (Figure 2.3B, right). Therefore, these results strongly suggest that c-Myc plays an important role in regulating miRNA expression during the reprogramming.

To further confirm that c-Myc is the primary factor antagonizing miRNA expression, cells were transduced with OSK with or without c-Myc, and miRNA expression was examined by real time quantitative reverse transcription polymerase chain reaction (RT-qPCR) at various time points post-transduction. In contrast to OSK, OSKM transduction greatly decreased expression of let-7a, miR-16, miR-21, miR-29a, miR-143 during reprogramming (Figure 2.3C), indicating that c-Myc plays a predominant role in regulating expression of MEF-enriched miRNAs, including the most abundant ones, let-7a, miR-21, and miR-29a. These data also suggest that c-Myc boosts reprogramming, in part, through miRNA downregulation.

c-Myc regulates miRNA expression at the transcriptional level during reprogramming

c-Myc has been shown to influence miRNA expression in multiple human and mouse cancer models (Chang *et al.*, 2008b; Chang *et al.*, 2009a) and Lin28b is one of the key intermediate modulators to posttranscriptionally regulate let-7 biogenesis (Chang *et al.*, 2009a). Therefore, we examined whether Lin28b-mediated regulation of miRNA expression plays a role during reprogramming. To address this question, we collected reprogrammed cells at various time intervals from day 3 to 15 post transduction of reprogramming factors. RT-qPCR analysis showed that mRNA expression of Lin28a and Lin28b were undetectable in MEF and during the reprogramming process while ES cells exhibited high level of Lin28a and Lin28b expression (Figures 2.4A and 2.4B). Control marker gene expression analysis established the successful progression of reprogramming process where the levels of Thy1 and Fibrillin-2 were downregulated and Nanog and Fbox15 were upregulated (Figure 2.4C). These findings strongly suggest that c-Myc regulation of miRNAs is Lin28-independent.

Figure 2.4

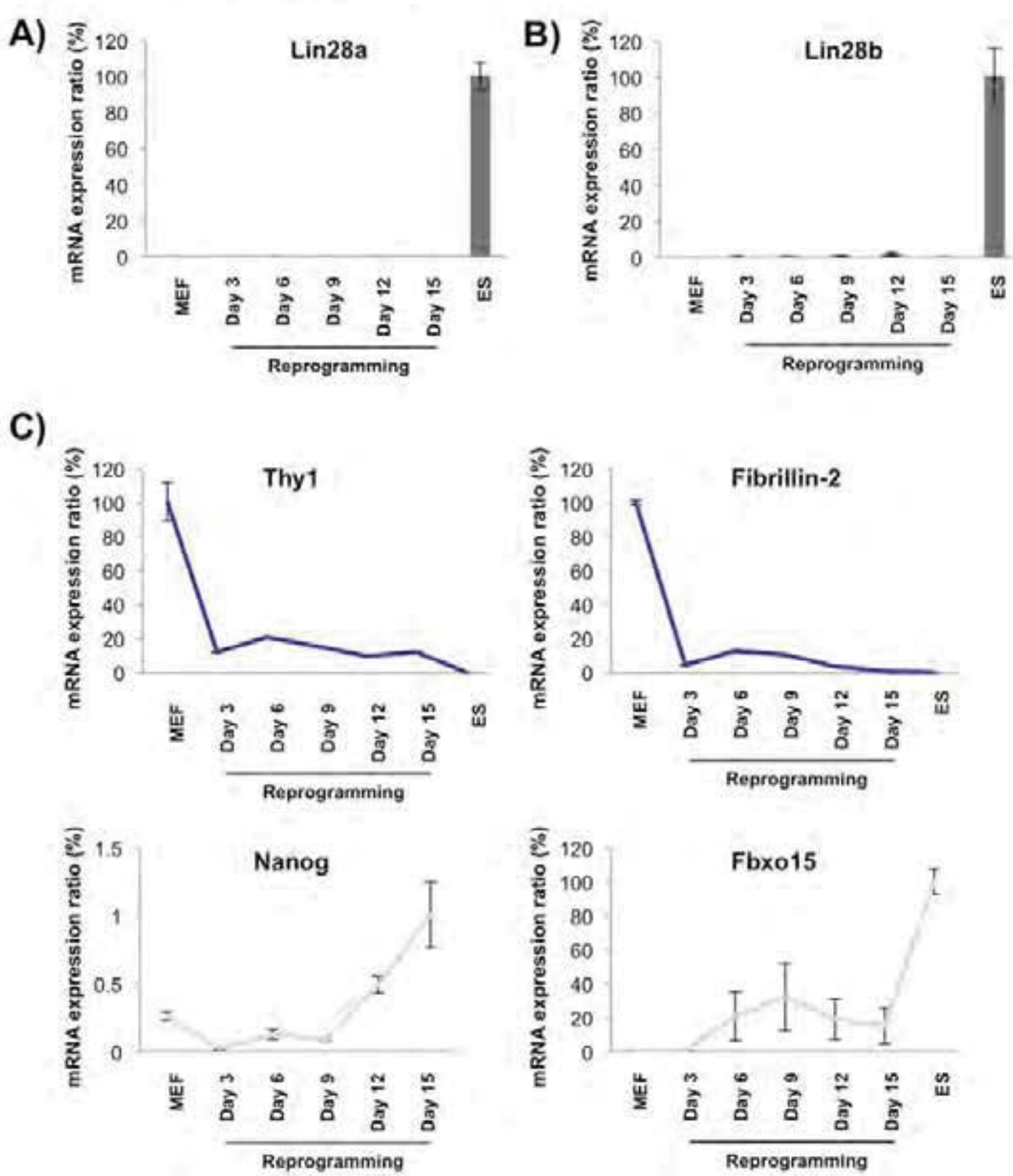

A)
Lin28a
mRNA expression ratio (%)
120
100
80
60
40
20
0
MEF
Day 3
Day 6
Day 9
Day 12
Day 15
ES
Reprogramming
B)
Lin28b
mRNA expression ratio (%)
120
100
80
60
40
20
0
MEF
Day 3
Day 6
Day 9
Day 12
Day 15
ES
Reprogramming
C)
Thy1
mRNA expression ratio (%)
120
100
80
60
40
20
0
MEF
Day 3
Day 6
Day 9
Day 12
Day 15
ES
Reprogramming
Fibrillin-2
mRNA expression ratio (%)
120
100
80
60
40
20
0
MEF
Day 3
Day 6
Day 9
Day 12
Day 15
ES
Reprogramming
Nanog
mRNA expression ratio (%)
1.5
1
0.5
0
MEF
Day 3
Day 6
Day 9
Day 12
Day 15
Reprogramming
Fbxo15
mRNA expression ratio (%)
120
100
80
60
40
20
0
MEF
Day 3
Day 6
Day 9
Day 12
Day 15
ES
Reprogramming

Figure 2.4

Reprogramming does not induce *Lin28a* and *Lin28b* expression.

Oct4-EGFP MEF were reprogrammed with OSKM retroviruses and transduced cells were collected at various time intervals during the reprogramming progress, as indicated. *Lin28a* **(A)** and *Lin28b* **(B)** expression levels were detected by RT-qPCR analysis. ES cells served as positive control. Error bars represent standard deviation of two independent experiments.

(C) Reprogramming progression is monitored by *Thy1, Fibrillin-2, Nanog*, and *Fbox15* expression. Thy1 and Fibrillin-2 are highly expressed in differentiated cell types such as MEFs. Nanog and Fbxo15 are highly expressed in pluripotent stem cells as iPS or ES cells. Gene expression level was quantified by RT-qPCR. Nanog expression level in ES cells is set to 100%, which is not shown in the plot. Error bars represent standard deviation of two independent experiments.

Next, to determine whether the c-Myc effect on MEF-enriched miRNAs is post-transcriptional, we examined miRNA biogenesis by Northern blotting and quantified the amounts of pre-miRNAs and mature miRNAs. Our analysis showed that the ratio between pre-miRNA and mature miRNA in the presence of OSKM (Figure 2.5) was not changed, suggesting that the miRNA maturation process of miR-21 and miR-29a was not compromised by c-Myc during reprogramming. Altogether, these data show that the c-Myc–mediated down-regulation of miR-21 and miR-29a is Lin28a/b-independent and occurs at the transcriptional level.

iPS cells derived via miRNA depletion attain pluripotency

To investigate whether blocking miR-21 or miR-29a compromises iPS cell pluripotency, we derived iPS cells treated with miR antagomirs and evaluated them for pluripotency (Li *et al.*, 2011). Since OSKM-derived iPS cells were already well characterized in numerous studies, we decided to thoroughly examine our OSKM/anti miR-29a and OSKM/anti miR21 iPS cells, as well as OSK/anti miR-21 clones. First, iPS

Figure 2.5

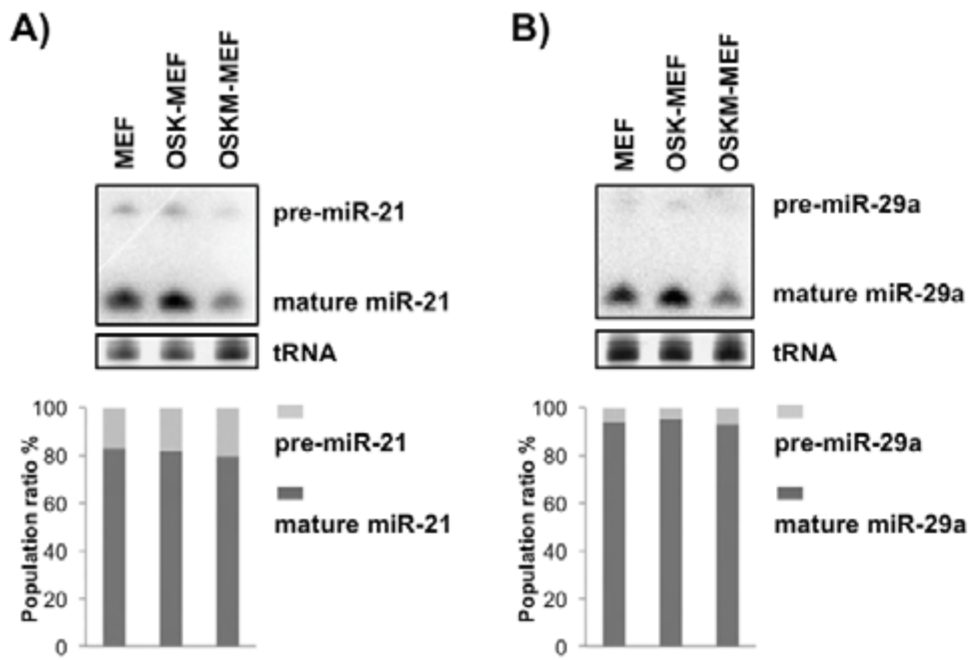

A)
MEF
OSK-MEF
OSKM-MEF
pre-miR-21
mature miR-21
tRNA
Population ratio %
100
80
60
40
20
0
pre-miR-21
mature miR-21
B)
MEF
OSK-MEF
OSKM-MEF
pre-miR-29a
mature miR-29a
tRNA
Population ratio %
100
80
60
40
20
0
pre-miR-29a
mature miR-29a

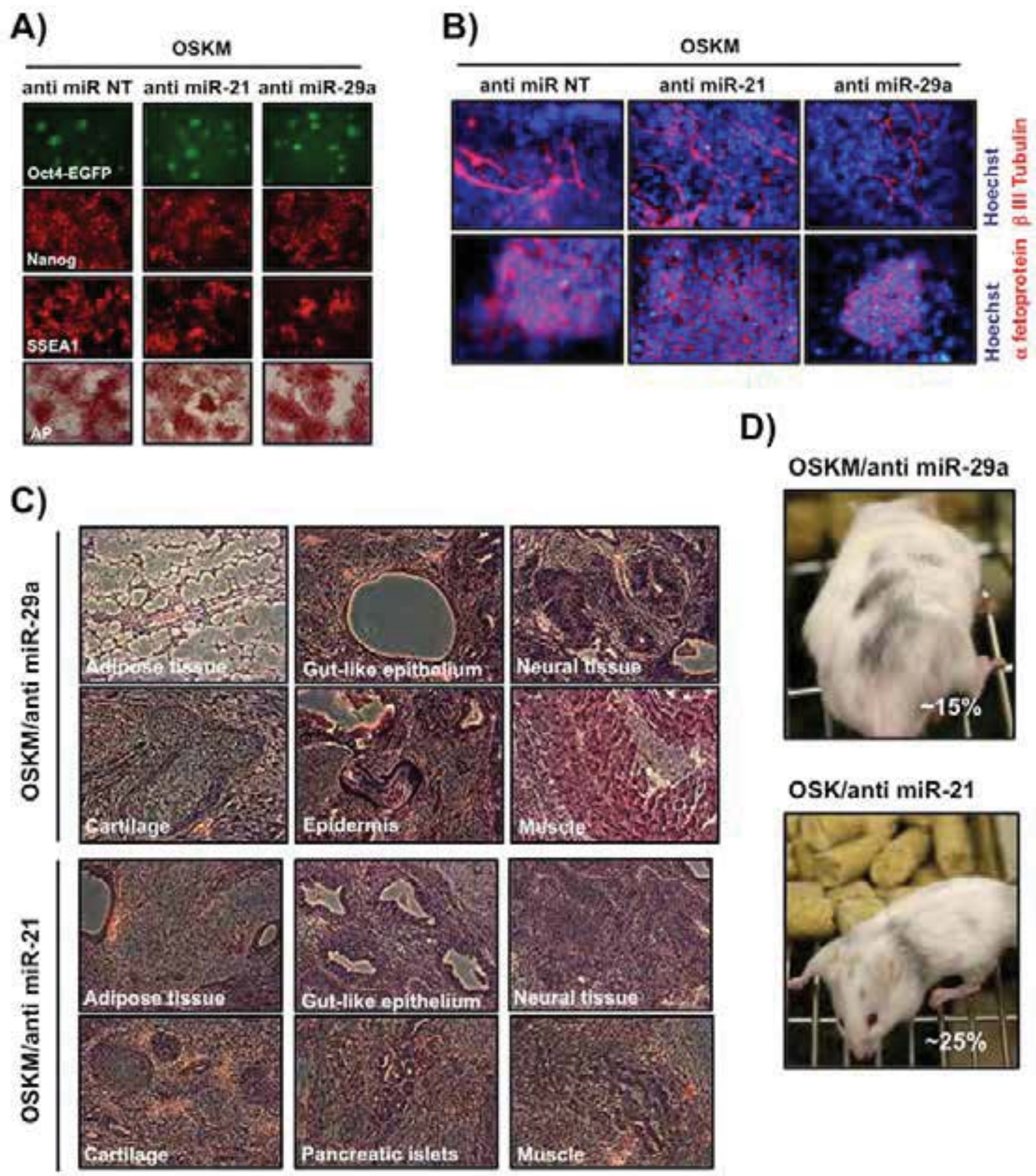
Figure 2.5

c-Myc does not affect mature miRNA processing of miR-21 and miR-29a during reprogramming.

Oct4-EGFP MEF were transduced with reprogramming factors, as indicated. Total RNAs were isolated at day 5 post transduction, and then were subjected to Northern blot analysis (A and B). Intensity of pre-miR and mature miR were measured and quantified by Multi Gauge V3.0 (Fujifilm). tRNAs serve as loading control. Experiments were repeated at three times and a representative blot is shown here.

cells were manually picked ~2 weeks after reprogramming and were expanded to examine morphology and expression of ES-specific markers. Cells exhibited an ES-like morphology and a highly expressed Oct4-EGFP (Figure 2.6A), indicating establishment of endogenous ES cell signaling. In addition, anti-miR-derived iPS cells expressed ES cell–specific markers, including Nanog and SSEA1, and exhibited alkaline phosphatase activity (Figure 2.6A). To test whether those iPS cells showed pluripotent potential comparable to that of ES cells, those iPS cells were induced to form embryoid bodies (EBs) (Figure 2.6B) or were injected into nude mice (Figure 2.6C) and allowed to differentiate into various tissues. After 2 weeks of *in vitro* differentiation, typical cell types derived from all three germ layers were observed (Figure 2.6B). Teratoma tumors, formed 3 weeks after injection, were subjected to histopathologic analysis. Various tissues originating from all three germ layers (Figure 2.6C) were generated, confirming that anti-miR-derived iPS cells obtained pluripotency. To use the most stringent test of pluripotency, iPS cells were injected into embryonic day (E) 3.5 blastocysts to create chimeric mice. Mouse derived from anti miR-29a iPS cells showed a significant ~15%

Figure 2.6



A)
OSKM
anti miR NT
anti miR-21
anti miR-29a
Oct4-EGFP
Nanog
SSEA1
AP
B)
OSKM
anti miR NT
anti miR-21
anti miR-29a
Hoechst β III Tubulin
Hoechst α fetoprotein
C)
OSKM/anti miR-29a
Adipose tissue
Gut-like epithelium
Neural tissue
Cartilage
Epidermis
Muscle
OSKM/anti miR-21
Adipose tissue
Gut-like epithelium
Neural tissue
Cartilage
Pancreatic islets
Muscle
D)
OSKM/anti miR-29a
~15%
OSK/anti miR-21
~25%

Figure 2.6

Mouse iPS cells derived with miR-21 and miR-29a inhibitors are pluripotent.

(A) Staining with ES cell markers of OSKM/anti miR-29a or miR-21 iPS cells. GFP+ colonies derived following OSKM and various miR inhibitor treatments were picked for further analysis. Representative colonies expressing the embryonic stem cell markers Nanog and SSEA1 are shown. Endogenous Oct3/4 was also activated, as indicated by the EGFP expression. Strong alkaline phosphatase (AP) activity is shown as one of the ES markers. Anti-miR NT (nontargeting) serves as miR inhibitor control.

(B) *In vitro* differentiation of OSKM/anti miR-29a or miR-21 iPS cells. Embryoid bodies were formed *in vitro* and cultured for 2 weeks. Cells were fixed and stained with anti-α fetoprotein (for mesoderm) and anti-β-tubulin III (for ectoderm). Nuclei are shown as counter stain by Hoescht staining.

(C) Teratoma formation analysis of OSKM/anti miR-29a or miR-21 iPS cells. We injected 1.5×10^6 iPS cells subcutaneously into athymic nude female mice. Tumor masses were collected at 3 weeks after injection and fixed for histopathologic analysis.

Figure 2.6 (continuation)

Various tissues derived from three germ layers were identified, including gut-like epithelium and pancreatic islet-like structure (endoderm); adipose tissue, cartilage, and muscle (mesoderm); and neural tissue and epidermis (ectoderm).

(D) Chimera analysis of OSKM/anti miR-29a and OSK/anti miR-21 iPS cells. Eight to 14 iPS cells were injected into E3.5 mouse blastocysts. iPS cell contribution to each chimera was estimated by assessing agouti coat color and is shown as a percentage.

black coat color attributable to iPS cells (Figure 2.6D). Since OSK in combination with miR-21 inhibitors resulted in high reprogramming efficiency (Figure 2.2), we also determined the pluripotency of OSK/anti miR-21 iPS cells by chimera analysis. Mouse generated from OSK/anti miR-21 iPS cells showed ~25% black coat color (Figure 2.6D). These data show that depleting miR-21 and miR-29a had no adverse effect on pluripotency of derived iPS cells.

Inhibiting miR-29a down-regulates p53 through p85α and CDC42 pathways

To understand the mechanisms underlying miR-29a's effect on reprogramming, we first examined expression of p85α and CDC42, which are reportedly direct targets of miR-29 in HeLa cells (Park *et al.*, 2009a). To do so, we transfected miRNA inhibitors into MEFs and analyzed p85α and CDC42 protein expression by western blot at day 5 post-transfection. As expected, p85α and CDC42 protein levels increased slightly following miR-29a block, whereas a let-7a inhibitor had little effect (Figures 2.7A and 2.7B). The transformation related protein 53 (Trp53 or p53) is also reportedly a direct target of p85α and CDC42 (Park *et al.*, 2009a). Therefore, we asked whether p53 is

Figure 2.7

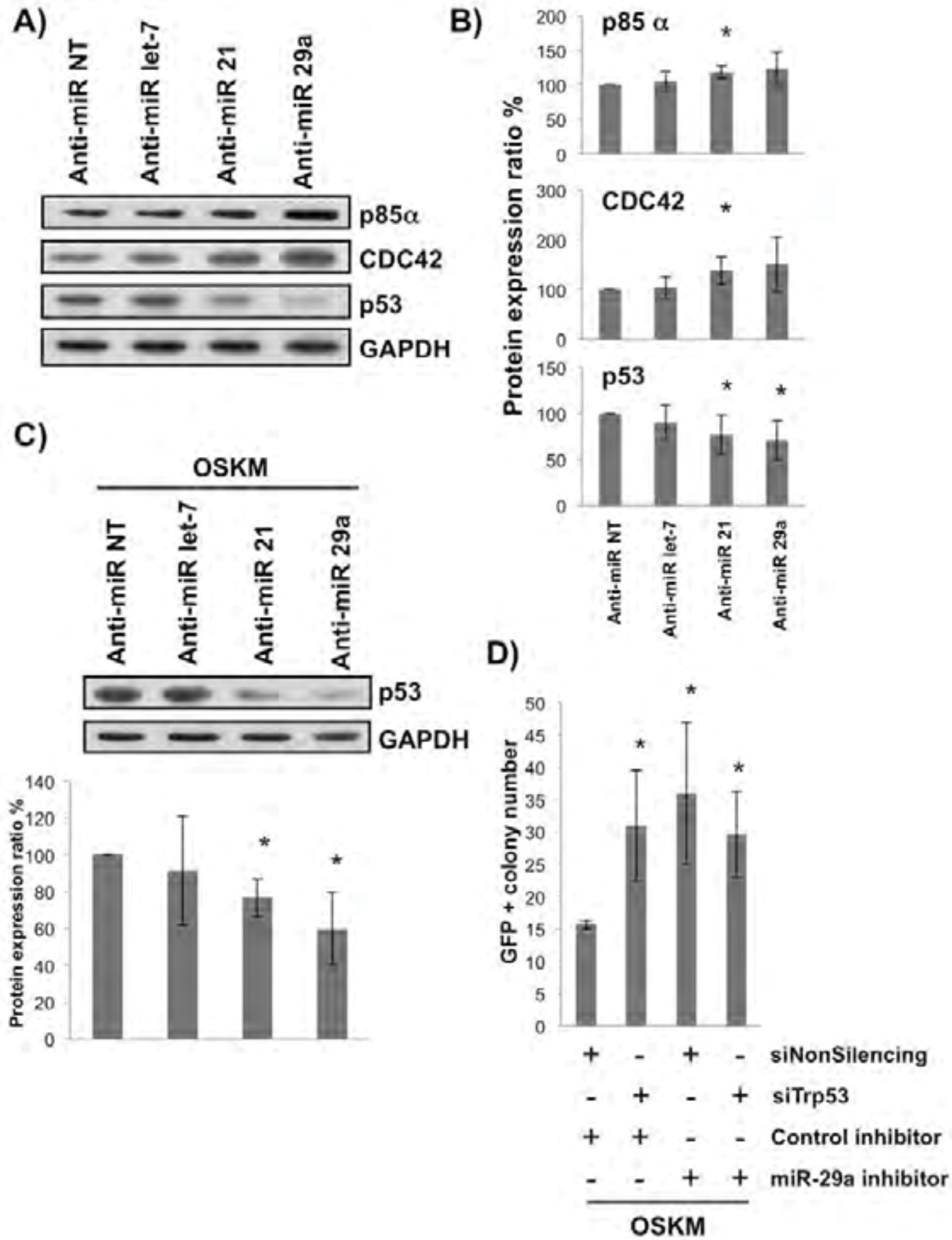

A)
Anti-miR NT
Anti-miR let-7
Anti-miR 21
Anti-miR 29a
p85α
CDC42
p53
GAPDH
B)
p85 α
CDC42
p53
Protein expression ratio %
C)
OSKM
p53
GAPDH
Protein expression ratio %
D)
GFP + colony number
siNonSilencing
siTrp53
Control inhibitor
miR-29a inhibitor
OSKM

Figure 2.7

Inhibition of miR-21 or miR-29a enhances iPS cell reprogramming by decreasing p53 protein levels and up-regulating p85α and CDC42 pathways.

(A) Western analysis of expression of p53, CDC42, and p85α following inhibition of various miRNAs. We transfected 1×10^5 Oct4-EGFP MEFs with the indicated miRNA inhibitors. Cells were harvested and analyzed 5 d later.

(B) Quantitative representation of protein expression in the presence of indicated miR inhibitors. Signal intensity was normalized to GAPDH intensity and is shown as a percentage relative to expression in control (NT) cells, which was set arbitrarily to 100. Error bars, SD of at least three independent experiments. **P*-value <0.05.

(C) Immunoblot analysis of p53, CDC42, and p85α expression following inhibition of various miRNAs and OSKM transduction. We transfected 1×10^5 Oct4-EGFP MEFs with the indicated miRNA inhibitors. Cells were harvested 5 d later and analyzed by immunoblot. Signal intensity was normalized as described in *B*. Error bars, SD of at least three independent experiments.**P*-value <0.05.

Figure 2.7 (continuation)

(D) Depleting miR-29a or p53 enhances reprogramming efficiency. We transfected 4×10^4 Oct4-EGFP MEFs with the indicated siRNAs and miRNA inhibitors, as well as OSKM reprogramming factors. GFP-positive cells were counted at day 12 after transduction. Error bars, SD of at least three independent experiments. **P*-value <0.05.

indirectly regulated by miR-29a in MEFs as well. To test that, MEFs were transfected with miRNA inhibitors and harvested 5 d for immunoblotting to evaluate expression of p53. p53 protein levels decreased by ~30% (Figures 2.7A and 2.7B) following miR-29a inhibition but were not altered by the NT control or by let-7a inhibition. Significantly, depleting miR-21 also released p85α and CDC42 protein repression, and consequently, the levels of p85α and CDC42 increased, which resulted in down-regulation of p53 expression by ~25% (Figures 2.7A and 2.7B).

To further confirm that p53 levels decrease with inhibition of miR-21 or miR-29a during reprogramming, we examined p53 expression at reprogramming day 5 by Western blot analysis. To initiate reprogramming we introduced miRNA inhibitors together with OSKM. Consistent with observations in MEFs alone, p53 protein levels decreased by ~25% or ~40% following miR-21 or miR-29a depletion, respectively, during reprogramming, compared with OSKM controls (Figure 2.7C). In summary, our data showed that blocking miR-29a reduced p53 protein levels by about 30%–40% through p85α and CDC42 pathways during reprogramming. In addition, depletion of miR-21 had a similar effect on both p85α and CDC42 and lowered p53 protein levels by about 25% to about 30%.

Inhibition of miR-29a enhances reprogramming efficiency through p53 down-regulation

It was recently reported that p53 deficiency can greatly increase reprogramming efficiency (Banito *et al.*, 2009b; Hong *et al.*, 2009; Judson *et al.*, 2009a; Kawamura *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009). Since depleting miR-29a significantly decreased p53 levels and increased reprogramming efficiency by about threefold (Figure 2.1), we asked whether the effect of miR-29a knockdown is mediated primarily by p53 down-regulation. To that end, we transfected p53 siRNA and/or the miR-29a inhibitor into Oct4-EGFP MEFs together with OSKM to initiate reprogramming. Down-regulation (~80%) of p53 by small interfering RNA (siRNA) had a similar positive effect on reprogramming efficiency as did miR-29a inhibition (Figure 2.7D). We did not observe an increase in reprogramming efficiency when miR inhibitors were added in the presence of p53 siRNA (Figure 2.7D). These results suggest that inhibition of miR-29a acts, in part (see below), through down-regulation of p53 to increase reprogramming efficiency.

Inhibition of miR-21 and miR-29a decreases phosphorylation of ERK1/2, but not GSK3β, to enhance reprogramming

miR21 reportedly activates MAPK/ERK through inhibition of the sprouty homologue 1 (Spry1) in cardiac fibroblasts (Thum *et al.*, 2008). Blocking MAPK/ERK activity promotes reprogramming of neural stem cells (Silva *et al.*, 2008b) and secures the ground state of ESC self-renewal (Nichols *et al.*, 2009; Ying *et al.*, 2008). Therefore, we asked whether miR-21 regulates the MAPK/ERK pathway during reprogramming by evaluating ERK1/2 phosphorylation in MEFs following the introduction of miRNA inhibitors. To test that, MEFs were transfected with miRNA inhibitors and then harvested for Western blot analysis to determine the phosphorylated ERK1/2 level. Western blot analysis showed that blocking miR-21 significantly decreased by ~45% the ERK1/2 phosphorylation relative to the NT controls, while let-7a inhibitors had no effect (Figure 2.8A). Interestingly, depleting MEFs of miR-29a also significantly reduced ERK1/2

Figure 2.8

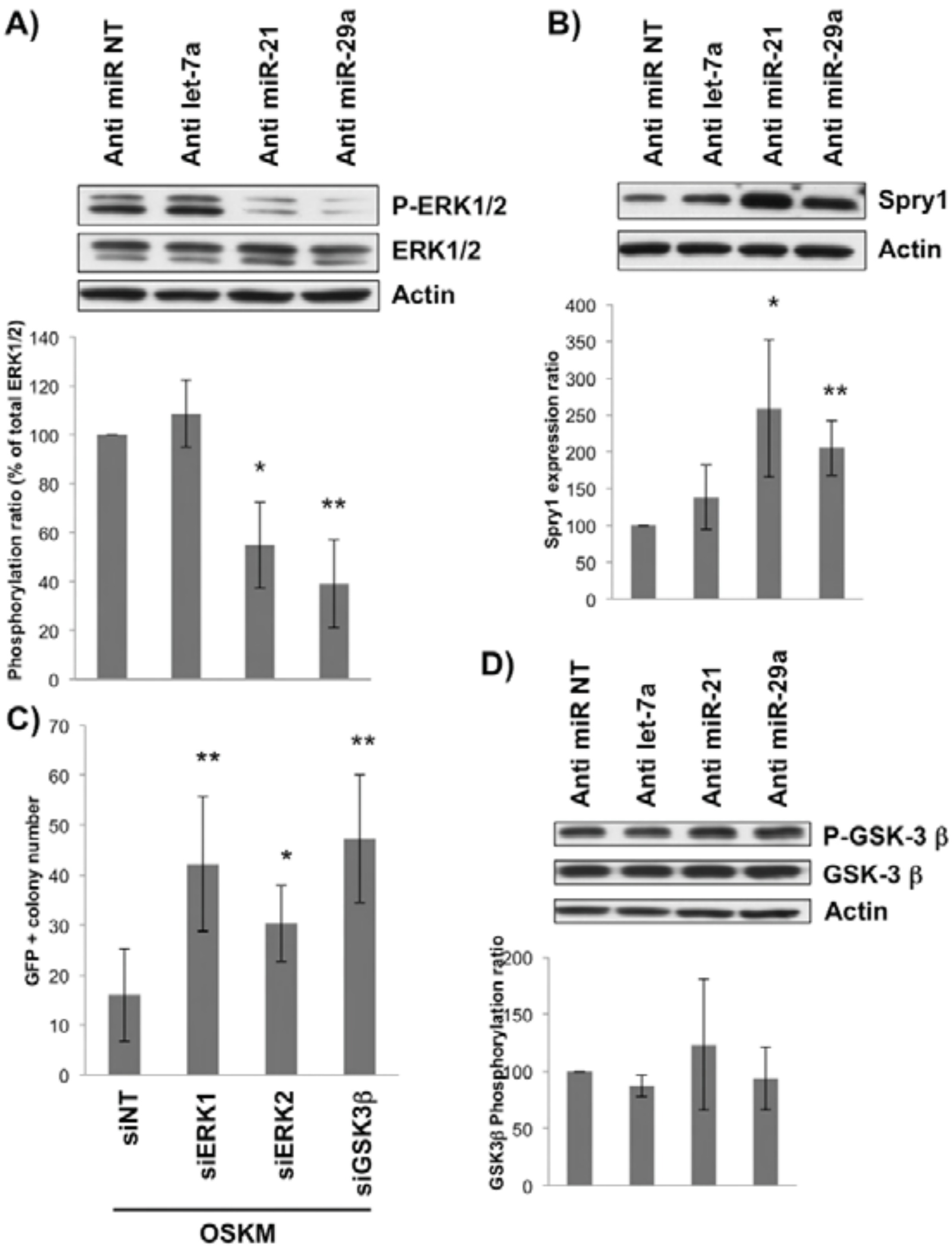

A)
Anti miR NT
Anti let-7a
Anti miR-21
Anti miR-29a
P-ERK1/2
ERK1/2
Actin
Phosphorylation ratio (% of total ERK1/2)
0
20
40
60
80
100
120
140
*
**
B)
Anti miR NT
Anti let-7a
Anti miR-21
Anti miR-29a
Spry1
Actin
Spry1 expression ratio
0
50
100
150
200
250
300
350
400
*
**
C)
GFP + colony number
0
10
20
30
40
50
60
70
**
*
**
siNT
siERK1
siERK2
siGSK3β
OSKM
D)
Anti miR NT
Anti let-7a
Anti miR-21
Anti miR-29a
P-GSK-3 β
GSK-3 β
Actin
GSK3β Phosphorylation ratio
0
50
100
150
200

Figure 2.8

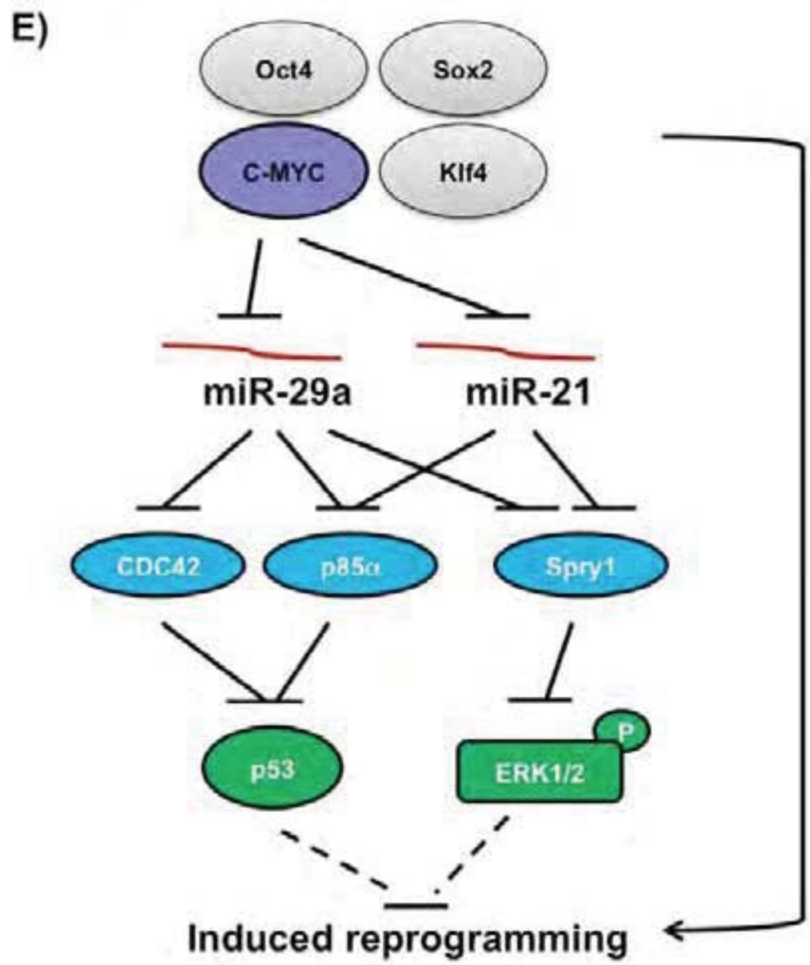

E)
Oct4
Sox2
C-MYC
Klf4
miR-29a
miR-21
CDC42
p85α
Spry1
p53
P
ERK1/2
Induced reprogramming

Figure 2.8

Depleting miR-21 and miR-29a promotes reprogramming efficiency by down-regulating the ERK1/2 pathway.

(A) Western analysis of phosphorylated and total ERK1/2 following inhibition of various miRNAs in MEFs. We transfected 1×10^5 Oct4-EGFP MEFs with the indicated miRNA inhibitors, harvested 5 d later, and immunoblotted. Signal intensity normalized to actin and shown as percentage relative to expression of anti-miR NT control. Error bars, SD of three independent experiments. *P-value <0.05; **P-value <0.005.

(B) Western blot analysis of Spry1 expression ratio shows that depleting miR-21 and miR-29a increases Spry1 protein levels. MEFs were transfected with various miRNA inhibitors as indicated. Cells were harvested at day 5 after transfection for Western blot analysis. Signal intensity normalized to actin and shown as described in *A*. Error bars, SD of three independent experiments. *P-value <0.05; **P-value <0.005.

(C) Fold-change in reprogramming efficiency following ERK1/2 or GSK3β knock-down. We transfected 4×10^4 Oct4-EGFP MEFs with the indicated siRNAs, as well as OSKM.

Figure 2.8 (continuation)

GFP-positive cells were counted 2 weeks later. Transfection with siNT serves as control for the reprogramming efficiency. Error bars, SD of three independent experiments. **P*-value <0.05; ***P*-value <0.005.

(D) Western analysis of phosphorylated and total GSK-3β following inhibition of various miRNAs in MEFs. We transfected 1×10^5 Oct4-EGFP MEFs with the indicated miRNA inhibitors, harvested 5 d later, and analyzed by immunoblot. Signal intensity normalized as described in *A*. Error bars, SD of three independent experiments.

(E) Schematic representation showing that c-Myc enhances reprogramming by down-regulating the MEF-enriched miRNAs, miR-21 and miR-29a. The p53 and ERK1/2 pathways function as barriers to reprogramming, and miR-21 and miR-29a indirectly activate those pathways through down-regulating CDC42, p85α, and Spry1. The cross-talk between miR-21/p53 and miR-29a/ERK1/2 pathways is also shown. c-Myc represses expression of these miRNAs and in turn compromises induction of ERK1/2 and p53. The dotted lines indicate p53 and ERK1/2 effects on iPS generation.

phosphorylation by 60% relative to the NT control (Figure 2.8A). Next we determined whether miR-21 and miR-29a affected ERK1/2 phosphorylation by altering Spry1 levels. We depleted miR-21 or miR-29a in MEFs by transfecting various miRNA inhibitors, and quantified Spry1 expression levels by immunoblotting. Our results showed that inhibiting miR-21 and miR-29a enhanced Spry1 expression levels (Figure 2.8B). Therefore, our data demonstrate that depleting miR-21 and miR-29a down-regulates phosphorylation of ERK1/2 by modulating Spry1 protein levels.

To address whether ERK1/2 down-regulation enhances reprogramming efficiency, we introduced siRNAs targeting ERK1 or ERK2 into Oct4-EGFP MEFs in the course of 4F-reprogramming. Depletion of either ERK1 or ERK2 significantly enhanced the generation of mature iPS cells (Figure 2.8C). As expected, our data showed that miR-21 acts as an inducer of ERK1/2 activation in MEFs, since blocking miR-21 reduced ERK1/2 phosphorylation. Depleting miR-29a also significantly diminished ERK1/2 phosphorylation. These results strongly suggest that miR-21 and miR-29a regulate ERK1/2 activity to modulate reprogramming efficiency (Figures 2.8A–C).

The GSK3β pathway also represses ES self-renewal and reprogramming of neural stem cells (Ying *et al.*, 2008). Depleting GSK3β with siRNA greatly increased mature iPS cell generation (Figure 2.8C). Therefore, we asked whether miRNA depletion regulated GSK3β activation. Immunoblotting showed that blocking miRNAs in Oct4-EGFP MEFs had no significant effect on GSK3β activation (Figure 2.8D). We then asked whether miRNA depletion alters apoptosis or cell proliferation during reprogramming by using flow cytometry to assess cell viability and replication rate. Blocking miRNA-21, miRNA-29a, or let-7 during reprogramming with OSKM did not alter apoptosis or proliferation rates (Figure 2.9). Overall, our results demonstrate that miR-29a and miR-21 modulate p53 and ERK1/2 pathways to regulate iPS cell reprogramming efficiency (Figure 2.8E).

Figure 2.9

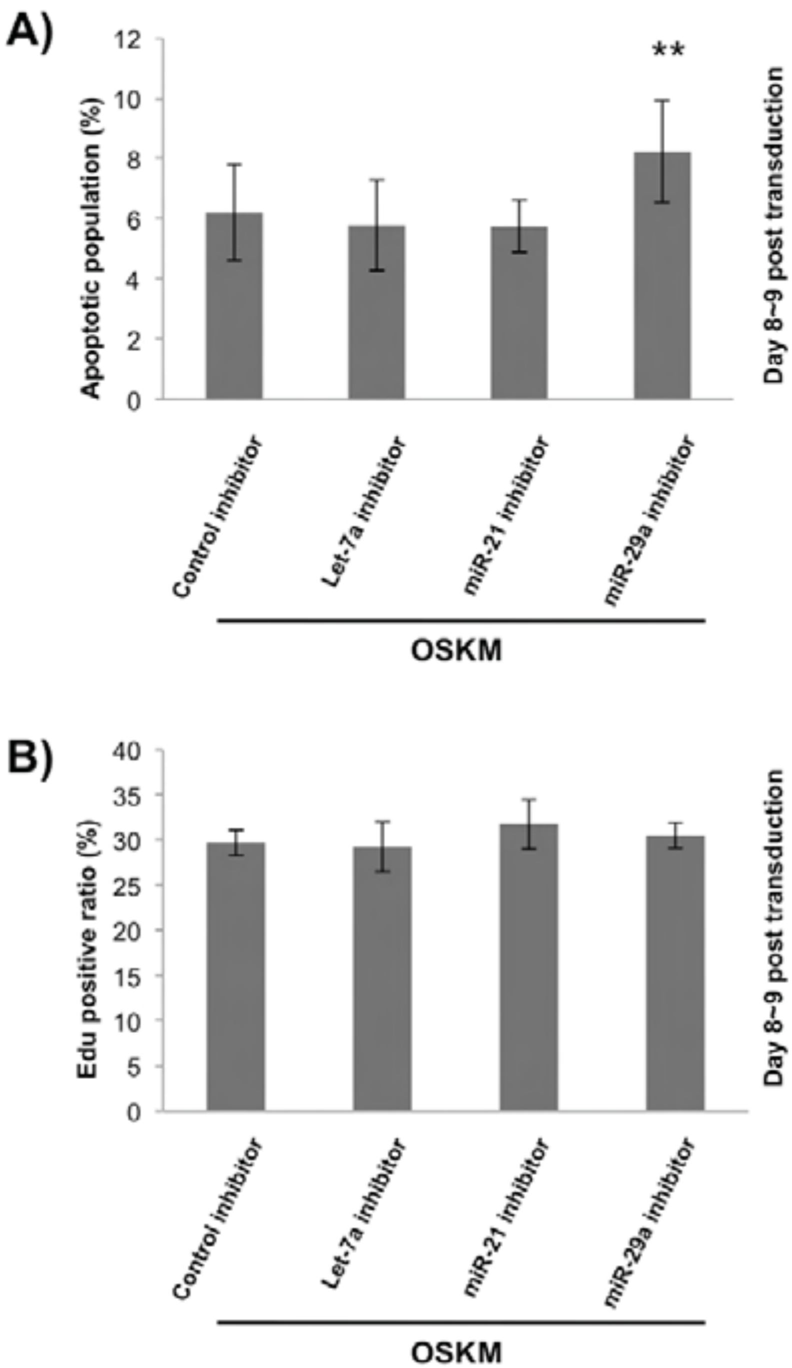

A)
Apoptotic population (%)
0
2
4
6
8
10
12
**
Day 8~9 post transduction
Control inhibitor
Let-7a inhibitor
miR-21 inhibitor
miR-29a inhibitor
OSKM
B)
Edu positive ratio (%)
0
5
10
15
20
25
30
35
40
Day 8~9 post transduction
Control inhibitor
Let-7a inhibitor
miR-21 inhibitor
miR-29a inhibitor
OSKM

Figure 2.9

Inhibition of miRNA does not alter apoptosis or proliferation rates during reprogramming.

(A) Inhibitors of miRNA were introduced into Oct4-MEFs during reprogramming with OSKM. Cells were collected at 8~9 days post transduction. Apoptosis was evaluated using a PE Annexin V Apoptosis Detection Kit I (BD Pharmingen; Cat# 559763) and 7-Amino-Actinomycin (7-AAD). The signal was detected by FACS. Error bars represent standard deviation of three independent experiments.

(B) miRNA inhibitors were introduced into Oct4-MEFs during reprogramming with OSKM. Cells were collected at 8~9 days post transduction. One day before collection, cells were treated with 5-ethynyl-2'-deoxyuridine (Edu) using Click-iT Edu Imaging Kits (Invitrogen; Cat# C10337). The signal was detected by FACS. Error bars represent standard deviation of three independent experiments.

Materials and Methods

MEF Derivation

Oct4-EGFP MEFs were derived from the mouse strain B6;129S4-*Pou5f1*$^{tm2(EGFP)Jae}$/J (Jackson Laboratory; stock no. 008214) using the protocol provided on the WiCell Research Institute website (http://www.wicell.org/). Oct4-EGFP MEFs were maintained in MEF complete medium (DMEM with 10% FBS, nonessential amino acids, L-glutamine, but without sodium pyruvate).

Reprogramming Using Retrovirus

Reprogramming was conducted as described (Takahashi and Yamanaka, 2006). In brief, 4×10^4 Oct4-EGFP MEFs were transduced with pMX retroviruses to overexpress Oct4, Sox2, Klf4, and c-Myc (Addgene). Two days later, transduced Oct4-EGFP MEFs were fed with ES medium (DMEM with 15% ES-screened FBS, nonessential amino acids, L-glutamine, monothioglycerol, and 1000 U/mL LIF), and the media were changed every other day. Reprogrammed pluripotent stem cells (defined as EGFP+ iPS cell colonies) were scored by fluorescence microscopy ~2 weeks after transduction, unless otherwise stated. To derive iPS cells, EGFP+ colonies were manually picked under a stereo microscope (Leica).

miRNA inhibitor or siRNA Transfection

Inhibitors of let-7a, miR-21, and miR-29a miRNAs were purchased from Dharmacon. We transfected 4×10^4 Oct4-EGFP MEFs with Lipofectamine and inhibitors according to manufacturer's instruction (Invitrogen). Three to 5 hours later, the medium was discarded and replaced with MEF complete medium; for reprogramming, retrovirus encoding reprogramming factors (Oct4, Sox2, Klf4, and c-Myc) was added and the medium was changed to complete medium the next day. Inhibitors or siRNAs were introduced again at day 5 after transfection/transduction, unless otherwise stated.

For Northern analysis, 1×10^5 Oct4-EGFP MEFs were transfected and harvested 5 day later. Total RNA was isolated by TRIZOL (Invitrogen) and ~9 µg of total RNA was resolved on a 14% denaturing polyacrylamide gel (National Diagnostics). RNAs were transferred onto Hybond-XL membranes (GE healthcare), and miRNAs were detected by isotopically labeled specific DNA probes. Signal intensity was visualized by phospho-imager and analyzed using Multi Gauge V3.0 (FUJIFILM). miRNA signal intensity was normalized to that of U6 snRNA. Experiments were performed in triplicate.

For Western analysis, 1×10^5 Oct4-EGFP MEFs were transfected and harvested 5 day later. Total proteins were prepared in M-PER buffer (Pierce), and equal amounts of total protein were separated on 10% SDS-PAGE gels. Proteins were transferred to PVDF membranes, and bands were detected using the following antibodies: GAPDH (Santa Cruz; catalog no. sc-20357), p53 (Santa Cruz; catalog no. sc-55476), PI3 kinase p85 (Cell Signaling; catalog no. 4257), Cdc42 (Santa Cruz; catalog no. sc-8401), p-ERK1/2 (Cell Signaling; catalog no. 9101), ERK1/2 (Cell Signaling; catalog no. 9102), p-GSK3β (Cell Signaling; catalog no. 9323), GSK3β (Cell Signaling; catalog no. 9315), and β-actin (Thermo Scientific; catalog no. MS-1295). Signal intensity was quantified by Multi Gauge V3.0 (FUJIFILM) and normalized to GAPDH or β-actin. Experiments were repeated three to five times.

In Vitro Differentiation and Teratoma Formation Assay

For *in vitro* differentiation, iPS cells were dissociated by trypsin/EDTA and re-suspended in EB medium (DMEM with 15% FBS, nonessential amino acid, L-glutamine) to a final concentration of 5×10^4 cells/mL. To induce EB formation, 1000 iPS cells in 20 µL were cultured in hanging drops on inverted Petri dish lids. Three to 5 d later, EBs were collected and transferred onto 0.1% gelatin-coated six-well plates at about 10 EBs per well. Two weeks after formation of EBs, beating cardiomyocytes (mesoderm) were identified by microscopy, and cells derived from endoderm and ectoderm were identified by α-fetoprotein (R&D; catalog no. MAB1368) and neuron-specific βIII-tubulin (abcam; catalog no. ab7751) antibodies, respectively.

For teratoma assays, 1.5×10^6 iPS cells were trypsinized and re-suspended in 150 µL and then injected subcutaneously into the dorsal hind limbs of athymic nude mice anesthetized with avertin. Three weeks later, mice were killed to collect teratomas. Tumor masses were fixed, dissected, and analyzed in the Cell Imaging-Histology core facility at the Sanford-Burnham Institute.

Chimera Analysis

iPS cell media was changed 2 hours before harvest. Trypsinized iPS cells were cultured on 0.1% gelatin-coated plates for 30 min to remove feeder cells. iPS cells were injected into E3.5 *C57BL/6-cBrd/cBrd* blastocysts and then transferred into pseudopregnant recipient females. After birth, the contribution of iPS cells was evaluated by pup coat color: agouti is from iPS cells.

Immunofluorescence and Alkaline Phosphatase Staining

iPS cells were seeded and cultured on 0.1% gelatin-coated six-well plates. Four days later, cells were fixed in 4% paraformaldehyde (Electron Microscopy Sciences; catalog no. 15710-S). For immunofluorescence staining, fixed cells were permeablized with 0.1% Triton X-100 in PBS and blocked in 5% BSA/PBS. Antibodies against SSEA-1 (R&D; catalog no. MAB2155) and Nanog (R&D; catalog no. AF2729) served as ES markers. Nuclei were visualized by Hoechst 33342 staining (Invitrogen). For alkaline phosphatase

(AP) staining, fixed cells were treated with AP substrate following the manufacturer's instruction (Vector Laboratories; catalog no. SK-5100).

CHAPTER III

Discovery of NSAID and anticancer drugs as reprogramming enhancers

Summary

Recent breakthroughs in creating induced pluripotent stem cells (iPS cells) provide alternative means to obtain embryonic stem-like cells without destroying embryos by introducing four reprogramming factors (*Oct3/4*, *Sox2*, and *Klf4*/*c-Myc or Nanog/Lin28*) into somatic cells. iPS cells are versatile tools for investigating early developmental processes and could become sources of tissues or cells for regenerative therapies. Here, for the first time, we describe a strategy to analyze genomics datasets of mouse embryonic fibroblasts (MEFs) and embryonic stem cells to identify genes constituting barriers to reprogramming. We further show that computational chemical biology combined with genomics analysis can be used to identify small molecules regulating reprogramming. Specific downregulation by small interfering RNAs (siRNAs) of several key MEF-specific genes encoding proteins with catalytic or regulatory functions, including *Wisp1, Prrx1, Hmga2, Nfix, Prkg2, Cox2,* and *Tgf-β3*, greatly increased

reprogramming efficiency. Based on this rationale, we screened only 17 small molecules in reprogramming assays and discovered that the non-steroidal anti-inflammatory drug Nabumetone and the anticancer drug 4-hydroxytamoxifen can generate iPS cells without Sox2. Nabumetone could also produce iPS cells in the absence of c-Myc or Sox2 without compromising self-renewal and pluripotency of derived iPS cells. In summary, we report a new concept of combining genomics and computational chemical biology to identify new drugs useful for iPS cell generation. This hypothesis-driven approach provides an alternative to shot-gun screening and accelerates understanding of molecular mechanisms underlying iPS cell induction.

Introduction

Embryonic stem (ES) cells are not only versatile tools for investigating early developmental events but provide a promising source of tissues potentially useful for regenerative therapies. Recent breakthroughs in generating induced pluripotent stem cells (iPS cells) provide alternative means to obtain ES-like cells without destroying embryos by introducing four reprogramming factors (*Oct3/4*, *Sox2*, and *Klf4*/*c-Myc or Nanog/*

Lin28) into somatic cells (Takahashi *et al.*, 2007; Takahashi and Yamanaka, 2006; Yu *et al.*, 2007). iPS cells share numerous traits with ES cells, such as colony morphology, transcriptome, self-renewal ability and pluripotency (Okita *et al.*, 2007; Yu *et al.*, 2007). Moreover, customized therapeutic applications of iPS cells have been reported (Hanna *et al.*, 2007; Soldner *et al.*, 2009; Staerk *et al.*, 2010). Nonetheless, the molecular basis of reprogramming remains unclear.

Reprogramming is a step-wise process moving from differentiated to ES-like stages (Brambrink *et al.*, 2008; Stadtfeld *et al.*, 2008a), a progression that can be monitored using various cellular markers. The differentiation marker, Thy1, is highly expressed in mouse embryonic fibroblasts (MEFs), and its expression in MEFs decreases within a few days of transduction with transgene Oct3/4, Sox2, Klf4, and c-Myc (denoted here 4F: OSKM). Consequently, expression of the stem cell marker SSEA1 increases, followed by activation of other ES markers, such as endogenous Nanog, Oct3/4, and X reactivation. During this process, iPS cells are enriched or selected (Hanna *et al.*, 2009). Increasing evidence indicates that the four reprogramming factors cooperatively initiate the transition of cell identity from somatic to iPS cells (Sridharan *et al.*, 2009). Based on these data, we reasoned that signature patterns of gene expression in MEFs constitute a barrier for induced reprogramming and that overcoming this barrier may be a rate-limiting step in the reprogramming process.

Here, for the first time, we describe a systematic strategy to analyze genomics datasets of MEFs and mouse embryonic stem cells (MESCs) to identify barriers to reprogramming. We show that computational drug screening combined with genomics analysis can identify small molecules that regulate reprogramming. We show that down-regulation by siRNAs of a several key MEF-specific genes encoding proteins with catalytic or regulatory functions, including *Wisp1, Prrx1, Hmga2, Nfix, Prkg2, Cox2,* and *Tgf-β3*, greatly increased reprogramming efficiency. Our drug screening results showed that: (a) the non-steroidal anti-inflammatory drug (NSAID) Nabumetone acts as a COX2 inhibitor to enhance reprogramming; (b) the anti-cancer drug OHTM can generate iPS cells without Sox2 during reprogramming by inducing endogenous Sox2 expression; and (c) Nabumetone can produce iPS cells in the absence of c-Myc or Sox2 without compromising self-renewal and pluripotency of derived iPS cells. In summary, our novel strategy combines genomics and computational drug screening to identify new drugs for reprogramming potentially leading to novel therapies.

Results

Silencing MEF-Specific Genes Encoding Catalytic or Regulatory Factors Enhance iPS cell Generation

To determine quantitatively which genes are specifically expressed in MEF and mouse embryonic stem cells (MESCs), we conducted mRNA a microarray analysis to examine mRNA expression profiles in both cell types. We focused on MEF-specific genes encoding catalytically active or regulatory proteins based on their important roles in cellular function, and selected *Wisp1, Prrx1, Hmga2, Nfix, Prkg2, Cox2, Tgf-β3, Lyzs,* and *6720477E09RIK* (Figure 3.1A) for further investigation. These genes are highly expressed in MEF but not MESC (Figure 3.1A & (Mikkelsen *et al.*, 2008)) and play key roles in various biological functions (please see Table 3.1 in Appendices). We

Figure 3.1

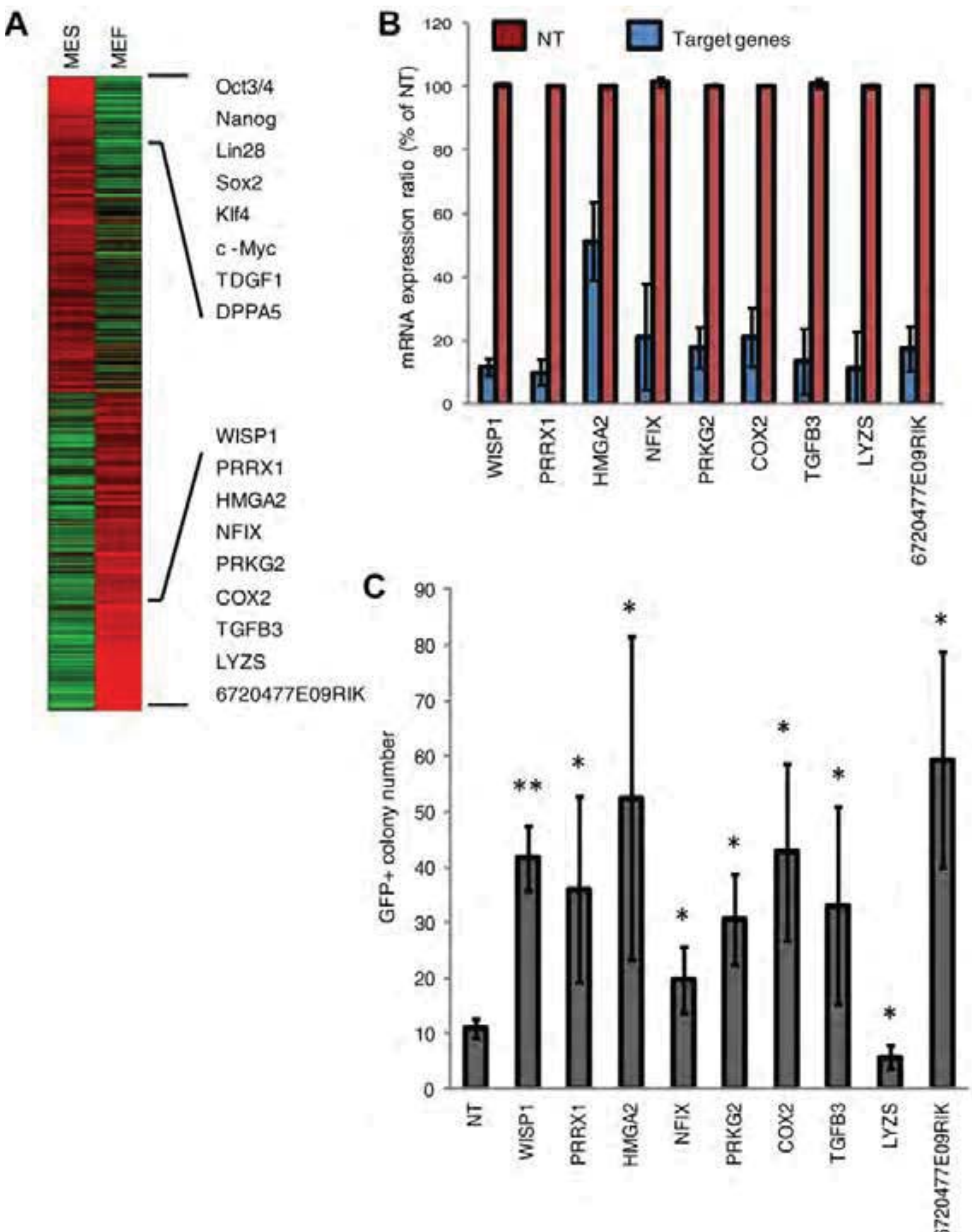

A
MES
MEF
Oct3/4
Nanog
Lin28
Sox2
Klf4
c -Myc
TDGF1
DPPA5
WISP1
PRRX1
HMGA2
NFIX
PRKG2
COX2
TGFB3
LYZS
6720477E09RIK
B
NT
Target genes
mRNA expression ratio (% of NT)
0
20
40
60
80
100
120
WISP1
PRRX1
HMGA2
NFIX
PRKG2
COX2
TGFB3
LYZS
6720477E09RIK
C
GFP+ colony number
0
10
20
30
40
50
60
70
80
90
NT
WISP1
PRRX1
HMGA2
NFIX
PRKG2
COX2
TGFB3
LYZS
6720477E09RIK

Figure 3.1

Inhibiting mouse embryonic fibroblast (MEF)-specific genes enhances induced pluripotent stem cell (iPS cell) reprogramming.

(A) Heat map representing mRNA microarray analysis of mouse embryonic stem cell (MESCs) and MEFs. Total RNA isolated from MEFs and MESCs was used for mRNA microarray analysis. The expression intensity of each gene is shown by colorimeter. Key genes encoding catalytic proteins from MEFs or self-renewal factors from MESCs were selected for further investigation.

(B) Efficient silencing of MEF-specific genes by small interfering RNAs (siRNAs). MEFs were transfected with siRNAs targeting indicated genes. Cells were harvested approximately 24 hours post-transfection for real time quantitative RT-PCR analysis. Nontargeting siRNA served as control. Error bars represent SDs of six independent experiments.

(C) Downregulation of MEF-specific genes significantly improves reprogramming. Oct4-EGFP MEFs were transduced with Oct3/4, Sox2, Klf4, and c-Myc and 5 days later

Figure 3.1 (continuation)

transfected with siRNAs targeting indicated genes. Mature reprogrammed iPS cells were identified as GFP+ colonies and counted by fluorescence microscopy at days 14–16. Error bars represent SDs of three independent experiments. *, $p < 0.05$; **, $p < 0.005$. Abbreviations: MEF, mouse embryonic fibroblast; MESC, mouse embryonic stem cell; NT, nontargeting; GFP, green fluorescent protein.

hypothesized that these factors may negatively regulate reprogramming from MEF to an ES-like stage by securing identities of fibroblasts and that down-regulation of these genes might enhance the reprogramming process. To test this hypothesis, we examined the effect of knockdown of these genes in Oct4-EGFP MEFs by specific siRNAs. Most genes were knocked down by at least 80% in siRNA-transfected Oct4-EGFP MEFs (Figure 3.1B), and that down-regulation persisted for at least five days post-transfection (data not shown). Since the duration of down-regulation was sufficient to exert an impact on reprogramming, we introduced the four reprogramming factors (4F or OSKM: Oct4, Sox2, Klf4, and c-Myc) into Oct4-EGFP MEFs followed by siRNA transfection five days later (Figures 3.1B & 3.1C). Two weeks later, mature reprogrammed iPS cells were identified based on EGFP-positivity and counted by fluorescence microscopy. Down-regulation of most of the MEF-specific genes encoding catalytic or regulatory factors greatly enhanced reprogramming efficiency by 2 to 6-fold (Figure 3.1C), compared with non-targeting (NT) control. The genes exhibiting barrier effects on reprogramming play distinct roles in cellular functions, such as signaling molecules

(*Wisp1* and *Tgf-β3*), transcriptional regulators (*Prrx1, Hmga2, Nfix*, and *6720477e09rik*), and catalytic enzymes (*Cox2* and *Prkg2*). Most of these identified genes are novel to reprogramming, except TGF-β pathway, which has been shown to act as a roadblock during reprogramming (Ichida *et al.*, 2009; Maherali and Hochedlinger, 2009a). Interestingly, *Lyzs* depletion showed reduction of iPS cells (Figure 3.1C). In addition, we examined quantitative expression of a selected set of MEF-specific genes during the reprogramming process (Figure 3.2). All the genes analyzed decreased upon induction of reprogramming, except *Cox2*, which increased at the early stage of reprogramming followed by a dramatic decrease (Figure 3.2A). Expression levels of all these genes were diminished in late stage of reprogramming (Day 12 or Day 15) as in ES cells. These gene expression patterns indicate that MEF-specific molecular network will be disrupted by 4F to achieve the cell fate transitions during reprogramming. In summary, these results support the idea that MEF-specific catalytic or regulatory proteins can negatively regulate reprogramming and also suggest that it is critical to modulate diverse biological functions during transition of cell identities such as MEFs to iPS cells.

Figure 3.2

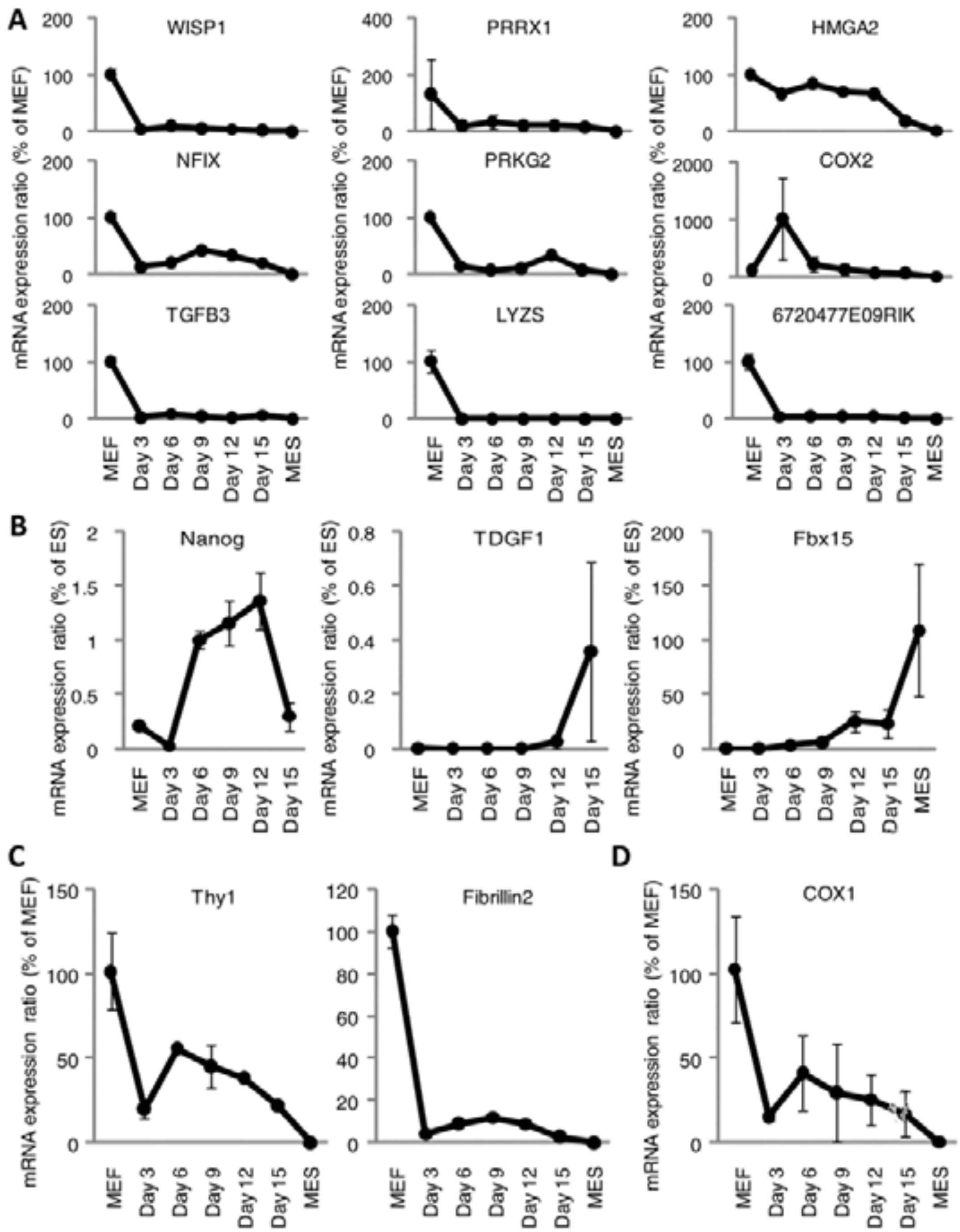

A
WISP1
PRRX1
HMGA2
NFIX
PRKG2
COX2
TGFB3
LYZS
6720477E09RIK
mRNA expression ratio (% of MEF)
MEF
Day 3
Day 6
Day 9
Day 12
Day 15
MES
B
Nanog
TDGF1
Fbx15
mRNA expression ratio (% of ES)
C
Thy1
Fibrillin2
D
COX1

Figure 3.2

Expression profiles of selected MEF-specific genes during reprogramming.

(A) Selected MEF-specific genes dramatically decrease during reprogramming, except *Cox2*. Real-time PCR analysis of a selected set of genes during reprogramming. Oct4-MEFs were transduced with OSKM to induce reprogramming. Transduced cells were collected at various time points for isolating total RNAs and real-time PCR analysis. GAPDH mRNA expression level served as internal control. Expression level of target genes was normalized to those in MEFs. MESC served as control. Error bars represent standard deviations of at least two independent experiments.

(B) Mouse embryonic stem cell (MESC)-specific genes were induced during reprogramming. Experiments were performed as described in A and served as indicators of reprogramming progress. Error bars represent standard deviations of at least two independent experiments.

(C) Differentiated markers Thy1 and Fibrillin2 were diminished during reprogramming. These data were created as described in panel A and served as indicators of

Figure 3.2 (continuation)

de-differentiation progress. Error bars represent standard deviations of at least two independent experiments.

(D) *Cox1* decreased dramatically upon induction of reprogramming. These data were created as described in panel A. Error bars represent standard deviations of at least two independent experiments.

The NSAID Nabumetone enhances iPS cell generation

Next, we developed a genomics database drug discovery strategy to identify small molecules that enhance reprogramming. To shorten the list without extensive shot-gun screening, we focused on candidate molecules that potentially either antagonized MEF-specific genes or upregulated MESC-specific/reprogramming genes (Figure 3.1A). To do so, we conducted computational screening by utilizing NextBio (www.nextbio.com) data-mining tools to collect information from public data sources (Kupershmidt *et al.*, 2010). NextBio provides an integrated platform to collect information from public databases, process these data using various pipelines, and then output analyzed results for customized purposes. Using highly enriched genes in either MESC or MEF (Figure 3.1A) as queries, we manually examined the information of meta-analysis and acquired 17 molecules (Table 3.2) that either negatively regulated MEF genes or positively affected MESC genes from various *in vitro* and *in vivo* studies deposited in public data base. We tested all 17 by examining alkaline phosphatase (AP) + colony formation during reprogramming while these molecules were applied. Molecules

Table 3.2. List of molecules for screening

ID	**Molecules**	**CAS #**	**Predicted targets**
1	Nickel sulfate hexahydrate ($NiSO_4$)	10101-97-0	WISP1, PRRX1, LYZS
2	2, 3, 7, 8-tetrachlorodibenzo-p-dioxin	1746-01-6	TGF-β3
3	Nabumetone	42924-53-8	COX2
4	4-hydroxytamoxifen (OHTM)	68047-06-3	Sox2
5	Moclobemide	71320-77-9	Nanog
6	Lectin		DPPA5
7	Corynanthine hydrochloride	66634-44-4	TDGF1
8	TGF-β		Oct3/4
9	Acitretin	55079-83-9	Oct3/4
10	Retinoic acid p-hydroxyanilide	65646-68-6	Oct3/4
11	Diacerein	13739-02-1	Nanog
12	Phorbol 12-myristate 13-acetate	16561-29-8	Nanog
13	Progesterone	57-83-0	Nanog
14	Tolazamide	1156-19-0	Nanog
15	15-deoxy-$\Delta^{12, 14}$-prostaglandin J_2	89886-60-2	Klf4
16	(-)-Norepinephrine	51-41-2	c-Myc
17	β-estradiol	50-28-2	c-Myc

not showing adverse effect on AP+ colony formation (data not shown) were picked for further study. To the end, we picked 6 molecules—Nabumetone, 4-hydroxytamoxifen (OHTM), Corynanthine, Moclobemide, NiSO4, and lectin—for further analysis (Figure 3.3A). To evaluate their effect on induction of mature GFP+ iPS cells, we treated OSKM-transduced Oct4-EGFP MEFs four days after transduction with each of these factors separately. Among the six, the NSAID prostaglandin-endoperoxide synthase (PTGS) and the cyclooxygenase (COX) inhibitor Nabumetone greatly increased the number of reprogrammed colonies by at least 2.8-fold (Figure 3.3B) compared with DMSO controls, while lectin showed minor but consistent improvement on iPS cell formation. Since MEFs mainly express the COX2 isozyme (verified by RT-qPCR, data not shown & (Mikkelsen *et al.*, 2008)), we proposed that COX2 is the primary Nabumetone target during reprogramming. To test that idea, we knocked down COX2 in Oct4-EGFP MEFs by siRNA with or without Nabumetone during reprogramming with OSKM. In the presence of control siRNA (siNT), Nabumetone alone enhanced reprogramming efficiency by more than 6-fold (Figure 3.3C) compared with DMSO

Figure 3.3

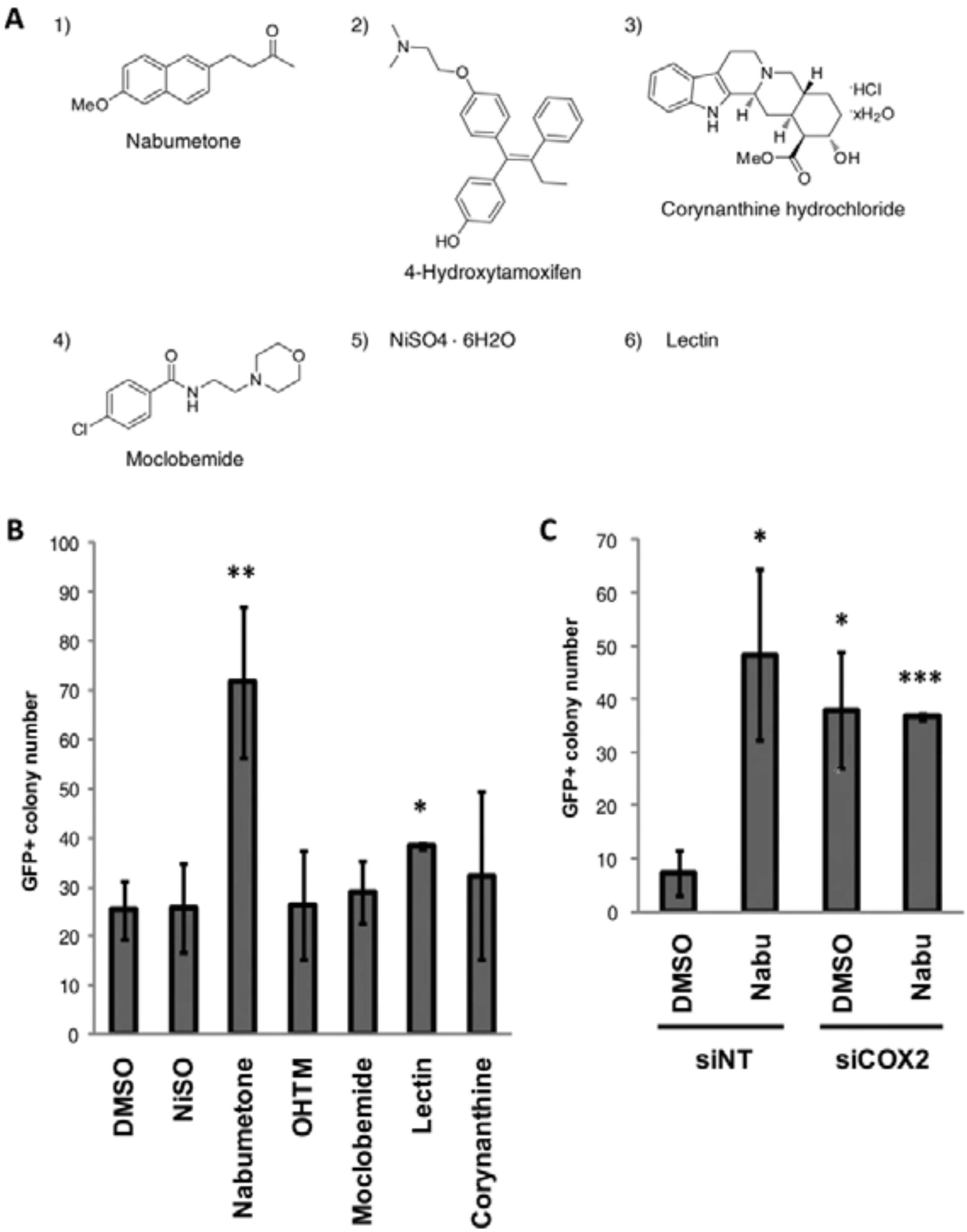

A
1)
Nabumetone
MeO
2)
4-Hydroxytamoxifen
HO
3)
Corynanthine hydrochloride
·HCl
·xH2O
MeO
OH
4)
Moclobemide
Cl
5) NiSO4 · 6H2O
6) Lectin
B
GFP+ colony number
DMSO
NiSO
Nabumetone
OHTM
Moclobemide
Lectin
Corynanthine
C
GFP+ colony number
DMSO
Nabu
DMSO
Nabu
siNT
siCOX2

Figure 3.3

Nabumetone significantly enhances iPS cell reprogramming by inhibiting COX2

(A) Structures of six small molecules used in iPS cell reprogramming. Small molecules were selected by analyzing MEF and MESC genomics data as described in text.

(B) Nabumetone significantly boosts OSKM-induced reprogramming while lectin showed minor but consistent increase as well. Oct4-EGFP MEFs were transduced with OSKM and four days later treated with individual small molecules for at least 10 days. GFP+ colonies were identified as described in Fig 1. Error bars represent standard deviations of three independent experiments. * *P* value < 0.05; ** *P* value < 0.005.

(C) Nabumetone improves reprogramming through blocking COX2. Oct4-EGFP MEFs were transduced with OSKM. Four days later, cells were treated with Nabumetone or DMSO. The next day, cells were transfected with various siRNAs as indicated. GFP+ colonies were identified as described in Fig 1 at day 12 ~ 14. Error bars represent

Figure 3.3 (continuation)

standard deviations of six independent experiments. * *P* value < 0.05; *** *P* value <

0.0005. siNT serves as control. Nabu is abbreviation of Nabumetone.

treatment. Transduction of cells with COX2 siRNA increased the number of GFP+ iPS cell colonies by over 5-fold compared with cells transduced with siNT control (Figure 3.3C). However, we observed no further enhancement of reprogramming efficiency in the presence of both siCOX2 and Nabumetone (Figure 3.3C), likely due to the maximal COX2 silencing effects by siRNA. To determine whether the COX2 is the main target instead of COX1, which is constitutively expressed in various tissues, we applied selective inhibitors targeting either COX1 or COX2 during reprogramming with OSKM or OSK (Futaki *et al.*, 1994; Laneuville *et al.*, 1994; Reddy *et al.*, 1996). Interestingly, only the selective COX2 inhibitors, Celecoxib and NS-398, showed similar effects on iPS cell generation as Nabumetone with OSKM or OSK pluripotency factors (Figure 3.4). On the other hand, selective COX1 inhibitor, Indomethacin, showed no effect to boost reprogramming with OSKM or OSK (Figure 3.4), although COX1 greatly decreased upon induction of reprogramming (Figure 3.2D). To further investigate the role of COX2 in reprogramming, we cloned and overexpressed COX2 along with OSKM during reprogramming. Our results show that overexpression of COX2 compromised

Figure 3.4

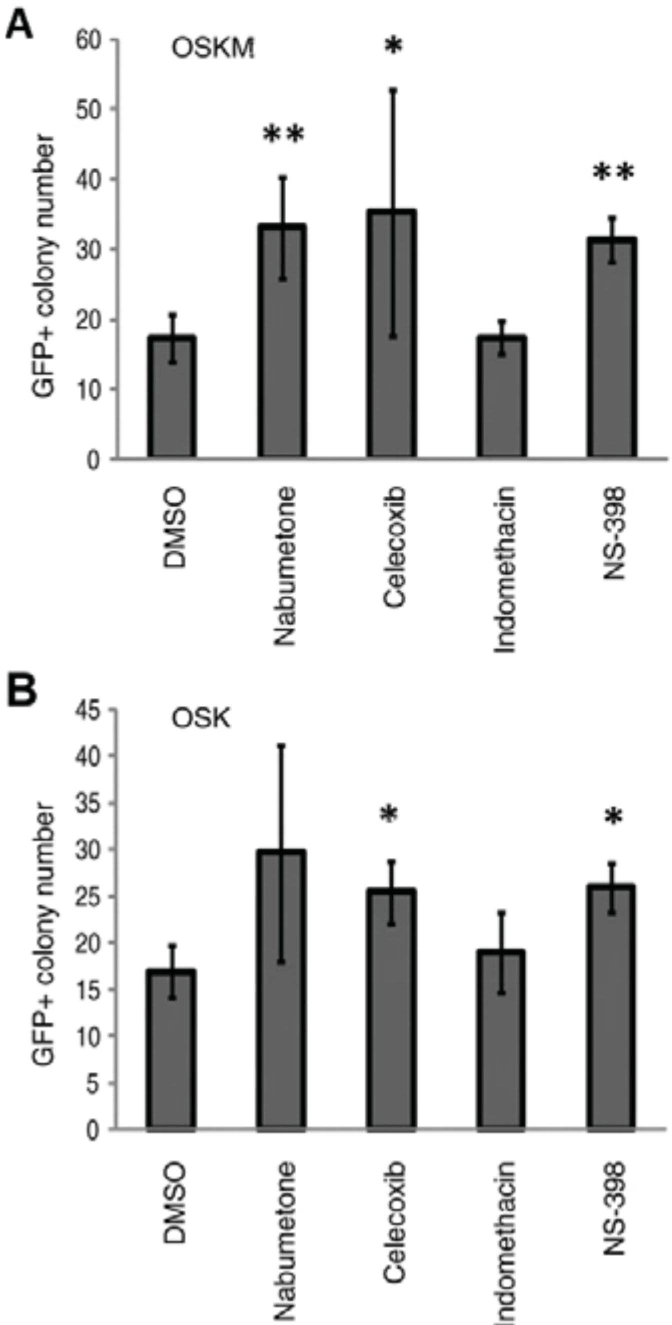

A
OSKM
GFP+ colony number
0
10
20
30
40
50
60
**
*
**
DMSO
Nabumetone
Celecoxib
Indomethacin
NS-398
B
OSK
GFP+ colony number
0
5
10
15
20
25
30
35
40
45
*
*
DMSO
Nabumetone
Celecoxib
Indomethacin
NS-398

Figure 3.4

Specific COX2 inhibitors significantly enhance OSKM and OSK reprogramming.

Oct4-MEFs were transduced with OSKM **(A)** or OSK **(B)** to induce reprogramming. Small molecules were applied at day 4~5 post transduction. EGFP+ colony number was scored under fluorescent microscopy at two weeks post transduction. Error bars represent standard deviations of at least three independent experiments. * P value < 0.05; ** P value < 0.005.

reprogramming with OSKM pluripotency factors (Figure 3.5). Overall, these results support the notion that COX2 is a barrier for reprogramming and that Nabumetone enhances reprogramming by mainly blocking COX2 activity.

Nabumetone can generate iPS cells in the absence of c-Myc

To further analyze Nabumetone reprogramming potential, we asked whether Nabumetone can replace the proto-oncogene c-Myc, which may greatly increase tumorigenesis *in vivo*. Oct4-EGFP MEFs were reprogrammed using either OSKM or OSK without c-Myc, and induced cells were treated with Nabumetone or DMSO four days later. Nabumetone treatment significantly enhanced reprogramming by OSK by ~2.5-fold as assessed at day 21 (Figure 3.6A) compared with control OSK+DMSO. This data suggests that Nabumetone not only improves OSKM reprogramming, likely by blocking COX2, but also can substitute c-Myc function in the process.

Figure 3.5

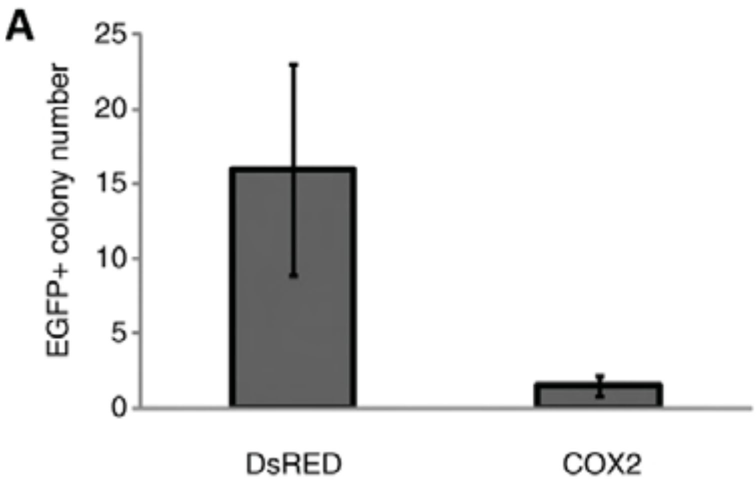


Figure 3.5

Overexpression of COX2 compromises OSKM reprogramming.

A) Oct4-MEFs were transduced with OSKM to induce reprogramming. Retroviruses overexpressing *COX2* transgene were transduced one-day post OSKM transduction. EGFP+ colony number was scored under fluorescent microscopy at two weeks post transduction. Error bars represent standard deviations of at least three independent experiments. DsRED transgene served as control.

Figure 3.6

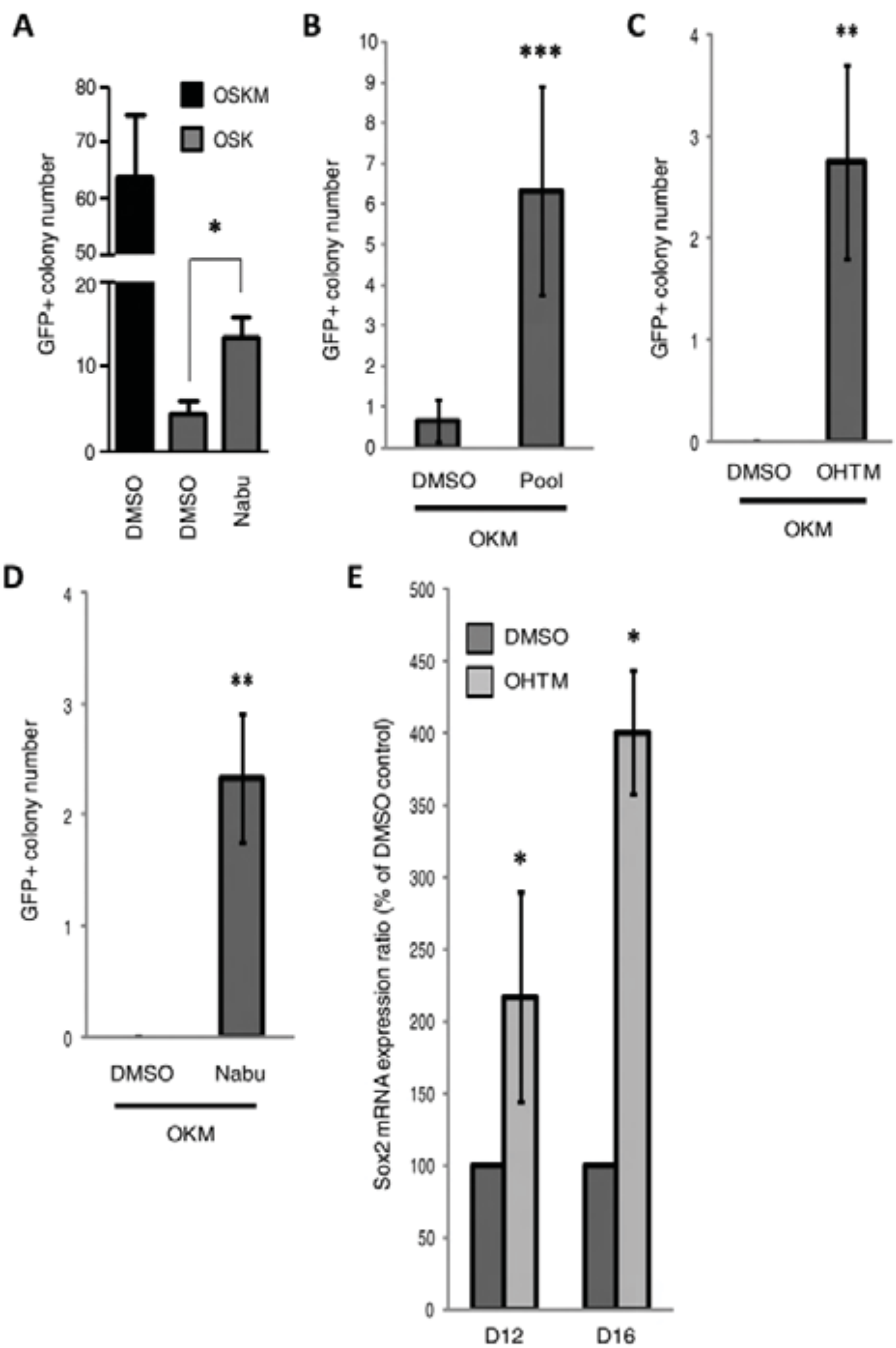

A
B
C
D
E
GFP+ colony number
OSKM
OSK
DMSO
DMSO
Nabu
Pool
OKM
OHTM
Sox2 mRNA expression ratio (% of DMSO control)
D12
D16

Figure 3.6

Small molecules can generate iPS cells in the absence of c-Myc and Sox2

(A) Nabumetone and OSK reprogram MEF. Oct4-EGFP MEFs were transduced with OSK without c-Myc and four days later treated with Nabumetone or DMSO for two weeks. Cells transduced with OSKM are shown for comparison. GFP+ colonies were identified as described in Fig. 1 at day 21. Error bars represent standard deviations of two independent experiments. * *P* value < 0.05.

(B) A pool of six molecules with OKM reprograms MEFs to iPS cells. Oct4-EGFP MEFs were transduced with OKM and treated with pool of 6 molecules, including $NiSO_4$, Nabumetone, OHTM, Moclobemide, Lectin, and Corynanthine, at day 4 for at least 10 days. GFP+ colonies were identified and counted as described in Fig. 1 at day 14. Error bars represent standard deviations of six independent experiments. *** *P* value < 0.0005.

(C) OHTM and OKM reprogram MEFs to iPS cells. Oct4-EGFP MEFs were transduced with OKM and four days later treated with 1.25 mM OHTM at least 10 days. GFP+ colonies were counted as described in Fig. 1 at day 15~21. Error bars represent standard

Figure 3.6 (continuation)

deviations of four independent experiments. ** *P* value < 0.005.

(D) Nabumetone plus OKM reprograms MEFs to iPS cells. Oct4-EGFP MEFs were transduced with OKM and four days later treated with 2.18 mM Nabumetone (Nabu) for at least 10 days. GFP+ colonies were counted as described in Fig. 1 at day 17~21. Error bars represent standard deviations of three independent experiments. ** *P* value < 0.005.

(E) Sox2 expression is significantly induced by OHTM during OKM-induced reprogramming. Oct4-EGFP MEFs were transduced with OKM and treated with OHTM four days later. Cells were harvested at indicated days (D) for real time RT-PCR analysis. β actin expression serves as an internal control. Error bars represent standard deviation of 3 independent experiments. * *P* value < 0.05.

OHTM and Nabumetone can produce iPS cells without Sox2

We next asked whether the small molecules identified in our analysis can replace the need for other reprogramming factors. To do so we tested a pool of the six candidate molecules for their ability to replace any single reprogramming factor. Strikingly, the pool replaced Sox2 during reprogramming of Oct4-EGFP MEF with OKM and significantly increased reprogramming efficiency by more than 10-fold (Figure 3.6B) compared with controls. To determine which molecule(s) exerted that effect, we individually tested each of the six small molecules in OKM reprogramming protocols. We found that the anti-cancer drug OHTM significantly improved OKM-induced reprogramming, while OKM+DMSO did not produce any mature iPS cell colonies (Figure 3.6C). Similarly, Nabumetone significantly improved OKM-induced reprogramming, which showed comparable effect with OHTM (Figure 3.6D). Overall, these results indicate that either OHTM or Nabumetone can substitute Sox2 function to generate iPS cells.

OHTM increases endogenous Sox2 expression during OKM reprogramming

To understand the molecular mechanism underlying OHTM's effect on reprogramming, we asked whether OHTM induces endogenous Sox2 expression. To do so, we applied OHTM or control DMSO to Oct4-EGFP MEF four days after transduction with OKM. Cells were harvested at indicated time points for total RNA isolation and real time PCR analysis (Figure 3.6E). Strikingly, endogenous Sox2 mRNA was significantly induced by 220% by OHTM in OKM-transduced cells at day 12 and by 400% at day 16 compared with OKM+DMSO controls, indicating that OHTM enhances reprogramming, at least partially, by increasing endogenous Sox2 expression. However, the direct targets of OHTM to affect Sox2 expression are not clear.

OKM+OHTM or OKM+Nabumetone iPS cells attain ES identity and pluripotency

To verify whether iPS cells derived with OKM in the presence of our pooled or individual molecules attain self-renewal and pluripotency, we analyzed iPS cells for these properties. Genomic DNAs were isolated from OKM plus the six-molecule pool (OKM+6), OKM+OHTM, or OKM+Nabumetone iPS cells to verify transgene integration by PCR analysis. OKM iPS cell clones showed no Sox2 transgene integration

(Figures 3.7B and 3.7C), demonstrating OKM iPS cells could be derived with pool of six molecules, OHTM or Nabumetone alone in the absence of Sox2 transgene. When we cultured OKM iPS cells for at least one month (> 10 passages) and fixed them for immunostaining, OKM+6 and OKM+Nabumetone iPS cells exhibited ES-like dome shape morphology with a clear boundary (Figures 3.7A and 3.8A), and they highly expressed endogenous Oct3/4 (EGFP) and Nanog (Figures 3.7A and 3.8A), indicating establishment of ES-like transcriptional networks. OKM+6 iPS cells expressed SSEA1 (Figure 3.7A), and OKM+Nabumetone iPS cells also acquired the stem cell marker alkaline phosphatase (AP) (Figure 3.8A). Importantly, endogenous Sox2 expression was activated in OKM+Nabumetone iPS cells (Figure 3.8A), suggesting that a full self-renewal circuit was restored. To confirm restoration of an ES-like transcriptome, we examined mRNA expression profiles of OKM+OHTM and OKM+Nabumetone iPS cells by microarray analysis. Representative clones from OKM+OHTM iPS cells showed a high degree of similarity with ES cells, but not MEFs (Figure 3.8B), as did OKM+Nabumetone iPS clones (Figure 3.8B).

Figure 3.7

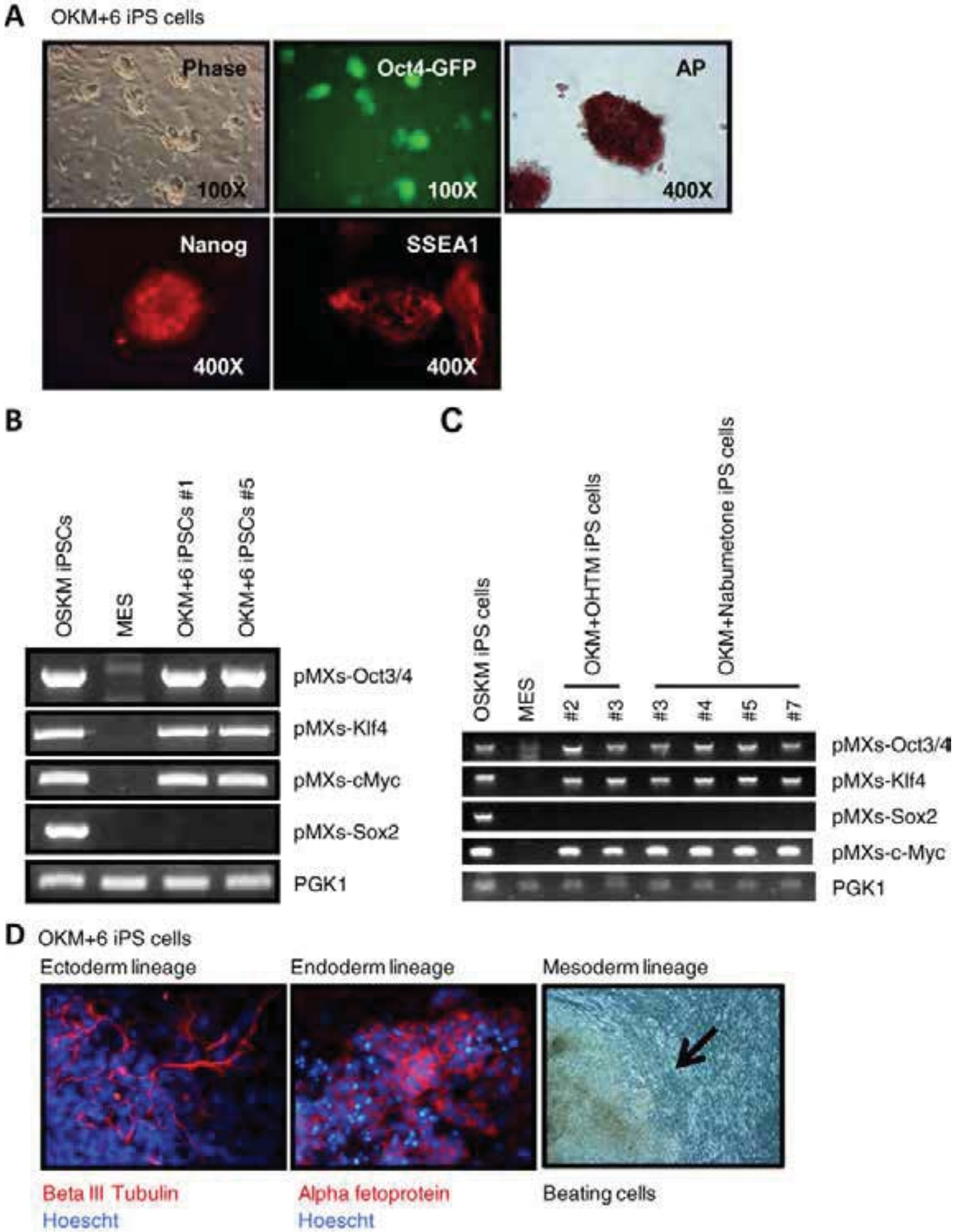

A
OKM+6 iPS cells
Phase
100X
Oct4-GFP
100X
AP
400X
Nanog
400X
SSEA1
400X
B
OSKM iPSCs
MES
OKM+6 iPSCs #1
OKM+6 iPSCs #5
pMXs-Oct3/4
pMXs-Klf4
pMXs-cMyc
pMXs-Sox2
PGK1
C
OSKM iPS cells
MES
OKM+OHTM iPS cells
OKM+Nabumetone iPS cells
#2
#3
#3
#4
#5
#7
pMXs-Oct3/4
pMXs-Klf4
pMXs-Sox2
pMXs-c-Myc
PGK1
D
OKM+6 iPS cells
Ectoderm lineage
Endoderm lineage
Mesoderm lineage
Beta III Tubulin
Hoescht
Alpha fetoprotein
Hoescht
Beating cells

Figure 3.7

Characterization of OKM+6 factor-derived iPS cells

(A) iPS cells derived by OKM plus six molecules express ES cell-specific markers. Immunostaining for ES markers of OKM+6 iPS cells. OKM+6 iPS cells were grown on gelatin-coated plates and fixed for immunostaining. Representative colonies express the stem cell markers Nanog, SSEA1, alkaline phosphatase (AP), and endogenous Oct3/4 (Oct4-EGFP). Magnification is indicated.

(B) OKM+6 iPS cells are derived without a Sox2 transgene. PCR analysis of pMXs transgene (pMXs is the plasmid name followed by transgenes of interests) integration. Genomic DNA (gDNA) was isolated from two different lines (#1 and #5) of OKM+6 iPS cells. Equivalent amounts of gDNA served as template for PCR assays using primers to detect pMXs retro transgenes. OSKM iPS serves as a positive control and MESC as a negative control for transgene integration. PGK1 served as internal control.

(C) OKM+Nabumetone and OKM+OHTM iPS cells are derived without the Sox2 transgene. PCR analysis of pMXs transgene integration. Genomic DNA was isolated

Figure 3.7 (continuation)

from different cell lines, such as OSKM, OKM+OHTM, and OKM+Nabumetone iPS cells. Equivalent gDNA was used for each PCR with primers specific for each pMXs retro transgenes. OSKM iPS serves as a positive control and MESC as negative control for transgene integration. PGK1 serves as an internal control.

(D) OKM+6 iPS cells can differentiate into three germ layers *in vitro*. Immunostaining for germ layer-specific differentiation markers in tissues derived from OKM+6 iPS cells. Embryoid bodies were formed *in vitro* and cultured for 2 weeks. Cells were fixed and stained with anti-AFP (endoderm) or anti-beta tubulin III (ectoderm). Beating cells derived from mesoderm are indicated by arrow.

Figure 3.8

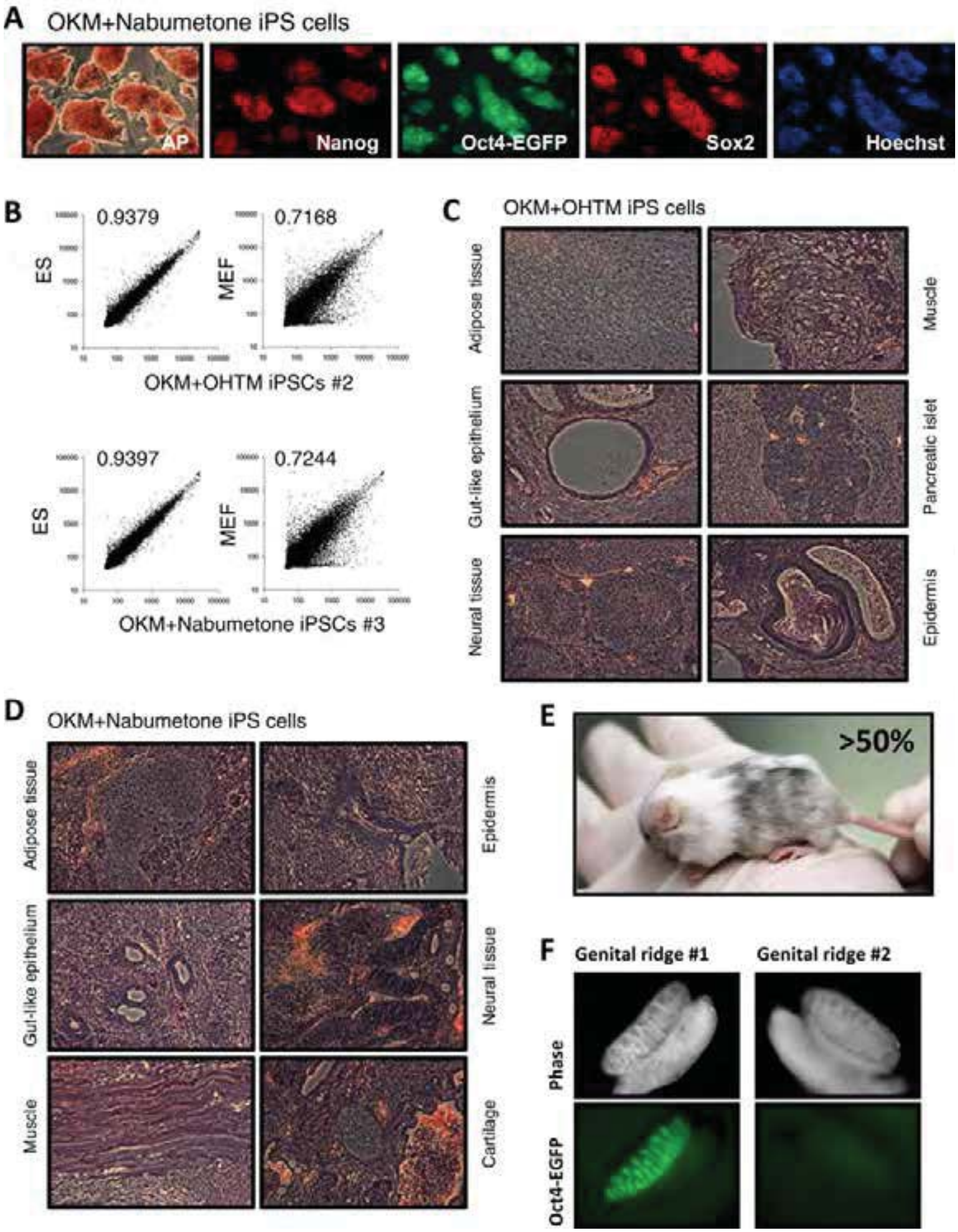

A
OKM+Nabumetone iPS cells
AP
Nanog
Oct4-EGFP
Sox2
Hoechst
B
0.9379
ES
0.7168
MEF
OKM+OHTM iPSCs #2
0.9397
ES
0.7244
MEF
OKM+Nabumetone iPSCs #3
C
OKM+OHTM iPS cells
Adipose tissue
Muscle
Gut-like epithelium
Pancreatic islet
Neural tissue
Epidermis
D
OKM+Nabumetone iPS cells
Adipose tissue
Epidermis
Gut-like epithelium
Neural tissue
Muscle
Cartilage
E
>50%
F
Genital ridge #1
Genital ridge #2
Phase
Oct4-EGFP

Figure 3.8

iPS cells derived by OKM + Nabumetone or OKM + OHTM acquire pluripotency

(A) Sox2 expression is reactivated in OKM+Nabumetone iPS cells. OKM+Nabumetone (OKM+Nab) iPS cells were fixed and immunostained for ES cell markers. Representative colonies express ES cell markers Nanog, alkaline phosphatase (AP), and endogenous Oct3/4 (Oct4-EGFP). Endogenous Sox2 was also activated. Hoechst counterstain marks nuclei.

(B) OKM+Nabumetone and OKM+OHTM iPS cells share transcriptional profiles similar to MES cells but not MEFs. Scatter plots show transcriptome comparison of iPS clones with ES or MEF cells. Total RNA was isolated from indicated iPS cells and subjected to mRNA microarray analysis. R^2 values are shown at the top of each panel.

(C) & (D) OKM+Nabumetone and OKM+OHTM iPS cells can differentiate into various cell types. Teratoma formation analysis of OKM+Nabumetone and OKM+OHTM iPS cells. $1.5X10^6$ iPS cells were injected subcutaneously into athymic nude female mice and tumor masses collected three weeks later. Histopathological analysis shows that tissues

Figure 3.8 (continuation)

derived from all three germ layers were identified, including gut-like epithelium and pancreatic islets (endoderm), adipose tissue, cartilage, and muscle (mesoderm), and neural tissue and epidermis (ectoderm).

(E) OKM+Nabumetone iPS cells contribute to chimera mice. OKM+Nabumetone iPS cells were injected into E3.5 blastocysts to create chimera mice. Seventeen days after birth, agouti coat color was used to determine OKM iPS cells contribution in chimera mice. The representative picture shows >50% contribution of OKM+Nabumetone iPS cells.

(F) OKM+Nabumetone iPS cells contribute to germline formation. OKM+Nabumetone iPS cells were injected into E3.5 blastocysts to create chimera mice. E13.5 embryos were collected from recipient mice for harvesting genital ridge. Germline transmission was determined by Oct4-EGFP expression, indicating contribution of OKM+Nabumetone iPS cells.

To determine whether OKM plus small molecule-derived iPS cells show pluripotency comparable to ES cells, we first tested *in vitro* differentiation capacity. OKM+6 iPS cells were induced to form embryoid bodies (EBs) for two weeks, and then fixed for immunostaining. After two weeks of *in vitro* differentiation, cell types typical of all three germ layers were observed (Figure 3.7D). To further assess differentiation potential, OKM+OHTM and OKM+Nabumetone iPS cells were injected into nude mice and allowed to differentiate into various tissues. Teratomas, which were observed three weeks post injection, were subjected to histopathological analysis. Tissues originating from all three germ layers were generated (Figures 3.8C and 3.8D), confirming that iPS cells were pluripotent. To vigorously test pluripotency of OKM iPS cells, OKM+Nabumetone iPS cells were injected into embryonic day (E) 3.5 blastocysts to create chimera. Contributions of OKM+Nabumetone iPS cells to chimera mice were accessed by black coat color at day 17 after birth. We obtained OKM+Nabumetone iPS cells contribution up to 50% (Figure 3.8E). We next examined the germline transmission capability of OKM+Nabumetone iPS cells. By analyzing E13.5 embryos after injecting

OKM+Nabumetone iPS cells into blastocysts, we found strong Oct4-EGFP expression in genital ridge (Figure 3.8F), showing germline contribution of OKM+Nabumetone iPS cells. In summary, our data demonstrate that small molecule with OKM derived iPS cells do attain ES identity and pluripotency.

Materials and Methods

MEF Derivation

Oct4-EGFP MEFs were derived from the mouse strain B6;129S4-*Pou5f1*$^{tm2(EGFP)Jae}$/J (The Jackson Laboratory, Bar Harbor, Maine, USA, http://www.jax.org/; stock #008214) following the protocol on the WiCell Research Institute, Madison, WI, USA, http://www.wicell.org/ website. In brief, embryonic day 13.5 (E13.5) embryos were collected from time-mated pregnant female mice and then tested for microbial contamination. Oct4-EGFP MEFs were maintained in MEF complete medium (Dulbecco's modified Eagle's medium [For DMEM or culture medium & materials: Gibco Cell Culture, Carlsbad, CA, USA, http://www.invitrogen.com/gibco] with 10% fetal bovine serum (FBS), nonessential amino acids, L-glutamine, and no sodium pyruvate). Cells passaged fewer than five times were used for induced reprogramming.

Reprogramming by Retrovirus-Mediated Transduction of Factors

Reprogramming was conducted as described (Takahashi and Yamanaka, 2006). In brief, 4×10^4 Oct4-enhanced green fluorescent protein (EGFP) MEFs were transduced with pMXs retroviruses for ectopic expression of *Oct4*, *Sox2*, *Klf4*, and *c-Myc* (Addgene). Three days later, cells were fed ESC medium (DMEM with 15% ESC-screened FBS, nonessential amino acids, L-glutamine, monothioglycerol, and 1,000 U/ml leukemia inhibitory factor (LIF)) and the media was changed every other day. Reprogrammed (EGFP+) cells were identified and scored by fluorescence microscopy 2–3 weeks post-transduction, unless otherwise stated. To derive iPS cells, EGFP+ colonies were manually picked under a stereomicroscope (Leica Microsystems, Buffalo Grove, IL, USA, http://www.leica-microsystems.com/). In the case of small molecule treatment, indicated small molecules were applied to reprogramming cells on day four post-transduction and fresh medium was added every other day for at least 2 weeks or until EGFP+ colonies appeared.

siRNA Transfection

Specific siRNAs were purchased from Dharmacon RNAi Technology, Lafayette, CO, USA. Approximately 4 × 10^4 Oct4-EGFP MEFs were transfected with Lipofectamine/siRNAs complexes according to the manufacturer's instruction (Invitrogen, Carlsbad, CA, USA, http://www.invitrogen.com/). After 3–5 hours later, the transfection reagent was discarded and MEF complete medium was added for culturing. Gene knockdown efficiency was evaluated by semi quantitative real time polymerase chain reaction (RT-PCR). Glyceraldehydes-3-phosphate dehydrogenase (GAPDH) served as an internal control to normalize mRNA expression signals.

For reprogramming, retrovirus expressing reprogramming factors (Oct4, Sox2, Klf4, and c-Myc) were added and the medium was then changed to complete medium the next day. For overexpression of *COX2* transgene, retroviruses expressing COX2 were added 1 day after OSKM transduction. siRNAs were introduced at day 5 post-transduction.

In Vitro Differentiation and Teratoma Formation Assay

For *in vitro* differentiation, iPS cells were dissociated by trypsin/EDTA and re-suspended in embryoid body (EB) medium (DMEM with 15% FBS, nonessential amino acid, L-glutamine) to final concentration at 5×10^4 cells per milliliter. To induce EB formation, 1,000 iPS cells in 20 µl were cultured in hanging drops on inverted Petri dish lids. Three to five days after EB formation, EBs were collected and transferred to 0.1% gelatin-coated 6-well plates at a density of ~ 10 EBs per well. Two weeks later, beating cardiomyocytes (mesoderm) were identified microscopically. Cells derived from endoderm and ectoderm were identified by α-fetoprotein (R&D systems, Minneapolis, MN, USA, http://www.rndsystems.com/; Cat#MAB1368) and neuron-specific βIII tubulin (Abcam, Cambridge, MA, USA, http://www.abcam.com/; Cat# ab7751) antibodies, respectively.

To assay teratoma formation, 1.5×10^6 iPS cells were trypsinized and re-suspended in 150 µl of culture medium, and then injected subcutaneously into the dorsal hind legs of athymic nude mice anesthetized with avertin. Three weeks later, mice were sacrificed to collect teratomas. Tumor masses were fixed, dissected, and analyzed in the Sanford-Burnham Medical Institute Cell Imaging-Histology Core Facility.

Immunofluorescence and AP Staining

iPS cells were seeded and cultured on 0.1% gelatin-coated six-well plates. After 4 days, cells were fixed with 4% paraformadehyde (Electron Microscopy Sciences, Hatfield, PA, USA, http://www.emsdiasum.com/microscopy/; Cat# 15710-S). For immunofluorescence, fixed cells were permeabilized with 0.1% Triton X-100 in PBS and blocked with 5% BSA in PBS. SSEA-1 (R&D; Cat# MAB2155), Sox2 (R&D; Cat#MAB2018), and Nanog (R&D; Cat# AF2729) antibodies were used to detect ESC markers. Nuclei were visualized by Hoechst 33342 (Invitrogen) staining. For alkaline phosphatase (AP) staining, fixed cells were treated with AP substrate following the manufacturer's instruction (Vector Laboratories, Burlingame, CA, http://www.vectorlabs.com/order.aspx; Cat# SK-5100).

Microarray Analysis

Total RNAs were isolated from indicated cells using TRIZOL reagent (Invitrogen). Gene expression was detected and normalized in the Sanford-Burnham Medical institute high-throughput screening and genomics core facilities. Heat maps were created using MultiExperiment View, Boston, MA, USA, (http://www.tm4.org). Scatter plots were created using Excel.

Meta-Analysis for Small Molecule Candidates

Select individual MEF or MESC genes served as queries to perform searches using the NextBio, Cupertino, CA, http://www.nextbio.com/ engine. The compounds identified were analyzed for specific activities, such as downregulation of the *COX2* gene by Nabumetone. Finally, 17 molecules (Table 3.2) were selected as potent inducers of MESC genes or inhibitors of MEF genes, as predicted by NextBio meta-analysis.

CHAPTER IV

Transcriptome Signatures During Reprogramming

Summary

Induced pluripotent stem (iPS) cells provide a valuable resource as an alternative to embryonic stem cells, especially in the field of regenerative medicine. To understand the mechanism of regulatory networks during reprogramming, we performed a genome wide RNAi screen and purified cellular populations during four key steps of reprogramming: We integrated genome-wide RNAi screen with step-wise transcriptome analysis to deeply analyze the molecular requirements in induced reprogramming. Our data suggest that to attain SSEA1+ stages is the rate-limiting step during reprogramming. *Nanog, Sall4, Esrrb, Dppa4, Dppa5a, Dnmt3b and Dnmt3l* are activated in $SSEA1^+$ cells, while more extensive interactions of embryonic stem cell core circuitry (ESCCC) regulators are established in mature iPS cells, including *Utf1, Nr6a1, Tdgf1, Gsc, Fgf10, T, Chrd, Dppa3, Fgf17, Eomes, Foxa2*. Remarkably, we found that genes with non-differential change play the most critical roles to the transitions of reprogramming, while analysis of

differential transcriptome might not comprehensively reveal the key regulators. Functional validation showed that genes, such as *Dmbx1*, *Gsc*, *Med21*, *Hnf4g*, *Mef2c*, *Psmd9*, *Tfdp1*, *Nfe2*, *Foxn3*, *Erf*, *Cdkn2aip*, *Msx3*, *Ssbp3*, *Dbx1*, *Hoxd4*, *Lzts1*, *Arx*, *Hoxd12*, *Gtf2i*, *Nkx6-2*, *Ankrd22*, and *Hoxc10*, act as essential or barrier roles to reprogramming. We also confirmed several genes required for maintaining ES cell properties, such as *Srsf2*, *Hcfc1*, *Ruvbl2*, *Asb4*, *Dmbx1*, *Gbx2*, *Gsc*, *Hnf4g*, *Klf5*, *L3mbtl2*, *Med21*, *Mef2c*, *Nobox*, *Pcgf6*, *Phox2a*, *Tcf15*, *Oct4/Pou5f1*, *Nanog*, and *Trim28*.

Introduction

Somatic reprogramming to pluripotent status can be achieved by introducing a limited number of transcription factors, including Oct4, Sox2, Klf4, c-Myc (OSKM), Nanog, and Lin28 (Takahashi *et al.*, 2007; Takahashi and Yamanaka, 2006; Yu *et al.*, 2007). Those induced pluripotent stem cells (iPS cells) highly resemble embryonic stem cells (ESCs) and hold promise to customized regenerative medicine (Grskovic et al., 2011; Jopling *et al.*, 2011; Robinton and Daley, 2012; Tiscornia *et al.*, 2011; Wu and Hochedlinger, 2011).

Primary obstacles to the successful application of iPS cells for medical purposes are their low reprogramming efficiency and lack of understanding the mechanisms of reprogramming. A few markers, including Thy1, alkaline phosphatase (AP), and SSEA1, activated in sequential stages, are required to identify cells that transform through the process of induced reprogramming, while embryonic stem cell-specific genes (*Nanog, Oct4, Tert*) are activated at later stages (Brambrink *et al.*, 2008; Stadtfeld *et al.*, 2008a). Further work suggests that induced reprogramming is a step-wise event, comprising initial, mature, and stabilization stages (Samavarchi-Tehrani *et al.*, 2010). Several key cellular events have been observed during reprogramming, such as mesenchymal-to-epithelial transition (Li *et al.*, 2010; Samavarchi-Tehrani *et al.*, 2010) and cell-cycle modulation (Banito *et al.*, 2009a; Hong *et al.*, 2009; Kawamura *et al.*, 2009b; Li *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009). Furthermore, the epigenome is reset upon induced reprogramming (Koche *et al.*, 2011; Maherali *et al.*, 2007), and several epigenetic regulators play important roles in the reprogramming process (Onder *et al.*, 2012). The cooperation of OSKM has also been considered as a critical factor to efficient reprogramming (Carey *et al.*, 2011; Soufi *et al.*, 2012; Sridharan *et al.*, 2009). Despite these efforts, we do not fully understand the molecular mechanisms of induced cellular reprogramming.

Here, by isolating pure populations of cells during various stages of reprogramming and combining with genome-wide RNAi screen and transcriptome analysis, we were able to discover key genes and cellular events involved in the transitions associated with the reprogramming process. Moreover, we functionally identified the critical genes required to modulate the reprogramming process. We further validated a series of genes that either block or enhance reprogramming process. Finally, we demonstrated that Pcgf6, Ruvbl2, Srsf2, and Hcfc1 play important roles not only in inducing somatic reprogramming, but also in maintaining embryonic stem (ES) cell identity.

Results

Distinct Stages of Reprogramming Defined by Signature Markers

To better elucidate the dynamic changes of molecular mechanisms during cellular reprogramming, we employed transcriptome analysis and shRNA library screening upon induced reprogramming in order to reveal mRNA changes of key molecules and to functionally validate their roles in a step-wise manner (Figure 4.1A). First, we established a set of markers to isolate desired cell populations in a highly heterogeneous pool of transformed/reprogrammed cells by OSKM reprogramming factors. Thy1 is highly expressed in mouse embryonic fibroblasts (MEFs) and subsequently diminishes in the progression of reprogramming, while SSEA1 is absent in MEFs, but gradually increases upon induced reprogramming (Brambrink *et al.*, 2008; Stadtfeld *et al.*, 2008a). Therefore, Thy1 can serve as an early-stage marker and SSEA1 can serve as a middle- and late-stage marker for assessing reprogramming progress. In addition, it has been shown that retroviral sequences are repressed in ES cells (Macfarlan *et al.*, 2011; Wolf and Goff, 2007, 2009); thus we used the *DsRed* gene driven by retroviral LTRs as a marker to

Figure 4.1

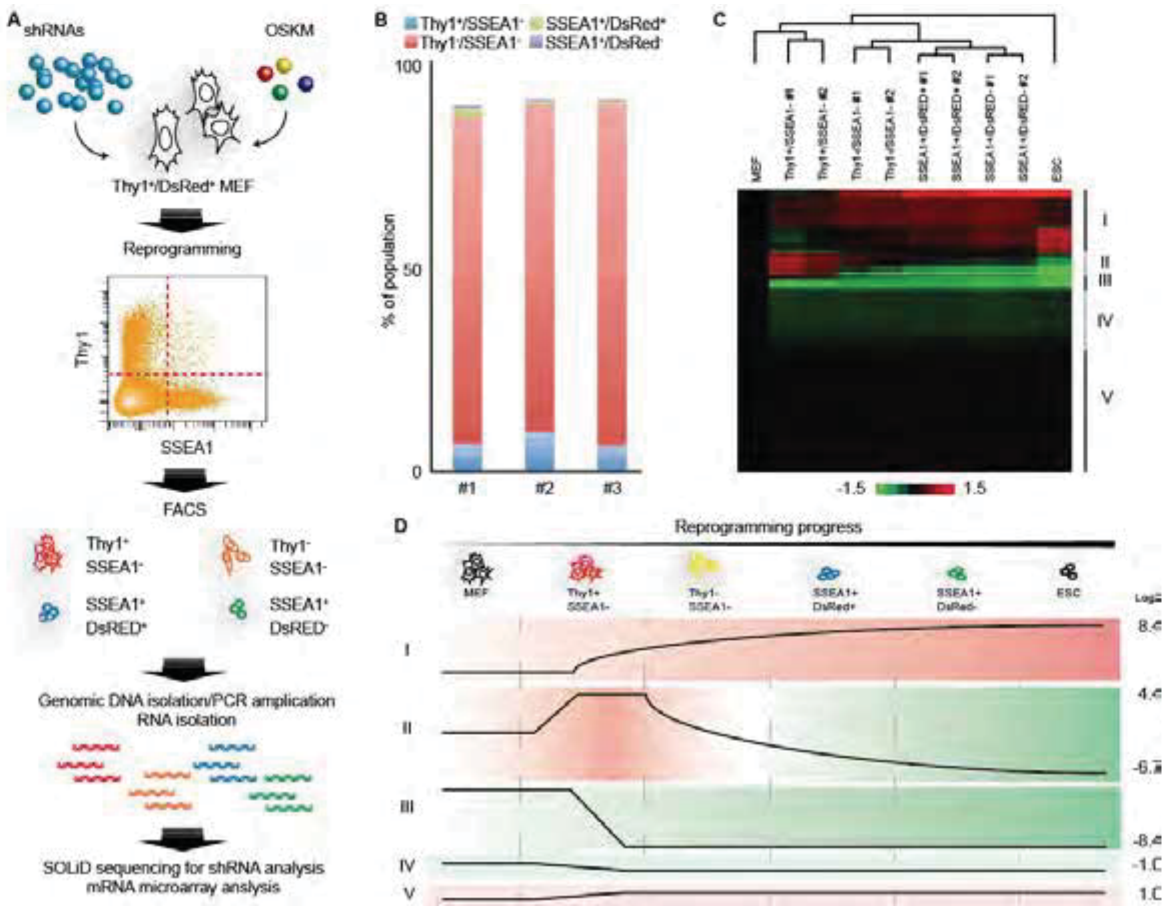

A
shRNAs
OSKM
Thy1+/DsRed+ MEF
Reprogramming
Thy1
SSEA1
FACS
Thy1+ SSEA1-
Thy1- SSEA1-
SSEA1+ DsRED+
SSEA1+ DsRED-
Genomic DNA isolation/PCR amplication
RNA isolation
SOLiD sequencing for shRNA analysis
mRNA microarray analysis
B
Thy1+/SSEA1-
SSEA1+/DsRed+
Thy1-/SSEA1-
SSEA1+/DsRed-
% of population
100
50
0
#1
#2
#3
C
MEF
ESC
I
II
III
IV
V
-1.5
1.5
D
Reprogramming progress
MEF
Thy1+ SSEA1-
Thy1- SSEA1-
SSEA1+ DsRed+
SSEA1+ DsRed-
ESC

Figure 4.1

Dissecting key molecular mechanisms during reprograming by genome-wide RNAi screening and transcriptome analysis

(A) Scheme of shRNA library screening strategy.

~57000 shRNAs were introduced into $Thy1^{+}$/$DsRed^{+}$ MEFs together with four reprogramming factors. Transduced cells were then sorted into four populations based on combinations of various markers, such as Thy1, SSEA-1, and DsRed. Isolated cells were subjected to DNA and RNA extractions for further analysis. Genomic DNA was extracted from isolated cells. Integrated shRNAs were amplified from gDNA and subject to high-throughput second-generation sequence analysis.

(B) Bar graph showing different proportions of sorted cell populations.

OSKM-reprogrammed cells were sorted according to established marker set at 2 weeks post reprogramming. Cell number was counted by flow cytometry and was plotted in percentage for each sorted population. Three independent experiments are shown here.

Figure 4.1 (continuation)

(C) Heat map of mRNA expression profiles during induced reprogramming.

RNA samples were extracted from cell populations in (b), and then were analyzed by mRNA microarray analysis. Data was processed and visualized by using Cluster and Java TreeView respectively. Distinct expression pattern of genes are clustered and grouped into five main groups as I to V. Hierarchical tree was created by Cluster. Duplicate samples were numbered as #1 and #2. Fold changes of mRNA level compared with MEF are represented in log_2 scale.

(D) Five distinct patterns of mRNA expression during reprogramming progress.

Scheme of mRNA expression pattern of each group in (a) during reprogramming. The fold changes (log_2 value) of transcriptome in each group were illustrated on the right side of the scheme. For group I, II, and III, the maximal fold changes are shown. For group IV and V, approximately 90% of genes have fold change within +/- 1 in log_2 scale, respectively.

differentiate incomplete reprogrammed cells from mature ones, as indicated by the arrows in Figure 4.2A.

Collectively, we used Thy1, SSEA1, and DsRed as markers to define four stages of the reprogramming process: $Thy1^{+}/SSEA1^{-}$ for the initial stage, $Thy1^{-}/SSEA1^{-}$ for the transition stage, $SSEA1^{+}/DsRed^{+}$ for the pre-determined (early-reprogrammed) stage, and $SSEA1^{+}/DsRed^{-}$ for the mature reprogrammed stage (Figure 4.1A).

To acquire a homogenous cell population for shRNA library screening and transcriptome analysis, we isolated high-purity MEFs (~98%) expressing both Thy1 and DsRed markers (Figure 4.2B) by fluorescence-activated cell sorting (FACS). We then used sorted $Thy1^{+}/DsRed^{+}$ cells as recipients and induced somatic reprogramming by transducing lentiviruses containing a whole-genome shRNA library together with retroviruses expressing OSKM (Figures 4.1A, 4.2C and 4.2D).

Keeping in mind that transformed cells have a high degree of both dynamic changes and randomness on mRNA profiles (Hanna *et al*., 2009; Yamanaka, 2009a), here we focused on "committed" or "trapped" cells at the end stage of reprogramming, where we

Figure 4.2

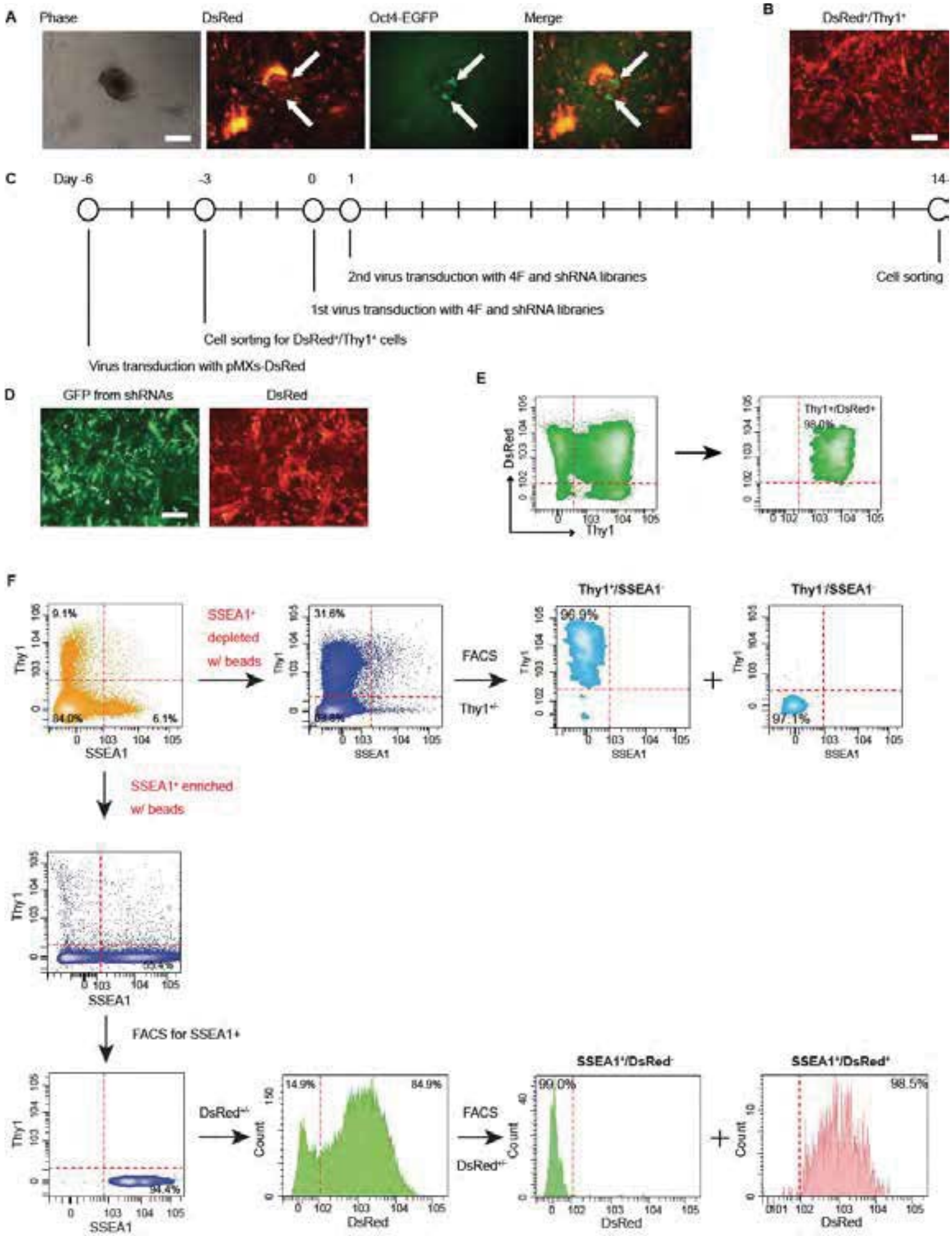

A
Phase
DsRed
Oct4-EGFP
Merge
B
DsRed+/Thy1+
C
Day -6
-3
0
1
14
2nd virus transduction with 4F and shRNA libraries
Cell sorting
1st virus transduction with 4F and shRNA libraries
Cell sorting for DsRed+/Thy1+ cells
Virus transduction with pMXs-DsRed
D
GFP from shRNAs
DsRed
E
DsRed
Thy1
Thy1+/DsRed+
F
SSEA1+ depleted w/ beads
FACS
Thy1+/-
Thy1+/SSEA1-
Thy1-/SSEA1-
SSEA1+ enriched w/ beads
FACS for SSEA1+
DsRed+/-
SSEA1+/DsRed-
SSEA1+/DsRed+
Thy1
SSEA1
Count
DsRed
9.1%
84.0%
6.1%
31.6%
96.9%
97.1%
14.9%
84.9%
99.0%
98.5%
94.4%

Figure 4.2

shRNA library screening strategy to dissect molecular requirements in induced reprogramming.

(A) Reciprocal expression of DsRed and Oct4-EGFP in reprogrammed cells.

DsRed was shut down where Oct4-EGFP was turned on in reprogrammed cells. DsRed and EGFP signals were detected by fluorescent microscopy. Images were taken at day 10 post induced reprogramming with OSKM. White arrows indicate reciprocal expression of DsRed and Oct4-EGFP. Scale bar denotes 100 μm.

(B) High purity of DsRed positive cells isolated by FACS.

DsRed and Thy1 double positive cells were sorted by FACS and cultured for three more days before subsequent virus transduction. DsRed signal was detected by fluorescent microscopy three days post transduction of pMXs-DsRed pseudo virus. Scale bar denotes 50 mm.

Figure 4.2 (continuation)

(C) Timeline of experimental procedure.

Key steps of experimental design are illustrated here as timeline. Whole experiment takes ~3 weeks to complete.

(D) High transduction efficiency of lentiviral shRNA library in MEFs.

$DsRed^{+}/Thy1^{+}$ MEFs were transduced with virus containing shRNA library and reprogramming factors, OSKM. shRNA library was constructed into pGIPz vectors, which constitutively express EGFP. shRNA library-transduced cells can be determined by detecting EGFP signal. DsRed and EGFP signals were detected by fluorescent microscopy. Images were taken at four days post second transduction of shRNA library. Scale bar denotes 50 mm.

(E) Cell sorting for high purity of $Thy1^{+}/DsRed^{+}$ MEFs.

CF-1 MEFs were transduced with pMXs-DsRed pseudo virus three days before sorting. Antibody against Thy1 was used to detect $Thy1^{+}$ cells. Thy1 and DsRed double positive cells were isolated by fluorescence-activated cell sorting (FACS). Purity of isolated cells

Figure 4.2 (continuation)

was confirmed by flow cytometry analysis after sorting and was shown in percentage.

(F) Four distinct cell populations sorted by FACS.

Sorted $DsRed^+/Thy1^+$ cells described above were used for shRNA screening during reprogramming. Two weeks post transduction with shRNA library and OSKM, cells were sorted by FACS to acquire four populations with distinct markers, as $Thy1^+$ only, $Thy1^-/SSEA1^-$, $SSEA1^+/DsRed^+$, and $SSEA1^+/DsRed^-$. Cells were first separated with magnetic beads conjugated with anti-SSEA1 antibodies (highlighted in red) to boost the recovery rate of sorting. Sorted cells were at least with > 95% purity for indicated markers, shown as percentage.

believe that a more defined/stable transcriptome is established in most cells and that cell fate is unlikely to be changed further. To acquire those "committed" cell populations, we sorted the cells at 14 days post virus transduction, the putative ending point of the reprogramming process for MEFs (Figure 4.2C). Desired cell populations with high purities were isolated by stringent sorting using the marker set described above (Figure 4.2E and 4.2F), including Thy1^{+}/SSEA1^{-} cells (>95% purity); Thy1^{-}/SSEA1^{-} cells (>96.5% purity); SSEA1^{+}/DsRed^{+} cells (~96% purity); and SSEA1^{+}/DsRed^{-} cells (~99% purity). As expected, only a small portion (1%–2.5%) of transduced cells attains the two later SSEA1^{+} stages (Figure 4.1B). Of those SSEA1^{+} cells, the mature iPS cells (SSEA1^{+}/DsRed^{-}) compose ~0.2–0.4% of total transduced cells (Appendix 1). In contrast, a much larger proportion of cells (6.5%–9.7%) is enriched in the Thy1^{+}/SSEA1^{-} stage (Figure 4.1B). Surprisingly, the majority (>80%) of the transduced cells are at the transition stage (Thy1^{-}/SSEA1^{-}) (Figure 4.1B and Appendix 1), which are neither fibroblast-like nor stem cell-like cells. The distinct distribution of this cell population suggests that dismantling somatic-molecular networks is relatively easier to achieve upon induced reprogramming, while re-establishing pluripotent networks is likely the rate-limiting step, with a higher threshold to overcome.

To confirm that these sorted populations are indeed representative cellular reprograming, we isolated total RNAs from the sorted cells and conducted mRNA-microarray analysis for those samples. As expected, we found that most key regulators of ES cell core circuitry (ESCCC), including *Esrrb, Nanog, Lin28a*, and *Sall4* (Figure 4.3A), are induced in the cells at the later stages (SSEA1$^+$/DsRed$^+$ and SSEA1$^+$/DsRed$^-$ populations). We also examined the genes involved in mesenchymal-to-epithelial transition (MET) in these four populations. Epithelial genes (*Cdh1, Ocln, Krt8*) are depleted in Thy1$^+$/SSEA1$^-$ cell population, but induced in the later stages (Figure 4.3A). In contrast, mesenchymal genes (*Snai1, Zeb1/2, Ncam1*) are highly expressed in the Thy1$^+$/SSEA1$^-$ population but repressed in the later stages (Figure 4.3A). Taken together, these data demonstrate that our sorted cell populations represent distinct stages along the normal induced-reprogramming process.

Figure 4.3

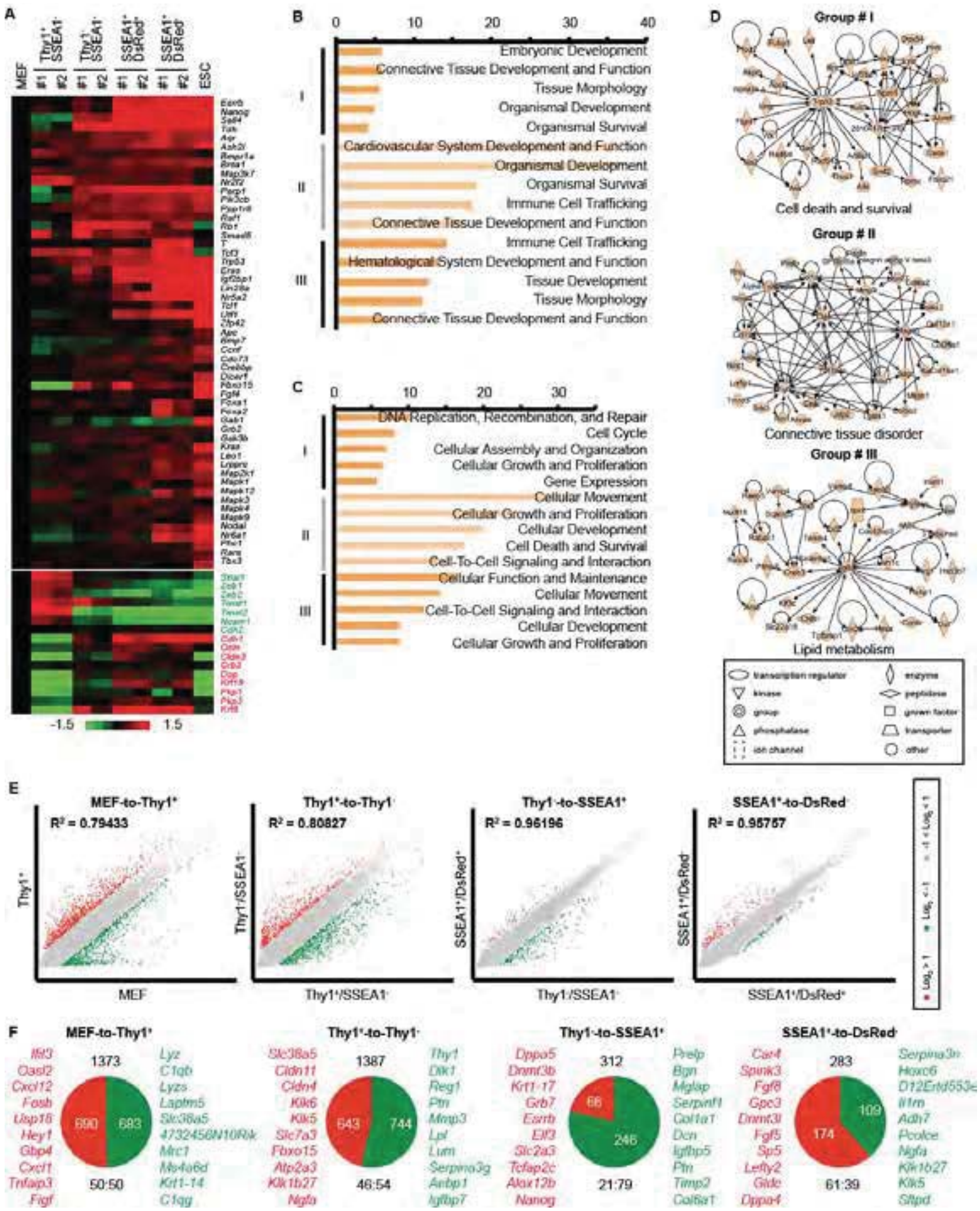

A
B
C
D
E
F
Group # I
Cell death and survival
Group # II
Connective tissue disorder
Group # III
Lipid metabolism
Embryonic Development
Connective Tissue Development and Function
Tissue Morphology
Organismal Development
Organismal Survival
Cardiovascular System Development and Function
Immune Cell Trafficking
Hematological System Development and Function
Tissue Development
DNA Replication, Recombination, and Repair
Cell Cycle
Cellular Assembly and Organization
Cellular Growth and Proliferation
Gene Expression
Cellular Movement
Cellular Development
Cell Death and Survival
Cell-To-Cell Signaling and Interaction
Cellular Function and Maintenance
MEF-to-Thy1+
R^2 = 0.79433
Thy1+-to-Thy1-
R^2 = 0.80827
Thy1-to-SSEA1+
R^2 = 0.96196
SSEA1+-to-DsRed-
R^2 = 0.96757
1373
690
683
50:50
1387
643
744
46:54
312
66
246
21:79
283
174
109
61:39

Figure 4.3

Transcriptome analysis reveals key differential genes and networks during reprogramming.

(A) Heat map of mRNA expression profile showing key ES cell and MET regulators during induced reprogramming.

Fold changes of mRNA expression from select molecules were examined for four cell populations during reprogramming. Four cell populations are indicated above the heat map. Replicate samples were labeled as #1 and #2. MEF and ESC serve as controls of two determined cell types. Fold changes of mRNA level compared with MEF are represented in $\log_2$ scale. Gene names in black are ES cell regulators, in green are mesenchymal regulators, and in red are epithelial regulators.

(B) Bar graph showing biological functions of group I, II, and III in transcriptome analysis

Gene ontology analysis is performed by using IPA. Only five most significant functions for each group were shown. Probability (Fishers' Exact test) was represented as $-\log_{10}$ (*p*

Figure 4.3 (continuation)

value) and shown above the bar graph.

(C) Bar graph showing physiological system development and functions of group I, II, and III in transcriptome analysis

Analysis was performed as described above using IPA. Only five most significant functions for each group were shown. Probability (Fishers' Exact test) was represented as $-\log_{10}$ (*p* value) and shown above the bar graph.

(D) Networks showing representative key genes of group I, II, and III in transcriptome analysis.

Analysis was performed as described above using IPA. Only one representative network for each group was shown here. Legends are shown inside the rectangle in the lower part of the panel.

(E) Scatter plots showing unique transcriptome changes between each cell populations from MEFs to iPS/ES cells.

Scatter plots of mRNA expression change between each transition steps during

Figure 4.3 (continuation)

reprogramming. Correlations of transcriptome between two cell populations are shown as R square value. Genes with two-fold reduction in mRNA level are shown in greed dots, while genes with two-fold induction shown in red dots. Genes within two-fold changes shown in grey dots. Figure legends are shown on the right side of the panel.

(F) Pie charts showing mRNA regulations crossing the transitions in reprogramming.

Cell type transitions are indicated above each chart. Total number of differential genes (> 2 fold change) is shown above the pie charts. Number of differential genes between distinct cell populations is shown within red (up-regulated) or green (down-regulated) part in pie chart. Relative ratio of differential genes (up-regulated genes versus down-regulated genes) is shown below the pie charts. Ten most differential genes in each transition are listed next to the corresponding pie charts. Gene names in red indicated up-regulated genes and in green indicate down-regulated ones.

K-Means Clustering Reveals Five Distinct Gene Patterns During Induced Reprogramming

To explore mRNA expression profiles in sorted populations, we first sought to determine the major transcriptome changes that occur during reprogramming; to identify these changes, we used k-means clustering to cluster all of the studied genes according to their expression patterns in sorted populations, finding five distinct groups (group I to V) of mRNA expression profiles along the reprogramming process (Figure 4.1C). Group-I genes gradually increase their expression level (log_2 value to 8.4) from the initial to mature stages during reprogramming (Figure 4.1D). In contrast, genes in group III exhibit significantly reduced expression (log_2 value to -8.4), even starting from the initial stage (Figure 4.1D). We found group-II genes to show a unique expression pattern in which they are first induced (log_2 value to 4.4) at the initial stage and then repressed (log_2 value to -6.7) in the subsequent stages (Figure 4.1D). Group IV and V have minor/no changes to mRNA expression, with a slight decrease ($log_2 > -1$) or increase ($log_2 < 1$), respectively, during reprogramming, as shown in Figure 4.1D. Please also see the

Appendix 2 for the complete gene list of transcriptome analysis and summary.

Highly Modulated Functions in Reprogramming Uncovered Among Three Highly differential Groups

To gain insight into the five distinct trends of mRNA expression described above, we performed comprehensive transcriptome analysis for each group of genes by using Ingenuity Pathways Analysis (IPA) (www.ingenuity.com), a platform that provides bioinformatics pipelines to conduct gene ontology (GO) analysis to discover over-representative genes for protein interactions, networks, and canonical pathways in sorted cells. In group I, genes involved in embryonic development (e.g., *Dnmt3b, Esrrb, Otx2, Fgf8, Tfap2c, Slc2a1, Lmnb1, Nes, Nasp, Klf2, Blm, Parp1Lig1, Nr5a2, Gsc*) are specifically enriched (Figure 4.3B), indicating that many important developmental regulators are induced alongside the reprogramming process.

Genes involved in cell-cycle (e.g., *Mdk, Fgf8, Sgol1, Top2a, Mcm2, Aurka, Ccnb1, Zic3, Mybl2, Spc25, Cdh1*) and DNA replication/recombination/repair (e.g., *Mcm2, 2810417H13Rik, Hmgb2, Nasp, Parp1, Cdt1, Dbf4, Lig1, Dut, Timeless, Foxm1, Cdc6,* *Trp53, Fen1*) are also enriched in group I (Figure 4.3C), showing increased activation among those networks. Furthermore, network analysis showed that cell death and its associated survival network (*Trp53, Rad54l, Npm1, Ung, Kiaa0101*) are highly up-regulated during reprogramming (Figure 4.3D). Those data suggest that under the stress of induced reprogramming, securing genome integrity by activating DNA repair pathways and cell-cycle control is a priority for cells when they respond to the massive changes induced by the four reprogramming factors described here. In addition, genes involved in cellular assembly and organization (*Uhrf1, Cdt1, Cdc6, Trp53, Lbr, Hmgn5, Hmgn2, Dnmt1, Rb1, Cdc7*) are also highly induced during reprogramming (Figure 4.3C), suggesting active cellular-structure remodeling. Numerous genes (e.g., *Trh, Dnmt3b, Nanog, Otx2, Sall4, Zscan10, Fosb, Mdk, F2rl1, Fgf8, Dnmt3l, Olig1, Tcf15, Foxd1*) involved in gene expression are enriched in group I (Figure 4.3C), suggesting that global transcriptional and translational changes happen along with the reprogramming process.

In group II, genes associated with cardiovascular system development and function (e.g., *Ptn, Col1a1, Mgp, Vcam1, Slit2, Pdgfra, Cav1, Mmp3, Dcn, Thbs2*) are highly enriched. These genes are induced in the initial stage (Thy1$^+$/SSEA1$^-$) and then subsequently decrease in later stages (Figure 4.3B) during reprogramming. Interestingly, genes involved in connective tissue development and other types of cellular interaction (e.g., *Ptn, Col1a1, Mgp, Cyp1b1, Vcam1, Slit2, Thbd, Pdgfra, Cav1, Mmp3, Dcn, Thbs2, Ptx3, Lsp1*) are also significantly enriched in group II (Figures 4.3B, 4.3C, and 4.3D), indicating that genes modulating cell-to-cell interactions/organizations may play a temporal role in the process of induced reprogramming.

In group III, where genes are repressed during the reprogramming process, genes involved in hematological system and connective tissue development are highly enriched (Figure 4.3B). Together with the findings in group II, these data indicate a cell identity change, in which genes associated with cellular reorganization become highly regulated. Interestingly, the lipid metabolism network is highly represented in this group (Figure 4.3D), suggesting changes of cellular metabolism, macromolecule biogenesis, or energy preference along the reprogramming process.

In addition to those group-specific functions/networks, some have more complex regulatory patterns, which are enriched in more than one trend/group. For example, cell growth and movement, including cell-to-cell signaling, is enriched in groups I, II, and III (Figures 4.3B and 4.3C). In addition, tissue morphology or organismal survival network (Figure 4.3C) exhibits two distinct expression trends (group I and III or group I and II, respectively). Gene ontology analysis of transcriptome changes is shown in Appendix 3.

Group-IV and -V genes showed no or minor changes at the mRNA level among all cell populations (Figures 4.1B and 4.1C). Those two groups cover the majority of genes, which contribute to a variety of cellular functions/networks (Appendix 3). Because changes at the mRNA expression level ($\log_2$ within 1 to -1) are limited in these two groups, it is difficult to evaluate the influence of those genes during reprogramming without combining with other analyses. Therefore, we will discuss the importance of those genes in Group IV and V later with shRNA library screening analysis.

To summarize, by analyzing mRNA profiles we were able to discover five distinct expression patterns (groups I to IV) that occur during the reprogramming process. In addition to known functions such as cell cycle and cell death, each highly regulated group

(I to III) exhibits significant regulation of novel networks, including cell-to-cell interaction/organization, gene regulation, and cellular-structural organization.

Revealing Key Molecules/Pathways in The Transitions to Different Stages of Reprogramming

It remains poorly understood which molecular hurdles are critical to overcome for cells to make a transition from initial to mature stages of reprogramming. To address this uncertainty, we examined the transcriptome difference that exists between cell populations of every two adjacent stages along the reprogramming progress, from MEF to SSEA1^{+}/DsRed^{-} cells. We found that the primary transcriptome changes (fold changes between two cell populations > +/- 1 in $\log_2$ scale) occurred at two early transitions, MEF-to-Thy1^{+}/SSEA1^{-} (1373 genes) and Thy1^{+}/SSEA1^{-}-to-Thy1^{-}/SSEA1^{-} (1387 genes) (Figures 4.3E and 4.3F). Fewer expression changes occurred in the two later stages of the reprogramming process (312 and 283 genes in Thy1^{-}/SSEA1^{-}-to-SSEA1^{+}/DsRed^{+} and SSEA1^{+}/DsRed^{+}-to-SSEA1^{+}/DsRed^{-} transitions, respectively). These results showed that massive transcriptome reconstruction primarily occurs in the early stages before cells obtain an $SSEA1^+$ marker, which refers committed cell populations toward pluripotency (Figure 4.3F).

Our data suggest that the first two transitions may be the cell-fate-reorganizing phases, comprising the respond-to-reprogramming stress step and the de-constructing-of-somatic-networks step. Following these steps, the later two transitions are cell-fate-committing phases where ES cell-specific regulatory networks are acquired to attain pluripotent status, in the context with dominant OSKM expression (Figures 4.3E and 4.3F).

Notably, the number of repressed and induced genes remains the similar, if not the same (ratio at 50:50 and 46:54), at the first two transitions (Figure 4.3F). In contrast, most differential-expression genes decrease (79%) at the $Thy1^-$/$SSEA1^-$-to-$SSEA1^+$/$DsRed^+$ transition, while others increase (61%) at the $SSEA1^+$/$DsRed^+$-to-$SSEA1^+$/$DsRed^-$ transition (Figure 4.3F). GO analysis of the differential genes at each transition suggests that it is important to modulate the genes associated with fibroblast property (Figure 4.4A) before cells reach the later two $SSEA1^+$

stages. Consistently, key molecules associated with fibrotic properties, *Lyz* and *Lyzs*, are among the top 20 differentiated genes at the first two transitions (Figure 4.3F). Genes involved in embryonic stem cell pluripotency are activated starting at the Thy1$^-$/SSEA1$^-$-to-SSEA1$^+$/DsRed$^+$ transition (Figure 4.4A). Additional ES cell-specific networks are activated in the final transition from the SSEA1$^+$/DsRed$^+$ to SSEA1$^+$/DsRed$^-$ stages (Figure 4.4A). The complete lists of differential genes in each transition step can be reviewed in Appendix 4.

Our data indicate that to reach the “early reprogrammed” SSEA1$^+$/DsRed$^+$ stage, it is important to activate many of the key players involved in embryonic stem cell core circuitry, including *Nanog, Sall4, Esrrb, Dppa4, Dppa5a, Dnmt3b, and Dnmt3l* (Figures 4.3F and 4.4B). For pre-determined cells (SSEA1$^+$/DsRed$^+$), in order to progress to a mature reprogrammed status (SSEA1$^+$/DsRed$^-$), those molecules are further induced to a higher expression level, possibly to acquire a complete pluripotent state (Figure 4.4C). Furthermore, when cells proceed from the SSEA1$^+$/DsRed$^+$ to SSEA1$^+$/DsRed$^-$ stages

Figure 4.4

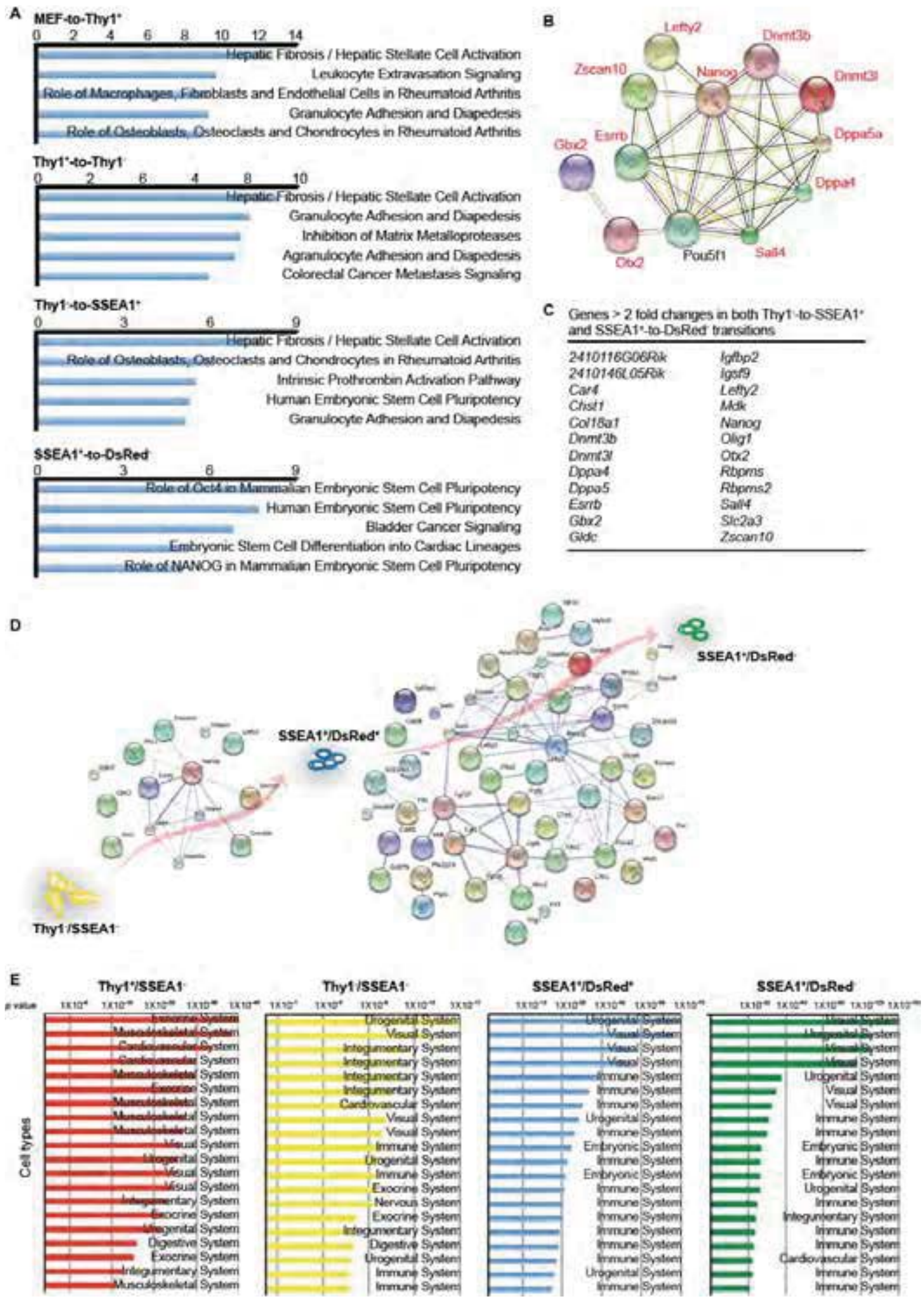

A
MEF-to-Thy1+
Hepatic Fibrosis / Hepatic Stellate Cell Activation
Leukocyte Extravasation Signaling
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis
Granulocyte Adhesion and Diapedesis
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis
Thy1+-to-Thy1-
Hepatic Fibrosis / Hepatic Stellate Cell Activation
Granulocyte Adhesion and Diapedesis
Inhibition of Matrix Metalloproteases
Agranulocyte Adhesion and Diapedesis
Colorectal Cancer Metastasis Signaling
Thy1-to-SSEA1+
Hepatic Fibrosis / Hepatic Stellate Cell Activation
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis
Intrinsic Prothrombin Activation Pathway
Human Embryonic Stem Cell Pluripotency
Granulocyte Adhesion and Diapedesis
SSEA1+-to-DsRed-
Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency
Human Embryonic Stem Cell Pluripotency
Bladder Cancer Signaling
Embryonic Stem Cell Differentiation into Cardiac Lineages
Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency
B
Lefty2
Dnmt3b
Zscan10
Nanog
Dnmt3l
Dppa5a
Gbx2
Esrrb
Dppa4
Otx2
Pou5f1
Sall4
C
Genes > 2 fold changes in both Thy1-to-SSEA1+ and SSEA1+-to-DsRed- transitions
2410116G06Rik
2410146L05Rik
Car4
Chst1
Col18a1
Dnmt3b
Dnmt3l
Dppa4
Dppa5
Esrrb
Gbx2
Gldc
Igfbp2
Igsf9
Lefty2
Mdk
Nanog
Olig1
Otx2
Rbpms
Rbpms2
Sall4
Slc2a3
Zscan10
D
SSEA1+/DsRed-
SSEA1+/DsRed+
Thy1-/SSEA1-
E
Thy1+/SSEA1-
Thy1-/SSEA1-
SSEA1+/DsRed+
SSEA1+/DsRed-
p value
Cell types

Figure 4.4

Expression cascades of epigenetics regulators during induced reprogramming

(A) Bar graphs showing key canonical pathways in the transition steps during reprogramming.

Gene ontology analysis was performed to analyze the differential genes between indicated two cell populations. Cell type transitions are shown above each bar graph. Only five most significant pathways are shown here. Probability (Fishers' Exact test) was represented as $-\log_{10}$ (*p* value) and shown above each bar graph.

(B) Scheme showing functional protein association networks of early-induced ES cell core circuitry (ESCCC) factors in SSEA1^{+} cell population.

Predicted protein interactive network was created in STRING by using the early-induced ES cell core factors identified in transcriptome analysis. Gene names in red are induced in both Thy1^{-}-to-SSEA1^{+} and SSEA1^{+}-to-DsRed^{-} transitions.

(C) Table listing induced genes in both Thy1^{-}-to-SSEA1^{+} and SSEA1^{+}-to-DsRed^{-} transitions.

Figure 4.4 (continuation)

The common induced genes (> 2 fold change) in both Thy1^{-}-to-SSEA1^{+} and SSEA1^{+}-to-DsRed^{-} transitions are listed.

(D) Scheme showing the expansion of ESCCC interactive networks when cells cross the transition step from SSEA1^{+}/DsRed^{+} to SSEA1^{+}/DsRed^{-} stage.

Predicted protein interactive networks were created in STRING by using up-regulated genes among the transitions as input.

(E) Bar graphs showing body atlas of four cell populations in reprogramming.

Transcriptome of each cell population was analyzed and calculated for the positive correlations of gene expression profiles to various tissue/cell types in mouse by using NextBio platform. Sorted cell populations used for analysis are shown above each bar graph. The twenty most significant correlated cell types are listed here. Probabilities (Fishers' Exact test) are presented as in *p* value and shown above each bar graph. Colors of bar graph are corresponding to the cell populations shown in Figure 4.1A.

(Figure 4.4D), more extensive interactions of ESCCC regulators are established, including *Utf1, Nr6a1, Tdgf1, Gsc, Fgf10, T, Chrd, Dppa3, Fgf17, Eomes, Foxa2*, and others; indicating that the final step of reprogramming is to reinforce the ES cell core circuitry. The complete lists of common and unique genes in the last two-transition steps can be reviewed in Appendix 5.

To summarize, we revealed major cellular networks based on dynamic trends of the transcriptome (Figures 4.1C and 4.1D) and on the transition steps of specific cell populations (Figures 4.3E and 4.3F). We identified key genes in highly differential groups (I, II, and II), which may serve as signature markers for reprogramming progression. We also listed numerous key differential genes for transition between distinct stages, which can be used as potential small-molecule targets to advance the reprogramming process.

Four Sorted Populations Indicate Cell-Fate Changes Along with Induced Reprogramming Progress

Because the markers used for sorting reflect the change of cell properties, we speculated that each sorted cell population might comprise certain representative cell type(s) along with the reprogramming process. To test this hypothesis, we conducted a meta-analysis by comparing our transcriptome profiles with numerous tissue types from whole body (Body Atlas analysis) using the NextBio platform (Kupershmidt *et al.*, 2010). This algorithm was designed to find correlations between genes of interest (queries) and normalized gene expression across all available tissues, cell types, cell lines, and stem cells in its library; this is accomplished by calculating mRNA expression profiles with a positive or negative correlation.

Using this algorithm, we found that Thy1+/SSEA1- cells have the highest correlation (p value $< 1X10^{-40}$) with cells derived from exocrine, musculoskeletal, and cardiovascular systems, which contain fibrotic cell types (Figure 4.4E). Conversely, we found SSEA1+/DsRed- cells have a very high correlation (p value $< 1X10^{-130}$) with cells derived from the urogenital system, which contain germ line stem cells (Figure 4.4E). We also found that the cells with the highest correlation (p value $< 1X10^{-153}$) to SSEA1+/DsRed- cells were derived from the visual system (Figure 4.4E). In addition, SSEA1+/DsRed+ cells were found to have a high correlation (p value < ~$1X10^{-70}$) with urogenital and visual systems, although with lower significance compared with SSEA1+/DsRed- cells; this finding supports the idea that SSEA1+/DsRed+ cells are in the “early reprogrammed/pre-determined” status before reaching full pluripotent status.

We also found that cells derived from the immune system have a significant correlation with SSEA1+/DsRed+ and SSEA1+/DsRed- cells. This finding of a higher transcriptome correlation to iPS/ES cells might explain how cells derived from the circulatory system are thought to provide better somatic cell sources for efficient induced reprogramming (Cahan and Daley, 2013; Eminli *et al.*, 2009; Gonzalez *et al.*, 2011; Polo *et al.*, 2010). Interestingly, Thy1-/SSEA1- cells have low significant correlations (p value < $1X10^{-9}$ to $1X10^{-17}$) with any tissue types (Figure 4.4E), suggesting a high degree of heterogeneity of cell contents in this status (Thy1-/SSEA1-).

In short, we found that cells derived from the visual, urogenital, and immune systems may serve best as the resource for efficient induced reprogramming. Thy1-/SSEA1- status might serve as the cell-fate-decisive stage prior to commitment of cell types, because of high heterogeneous tissue types with low mRNA expression correlations. Finally, we showed that cells from the visual system and immune system might serve as great resources for better efficiency of reprogramming due to high correlativity of transcriptome.

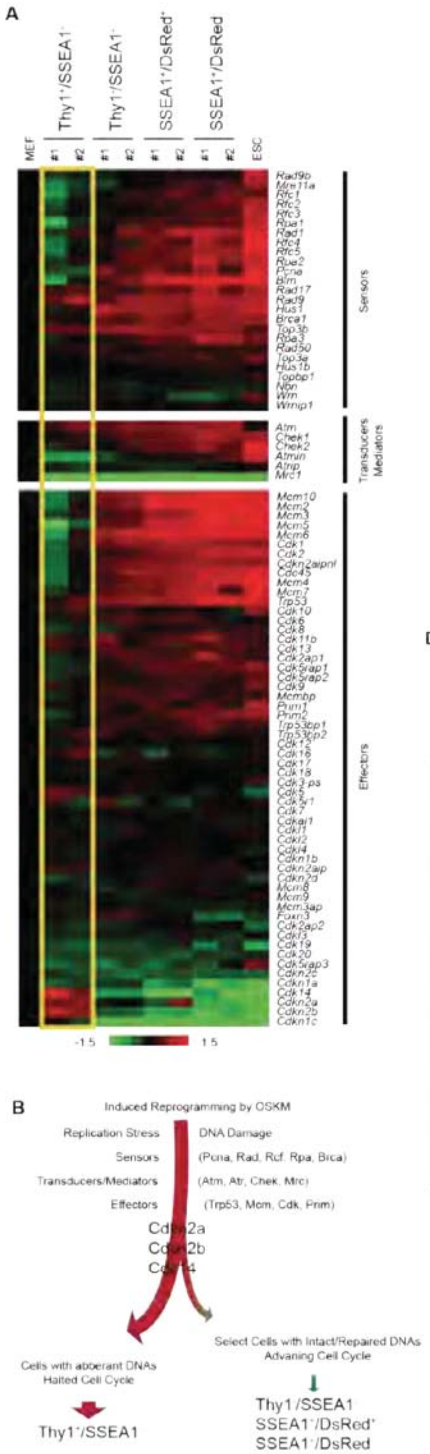
Deeper Insight into Key Molecular Events of Reprogramming

It has been shown that several events are critical for the reprogramming process, including cell cycle regulation, epigenetics changes, and pluripotency restoring (Banito *et al.*, 2009a; Brambrink *et al.*, 2008; Hong *et al.*, 2009; Kawamura *et al.*, 2009b; Li *et al.*, 2009a; Marion *et al.*, 2009; Onder *et al.*, 2012; Papp and Plath, 2013; Stadtfeld *et al.*, 2008a; Utikal *et al.*, 2009). However, the specifics of the molecular regulation and dynamic changes associated with these key events remain poorly understood.

To obtain greater insight into these events, we first examined the mRNA expression profiles for genes associated with cell cycle regulation, including DNA damage, G1/S checkpoint, G2/M checkpoint, Cyclin regulation, and DNA replication. As shown in Figure 4.5A, we observed that the majority of the sensors and transducers/mediators are induced in cell populations with Thy1$^-$/SSEA1$^-$ markers. Those upstream regulators are in turn up-regulated further throughout the reprogramming process, up until the end of reprogramming stage (Figure 4.5A). As expected, key effector Trp53 is induced upon initiation of reprogramming. In the initial reprogramming stage, the majority of the observed mini-chromosome maintenance (MCM) helicases are already induced Thy1$^-$/SSEA1$^-$ cells (Figure 4.5A), suggesting that DNA replication machinery is activated early on in the reprogramming process. In contrast, senescence genes *Cdkn2a/Arf-Ink4a*, *Cdkn2b/Ink4b*, and *Cdk14* are depleted, while most effectors are greatly induced in the initial stage of reprogramming (Figure 4.5A).

The main difference between the mRNA expression level of cell cycle regulators is established in the initial stage (Thy1$^+$/SSEA1$^-$) versus later cell populations, as indicated by the yellow rectangle in Figure 4.5A; this suggests that DNA damage and replication checkpoints may serve as gatekeepers to prevent cells with aberrant DNAs from progressing further during induced reprogramming, possibly by activating *Cdk14* and

Figure 4.5



C

Histone Lysine Methylase Complexes (HKMT) and Polycomb Complexes (PRC)

Complexes (Substrate)	Regulatory Effects	Main Components
HKMT1a/b/c/d/e (H3K9)	Repressive	Suv39h1, Suv39h2, Ehmt2/G9a, Ehmt1/Glp, Setdb1, Atf7ip, Chaf1a/Caf1, Cbx5/Hp1
HKMT2a/b/c/d/f/g (H3K4) Trx Complexes	Active	Mll1, Mll2, Ash2l, Men1, Wdr5, Rbbp5, Dpy30, Mll3, Mll4, Hcfc1, Kdm6a/Utx, Pagr1a/Pa1, Paxip1/Ptip, Ncoa6, Wdr5, Rbbp5, Dpy30, Ash2l, Setd1a, Setd1b, Wdr82, Wdr5, Rbbp5, Dpy30, Ash2l, Cxxc1
HKMT3 (H3K36)	Active	Setd2; Whsc1
HKMT4 (H3K79)	Active	Dot1, Mllt3/Af9, Mllt10/Af10, Mllt1/Enl, Mllt6/Af17, Trrap
HKMT5a/b/c (H4K20)	Repressive	Setd8/Pr-set7; Suv420h1, Suv420h2
HKMT6/PRC2 (H3K27)	Repressive	Ezh1, Ezh2, Suz12, Eed, Rbbp4, Rbbp7
PRC1 (H2AK119Ub)	Repressive	Ring1, Rnf2, Cbx2, Cbx4, Cbx7, Cbx8, Pcgf1, Pcgf2, Pcgf3, Pcgf4, Pcgf5, Pcgf6

‡Adapted from Cell SnapShot: Histone Lysine Methylase Complexes (Cell 149, April 13, 2012)

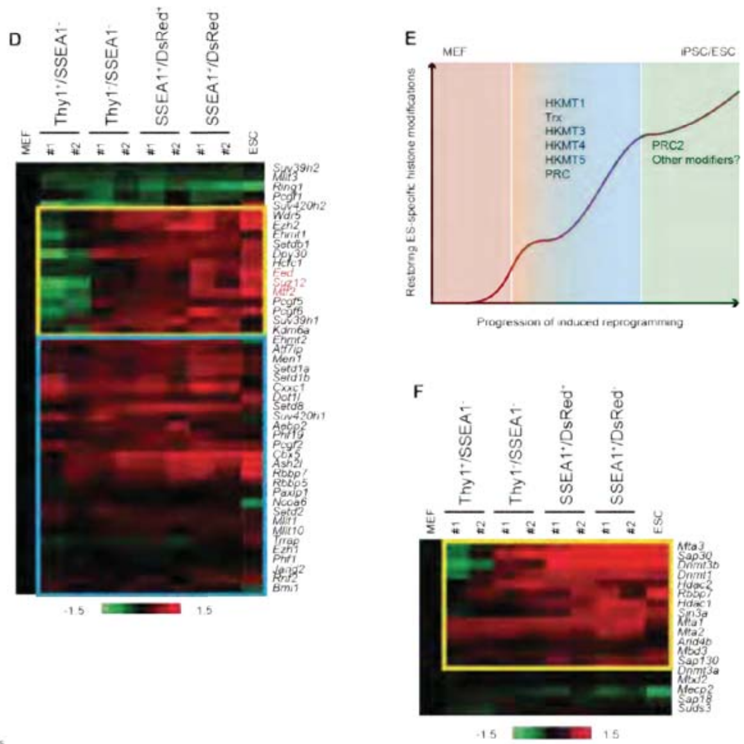


Figure 4.5

Cdk14 and Cdkn2a/b are the gatekeepers in the initial stage of reprogramming and PRC2 complexes are the last to be restored until in the mature iPS cells.

(A) Heat map of mRNA expression profiles showing distinct activation patterns for cell cycle regulators.

Genes are grouped into three functional categories are shown in the right side of heat map. Genes are further clustered by K-mean clustering analysis. Distinct expression patterns are highlighted with yellow rectangle. Fold changes of mRNA level compared with MEF are represented in $\log_2$ scale.

(B) Scheme showing cell cycle regulation during induced reprogramming progress.

Various regulators are shown next to the reprogramming progressing line. Three key decisive factors are enlarged and bold. Red arrows indicate incomplete induced reprogramming and green arrows indicate further reprogrammed cell populations.

Figure 4.5 (continuation)

(C) Table listing the main components of histone lysine methylase complexes and polycomb repressive complexes.

Gene lists are adopted from SnapShot archive in Cell journal.

(D) Heat map of mRNA expression profiles showing sequential activation patterns of histone lysine methylation modifiers/transferases (HKMTs)

HKMTs mRNA expression profiles were processed as described above. Two distinct activation patterns are highlighted in yellow and blue rectangles. Genes with activation latency are highlighted in red texts. Fold changes of mRNA level compared with MEF are represented in $\log_2$ scale.

(E) Scheme showing sequential activations of epigenetics regulators

Cell fate change is shown on the top of the scheme based on the progression of induced reprogramming. Main HKMT complexes are listed and positioned corresponding to the activation patterns in (d). Red line shows the re-establishment of epigenetic regulators.

Figure 4.5 (continuation)

(F) Heat map of mRNA expression profiles showing sequential activation patterns for DNA methylation regulators

mRNA expression profiles of DNA methylation regulators were processed as described above. Activation of mRNA level is highlighted in yellow rectangle. Fold changes of mRNA level compared with MEF are represented in log_2 scale.

Cdkn2a/b early as in the initial stage (Figure 4.5B).

Cells have been shown to acquire significant epigenetics changes upon induced reprogramming, such as histone modifications and DNA methylations (Koche *et al*., 2011; Maherali *et al*., 2007). Several epigenetic regulators haven been proved to influence reprogramming efficiency, such as PRC1, PRC2, *Suv39h1, Yy1*, and *Dot1l* (Onder *et al*., 2012). However, the dynamics required to activate this epigenetic-modifying mechanism remains unclear with regard to transitions between reprogramming stages. We thus examined the mRNA expression profile of epigenetics regulators, including histone lysine methylase/methyltransferase (HKMT) complexes, polycomb repressive complexes (PRCs), and DNA methylation modulators (Figure 4.5C).

The majority of the genes associated with HKMT complexes are induced upon initiation of the reprogramming process, as indicated by the blue rectangle in Figure 4.5D. In contrast, only a few components decrease in the majority of the stages during reprogramming, including *Suv39h2, Mllt3, Ring1, Pcgf1*, and *Suv420h2* (Figure 4.5D). Notably, many of the down-regulated components are involved in repressive transcriptional regulations, such as *Suv39h2, Ring1, Pcgf1*, and *Suv420h2* (Figure 4.5C). Key components of HKMT1 complexes (*Setdb1, Ehmt1*, and *Suv39h1*) and of HKMT2, aka Trx complexes (*Wdr5, Dpy30, Hcfc1, Kdm6a*), shared a similar expression profile with high induction at later stages during reprogramming (Figure 4.5D). In addition, the main components of PRC2 (*Ezh2, Eed, Suz12, Mtf2*) are not induced until cells reach the early-reprogrammed stage (SSEA1$^+$/DsRed$^+$), as indicated by the yellow rectangle in Figure 4.5D. These findings suggest that restoring the bivalent status in iPS/ES cells is one of the late events to take place in the reprogramming process (Figure 4.5E). Similarly, some known factors of PRC1, such as *Pcgf5* and *Pcgf6*, are also induced at later stages (Figure 4.5D).

Consistent with histone modifiers, molecules involved in DNA methylation are induced gradually during the reprogramming process (Figure 4.5F). Thus, our results clarify a distinct re-activating dynamics of histone modifiers in the reprogramming process. Furthermore, our data suggest that the main scaffold used for histone modifications is first established in the re-constructing stage of reprogramming

(Thy1^{-}/SSEA1^{-}), but the complete mechanisms of histone modifications are restored in only the mature iPS/ES cells. Most importantly, our data provide deeper insight into understanding dynamic regulations of key molecular events.

CHAPTER V

Functional Dissection of the Molecular Requirements of Induced Reprogramming

Results

Genome-Wide shRNA Screening Identifies Key Factors in Induced Reprogramming

In addition to the extensive transcriptome analysis described in Chapter IV, we also developed a genome-wide shRNA library screening to identify functionally important genes in reprogramming. To do this, we first isolated genomic DNA from sorted cells, where a genome-wide shRNA library has been introduced after induced reprogramming (shown in Figure 4.1A). Specific primers flanking the stem loop regions of shRNAs were used to amplify genome-integrated shRNAs in each cell population. To identify the enriched shRNA targets, we sequenced those amplified fragments in each sorted population by Sequencing by Oligonucleotide Ligation and Detection (SOLiD sequencing).

We assumed that shRNAs targeting essential genes would be enriched in distinct cell populations, and depleting those factors by shRNAs would compromise or enhance the reprogramming progress. Based on this assumption, we aimed to identify shRNA targets that are enriched specifically in each cell population. To this end, we performed K-means clustering for identified reads from sorted populations based on the relative enrichments in different cell populations. We obtained four distinct gene clusters (A, B, C, D) enriched specifically in each cell population and one cluster (E) containing non-specific enrichments (Figure 5.1A).

To further understand which reprogramming-associated modulations could be revealed through our shRNA library screening. We thus conducted a meta-analysis of those enriched hits from shRNA screening (Figure 5.1A) by using IPA software. Over-representative molecular and cellular functions were revealed by gene ontology (GO) analysis for each cluster (Figures 5.2A, 5.2B and Appendix 6). Consistent with our transcriptome analysis, we found that cell cycle regulation plays a significant role in the initial stage (Figures 5.2B, Group A), while cell death is critical to successful reprogramming (Figures 5.2B, Group D). Notably, cell-to-cell interactions are important for the initial, transition, and early reprogrammed stages (Figures 5.2B and

Figure 5.1

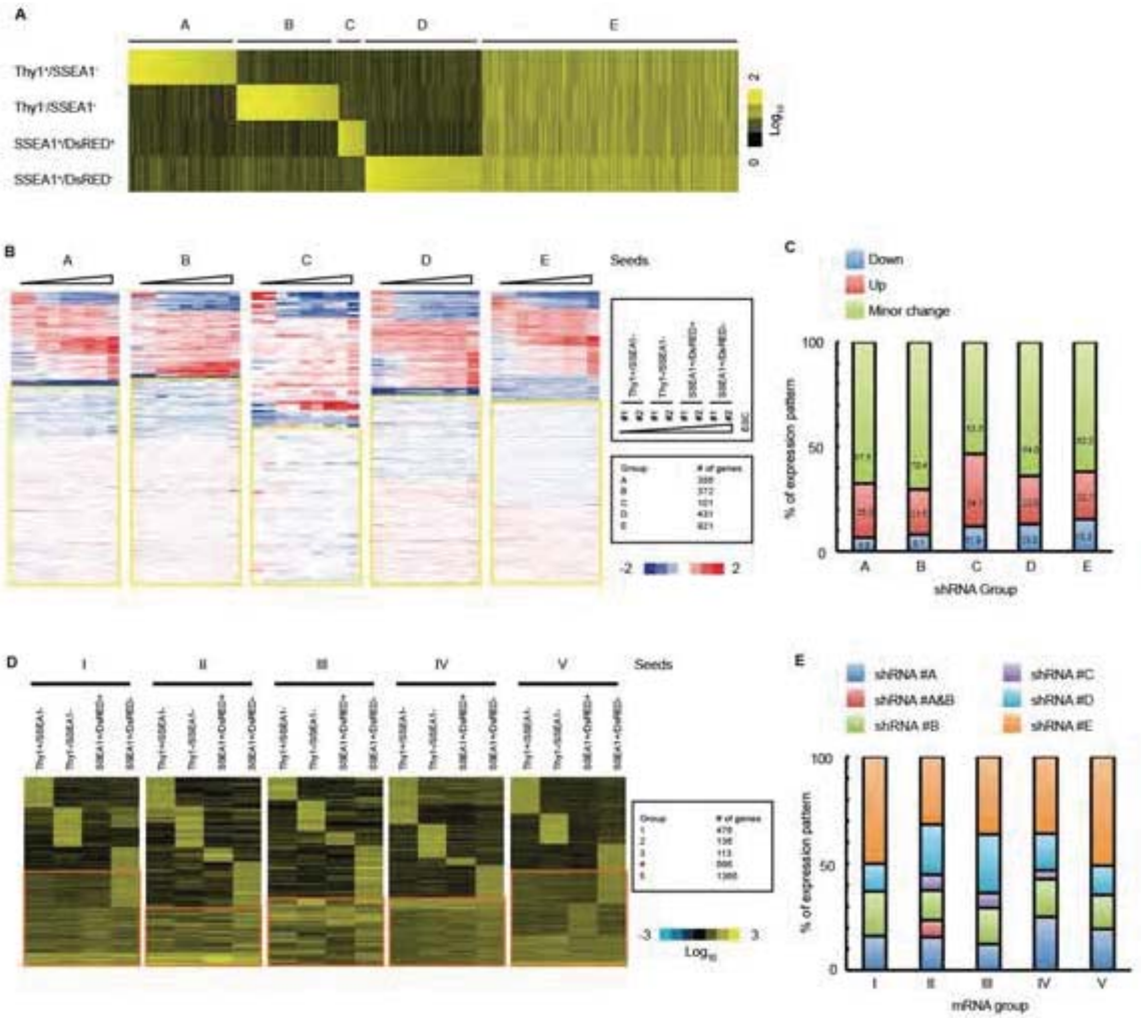

A
B
C
D
E
Thy1+/SSEA1-
Thy1-/SSEA1-
SSEA1+/DsRED+
SSEA1+/DsRED-
Log10
Seeds
Down
Up
Minor change
% of expression pattern
shRNA Group
Group
# of genes
I
II
III
IV
V
shRNA #A
shRNA #A&B
shRNA #B
shRNA #C
shRNA #D
shRNA #E
mRNA group

Figure 5.1

Revealing unique sets of molecules that play critical roles during reprogramming by integrated analysis of shRNA library screening and transcriptome profiling.

(A) Heat map demonstrating specific enriched shRNA targets in distinct populations along the reprogramming process.

Identified targets by shRNA reads were clustered by using Gene Cluster 3.0 and visualized with Java TreeView. Letter A to E were designated to mark five distinct clusters. Gene ontology was generated for each cluster with IPA (Ingenuity systems). Please note that reads of shRNA-identified targets are shown in log_{10} scale.

(B) Heat map illustrating mRNA expression profile of genes identified from shRNA library screening in Figure 5.1A.

Genes identified by shRNA library screening were clustered into five groups and only qualified genes having reads > 1.5 (log_{10} scale) were kept for further analysis. mRNA expression profile (Figure 4.1C) of those qualified genes was examined, clustered, and illustrated into five groups as the hits of shRNA library screening in (A). From left side to

Figure 5.1 (continuation)

right of heat map, mRNA expression trends were presented from initiation stage to maturation stage of reprogramming (upper right rectangle). Number of qualified targets from shRNA library screening are listed in the lower right rectangle. Minor or none changed genes were highlighted with yellow rectangle. Fold change of mRNA level compared with MEF was shown in log_2 scale.

(C) Bar graph showing the proportion of mRNA expression profiling corresponding to shRNA-identified genes in Figure 5.1A.

Genes in (B) were shown in percentage corresponding each group of shRNA-identified targets. Genes down-regulated are colored in blue, up-regulated in red, and minor changed in green. Relative ratio for each mRNA expression pattern is indicated.

(D) Heat map illustrating shRNA reads of distinct mRNA expression pattern groups in Figure 4.1C.

Reads from shRNA library screening were extracted and examined by using gene lists of each group from Figure 4.1C. Only qualified targets (shRNA reads > 1.5 in log_{10} scale)

Figure 5.1 (continuation)

were kept for further analysis. Select genes was examined, clustered, and illustrated into five groups as the groups in Figure 4.1D. From left side to right of heat map, shRNA reads were presented from initiation stage to maturation stage of reprogramming as indicated above the heat maps. Number of qualified genes from mRNA microarray analysis and shRNA library screening was listed in the lower right rectangle. Genes enriched in cluster C were highlighted with purple rectangle. Genes enriched in both cluster A and B were highlighted with red rectangle. Please note that reads of shRNA library were shown in log_{10} scale.

(E) Bar graph demonstrating proportion of enriched shRNA-identified targets corresponding each mRNA expression group in Figure 4.1C.

shRNA-identified genes in (D) were shown in percentage corresponding each mRNA expression group clustered in Figure 1C. Enriched shRNA targets are shown in different colors as legends shown above the chart.

Figure 5.2

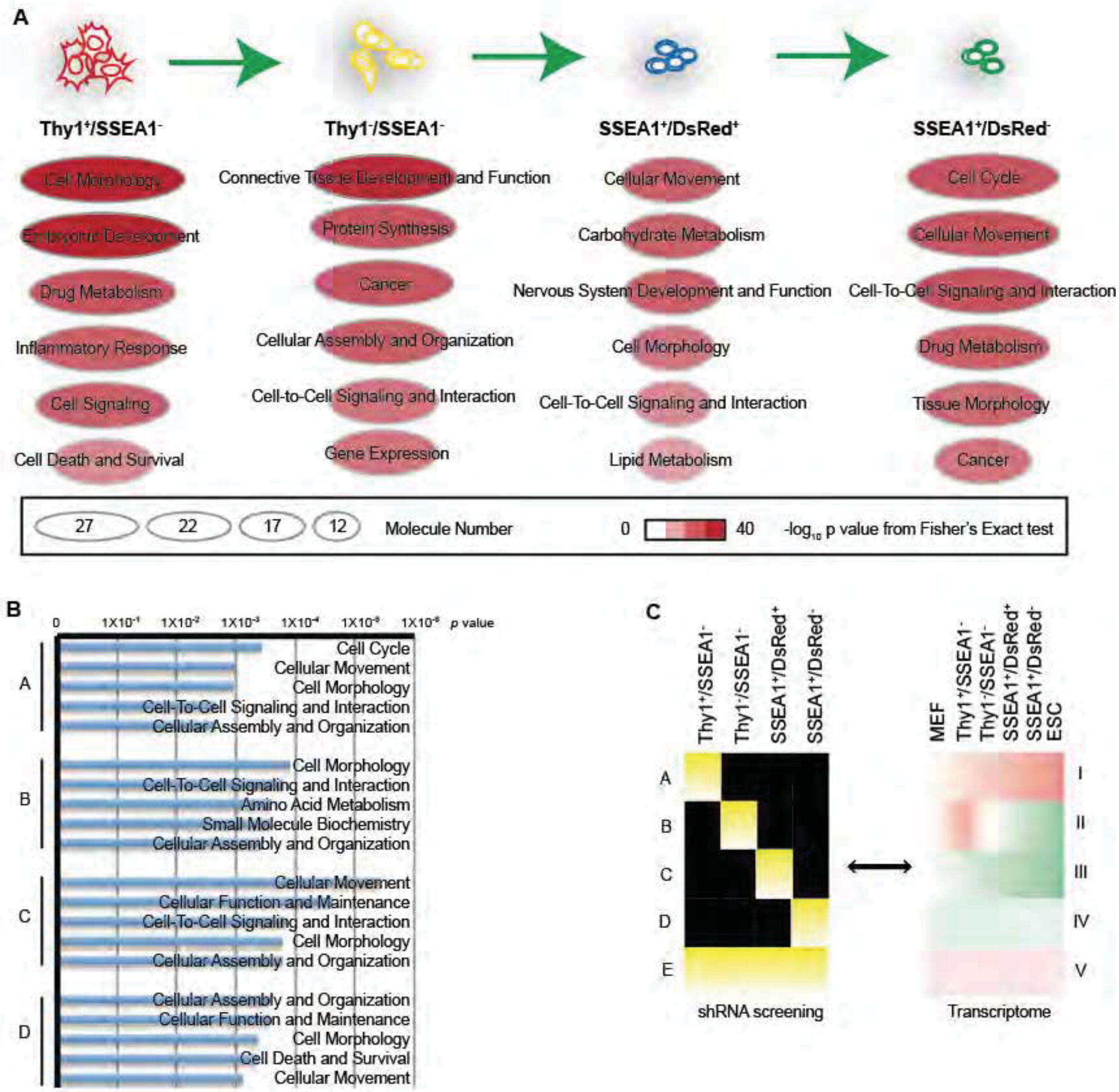

A
Thy1+/SSEA1-
Thy1-/SSEA1-
SSEA1+/DsRed+
SSEA1+/DsRed-
Cell Morphology
Embryonic Development
Drug Metabolism
Inflammatory Response
Cell Signaling
Cell Death and Survival
Connective Tissue Development and Function
Protein Synthesis
Cancer
Cellular Assembly and Organization
Cell-to-Cell Signaling and Interaction
Gene Expression
Cellular Movement
Carbohydrate Metabolism
Nervous System Development and Function
Cell Morphology
Cell-To-Cell Signaling and Interaction
Lipid Metabolism
Cell Cycle
Cellular Movement
Cell-To-Cell Signaling and Interaction
Drug Metabolism
Tissue Morphology
Cancer
27
22
17
12
Molecule Number
0
40
-log10 p value from Fisher's Exact test
B
0
1X10-1
1X10-2
1X10-3
1X10-4
1X10-5
1X10-6
p value
A
Cell Cycle
Cellular Movement
Cell Morphology
Cell-To-Cell Signaling and Interaction
Cellular Assembly and Organization
B
Cell Morphology
Cell-To-Cell Signaling and Interaction
Amino Acid Metabolism
Small Molecule Biochemistry
Cellular Assembly and Organization
C
Cellular Movement
Cellular Function and Maintenance
Cell-To-Cell Signaling and Interaction
Cell Morphology
Cellular Assembly and Organization
D
Cellular Assembly and Organization
Cellular Function and Maintenance
Cell Morphology
Cell Death and Survival
Cellular Movement
C
Thy1+/SSEA1-
Thy1-/SSEA1-
SSEA1+/DsRed+
SSEA1+/DsRed-
A
B
C
D
E
shRNA screening
MEF
Thy1+/SSEA1-
Thy1-/SSEA1-
SSEA1+/DsRed+
SSEA1+/DsRed-
ESC
I
II
III
IV
V
Transcriptome

Figure 5.2

Revealing genes/networks critical to induced reprogramming by integrated analysis of shRNA library screening and transcriptome profiling.

(A) Scheme showing representative networks identified by shRNA screening in each isolated cell population

Qualified hits (shRNA reads > 1.5 in $\log_{10}$ scale) were analyzed by using IPA to discover over-represented networks/functions/pathways. The six most significant networks are shown in each cell population from initial stage ($Thy1^{+}/SSEA1^{-}$) to mature stage ($SSEA1^{+}/DsRed^{-}$) during reprogramming. The size of the oval shape is proportional to the number of molecules involved in each network. Color codes denote probability (Fishers' Exact test) as in $-\log_{10}$ (*p* value).

(B) Bar graph showing key molecular and cellular functions identified by shRNA library screening.

Cluster identifications are shown on the left side of the plot. Probability (Fishers' Exact test) is shown in *p* value.

Figure 5.2 (continuation)

(C) Strategy scheme demonstrating the integration analysis of shRNA library screening and transcriptome data.

Identified gene lists from each cluster of both data sets are used as the seeds (queries) for integrative comparison analysis. mRNA expression profiles were analyzed in correspondence with gene lists identified by shRNA screening (A to E); in contrast, enrichments of shRNA-targeted genes were examined corresponding groups in transcriptome data (I to V).

Appendix 6), supporting our observation from the earlier transcriptome analysis (Figure 4.1). Similarly, the organization of cellular structures (Cellular movement/morphology/assembly and organization) significantly influences all studied cell populations (Figure 5.2B and Appendix 6). Furthermore, genes associated with cellular metabolisms (amino acid metabolism and small molecule biochemistry) are critical specifically in the "transition" stage of reprogramming. Modulation of cellular function and maintenance are critical to cells' ability to reach the later stages of reprogramming (i.e., pre-determined and mature reprogrammed stages), as shown in Figure 5.2B. The complete list of shRNA-identified genes is shown in Appendix 6.

Networks associated with cell morphology and embryonic development are highly targeted in $Thy1^{+}/SSEA1^{-}$ cell populations, suggesting that those two networks play critical roles in determining the early-stage cell fate transition. Consistent with our transcriptome analysis (Figure 4.1), networks of cell survival (inflammatory response and cell death) are keys to the transition from $Thy1^{+}/SSEA1^{-}$ to $Thy1^{-}/SSEA1^{-}$ status. Similarly, genes involved in cellular structure organization and cell-to-cell interaction are also specifically targeted at the transitions from Thy1$^-$/SSEA1$^-$ to SSEA1$^+$/DsRed$^-$ populations (Figure 5.2A). We also found that genes associated with cell cycle and cancer networks are selectively targeted in mature reprogrammed cells (Figure 5.2A), suggesting the repressive roles of identified targets to reprogramming. Finally, genes associated with drug-, carbohydrate-, and lipid-metabolisms play important roles in modulating the reprogramming process (Figure 5.2A). In short, our RNAi screen was able to identify many well-known molecular and cellular functions important to reprogramming, such as cell cycle, cell death, and metabolism. In addition to the known functions, our screening data showed several novel modulations critical to induced reprogramming, including cell-to-cell communications, cellular movement, cell morphology and structural organizations.

Integrating shRNA Library Screening and Transcriptome Analysis to Define Important Genes in Reprogramming

Studying cell-/tissue-specific mRNA expression profiles/changes helps to identify important genes in certain biological conditions. However, we speculated that solely examining mRNA levels during the reprogramming process might cause researchers to miss many key regulators, specifically because of the high heterogeneity of OSKM-transformed/-reprogrammed cell populations. We also wondered whether our shRNA library screening could identify certain hidden modulators masked by noise in the heterogeneous transcriptome.

To address these hypotheses, we further exploited two data sets generated from shRNA library screening and transcriptome analysis (Figure 5.2C). First, we tested whether we could recognize specific mRNA expression patterns for the identified shRNA targets. We utilized the target lists developed via shRNA library screening (Figure 5.1A) as seeds (queries) to find the expression profiles from transcriptome analysis (Figure 4.1C). To this end, we accessed five groups of mRNA expression profiles corresponding to the five clusters of shRNA-identified targets (Figure 5.1B). We did not find distinct expression patterns among those five shRNA groups (Figure 5.1B). This finding implies that mRNA expression profiling might not serve as a precise indicator/predictor to explain stage-specific functions of genes during reprogramming, although transcriptome analysis does reveal signature molecular networks at each stage of sorted cell populations.

Interestingly, we found that the majority of identified shRNA targets (~53% to 70%) are not highly regulated during the reprogramming process (as indicated by the yellow rectangle in Figures 5.1B, 5.1C, and Appendix 7), suggesting that genes without significant change upon reprogramming are the most significant to the transition of reprogramming. Among those genes with expression changes, more genes are up-regulated (21.5%~34.6%) than down-regulated (6.5%~15.3%) (Figure 5.1C and Appendix 7). Notably, the proportion of down-regulated genes increases (from ~6.5% to ~13%) from group A to group D (Figure 5.1C and Appendix 7), suggesting that further suppressing the decreased genes by shRNAs is beneficial to promoting reprogramming progress. We found that the ratio of up-regulated genes is especially high in group C ($SSEA1^+$/$DsRed^+$) even with a low number of shRNA-identified targets in group C (Figure 5.1C and Appendix 7), indicating that induced genes play more significant roles in the transition to or from the early-reprogrammed (pre-determined) stage

(SSEA1$^+$/DsRed$^+$).

We further tested whether mRNA expression profiles could be used to predict gene functions associated with induced reprogramming. To address this question, we used a similar approach to that described above, but using gene lists from transcriptome analysis (Figure 4.1C) as queries to find specific patterns of the enriched shRNA targets. Surprisingly, we found that half of the genes in group I can be identified as shRNA targets in group E (as indicated by the orange rectangle in Figure 5.1D), suggesting that a large portion (> 50%) of induced genes have little functional influence (in group E) on the process of induced reprogramming; this is the case even though those genes are induced significantly upon induced reprogramming.

As expected, more than 50% of matched genes in the mRNA group V (low changed) are identified in shRNA group E (Figure 5.1D and 5.1E), showing that a large proportion of low or un-changed genes contribute little to induced reprogramming. Furthermore, down-regulated genes, including mRNA groups II, III, and IV, matched a higher proportion of shRNA group D (~17% to 27% compared with 13%; Figure 5.1E and

Appendix 7), suggesting that further depletion of those targets facilitates maturation from the SSEA1^{+}/DsRed^{+} to SSEA1^{+}/DsRed^{-} stages. The complete gene lists and summary of each shRNA-identified targets can be reviewed in Appendix 8.

To summarize, we first integrated a genome-wide shRNA library screening with step-wise transcriptome analysis to extensively analyze the molecular mechanisms of induced reprogramming. We discovered that genes with minor expression-level changes play the most important roles during reprogramming. Our data also suggest that analysis of differential transcriptome might not comprehensively reveal the key regulators, because no shRNA-targeted groups show specific mRNA expression patterns.

Validation of Select Targets Demonstrates a High Discovery Rate for Key Reprogramming Molecules

To validate the identified targets from either transcriptome analysis or shRNA library screening, we selected several targets from both assays for testing the influence of these genes on reprogramming efficiency. To test shRNA-identified targets, we selected stage-specifically enriched targets (reads with log10 value > 1.5; Appendix 6) from the initial stage (Thy1$^+$/SSEA1$^-$) and the mature reprogrammed stage (SSEA1$^+$/DsRed$^-$). To test targets from transcriptome analysis, we selected highly induced genes in group I (Figure 4.1C). The majority of the selected genes from both assays are transcription regulators.

We first focused on shRNA-identified genes with a somatic reprogramming system. We speculated that genes, which are highly targeted in specific populations, might either promote or comprise the reprogramming progress. To test this, we first examined the effects of genes selectively targeted in a Thy1$^+$/SSEA1$^-$ cell population (group A) on reprogramming efficiency. Those genes are involved in the various key networks described above (Figure 5.2); Two examples are shown in Figure 5.3A to 5.3D. We knocked down select targets by siRNAs at the early time point of reprogramming and examined reprogramming efficiency by scoring the Oct4-GFP positive colonies two weeks after virus transduction. Of nine selected genes, depletion of six targets (~66.7%), *Dmbx1, Gsc, Med21, Hnf4g, Mef2c*, and *Psmd9*, showed significant reduction (p value < 0.05) on reprogramming efficiency with siRNA knockdown (Figure 5.4A). Furthermore, depleting *Dmbx1, Gsc, Zeb2, Med21, Hnf4g*, and *Mef2c* (six out of nine genes) showed a greater influence on compromising reprogramming efficiency compared with Oct4 knockdown (red-dotted line in Figure 5.4A).

Notably, Dmbx1- and Gsc-depleted cells showed the most evident phenotype (Figure 5.4A). As shown in Figure 5.3E, these putatively essential genes showed diverse mRNA expression patterns during the reprogramming process, again supporting the hypothesis that an mRNA expression trend might not be a precise predictor of critical functionalities to induced reprogramming. To summarize, most targets identified by our sorted shRNA-library screening act as essential players to induced reprogramming.

Conversely, we also tested genes (group D) selectively targeted by shRNAs in mature reprogrammed cells ($SSEA1^{+}/DsRed^{-}$), assuming that those genes might be barriers to induced reprogramming; one example is shown as in Figures 5.3B and 5.3D. We again knocked down select targets by siRNAs at the early time point of induced reprogramming

Figure 5.3

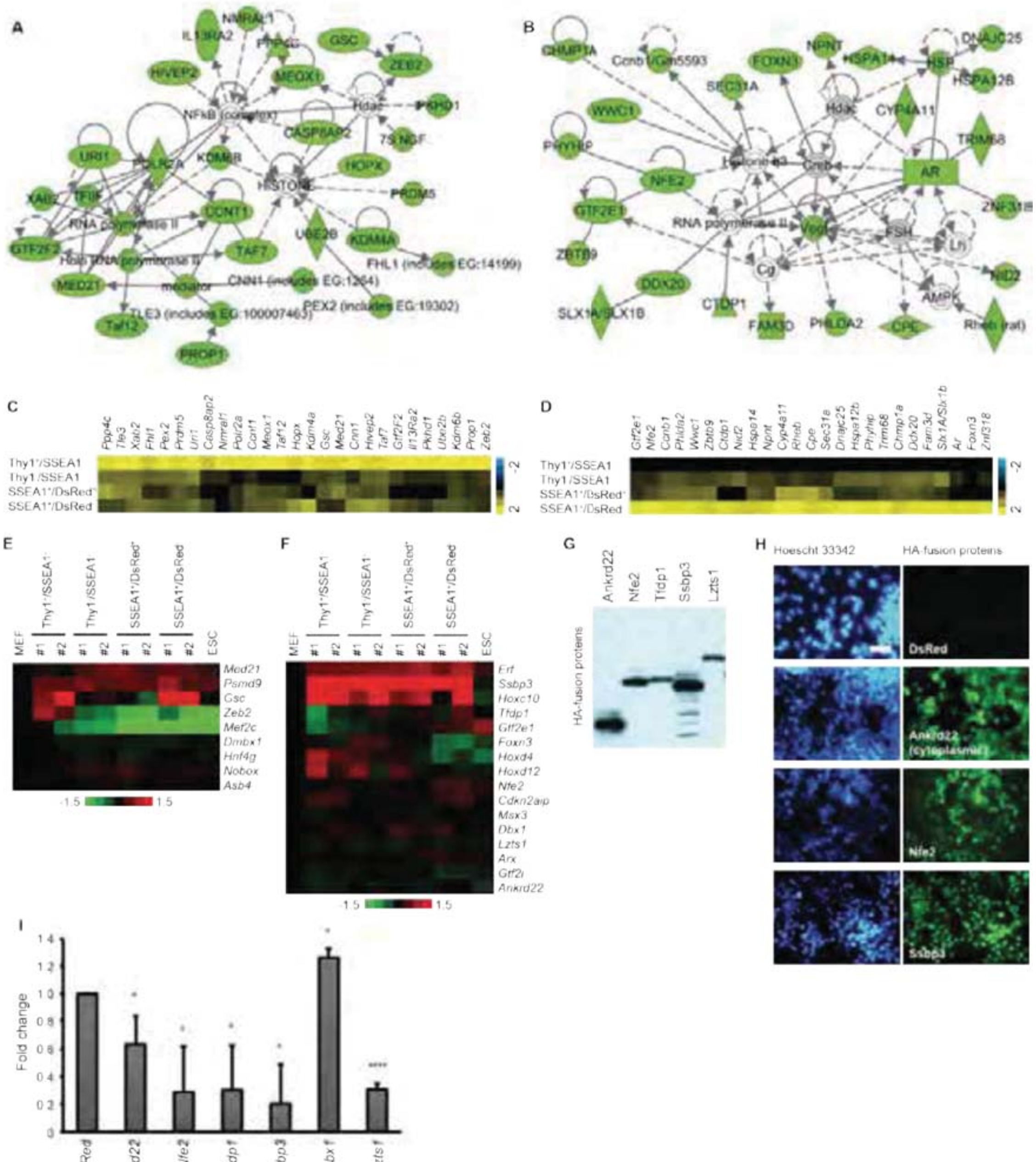

A
B
C
D
E
F
G
H
I
Thy1⁺/SSEA1⁻
Thy1⁻/SSEA1
SSEA1⁺/DsRed⁺
SSEA1⁺/DsRed
MEF
ESC
Med21
Psmd9
Gsc
Zeb2
Mef2c
Dmbx1
Hnf4g
Nobox
Asb4
Erf
Ssbp3
Hoxc10
Tfdp1
Gtf2e1
Foxn3
Hoxd4
Hoxd12
Nfe2
Cdkn2aip
Msx3
Dbx1
Lzts1
Arx
Gtf2i
Ankrd22
HA-fusion proteins
Hoescht 33342
DsRed
Ankrd22 (cytoplasmic)
Nfe2
Ssbp3
Fold change
DsRed
Ankrd22
Nfe2
Tfdp1
Ssbp3
Dbx1
Lzts1

Figure 5.3

shRNA-identified targets play critical roles during induced reprogramming.

(A) to (D) Scheme showing representative networks identified in shRNA-group A and D

(A) and (B), shRNA-identified molecules are highlighted in green color. Non-enriched/identified molecules were shown in grey/white colors. (C) and (D), Number of reads for shRNA-identified genes are shown as heat maps corresponding (A) and (B) respectively. Number is shown in log_{10} scale.

(E) Heat map showing mRNA expression profiling for putative essential genes to reprogramming

mRNA expression change of select genes were examined during reprogramming. MEF and ESC serve as controls for two determined cell types. Replicate samples were labeled as #1 and #2. Fold change value is presented in log_2 scale.

(F) Heat map showing mRNA expression profiling for putative barrier genes to reprogramming.

Figure 5.3 (continuation)

mRNA expression change of select genes were examined during reprogramming. MEF and ESC serve as controls for two determined cell types. Replicate samples were labeled as #1 and #2. Fold change value is presented in $\log_2$ scale.

(G) Western blot analysis showing overexpression of select targets from putative barriers

Select genes were cloned into pMXs vector. Overexpression of those proteins were examined in 297FT cells and detected with anti-HA antibody by western blot analysis.

(H) Immuno-fluorescent staining showing proper functionality of exogenous proteins during reprogramming.

Transgenes were introduced into Oct4-EGFP MEFs together with four reprogramming factors OSKM. Exogenous proteins were detected with anti-HA antibody and visualized by fluorescence microscopy. Hoescht 33342 serves as counterstaining for nuclei. Scale bar denotes 25 mm.

Figure 5.3 (continuation)

(I) Bar graph showing fold changes of MEF reprogramming efficiency with forced-expression of barrier genes.

Transgenes were introduced into Oct4-EGFP MEFs with OSKM and the same assay was conducted as in Fig. 3a to d. Probabilities (Student *t*-test) are shown as * p value < 0.05 and **** $p < 0.00005$.

Figure 5.4

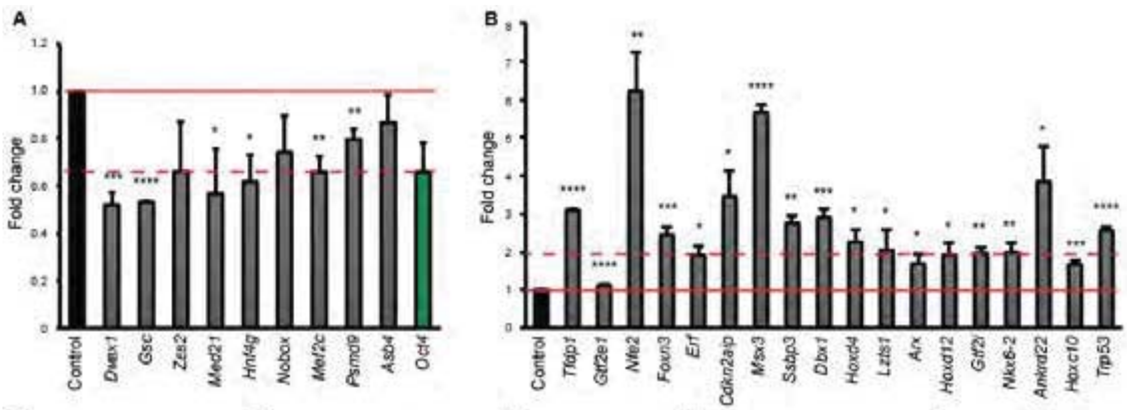

A
Fold change
Control
Dvex1
Gsc
Zes2
Med21
Hnf4g
Nobox
Mef2c
Psmd9
Asb4
Oct4
B
Fold change
Control
Tfdp1
Gtf2e1
Nfe2
Foxn3
Erf
Cdkn2aip
Msx3
Ssbp3
Dbx1
Hoxd4
Lzts1
Arx
Hoxd12
Gtf2i
Nkx6-2
Ankrd22
Hoxc10
Trp53

Figure 5.4

Functional genomic screening and transcriptome analysis reveal key regulators of induced reprogramming and ES cell properties.

(A) Bar graph showing fold change of MEF reprogramming efficiency with depletion of various essential genes.

siRNAs against select targets were introduced into Oct4-EGFP MEFs while cells were reprogrammed with OSKM. Fully reprogrammed colonies were identified and scored as EGFP positive colonies. Relative efficiency of reprogramming was calculated by normalized to none-targeting siRNA control (Control; black bar). Temporary knock-down of Oct4 by siRNA serves as positive control (green bar). Error bars denote standard error of the mean (S.E.M.), $n >= 3$. Red solid line marks the level of Control value and red dot line marks the cutoff value based on positive control (Oct4 knock-down). Probabilities (Student *t*-test) are shown as * p value < 0.05; ** $p < 0.005$; *** $p < 0.0005$; **** $p < 0.00005$.

Figure 5.4 (continuation)

(B) Fold change of MEF reprogramming efficiency with depletion of various barrier genes.

Same assay was conducted as in (E). p53 knock-down serves as positive control. Error bars denote S.E.M., $n \geqq 3$. Red solid line marks the level of Control value and red dot line marks the cutoff value. Probabilities (Student *t*-test) are shown as * p value < 0.05; ** $p < 0.005$; *** $p < 0.0005$; **** $p < 0.00005$.

and examined reprogramming efficiency by scoring the Oct4-EGFP positive colonies. Depleting 16 out of 17 tested genes (~94%; except *Gtf2e1*) showed significantly improved reprogramming efficiency compared with non-targeting siRNA control (Figure 5.4B). Furthermore, knockdown of 13 genes (~76.5%) exerted at least a two-fold induction of reprogramming efficiency (marked as red dotted line in Figure 5.4B), compared with non-targeting siRNA control. Those genes are *Tfdp1, Nfe2, Foxn3, Erf, Cdkn2aip, Msx3, Ssbp3, Dbx1, Hoxd4, Lzts1, Arx, Hoxd12, Gtf2i, Nkx6-2, Ankrd22*, and *Hoxc10*. The expression profile of these potential barriers again showed no specific trend (Figure 5.3F). To further validate the roles of these barriers, we tested their influence on reprogramming by forced-expressing transgenes with OSKM. We examined the protein expression of select transgenes by western blot analysis or immunofluorescence staining (Figure 5.3G and 5.3H). As expected, overexpression of the majority of putative barriers significantly compromised reprogramming efficiency, by ~40% to 80%, compared with DsRed control (Figure 5.3I). In summary, validation results showed that our RNAi screen identified meaningful targets serving as either positive or negative regulators during reprogramming.

Pcgf6, Ruvbl2, Hcfc1, and Srsf2 Play Critical Roles in Both ES Cell Identity and Induced Reprogramming

Finally, we sought to functionally test genes from transcriptome analysis (Figures 4.1C and 4.1D). To do this, we first asked whether genes highly induced during reprogramming (group I) could also contribute to ES cell identity. Many known ES-cell regulators, such as Nanog, Esrrb, and Lin28, are clustered into group I, indicating the high functional relevance of this group. Among group-I genes, we picked a panel of transcription factors with little-known functions in embryonic stem cells for further study (Figure 5.5A). We first tested the roles of these genes in maintaining ES cell self-renewal; this was accomplished by treating Oct4-EGFP ES cells with specific siRNAs to examine the loss of pluripotency by detecting EGFP signal with flow cytometry analysis, which was conducted four days after siRNA transfection. Sixteen of 64 tested genes (25%) showed a significant reduction (Z score >2) of Oct4-EGFP signal after depletion with siRNAs (Figure 5.5A), such as *Asb4, Dmbx1, Gbx2, Gsc, Hnf4g, Klf5, L3mbtl2, Med21,*

Figure 5.5

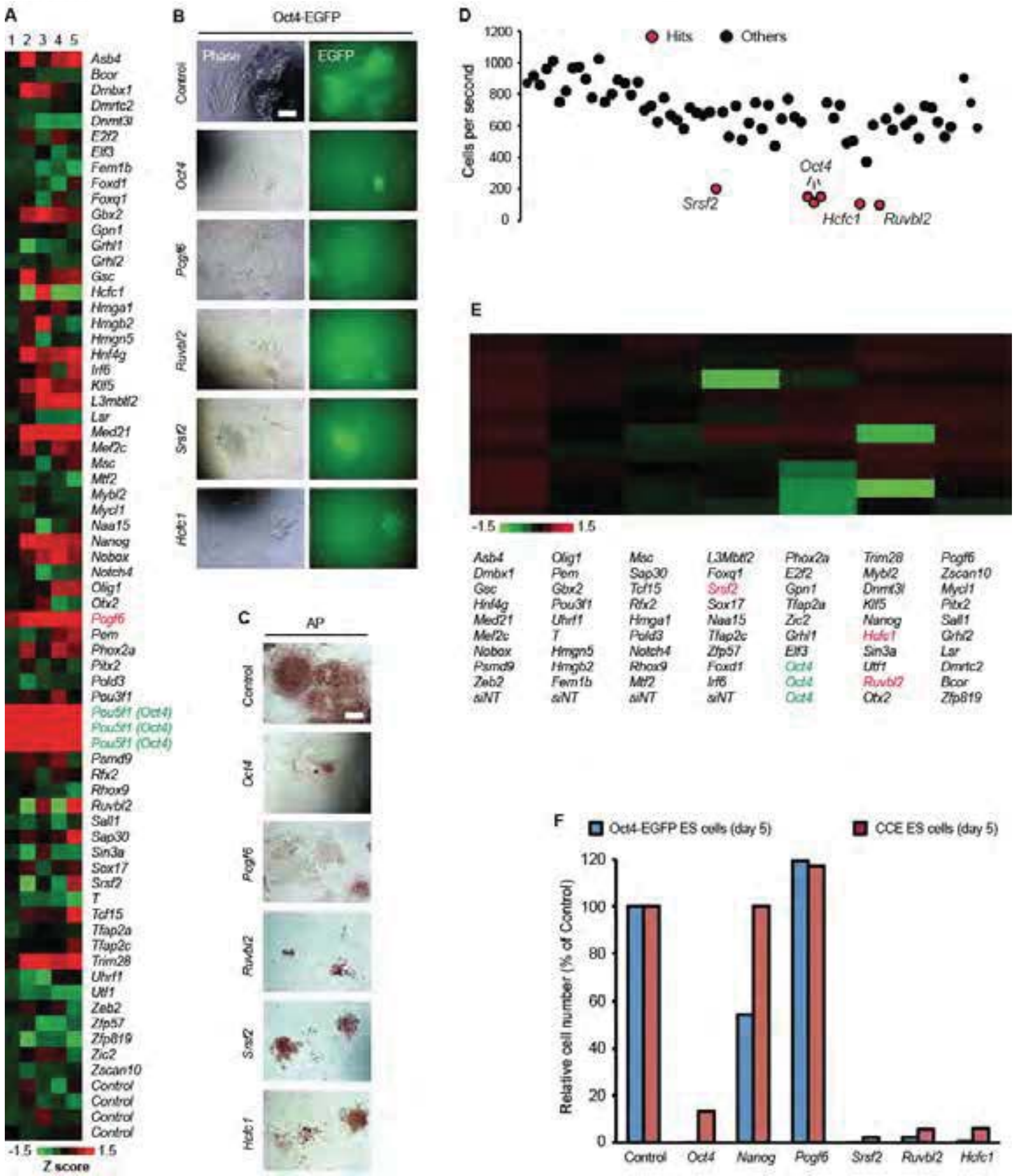

A
1 2 3 4 5
Asb4
Bcor
Dmbx1
Dmrtc2
Dnmt3l
E2f2
Elf3
Fem1b
Foxd1
Foxq1
Gbx2
Gpn1
Grhl1
Grhl2
Gsc
Hcfc1
Hmga1
Hmgb2
Hmgn5
Hnf4g
Irf6
Klf5
L3mbtl2
Lar
Med21
Mef2c
Msc
Mtf2
Mybl2
Mycl1
Naa15
Nanog
Nobox
Notch4
Olig1
Otx2
Pcgf6
Pem
Phox2a
Pitx2
Pold3
Pou3f1
Pou5f1 (Oct4)
Pou5f1 (Oct4)
Pou5f1 (Oct4)
Psmd9
Rfx2
Rhox9
Ruvbl2
Sall1
Sap30
Sin3a
Sox17
Srsf2
T
Tcf15
Tfap2a
Tfap2c
Trim28
Uhrf1
Utf1
Zeb2
Zfp57
Zfp819
Zic2
Zscan10
Control
Control
Control
Control
-1.5 1.5
Z score
B
Oct4-EGFP
Phase
EGFP
Control
Oct4
Pcgf6
Ruvbl2
Srsf2
Hcfc1
C
AP
Control
Oct4
Pcgf6
Ruvbl2
Srsf2
Hcfc1
D
Hits
Others
Cells per second
1200
1000
800
600
400
200
0
Srsf2
Oct4
Hcfc1
Ruvbl2
E
-1.5 1.5
Asb4 Dmbx1 Gsc Hnf4g Med21 Mef2c Nobox Psmd9 Zeb2 siNT
Olig1 Pem Gbx2 Pou3f1 Uhrf1 T Hmgn5 Hmgb2 Fem1b siNT
Msc Sap30 Tcf15 Rfx2 Hmga1 Pold3 Notch4 Rhox9 Mtf2 siNT
L3Mbtl2 Foxq1 Srsf2 Sox17 Naa15 Tfap2c Zfp57 Foxd1 Irf6 siNT
Phox2a E2f2 Gpn1 Tfap2a Zic2 Grhl1 Elf3 Oct4 Oct4 Oct4
Trim28 Mybl2 Dnmt3l Klf5 Nanog Hcfc1 Sin3a Utf1 Ruvbl2 Otx2
Pcgf6 Zscan10 Mycl1 Pitx2 Sall1 Grhl2 Lar Dmrtc2 Bcor Zfp819
F
Oct4-EGFP ES cells (day 5)
CCE ES cells (day 5)
Relative cell number (% of Control)
120
100
80
60
40
20
0
Control
Oct4
Nanog
Pcgf6
Srsf2
Ruvbl2
Hcfc1

Figure 5.5

Pcgf6, Srsf2, Hcfc1, and Ruvbl2 are required for maintaining ES cell property.

(A) Heat map showing Z score profiling of five independent siRNA screening assays.

Five individual experiments of siRNA screening assays in Oct4-EGFP ES cells were represented. Select target Pcgf6 for further study was highlighted in red. Positive control *Oct4* was highlighted in green. Z score value was shown here as in color code.

(B) Microscopy images showing *Pcgf6* depletion with siRNA reduced EGFP signal in Oct4-EGFP ES cells.

Oct4-EGFP ES cells were transfected with various siRNAs and EGFP signal was detected four days post transfection by fluorescent microscopy. Non-targeting siRNA serves as a negative control (Control) and *Oct4* siRNA serves as a positive control. Scale bar denotes 100 mm.

(C) Microscopy images showing *Pcgf6* depletion with siRNA reduced alkaline phosphatase (AP) activity in CCE ES cells.

CCE ES cells were transfected with various siRNAs and alkaline phosphatase activity

Figure 5.5A (continuation)

(AP) was detected four days post transfection by using Vector Red Alkaline Phosphatase Substrate Kit I (Vector cat# SK-5100). Non-targeting siRNA serves as a negative control (Control) and *Oct4* siRNA serves as a positive control. Scale bar denotes 100 μm.

(D) Scatter plot showing cell number counts of cells treated with various siRNAs.

Oct4-EGFP ES cells were transfected as described in (A). Cell number was measured by flow cytometry four days later. *Oct4* knock-down samples serve as positive controls. Experiments have been repeated five times and only one representative example is shown here.

(E) Heat map showing relative cell growth of ES cells treated with siRNAs.

Various siRNAs were transfected into Oct4-EGFP ES cells. Four days after transfection, cell growth was measured by using CellTiter 96 Aqueous One Solution Cell Proliferation Assay (MTS) kit (Promega). Relative ratio of cell growth was shown in color code. Corresponding target IDs were listed below the heat map. Select targets for further study were highlighted in red. Positive control *Oct4* was highlighted in green.

Figure 5.5A (continuation)

(F) Bar graph showing that Srsf2, Ruvbl2, and Hcfc1 are required to maintain proper cell growth in both Oct4-EGFP and CCE ES cells.

Both cells were treated with indicated siRNAs and cell growth was measured five days post transfection as described above.

Mef2c, Nobox, Pcgf6, Phox2a, Tcf15, Oct4/Pou5f1, Nanog, and *Trim28*. Among those genes and excluding si*Oct4* control, *Pcgf6* depletion had the most significant and consistent reduction of Oct4-EGFP signal (Figure 5.5A). The requirement of Pcgf6 to maintain ES self-renewal has been further confirmed under microscopy analysis, showing that ES markers (Oct4-EGFP or alkaline phosphatase activity) diminished with *Pcgf6* depletion in ES cells (Figures 5.5B and 5.5C).

We also examined whether depleting those genes might influence cell number in ES cells. Oct4-EGFP ES cells were treated with siRNAs as described in Figure 5.5A, and cells were counted by flow cytometry analysis. Strikingly, down-regulation of *Srsf2, Hcfc1*, and *Ruvbl2* caused a consistent and severe reduction in ES cell number (Figure 5.5D), comparable to Oct4 knockdown. ES cell growth was further examined with siRNA treatments, showing that ES cells require *Srsf2, Hcfc1*, or *Ruvbl2* to maintain a normal growth rate (Figure 5.5E). The effect of those three genes was further confirmed in a different ES cell line (Figure 5.5F). Notably, although depletion of *Ruvbl2, Srsf2*, and *Hcfc1*, colony size of ES cells was smaller, cells still retained the ES property with strong

Oct4-EGFP signal and alkaline phosphatase (AP) activity, in contrast to *Pcgf6*-depleted cells showing reduced EGFP signal and AP activity (Figures 5.5B and 5.5C).

To summarize, the targets identified by sorted shRNA-library screening indeed play critical roles (essentials or barriers) in modulating the progress of induced reprogramming by regulating various aspects of cellular functions. Further validation with siRNAs in ES cells showed that several genes are critical to maintaining ES cell self-renewal, including *Pcgf6, Asb4, Dmbx1, Gbx2, Gsc, Hnf4g, Klf5, L3mbtl2, Med21, Mef2c, Nobox, Phox2a, Tcf15*, and *Trim28*. Among these genes, Pcgf6 plays an essential role in maintaining ES cell renewal, while *Srsf2, Hcfc1*, and *Ruvbl2* are critical to ES cell proliferation. Finally, Our approaches comprehensively reveal numerous novel key modulations, by combining genome-wide shRNA library screening with transcriptome analysis (Figure 5.6).

Figure 5.6

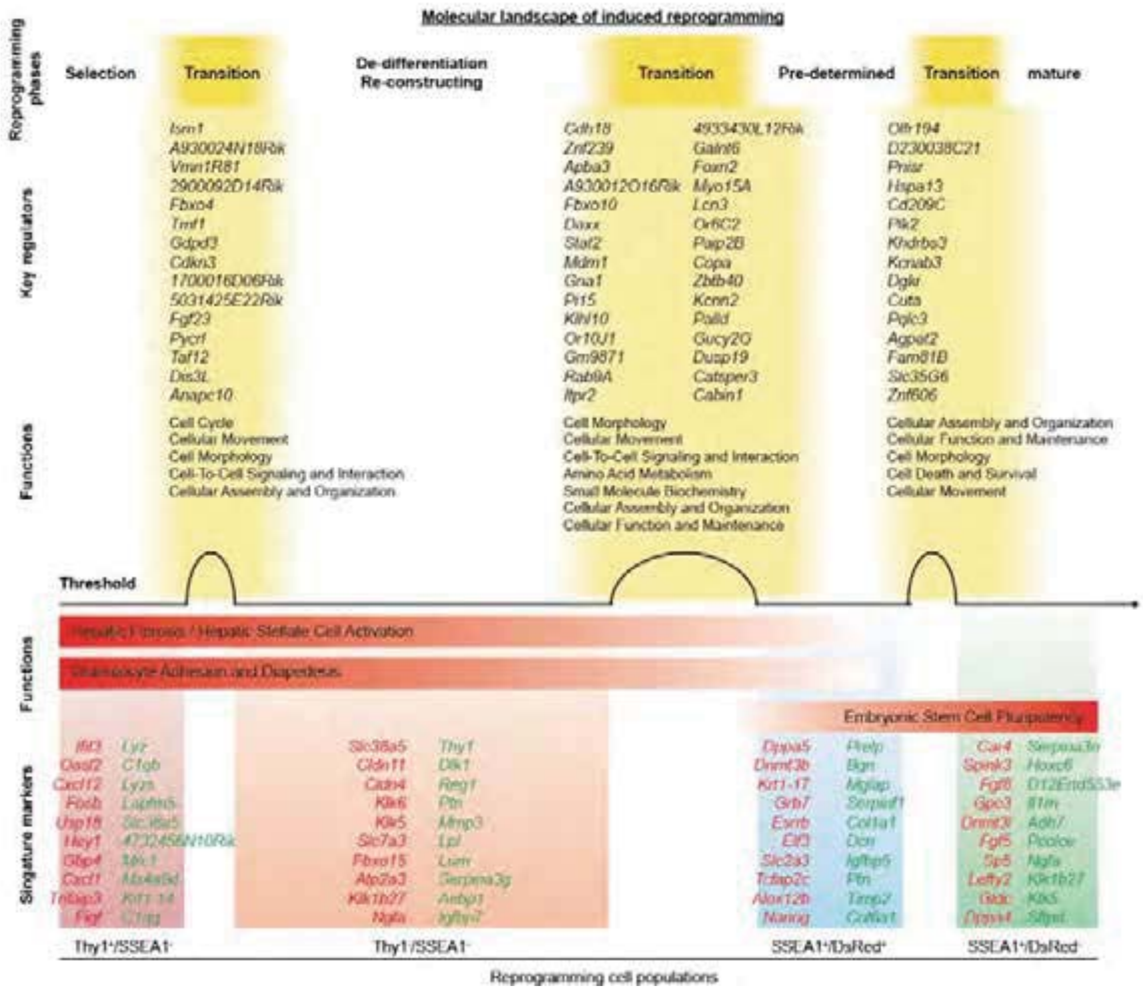

Molecular landscape of induced reprogramming
Reprogramming phases
Selection
Transition
De-differentiation
Re-constructing
Transition
Pre-determined
Transition
mature
Key regulators
Ism1
A930024N18Rik
Vmn1R81
2900092D14Rik
Fbxo4
Trmt1
Gdpd3
Cdkn3
1700016D06Rik
5031425E22Rik
Fgf23
Pycrl
Taf12
Dis3L
Anapc10
Cdh18
Znf239
Apba3
A930012O16Rik
Fbxo10
Daxx
Stat2
Mdm1
Gna1
Pri15
Klhl10
Or10J1
Gm9871
Rab9A
Itpr2
4933430L12Rik
Galnt6
Foxn2
Myo15A
Lcn3
Or6C2
Paip2B
Copa
Zbtb40
Kcnn2
Palld
Gucy2G
Dusp19
Catsper3
Cabin1
Olfr194
D230038C21
Pnisr
Hspa13
Cd209C
Plk2
Khdrbs3
Kcnab3
Dgki
Cuta
Pqlc3
Agpat2
Fam81B
Slc35G6
Znf606
Functions
Cell Cycle
Cellular Movement
Cell Morphology
Cell-To-Cell Signaling and Interaction
Cellular Assembly and Organization
Cell Morphology
Cellular Movement
Cell-To-Cell Signaling and Interaction
Amino Acid Metabolism
Small Molecule Biochemistry
Cellular Assembly and Organization
Cellular Function and Maintenance
Cellular Assembly and Organization
Cellular Function and Maintenance
Cell Morphology
Cell Death and Survival
Cellular Movement
Threshold
Functions
Hepatic Fibrosis / Hepatic Stellate Cell Activation
Leukocyte Adhesion and Diapedesis
Embryonic Stem Cell Pluripotency
Singature markers
Slc38a5
Cldn11
Cldn4
Klk6
Klk5
Slc7a3
Fbxo15
Atp2a3
Klk1b27
Ngfa
Thy1
Dlk1
Reg1
Ptn
Mmp3
Lpl
Lum
Serpina3g
Dppa5
Dnmt3b
Krt1-17
Grb7
Esrrb
Slc2a3
Tcfap2c
Alox12b
Nanog
Prelp
Bgn
Mglap
Col1a1
Dcn
Igfbp5
Ptn
Timp2
Car4
Spink3
Fgf8
Gpc3
Fgf5
Sp5
Lefty2
Hoxc6
Adh7
Nefa
Klk1b27
Klk5
Thy1⁺/SSEA1⁻
Thy1⁻/SSEA1⁻
SSEA1⁺/DsRed⁺
SSEA1⁺/DsRed⁻
Reprogramming cell populations

Figure 5.6

Model showing molecular requirements to induced reprogramming.

Reprogramming phases are shown on the top of the chart. The transitions between each stage are highlighted in dark yellow patches. Key molecules and functions identified by shRNA library screening are summarized and shown above the threshold line. Those identified by transcriptome analysis are shown below the threshold line. The bulges of threshold line represent the transition steps in induced reprogramming progress. The dynamics of representative functions identified by transcriptome analysis is represented in gradient red along the progression of reprogramming. Up-regulated genes are highlighted in red and down-regulated ones are in green. The corresponding-sorted cell populations are shown on the bottom of the chart.

Materials and Methods

FACS and Whole-genome shRNA Library Screening

To establish a marker set for isolating four distinct cell populations in reprogramming (Figure 4.1A). First, cells were transduced with retroviruses containing pMXs-DsRed plasmids. Three days later, transduced cells were harvested and stained with phycoerythrin-Cy7 (PE-Cy7)-conjugated antibodies targeting Thy1 (25-0902, eBioscience). Thy1 and DsRed double-positive cells ($Thy1^+/DsRed^+$) were isolated by FACS. Isolated $Thy1^+/DsRed^+$ cells were recovered for three days before introduction of shRNA library and OSKM for induced reprogramming. Pseudo viruses expressing pGIPz-shRNA library and pMXs-OSKM were generated in 293FT and Plate-E cells, respectively. Pseudo viruses were administrated at day 0 and day 1 during reprogramming to maximize the transduction efficiency. ES cell medium was used for culturing transformed cells at day 3 post induced reprogramming. Two weeks after reprogramming, cells were harvested and dissociated with trypsin/EDTA. PE-Cy7-conjugated antibodies targeting Thy1 (25-0902, eBioscience) and Alexa

Fluor®647-conjugated SSEA1 antibodies (51-8813, eBioscience) were used to detect surface markers Thy1 and SSEA1. Before isolating cells with FACS, $SSEA1^{+}$ cells were enriched using Anti-SSEA-1 (CD15) MicroBeads (130-094-530, Miltenyi Biotec GmbH). SSEA1-enriched cells were used for sorting $SSEA1^{+}/DsRed^{+}$ and $SSEA1^{+}/DsRed^{-}$ cell populations. SSEA1-depleted cells were used for sorting $Thy1^{+}/SSEA1^{-}$ and $Thy1^{-}/SSEA1^{-}$ cell populations. The shRNA-library screening in reprogramming was independently conducted three times. Total RNAs and genomic DNAs were extracted from sorted populations for mRNA microarray analysis and SOLiD sequencing analysis.

Oct4-EGFP Mouse Embryonic Fibroblast Derivation

Oct4-EGFP MEFs were derived from the mouse strain B6;129S4-$Pou5f1^{tm2(EGFP)Jae}$/J (Jackson Laboratory; stock #008214) using the protocol provided on the WiCell Research Institute website (http://www.wicell.org/). In brief, E13.5 embryos were collected from time-mated pregnant female mice. Cells isolated from embryos then were tested for microbial contamination. Oct4-EGFP MEFs were maintained in MEF complete medium (DMEM with 10% FBS, nonessential amino acids, L-glutamine, and no sodium pyruvate).

Robust-growing cells (usually < 4 passages) were used for induced reprogramming.

Construction of Retroviral Vectors Expressing Transgenes

Complementary DNAs of select targets were amplified by using total RNAs of ES cells and inserted into retroviral vector pMXs (Addgene; http://www.addgene.org/). All transgenes in this study were tagged with HA sequence, including *Ankrd22, Nfe2, Tfdp1, Ssbp3, Lzts1, Dbx1, Pcgf6, Hcfc1, Srsf2, and Ruvbl2*. Retroviruses expressing transgenes were produced in ecotropic version using Plat-E cells (RV-101, Cell Biolabs) or amphotropic version using Plat-A cells (RV-102, Cell Biolabs) to transduce mouse or human somatic cells, respectively. Virus supernatant was collected at two days post transfection. Virus supernatant was added with 6 mg/ml of polybrene (Millipore) to enhance transduction efficiency.

Human Induced Pluripotent Stem Cell Culture

Derived human iPS cells were cultured following the protocols available on the WiCell Research Institute website (http://www.wicell.org/). Briefly, cells were grown in DMEM/F12 medium (Invitrogen; Cat# 11330-032) containing 20% knockout serum replacer (Invitrogen; Cat# 10828), 4ng/ml of human recombinant basic fibroblast growth factor (bFGF; Invitrogen; Cat# 13256-029), 1 mM L-glutamine (Invitrogen; Cat# 25030081), and 1% non-essential amino acids (Invitrogen; Cat# 11140-050). Human iPS cells were seeded on a feeder layer of mouse embryonic fibroblasts (MEF) at young passages (1 to 4). MEF were irradiated and seeded at 1.88 X 105 cells per well in a six-well plate. For the long-term process of human reprogramming, hES cell culture medium was conditioned for 24 h on MEF at 2.12 X 105 cells/ml, and bFGF was added before use.

Immunofluorescence and Alkaline Phosphatase (AP) Staining

Human iPS cells were characterized for pluripotency by staining pluripotency markers as described (Cao *et al.*, 2008). Briefly, hiPS/ES cells were fixed with 4% paraformaldehyde (Electron Microscopy Sciences; Cat# 15710-S) in PBS for 30 min at room temperature (RT), and permeabilized for 5 min at RT by treating with 0.1% Triton X-100 in PBS. Permeabilized cells were blocked with 5% goat serum in PBS for 30 min at RT. Cells were incubated for 1 h at RT with antibodies specifically targeting SSEA-4 (sc-21704, Santa Cruz), Tra-1-60 (4746, Cell Signaling), Tra-1-81 (4745, Cell Signaling), and Nanog (AF1997, R&D systems) in 1.5% goat serum in PBS at 1:500 dilutions. After washing three times with 1 ml of PBS, cells were treated with secondary antibodies (Alexa Fluor 488 and 546) diluted 1:200 in 1.5% goat serum in PBS for 1 h at RT. Cell nuclei were stained with DAPI (4',6 diamidino-2-phenylindole) in PBS. Fluorescence images were captured by fluorescence microscopy. For AP staining, fixed cells were treated with alkaline phosphatase substrate following the manufacturer's instruction (Vector Laboratories; Cat# SK-5100).

Western Blot Analysis

Protein expression of HA-tagged transgenes, including *Ankrd22, Nfe2, Tfdp1, Ssbp3, Lzts1, Dbx1, Pcgf6, Hcfc1, Srsf2, and Ruvbl2*, were tested in reprogrammed cells or iPS/ES cells. Cells transfected with transgenes were harvested and total proteins were prepared in M-PER buffer (Pierce). Equal amounts of total protein were separated on 10% SDS-PAGE gels. Proteins were transferred to PVDF membranes, and specific proteins were detected using anti-HA antibody (11867423001, Roche Applied Science).

GAPDH (sc-20357, Santa Cruz) and β Actin (MS-1295, Thermo Scientific) served as loading controls. Signal of target proteins was visualized and detected with SuperSignal West Femto Chemiluminescent Substrate (34094, Thermo Scientific).

Gene Knockdown with siRNA Transfection for Testing Reprogramming Efficiency

Specific siRNAs against select targets were purchased from Dharmacon (Thermo Scientific). Before treated with retroviruses for reprogramming, $4X10^4$ Oct4-EGFP MEFs were transfected with Lipofectamine/siRNAs complexes according to the manufacturer's instruction (Invitrogen). In general, at least 25 nano molar of siRNAs in final concentration was used to effectively deplete target genes. Three to five hours later, the transfection reagent was discarded and retrovirus-containing supernatant was added for induced reprogramming. Gene knockdown efficiency was evaluated by semi-quantitative real time RT-PCR ~24 hours later (data not shown). *Gapdh* served as an internal control to normalize mRNA expression signals.

Gene Knockdown with siRNA Transfection in ES cells for Examining ES cell Identity

Oct4-EGFP or CCE ES cells were seeded at the concentration of $1X10^5$ cells/well in 12-well plates coated with 0.1% gelatin one day before transfection. The next day, cells were transfected with Lipofectamine/siRNAs complexes (25 ~50 nM in final concentration) as described above. Three to five hours later, the transfection reagent was discarded and ES-cell culture medium was added. Four days after transfection, Oct4-EGFP signal and alkaline phosphatase activity were examined under microscopy as described above.

Microarray Analysis

To analyze transcriptome changes during reprogramming, total RNAs were isolated from four sorted cell populations using TRIZOL reagent (Invitrogen). Gene expression was detected and normalized in the SBMRI HT screening and genomics core facilities. Gene clusters were created using Cluster 3.0, and heat maps were created using Java TreeView. Scatter plots were created using Excel.

SOLiD Sequencing for Genome-wide shRNA Library Screening

To acquire enriched shRNAs in each sorted cell population, primer X76

(5'-acgtcgaggtgcccgaagga-3') and M100 (5'-aagcagcgtatccacatagcgt-3') were used to amplify the integrated shRNA hairpins from isolated genomic DNAs using Phusion Hot Start DNA polymerase (#F-549, Thermo Scientific). Desired PCR products (~700bp) were purified with QIAEX II Gel Extraction Kit (20021, Qiagen). PCR products were digested with restriction enzymes EcoRI and XhoI to remove the flanking fragments. Digested PCR products (~180bp) were purified again using a QIAEX II Gel Extraction Kit.

To perform SOLiD sequencing, the samples were sent to the SBMRI Analytical Genomics Core Facility. In brief, PCR products were purified again in 3% Agarose gel and purified bands were confirmed by 2100 Bioanalyzer analysis (Agilent Technologies) prior to preparation of SOLiD-sequencing amplicons. After SOLiD sequencing, the contaminated sequences with repeating nucleotides were filtered, and reads were mapped to the parental sequences of pGIPz shRNA library provided from Thermo Scientific. The mapping parameters were set to have at least 19-matched nucleotides and with only one-mismatched base pair allowed in a 25-nucleotide long context. For each sorted cell population, the numbers of mapped/filtered reads are 708,344/2,531,068 ($Thy1^+$ and $SSEA1^-$), 274,690/1,542,129 ($Thy1^-$ and $SSEA1^-$), 456,349/1,168,247 ($SSEA1^+$ and $DsRed^+$), and 681,455/5,187,301 ($SSEA1^+$ and $DsRed^-$).

We consolidated several shRNA-sequencing reads to a single target, as multiple shRNAs can target the same genes. Target genes with less than 10 shRNA reads (log_{10} <1) were considered as background noises and discarded. To discover over-representative molecules and functions in shRNA-identified targets, we set the cutoff value for shRNA reads at 1.5 in log_{10} scale using IPA platform. Consolidated data of target genes in each sorted cell population are listed in Appendix 3. In each sorted cell population, the numbers of shRNA-identified genes are 829 ($Thy1^+$ and $SSEA1^-$), 784 ($Thy1^-$ and $SSEA1^-$), 206 ($SSEA1^+$ and $DsRed^+$), and 898 ($SSEA1^+$ and $DsRed^-$).

High-through-put siRNAs Screening in Oct4-EGFP ES Cells

To retro-transfect Oct4-EGFP ES cells in 96-well plates, Lipofectamine 2000 (L2K) and siRNA transfection complexes were first prepared in each well with a volume ratio of L2K versus siRNA (10 mM) of 0.6:1. Approximately 70 ng of siRNAs in ~15 ml of

OptiMEM was used in each well coated with 0.1% gelatin.

To perform siRNA retro-transfection, Oct4-EGFP ES cells were then seeded at the density of 4000-cells/150 ml/well in 96-well plates containing siRNA transfection complexes. The next day, the transfection reagent was discarded and ES-cell culture medium was used and subsequently changed every other day. To detect the Oct4-EGFP signal, four days after transfection, cells were dissociated with 0.25% trypsin for ~3 minutes and re-suspended in 200 ml of ES medium for flow cytometry analysis.

Meta-Analysis Using IPA and NextBio Platforms

To analyze transcriptome changes, normalized mRNA expression data were uploaded onto the IPA server using an IPA browser. For the four-sorted cell populations, the cut off value for fold change in $\log_2$ scale and *p*-value were set as 1 and 0.05, respectively. Over-representative genes, networks, and pathways were identified using the IPA platform.

To analyze shRNA-enriched targets in the four-sorted cell populations, the number of shRNA reads was converted into a $\log_{10}$ scale. Gene IDs with sequencing reads were then uploaded onto the IPA server. The cut off value for shRNA-enrichment was arbitrarily set at 1.5 in $\log_{10}$ scale, and the *p*-value (Fishers' Exact test) was set at 0.05. Over-representative genes, networks, and pathways were identified using IPA platform.

To analyze cell-type correlations of the four-sorted populations, normalized mRNA expression data were uploaded onto the NextBio server and processed using the BodyAtlas algorithm.

CHAPTER VI

Discussion

The new era of reprogramming was initiated by the ectopic expression of four transcription factors in somatic cells, first demonstrated by Yamanaka's group (Takahashi and Yamanaka, 2006) in mouse cells and later in human cells by Thomson's[2] and Yamanaka's[3] groups. Using retroviral or lentiviral systems, these four factors, Oct4, Sox2, Klf4/Lin28, and c-Myc/Nanog (also referred to as OSKM or OSLN) can be easily introduced into somatic cells to induce reprogramming to an embryonic stem (ES) cell-like pluripotent state. The induced pluripotent stem cells (iPS cells) generated by this breakthrough technology have provided a valuable alternative resource to human embryonic stem cells (Yamanaka, 2007). However, the low efficiency of reprogramming and concerns of genetic modification by the transgenes remain major hurdles in the therapeutic application of iPS cells (Stadtfeld and Hochedlinger, 2010; Takahashi *et al.*, 2007; Yamanaka, 2007; Yu *et al.*, 2007). In recent years, substantial progress has been made in improving reprogramming efficiency and in substituting select transcription factors (Ho *et al.*, 2011; Hochedlinger and Plath, 2009; Plath and Lowry, 2011; Stadtfeld and Hochedlinger, 2010). Although many windows have been opened to improve the efficiency of reprogramming and to minimize transgenic integrations into the genome, we have only just begun to understand the molecular mechanisms that control reprogramming beyond the four factors. Many studies have shown that reprogramming can be defined and achieved as a step-wise process (Brambrink *et al.*, 2008; Sridharan *et al.*, 2009; Stadtfeld *et al.*, 2008a). Several genes and proteins have been identified that have greatly impacted reprogramming efficiency, including Ink4a/ARF, p53/p21 (Banito *et al.*, 2009a; Hong *et al.*, 2009; Kawamura *et al.*, 2009b; Li *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009), TGF-β (Ichida *et al.*, 2009; Maherali and Hochedlinger, 2009b), and miRNAs (Judson *et al.*, 2009b; Li *et al.*, 2011; Liao *et al.*, 2011; Lin *et al.*, 2010; Lipchina *et al.*, 2011; Melton *et al.*, 2010; Pfaff *et al.*, 2011; Subramanyam *et al.*, 2011; Yang *et al.*, 2011a). Despite these advances, the molecular events occurring during reprogramming remain largely unknown. Therefore, we utilized several different approaches to decipher the mechanisms underlying the induced reprogramming progress.

MicroRNAs Serve as Key Regulators in Induced Reprogramming

We are the first to report that c-Myc represses MEF-enriched miRNAs, such as miR-21, let-7a, and miR-29a, during reprogramming. Depleting miR-29a with inhibitors decreased p53 protein levels most likely by releasing p85α and CDC42 repression. In addition, depleting miR-21 decreased ERK1/2 phosphorylation. Interestingly, we found that miR-21 inhibition reduced p53 protein levels and that inhibiting miR-29a also reduced ERK1/2 phosphorylation level. Both p53 and ERK1/2 signaling antagonizes reprogramming (Banito *et al.*, 2009b; Hong *et al.*, 2009; Judson *et al.*, 2009a; Kawamura *et al.*, 2009a; Marion *et al.*, 2009; Silva *et al.*, 2008b; Utikal *et al.*, 2009). Blocking miR-21 and miR-29a or knockdown of p53 and ERK1/2 can enhance reprogramming efficiency. Thus, we propose that c-Myc facilitates reprogramming in part by suppressing the MEF-enriched miRNAs, miR-21 and miR-29a, which act as reprogramming barriers through induction of p53 protein levels and ERK1/2 activation.

Forced expression of ES-specific miRNAs of the miR-290 family can replace c-Myc to promote reprogramming (Judson *et al.*, 2009a). c-Myc also binds the promoter region of the miR-290 cluster (Chen *et al.*, 2008; Judson *et al.*, 2009a). However, early expression of the c-Myc transgene is effective to initiate reprogramming but dispensable at the transition stage or later in mature iPS cells (Sridharan *et al.*, 2009), where miR-290 clusters start to express. Therefore, it is unlikely that c-Myc promotes early stages of reprogramming through activating the miR-290 family.

We also found that expression level of MEF-enriched miRNAs, including miR-29a, miR-21, miR-143 and let-7a, decreases when c-Myc is introduced for reprogramming. c-Myc has a profound transcriptional effect (Wanzel *et al.*, 2003a) on miRNAs in promoting tumorigenesis (Chang *et al.*, 2008b; Chang *et al.*, 2009a) or sustaining the pluripotency ground state (Lin *et al.*, 2009a; Smith *et al.*, 2010). Therefore, c-Myc repression of miRNA expression is the likely mechanism underlying reprogramming.

miR-21 acts as positive mediator to enhance fibrogenic activity through the TGF-β1 (Liu *et al.*, 2010a) and ERK1/2 (Thum *et al.*, 2008) pathways, both of which have been shown to influence reprogramming and the ES cell ground state (Ichida *et al.*, 2009; Nichols *et al.*, 2009; Ying *et al.*, 2008). Notably, among validated miR-29a targets, protein level of p53 is indirectly induced by miR-29a (Park *et al.*, 2009a). In addition, recent studies show that the Ink4-Arf/p53/p21 pathway compromises reprogramming, and p53 deficiency greatly enhances reprogramming efficiency (Banito *et al.*, 2009b; Hong *et al.*, 2009; Judson *et al.*, 2009a; Kawamura *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009). Thus these signaling pathways are likely the primary barriers to the reprogramming process.

Depleting the c-Myc-targeted miRNAs, miR-21 and miR-29a, enhanced reprogramming efficiency ~2.4- to ~3-fold, suggesting that MEF-enriched miRNAs also function as reprogramming barriers. Let-7 inhibition has been recently reported to enhance reprogramming (Melton *et al.*, 2010), however, by several attempts we observed a minor effect in reprogramming when let-7 was inhibited by antagomirs. Moreover, our data showed that the induction of p53 during reprogramming was compromised by miR-29a inhibition, enhancing reprogramming efficiency. Similarly, reprogramming can be greatly promoted by either depleting miR-21 or ERK1/2. c-Myc is a major contributor to the early stage of reprogramming and is not required to sustain the process at transition and late stages (Sridharan *et al.*, 2009), indicating that c-Myc-regulated miRNAs may be employed to initiate high efficiency reprogramming.

c-Myc reportedly directly binds to and represses the miR-29a promoter (Chang *et al.*, 2008b). However, further studies are needed to understand how c-Myc regulates miR-21 expression. Our data show that c-Myc can be only partially replaced by depleting miR-21 and suggest that c-Myc has other functions in reprogramming. Thus regulation of multiple pathways or wide repression of MEF-enriched miRNAs may be required to replace c-Myc function during reprogramming.

c-Myc plays a key role in establishing the early transition stage

We demonstrated that c-Myc disturbs the fibroblastic network by inhibiting the mouse embryonic fibroblast (MEF)-enriched miRNAs, miR-21 and miR-29a, to lower the threshold for reprogramming (Yang *et al.*, 2011a). Thus, c-Myc establishes the early molecular context of reprogramming, not only by directly interacting with promoter regions of target genes, but also by exerting inhibitory effects on somatic networks by regulating miRNAs.

The cellular phenotypes associated with the reprogramming transitions have been reported in recent studies (Li *et al.*, 2010; Samavarchi-Tehrani *et al.*, 2010), but a clear picture of the detailed molecular events driving the transitions is still lacking. Among the four reprogramming factors, c-Myc has been shown to play the dominant role in initiating the early transitional stage (Koche *et al.*, 2011; Sridharan *et al.*, 2009). Expression of c-Myc alone can downregulate the expression of fibroblast-specific genes and induce the molecular context of the embryonic status within 3 days of transduction (Sridharan *et al.*, 2009). In addition to regulating the expression of hundreds of genes, as shown in previous reports (Sridharan *et al.*, 2009; Wanzel *et al.*, 2003b), c-Myc regulates numerous miRNAs to promote tumorigenesis (Chang *et al.*, 2008a; Chang *et al.*, 2009b; Gao *et al.*, 2009; Lotterman *et al.*, 2008) and to maintain pluripotency in ES cells (Lin *et al.*, 2009b; Lin *et al.*, 2009c; Smith and Dalton, 2010; Smith *et al.*, 2010).

The MEF-enriched miRNAs, miR-21, miR-29a, and let-7, act as barriers to the

initial stage of reprogramming

We previously demonstrated that the miRNA expression profile changes dramatically upon OSKM introduction into MEFs, with c-Myc playing the dominant regulatory role in this process (Yang *et al.*, 2011a). Furthermore, we have shown that c-Myc decreases the expression of MEF-enriched miRNAs, such as miR-21 and miR-29a. c-Myc transcriptionally suppresses miR-29 expression by binding to its promoter (Mott *et al.*, 2010), while the molecular mechanism by which c-Myc regulates miR-21 expression is still unclear. miR-21 positively regulates the TGF-β1 (Liu *et al.*, 2010b) and MAP kinase (Thum *et al.*, 2008) pathways, which have been shown to act as roadblocks to reprogramming (Ichida *et al.*, 2009; Li *et al.*, 2010; Li *et al.*, 2011; Liao *et al.*, 2011; Maherali and Hochedlinger, 2009b; Nichols *et al.*, 2009; Wray *et al.*, 2010; Yang *et al.*, 2010; Ying *et al.*, 2008). miR-29a has been shown to indirectly induce p53 protein levels by post-transcriptionally inhibiting CDC42 and p85a (Park *et al.*, 2009b). Consistent with these observations, depleting miR-21 or miR-29a dramatically (2 to 3 fold) increases reprogramming efficiency, suggesting that MEF-enriched miRNAs act as barriers to reprogramming (Yang *et al.*, 2011a). We also showed that miR-21 and miR-29a modulate reprogramming by regulating phosphorylation of ERK1/2 by 45~60% through Spry1 protein expression. In addition, depletion of miR-21 and miR-29a downregulates p53 protein levels by 25~40% through elevation of CDC42/p85a expression, which consequently enhances reprogramming efficiency. These data provide evidence for new regulatory networks during reprogramming involving c-Myc, miR-21, and miR-29a.

Another abundant miRNA in MEFs, let-7, has been shown to act as a barrier to reprogramming, since depleting let-7 enhanced the reprogramming efficiency by 4.3 fold with only the OSK reprogramming factors (Melton *et al.*, 2010). Ectopic expression of c-Myc reduces let-7a expression in MEFs during reprogramming, although to a relatively modest degree (Yang *et al.*, 2011a). It has been reported that c-Myc represses let-7 through Lin-28b transactivation (Chang *et al.*, 2009b); however, Lin-28b mRNA is undetectable during the early stage of reprogramming (Yang *et al.*, 2011a), suggesting other indirect mechanisms may be involved. The let-7 family may exert negative effects on reprogramming, because they are known to repress numerous pluripotent regulators, including Myc, Hmga2, Lin-28, and Sall4 (Kim *et al.*, 2009a; Melton *et al.*, 2010; Park *et al.*, 2007; Rybak *et al.*, 2008; Sampson *et al.*, 2007). To summarize, the MEF-enriched miRNAs, miR-21, miR-29a, and let-7a modulate various pathways to antagonize the reprogramming process. Furthermore, c-Myc has an intrinsic ability to initiate the reprogramming transition, not only by targeting the promoter regions of numerous genes, but also by inhibiting MEF-enriched miRNAs in the initial stage of reprogramming.

p53-regulated miRNA miR-34 and miR145 play important roles in reprogramming

The introduction of reprogramming factors into somatic cells initiates the cellular stress response to viral infection and oncogenes. Among the stress response molecules, transformation-related protein 53 (Trp53 or p53) plays a critical role as a gate-keeper to ensure that only cells with genomic integrity will survive to reach the pluripotent status, while stochastic nuclear reprogramming is induced (Banito *et al.*, 2009a; Hong *et al.*, 2009; Kawamura *et al.*, 2009b; Li *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009). miR-34 has been identified as a downstream target of p53 and contributes significantly to p53-mediated cell cycle arrest and apoptosis (Chang *et al.*, 2007; He *et al.*, 2007;

Raver-Shapira *et al.*, 2007). miR-34a deficiency in murine somatic cells improves the efficiency (by more than 4 fold) and kinetics (by two days earlier) of reprogramming (Choi *et al.*, 2011). Consistent with this observation, p53-induced miR-34a/b/c act as negative regulators of reprogramming, in part through the repression of pluripotency genes such as Lin28a (Jain *et al.*, 2012), Nanog, Sox2, N-Myc (Choi *et al.*, 2011), and c-Myc (Siemens *et al.*, 2011).

After initiation of reprogramming, mesenchymal-to-epithelial transition (MET) is the next step towards pluripotency (Li *et al.*, 2010; Samavarchi-Tehrani *et al.*, 2010). Approximately 5 days after OSKM induction, transformed cells undergo dramatic morphological changes from mesenchymal-like (polarized and mono-adherent) to epithelial-like (densely packed) cells. MET is critical for somatic cells to complete the first step of de-differentiation. Interestingly, miR-34a/b/c have been shown to compromise Snail1-dependent EMT (the reverse transition to MET) in cancer cells by targeting the 3' untranslated region (UTR) of Snail1 (Kim *et al.*, 2011b), while Snail1 and ZEB1 impose a negative feedback loop on miR-34a/b/c by binding the E-boxes of the miR-34a/b/c promoters (Siemens *et al.*, 2011). miR-34a also decreases other EMT factors, such as β-catenin, LEF1, Axin2 (Kim *et al.*, 2011b), Slug, and ZEB1 (Siemens *et al.*, 2011), and ectopic expression of miR-34a also prevents TGF-β-induced EMT (Siemens *et al.*, 2011). Therefore, short-term introduction of miR-34a/b/c may suppress the EMT in the early reprogramming process, while reprogramming factors coordinately affect MET to de-differentiate somatic cells. Since miR-34 modulate various functional pathways, miR-34 may play dual roles to secure cell integrity and promote MET in the cell-context-dependent manner.

miR-145, suggested to be the direct target of p53 (Jain *et al.*, 2012), plays critical roles to direct differentiation of ES cells (Xu *et al.*, 2009). miR-145 has been reported to downregulate Sox2 (Liu *et al.*, 2012), Klf4 (Jain *et al.*, 2012), and Oct4 to promote mesoderm and ectoderm differentiation in ES cells (Xu *et al.*, 2009). Furthermore, miR-145 promoter region is bound and repressed by Oct4 in ES cells (Xu *et al.*, 2009), suggesting Oct4 may lift the suppression of endogenous OSK by miR-145 during reprogramming. However, regulatory networks of miR-145 during reprogramming need to be vigorously interrogated, since this hasn't been tested during the process of reprogramming.

EMT/MET-associated miRNAs play important roles in modulating the transitional stage of reprogramming

During the MET stage of reprogramming, pro-mesenchymal miRNAs miR-10b (Ma *et al.*, 2007) and miR-155 (Kong *et al.*, 2008) decrease (Li *et al.*, 2010), and pro-epithelial miRNAs miR-205 (Gregory *et al.*, 2008a; Wiklund *et al.*, 2010a) and miR-429 (miR-200 family) (Burk *et al.*, 2008; Chen *et al.*, 2012; Chen *et al.*, 2011b; Wellner *et al.*, 2009) increase (Li *et al.*, 2010; Samavarchi-Tehrani *et al.*, 2010). miR-10b promotes EMT in cancer metastases by targeting homeobox D10 (Ma *et al.*, 2007), and miR-10b antagomirs suppress metastases *in vivo* (Ma *et al.*, 2010). miR-155 plays an important role in TGF-β–induced EMT by targeting RhoA (Kong *et al.*, 2008), one of the key factors maintaining junction formation and stabilization (Wang *et al.*, 2003). However, a recent report showed that miR-155 may have dual functions in modulating EMT depending on the microenvironment of the tumor (Xiang *et al.*, 2011), suggesting that the functions of miRNAs are cell and/or tissue context-dependent.

Conversely, the miR-200 family and miR-205 have been shown to positively regulate MET by targeting ZEB1 and ZEB2 (Chen *et al.*, 2011b; Gregory *et al.*, 2008b; Park *et al.*, 2008b; Wiklund *et al.*, 2010b), while ZEB1 reciprocally represses the miR-200 family (Burk *et al.*, 2008; Wellner *et al.*, 2009). In addition, bone morphogenetic protein (BMP), which is required for efficient reprogramming with OSKM, promotes MET and also induces expression of miR-205 and the miR-200 family during OSKM-induced reprogramming (Samavarchi-Tehrani *et al.*, 2010). Introduction of miR-200b/c mimics synergize with OSKM to promote more efficient reprogramming (Samavarchi-Tehrani *et al.*, 2010). Notably, c-Myc may boost reprogramming efficiency by directly inducing expression of the miR-200 family (miR-200, miR-141, and miR-429), and possibly coordinating with Klf4 to initiate MET (Chen *et al.*, 2011a; Li *et al.*, 2010).

The miR-290/302 seed family plays significant roles during the programming progress

It has been shown that microRNAs maintain the murine ES property by promoting the G1-S transition of the cell cycle and that aberrant miRNA biogenesis impairs proliferation of ES cells, which accumulate in the G1 phase (Kanellopoulou *et al.*, 2005; Murchison *et al.*, 2005; Wang *et al.*, 2008). The key miRNAs for these functions are the miR-290 and miR-302 clusters, which are the most abundant miRNAs in mouse and human ES cells respectively (Houbaviy *et al.*, 2003; Landgraf *et al.*, 2007; Suh *et al.*, 2004). These two clusters have almost identical seed regions (miR-290/302 seed family), suggesting they have highly similar target and/or regulatory networks. In human ES cells, the miR-302 cluster is regulated by Oct4/Sox2 to post-transcriptionally modulate cyclin D1, a key regulator of cell cycle progression (Card *et al.*, 2008; Marson *et al.*, 2008). The miR-290/302 seed family modulates cell cycle progression by targeting diverse regulators of the cell cycle, including p21 and other inhibitors of the cyclin E/Cdk2 pathway (Wang *et al.*, 2008). Numerous targets of the miR-302 cluster were uncovered using the photoactivatable ribonucleoside-enhanced cross-linking and immunoprecipitation method (PAR-CLIP); these included modulation of BMP signaling through suppression of Tob2, Dazap2, and Slain1 (Lipchina *et al.*, 2011). miR-302a is known to target Lefty1/2, which is an agonist of the TGF-β/Nodal signaling pathway in embryogenesis (Rosa *et al.*, 2009). In mouse ES cells, the miR-290 family controls de novo methylation through Rbl2-dependent regulation of DNA methyltransferase (Dnmts) (Benetti *et al.*, 2008; Sinkkonen *et al.*, 2008). Based on these findings, it appears that the main function of the miR-290/302 seed family is to shorten the G1 phase of the cell cycle to support self-renewal, and to secure the epigenetic status that maintains the pluripotency of ES cells.

During MET stage of OSKM-induced reprogramming, aggregates and colonies of reprogrammed cells become visible under low magnification microscopy as reprogrammed cells acquire epithelial cell features. These cells begin to express pluripotency markers, of which SSEA-1 is the earliest surface marker to indicate the potential iPS cells (Brambrink *et al.*, 2008; Stadtfeld *et al.*, 2008a). As the reprogrammed cells move towards a state of pluripotency, Nanog, Esrrb, Lin28, Dppa4, Tert, Sox2, and Oct-4 are endogenously expressed, demonstrating that the core circuit of pluripotency has been established (Brambrink *et al.*, 2008; Samavarchi-Tehrani *et al.*, 2010; Sridharan *et al.*, 2009; Stadtfeld *et al.*, 2008a). The embryonic stem cell cell-cycle-regulating (ESCC) miRNAs, the miR-302 clusters, are also expressed during the transition stage day 4 to day 7 post induced reprogramming (Kamata *et al.*, 2010; Li *et al.*, 2011), mainly induced by the reprogramming factor c-Myc (Judson *et al.*, 2009b; Liao *et al.*, 2011). Recent study has shown that the promoter of miR-302 cluster can be bound and that the expression of miR-302 can be induced by vitamin C-dependent Oct4/Jhdm1b cooperation during reprogramming (Wang *et al.*, 2011). The biogenesis of miRNAs has been shown to be critical to efficient reprogramming, because Ago2 downregulation reduces the number of iPS cell colonies (Li *et al.*, 2011). Depletion of the miR-302 family reduces reprogramming efficiency in response to OSK or OSKM (Liao *et al.*, 2011; Wang *et al.*, 2011), suggesting that the miR-302 family plays essential roles in the reprogramming process. Ectopic expression of the miR-290 or miR-302 clusters has been shown to improve OSKM- or OSK-reprogramming (Judson *et al.*, 2009b; Subramanyam *et al.*, 2011) by promoting MET through inhibition of the TGF-β receptor (Li *et al.*, 2011; Liao *et al.*, 2011; Subramanyam *et al.*, 2011). Recent finding (Luningschror *et al.*, 2012) also demonstrated that miR-290 cluster maintain pluripotency by repressing nuclear factor kappa B (NF-kB) signaling pathway, which in turn restricts epithelial to mesenchymal transition in ES cells. Furthermore, the miR-290/302 seed family targets diverse functional groups to positively enhance induced reprogramming, including cell cycle regulation, (Cdkn1a, Rbl2, and Cdc2l6) and epigenetic regulation (Aof1, Aof2, Mecp1-p66, MECP2, Mbd2, and Smarcc2) (Lin *et al.*, 2011; Subramanyam *et al.*, 2011).

Other miRNAs have been identified to enhance reprogramming. For example, miR-17/92, miR-106b/25, and miR-106a/363 clusters boost reprogramming by targeting TGF-βr2 and p21 (Li *et al.*, 2011). Notably, miR-17, miR-93, and miR-106a have also been induced during the MET stage (day 4 post reprogramming) (Chen *et al.*, 2012; Li *et al.*, 2011). Moreover, introduction of miR-106b and miR-93 miRNA mimics can promote MET to boost reprogramming efficiency (Li *et al.*, 2011). The miR-130/301/721 family, identified by miRNA screening, target the homeobox transcription factor Meox2 (also known as Gax) to achieve ~2-fold increase in reprogramming (Pfaff *et al.*, 2011). All those miRNAs (miR-17, 106a, 106b clusters, and miR-130/301/721 family) share a similar seed region with the miR-290/302 family, suggesting that an abundance of miRNAs containing the miR-290/302 seed region play significant roles in various biological functions and intrinsically act as positive regulator to reprogramming.

Reprogramming with miRNAs only

A few reports have shown the great promise of inducing reprogramming with only microRNAs (miRNAs) (Anokye-Danso *et al.*, 2011; Lin *et al.*, 2008; Lin *et al.*, 2011; Miyoshi *et al.*, 2011; Warren *et al.*, 2010). The miR-290/302 seed family plays multiple roles at the ES stage (Marson *et al.*, 2008) and during the reprogramming process, and the miR-290 and miR-302 clusters are the predominant miRNA population expressed in mammalian ES cells. Therefore, the miR-290/302 seed family may have the potential to induce somatic cell reprogramming in the absence of transgenes OSKM. The reprogramming potential of the miR-302 cluster was first tested in human cancer cells, which showed that the signature properties of pluripotent stem cells are acquired in miR-iPS cells (Lin *et al.*, 2008). Following this finding, several reports demonstrated that the miR-302 cluster can reprogram various primary cell types into pluripotent stem cells (Anokye-Danso *et al.*, 2011; Lin *et al.*, 2011; Miyoshi *et al.*, 2011). Among these, Morrisey's group demonstrated that miRNA-induced reprogramming is more efficient than transcription factor-mediated one in both mouse (81.5% versus 17.9%) and human somatic cells (10% versus 0.004%) (Anokye-Danso *et al.*, 2011). But to achieve this striking efficiency, suppression or low level of Hdac2 seems to be required in both mouse and human cells (Anokye-Danso *et al.*, 2011; Miyoshi *et al.*, 2011). Mori's group further demonstrated that clinical-applicable iPS cells can be generated by introducing only a group of mature miRNAs (miR-200c, miR-302 family, and miR-369s), without retro-viral integration in genome (Miyoshi *et al.*, 2011). However, this transfection-base reprogramming can only reach 0.01% reprogramming efficiency in mouse cells, and even lower (0.001%) in human cells (Miyoshi *et al.*, 2011). The methodology of administrating miRNAs may be one of the main reasons to cause the great discrepancy of miR-induced reprogramming efficiency between Morrisey (virus transduction) (Anokye-Danso *et al.*, 2011) and Mori (small RNA transfection) (Miyoshi *et al.*, 2011) groups. They also used distinct combination of miRNAs for reprogramming. miR-302 cluster combined with valproic acid (VPA) treatment were employed in Morrisey's group, while miR-200c, miR-302abcd, and miR-369s were used in Mori's group. Moreover, VPA for Hdac2 suppression and miR-367 are required in Morrisey's study, but both are dispensable in Mori's one. Those inconsistencies may need to be clarified to further improve the efficiency of reprogramming and clinical applicability of iPS cells. Despite the phenomenon of miR-induced somatic reprograming, how microRNAs can perturb somatic molecular networks and then launch pluripotent regulatory networks remains unknown (Anokye-Danso *et al.*, 2011; Miyoshi *et al.*, 2011).

The mechanisms in miRNA-only reprogramming

As described above, numerous miR-290/302 seed family targets have been identified, but these molecular networks have only been shown in the ES cell context or with forced expression of reprogramming factors OSKM. Wu's group provided the molecular evidence of miRNA-only induced reprogramming by demonstrating that the miR-302 cluster reactivates Oct4 and Nanog through releasing epigenetic repression on the promoter regions by targeting lysine-specific histone demethylases 1 and 2 (AOF1/2), which regulate histone lysine 3 methylation level, and also by targeting methyl-CpG binding proteins 1 and 2 (MECP1/2), which coordinate with DNMT1-mediated gene regulations (Lin *et al*., 2011). However, Blelloch's group showed that only TGF-β2r was detectably changed under the same miR-only reprogramming conditions (Subramanyam *et al*., 2011). A change in expression of MECP2 and other known targets of miR-302 could only be detected in the presence of three or four reprogramming factors (Subramanyam *et al*., 2011), suggesting that the reprogramming effect of miR-302 is likely as a cell context-dependent modulator. Therefore, the miR-302 cluster may exert its reprogramming potential through distinct routes from those of Yamanaka's factors, but can induce reprogrammed cells to eventually reach a similar, if not identical, stage of pluripotency.

Small Chemical Molecules Targeting MEF-Enriched Genes Increase Induced Reprogramming

Based on knowledge of the reprogramming steps, we hypothesized that overcoming MEF-specific networks is the first step in the process. We observed that specific siRNA-mediated knockdown of MEF genes encoding catalytic or regulatory proteins, including *Wisp1, Prrx1, Hmga2, Nfix, Prkg2, Cox2, 6720477e09rik,* and *Tgf*-β3, significantly enhanced reprogramming. To accelerate screening of small molecules, we used a computational screening method using the NextBio data-mining framework (Kupershmidt *et al.*, 2010) and identified six molecules, including Nabumetone, OHTM, Corynanthine, Moclobemide, NiSO4, and lectin, which function together to reprogram MEFs without Sox2. One of those factors alone, OHTM, could partially replace the Sox2 transgene during reprogramming by inducing endogenous Sox2 expression. We further showed that Nabumetone enhances reprogramming by inhibiting COX2 activity. Finally, we showed that Nabumetone also promotes reprogramming in the absence of c-Myc or Sox2 function without compromising self-renewal and pluripotency of small molecule-derived iPS cells.

New Life for FDA-approved Drugs in Induced Reprogramming

Nabumetone is a non-steroidal anti-inflammatory drug (NSAID) clinically used primarily to treat pain and inflammation associated with osteoarthritis or rheumatoid arthritis (Hedner *et al.*, 2004; Moore *et al.*, 2009). Nabumetone exerts anti-inflammatory activity by inhibiting COX2 function through its metabolite 6-methoxy-2-naphthylacetic acid. Moreover, it is reported that NSAIDs compromise tumor growth in clinical cases and experimental models of cancer and also that two isoforms cyclooxygenase-1 and -2 function in a variety of pathophysiological processes, such as modulating apoptosis, angiogenesis, invasion, and carcinogenesis (Boonsoda and Wanikiat, 2008; Elrod *et al.*, 2009; Hashitani *et al.*, 2003; Hida *et al.*, 2002; Hida *et al.*, 2000; Meric *et al.*, 2006). Preliminary *in vitro* and *in vivo* studies show that following COX inhibition, signals regulating cell proliferation and apoptosis networks, including EGFR, KRas, PI3K, JAK1, STAT3, c-jun, PCNA, TGF-β3, BAX, TUNEL, Bcl-2, c-jun, p21, p27, p53, and NM23, are widely altered in tumor cells (Axelsson *et al.*, 2010). However, the roles of COX inhibitors in tumorigenesis remain controversial, as COX2 expression differs widely in different types of cancer cells (Meric *et al.*, 2006). In this study, we showed that COX2 is highly expressed in MEFs and serves as a barrier to reprogramming. Therefore, further analysis is required to understand the biological function and molecular regulation of COX2 in both cancer and reprogramming biology.

Tamoxifen is a standard chemotherapy used to treat primary and advanced breast cancer by blocking the estrogen receptor (ER) via its metabolites OHTM and endoxifen. OHTM activity has been addressed primarily through its effect on the ER (Brauch *et al.*, 2009). However, we did not observe detectable levels of ER expression in MEFs (data not shown). OHTM-induced programmed cell death can reportedly be induced through ER-independent pathways in HeLa cells (Obrero *et al.*, 2002), suggesting that other factors respond to OHTM. Moreover, 3,4-dihydroxytamoxifen, a more hydroxylated form of OHTM, can interact with both proteins and DNA (Brauch *et al.*, 2009), suggesting the possibility of numerous targets *in vivo*.

Chemically Induced Reprogramming with Small Molecules

Reprogramming of somatic cells to iPS cells by small molecules could facilitate pharmaceutical and medical applications of pluripotent stem cells (Feng *et al.*, 2009;

Yamanaka, 2009b). A number of studies have identified small molecules that enhance reprogramming by targeting various pathways including TGF-β and GSK3 (Ichida *et al.*, 2009; Li *et al.*, 2009b; Liang *et al.*, 2010; Lyssiotis *et al.*, 2009; Maherali and Hochedlinger, 2009a; Mali *et al.*, 2010; Shi *et al.*, 2008a; Shi *et al.*, 2008b). Although iPS cells can be generated in the absence of Sox2 (Ichida *et al.*, 2009; Maherali and Hochedlinger, 2009a; Shi *et al.*, 2008a), only RepSox has been shown to partially induce Nanog expression in partial iPS cells (Ichida *et al.*, 2009). Here, we are the first to report that Sox2 can be induced by OHTM treatment during reprogramming. Further investigation is required to identify pathways modulated by OHTM in MEFs during reprogramming.

Increasing evidence shows that overcoming the security of somatic cell identity is a critical step initiating the transition from mesenchymal to epithelial status (Li *et al.*, 2010; Loh and Lim, 2010; Samavarchi-Tehrani *et al.*, 2010; Silva *et al.*, 2008b; Silva *et al.*, 2009). This step requires large-scale regulation of opposing genes within only few days during the first 8 days of reprogramming, including *Cdh1, Epcam, Crb3, Ocln, Snail,* *Slug*, *Zeb1*, *Zeb2*, BMP, and TGF-β pathways (Li *et al.*, 2010; Samavarchi-Tehrani *et al.*, 2010). As TGF-β3 is also in our list and TGF-β3 knockdown greatly enhances reprogramming efficiency, these data support our idea that down-regulating MEF regulatory factors is an effective approach to enhance reprogramming. Furthermore, our study confirms that downregulation of MEF genes encoding catalytic factors constitutes some of the earliest steps of reprogramming and that attenuating key somatic genes is critical to enhance reprogramming efficiency. Further study is needed to reveal how the individual network of these MEF-enriched enzymes functions in the process.

Converging regulations of miRNAs and small molecule Nabumetone

OSKM-transformed cells need to overcome thresholds to initiate cell fate transitions (Figure 6.1). MEF-enriched miRNAs and genes function as barriers to induced reprogramming. With inhibitors of miRNAs or chemicals, reprogramming efficiency will be improved with lower threshold (Figure 6.1). MEF-enriched miRNAs, miR-21 and miR-29a, act as indirect positive-regulators of p53 and ERK1/2 pathways (Figure 6.2). miR-21 and miR-29a share downstream targets may provide explanations of that

Figure 6.1

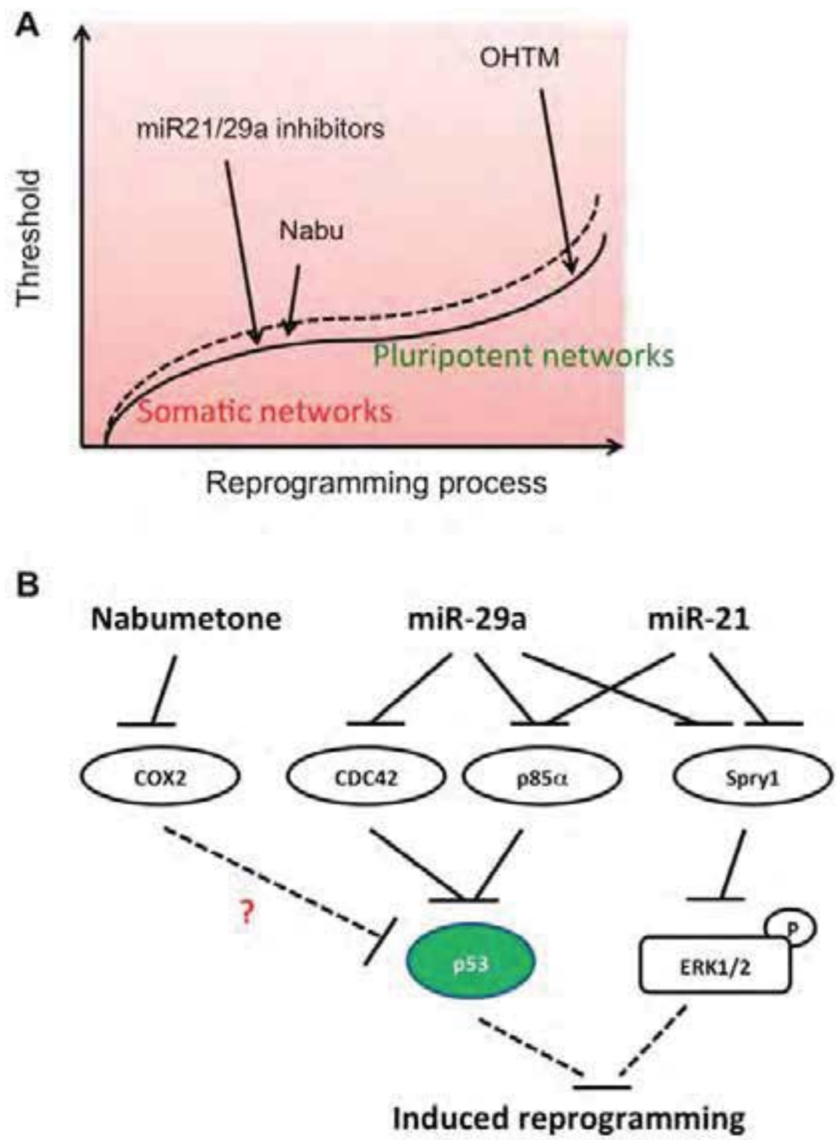

A
OHTM
miR21/29a inhibitors
Nabu
Threshold
Pluripotent networks
Somatic networks
Reprogramming process
B
Nabumetone
miR-29a
miR-21
COX2
CDC42
p85α
Spry1
?
p53
P
ERK1/2
Induced reprogramming

Figure 6.1

Correlation of miRNA inhibitor and small molecule effects in enhancing induced reprogramming

(A) Scheme showing reprogramming potential with various treatments.

Threshold of reprogramming potential is represented as dotted curve line (without treatment), or solid curve line (with treatments). The major effective stages of each treatment are indicated with arrows. Reprogramming process is shown from "somatic networks" to "pluripotent networks". Nabu abbreviates Nabumetone. OHTM denotes 4-hydroxytamoxifen.

(B) Converging target of miRNA inhibitors and Nabumetone.

The direct inhibitory regulations are shown in solid lines and indirect regulations are shown in dotted lines. The converging target p53 is highlighted in green.

co-inhibiting miR-21 and miR-29a show little additive effect in enhancing reprogramming efficiency (data not shown). Interestingly, specific target of Nabumetone, COX2, has been shown regulating p53 expression in cancer cells and depletion of COX2 shows increased iPS cell generation. Although COX2's regulatory mechanisms of p53 are unclear, p53 might be the converging target for both miRNAs and Nabumetone during reprogramming.

Probing the Molecular Mechanism of Induced Reprogramming with Integrative Genome-Wide Studies

We examined the molecular mechanism in a step-wise manner by applying FACS to a group of distinct cell populations, representing four critical steps from initiation to maturation of induced reprogramming. We first clustered genes into five categories (I–V) based on their expression patterns along the pathway to induced reprogramming. Numerous genes were shown to be key players at each transition stage from mouse embryonic fibroblast to induced pluripotent stem cells. We employed genome-wide RNAi screen to independently identify critical functionalities of molecules/pathways, which modulate the progress of induced reprogramming. Select genes were tested individually to further confirm their roles during reprogramming.

The high validation rate of this two-pronged study suggests that our new strategy is highly valuable to discovering key regulatory molecules/networks in the reprogramming process. By successfully combining whole-genome shRNA library screening with FACS analysis, we were able to shed light on the molecular basis contributing to modulating induced reprogramming.

Deeper Insight of Regulatory Networks in Reprogramming

Several transition events may prove decisive step for cells as they proceed to the next phase of induced reprogramming. For example, we showed that most key players involved in DNA damage/cell cycle regulation are activated upon induced reprogramming, consistent with previous reports (Banito *et al.*, 2009a; Hong *et al.*, 2009; Kawamura *et al.*, 2009b; Li *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009). Furthermore, cells escaping from this surveillance system showed a positive influence on reprogramming progress (Banito *et al.*, 2009a; Hong *et al.*, 2009; Kawamura *et al.*, 2009b; Li *et al.*, 2009a; Marion *et al.*, 2009; Utikal *et al.*, 2009).

However, it is critical to resume the cell cycle by overcoming senescence for cells to leave the somatic status, which is supported by our findings that Ink4/Arf is only enriched in the initial cell population, as well as by previous findings (Banito *et al.*, 2009a; Li *et al.*, 2009a). The new identified gene Cdk14 may modulate the reprogramming progress by regulating cell cycle progression and cell proliferation (Shu *et al.*, 2007). Re-entry into the cell cycle might generally boost the cell transformation and transition away from fibrotic/somatic status, but may not necessarily push cells specifically toward pluripotent status. The majority of transformed cells are “trapped” in the transition stage ($Thy1^-$/$SSEA1^-$), with divergent transcriptome showing correlations to various tissue types; this implies that cells are reset at this re-constructing phase where cells might have the potential to adopt distinct cell fates until the “right” molecular networks are further re-built. This notion is supported by recent studies (Polo *et al.*, 2012; Shu *et al.*, 2013) showing that re-administration of OSKM or lineage specifiers into those transitioning cells drove more cells into pluripotent or other desired states. The potential diversity of cell fates at the Thy1$^-$/SSEA1$^-$ stage is usually ignored, probably because the only desired cell type here is the pluripotent stem cells. But, these "transitioning" cells with high plasticity may provide a good starting point for various cell-fate inter-conversions.

To reach the specific path toward pluripotency (the pre-determined stage), transitioning cells (Thy1$^-$/SSEA1$^-$) need to activate several preliminary factors, such as *Nanog, Sall4, Esrrb, Dppa4, Dppa5a, Dnmt3b and Dnmt3l.* These "pre-determined" SSEA1$^+$/DsRed$^+$ cells show a strong resemblance to ES cells in the transcriptome profile but with lower expression level and incomplete induction of the majority of the key regulators in ES cells. Despite this discrepancy, this observation raises the possibility of deriving certain progenitors/adult stem cells from the SSEA1$^+$/DsRed$^+$ population, although vigorous tests are required to obtain practical evidence.

To fully acquire pluripotency, cells will need stronger induction of the preliminary factors and will also need to further re-establish the ES core circuitry with additional activation of numerous factors, including *Utf1, Nr6a1, Tdgf1, Gsc, Fgf10, T, Chrd, Dppa3, Fgf17, Eomes, Foxa2*, and others. Upon induced reprogramming, the deconstruction of molecular networks in Thy1^{+} cells takes place in order for cells to de-differentiate to Thy1^{-} status. However, our data point to the possibility that Thy1^{+}/SSEA1^{-} cells represent the cells that either developed into other cell types or failed to progress properly. Cells in this prior-determined stage might be directed further to attain the desired cell type if specific barriers are overcome.

Novel Key Regulators in Maintaining ESC Identity

Srsf2, Hcfc1, and Ruvbl2 play important roles in various cell types (Dejosez *et al.*, 2010; Ding *et al.*, 2009; Xiao *et al.*, 2007). Furthermore, Pcgf6, Hcfc1, and Ruvbl2 have been shown to associate with epigenetic-modifying complexes (Akasaka *et al.*, 2002; Jha *et al.*, 2013; Tyagi *et al.*, 2007; Tyagi and Herr, 2009). We found that Pcgf6, Srsf2, Hcfc1, and Ruvbl2 all play important roles in both ES cell maintenance and induced reprogramming progress. Interestingly, depletion of Pcgf6 greatly compromised self-renewal, but not cell growth, in ES cells, while Srsf2, Hcfc1, and Ruvbl2 have reciprocal effects. This finding demonstrates that those four genes may enhance reprogramming efficiency through different pathways.

Determinative Factors in reprogramming Identified in Our Functional Genomics Study

Somatic reprogramming with OSKM leads to great dynamic changes of transcriptome (Buganim *et al.*, 2012; Hanna *et al.*, 2009; MacArthur *et al.*, 2008; Yamanaka, 2009a), while cell fate is gradually determined along the reprogramming process (Brambrink *et al.*, 2008; Stadtfeld *et al.*, 2008a). Distinct from previous strategies, we focused on the end stage of induced reprogramming, where molecular contents are defined/fixed in those trapped cells. From this new point of view, we are able to identify several novel modulators that influence the cell-fate decision, which might be missed by collecting transient cell types during reprogramming. Furthermore, previous studies all focused on the genes enriched/activated in iPS/ES cells by mRNA analysis; solely analyzing transcriptome changes in this fashion may miss several important modulators at the transition steps during reprogramming, as the posttranscriptional/translational regulations also play significant roles even with little change in mRNA level. Indeed, whole-genome shRNA library screening in this study provides an unbiased method to identify those "hidden" factors in the reprogramming process, regardless of the mRNA expression change.

Two important findings with similar cell sorting approaches were published by Jaenisch's lab and Hochedlinger's lab (Buganim *et al.*, 2012; Polo *et al.*, 2012). Jaenisch's group suggested two sequential phases (probabilistic and hierarchical phases) of induced reprogramming, which highly resembles our findings of a de-constructing/re-constructing phase and a pre-determined phase. Both studies showed that Esrrb, Nanog, and Sall4 are more reliable indicators for successful reprogramming, which is consistent with our results. More importantly, our work further advanced the field by identifying numerous novel key modulations, by combining genome-wide shRNA library screening with transcriptome analysis. In addition, our shRNA screening revealed a large number of genes that functionally contribute to induced reprogramming, such as numerous identified barrier or essential factors, regardless of the complex nature of mixed transcriptome. We thus believe that this pioneering study, which applies shRNA library screening to elucidate the reprogramming mechanism, will serve as a strong foundation for various applications in this field, such as small molecule targeting, cell-fate manipulation, and progenitor derivation. Most importantly, it will help researchers better understand the molecular basis of induced reprogramming.

New Approaches Shed Lights on the Mechanisms of Different Reprogramming Processes

Destabilization of somatic networks is the first cellular event in reprogramming before re-construction of the ES-specific networks. In contrast to most studies that investigate the ES cell-specific genes in reprogramming, our work first focused on the function of MEF-enriched miRNAs and genes in early reprogramming process. Furthermore, to minimize the cost and effort by shotgun screening approaches, we combine genomics and computational drug screening to identify new drugs for reprogramming potentially. Focusing on the catalytic proteins enriched in MEF, we only tested limited number of small molecules to identify active chemicals in reprogramming process. Therefore, we believe that this new aspect of screening approach will inspire future studies to select potential targets predicted by bioinformatics analysis for further investigation, as opposed to large scale screening.

High degree of cell complexity is the major obstacle to understand step-wise regulatory networks in reprogramming process. Therefore, we established a new system to distinguish different cell populations by using cell-fate specific markers. This system allows us to isolate the cells in transition stages, which provide more information about the cellular events step-wisely in reprogramming. We further utilized genome-wide RNAi screen to perform loss-of-function analysis. By combining cell sorting, we were able to identify gene required for each cell-fate transition. The information of temporal regulations and requirements of stage-specific genes will provide solid foundation to advance the understanding of cell-fate transitions. Furthermore, we found that cell plasticity is altered along the reprogramming process, suggesting trans-differentiation might be possible along the induced reprogramming. And epithelial cells derived from visual system show highly correlated transcriptome profiles with ES/iPS cells, providing another cell resource for efficient induced reprogramming.

Transcriptome analysis is the most common way to understand the expression changes and to predict the key regulatory molecules or networks in various biological processes, including induced reprogramming. But differentially expressed genes may only serve as markers, because of insufficient functional validation. Therefore, our integrative approach creates a unique opportunity to analyze genome-wide data by RNAi screen and combining transcriptome analysis. We identified differentially expressed genes in each transition step, providing cell-fate markers from the initial to mature-reprogrammed status. In addition, the functional requirements during the cell-fate transition are also identified by RNAi screen. Surprisingly, our integrative analysis reveals that a group of genes, with little expression changes, play critical roles in each reprogramming stage. This finding raises the notion that “non-induced or changed” genes may play important roles in various physiological conditions, even though these genes are likely to be neglected in transcriptome analysis.

Prospective Development in Induced Reprogramming

Transcriptome changes and functional impacts of stage-specific genes are revealed in our study, but the mediators of four reprogramming factors are still unclear. This missing link between OSKM and downstream effectors is the key to understand the direct regulatory networks and pathways of reprogramming factors. To investigate that, tetracycline inducible system can be used to temporarily express each reprogramming factor and differentially expressed genes can be examined to elucidate potential mediators. Analyze the genomic binding sites of each reprogramming factor will also provide insights into the mediators during reprogramming process. To the end, we might be able to construct hierarchical regulatory pathways of each reprogramming factor and understand how this stochastic process of iPS cell generation can be directed.

Generation of iPS cells with a safe and efficient way is required to expedite the clinical applications in regenerative medicine. Among various methods to create iPS cells, small molecule treatment provides a safe way with no genomic modifications. Since our genome-wide study provides wealthy information of signature markers or determinant molecules during reprogramming process, we should utilize small molecules specifically targeting identified proteins to direct the cell fate changes in higher efficiency.

APPENDICES

I. Table 3.1

II. Appendix 1. Proportion of sorted cells

III. Appendix 2. Whole genome transcriptome analysis

IV. Appendix 3. Top Biological Functions of mRNA group I to V

V. Appendix 4. Transcriptome changes in each transition step during reprogramming.

VI. Appendix 5. Common and unique gene lists for last two transition steps.

VII. Appendix 6. Genome-wide RNAi screen and analysis.

VIII. Appendix 7. Gene number and ratio in each shRNA-enriched group

IX. Appendix 8. Summary of shRNA-identified genes

Table 3.1. Function Summary of Select MEF-enriched genes

Common Name	Reference Sequence
WISP1	NM_018865
Function Summary*: This gene encodes a member of the WNT1 inducible signaling pathway (WISP) protein subfamily, which belongs to the connective tissue growth factor (CTGF) family. WNT1 is a member of a family of cysteine-rich, glycosylated signaling proteins that mediate diverse developmental processes. The CTGF family members are characterized by four conserved cysteine-rich domains: insulin-like growth factor-binding domain, von Willebrand factor type C module, thrombospondin domain and C-terminal cystine knot-like domain. This gene may be downstream in the WNT1 signaling pathway that is relevant to malignant transformation. It is expressed at a high level in fibroblast cells, and overexpressed in colon tumors. The encoded protein binds to decorin and biglycan, two members of a family of small leucine-rich proteoglycans present in the extracellular matrix of connective tissue, and possibly prevents the inhibitory activity of decorin and biglycan in tumor cell proliferation. It also attenuates p53-mediated apoptosis in response to DNA damage through activation of the Akt kinase. It is 83% identical to the mouse protein at the amino acid level. Alternative splicing of this gene generates 2 transcript variants.	

Common Name	Reference Sequence
PRRX1	NM_011127

Function Summary*:

The DNA-associated protein encoded by this gene is a member of the paired family of homeobox proteins localized to the nucleus. The protein functions as a transcription co-activator, enhancing the DNA-binding activity of serum response factor, a protein required for the induction of genes by growth and differentiation factors. The protein regulates muscle creatine kinase, indicating a role in the establishment of diverse mesodermal muscle types. Alternative splicing yields two isoforms that differ in abundance and expression patterns.

Common Name	Reference Sequence
HMGA2	NM_010441

Function Summary*:

This gene encodes a protein that belongs to the non-histone chromosomal high mobility group (HMG) protein family. HMG proteins function as architectural factors and are essential components of the enhancesome. This protein contains structural DNA-binding domains and may act as a transcriptional regulating factor. Identification of the deletion, amplification, and rearrangement of this gene that are associated with myxoid liposarcoma suggests a role in adipogenesis and mesenchymal differentiation. A gene knock out study of the mouse counterpart demonstrated that this gene is involved in diet-induced obesity. Alternate transcriptional splice variants, encoding different isoforms, have been characterized.

Common Name	Reference Sequence
NFIX	NM_001081982
Function Summary[¶]: Recognizes and binds the palindromic sequence 5'-TTGGCNNNNNGCCAA-3' present in viral and cellular promoters and in the origin of replication of adenovirus type 2. These proteins are individually capable of activating transcription and replication.	

Common Name	Reference Sequence
PRKG2	NM_008926
Function Summary[§]: AMP-activated protein kinase (AMPK) is a heterodimeric protein serine/threonine kinase that is composed of alpha- (catalytic) and beta/gamma- (regulatory) subunits. AMPK acts as a sensor of the energy status of cells and ensures survival at times of metabolic stress. AMPK phosphorylates many metabolic enzymes to stimulate catabolic pathways, such as ketogenesis, and inhibit anabolic pathways, such as protein synthesis. The long-term activation of AMPK increases the capacity of cells to produce ATP. AMPK is regulated by phosphorylation at the Thr-172 residue of the alpha-subunit by AMPKK and by phosphorylation by calmodulin-dependent protein kinase kinase-beta (CamKKbeta). In addition, the ratio of AMP:ATP mediates allosteric activation of the enzyme. AMPK is found throughout the body with high concentrations in metabolically active tissues such as the skeletal muscles and liver.	

Common Name	Reference Sequence
COX2 (PTGS2)	NM_011198

Function Summary*:

Prostaglandin-endoperoxide synthase (PTGS), also known as cyclooxygenase, is the key enzyme in prostaglandin biosynthesis, and acts both as a dioxygenase and as a peroxidase. There are two isozymes of PTGS: a constitutive PTGS1 and an inducible PTGS2, which differ in their regulation of expression and tissue distribution. This gene encodes the inducible isozyme. It is regulated by specific stimulatory events, suggesting that it is responsible for the prostanoid biosynthesis involved in inflammation and mitogenesis.

Common Name	Reference Sequence
TGF-β3	NM_009368

Function Summary*:

This gene encodes a member of the TGF-β family of proteins. The encoded protein is secreted and is involved in embryogenesis and cell differentiation. Defects in this gene are a cause of familial arrhythmogenic right ventricular dysplasia 1.

Common Name	Reference Sequence
LZYS	NM_017372

Function Summary*:

C-type lysozyme (1, 4-beta-N-acetylmuramidase, LYZ) and alpha-lactalbumin (lactose synthase B protein, LA). They have a close evolutionary relationship and similar tertiary structure, however, functionally they are quite different. Lysozymes have primarily bacteriolytic function; hydrolysis of peptidoglycan of prokaryotic cell walls and transglycosylation. LA is a calcium-binding metalloprotein that is expressed exclusively in the mammary gland during lactation. LA is the regulatory subunit of the enzyme lactose synthase. The association of LA with the catalytic component of lactose synthase, galactosyltransferase, alters the acceptor substrate specificity of this glycosyltransferase, facilitating biosynthesis of lactose.

Common Name	Reference Sequence
6720477E09RIK	NM_001172121
Function Summary*: This gene encodes an RNA-binding protein that belongs to the c-myc gene single-strand binding protein family. These proteins are characterized by the presence of two sets of ribonucleoprotein consensus sequence (RNP-CS) that contain conserved motifs, RNP1 and RNP2, originally described in RNA binding proteins, and required for DNA binding. These proteins have been implicated in such diverse functions as DNA replication, gene transcription, cell cycle progression and apoptosis. The encoded protein was isolated by virtue of its binding to an upstream element of the alpha2(I) collagen promoter. The observation that this protein localizes mostly in the cytoplasm suggests that it may be involved in a cytoplasmic function such as controlling RNA metabolism, rather than transcription. Multiple alternatively spliced transcript variants encoding different isoforms have been found for this gene.	

* Information is collected through NCBI RefSeq, unless otherwise stated.

¶ Information is collected from Protein Knowledgebase in UniProt.

§ Information is collected from TOCRIS bioscience (http://www.tocris.com).

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Appendix 1. Proportion of sorted cells

%	Thy1+	Thy1-SSEA1-	EA1+DsRed+	EA1+DsRed-	Total %*
Experiment #1	6.733	80.665	2.138	0.427	89.96257155
Experiment #2	9.738	80.640	0.870	0.222	91.47
Experiment #3	6.560	83.682	0.942	0.216	91.4

* Cells were gated with stringent parameter to make sure high purity of each population was acquired (please see Supplemental Figure 1). Therefore, ~9 to 10% of cells were ommitted by gating.

Appendix 2. Whole genome transcriptome analysis

Group #	Subgroup #	Gene	MEF	Thy1+SSEA1- #1	Thy1+SSEA1- #2	Thy1-SSEA1- #1	Thy1-SSEA1- #2	SSEA1+DsRed+ #1	SSEA1+DsRed+ #2	SSEA1+DsRed- #1	SSEA1+DsRed- #2	ESC
1	1	1110012J17Rik		[illegible]	0.6191	0.5112	0.4276	1.2524	0.9441	2.1685	1.7195	1.3951
1	1	1700019D03Rik		-1.3495	-0.6718	1.5939	0.8652	1.3221	0.7789	0.7102	0.9176	0.8481
1	1	1700029P11Rik		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.777	[illegible]	3.7904
1	1	Fuom		-1.1738	-0.9884	0.4884	[illegible]	0.8835	0.7673	2.0272	1.5122	1.9566
1	1	1810064F22Rik		0.2895	0.6891	0.7498	1.1216	1.0876	1.0728	1.4127	1.1494	0.9245
1	1	2010001M09Rik		-0.128	[illegible]	1.1444	0.8493	2.5187	2.2562	1.833	1.6215	[illegible]
1	1	2410137M14Rik		[illegible]	[illegible]	1.6142	1.9432	2.206	2.7203	1.8933	2.5973	1.6216
1	1	2610019F03Rik		-0.3125	-0.5937	1.3719	1.5283	2.0237	1.9213	1.4007	1.7347	1.3698
1	1	2700097O09Rik		-0.7503	-0.156	0.5856	0.9799	1.0813	1.0389	1.1791	1.0809	1.4288
1	1	2810417H13Rik		-0.4344	0.599	1.1729	1.2294	1.856	1.4317	2.1286	1.8502	[illegible]
1	1	3200002M19Rik		[illegible]	[illegible]	0.5826	0.865	0.9106	1.2371	1.1659	0.8677	1.7587
1	1	8430410A17Rik		-0.6759	-0.5045	0.7848	0.7754	1.1835	1.0749	1.0345	0.9734	1.0096
1	1	Abcf2		[illegible]	0.7153	0.674	0.9887	0.8654	1.1315	1.0034	0.7717	1.8168
1	1	Acp6		-0.999	-0.6133	1.3424	1.0396	1.8558	1.6445	1.6606	1.637	0.9535
1	1	Acsbg1		-0.357	0.5452	2.8886	2.6894	2.325	1.8804	1.0605	1.2663	[illegible]
1	1	Acsl3		[illegible]	[illegible]	[illegible]	[illegible]	0.8679	[illegible]	1.5007	1.2665	1.3458
1	1	Actb		1.9501	1.2432	1.0659	1.3872	0.8226	1.9286	1.9294	2.2891	1.4093
1	1	Actl6a		[illegible]	-0.158	0.6039	0.5312	0.9448	0.9387	1.7388	1.1809	1.7035
1	1	Acvr2b		-1.3741	-0.692	[illegible]	0.4728	0.8472	0.9346	2.1507	1.3167	2.6494
1	1	Adat1		-0.0499	0.4267	0.2444	0.6166	0.7744	0.9655	1.3898	1.1857	1.0788
1	1	Akap12		0.555	-0.1602	0.1297	0.1458	0.7843	0.9934	1.1386	1.4276	1.5535
1	1	Alpl		-0.5442	-0.0628	1.7344	1.7446	1.8358	1.66	1.5192	1.7094	1.754
1	1	Alyref		-0.5217	0.1398	0.6326	0.8527	0.9878	1.2583	1.1251	1.1341	0.973
1	1	Anln		-0.9005	0.2603	0.9271	0.8563	1.1831	1.0981	[illegible]	0.935	1.2039
1	1	Ap1m2		-0.2438	-0.3669	0.099	0.2764	0.9579	1.0329	1.244	1.3225	1.1659
1	1	Arhgap8		0.214	0.2351	0.2893	0.4829	1.3362	1.4901	1.6428	2.0549	1.9294
1	1	Arid3b		-0.3965	-0.2378	0.3215	0.3071	0.6864	[illegible]	2.1062	1.263	2.0629
1	1	Armcx1		1.4573	1.8564	2.3787	2.1971	1.3	0.6704	1.5901	1.12	1.5276
1	1	As3mt		0.0601	0.0846	0.6179	0.7505	0.9739	0.8946	1.016	0.805	1.7761
1	1	Ash2l		0.1649	0.6492	0.5281	0.8386	0.7607	1.0448	1.2324	0.8709	1.9472
1	1	Asna1		0.8917	0.3393	1.1346	1.0324	1.2311	1.3658	1.8891	1.3636	2.1537
1	1	Aspm		-0.2742	0.1701	0.4902	0.8348	1.3236	1.136	1.256	1.2672	1.3073
1	1	Atad5		-0.5417	-0.0896	0.3867	0.5957	1.0231	0.5901	1.4082	1.4576	1.4143
1	1	Atic		0.2695	0.9301	0.9706	1.3206	1.0693	1.6279	1.477	1.187	1.0095
1	1	Atp12a		-0.3013	-0.125	2.7814	2.5445	2.8441	2.2917	1.8537	2.5132	[illegible]
1	1	Atp1b1		1.5995	1.445	0.1185	[illegible]	0.7015	0.5896	1.7034	0.8752	2.898
1	1	AU018091		-0.3539	-0.2953	0.3481	0.3632	0.912	1.1214	1.3886	1.5057	1.823
1	1	Aurka		-0.8506	0.2383	0.7287	1.0583	1.2914	1.4599	1.5792	1.8429	1.8795
1	1	B3gnt7		[illegible]	0.0958	0.4084	0.2285	1.0771	1.0598	1.8031	1.3896	1.316
1	1	BC052040		-0.0894	-0.2174	0.4468	0.2578	0.8306	0.8804	1.0654	0.9318	1.94
1	1	BC085271		-0.9574	-0.194	0.471	0.7283	0.9076	0.9867	1.2362	0.737	1.9474
1	1	Bcat1		-0.6725	0.5755	-0.2741	0.1001	[illegible]	0.8169	1.1071	1.4198	1.9095
1	1	Bcat2		0.2675	0.3318	1.1474	1.036	1.5681	1.598	1.9687	2.0343	1.5734
1	1	Bend3		0.2865	0.1377	0.501	0.676	0.9682	0.9514	1.6716	1.211	1.1271
1	1	Bex2		-0.9755	-0.8424	-0.2614	0.1156	0.6657	0.916	2.4789	1.4842	2.7752
1	1	Bex4		-1.1069	-1.202	0.2551	0.4276	0.9364	1.2556	2.7708	2.2925	4.4697
1	1	Birc5		-0.8969	0.327	0.4144	0.8225	1.3357	1.4203	1.6948	1.3738	1.4163
1	1	Blm		-1.0163	-0.0806	0.4212	0.7908	1.1842	1.401	2.1207	1.5738	3.2545
1	1	Bub1b		-0.8453	[illegible]	0.3202	0.4028	0.7437	0.7716	1.0398	0.8086	2.0045
1	1	C80913		0.6083	0.6965	0.5979	0.7573	0.9354	1.0563	1.336	1.2391	1.9016
1	1	Capsl		-0.3109	-0.1918	0.4896	0.3278	1.242	1.1836	1.383	1.6927	1.5492
1	1	Car14		0.585	0.5895	0.5206	0.4285	[illegible]	[illegible]	2.2084	1.3165	1.1258
1	1	Car2		-0.343	-0.2171	0.3667	0.1836	0.7558	0.7196	1.6842	1.5	1.1696
1	1	Car4		-0.0297	0.1535	0.5269	0.616	1.5279	0.4557	5.0636	3.7629	1.5289
1	1	Cbx5		0.1335	0.5106	0.6333	1.0949	0.963	1.3307	1.3265	1.2319	1.9062
1	1	Cbx7		-0.4559	-0.6267	0.4625	0.2728	0.7754	0.5109	1.4392	0.8292	2.9466
1	1	Ccdc114		-0.0812	0.2057	0.3345	0.3092	0.8649	0.8892	1.5258	1.305	1.6392
1	1	Ccdc99		-0.558	0.3002	0.2069	0.8446	0.6501	0.9549	1.0235	1.038	1.7816
1	1	Ccnb1		-1.0942	[illegible]	1.0545	1.0027	1.7368	1.5998	2.1934	1.7778	1.3949
1	1	Cd59b		-0.1518	-0.6165	1.0644	1.047	1.4656	1.4855	1.9239	1.8268	[illegible]
1	1	Cdc20		-0.4309	0.3761	0.2392	0.6328	0.7191	1.1934	1.1362	0.9741	1.7328
1	1	Cdc34		0.3554	0.4533	1.0585	1.2428	1.4156	1.4996	1.9895	1.6387	1.5806
1	1	Cdc45		-0.6876	0.0831	0.4382	0.9367	0.9326	1.0185	1.2757	1.2062	1.8249
1	1	Cdc5l		-0.2348	-0.2059	0.5485	0.1961	0.8465	0.7564	1.1308	0.7535	1.6001
1	1	Cdc6		-0.5874	0.0533	0.6685	0.977	1.2194	1.1986	1.7733	1.4559	2.1269
1	1	Cdc7		-0.7885	0.1409	-0.0612	0.7902	0.6772	0.9162	1.2743	1.0444	2.068
1	1	Cdca2		-1.2162	-0.088	0.4834	0.8376	1.0703	1.4045	1.1856	1.2077	1.9847
1	1	Cdca5		-0.1413	0.2187	0.6919	0.807	1.2967	1.0199	1.6853	1.1639	1.3532
1	1	Cdca7		-2.2481	[illegible]	-0.0788	0.7584	0.8059	1.0527	1.6919	1.4602	1.9583
1	1	Cdca8		-0.966	-0.0752	0.1794	0.4865	0.952	1.0768	1.3711	0.5622	2.0464
1	1	Cdh1		-1.3404	-1.4337	0.569	-0.0371	1.45	0.9846	1.8721	1.6777	1.9529
1	1	Cdk2		-0.5866	[illegible]	0.3178	0.452	0.7655	0.8697	1.185	1.1537	1.1754
1	1	Cdt1		-0.3555	-0.1942	0.7012	0.9958	1.23	1.2773	1.7802	1.5559	2.941
1	1	Cenph		-0.3019	[illegible]	0.2625	0.4346	0.9044	0.5962	1.219	1.0397	1.5654
1	1	Cenpi		-0.1068	0.6655	0.6116	0.7806	0.9169	0.9017	1.0552	0.9712	1.4113
1	1	Cenpm		-0.1099	0.5954	0.3553	0.7873	0.7884	1.0707	1.0874	1.274	1.3275
1	1	Cenpn		-0.137	0.4266	0.5639	0.7261	1.036	0.965	1.4026	1.3319	1.9381
1	1	Cenpp		-0.2533	0.0604	0.2142	0.5304	0.7527	0.4904	1.0284	1.0638	1.8561
1	1	Cenpt		0.3261	0.8366	0.5905	0.6304	1.0409	1.0748	0.909	1.4095	1.579
1	1	Chaf1a		-0.4975	0.2638	0.5103	1.0243	1.0073	1.2005	1.0209	1.3481	1.4309
1	1	Chaf1b		-0.8286	-0.1277	0.2324	0.3805	0.6605	0.5266	1.2467	1.2011	2.2774
1	1	Chchd10		-1.6034	-0.8673	0.3478	0.1262	1.1462	0.6228	2.2651	1.6031	4.0279
1	1	Chtf18		-0.3118	0.1795	0.6706	0.8655	1.3001	1.4227	1.6667	1.4906	1.9376
1	1	Ckap5		0.3507	0.3722	0.946	0.6642	1.1647	1.1591	1.5031	1.4284	0.8796
1	1	Cldn4		-2.6348	-3.0339	1.4473	-0.7365	2.2291	1.0544	1.4022	1.6557	0.6776
1	1	Cldn6		[illegible]	-0.1069	0.6541	0.6036	1.5922	1.6067	3.966	3.1479	3.3959
1	1	Clspn		-0.4147	0.0637	0.2587	0.6695	0.8563	1.2257	1.2414	1.2625	1.3392
1	1	Cox4nb		-0.0533	0.173	0.2884	0.2446	0.7746	0.8519	1.0088	0.9301	1.7291
1	1	Cpsf4l		-0.5975	-0.6112	0.9691	0.4263	1.6542	1.2045	1.9052	1.701	3.4187
1	1	Csda		-0.5003	0.1675	0.5271	0.9236	0.741	1.0484	0.91	1.0109	1.097
1	1	Csrp2		0.4091	0.7666	-0.2445	[illegible]	0.4664	1.1415	1.2052	1.2968	2.1807
1	1	Cth		-1.4117	-0.456	1.5641	1.4576	1.5538	1.5075	0.9971	1.1594	0.5348
1	1	Cul4b		0.1288	0.2524	0.4067	0.3184	0.9721	0.363	1.1715	0.9841	1.5301
1	1	D2Ertd750e		-0.2362	0.3129	0.6443	0.7331	1.2046	0.9581	1.3406	1.076	0.805
1	1	Dact2		-0.2493	-0.1976	0.6286	0.8414	1.1462	1.42	0.8373	1.0626	0.8707
1	1	Dbf4		0.1107	0.3339	1.3303	1.0988	1.6475	1.4267	2.245	1.5102	2.0982
1	1	Dcbld1		0.0845	0.5292	0.7642	0.7292	0.6827	0.5176	0.8923	0.6224	1.9511
1	1	Ddc		0.3006	0.9345	2.1699	2.2593	2.6507	3.0392	2.1779	2.6436	2.8101
1	1	Ddx18		-0.4949	0.1207	0.2511	0.9185	0.761	1.003	1.2645	1.0967	1.2419
1	1	Ddx21		-0.1088	0.3442	0.8298	0.7105	0.9062	0.8701	1.3354	1.0388	1.3549
1	1	Ddx25		-0.3649	-0.4822	[illegible]	0.2255	0.4408	1.0306	1.6937	1.34	2.1268
1	1	Ddx27		-0.6317	0.0698	0.4619	0.8235	0.5818	0.8803	0.9721	1.0699	1.234
1	1	Ddx39b		0.4126	1.2892	1.4254	1.3224	1.7428	1.5636	1.7471	1.6012	0.5762
1	1	Depdc1b		-0.7387	-0.047	0.2053	0.8698	1.0913	1.1038	1.3822	1.2964	1.4059
1	1	Dmrtc2		-0.3391	0.0867	2.9658	3.0299	3.095	2.7778	1.956	2.6749	1.0743
1	1	Dnajc2		-0.0287	0.2492	0.5058	0.7243	0.7399	0.8029	1.2719	0.9101	1.3379
1	1	Dnmt1		-0.6742	0.2524	0.5076	0.8744	1.1507	1.0998	1.0691	1.1622	0.9309
1	1	Dnmt3b		-0.9365	-0.629	0.6095	0.3878	2.7488	1.8878	5.0718	4.3591	3.4893
1	1	Dnmt3l		0.1885	0.5949	0.225	-0.1288	1.5949	[illegible]	4.3595	2.6381	5.8
1	1	Dpp4		0.5944	0.9384	2.8878	1.5683	1.9531	0.7374	1.5089	0.8308	1.321
1	1	Dppa3		0.0798	0.0241	0.0603	-0.0241	[illegible]	[illegible]	1.6098	0.9828	2.854
1	1	Dppa4		0.0318	[illegible]	0.1957	-0.0679	1.4824	[illegible]	4.1133	2.7029	6.5911
1	1	Dppa5a		-0.1123	0.074	2.4103	1.4821	4.4694	3.275	6.5816	5.4637	8.4132
1	1	Dusp4		-0.0747	-0.106	1.3463	0.6359	[illegible]	0.8627	1.1422	0.7573	1.2834
1	1	Dut		0.0911	0.3782	1.7519	1.5569	1.8106	1.3463	1.9612	1.4872	0.5849
1	1	Dyrk3		-0.592	-0.7244	0.5519	1.1719	1.1915	1.1746	1.2332	1.2155	1.2137
1	1	E130012A19Rik		-1.7507	-0.8555	0.9247	1.3273	1.3858	1.8476	1.8252	1.8409	2.4809
1	1	E130306D19Rik		-0.5378	-0.0392	-0.0848	0.336	0.9285	1.1007	1.3558	1.3979	1.3767
1	1	E2f5		0.4763	0.0983	0.2359	0.3645	0.564	0.4465	1.5542	1.0119	1.4432
1	1	Lefty1		0.125	-0.0979	[illegible]	-0.0979	0.8828	0.9383	2.6853	1.7839	4.6406
1	1	Eif2s3y		1.1123	0.6107	1.0214	0.5691	0.8933	0.6696	1.2164	0.9037	2.53
1	1	Eif4ebp2		0.421	0.8359	0.8839	1.0994	1.2109	1.389	1.6923	1.4442	0.8659
1	1	Eif4enif1		0.5488	0.5414	0.8476	0.6427	1.1559	0.9216	1.2227	1.2151	1.1587
1	1	Eif5		1.1399	1.0775	1.4676	1.4911	1.258	1.3186	1.7405	0.9705	1.8168
1	1	Eif5a		0.2378	0.9179	1.0036	1.4431	1.249	1.6484	1.6482	1.2601	1.8614
1	1	Ell3		0.2169	0.245	0.5154	0.4157	0.6408	0.7691	1.0327	0.941	2.6688
1	1	Elovl6		-0.1846	0.4363	0.463	1.0298	0.9514	1.0572	1.3488	0.6129	1.1153
1	1	Enoph1		[illegible]	0.3394	0.3533	0.454	0.6941	0.5266	1.1921	1.091	1.7972
1	1	Epb4.9		0.2112	0.1676	0.0929	[illegible]	[illegible]	[illegible]	1.2816	1.0282	4.0231
1	1	Epha2		[illegible]	0.3028	0.8266	0.9657	1.21	1.5466	1.6968	1.7844	1.3233
1	1	Eras		[illegible]	-0.1729	1.0862	0.4276	1.8916	1.3355	2.8263	1.9263	2.8984
1	1	Erh		-0.2957	0.7955	0.7194	1.2192	0.6954	1.3191	1.1121	0.7495	1.2903
1	1	Esco2		-0.2337	0.2633	0.5224	0.9259	1.2272	1.1409	1.6959	1.3094	2.6211
1	1	Espl1		-0.8325	[illegible]	0.3374	0.7718	1.1416	1.2065	1.5071	1.5465	1.9104
1	1	Esrp1		-1.9858	-1.9594	0.1756	0.4551	1.6862	1.8534	1.9638	2.2915	1.1027
1	1	Esrrb		-0.0593	[illegible]	0.6074	0.1325	2.3998	1.1774	4.665	3.5893	7.0464
1	1	Etaa1		-0.7077	0.2807	0.3961	0.7577	1.1048	0.9786	1.4434	0.9756	2.1675
1	1	Exosc2		-0.0713	0.305	0.8201	0.9273	1.2765	0.9888	1.8172	0.9955	1.2518
1	1	Ezh2		-0.4101	[illegible]	0.3689	0.7763	0.7509	1.266	1.54	[illegible]	2.2155
1	1	F2rl1		-0.4038	0.215	2.0844	1.4514	2.222	2.1849	2.4067	2.6928	1.0628
1	1	Fabp3		0.687	0.3335	0.1565	-0.3326	[illegible]	[illegible]	2.1744	1.3737	4.784
1	1	Fam25c		-0.9299	-0.9109	2.065	1.2475	2.8462	2.1533	2.4351	1.5927	2.3712
1	1	Fancd2		-0.5904	0.1154	0.4177	0.6887	0.8628	1.0128	1.4086	1.2068	2.1401
1	1	Fblim1		1.4821	1.9281	1.7229	1.0317	1.4001	0.7806	1.9608	1.2048	2.6176
1	1	Fen1		-0.7643	0.1838	0.4839	0.9131	1.2285	1.2052	1.2941	1.3921	1.1663
1	1	Fgf15		0.2994	0.4184	0.2748	0.2567	[illegible]	[illegible]	1.7027	1.2103	1.5113
1	1	Fgf17		0.222	-0.0884	0.335	0.088	[illegible]	[illegible]	1.3179	0.9914	2.8131
1	1	Fgf5		0.2944	-0.0745	[illegible]	0.1328	0.9648	0.5329	3.7139	3.1989	[illegible]
1	1	Fgf8		-0.1715	[illegible]	-0.112	[illegible]	[illegible]	[illegible]	3.4481	2.6399	[illegible]
1	1	Fignl1		-0.7249	0.4984	0.4499	0.9752	1.2808	1.3111	1.8593	1.8155	2.4301
1	1	Fiz1		0.4012	0.4724	0.8832	0.9184	1.2574	1.0852	1.4301	1.3085	1.1794
1	1	Fkbp4		-0.4892	0.312	0.5479	1.0284	0.9653	1.0934	1.5417	1.5416	1.333
1	1	Foxd1		0.4046	0.8993	2.8958	2.7016	3.1717	2.3015	1.9525	2.3436	[illegible]
1	1	Foxm1		-0.0713	0.6406	1.3222	1.2413	1.4288	1.1575	1.5317	1.4711	1.0089
1	1	Frat2		0.7303	0.4423	2.1203	1.6112	1.5971	1.0821	1.205	1.0872	0.9362
1	1	Fubp1		-0.172	0.4118	0.8401	0.7756	1.0573	1.0039	1.6266	1.1594	1.6218
1	1	Fxn		-0.0524	0.6097	0.6823	1.0934	1.0568	0.8415	1.1804	1.1963	1.239
1	1	Fzd5		-0.4355	-0.4501	1.3935	1.3255	1.3597	1.1452	1.2558	1.0252	1.8458
1	1	G3bp1		0.4681	1.2621	1.0791	1.4847	1.1544	1.9245	1.505	0.9435	2.1544
1	1	G3bp2		-0.3013	0.0582	0.4027	0.4944	0.8819	1.1774	1.2663	0.9757	1.2247

1	1	Gart		-0.8783	0.1144	0.2157	0.9234	0.6369	1.0559	1.0373	1.0808	1.7993
1	1	Gbx2		0.0701	0.0605	0.7445	0.9046	1.8074	2.465	3.5221	3.2196	5.1157
1	1	Gcnt2		2.5864	1.6104	2.4108	1.2746	1.8643	1.4982	1.8706	1.5002	3.1429
1	1	Gdf3		-0.2266	-0.3475	1.5214	1.1948	2.1699	2.016	2.6466	2.1383	4.105
1	1	Gemin6		-0.5987	0.337	0.0885	0.7204	0.391	0.999	0.7981	1.063	1.8251
1	1	Gjb3		0.2753	0.9424	1.257	0.1898	1.2189	0.766	2.0022	1.3746	2.8894
1	1	Gldc		-1.2975	-1.1582	-0.635	-0.2919	0.5373	0.1895	3.193	2.1855	4.7424
1	1	Glud1		0.5894	0.9918	1.3931	1.0153	1.1197	0.8995	1.2367	0.8063	1.6697
1	1	Gnpda1		0.1642	0.4539	0.4401	0.9571	0.7463	1.143	0.8438	0.5912	2.2392
1	1	Gpx2		-0.4944	-0.4091	0.9525	0.9175	2.5935	2.0621	2.159	2.4452	0.4611
1	1	Grhl2		-0.6374	-0.4714	[illegible]	-0.2945	0.9987	0.8547	1.3488	1.2935	1.4369
1	1	Grwd1		-0.1818	0.0422	0.4112	0.5158	0.4782	0.62	0.8855	0.926	2.3217
1	1	Gsg2		-0.3862	0.3957	0.4455	0.7204	0.9662	1.2493	1.1716	1.1432	1.7339
1	1	Gsta4		-0.1392	0.1289	1.0392	1.8809	1.5686	2.1113	1.59	2.169	2.1526
1	1	Gtse1		-0.2853	0.4062	0.4311	0.8219	0.7369	1.0292	0.7699	1.0505	1.4028
1	1	Gtsf1l		-0.2426	-0.2562	-0.1287	0.0726	0.5792	0.4172	1.5196	1.2297	3.1165
1	1	Gyltl1b		-0.128	-0.2975	0.58	0.3105	1.3297	1.4072	1.7715	1.8761	1.8671
1	1	H1fx		0.545	0.9158	1.5206	1.3533	1.8295	1.416	2.5259	2.0571	0.9277
1	1	H2afx		0.1895	0.7021	1.439	1.2722	2.2528	1.8605	2.6979	2.4468	1.9728
1	1	H2afz		-1.1608	-0.4535	1.1083	0.9196	1.2836	1.2784	1.648	1.0944	1.1108
1	1	H2-Bl		-0.1955	-0.2451	[illegible]	-0.1643	1.1155	0.4649	2.0892	1.2792	1.3359
1	1	Hat1		-0.8465	[illegible]	0.456	0.552	0.7898	0.922	1.2367	1.2101	2.4613
1	1	Haus6		-0.3017	0.2843	0.4673	0.6597	0.727	0.6706	1.1136	0.7799	1.6741
1	1	Haus8		-0.3508	0.3492	0.576	0.9349	0.9865	0.7968	0.8442	1.4112	1.0029
1	1	Hdgf		0.1507	0.2753	0.9055	0.8071	1.2424	1.0902	1.1311	1.1836	1.3003
1	1	Heatr1		-0.3303	0.2079	0.2775	0.4907	0.7122	0.7271	1.6338	1.2714	1.8292
1	1	Hic2		[illegible]	-0.1952	0.9139	0.0967	1.0218	0.6834	1.6279	1.4205	1.7441
1	1	Hirip3		-0.6699	0.3718	0.5822	0.8669	1.2809	1.3748	1.4674	1.5872	2.2389
1	1	Hist1h2ad		-0.2258	0.8382	1.4107	1.8748	1.9417	2.1402	2.1056	2.1508	2.2199
1	1	Hist1h2af		-0.182	0.8658	1.3391	1.6594	1.7354	1.6774	1.9025	1.8369	2.0205
1	1	Hist1h2ag		-0.1693	0.8494	1.1798	1.7539	1.7878	1.9464	2.0413	2.0383	2.2014
1	1	Hist1h2ah		-0.3827	0.8533	1.3818	1.6526	1.9329	1.9539	1.9385	2.1132	2.3456
1	1	Hist1h2ak		-0.3501	0.9244	1.4777	1.7758	1.9578	2.0571	1.9003	2.0796	2.5944
1	1	Hist1h2an		-0.3007	0.8231	1.2838	1.5633	1.847	1.6938	1.7432	1.8517	1.7866
1	1	Hist1h2ao		-0.7659	0.5908	0.9702	1.4002	1.4165	1.7211	1.7573	1.8989	1.3379
1	1	Hist1h3a		0.3262	0.143	0.7433	0.7767	1.1365	0.8764	1.9871	1.3835	1.9358
1	1	Hist1h3d		0.2932	0.1779	0.404	0.9133	0.9872	0.6253	1.8452	1.1382	1.6832
1	1	Hist1h3e		0.8435	0.474	1.1511	0.5471	1.3669	0.8827	2.0106	1.5253	1.9074
1	1	Hist2h2ab		-0.4352	0.2436	0.6613	1.1277	1.4989	1.3102	1.8523	1.7241	2.1249
1	1	Hist2h2ac		-0.4112	0.5216	0.9207	1.4652	1.524	1.5398	1.5167	1.9287	1.6536
1	1	Hist2h3b		1.1837	0.9432	1.5122	1.0706	1.5673	0.9037	1.8062	1.3132	0.8428
1	1	Hmga1		-0.2601	0.5591	1.4798	1.5209	1.7499	1.6808	2.0447	2.0261	1.4087
1	1	Hmgb2		[illegible]	0.3812	1.3417	1.3616	1.796	1.7857	2.4073	1.7634	2.4852
1	1	Hmgn5		-0.5728	0.1064	1.2426	1.2272	1.4747	1.4197	1.9185	1.3427	0.7678
1	1	Hn1l		0.3219	0.8777	0.7424	0.7753	0.9236	1.2059	1.7373	1.3598	1.1192
1	1	Hnrnpa2b1		0.6036	0.5979	1.4755	1.1231	1.5494	0.9358	1.9346	1.4698	1.1151
1	1	Hook2		-0.0677	-0.1592	0.2151	0.5772	0.7437	0.8362	1.0557	0.831	1.7646
1	1	Hsp90aa1		0.2107	0.0809	0.8958	0.5931	1.0945	0.6408	1.65	1.1761	1.7894
1	1	Hsp90ab1		-0.2859	[illegible]	0.6359	0.8896	1.0673	1.0728	1.2188	0.6589	1.2675
1	1	Hspa4		0.2118	0.1394	0.7333	0.4189	0.9773	0.5469	1.3329	0.7327	1.3957
1	1	Hspa8		0.3503	0.6186	0.7169	1.3089	0.9735	1.5254	1.4071	0.4072	1.7803
1	1	Hspb1		-0.2396	-0.3875	0.9007	0.4789	1.5861	0.9421	1.1644	1.2365	1.0567
1	1	Hspd1		[illegible]	1.0299	0.946	1.6929	1.0555	2.1602	1.1533	0.7757	2.4157
1	1	Hus1		-0.1554	0.2246	1.1184	0.9334	0.9798	0.7837	0.9344	0.9769	1.2368
1	1	Iap		-0.5097	[illegible]	1.4351	0.8786	1.9989	1.0257	1.7273	1.2455	[illegible]
1	1	Ifitm1		1.0678	0.7193	1.715	0.7205	2.2893	1.2444	2.4029	1.9374	2.5042
1	1	Igf2bp1		0.5004	0.1172	0.6627	0.2514	1.3746	1.3371	2.5946	2.0084	3.2869
1	1	Igf2bp3		0.5252	0.4616	0.4974	0.6727	0.8627	0.8365	1.4155	1.3515	0.9776
1	1	Igsf9		-0.4861	-0.3763	-0.3718	-0.2166	0.8647	0.6593	2.2106	1.5169	2.2559
1	1	Incenp		-0.4148	0.3263	1.0044	0.9069	1.4233	1.5533	1.8071	1.6256	1.5086
1	1	Ipo5		0.1913	0.4537	0.6924	0.5948	0.9871	1.0126	1.5729	1.2599	1.4332
1	1	Irgm1		0.9001	0.8376	1.2143	1.4548	1.4166	1.3423	1.6266	1.4487	1.3027
1	1	Jam2		0.6119	0.6767	1.8902	1.3844	1.102	0.4455	0.2813	0.3743	3.1711
1	1	Kdm1a		-0.2946	-0.1378	0.6511	0.5012	0.7689	0.7086	0.9948	1.1503	1.3577
1	1	Kdm4c		0.1277	-0.0646	0.838	0.6141	1.0704	0.7592	1.2445	1.125	1.0963
1	1	Kif11		-0.4183	0.436	0.7579	0.8372	1.6032	1.3591	1.5377	1.5648	1.5181
1	1	Kif18a		-0.4342	-0.2699	0.1661	0.4532	0.8603	0.6996	1.0311	0.7751	2.0061
1	1	Kif18b		-0.2894	0.4502	0.8538	1.0159	1.3916	1.4478	1.8214	1.6947	2.0139
1	1	Kif22		-1.2214	-0.2419	-0.1121	0.5322	0.8961	0.9616	1.2706	1.0107	2.0209
1	1	Kif23		0.0769	1.1267	1.118	1.216	1.4015	1.4381	1.6757	1.424	1.2684
1	1	Kif2c		-1.1937	-0.1967	-0.1073	0.358	0.8779	0.8696	1.0587	1.1875	1.6994
1	1	Kif4		0.0945	0.4366	0.7116	0.6808	1.0934	1.0522	1.3301	1.2792	1.4493
1	1	Klf2		1.7436	0.2106	1.2149	-0.3583	1.8947	0.8999	1.9552	1.5838	3.2279
1	1	Klf5		0.5937	-0.4198	0.9167	0.1991	1.4064	0.8548	1.637	1.1388	3.717
1	1	Kntc1		-0.4064	0.5896	0.7147	1.145	1.5284	1.2932	1.6567	1.6589	2.0184
1	1	Kpna2		-0.0896	0.531	0.7061	0.7509	0.66	0.9592	0.7721	0.9339	1.8785
1	1	Krt17		-3.1928	-2.302	[illegible]	0.3492	1.8635	2.0929	1.9703	2.7663	-0.3923
1	1	Krt18		-0.4097	-0.2354	0.9743	0.2595	1.5266	1.0745	2.2522	1.4324	1.2728
1	1	Krt42		-0.1249	-0.1641	0.9765	0.9168	1.8629	2.2924	2.3404	2.4442	3.1836
1	1	Krt8		-2.4713	-1.7985	1.2618	0.3623	1.9796	1.5445	1.8332	1.6719	-0.3038
1	1	L1td1		-2.6649	-1.5985	0.8159	1.141	1.8841	1.8973	1.8881	1.6568	0.7937
1	1	L3mbtl2		-0.3439	0.1663	0.6524	0.6524	0.8799	0.9457	1.5108	1.1851	1.3323
1	1	Lad1		-0.8084	-0.6696	0.5583	0.5611	1.4805	1.6256	1.2215	1.7748	[illegible]
1	1	Lama1		-0.0788	0.481	0.5944	1.1825	1.1393	1.767	1.1862	1.7729	3.2449
1	1	Lbr		-0.3965	[illegible]	0.4812	0.4701	1.0425	0.8846	1.7928	1.3742	1.439
1	1	Lck		-0.0562	0.2522	0.6286	0.4854	1.1696	0.7121	2.0313	1.5388	2.4191
1	1	Ldoc1		0.2898	0.1064	0.8625	0.074	1.0223	0.6546	1.5512	0.5664	1.4651
1	1	Lefty2		0.8454	0.5472	0.2213	0.1448	1.5753	0.9125	4.3082	3.6843	4.7721
1	1	Lig1		-1.0655	0.1124	0.4	0.8863	1.1604	1.1782	1.5697	1.51	1.7733
1	1	Lin28a		0.1074	-0.0496	0.1457	0.078	0.7453	0.2013	3.0425	1.9904	2.8398
1	1	Llgl2		-1.2839	-1.392	0.3212	-0.1448	0.9986	0.8817	1.5156	1.4466	2.6084
1	1	Lmnb1		-1.2215	0.5769	1.0742	1.4781	1.6021	2.4848	1.7262	1.8575	2.1209
1	1	Lrp11		0.5283	-0.0644	-0.2271	-0.1598	0.3281	0.3677	1.5176	1.2639	2.1665
1	1	Lrrc34		[illegible]	-0.0787	0.1972	[illegible]	0.6282	0.8985	1.0452	1.0732	2.9302
1	1	Lsm2		0.1025	0.3308	0.6736	0.944	1.1945	1.4969	1.5886	1.5852	1.1323
1	1	Lsr		-0.4621	-0.3848	0.2295	0.225	0.801	1.1818	1.4837	1.1133	1.1468
1	1	Lss		0.6412	0.8667	0.7106	0.8052	0.878	0.8974	1.6044	1.3245	1.4565
1	1	Ly6g6e		-0.1978	0.0455	-0.0538	0.316	0.6144	0.4976	1.4573	1.0082	3.4699
1	1	Lyar		-0.2729	0.0459	0.3193	0.7087	0.7839	1.0749	1.2879	1.1955	1.7153
1	1	Mad2l1		-0.571	0.1484	0.5731	0.9804	1.1724	1.419	1.2892	1.2049	1.5909
1	1	Mapk6		1.4704	0.601	1.9908	1.1941	1.5533	1.4202	1.5277	1.2493	0.904
1	1	Marcksl1		0.5956	0.2518	0.3567	0.1214	0.8823	0.4722	2.1173	1.3559	1.4097
1	1	Mcam		1.1639	1.2843	0.9316	1.2187	1.3728	1.5468	1.6232	2.0074	1.3593
1	1	Mcm10		-0.7649	-0.1668	0.8012	0.8924	1.3625	1.2067	1.6514	1.4579	2.4714
1	1	Mcm2		-0.7107	0.1307	0.6533	0.823	1.4162	1.3476	2.0276	1.921	2.2602
1	1	Mcm3		-0.3867	0.2891	0.3791	0.5858	0.9514	0.9796	1.6734	1.5794	2.403
1	1	Mcm4		-0.6473	0.0611	0.4042	0.6491	0.7808	0.9327	1.2095	1.2493	1.5201
1	1	Mcm5		-1.6652	-0.5593	0.5821	0.6354	1.1912	1.2189	1.5072	1.3016	1.9008
1	1	Mcm6		-0.9508	0.2823	0.9428	1.1849	1.3415	1.3257	1.8177	1.6815	1.6108
1	1	Mcm7		-0.3419	0.1001	0.5612	0.7317	0.694	1.1427	1.1297	0.4542	1.9403
1	1	Mdk		0.9483	0.2969	0.7849	0.4082	1.722	1.3079	3.5408	2.7618	4.5825
1	1	Melk		-0.2728	0.2586	0.4793	0.585	0.8689	0.8543	1.2294	0.8039	1.2241
1	1	Mis18bp1		-0.1481	0.2955	0.6775	0.9191	1.3295	1.075	1.7143	1.452	1.4838
1	1	Mkrn1		0.0725	-0.2598	0.4671	0.1135	0.8384	0.4949	1.4931	0.8786	2.2826
1	1	Mlf2		0.8273	1.3228	1.2951	1.3822	1.2209	1.6794	1.8066	0.9901	0.6977
1	1	Mms22l		-0.2427	0.3392	0.6	0.5595	0.9991	0.9371	1.1703	1.0801	1.699
1	1	Mnd1		-0.5615	-0.1539	0.1058	[illegible]	0.5711	0.6132	1.594	1.0841	2.3304
1	1	Mns1		-0.6697	-0.1266	0.422	0.7506	1.3104	1.4259	1.5598	1.6487	1.7088
1	1	Mov10		0.6598	0.4134	0.9326	0.5842	1.0153	1.1421	1.1579	1.4747	1.1401
1	1	Mre11a		-0.3358	0.1276	0.4042	0.6572	0.9771	1.0579	1.3226	1.1228	1.8827
1	1	Mreg		-0.7902	-0.2221	0.0996	0.4367	0.5481	0.5518	1.3197	0.8032	3.1524
1	1	Mrps5		-0.3414	0.2531	0.195	0.496	0.6758	1.3629	1.2719	1.0474	1.8765
1	1	Msc		-1.2828	-0.3336	2.3709	3.1245	2.3335	2.4039	1.0758	1.6165	0.4225
1	1	Msh6		-0.6548	-0.2007	0.5815	0.7415	1.321	1.2762	1.6967	1.5583	2.3551
1	1	Mta3		-0.7103	-0.1653	0.631	0.7639	1.1164	1.501	1.7295	1.6543	1.405
1	1	Mtap7		-0.822	-0.377	0.9892	1.1311	1.5217	1.7752	1.0549	1.4421	1.3369
1	1	Mthfd1		-0.2887	0.6129	1.4535	1.5248	2.1442	2.0574	2.4559	2.6892	1.0662
1	1	Mum1		-0.0287	0.5383	0.3211	0.9334	0.6738	0.9372	1.3199	0.9916	1.6602
1	1	Mup6		0.0563	[illegible]	0.5251	0.154	1.4025	1.3266	3.0128	2.6371	2.5019
1	1	Mutyh		-0.1527	0.2981	0.3101	0.545	0.8653	0.6692	1.418	1.2738	1.7275
1	1	Mybl2		-0.9468	-0.1517	1.1889	0.9613	1.7576	1.7195	2.4237	1.7351	4.2576
1	1	Myef2		0.2086	0.5471	0.862	1.1448	0.9987	0.9566	1.1823	1.1357	1.6587
1	1	Mylpf		-0.4864	-0.156	0.3867	0.2326	1.2249	0.8197	2.1459	1.1534	2.9697
1	1	Myst2		0.2978	0.0967	1.0913	0.5468	1.0644	0.9508	1.1493	0.9963	1.2405
1	1	Nacc1		0.3651	0.3347	0.7214	0.4874	0.8836	0.7144	1.3818	0.9954	1.1659
1	1	Nanog		0.415	0.0808	0.5883	0.09	2.2891	1.4175	4.5034	3.4946	5.032
1	1	Nap1l1		[illegible]	0.5189	0.7206	0.8652	0.5608	0.6815	1.3728	1.0027	1.2726
1	1	Nasp		-1.1614	-0.3635	0.2949	0.5065	0.9325	1.0838	1.7111	1.5948	2.3083
1	1	Ncapd2		-0.4144	0.3774	0.8424	1.0652	1.7054	1.356	1.7438	1.6702	1.3467
1	1	Ncaph		-0.7204	0.2466	0.888	1.0631	1.4137	1.3112	1.2092	1.3224	1.2624
1	1	Ncl		-0.3366	[illegible]	0.694	0.6184	1.2075	1.0332	1.6385	1.3259	0.9558
1	1	Nde1		[illegible]	0.7	0.6751	0.7819	0.9915	0.9633	1.2087	0.8814	1.2689
1	1	Nfatc2ip		-0.3705	-0.411	0.813	0.5958	1.0835	0.934	1.1164	0.8032	1.7221
1	1	Ngfr		-1.5016	-0.7942	1.0052	0.895	1.7125	1.8314	1.2973	1.4348	-0.1039
1	1	Ngfrap1		0.3844	0.5547	0.597	0.6281	0.8925	0.8653	1.6063	1.4212	1.4283
1	1	Nhp2		-0.3829	0.2869	0.7589	1.149	1.1854	1.0095	1.3667	1.2876	1.0444
1	1	Notch4		-0.7755	0.094	1.0891	1.8973	1.3989	1.9266	1.3697	1.9259	1.9661
1	1	Npy		-0.4489	-0.2607	2.7256	2.2091	3.0643	2.5126	1.9361	1.8543	-0.4943
1	1	Nr5a2		[illegible]	[illegible]	0.2647	0.2366	0.7667	1.2689	1.3666	1.4509	2.7848
1	1	Nudt21		0.4689	0.6413	0.8798	1.0095	1.5329	0.897	1.5054	1.2957	1.4963
1	1	Nup133		-0.285	0.1376	0.3264	0.5821	0.8449	0.9629	1.3247	1.2008	1.9909
1	1	Nup155		0.4049	0.8608	0.7945	1.1705	1.045	1.323	1.1983	1.3138	1.5227
1	1	Nup43		-0.6211	0.2433	0.131	0.8336	1.0209	1.0976	1.7434	1.4425	2.0913
1	1	Nup62		-0.0782	-0.0842	0.5396	0.5283	0.8795	1.0363	1.3972	0.9414	1.5629
1	1	Nusap1		-1.2357	-0.3594	0.411	0.7164	1.2819	1.1734	1.1673	1.2135	1.1474
1	1	Odc1		-0.1527	0.2482	0.5251	0.7249	0.9628	1.0254	1.4753	1.2658	1.8448
1	1	Olfr985		-0.0423	-0.0884	0.909	0.6434	1.0658	1.1902	0.5644	0.9975	2.3042
1	1	Olig1		-1.3297	-1.4311	0.1003	0.2757	1.5901	2.0765	2.715	2.4936	-0.1869
1	1	Ooep		-0.1477	-0.1411	1.249	0.9343	2.6658	2.0827	3.9957	2.8061	5.9581
1	1	Orc1		[illegible]	-0.1699	0.6137	0.3547	0.8844	0.8332	1.3315	1.0646	2.0606
1	1	Orc5		-0.2017	0.1998	-0.1241	0.5432	0.8048	1.031	1.3428	1.1038	1.1745
1	1	Otx2		0.0815	0.0973	0.7477	0.4167	2.2002	1.3057	4.7891	3.3145	3.6151
1	1	Pa2g4		-0.5018	0.3497	0.7751	0.9458	0.8713	1.1777	1.0418	1.0909	0.8409
1	1	Parp1		-0.9679	[illegible]	0.8922	1.2029	1.4437	1.4248	1.5742	1.5565	1.6554

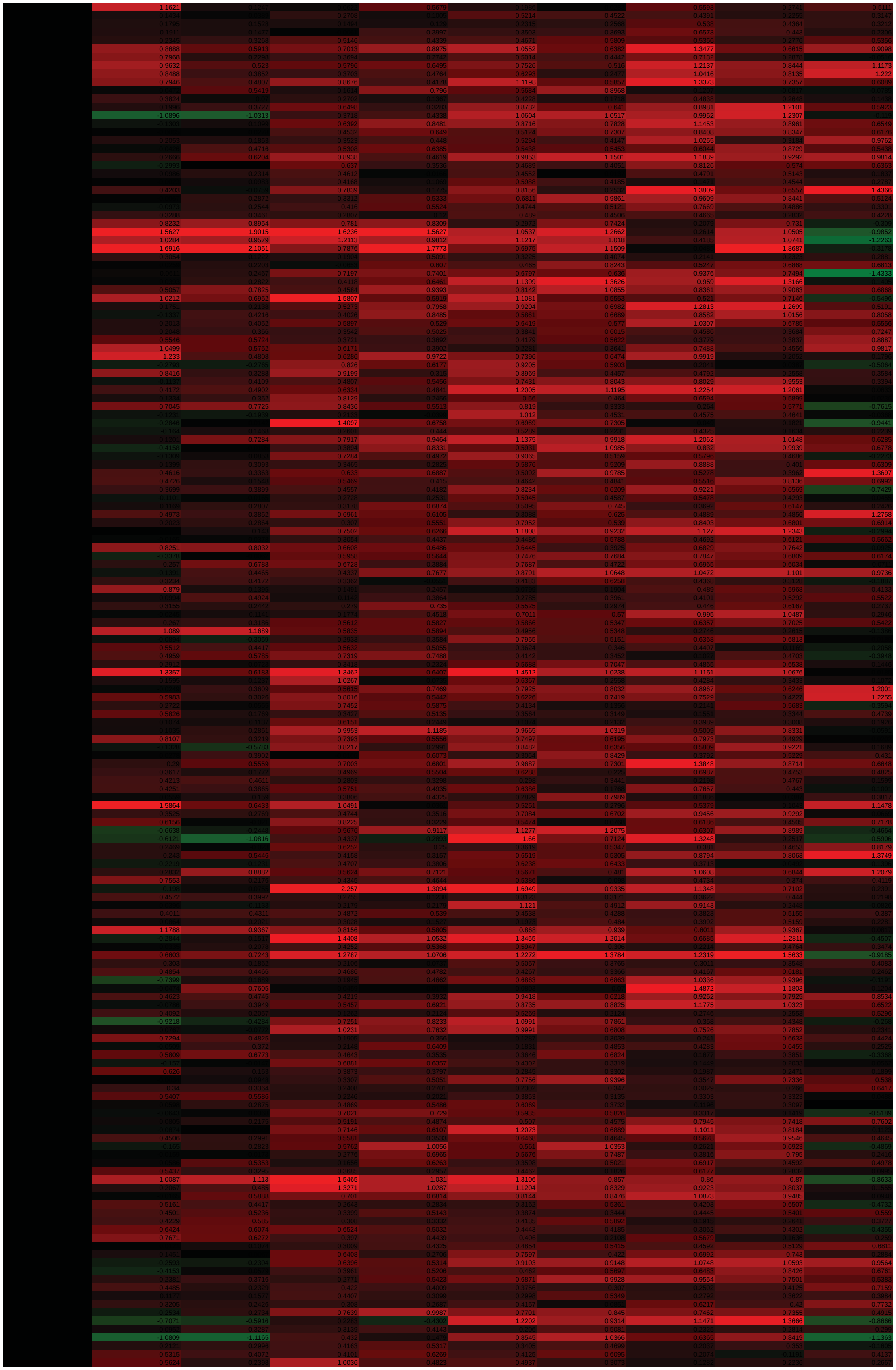
1	1	Pcyt1b	-0.4605	-0.3272	0.7649	0.7097	0.7025	0.7435	1.038	0.9812	1.267
1	1	Pdlim3	0.921	0.2179	0.4353	0.802	0.6201	0.5208	1.5808	1.4001	1.4798
1	1	Peg3	1.408	0.68	1.3498	1.2315	2.1115	2.1455	2.209	2.5691	[illegible]
1	1	Pga5	[illegible]	-0.1212	1.566	1.3421	1.2091	0.9744	1.2511	0.8853	1.7885
1	1	Phox2a	0.2455	0.1011	0.8771	1.3312	1.5407	2.0854	1.6383	2.0373	0.8418
1	1	Pif1	-0.3325	0.1101	0.1576	0.6394	0.8399	0.9879	0.9448	1.0278	1.9985
1	1	Pik3cb	-0.6594	-0.3467	0.9277	0.6321	0.9749	0.8432	1.0294	0.8707	1.2371
1	1	Pim3	-0.148	-0.2057	0.6792	1.0237	0.9852	1.2597	0.6592	0.7819	2.1513
1	1	Pkp2	-0.1787	-0.1138	0.9424	0.4654	1.335	1.1636	1.4861	1.4106	2.1233
1	1	Pla2g10	-0.043	0.0823	0.0588	[illegible]	0.9876	0.6347	2.1274	1.4814	3.9755
1	1	Pla2g1b	[illegible]	-0.0624	[illegible]	-0.1464	0.2345	[illegible]	2.2207	0.9411	3.4933
1	1	Plekhf2	-0.6421	-0.6211	1.2271	0.7158	1.6421	1.5824	2.1628	2.1552	1.7271
1	1	Plk4	0.1648	0.6668	0.3924	0.5361	0.9305	0.7417	1.1496	1.0581	1.7213
1	1	Pmf1	0.1702	0.5786	0.8083	0.7501	1.2819	1.1329	1.5885	1.3459	0.8311
1	1	Pml	1.0706	1.142	0.7457	0.7176	1.2569	1.3893	1.185	1.335	1.5745
1	1	Pold1	-0.7691	-0.0645	[illegible]	0.3068	0.747	0.7838	1.329	1.2762	1.4435
1	1	Pold2	-0.7496	0.302	0.5374	0.8962	0.9493	1.5304	0.8115	1.2243	1.6404
1	1	Pold3	-0.513	-0.0646	0.3562	0.5105	0.9877	0.6997	1.0863	1.29	1.2138
1	1	Pole	-0.0427	0.3887	0.8703	1.0014	1.1992	0.9733	1.5704	1.3746	1.5695
1	1	Porcn	-0.4222	-0.3786	1.5396	1.3761	2.0406	2.3839	1.4352	2.0487	[illegible]
1	1	Pou3f1	-0.5936	-0.6635	-0.2665	-0.3059	0.727	[illegible]	2.6295	1.7931	1.1168
1	1	Ppa1	-0.3223	0.1545	0.7905	1.1186	1.007	1.1565	1.5645	1.6332	1.5198
1	1	Ppat	-0.291	0.1889	1.1273	1.0604	0.9286	0.8949	1.1714	0.8858	1.849
1	1	Ppfibp2	0.3208	-0.1792	1.3458	0.7911	1.5449	1.1594	0.9776	0.952	1.1301
1	1	Ppp1r1a	-0.0519	0.0745	0.0805	0.1424	0.6665	0.5298	2.2407	1.6534	2.6483
1	1	Ppp2r2d	0.1535	0.3488	1.5237	1.0338	1.5758	1.0743	1.5041	1.1718	1.1107
1	1	Prc1	-0.7315	0.6843	0.7971	1.1443	1.3975	1.5068	1.3578	1.5209	1.8021
1	1	Prmt7	-0.5512	0.56	0.3864	0.6393	0.5908	1.0878	0.8306	0.9904	1.9187
1	1	Prpf3	0.1253	0.3599	0.6079	0.7257	0.6114	0.9635	0.7827	0.5489	1.9566
1	1	Prpf8	0.8781	0.7183	1.0848	0.9655	1.4513	0.9877	1.9796	1.5113	1.1093
1	1	Prps1	-0.9884	-0.3974	0.3803	0.6458	0.7651	0.9254	1.2265	1.0724	1.2182
1	1	Psip1	-0.3012	[illegible]	0.493	0.2691	0.8295	0.4758	1.5629	1.0286	1.1751
1	1	Psmc3ip	-0.5443	0.0876	[illegible]	0.454	0.8559	1.1502	1.3103	1.1976	2.0224
1	1	Psmd14	0.2839	0.5826	0.95	0.8489	1.2617	0.8489	1.6545	1.1275	0.7132
1	1	Ptma	0.3449	0.3543	1.2138	0.8103	1.5145	0.859	1.3142	1.5108	0.692
1	1	Pycr2	-0.5952	-0.0803	0.3299	0.8258	0.5183	0.9426	1.1496	1.3078	1.3207
1	1	Rab15	0.2947	0.3178	0.4526	0.1362	1.7615	1.2413	2.264	1.6018	1.9614
1	1	Rad1	-0.329	0.4097	0.0798	0.7944	0.6772	1.0851	1.1265	0.9779	1.6295
1	1	Rad51	-0.6311	0.1536	0.384	0.6443	0.4675	1.131	1.1351	0.8861	2.2224
1	1	Rad54b	-0.7443	0.3006	0.4804	0.8479	1.389	1.1257	1.8515	1.5277	2.9987
1	1	Rad54l	-0.8136	[illegible]	0.4052	0.8732	1.1111	1.4772	1.6346	1.15	2.2426
1	1	Ranbp1	-1.0926	0.0386	0.5938	0.8979	0.8988	1.0601	1.1908	1.1591	0.9573
1	1	Rasgrp1	-0.6333	-0.1405	1.5402	1.7044	1.4328	1.4548	0.5702	1.3578	1.3619
1	1	Rbm38	-0.1479	0.4967	1.2781	1.8304	1.5205	1.6536	1.6458	1.7529	1.6722
1	1	Rbmxl2	[illegible]	[illegible]	[illegible]	-0.0904	0.3111	-0.0655	1.8397	0.9932	3.9764
1	1	Rbpms	0.5569	0.68	0.0612	0.1867	0.8274	0.8197	1.5563	1.2639	2.4002
1	1	Rbpms2	0.3575	0.5744	0.9668	0.3508	2.056	1.0993	3.738	3.1417	4.032
1	1	Rcc1	-0.1195	[illegible]	0.2601	0.8917	0.6584	0.9904	1.2045	1.1366	1.1851
1	1	Rdm1	-0.7422	-0.533	0.5597	0.8359	0.9378	1.034	0.8357	1.0751	1.8454
1	1	Reep6	-0.3569	0.3544	0.4432	0.7083	1.1855	1.1978	1.3963	1.3507	0.7851
1	1	Rfc5	-0.7404	[illegible]	0.1398	0.4978	0.5918	0.7799	1.0131	0.8876	2.273
1	1	Rfx2	0.2378	-0.072	1.6061	0.9472	2.0556	1.5651	2.5519	2.0848	2.941
1	1	Rhox9	0.2188	0.0985	1.1987	0.2761	1.598	0.9564	2.2879	1.899	2.351
1	1	Robo4	-0.2591	-0.2093	0.1777	0.2412	0.452	0.698	1.5106	1.3876	2.1721
1	1	Rpf1	-0.0545	-0.1965	0.5036	0.763	0.9349	0.6543	1.3012	0.9747	1.2896
1	1	Rpp25	-0.2028	-0.0862	1.9586	1.9784	2.2972	2.8575	2.4951	2.3397	2.367
1	1	Rps4y2	0.5856	0.5783	0.8233	0.7802	1.2391	1.1345	1.7118	0.8305	3.3007
1	1	Rrm2	-0.3058	0.2241	0.8063	1.3292	1.0311	1.674	1.0636	1.6486	1.5065
1	1	Rrp12	-0.5037	0.1881	0.3293	0.4901	0.8618	1.0996	1.6503	1.2308	1.6224
1	1	Rrp1b	-0.3228	0.0613	0.3421	0.6557	0.6117	1.0181	1.0237	1.0265	2.3339
1	1	Rrp9	[illegible]	0.5825	0.5431	1.0501	0.8685	1.1556	1.6062	1.4909	1.6407
1	1	Rsl24d1	0.8742	0.7429	1.4329	1.8307	1.5171	1.8053	1.5711	1.4321	2.3544
1	1	Rtel1	-0.0521	0.3081	0.4051	0.4561	0.9002	0.7229	0.8844	0.9265	1.5956
1	1	Sall1	-0.129	-0.1258	0.4202	0.4698	1.0758	1.0925	1.7079	1.4025	2.3596
1	1	Sall4	-0.6732	-0.7916	1.0471	0.8577	2.6072	2.0594	4.3392	3.2372	4.1339
1	1	Sap30	-0.6428	0.2096	1.0538	1.5878	1.5998	1.7233	1.6966	1.8663	2.2856
1	1	Sart3	0.1519	0.3912	0.8811	0.9229	1.0558	1.2795	1.426	1.2789	1.1202
1	1	Sec14l1	0.9402	0.9674	1.8042	1.4976	1.9344	1.5552	1.3813	1.776	0.1726
1	1	Setd6	-0.422	0.5317	0.4791	0.9679	0.348	0.9138	0.6363	1.0416	2.2634
1	1	Sf3a1	-0.11	0.2467	0.6058	0.6992	0.7945	1.1059	1.0064	1.2167	1.0158
1	1	Sf3b3	0.3332	0.5322	0.5079	0.9025	0.9378	0.9367	0.9661	1.1836	1.3682
1	1	Sftpd	-0.2074	-0.2766	1.5937	1.5986	2.3657	1.5554	0.9203	1.3799	[illegible]
1	1	Sgol1	-0.0827	0.8143	0.6612	1.4431	1.6366	1.9101	2.0358	2.009	2.5842
1	1	Sh3gl2	-1.208	-1.1318	0.3292	0.5151	1.2528	1.9012	1.072	1.8168	2.2907
1	1	Siah1b	0.0072	-0.0615	0.5978	0.6698	0.6535	0.8984	1.5619	0.9571	1.9722
1	1	Sirt1	0.5021	-0.0355	1.0729	0.51	0.9173	0.4879	1.9107	0.9409	2.0216
1	1	Skp2	-0.7542	0.0841	0.1197	0.7176	0.8923	1.0635	1.1657	1.1551	1.2243
1	1	Slc17a6	0.238	0.2707	3.2046	2.996	3.8137	3.0044	2.5587	2.5985	0.1953
1	1	Slc28a1	-0.535	-0.4198	1.0094	1.3903	1.6414	1.8195	1.2442	1.5254	1.1892
1	1	Slc2a1	-1.4068	-1.196	0.6644	0.4346	1.4899	1.7455	2.0387	2.1149	0.819
1	1	Slc2a3	-0.2307	0.5346	2.066	1.6397	3.8453	3.4712	5.2043	4.9302	5.5343
1	1	Slc39a4	-0.255	-0.2762	0.1412	[illegible]	0.5883	0.6328	1.7177	1.1959	2.5979
1	1	Slc47a1	-0.0716	0.1699	[illegible]	0.6345	0.3745	0.5908	0.4424	0.6042	3.8084
1	1	Slc7a3	-0.874	-0.0282	3.099	3.0624	3.9763	3.4049	3.4948	2.9204	3.1495
1	1	Slc9a3r1	-0.7251	-0.4649	1.3096	0.9186	1.5254	1.5103	2.0086	1.9273	0.5103
1	1	Slco4a1	0.2809	0.2591	0.4539	0.3172	1.3464	1.0617	1.5611	1.6239	2.5214
1	1	Smarcad1	-0.7383	-0.1057	-0.3353	0.1803	0.5466	0.7939	1.214	0.9944	2.2684
1	1	Smarcc1	0.6086	0.7325	0.9912	1.3464	1.3109	1.5136	1.454	1.4385	2.094
1	1	Smg7	0.9845	0.5624	1.7181	1.1872	1.4868	1.4115	1.4583	1.5166	1.0662
1	1	Snrpa	0.294	0.2969	0.697	0.6533	1.0276	1.0156	1.6757	0.6898	1.1618
1	1	Snrpd1	-0.2285	0.287	0.5585	0.7331	0.6968	1.1718	1.2004	0.9066	1.5066
1	1	Snrpn	0.1571	0.0865	1.3186	1.2218	1.5049	1.2795	1.902	1.5013	1.7494
1	1	Sox15	[illegible]	0.0889	0.453	0.4483	1.2169	1.1243	1.5126	1.1036	0.9577
1	1	Sox21	-0.1112	0.5108	2.0484	1.9315	0.7635	0.217	1.4611	0.8373	1.1045
1	1	Sp5	-0.2674	-0.2251	0.3054	0.3448	0.9917	0.8391	3.733	3.3673	1.4983
1	1	Spag5	-0.371	0.3656	0.4479	0.7322	1.1484	0.8811	1.2625	0.9864	1.7053
1	1	Spc25	0.3215	0.7327	0.7623	1.2495	1.2908	1.3577	1.9869	1.6999	2.1135
1	1	Spink3	0.1642	-0.122	1.774	1.5331	0.6038	-0.1285	4.079	2.5552	2.7862
1	1	Spire2	0.6174	0.8535	0.6085	1.0041	1.4037	1.4252	1.5377	1.718	1.3661
1	1	Spnb3	-0.159	-0.121	0.2071	-0.0576	1.3869	0.7338	1.7544	1.4248	1.5241
1	1	Srm	-0.1325	0.5318	0.5504	1.0257	0.8023	1.184	1.2698	0.7435	1.0412
1	1	Srrt	0.6535	0.7278	0.8681	0.9774	1.2732	0.873	1.4801	1.2116	0.8396
1	1	Srsf1	-0.3892	0.2967	0.5337	0.9947	0.9573	0.9757	1.4478	0.8992	1.2509
1	1	Srsf2	-0.0911	0.1742	0.9534	0.9916	1.3497	0.7713	1.6299	1.2537	0.8032
1	1	Ssbp3	2.0389	1.7151	1.5708	1.4638	1.7535	1.7226	2.0438	1.7703	-0.0787
1	1	Stip1	-0.3865	0.301	0.5979	0.5897	0.9081	0.7332	1.0887	1.1348	1.2319
1	1	Stx3	0.461	0.3019	0.3324	0.1628	0.7152	0.6441	1.4977	1.0768	2.0509
1	1	Taf5	-0.2885	-0.0412	0.3038	0.433	0.7649	0.8517	0.9927	1.1548	1.5857
1	1	Taf9	0.8876	0.4964	0.8863	0.8745	0.8247	0.7266	1.2627	0.8913	1.4284
1	1	Tcf15	-0.0277	-0.0958	0.5748	0.2035	1.4658	1.7033	2.2886	2.4213	3.9865
1	1	Tcl1	0.075	-0.0597	[illegible]	0.0598	0.2058	0.1317	0.8498	0.2869	4.8491
1	1	Tcp1	0.4155	0.4923	0.5998	0.7521	0.9756	1.0189	1.2234	0.6491	1.8544
1	1	Tdg	-0.6677	[illegible]	0.4171	1.0406	0.6677	1.1078	0.9311	0.807	1.6433
1	1	Tdgf1	-0.5955	-0.644	-0.2749	-0.1741	0.6086	0.4437	1.9156	1.3909	2.8262
1	1	Tdh	-0.4598	0.0943	2.9549	2.4853	2.9353	2.6985	2.9004	2.661	4.055
1	1	Tdrd12	0.1372	0.0673	0.0792	0.171	0.3826	0.4298	1.6139	1.1128	3.8238
1	1	Tex9	0.0965	-0.0761	0.4179	0.6699	0.8443	0.8773	1.5233	1.2301	1.1177
1	1	Tfap2c	-0.9764	-0.9609	0.7226	0.5382	2.1799	1.874	2.8443	2.1463	2.3758
1	1	Tfrc	-2.3377	-1.2644	0.2175	0.7788	0.8456	1.1291	0.9522	1.3219	1.4465
1	1	Tgif1	0.7176	0.4597	0.5688	0.6047	0.4221	0.854	1.1196	0.7244	1.8865
1	1	Timeless	-0.2492	0.6088	0.613	0.7735	1.3017	1.2108	1.8476	1.4778	1.8909
1	1	Tipin	-0.3748	0.3722	0.3781	0.6986	0.9944	0.9524	1.0644	1.0716	1.7228
1	1	Tjp2	-0.6596	-0.0335	1.5065	1.0006	1.1715	0.9412	1.6042	1.2242	1.6065
1	1	Tk1	-0.7885	0.6315	0.7318	1.0081	1.3215	1.227	1.1837	1.4562	0.5661
1	1	Tle4	-0.4164	-0.1563	2.0366	1.8456	2.0998	1.9291	2.1174	1.931	1.186
1	1	Tmem180	-1.0361	-0.8026	0.779	0.9656	1.215	1.3468	1.7356	1.7023	0.7343
1	1	Tmsb10	1.1574	1.1857	1.6702	1.4244	1.4823	1.6711	0.9972	1.4212	0.7084
1	1	Tonsl	0.4267	0.4482	0.7223	0.8428	1.2924	1.0145	1.5213	1.3859	1.2291
1	1	Top2a	-0.3883	0.5986	0.9358	0.6547	1.6004	1.4071	2.1792	1.9572	2.6074
1	1	Tpx2	-0.5327	0.228	0.4561	0.4673	0.9764	1.0695	1.2456	0.8151	1.4712
1	1	Trh	0.0714	0.1311	3.8429	2.6941	4.5025	3.4988	6.7616	6.043	6.4836
1	1	Trim28	-0.1438	0.3304	0.6591	0.6362	0.8252	0.7279	1.6294	1.4114	1.3659
1	1	Trp53	0.1813	0.6431	0.7586	0.863	1.0308	1.0048	1.399	1.3945	1.3473
1	1	Trub2	-0.0667	[illegible]	0.3012	0.8258	0.8976	0.8042	1.3967	1.1706	1.5417
1	1	Tyms	-0.2614	0.5109	0.5131	1.0858	1.0031	1.1865	1.2678	1.274	1.6528
1	1	Tyms-ps	-0.3714	0.5203	0.5097	0.8626	0.7192	0.8641	0.9905	0.8956	1.4461
1	1	Uba2	-0.2804	0.2906	1.0247	1.3682	1.3631	1.4364	1.4475	1.2577	1.499
1	1	Ubqln4	-0.0258	0.4766	1.1025	1.1937	1.1564	1.1943	1.1479	1.5412	1.1222
1	1	Uchl5	-0.1865	0.4651	0.7273	0.9927	0.8611	1.0413	1.2334	0.9481	1.0437
1	1	Uhrf1	-1.2724	-0.114	1.2017	1.4498	1.5641	1.7557	1.8127	1.752	1.5317
1	1	Umps	-0.2793	0.5488	0.7714	1.136	0.8896	1.4853	0.8514	0.8498	1.6018
1	1	Ung	-0.7774	0.1089	0.5824	0.9889	1.2615	1.6942	2.2438	1.9612	2.7941
1	1	Upp1	-0.5318	0.7921	3.0927	2.9374	3.1431	2.6917	3.5323	2.8753	4.3456
1	1	Usp28	-0.0778	0.2057	0.8103	0.9673	1.3435	1.3726	1.7578	1.6814	2.5657
1	1	Usp39	0.2854	0.7241	0.8714	0.8891	0.8173	1.0921	1.3164	1.0476	1.5173
1	1	Usp7	0.0609	-0.1037	0.6445	0.4752	0.7257	0.611	0.9807	0.7895	1.7145
1	1	Utf1	-0.3327	-0.212	0.1231	0.0957	1.11	0.8887	3.0199	2.1664	3.8262
1	1	Vbp1	0.1668	0.1202	0.8237	0.741	1.2183	0.6507	1.5597	0.9785	1.1254
1	1	Wasf1	-1.2078	-0.4225	0.925	0.9784	0.8643	0.9589	0.8814	1.0646	0.8955
1	1	Wdhd1	-0.3429	0.3732	0.3341	0.9812	0.8441	1.1463	1.1718	1.274	1.6219
1	1	Wdr5	-0.2251	[illegible]	0.3609	0.8439	1.0175	0.8144	1.2199	0.7719	1.3119
1	1	Wdr76	-0.9107	-0.4417	0.2202	0.8252	1.0348	1.0155	1.4268	1.241	2.4578
1	1	Wdr86	-0.2248	-0.1095	0.0777	-0.1984	0.2482	0.2118	1.5706	1.0641	2.4892
1	1	Wfdc2	-2.5361	-1.7526	1.1074	0.1612	1.7564	1.4158	1.7359	1.1122	1.3321
1	1	Wnk1	0.2899	0.4278	0.9125	0.7309	0.9977	0.9813	1.1864	1.3954	1.4182
1	1	Wwc1	-0.8153	-0.3288	0.4746	0.762	1.1347	1.2974	1.0498	1.0173	1.0428
1	1	Zbtb8a	0.2309	0.501	[illegible]	0.3154	0.7641	0.376	1.6447	0.936	1.657
1	1	Zfp296	-0.2419	0.2157	0.8112	1.2731	1.4144	1.6675	1.3224	1.5337	2.8207
1	1	Zfp473	-0.1171	-0.3158	0.0976	0.6456	0.9	1.1241	1.3944	1.3317	2.0031
1	1	Zfp57	-0.0781	[illegible]	0.898	1.4805	1.2776	1.8923	1.4707	1.6652	1.7621
1	1	Zfp819	-0.0738	-0.1399	0.595	0.4339	0.6579	0.478	1.1276	0.8667	2.6746
1	1	Zic3	-1.503	-1.3346	0.4936	0.3289	1.4241	1.0063	2.1734	1.7352	2.6264
1	1	Zscan10	-0.0406	0.3153	0.6835	0.7363	2.0769	2.0634	3.7995	3.174	3.1729
1	2	0610007P14Rik	0.8399	0.823	0.477	0.4119	0.7281	0.444	0.8224	1.0582	0.4721

1	2 1110057K04Rik		[illegible]	0.2545	0.364	0.3726	0.4788	0.4827	0.5432	[illegible]	0.6874
1	2 Ctc1		[illegible]	[illegible]	0.3118	0.5218	0.7162	0.8044	0.8451	1.2136	0.7422
1	2 1700019G17Rik		[illegible]	[illegible]	0.8378	0.6658	1.1037	0.7558	0.932	0.5443	0.5618
1	2 1700027A23Rik		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.9143	0.7363	0.3487
1	2 1700093K21Rik		[illegible]	[illegible]	0.3547	[illegible]	0.5358	[illegible]	0.6969	[illegible]	[illegible]
1	2 1810009A15Rik		[illegible]	[illegible]	0.4866	0.4799	0.7152	0.4252	0.9042	0.9975	0.524
1	2 1810035L17Rik		0.4681	0.3639	0.691	0.3276	0.455	0.2975	0.7822	0.5062	[illegible]
1	2 2010107G12Rik		0.3058	0.6179	0.5211	0.5812	0.7351	0.5578	0.7048	0.5255	[illegible]
1	2 Tceanc2		[illegible]	[illegible]	0.3774	0.4656	0.3859	0.6583	0.3663	0.3855	[illegible]
1	2 2210016L21Rik		0.296	0.4521	[illegible]	[illegible]	[illegible]	0.3223	0.5294	0.3312	0.5771
1	2 2210404J11Rik		[illegible]	-0.4216	0.5689	[illegible]	0.9115	0.5452	[illegible]	0.4569	[illegible]
1	2 2310003C23Rik		0.396	0.5349	0.6887	0.7603	0.8627	0.6468	0.8111	0.8224	1.0194
1	2 2310003F16Rik		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.5673	[illegible]	0.5806	[illegible]
1	2 2310007B03Rik		-0.2605	-0.2752	0.2764	[illegible]	0.6282	0.4584	0.3566	0.6989	[illegible]
1	2 2310008H09Rik		-0.2762	[illegible]	0.3278	0.7153	0.6748	1.0979	0.4503	0.6223	0.7748
1	2 2310014L17Rik		0.3121	[illegible]	0.527	0.4057	0.4414	[illegible]	0.7836	0.3504	[illegible]
1	2 2310022A10Rik		[illegible]	[illegible]	0.2689	0.3205	0.5087	0.5589	0.5982	0.6059	0.6499
1	2 2310035C23Rik		0.6288	0.4034	0.4201	0.4174	0.4812	0.5811	0.2872	0.3182	0.3029
1	2 Kansl2		0.3954	0.6568	0.3826	0.7723	[illegible]	0.8241	0.4744	0.4359	0.9524
1	2 2310067B10Rik		0.5761	0.6808	1.3213	1.1316	1.4078	1.3871	1.0479	1.3915	0.4909
1	2 2310079F23Rik		[illegible]	0.4053	[illegible]	0.3593	[illegible]	0.5968	0.3628	0.4518	[illegible]
1	2 2410002O22Rik		0.2922	0.5338	0.3751	0.4962	0.6798	0.5095	0.6822	0.3923	[illegible]
1	2 2410004B18Rik		0.5674	0.3881	0.6293	0.3203	0.8702	0.4349	0.903	0.8596	0.8657
1	2 2410042D21Rik		0.4537	0.2312	0.6537	0.5054	0.3866	0.3626	0.3191	0.3744	1.0986
1	2 2410127L17Rik		0.2952	[illegible]	1.0394	0.7812	0.6971	0.8642	1.0363	0.8379	0.9438
1	2 2510003E04Rik		0.4906	0.2176	0.3201	0.3458	0.2994	[illegible]	0.3058	0.4554	0.69
1	2 Cactin		0.7172	0.5821	0.2548	0.5727	0.4729	0.5742	0.4977	0.6035	0.6318
1	2 2510039O18Rik		0.3755	0.2485	0.4153	0.3633	0.5943	0.5196	0.3871	0.7032	[illegible]
1	2 2610027L16Rik		0.3149	0.3151	0.7234	0.7828	0.7798	0.5788	0.8742	1.1551	0.949
1	2 2610318N02Rik		0.3535	0.5365	0.5066	0.5182	0.5313	0.7489	0.6884	0.6058	0.9664
1	2 2810046L04Rik		[illegible]	0.3742	0.4243	0.3501	0.433	0.7188	0.7028	0.7153	0.6159
1	2 2810432D09Rik		[illegible]	0.3961	[illegible]	0.5012	0.4736	0.7202	0.555	0.6042	0.525
1	2 2810453I06Rik		0.6539	0.5695	0.6073	0.4111	0.3791	0.2981	0.4389	0.3213	[illegible]
1	2 3230401D17Rik		0.3221	[illegible]	1.4205	0.2752	0.7248	0.2731	0.5978	0.3101	0.5147
1	2 4732418C07Rik		0.6169	0.6117	0.5519	0.4391	0.4863	0.196	0.2377	0.3724	[illegible]
1	2 4833439L19Rik		0.3209	[illegible]	0.4272	0.3672	0.3142	0.2553	0.2336	0.5026	0.5795
1	2 4921501E09Rik		0.5521	0.6217	0.428	0.5965	0.4124	0.4537	0.4988	0.5896	0.3965
1	2 4930432K21Rik		-0.5384	-0.2764	0.837	0.3348	1.2593	0.866	0.4306	0.7438	0.4528
1	2 4930453N24Rik		0.6436	0.4618	0.851	0.4946	0.6519	0.7049	0.7293	0.4448	0.6456
1	2 4930455C21Rik		0.5384	0.4527	0.4056	0.8533	0.7501	0.3813	0.6217	0.3672	1.0515
1	2 4930572J05Rik		-0.9343	[illegible]	0.6845	1.1003	0.7718	1.2187	0.8376	1.0069	[illegible]
1	2 4931406P16Rik		0.4176	0.2836	0.9548	0.6472	0.8092	0.4556	0.5216	0.9804	[illegible]
1	2 Cabs1		0.2205	[illegible]	0.5993	0.589	0.7784	1.0196	0.418	0.7872	[illegible]
1	2 4933424B01Rik		0.3508	0.4738	0.9945	0.6727	0.959	0.7465	0.9945	0.8551	0.652
1	2 5730494M16Rik		0.4623	0.5546	0.2971	0.5086	0.3604	[illegible]	0.6606	0.3072	0.8789
1	2 5830415F09Rik		0.4257	0.2729	0.1037	0.387	0.3736	0.3157	[illegible]	0.4022	0.4695
1	2 5830433M19Rik		0.2549	[illegible]	[illegible]	[illegible]	0.5104	[illegible]	0.6151	0.4196	0.7341
1	2 6030405A18Rik		-0.7547	-0.4652	1.4388	1.723	1.4594	0.9903	0.63	0.0926	-0.6433
1	2 8430408G22Rik		0.4064	[illegible]	1.734	0.7546	1.7653	0.6009	1.0213	0.7875	[illegible]
1	2 9030025P20Rik		-0.3953	-0.4844	0.4206	0.4623	0.694	0.6013	0.2962	0.5398	[illegible]
1	2 9030624J02Rik		0.3573	0.3067	0.4703	0.4104	0.4701	0.1931	0.2186	0.4072	[illegible]
1	2 9130011E15Rik		0.5072	[illegible]	0.4464	0.3161	0.4871	0.579	0.3674	0.5206	0.5709
1	2 9430015G10Rik		-0.2106	0.339	0.6043	0.5902	0.5900	0.9819	0.963	0.9956	0.7558
1	2 9930023K05Rik		-0.378	[illegible]	1.1036	1.3495	1.0894	1.3113	0.2586	1.0151	-0.4256
1	2 A230091H23		[illegible]	0.9205	1.6624	1.7299	0.5928	0.5521	0.1367	0.1450	[illegible]
1	2 A830093I24Rik		0.5496	0.6765	0.4717	0.6074	0.6532	0.5517	0.4884	0.724	0.6033
1	2 A930038C07Rik		0.3626	0.3436	0.4266	0.3867	0.6079	0.1572	0.2752	0.3946	0.428
1	2 Aaas		0.647	1.1013	0.4053	0.7492	0.6833	0.8592	1.258	1.0698	0.969
1	2 Aatf		0.3967	0.2986	0.3321	0.6796	0.3639	0.5208	0.3797	0.5858	0.768
1	2 Abca7		-0.2943	-0.2497	0.578	0.316	0.7456	0.5864	0.2425	0.7537	-0.5168
1	2 Abcb10		0.5313	0.7018	0.5018	0.369	0.6253	0.5071	0.584	0.4954	0.3952
1	2 Abcc10		0.3633	0.2688	0.4009	0.7217	0.5781	0.5723	0.2836	0.3647	0.4009
1	2 Abce1		0.1732	0.496	0.3297	0.4019	0.659	0.151	0.7382	0.4343	0.5705
1	2 Abhd2		0.1528	[illegible]	0.2345	0.5608	0.5037	0.6257	0.131	0.3397	[illegible]
1	2 Abo		[illegible]	0.2219	0.4111	0.5073	0.7755	0.4909	[illegible]	0.5202	[illegible]
1	2 Abp1		-0.9712	-1.0077	0.5226	0.9514	1.648	1.6664	1.893	1.2233	-0.9802
1	2 Abr		-0.4057	-0.4149	0.6589	0.4678	0.9639	0.7812	0.2554	0.4394	-0.4675
1	2 Acads		[illegible]	0.4899	0.314	0.3531	0.2675	0.7071	[illegible]	0.3957	0.6815
1	2 Acbd4		0.2063	0.1956	0.3578	0.3654	0.4922	0.4724	0.2101	0.3611	0.1774
1	2 Acin1		0.3017	0.418	0.7457	0.6105	0.6027	0.4192	0.6377	0.6948	0.8112
1	2 Acot10		[illegible]	[illegible]	0.8067	0.5744	0.5515	0.5482	[illegible]	0.3715	[illegible]
1	2 Acpp		-1.4973	-1.439	1.3153	1.0455	1.7463	1.2352	0.5432	0.6358	-1.3882
1	2 Acsf3		0.1209	0.2256	0.2839	0.3174	0.3469	0.5806	0.2063	0.4312	0.4213
1	2 Actn4		0.4752	0.8239	0.7641	0.6456	0.5115	0.5536	0.1949	0.1659	0.1962
1	2 Actr1b		0.108	0.5626	0.3674	0.471	0.2648	0.4289	0.2958	0.3274	0.3974
1	2 Adal		0.3697	0.2338	0.2828	0.3298	0.3102	0.276	0.3261	0.3368	0.3625
1	2 Adam10		0.3166	0.3456	0.4679	0.1303	0.4142	0.2789	0.2617	0.1647	0.3166
1	2 Adam23		0.3523	[illegible]	0.9837	0.4464	0.5139	0.5499	0.3855	0.6994	0.74
1	2 Adamts7		0.3126	0.3422	1.2536	0.957	0.7048	0.7671	0.7507	0.3177	-0.737
1	2 Adap1		[illegible]	0.2254	0.2659	0.6017	0.5478	0.7612	0.1101	0.3449	[illegible]
1	2 Adar		1.7234	0.3957	0.9642	0.1076	0.4184	[illegible]	0.6177	0.3786	0.2805
1	2 Add3		0.8314	0.3676	0.3697	0.2812	0.4221	0.3946	0.3271	0.6975	[illegible]
1	2 Adi1		0.2891	0.3267	0.795	0.7578	0.6769	0.5341	0.8057	0.6839	0.5059
1	2 Adipor1		[illegible]	[illegible]	0.8592	0.755	0.8051	0.8334	0.3542	0.6929	-0.7517
1	2 Adipor2		[illegible]	0.2759	0.9763	0.7602	0.6379	0.5715	0.5839	0.3358	0.8456
1	2 Adk		0.8144	0.8589	0.488	0.7129	0.4781	0.6792	0.6676	0.6563	0.1893
1	2 Ado		0.1553	0.4713	0.3899	0.2968	0.4423	0.418	0.2231	0.3409	0.1182
1	2 Adora1		[illegible]	[illegible]	0.1723	0.2195	0.5994	0.4343	0.1278	0.5653	[illegible]
1	2 Adra1a		0.526	0.2214	0.2357	0.3246	0.2946	0.5983	0.3823	0.4132	0.3546
1	2 Adra2b		0.4736	0.5017	0.2902	0.6861	0.6318	0.5415	0.3807	0.3589	0.319
1	2 Aebp2		0.0676	0.2507	0.4753	0.542	0.3736	0.9002	0.1868	0.2459	0.782
1	2 Agfg1		0.4193	[illegible]	0.2312	0.3869	0.5574	0.6773	0.6227	0.707	0.6955
1	2 Agpat9		0.3413	0.3798	0.3219	0.1658	0.4702	0.656	0.2446	[illegible]	[illegible]
1	2 Ahctf1		0.2549	0.2626	0.4521	0.2676	0.6518	0.6421	0.8563	0.9469	0.961
1	2 Ahcyl1		0.4006	0.6839	0.3374	0.5775	0.2973	0.4481	0.1245	0.2698	0.3282
1	2 Ahdc1		0.9038	0.7157	0.5506	0.4625	0.953	0.8062	1.2073	1.0573	0.337
1	2 Ahsa2		0.1208	0.2718	0.3276	0.2059	0.4477	0.6365	0.3687	0.204	0.1386
1	2 Ahsg		-0.4535	-0.3806	0.709	0.8632	0.806	1.5905	0.2329	0.9976	[illegible]
1	2 AI593442		0.9807	0.6531	0.8229	0.7546	1.3506	1.7874	1.4629	1.868	[illegible]
1	2 AI661453		0.1418	[illegible]	0.7488	0.1419	0.8575	0.7422	0.8799	0.9039	0.2262
1	2 AI846148		0.3343	[illegible]	0.7131	0.8432	0.7678	0.7387	0.5606	0.4936	0.2277
1	2 Aig1		0.2586	0.7139	0.923	0.8409	1.0743	0.9951	[illegible]	0.6651	-0.8166
1	2 Aip		0.6285	0.5341	0.1478	0.3376	0.2543	0.3905	0.2754	0.5782	[illegible]
1	2 Akap1		0.254	0.6091	0.4544	0.4974	0.4626	0.4856	0.8854	0.5256	1.2104
1	2 Akap8		0.3014	0.3975	0.4939	0.445	0.6141	0.36	0.6248	0.1677	0.2197
1	2 Akt1s1		1.0181	0.8993	0.7755	0.6145	0.7253	0.6918	0.3069	0.5497	-0.6148
1	2 Aldh4a1		0.7711	0.6099	0.7423	0.2219	0.3446	0.2952	0.2218	0.362	0.7225
1	2 Alg3		0.2009	0.5526	0.4664	0.8798	0.3926	0.6456	0.5942	0.6029	[illegible]
1	2 Alg9		0.2151	0.5086	0.3196	0.4683	0.4119	0.5048	0.1754	0.4545	0.352
1	2 Alkbh5		0.1571	0.388	0.4423	0.2859	0.5686	0.4091	0.6784	0.8004	0.3356
1	2 Alox12e		0.2046	0.3218	0.4166	[illegible]	0.6119	0.7526	0.6563	0.6221	[illegible]
1	2 Amd2		0.2864	0.3601	0.3618	0.374	0.4647	0.7356	0.8597	0.4401	1.2396
1	2 Amhr2		0.1895	0.3274	0.5316	0.5005	0.3874	0.3151	0.2447	0.3952	0.4159
1	2 Amz2		0.3211	0.4164	0.1824	0.2141	0.3774	0.3653	0.3609	0.4965	0.5609
1	2 Anapc5		0.317	0.5625	0.2506	0.6716	0.3296	0.7997	0.36	0.4487	0.7901
1	2 Ankrd13a		0.2175	0.388	0.7636	0.783	0.5519	0.6018	0.4481	0.5561	0.2602
1	2 Ankrd13c		0.1891	0.6	0.8603	0.6565	0.5698	0.5871	0.6524	0.5893	0.5569
1	2 Ankrd17		0.7653	0.3607	0.5606	0.1959	0.5738	[illegible]	0.4664	0.3935	0.3539
1	2 Ankrd40		0.6813	0.3166	0.4754	0.3686	0.3633	0.5629	0.2189	0.3536	0.5434
1	2 Ankrd54		0.2153	0.1145	0.2277	0.4048	0.3504	0.5468	0.41	0.3244	0.2612
1	2 Ano1		0.3054	1.1435	2.4576	2.6626	2.2254	1.7909	1.3307	1.271	-1.1918
1	2 Ano4		[illegible]	0.3091	1.9322	1.7881	1.6738	1.3147	0.8282	1.0016	[illegible]
1	2 Anp32e		-0.718	[illegible]	0.4923	0.7006	0.7331	0.9544	1.064	0.5766	0.7631
1	2 Anxa11		0.4696	0.4808	0.4357	0.3241	0.3706	0.2868	0.3696	0.6309	0.2646
1	2 Aoah		-0.3769	0.3081	1.7633	1.1857	1.0869	0.1415	0.4779	0.3752	-0.5105
1	2 Ap1g1		[illegible]	0.2052	0.3542	0.3168	0.2703	0.3818	0.4229	0.2796	0.344
1	2 Ap2a1		0.5945	0.86	0.7132	0.676	0.9437	0.9044	1.1119	0.9714	0.3978
1	2 Ap2b1		0.2441	0.2312	0.5374	0.5768	0.922	0.8021	0.5604	0.8782	0.6317
1	2 Ap3b1		0.1843	0.149	1.004	0.5922	0.5206	0.4202	[illegible]	[illegible]	[illegible]
1	2 Ap3d1		0.8376	0.6008	0.3965	0.1939	0.5245	[illegible]	0.5601	0.2248	[illegible]
1	2 Ap4b1		0.5486	0.4695	0.5861	0.8211	0.7494	0.5784	0.4578	0.5834	0.33
1	2 Ap4s1		0.5337	0.4513	0.5457	0.4931	0.3936	0.3598	0.7011	0.4313	0.2756
1	2 Apbb3		0.2452	0.2991	0.2484	0.4007	0.2462	0.3525	0.4261	0.32	0.3102
1	2 Apcs		0.1645	0.6142	0.1543	0.2588	0.5356	0.4059	0.1849	0.2093	0.3022
1	2 Apex1		-0.4461	[illegible]	[illegible]	0.6033	0.4949	0.686	1.1678	0.7589	0.4073
1	2 Apip		0.0429	[illegible]	0.3782	0.1737	0.7669	0.3075	0.1693	0.416	0.3322
1	2 Aplnr		0.2797	0.3467	0.2444	0.2469	0.2947	0.32	1.2513	0.8978	0.2737
1	2 Apobec3		0.2444	0.1885	0.8348	0.6455	1.0504	0.7569	1.0619	0.8495	1.1062
1	2 Aqr		0.5	0.3504	0.4416	0.8145	0.7776	0.747	1.3013	0.9444	0.9817
1	2 Arf5		1.1317	0.7725	0.8263	1.1601	0.8414	0.8977	0.8373	0.5774	0.4585
1	2 Arfgap2		0.3605	0.3758	0.6919	0.3165	0.7007	0.5379	0.4046	0.756	-0.5227
1	2 Arhgap26		-0.1513	-0.2466	0.9072	0.6236	0.9141	0.4125	0.1233	0.3418	-0.2558
1	2 Arhgap27		-0.3273	0.1530	0.3029	0.2945	0.3946	0.5812	0.3224	0.766	[illegible]
1	2 Arhgef1		0.1561	0.7142	0.2946	0.6362	0.6606	0.4957	0.4903	0.5554	-0.3622
1	2 Arid2		0.1557	0.1878	0.57	0.7502	0.7071	0.378	0.8252	0.5743	0.5229
1	2 Arih1		1.1042	0.4866	0.7542	0.7141	0.8964	0.6863	0.8964	0.5343	0.7064
1	2 Arih2		0.2957	0.2314	0.6467	0.3243	0.3548	[illegible]	0.5067	0.3048	0.4748
1	2 Arl4a		0.0958	[illegible]	0.9468	1.1576	1.2484	0.7561	0.4379	0.9131	[illegible]
1	2 Arl6		0.1597	[illegible]	0.6104	0.5141	0.6624	0.9887	0.8748	1.1667	1.2557
1	2 Arl6ip1		-0.4423	0.3256	0.6369	0.7555	1.2438	0.934	1.13	1.0339	0.8372
1	2 Arl6ip4		[illegible]	0.2662	0.514	0.5891	0.6014	0.4756	0.7283	0.8144	[illegible]
1	2 Armc6		0.2868	0.4942	0.3737	0.4812	0.452	0.4926	0.7705	0.5979	0.5633
1	2 Armc9		0.4229	0.3152	0.3097	0.2123	0.3767	0.4463	0.1441	0.4193	0.3732
1	2 Armcx2		1.2038	1.0429	0.3142	0.2616	-0.2218	0.2728	1.1422	0.5127	0.6124
1	2 Armcx5		0.9578	0.2678	0.5171	0.2475	0.4437	0.2798	0.6573	0.2894	0.4958
1	2 Arnt		0.2116	[illegible]	0.5361	0.2187	0.3636	0.5983	0.3243	0.2148	[illegible]
1	2 Arntl		0.5935	0.5674	1.0022	0.6945	0.7669	0.2762	0.1062	0.4355	0.2679
1	2 Arntl2		0.3144	0.3655	0.2596	0.3665	0.8275	1.0485	0.8094	0.6631	-0.2599
1	2 Arpc1a		0.2202	[illegible]	0.4597	0.2064	0.4637	0.3962	0.4432	0.1646	0.1446
1	2 Arpp21		0.1740	0.4171	1.3451	0.8575	0.3943	0.3069	0.24	0.3225	[illegible]
1	2 Arrdc2		0.4458	0.4699	0.1552	0.269	0.4619	0.5739	0.4898	0.373	0.9664
1	2 Asah1		1.0394	0.9877	0.6139	0.8202	0.5696	0.5711	[illegible]	0.4267	0.5634
1	2 Asap2		0.2213	0.3749	1.5264	1.3714	1.6968	1.5108	1.28	1.4309	-0.29
1	2 Asb12		0.2173	0.4396	0.444	0.1962	0.3172	0.3752	0.1942	0.2806	0.2464

1	2	Asb3	0.8231	0.458	0.4135	0.3991	0.2762	0.6039	0.4476	0.3502	0.6399
1	2	Ascc1	0.1515	0.5085	0.3982	0.5646	0.5792	0.6759	0.6008	0.7133	0.2794
1	2	Asf1a	0.0735	0.0632	0.4417	0.4056	0.217	0.2308	0.2445	0.4377	0.4437
1	2	Asph	0.1684	0.4021	0.297	0.1186	0.3943	0.2046	0.3109	0.3759	0.1715
1	2	Asprv1	-0.5893	-0.7711	0.1555	0.0682	1.0922	1.2496	0.8079	1.4283	-0.6483
1	2	Aspscr1	0.2812	[illegible]	0.5095	0.303	0.6306	0.2101	0.7812	0.5742	0.9354
1	2	Aste1	0.6535	[illegible]	0.6681	0.2848	0.4981	0.2478	0.3858	0.2216	0.3146
1	2	Atad2	0.2924	0.1284	0.4546	0.7027	0.507	0.9389	0.859	0.369	1.1069
1	2	Ate1	0.4085	0.1982	0.4192	0.2024	0.3942	0.396	0.4139	0.4454	0.8845
1	2	Atf2	0.644	0.2329	0.7271	0.7795	0.6571	0.8621	0.6752	0.7747	0.759
1	2	Atf7ip	0.2547	0.0938	0.5041	0.5459	0.601	0.5316	0.7209	0.4117	0.1945
1	2	Atg3	1.3182	0.7552	0.789	0.9692	0.7561	0.3358	0.5566	0.3339	-0.2087
1	2	Atg5	-0.1215	0.2186	0.3024	0.5803	0.561	0.4213	0.6496	0.4505	0.2228
1	2	Athl1	0.7596	0.3323	0.6706	0.5372	0.4798	[illegible]	0.2597	0.3303	0.2452
1	2	Atl2	0.0971	0.1976	0.3602	0.3376	0.2558	0.2767	0.2618	0.3933	0.3031
1	2	Atl3	0.9029	0.6655	0.5755	0.6276	0.5086	0.3337	0.2848	0.3626	-0.2812
1	2	Atm	0.4335	0.8107	0.5803	0.8	0.7051	0.8133	0.9432	0.9988	0.118
1	2	Atn1	1.9084	1.1611	1.3746	0.9262	1.0904	0.4496	0.8556	0.8734	-0.4163
1	2	Atp10a	0.3646	0.4001	1.1605	0.9767	0.7409	0.5275	0.2538	0.388	-0.5949
1	2	Atp2c1	0.1437	0.2457	0.6399	0.7604	0.4104	0.8867	0.0703	0.149	0.2596
1	2	Atp5g2	0.1224	0.3832	0.4363	0.392	0.5011	0.7203	0.6072	0.5653	0.4104
1	2	Atp5j	0.219	0.4054	0.4194	0.7062	0.479	0.6982	0.5545	0.6046	0.6484
1	2	Atp5l	0.5419	0.0872	1.073	0.5235	0.2885	[illegible]	0.5452	0.273	0.3154
1	2	Atp6ap2	0.5518	0.246	0.4659	0.5426	0.3003	0.3758	0.5375	-0.1359	0.8022
1	2	Atp6v0d1	0.7578	0.4834	0.2257	0.0745	0.3703	0.282	0.2856	[illegible]	0.9084
1	2	Atrx	0.3028	0.7157	0.4489	0.5093	0.5838	0.7007	0.6185	0.5289	0.8366
1	2	Atxn10	0.5457	0.6985	0.1506	[illegible]	0.3409	[illegible]	0.7533	0.1012	0.448
1	2	Atxn2l	0.4522	0.3489	0.4782	0.2558	0.4627	0.4042	0.4713	0.461	0.5503
1	2	Mipol1	-0.3709	0.0549	0.3206	0.7464	0.4074	0.5415	0.6169	0.3916	0.504
1	2	Aup1	0.4749	0.8527	0.5658	0.8886	0.6704	0.7615	0.2855	0.1848	[illegible]
1	2	Azi2	0.6766	0.4214	0.3736	0.3897	0.2766	0.431	0.1145	0.2236	0.3654
1	2	B230118H07Rik	0.2343	0.3921	0.4358	0.3212	0.2588	0.2918	0.4223	0.35	0.1515
1	2	B3gnt3	-0.2305	-0.2242	0.3754	0.4265	0.8405	0.9659	0.4424	0.7407	-0.2886
1	2	B4galt3	-0.0402	0.248	-0.0948	0.4456	0.6163	0.6111	0.4882	0.3896	0.5074
1	2	B630005N14Rik	0.6288	0.5076	0.6873	0.7528	0.7158	0.4858	0.5986	0.6567	0.1694
1	2	Bach2	0.5373	0.3728	0.6286	0.3728	0.4073	0.5086	0.3538	0.7222	-0.7335
1	2	Bag6	0.3605	0.0738	0.2682	0.301	0.2896	0.4529	0.4004	0.7402	0.6351
1	2	Bahcc1	1.0751	0.8518	0.4141	0.4542	0.1665	0.3463	0.3103	0.8054	1.0613
1	2	Banf1	0.0341	0.275	0.4457	0.719	0.5499	0.9889	0.6763	0.8437	1.3497
1	2	Bap1	0.2291	0.0756	0.4013	0.1804	0.4556	0.0945	0.599	0.4517	0.3346
1	2	Baz1a	-0.8597	-0.3583	1.1015	1.0625	0.8293	1.0028	0.2085	0.7539	-0.5401
1	2	Bbc3	1.1364	0.3202	1.3317	0.6738	0.9014	0.8388	0.7917	0.9736	0.8986
1	2	BC016423	0.3686	0.2836	[illegible]	0.2687	0.3451	0.5037	0.8375	0.5051	0.4591
1	2	BC026585	-0.5528	[illegible]	0.2327	0.4695	0.7691	0.6824	0.3424	0.4117	[illegible]
1	2	BC027231	[illegible]	0.1893	0.6117	0.3636	0.8067	0.5159	0.9345	0.7703	0.6422
1	2	BC030867	0.1409	0.5189	0.3327	0.5468	0.4357	0.655	0.9198	0.5596	1.0824
1	2	BC046331	-0.0749	0.1427	0.3815	0.6269	0.7746	0.8445	0.719	0.6992	0.0992
1	2	BC053749	0.09	0.1041	0.242	[illegible]	0.3878	0.2799	1.0011	0.5835	0.3578
1	2	Bcar1	0.6678	0.5257	0.6692	0.5655	0.6405	0.4647	0.8894	0.8987	0.373
1	2	Bckdhb	0.5484	0.4099	0.6966	0.7926	0.9629	0.5879	1.3108	0.7859	0.34
1	2	Bckdk	-0.1096	0.1861	0.1569	0.1878	0.4687	0.5971	0.4166	0.5351	0.4152
1	2	Bcl2l1	0.8488	0.8018	0.4655	0.5012	0.2894	0.2814	0.5775	0.2665	[illegible]
1	2	Bcl2l12	-0.2054	-0.0831	0.225	0.3136	0.4059	0.6733	0.4447	0.7	-0.3858
1	2	Bcor	0.3538	0.2218	1.022	0.9072	1.2412	1.1675	1.2394	1.1477	0.0736
1	2	Becn1	[illegible]	[illegible]	0.4772	0.5091	0.4525	0.282	0.1583	0.2061	0.2128
1	2	Bhmt2	0.0377	0.0742	0.947	0.8014	1.0793	0.6854	0.5163	0.6079	0.4795
1	2	Bicd2	0.5934	0.4507	0.6574	0.5141	0.5525	0.126	0.1649	0.447	-0.1325
1	2	Bmp8b	0.0857	0.152	0.3187	0.8282	0.2895	0.7984	0.2895	0.9089	0.0673
1	2	Bmpr1a	0.8442	0.579	0.4173	0.3016	0.4184	0.561	0.562	0.5046	0.1613
1	2	Bnc2	1.3122	0.1926	0.1348	0.0985	0.2326	0.5873	0.3893	0.4567	0.7531
1	2	Bok	0.2325	0.5412	0.3963	0.1878	0.1649	0.4983	0.3463	0.4891	0.3102
1	2	Bpnt1	0.1432	0.1529	0.401	0.8684	0.3496	0.6252	0.3085	0.2135	0.5077
1	2	Brca1	0.1321	0.0765	0.615	0.5283	0.877	0.6374	0.9488	0.8667	0.9537
1	2	Brcc3	0.4894	0.342	0.3773	0.5765	0.7043	0.342	0.6248	0.6231	0.5748
1	2	Brd2	0.5231	0.3221	0.9568	0.4411	0.3904	0.4338	0.4848	0.4712	[illegible]
1	2	Brd4	0.3688	0.4457	0.585	0.4367	0.5016	0.9033	0.7601	0.7238	0.8771
1	2	Bre	0.4602	0.414	0.4789	0.3454	0.5202	0.2894	0.3626	0.4824	-0.3102
1	2	Brix1	-0.211	0.1167	0.4494	0.5566	0.4078	0.7112	0.5328	0.5674	0.7821
1	2	Btbd3	0.4979	0.3336	1.1332	0.9333	0.3374	0.5057	[illegible]	[illegible]	-0.1692
1	2	Btla	0.2867	0.2705	1.1568	0.6896	0.6364	0.1643	0.2844	[illegible]	0.1159
1	2	Btrc	0.3163	0.3253	0.1841	[illegible]	0.411	0.1047	0.7804	0.4438	-0.1518
1	2	Bub3	0.3448	0.55	0.7948	0.9946	0.96	1.1705	1.2335	1.2213	0.3595
1	2	Bzw1	-0.1579	[illegible]	0.2985	0.2838	0.5136	0.5993	0.4292	0.2921	-0.1869
1	2	C230029F24Rik	0.4497	0.485	0.5364	0.5737	0.5819	0.4652	0.314	0.3599	0.3286
1	2	Emc1	[illegible]	-0.0551	0.3322	0.4311	0.3844	0.3199	0.5918	0.465	0.1234
1	2	C2cd3	0.1339	0.1199	0.3149	0.3593	0.5855	0.2941	0.7427	0.5823	0.1606
1	2	Prr14l	-0.0968	[illegible]	0.2186	0.2497	0.6018	0.2802	0.2343	0.4685	0.0565
1	2	Cabp4	0.0885	0.2074	0.1011	0.1837	0.3912	0.1778	0.5075	0.531	0.0885
1	2	Cacnb3	0.6466	0.7162	0.7776	1.0114	0.478	0.1546	0.2175	0.0834	-0.1009
1	2	Cacybp	0.1577	0.1003	0.834	0.8406	1.0463	1.0911	1.0819	1.0939	0.6724
1	2	Cad	-0.4208	0.5183	0.4876	0.7735	0.6186	0.752	0.7882	1.0758	0.5295
1	2	Calm2	1.2185	0.986	1.146	0.8147	1.0497	0.4568	1.2806	0.8805	0.7315
1	2	Calr	1.5158	1.1635	1.3692	0.9524	0.8513	1.1112	0.8342	0.8398	0.9203
1	2	Camk2d	0.9778	0.6158	1.2236	0.9137	1.0178	0.8241	0.3225	0.5346	-1.0849
1	2	Capn7	0.2875	0.197	0.5098	0.4918	0.4192	0.1421	0.3702	0.2634	0.4001
1	2	Capn8	0.1478	0.129	0.4909	0.3994	0.1634	0.3595	0.415	0.4176	0.2327
1	2	Caprin1	[illegible]	[illegible]	0.4168	0.4243	0.6482	0.1899	1.1342	0.605	0.5687
1	2	Card10	-0.3476	0.1294	0.9978	0.607	1.0661	1.0736	0.8438	1.3373	-0.594
1	2	Carm1	0.6194	0.5823	0.5806	0.7407	0.6449	0.9366	0.8709	0.8368	0.2991
1	2	Cbx2	-0.1615	0.4439	0.0622	0.5564	0.3236	0.4854	1.0784	0.9786	0.8829
1	2	Ccdc109a	0.3531	0.2737	0.4961	0.5352	0.4866	0.6484	-0.0433	0.1826	[illegible]
1	2	Ccdc125	-0.057	-0.025	0.3484	0.3063	0.4987	0.5291	0.6004	0.5901	0.5504
1	2	Ccdc25	0.3351	0.1626	0.2262	0.3403	0.3799	[illegible]	0.7864	0.5064	0.4445
1	2	Ccdc66	0.4511	0.5211	0.3975	0.4966	0.5104	0.1509	0.1932	0.7313	0.7701
1	2	Ccdc72	0.2666	0.3815	0.4273	-0.067	0.6322	0.064	0.9132	0.6676	0.6045
1	2	Ccdc86	-0.1806	0.0994	0.3527	0.649	0.5797	0.5845	0.9004	0.6351	0.2413
1	2	Ccdc90b	0.5798	0.4312	0.1062	-0.1221	0.4335	[illegible]	0.4805	0.2928	0.5549
1	2	Cchcr1	0.4333	0.6179	0.4164	0.4366	0.6855	0.7527	0.705	0.6663	0.4469
1	2	Ccnd3	0.7638	0.6818	0.5876	0.666	0.3391	0.7913	0.1981	[illegible]	0.9794
1	2	Ccng1	0.466	0.9041	[illegible]	0.8573	0.5758	0.8544	0.6664	0.8494	0.8361
1	2	Ccnl1	1.3902	0.449	1.4936	0.3661	1.1461	0.3971	0.7024	0.449	-0.1426
1	2	Ccnt1	0.3727	0.248	0.4424	0.1394	0.6064	0.4454	0.5891	0.6867	-0.1744
1	2	Ccrn4l	1.4386	-0.1739	1.2497	-0.1992	[illegible]	-0.1555	0.5926	[illegible]	0.6446
1	2	Cct2	0.1343	0.302	0.4638	0.4046	0.4404	0.2219	0.2837	0.2572	0.7903
1	2	Cct5	0.3452	0.295	0.5855	0.4732	0.7998	0.6452	0.8299	0.6777	0.6088
1	2	Cct8	-0.1732	0.4391	0.6009	0.6258	0.8643	0.7066	0.9775	0.6368	0.9846
1	2	Ccz1	0.1068	[illegible]	0.358	0.3227	0.7697	0.3413	0.4781	0.4387	0.3837
1	2	Cd24a	-0.0754	[illegible]	0.6092	0.2892	0.6208	0.4246	0.2278	0.306	-0.178
1	2	Cd3eap	-0.3316	0.5202	0.4431	0.5255	0.3135	0.894	0.0721	0.078	0.4071
1	2	Cd3g	0.1123	0.0698	1.1851	0.3759	0.8113	0.2194	0.5549	0.2659	0.2716
1	2	Cd44	-0.1593	-0.1377	0.4338	0.4851	0.4764	1.0241	0.0712	0.3504	-0.4404
1	2	Cd59a	-0.3047	-0.2998	1.0466	1.2253	1.2588	1.0947	1.0676	1.1803	-1.2528
1	2	Cd80	0.4394	1.0129	0.4093	0.9153	0.2141	0.5984	0.1296	0.3403	-0.1392
1	2	Cdc25a	-0.0466	[illegible]	0.3633	0.5824	0.6157	1.043	0.8331	0.8314	1.2731
1	2	Cdc25b	-0.4331	0.2342	0.4896	0.4523	0.4733	0.766	0.1171	0.5245	-0.0867
1	2	Cdc37l1	0.5177	0.2989	0.1787	0.1131	0.215	0.1541	0.4685	0.5031	0.324
1	2	Cdc42ep5	0.7364	0.8285	1.2379	1.3624	1.0486	1.1401	0.5694	1.087	-1.3066
1	2	Cdc42se1	0.181	0.2233	0.3691	0.4005	0.6752	0.6367	0.154	0.4301	-0.2373
1	2	Cdca4	[illegible]	0.9039	0.6765	0.7764	0.5897	1.0019	0.7207	0.7614	1.218
1	2	Cdk1	-0.5821	[illegible]	0.6858	0.9372	0.8936	1.0866	0.9909	0.9587	0.8269
1	2	Cdk11b	0.4448	0.2436	0.7333	[illegible]	0.4832	0.557	0.9407	0.5225	[illegible]
1	2	Cdk13	0.3732	[illegible]	0.5649	0.3083	0.4791	0.4405	0.5418	0.5104	0.3713
1	2	Cdk2ap1	[illegible]	[illegible]	[illegible]	0.5508	0.395	0.4568	0.9919	0.5135	[illegible]
1	2	Cdk5rap1	0.213	[illegible]	[illegible]	0.456	0.3436	0.5974	[illegible]	0.4337	0.7666
1	2	Cdkn2aipnl	-0.5944	[illegible]	0.4977	0.6719	0.7387	0.8589	0.9165	0.8893	0.9015
1	2	Cdr2	1.0679	0.9855	0.2329	0.3711	-0.1411	0.3221	0.3464	0.283	0.6794
1	2	Cdv3	[illegible]	[illegible]	0.6319	0.463	0.7468	0.4737	1.2609	0.887	0.4962
1	2	Cdyl	0.1288	0.2695	0.9529	1.0119	0.9595	1.1397	0.7356	1.165	0.5654
1	2	Celsr2	-0.7117	-0.2085	0.5419	0.4849	0.3612	0.2945	0.3316	0.3633	-0.5165
1	2	Cend1	0.477	0.1574	0.1807	0.5041	0.4133	0.2084	0.2854	0.1988	0.3764
1	2	Cep164	0.1476	0.21	0.568	0.2679	0.2987	0.3529	0.3552	0.5236	0.5336
1	2	Cep57	[illegible]	0.1299	0.5402	0.4431	0.6828	0.6783	0.7508	0.8415	1.2136
1	2	Cep63	0.3834	0.3654	0.3776	0.518	0.2828	0.5132	[illegible]	[illegible]	[illegible]
1	2	Cetn2	[illegible]	[illegible]	0.3515	0.2365	0.3727	0.1333	0.0686	0.5542	0.3059
1	2	Cfl1	0.8545	0.8848	1.6404	1.1933	1.1016	0.9856	0.8417	0.912	-0.5611
1	2	Chchd7	0.6682	0.1101	0.4441	0.2815	0.7739	0.3224	1.0612	0.84	0.2531
1	2	Chd1	0.5798	[illegible]	0.323	0.3904	0.7483	0.8054	0.7772	0.6956	-0.4969
1	2	Chd1l	-0.1655	-0.2126	0.5569	0.7685	0.5131	0.6383	0.3455	0.683	0.9679
1	2	Chd4	-0.2463	-0.1478	0.2064	0.2862	0.5903	0.4613	0.7501	0.5095	[illegible]
1	2	Chek1	[illegible]	0.3321	0.2582	0.5602	0.6037	0.7267	1.1037	0.8989	0.9185
1	2	Chga	0.5005	0.3656	0.3492	0.36	0.3776	0.4096	0.452	[illegible]	0.4179
1	2	Chic2	0.7406	0.6419	0.5488	0.8083	0.5544	0.7885	0.4819	0.4537	[illegible]
1	2	Chrnb1	-0.2744	[illegible]	0.934	0.7426	0.5867	0.4042	0.3912	0.4791	[illegible]
1	2	Chst1	-0.2722	0.7736	[illegible]	-0.3076	1.0078	0.3617	2.7294	1.8909	-0.496
1	2	Chst3	0.5316	1.457	1.5974	1.8158	0.6119	0.8708	0.4739	0.9229	0.7725
1	2	Chtf8	[illegible]	[illegible]	[illegible]	0.629	0.4211	[illegible]	[illegible]	[illegible]	[illegible]
1	2	Chuk	0.6064	0.2828	0.4221	0.3786	0.3483	[illegible]	0.5766	[illegible]	0.6363
1	2	Cic	0.9196	0.3481	0.437	0.2406	0.6263	0.3182	0.5455	0.6111	[illegible]
1	2	Cited2	0.7927	0.5041	0.9106	0.4254	0.5866	0.363	0.7019	[illegible]	[illegible]
1	2	Cited4	[illegible]	[illegible]	[illegible]	[illegible]	0.7049	0.6212	0.8926	0.7363	[illegible]
1	2	Clasrp	0.5326	0.5594	0.3467	0.6402	0.7257	0.6559	0.5792	0.5743	[illegible]
1	2	Clcn2	0.2236	[illegible]	0.3748	0.3806	0.5446	0.602	0.0609	1.0958	0.9174
1	2	Cldn25	1.1138	0.8898	0.6996	0.4759	0.5762	0.5942	0.3456	0.3671	-0.4515
1	2	Cldn5	[illegible]	0.33	1.8594	1.0811	2.3024	1.6372	1.1195	0.6899	[illegible]
1	2	Clec16a	0.8857	0.5987	0.4436	0.3534	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
1	2	Clic3	-0.7759	0.4621	1.044	1.1591	1.2032	1.295	0.3209	1.5288	-1.1875
1	2	Clock	0.5636	0.3077	1.3299	0.6024	0.8963	0.5033	[illegible]	0.4298	-0.3855
1	2	Clstn1	0.9546	0.7228	0.5309	0.7797	0.6026	0.7309	0.5227	0.4656	[illegible]
1	2	Cltb	0.2466	[illegible]	0.982	1.1358	0.9625	1.0153	0.4286	0.8336	-0.9647
1	2	Cml2	[illegible]	[illegible]	0.5099	0.5236	0.5752	[illegible]	0.4411	0.3254	[illegible]
1	2	Cml3	0.1377	0.1326	0.9193	1.0181	0.5113	0.8581	0.4052	0.1868	[illegible]
1	2	Cmtm7	0.1898	0.3101	0.9081	0.9353	0.907	0.6503	-0.2906	0.2941	-0.47
1	2	Cnnm2	0.2801	0.1788	0.9057	0.4217	0.8279	0.5686	0.4409	0.3476	1.0021
1	2	Cnnm3	0.1001	[illegible]	0.3828	0.3622	0.5408	0.8724	0.3397	0.4202	[illegible]

1	2	Cnot3	0.2314	0.4624	0.6218	0.7262	1.0833	1.0139	0.9699	1.2611	0.3912
1	2	Cntf	0.7496	0.5002	1.134	0.8648	0.8282	0.8359	0.7031	0.7238	0.6215
1	2	Cobl	-0.7698	0.0794	1.5639	1.5052	0.9362	0.4745	0.0459	0.1823	0.9014
1	2	Cog2	0.3895	0.1018	0.3194	0.3462	0.4039	0.2973	0.3536	0.3495	0.6985
1	2	Col4a3bp	0.3562	0.4225	0.351	0.3352	0.3562	0.3795	0.4472	0.3139	0.3718
1	2	Cops4	-0.3055	-0.1507	0.6985	0.6623	0.6858	0.7754	0.4798	0.4916	-0.2808
1	2	Cops5	0.0436	[illegible]	0.2703	0.3417	0.36	0.4571	0.6203	0.7055	0.2193
1	2	Cops7a	-0.1012	0.1537	0.3677	0.3578	0.4493	0.6039	0.2984	0.5083	-0.0508
1	2	Cops7b	0.2475	0.5963	0.3778	0.4275	0.4579	0.5979	0.5842	0.5203	0.9103
1	2	Copz1	0.2471	0.6199	0.3548	0.3641	0.548	0.5141	0.7825	0.6704	0.4998
1	2	Cox18	0.2161	0.3655	0.4021	0.5542	0.6092	0.7267	0.5403	0.4161	0.6006
1	2	Cox6b2	0.8629	0.8697	0.5165	0.6079	0.4971	0.9118	0.6857	0.9717	1.2999
1	2	Cox6c	0.702	0.5388	0.7492	0.2532	0.4792	0.1861	0.6076	0.3059	0.4316
1	2	Cox7a2	0.0697	[illegible]	0.4659	0.4682	0.5473	0.4442	0.905	0.5847	0.6378
1	2	Cpox	0.3213	0.1142	0.2946	0.4477	0.2341	0.1563	0.575	0.3292	0.1914
1	2	Cpsf1	-0.0532	0.4549	0.3055	0.5189	0.8375	0.5224	1.3161	0.5103	0.933
1	2	Cpsf2	[illegible]	0.3949	0.2343	0.3642	0.5218	0.7024	0.5593	0.6006	0.4677
1	2	Cpsf3	0.2415	0.4191	0.5484	0.4191	0.4627	0.484	0.5991	0.6895	0.6854
1	2	Cpsf6	0.1694	0.3785	0.585	0.4617	0.4525	0.6954	0.8841	0.4709	1.074
1	2	Cpsf7	0.3246	0.1934	0.2247	0.1203	0.3335	0.2484	0.5386	0.6839	0.3063
1	2	Crebbp	0.1879	0.1058	0.3169	0.3219	0.2812	0.1824	0.3068	0.4491	0.2473
1	2	Cript	0.4999	0.4036	0.5391	0.323	0.3222	0.1833	0.4862	[illegible]	[illegible]
1	2	Crkl	0.6048	0.6438	0.743	0.5949	0.8192	0.9205	0.8319	0.9387	1.1516
1	2	Crocc	0.3643	0.1384	[illegible]	[illegible]	0.4776	0.3865	1.0407	0.7492	[illegible]
1	2	Crybg3	0.4119	0.3251	1.3439	0.8248	1.1101	0.8583	0.6027	0.9551	[illegible]
1	2	Cryz	[illegible]	[illegible]	0.6064	0.7807	0.4324	0.4164	[illegible]	[illegible]	[illegible]
1	2	Cse1l	0.4556	0.2935	0.4664	0.6223	1.0964	0.5822	1.1858	1.1352	0.8816
1	2	Csnk1d	0.3674	0.2493	0.4287	0.459	0.6596	0.9499	0.5625	0.2843	0.8534
1	2	Csrnp1	2.948	1.019	3.4073	1.2576	2.3362	1.1397	1.2623	1.4228	-0.5836
1	2	Ctdp1	[illegible]	[illegible]	0.5229	0.5381	0.3217	[illegible]	1.0198	0.4472	[illegible]
1	2	Ctnnbip1	0.9689	0.7293	0.5672	0.6407	0.3415	0.7241	0.9117	0.9096	0.3726
1	2	Ctnnbl1	[illegible]	0.2778	0.6793	0.4978	0.46	0.854	0.8104	0.9657	1.0543
1	2	Ctps	[illegible]	0.5318	0.2923	0.5262	0.3975	0.4857	0.2644	0.5267	0.6642
1	2	Cuedc2	0.6372	0.6033	0.4223	0.5977	0.8111	0.4635	0.6072	0.3587	0.2268
1	2	Cul1	0.3882	0.2975	0.6439	0.334	0.4812	[illegible]	0.5832	0.3305	[illegible]
1	2	Cul3	0.5385	0.4687	1.1462	0.6444	1.0237	0.6815	0.6588	0.5798	0.5165
1	2	Cuta	0.6989	0.3803	0.4406	0.3792	0.4278	0.2405	0.6822	0.6323	[illegible]
1	2	Cuzd1	0.2858	[illegible]	0.268	0.6012	0.5989	0.393	[illegible]	0.3656	[illegible]
1	2	Cxadr	[illegible]	-0.5815	0.8271	0.6365	0.6186	0.7052	0.4171	0.5526	[illegible]
1	2	Cxxc1	1.1513	0.7733	0.7483	0.8379	1.0042	0.7207	1.4916	1.0446	[illegible]
1	2	Cyb561	[illegible]	[illegible]	0.4827	0.3367	0.6118	0.5622	[illegible]	0.8278	[illegible]
1	2	Cyb5b	[illegible]	0.5535	0.4368	0.6131	0.2427	0.2514	0.3333	0.3765	[illegible]
1	2	Cyc1	[illegible]	[illegible]	0.3583	0.4879	0.7128	0.6463	0.6959	0.9773	0.8158
1	2	Cycs	[illegible]	[illegible]	0.3686	0.5654	0.8561	0.4356	0.7928	0.8163	[illegible]
1	2	Cyfip1	0.0997	0.415	0.6418	0.7115	0.3382	0.7873	0.2954	0.7854	[illegible]
1	2	Cyp20a1	0.442	0.9887	0.7625	0.6731	0.858	0.8953	0.5636	0.4472	[illegible]
1	2	Cyp2b23	[illegible]	[illegible]	[illegible]	[illegible]	0.7176	1.0819	0.7508	0.8068	[illegible]
1	2	Cyp2j9	1.2258	0.3955	1.0914	0.5962	0.9939	[illegible]	[illegible]	[illegible]	[illegible]
1	2	Cyp2s1	-1.6384	-1.415	[illegible]	0.4971	0.9412	1.6274	1.2538	1.6927	-0.6614
1	2	D10Wsu102e	[illegible]	[illegible]	0.6543	0.3624	0.6966	0.5012	0.6193	0.6573	[illegible]
1	2	D10Wsu52e	[illegible]	0.1956	0.3725	0.571	0.2789	0.4523	0.4899	0.405	[illegible]
1	2	D130040H23Rik	0.6212	0.4127	[illegible]	0.1986	0.3425	0.5881	0.4338	0.5309	[illegible]
1	2	D14Ertd668e	1.9978	0.4413	1.3313	[illegible]	0.4201	[illegible]	0.5155	[illegible]	2.2011
1	2	D17H6S56E-5	0.588	0.6067	0.7035	0.4407	0.619	0.4817	[illegible]	[illegible]	[illegible]
1	2	D19Ertd737e	0.2296	0.3743	0.4005	0.1308	0.342	0.1276	0.406	0.3785	0.2185
1	2	D230037D09Rik	[illegible]	[illegible]	0.6094	0.2959	0.3367	0.2952	0.2027	0.3775	0.4392
1	2	D3Ertd751e	0.46	0.2786	0.3626	0.3097	0.3421	0.2765	0.3457	0.3206	0.5386
1	2	D8Ertd82e	0.7972	0.2205	1.2815	0.4408	0.751	0.7236	0.7033	0.9417	[illegible]
1	2	D930014E17Rik	0.713	0.5832	0.5127	0.5283	0.6198	0.5902	0.3789	0.6671	0.4722
1	2	D930015E06Rik	[illegible]	[illegible]	0.8195	1.0107	1.0129	1.2283	0.4816	1.1781	-0.536
1	2	Dab1	[illegible]	0.1975	0.7776	0.5384	[illegible]	[illegible]	0.4944	[illegible]	[illegible]
1	2	Dapk1	0.6282	0.224	0.3053	0.6258	0.224	0.2926	0.8565	0.8043	[illegible]
1	2	Dars	0.3898	0.2656	0.6308	0.4999	0.7021	0.7612	0.7797	0.6192	0.816
1	2	Daxx	0.9963	0.3864	0.886	0.5345	0.9526	0.632	1.0027	0.9787	1.0147
1	2	Dazap1	[illegible]	[illegible]	0.5958	0.5005	0.985	0.7501	1.0878	0.7847	0.9647
1	2	Dcaf10	0.7415	0.3869	0.4855	0.4299	0.4561	0.4218	0.4167	0.3137	[illegible]
1	2	Dcaf13	[illegible]	0.3143	0.4341	0.3229	0.8181	0.5851	1.1699	0.6146	0.6709
1	2	Dcaf4	0.6009	0.5764	0.3619	0.5679	0.8328	0.6181	1.1028	0.6144	1.1533
1	2	Dclk2	[illegible]	[illegible]	0.8491	1.0502	0.4394	0.311	[illegible]	[illegible]	0.8573
1	2	Dcp1a	[illegible]	[illegible]	0.3488	0.3298	0.4322	0.3219	0.5191	0.5547	0.3323
1	2	Ddi2	0.3452	0.2198	0.4438	0.4106	0.3842	0.3078	[illegible]	0.2862	0.5436
1	2	Ddx1	[illegible]	0.5201	0.4442	0.3979	0.7293	0.7656	0.9358	0.9328	0.4676
1	2	Ddx19a	0.6244	0.6201	0.5753	0.7565	1.0218	0.6846	1.1951	0.9011	0.2848
1	2	Ddx24	0.7392	0.8895	0.9568	0.8659	0.7197	0.8552	0.6735	[illegible]	0.7114
1	2	Ddx46	[illegible]	[illegible]	0.6131	0.3952	0.8088	0.7012	1.0455	0.8492	1.0659
1	2	Ddx5	0.8587	0.8053	0.8378	0.915	0.7445	1.2185	0.6754	[illegible]	1.5126
1	2	Ddx51	0.2601	[illegible]	0.4348	0.5226	0.7804	0.7295	0.7577	0.7197	0.6711
1	2	Ddx52	0.3609	0.2292	0.7566	0.4634	0.8952	0.8329	0.604	0.9016	0.7973
1	2	Ddx54	[illegible]	[illegible]	[illegible]	0.4582	0.9033	0.7958	0.8516	1.1074	1.0094
1	2	Ddx58	1.651	[illegible]	1.0576	[illegible]	0.6946	[illegible]	0.4741	[illegible]	[illegible]
1	2	Dedd2	-0.6133	-0.6705	0.7218	0.1336	0.9218	[illegible]	[illegible]	0.4599	[illegible]
1	2	Defa-rs2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.4979	0.5153	[illegible]
1	2	Dek	[illegible]	[illegible]	[illegible]	0.4502	0.7044	[illegible]	[illegible]	0.3727	0.507
1	2	Dgka	-0.9192	-0.5007	1.1674	1.101	1.1951	1.1121	[illegible]	0.7964	-0.8243
1	2	Dgkk	0.4553	0.5171	[illegible]	[illegible]	[illegible]	[illegible]	2.446	1.4507	[illegible]
1	2	Dhcr24	0.2704	[illegible]	0.3454	0.3731	0.3866	0.4552	1.1919	0.598	0.3887
1	2	Dhcr7	0.3716	[illegible]	0.5327	0.644	0.5406	0.6007	0.9851	1.014	0.8248
1	2	Dhrs11	-0.1546	0.3615	1.0039	0.9692	0.6779	[illegible]	[illegible]	0.4698	[illegible]
1	2	Dhrsx	0.444	0.4685	0.9507	0.7581	1.0799	0.9835	1.2769	0.7148	-0.4352
1	2	Dhx29	0.3318	0.5735	0.4531	0.4977	0.4364	0.6472	0.7702	0.7342	1.2009
1	2	Dhx35	0.3923	0.2144	0.6797	0.5098	0.6247	0.756	0.8258	0.8216	0.6455
1	2	Dhx9	0.5065	0.4619	0.4225	0.5314	0.4488	0.7855	0.9392	0.496	0.8693
1	2	Diap1	-0.081	[illegible]	0.7883	0.755	0.7065	0.9101	0.863	0.742	1.3567
1	2	Dido1	0.0663	-0.1939	0.5661	0.5426	0.8713	0.2106	0.4042	0.5426	0.5111
1	2	Dis3	0.6145	0.5315	0.8297	0.5506	1.0062	0.499	1.2543	1.1086	1.0913
1	2	Dis3l2	-0.5549	-0.2137	1.2117	1.1451	0.7421	0.96	0.0963	0.36	-0.0984
1	2	Dmrtc1b	-0.1424	-0.1141	0.2727	-0.0865	0.439	0.4485	0.7902	0.4485	0.1442
1	2	Dmtf1	0.3012	0.139	0.5949	0.1147	0.5275	0.1688	0.4972	[illegible]	0.4831
1	2	Dmwd	0.2915	0.5817	0.6108	0.4489	0.5004	0.7237	0.7653	0.8681	0.6357
1	2	Dnaja2	0.3442	0.1664	0.7068	0.4961	0.4277	0.3716	0.5563	0.1987	0.6277
1	2	Dnajb6	[illegible]	0.3641	0.3282	0.3082	0.5802	0.6505	0.7201	0.6732	0.9836
1	2	Dnajc15	0.1904	-0.079	0.6131	0.457	0.8527	0.4969	0.6891	0.631	0.2216
1	2	Dnajc8	0.187	0.293	0.4884	0.6866	0.9676	0.6309	0.7746	0.5939	1.0498
1	2	Dock1	0.4877	0.5821	0.3642	0.4703	0.4349	0.4474	0.465	0.5813	-0.2754
1	2	Dok2	-1.3806	-1.305	0.5285	0.2614	1.0053	1.3573	0.9671	1.5207	-0.3504
1	2	Dos	0.4462	0.2368	0.5694	0.1848	0.6166	0.4157	0.5168	0.428	-0.193
1	2	Dot1l	0.6222	0.301	0.5107	0.4425	0.5895	0.3532	0.4071	0.3461	0.9761
1	2	Dph5	0.4428	0.3364	0.3219	0.6346	0.2925	0.4316	0.4583	0.3813	0.5461
1	2	Dpp9	0.4065	0.3519	0.063	0.2243	0.3911	0.2987	0.6633	0.2049	[illegible]
1	2	Dpysl2	0.087	0.3879	0.1072	0.4204	0.1818	0.4522	0.2438	0.556	0.1496
1	2	Drg2	0.1269	0.4292	0.3417	0.5863	0.0875	0.5454	0.4709	0.6909	0.103
1	2	Drosha	0.0841	0.29	0.4711	0.5736	0.41	0.354	0.5177	0.6519	0.6972
1	2	Dst	0.1847	0.3015	1.3052	0.6552	1.228	0.1789	0.5414	0.2825	-0.5726
1	2	Dus2l	0.4523	0.5046	0.2787	0.5458	0.5084	0.1485	0.575	0.4305	0.673
1	2	Dus3l	0.2496	0.2202	0.2749	0.1826	0.3932	0.3515	0.4873	0.3549	0.5814
1	2	Dusp10	1.206	0.5295	1.3297	0.5205	0.7611	0.542	0.3173	0.4653	-0.1328
1	2	Dusp18	0.3855	0.3141	0.6171	0.383	0.3805	0.5871	0.214	0.3141	-0.1185
1	2	Dusp6	1.216	0.7275	0.2755	0.2028	0.0948	0.2712	0.9638	0.6462	0.2541
1	2	Dvl2	0.3677	0.4695	0.2432	0.1169	0.3538	0.2702	0.5052	0.3111	0.7924
1	2	Dync1li1	0.6913	0.6679	1.003	0.7743	0.7546	1.0196	0.7275	0.7995	0.5704
1	2	Dynll1	0.2523	0.1066	0.3474	0.4319	0.6476	0.318	0.6986	0.6948	0.3144
1	2	Dyrk1a	0.6436	0.6137	0.7017	0.7527	0.7543	0.5276	0.7783	0.7972	0.6012
1	2	Dyrk2	0.941	0.283	0.4794	0.3502	0.2503	0.3366	0.4089	0.3463	0.317
1	2	E130308A19Rik	0.0686	0.2297	0.3622	0.5063	0.0807	0.1742	0.4536	0.5197	0.2699
1	2	E2f1	0.6696	1.0909	0.6321	0.7037	0.6092	1.0005	0.8594	0.9005	1.3641
1	2	E2f3	0.2187	0.3409	[illegible]	0.429	0.3337	0.5013	0.4612	0.5352	0.6302
1	2	E2f4	-0.0662	0.3907	0.4241	0.5101	0.7932	0.647	1.3496	1.1113	1.0749
1	2	E330018D03Rik	0.4032	0.2962	0.6569	0.5827	0.3629	0.5264	0.7845	0.1263	0.5797
1	2	Ebag9	0.1815	0.1203	0.4877	0.6547	0.4499	0.616	0.7649	0.5353	0.1838
1	2	Ebp	-0.1993	[illegible]	1.0164	0.9578	0.9102	1.0316	0.3806	1.0441	-0.5495
1	2	Ecd	[illegible]	0.0959	0.3178	0.7003	0.5378	0.6937	0.5749	0.665	0.4678
1	2	Eci1	-0.2609	0.1215	0.4762	0.4646	0.6993	0.6127	0.3056	0.613	-0.0566
1	2	Eda2r	0.7337	0.4785	0.8976	0.7892	0.5107	0.8244	0.7396	0.586	0.4621
1	2	Edf1	0.2323	0.3765	0.2489	0.5117	0.3545	0.3951	0.5942	0.4592	0.549
1	2	Eef1b2	0.3081	0.3627	0.6978	0.4013	0.5691	0.2249	0.6407	0.4122	[illegible]
1	2	Eef1d	-0.5433	[illegible]	0.4113	0.75	0.6518	0.9268	0.7073	0.8631	0.4264
1	2	Efna5	0.8881	0.3933	1.1627	1.1369	1.2905	0.9819	0.2777	0.7988	-0.5218
1	2	Efr3a	0.4408	0.3692	0.2518	0.6132	0.107	0.3502	0.1808	0.0745	0.4844
1	2	Efs	1.6978	1.5668	0.3231	0.2542	0.5629	0.1731	1.2791	1.0463	1.2673
1	2	Eftud2	-0.0575	0.4851	0.5133	0.5181	0.6919	0.6994	0.9339	0.9922	1.1966
1	2	Egln3	-0.219	-0.1982	0.3235	0.181	0.8454	0.5841	0.6739	0.8165	-0.1835
1	2	Ehmt1	-0.0867	0.3187	0.2686	0.6236	0.415	0.7577	0.3155	0.0576	0.5724
1	2	Ehmt2	0.5446	0.5343	0.6148	0.4889	0.9213	0.8425	0.708	0.7781	-0.5659
1	2	Ei24	0.1988	0.6623	0.4878	1.1052	0.8067	1.2033	0.4517	0.6578	[illegible]
1	2	Eif2b2	0.117	0.2163	0.2745	0.2691	0.4174	0.4587	0.5352	0.4795	0.3126
1	2	Eif2b4	[illegible]	[illegible]	0.4073	0.3675	0.5135	0.6479	0.6966	0.4705	0.8467
1	2	Eif2s3x	-0.3124	0.3694	0.1637	0.6625	0.6217	1.0379	0.9864	0.6283	[illegible]
1	2	Eif3a	0.6506	0.6066	1.0769	0.8921	0.9265	0.7294	1.0747	1.0288	1.093
1	2	Eif3b	[illegible]	0.4791	0.7374	0.5038	0.7486	1.1731	1.0758	0.8226	0.5294
1	2	Eif3h	0.2256	0.173	0.1391	0.2491	0.5083	0.4319	0.2888	0.173	0.2868
1	2	Eif4g1	0.1417	0.5991	0.46	0.7176	0.8823	0.8097	0.6942	0.8789	0.3495
1	2	Eif4g2	0.8384	0.7516	0.8645	0.5126	0.8198	0.5836	1.1264	0.9064	0.4961
1	2	Elavl1	0.1363	0.2035	0.5784	0.5819	0.6048	0.5682	1.3237	0.5527	0.7632
1	2	Elmod1	0.0993	0.1592	0.374	0.563	0.2326	0.4916	0.2744	0.3025	0.1703
1	2	Elovl5	[illegible]	0.3525	0.7191	0.5674	0.5765	0.6625	0.3849	0.4819	[illegible]
1	2	Elp2	[illegible]	0.3094	0.2703	0.2815	0.4235	0.3395	0.8782	0.592	0.4492
1	2	Elp3	-0.1126	0.4446	0.354	0.0985	0.5555	0.1417	0.93	0.8225	0.1794
1	2	Emg1	-0.2698	-0.0975	0.3717	0.3207	0.6908	0.7087	0.9783	1.1029	0.875
1	2	Enah	0.0906	0.4497	0.1124	0.149	0.3031	0.0621	0.7148	0.4643	0.4423
1	2	Enox2	[illegible]	-0.2252	0.7651	0.5474	0.6415	0.4945	0.5392	0.7284	-0.2903
1	2	Enpp4	0.0716	0.1128	0.5658	0.7689	0.497	0.6576	0.1249	0.5833	[illegible]
1	2	Epas1	0.1358	0.2032	0.2876	0.0738	0.3649	0.5314	0.4759	0.1164	0.19
1	2	Epb4.1l2	1.4555	1.2237	1.4405	1.1747	0.8346	0.6444	0.7384	0.4711	0.2592
1	2	Epc1	0.6563	0.4508	0.2492	0.5019	0.6507	0.6882	0.6462	0.6524	0.3014

1	2 Epn1	0.5577	0.3522	0.8483	0.6156	0.7572	0.8231	0.7923	0.8878	0.1669
1	2 Epn2	0.3567	[illegible]	0.3526	0.415	0.5718	0.4404	0.4881	0.4616	0.6559
1	2 Eps15l1	0.0936	0.2889	0.7325	0.4963	0.8878	0.4626	0.607	0.5284	0.1132
1	2 Eps8	1.6454	1.7211	1.5142	1.1389	0.9965	0.8578	0.2494	0.1828	0.1332
1	2 Ept1	-0.2666	0.1451	0.3806	0.3769	0.4899	0.572	0.5032	0.7178	0.2843
1	2 Ercc3	0.267	0.2817	0.2242	0.2699	0.3978	0.2998	0.3358	0.3415	0.3004
1	2 Ercc4	0.3013	-0.0439	0.3037	0.439	0.5565	0.1679	0.2129	0.2565	0.3542
1	2 Ercc6l	-0.0938	0.1219	0.3669	0.557	0.6641	0.4679	0.8965	0.987	1.1147
1	2 Erf	0.6445	0.6894	0.7	0.7568	0.7786	0.9986	0.6947	1.0408	0.3412
1	2 Ergic2	0.3434	0.1875	0.5042	0.131	0.7089	0.2843	0.5948	0.3088	[illegible]
1	2 Eri2	0.2312	0.4963	0.3066	0.4776	0.6102	0.7812	0.8005	0.9024	0.929
1	2 Erlin2	0.4003	0.5463	0.3504	0.2625	0.2178	0.5463	0.1479	0.355	0.5137
1	2 Esco1	0.2745	-0.1202	0.2532	0.3018	0.3224	0.4367	0.3101	0.3728	0.4942
1	2 Etf1	0.3329	-0.0791	0.7275	0.3699	0.731	0.4459	1.0652	0.8166	1.1208
1	2 Etfa	0.3773	0.4402	0.6736	0.7	0.7573	0.7319	0.5282	0.6275	0.7009
1	2 Etv1	0.3829	[illegible]	0.4277	0.737	0.2102	0.7488	0.3872	0.3958	1.0404
1	2 Etv4	0.3854	0.9897	0.9805	1.365	0.9961	1.1869	0.318	0.6359	1.3863
1	2 Evc	0.9945	1.1101	0.9361	0.825	0.5569	0.6789	0.2347	0.3254	-0.2334
1	2 Exoc2	0.4676	0.6055	0.387	0.2845	0.4407	0.3883	0.4296	0.544	-0.2604
1	2 Exoc6	-0.4372	-0.4325	0.585	0.3892	0.8451	0.4024	0.6595	0.4978	0.3016
1	2 Exosc1	-0.0481	0.263	0.289	0.7216	0.4122	0.836	0.4845	0.6537	1.0051
1	2 Exosc6	[illegible]	0.2983	0.6564	0.6872	0.9156	0.6614	1.1797	0.6465	1.0293
1	2 Eya3	0.1587	-0.1159	0.585	0.5216	0.8516	0.687	0.7518	1.0121	0.3916
1	2 Ezr	-0.9072	-0.3761	0.5143	0.3438	1.0958	0.9596	1.1164	1.2416	0.4437
1	2 Faf2	1.2597	1.0496	0.7339	0.6751	0.727	0.4217	0.8047	0.9711	-0.3226
1	2 Faim	0.0377	[illegible]	0.3587	0.3138	0.4277	0.2363	0.3528	0.3629	0.1373
1	2 Fam108a	0.3876	0.3526	0.3333	0.6299	0.5276	0.4251	0.7554	0.7471	-0.1584
1	2 Fam108b	0.2779	0.0872	0.3209	0.2382	0.2736	0.2538	0.3971	0.2714	0.4618
1	2 Fam110a	0.4435	0.8802	0.4577	0.8907	0.7114	1.0489	0.7106	0.6568	0.201
1	2 Fam110b	1.3891	0.7565	0.8721	0.4186	0.892	0.6674	0.7099	0.4748	0.427
1	2 Fam177a	0.3039	0.4134	0.8424	1.2498	0.7782	0.811	-0.383	0.353	-0.6737
1	2 Fam178a	0.6906	0.3739	[illegible]	0.1705	0.3778	0.5231	0.4936	0.5978	0.7963
1	2 Fam188a	0.1724	0.2317	0.2843	0.5217	0.6174	0.4614	0.5121	0.2153	0.485
1	2 Fam203a	0.2709	0.3691	0.3429	0.4508	0.5009	0.753	0.5185	0.491	0.5775
1	2 Ska2	-0.2834	0.1241	0.4299	0.7004	0.914	1.0996	0.8125	0.903	0.4027
1	2 Fam45a	0.8851	0.8511	0.2368	0.4006	0.5007	0.2468	0.149	0.1366	0.4975
1	2 Fam46b	0.7119	0.4011	1.1276	0.7037	0.7334	0.4733	0.1071	0.4128	-0.3142
1	2 Fam54b	0.3331	0.4543	0.5949	0.5354	0.1795	0.6159	0.1828	0.2832	[illegible]
1	2 Fam63a	-0.3325	-0.0744	0.741	0.7207	0.6472	0.98	0.3404	0.1998	[illegible]
1	2 Fam83e	0.1295	0.2012	0.2329	0.4851	0.4179	0.6017	1.1566	0.8513	0.2752
1	2 Fam83g	[illegible]	[illegible]	0.4644	0.1842	0.7646	0.6002	0.8901	0.8064	0.574
1	2 Fam96b	0.3025	0.2736	0.1448	0.4299	0.4315	0.4523	0.4404	0.4904	0.788
1	2 Fastk	0.5477	0.4577	0.2084	0.1917	0.1473	0.2384	0.4296	0.5506	0.4017
1	2 Fat2	0.3118	0.3405	0.3518	0.2973	0.2069	0.2528	0.4069	0.2944	0.1627
1	2 Fbxl14	0.1343	-0.0695	0.4046	0.2866	0.477	0.385	0.3514	0.298	0.1505
1	2 Fbxo21	0.7131	0.8193	0.5285	0.5582	0.4885	0.7422	0.9098	1.0677	[illegible]
1	2 Fbxo28	-0.3549	0.0714	0.4308	0.6511	0.5213	0.782	0.3912	0.7704	0.5586
1	2 Fbxo34	0.5197	0.499	0.1259	0.307	0.1753	0.2779	0.4192	0.2956	0.4863
1	2 Fbxo38	0.2681	0.3614	0.4177	0.3011	0.3179	[illegible]	0.4969	0.3934	0.3345
1	2 Fbxo42	0.2089	0.204	0.354	0.169	0.6634	0.4404	0.5377	[illegible]	[illegible]
1	2 Fem1c	0.7127	0.2021	0.9089	0.1882	0.6065	0.4303	0.718	0.5515	0.6201
1	2 Fez1	1.2915	1.5483	0.8289	1.1129	0.8348	0.9339	0.3891	1.0243	-0.9461
1	2 Fgd5	[illegible]	0.306	0.3687	0.358	0.1961	0.2976	0.3171	0.2976	0.187
1	2 Fgfbp3	0.2093	0.3989	0.7593	0.7434	0.2323	0.2475	0.1184	0.1167	0.1001
1	2 Fgfr1op	-0.0742	-0.0619	0.5097	0.5241	0.7674	0.4909	0.7455	0.6176	0.8848
1	2 Fgfr2	1.0431	0.6893	0.3405	[illegible]	0.3674	[illegible]	0.656	0.0908	0.1454
1	2 Fhdc1	0.1374	0.1657	0.875	1.1416	0.9965	1.4545	0.3584	0.9712	-0.87
1	2 Fig4	0.2329	0.1645	0.3472	0.2841	0.426	0.3759	0.3239	0.0624	0.5602
1	2 Fip1l1	0.3351	0.3877	0.6265	0.338	0.7003	0.528	0.6764	0.5537	0.2885
1	2 Fkbp8	0.3182	0.4577	0.3463	0.4522	0.4708	0.3995	0.5013	0.548	[illegible]
1	2 Flot1	1.1917	0.9368	0.8526	0.6612	0.6027	0.6216	0.1375	0.13	0.1998
1	2 Fmn2	-0.1012	[illegible]	0.3863	0.5126	1.1021	0.7245	1.279	1.1616	0.1543
1	2 Fnbp1	0.3732	0.0487	0.3658	0.3147	0.5172	0.5071	0.4575	0.2458	0.4329
1	2 Fndc3c1	0.6362	0.1802	0.2976	0.3598	0.3375	0.1676	0.6247	0.5659	0.1258
1	2 Fosb	3.8348	2.0735	3.1203	2.139	3.1832	2.2177	2.9131	2.9514	-2.2479
1	2 Foxa1	0.3777	0.0885	0.3858	0.1436	0.2828	0.1404	1.261	0.7072	0.175
1	2 Foxa2	[illegible]	0.185	[illegible]	0.1466	[illegible]	-0.0474	1.3176	0.5945	[illegible]
1	2 Foxj1	0.4243	0.5589	0.514	0.3749	0.4541	0.4765	0.3773	0.5483	0.5398
1	2 Foxk1	0.181	0.1333	0.2719	0.3806	0.4381	0.3907	0.1868	0.4745	0.2328
1	2 Foxl1	0.2711	0.2391	0.4569	0.1544	0.2034	0.5663	0.2768	0.467	0.371
1	2 Foxp1	0.6115	0.5294	1.2365	0.6658	0.9231	0.9138	[illegible]	0.4704	-0.6038
1	2 Frs2	0.9218	0.6907	0.3374	0.3365	0.4211	0.5042	0.5081	0.3295	0.2662
1	2 Frs3	0.0687	0.2949	0.0953	0.1375	0.3866	0.3785	0.5803	0.4317	0.2921
1	2 Fry	-1.1641	-0.6656	1.1857	1.1009	1.2332	1.3753	0.6859	1.1303	[illegible]
1	2 Fryl	0.3456	0.4485	0.736	0.376	0.2561	0.5742	0.2329	0.2619	-0.1197
1	2 Frzb	0.4976	0.2544	0.1375	0.1561	0.2224	[illegible]	0.8113	0.4903	[illegible]
1	2 Fscn1	0.9258	0.9261	0.6568	0.192	0.4541	0.3192	1.1599	1.09	-0.1491
1	2 Ftsj1	[illegible]	-0.0722	0.2503	0.6289	0.8091	1.0307	0.5377	0.9784	0.0779
1	2 Furin	0.9262	0.6559	0.9323	0.4005	0.6261	0.2661	0.225	0.5022	-0.1159
1	2 Fzd6	0.6773	0.7375	0.5548	0.4676	0.8621	0.4883	0.5149	0.797	[illegible]
1	2 Fzr1	-0.163	0.4338	0.4318	0.9092	1.0948	1.1139	1.1219	1.0863	0.5474
1	2 G430049J08Rik	0.4558	0.2523	0.3102	0.1288	0.1091	0.3965	0.1919	0.5488	0.2368
1	2 G6pc2	0.2646	0.4924	0.428	0.3605	0.3341	0.2923	0.1672	0.3747	0.3365
1	2 Gadd45a	0.8084	[illegible]	0.9211	-0.4871	0.4846	[illegible]	1.1951	0.4696	0.625
1	2 Galnt1	[illegible]	0.5237	[illegible]	0.5601	0.1742	1.038	0.2199	0.0954	[illegible]
1	2 Ganab	0.1562	0.5216	0.4177	0.216	0.3432	0.7023	0.5937	0.2058	0.9895
1	2 Gas2l1	0.6535	0.7831	0.3655	0.6401	0.5148	0.3261	0.4411	0.2835	-0.0896
1	2 Gatad1	0.1271	[illegible]	0.521	0.2846	0.465	0.3493	0.5921	0.2257	0.3573
1	2 Gbp1	1.7796	-0.3689	0.5452	-0.2602	1.1993	0.6011	1.5199	1.3649	0.9325
1	2 Gbp2	2.2523	-0.1847	1.0788	-0.3895	1.3273	0.3246	2.0225	1.585	[illegible]
1	2 Gcap14	1.0688	1.0591	0.9163	0.6536	0.7513	0.803	0.2206	0.7241	-0.1281
1	2 Gclc	0.3953	0.2844	0.3275	0.2352	0.2518	0.194	0.3253	0.314	0.3342
1	2 Gclm	0.6214	0.5548	0.8548	0.6629	1.2614	1.035	1.089	0.7583	1.049
1	2 Gdi1	1.0739	0.9418	1.1926	1.1424	0.9043	1.1503	0.9397	0.83	0.3582
1	2 Gemin4	-0.0418	0.3543	0.1493	0.8055	0.7947	0.8775	1.3543	1.0337	0.7445
1	2 Get4	0.107	-0.2673	0.2481	0.4039	0.7277	1.1881	1.08	0.8334	1.0562
1	2 Gip	0.1939	0.0676	0.3941	0.544	0.3809	0.402	0.3268	0.3729	0.2791
1	2 Git1	0.6613	0.4976	0.4681	0.4332	0.5892	0.4449	0.79	0.606	0.1479
1	2 Gkap1	0.1546	0.2598	0.5217	0.3477	0.4033	0.4886	0.1585	0.1969	0.6703
1	2 Glis2	0.5966	0.2794	0.2356	0.4165	0.2332	0.2985	0.2985	0.3196	0.2232
1	2 Glod5	[illegible]	0.3353	0.1654	0.1594	0.5347	0.537	0.2837	0.2444	0.2358
1	2 Glrx2	0.4028	0.3042	0.3677	0.1995	0.5401	0.286	0.4235	0.2989	0.3085
1	2 Glrx3	[illegible]	0.0929	0.7442	0.3954	0.5253	0.2979	0.4843	0.3351	[illegible]
1	2 Glrx5	0.0852	0.58	0.5056	0.6703	0.3049	0.3583	0.5173	0.5681	-0.4935
1	2 Glyat	0.2481	0.5838	0.1868	0.2451	0.2361	0.2866	0.2719	0.4363	0.2895
1	2 Gm12657	0.739	0.3265	0.5553	0.4515	1.0709	-0.1482	0.9705	0.6382	0.6841
1	2 Gm129	1.359	0.6174	1.2833	0.6642	0.271	0.2869	0.4745	0.6472	1.421
1	2 Gm13034	0.2688	0.202	0.5218	0.4614	0.34	0.3326	0.4127	0.3276	0.5196
1	2 Gm14325	0.259	0.1832	0.4297	0.2746	0.2944	0.1402	0.5164	0.2433	0.2319
1	2 Gm1698	-0.1606	0.4743	1.1276	2.1347	1.3051	0.9907	0.3629	1.0931	[illegible]
1	2 Gm5458	0.3852	0.3697	0.1684	0.5669	0.4607	0.204	0.2301	0.4607	0.2272
1	2 Gm5662	0.4358	0.3726	0.357	0.2257	0.37	0.2901	0.4058	0.4108	0.2257
1	2 Gm5797	0.0971	0.304	0.3601	0.4113	0.2266	0.1416	0.3944	0.648	0.5345
1	2 Gm6578	0.664	0.3831	0.2592	0.5935	0.3699	0.4329	0.0997	0.4093	0.3294
1	2 Gmcl1	0.2535	0.2236	0.4561	0.5765	0.7526	0.6155	0.7422	0.6241	0.9337
1	2 Gmppa	0.6971	0.4887	0.2632	0.2579	0.3759	0.3122	0.4089	0.4553	[illegible]
1	2 Gnai2	0.8363	0.7732	0.7799	0.4999	0.9261	0.6653	1.2477	1.4484	-1.1533
1	2 Gnal	0.224	0.1597	0.1432	0.2885	0.2208	0.4423	0.3589	0.3474	0.2643
1	2 Gng5	0.7442	0.1277	0.5987	0.3631	0.6028	0.2203	1.0731	0.7343	0.7999
1	2 Gnptab	-0.0699	0.3557	1.0985	0.9483	0.9092	0.7554	0.1781	0.5547	-0.3443
1	2 Golm1	-0.0418	0.5839	1.3268	1.1994	0.7241	0.3429	0.5195	0.3931	[illegible]
1	2 Golt1b	0.8618	1.0885	0.1731	0.3222	0.4133	0.473	0.2827	0.4405	0.8102
1	2 Gorasp2	0.6664	0.6561	0.5511	0.8121	0.6264	0.6979	0.7345	0.7473	0.8095
1	2 Gpatch1	0.195	0.0885	0.3079	0.4518	0.5403	0.0907	0.2943	0.2405	0.5713
1	2 Gpatch4	-0.2795	0.3303	[illegible]	0.5469	0.5148	0.4353	0.6105	0.5605	0.5271
1	2 Gphn	-0.2467	0.0838	0.7488	0.8305	0.7722	0.4412	0.4186	0.5153	-0.7974
1	2 Gpr1	-0.2002	[illegible]	0.3307	0.3131	0.4594	0.5923	0.2754	0.3498	-0.0978
1	2 Gpr143	0.0564	0.0736	0.8058	0.3183	0.7662	0.1339	0.2321	0.1174	0.1273
1	2 Gprc5a	1.4157	1.0291	1.9694	0.8429	1.0819	0.6624	1.1667	0.8736	-0.4831
1	2 Gps1	-0.0649	0.4121	0.5364	0.3584	0.631	0.5137	0.5245	0.3294	0.5145
1	2 Grb2	0.1832	0.2437	0.3058	0.2875	0.2542	0.2181	0.3379	0.4188	0.3199
1	2 Grhl1	-0.2727	-0.5329	1.1694	0.5464	1.2572	0.8908	0.7909	0.8482	0.1207
1	2 Gria1	0.3427	0.3966	0.183	0.5615	0.2578	0.3372	0.3536	0.2013	0.2373
1	2 Grk6	-0.3164	[illegible]	0.5393	0.6713	0.7637	1.1355	0.6995	0.6729	0.5283
1	2 Gsc	0.7205	1.7459	0.091	0.2734	[illegible]	-0.5156	1.7372	1.4002	[illegible]
1	2 Gse1	0.6959	0.4637	0.4835	0.379	0.7119	0.4709	0.732	0.9218	0.3147
1	2 Gsk3a	0.6631	0.588	0.8473	0.7309	0.8285	0.7068	0.849	0.8268	0.2123
1	2 Gsk3b	0.2099	0.2717	0.5476	0.3443	0.4434	0.5524	[illegible]	0.4557	-0.0959
1	2 Gsta3	-0.4375	0.2353	0.9758	0.8154	1.3168	0.6394	0.7547	0.7476	0.9387
1	2 Gstk1	0.3893	0.3639	0.6179	0.4534	1.3238	1.5313	0.805	1.7097	-0.2836
1	2 Gtf2a1	-0.1071	[illegible]	0.4261	0.3517	0.4905	0.2951	0.6286	0.2337	0.4172
1	2 Gtf2ird1	0.2731	0.072	0.3517	0.2084	0.3702	0.482	0.3824	0.2578	0.4989
1	2 Gtf3c1	0.5372	0.516	0.6984	0.5902	0.7836	0.7176	0.5591	0.8238	-0.7074
1	2 Gtf3c2	0.34	0.688	0.6046	0.8751	0.9304	1.0307	1.2895	0.7588	0.7795
1	2 Gtf3c5	0.4931	0.1991	0.2652	0.0977	0.2189	0.4895	0.6812	0.7111	0.3892
1	2 Gtf3c6	0.0505	0.3719	0.4549	0.4465	0.8805	0.9683	1.3449	1.2222	0.4883
1	2 H2afj	0.4759	0.5343	0.8332	0.7665	0.4827	0.6907	0.4239	0.7553	-0.4954
1	2 H2-Q1	0.6993	0.3787	0.4915	0.4452	0.5981	0.463	0.4697	0.2358	0.5002
1	2 Hal	-0.5408	-0.2949	1.0767	0.7272	1.1086	0.8263	0.7404	0.7973	-0.3557
1	2 Haus4	[illegible]	-0.0641	0.3672	0.4893	0.485	0.8086	0.4613	0.7062	0.5599
1	2 Hcfc1r1	0.536	0.6119	0.5946	0.4654	0.6609	0.2591	0.2938	0.3381	-0.1494
1	2 Hdac1	-0.0708	0.1983	0.2089	0.4661	0.7156	0.6846	1.2969	1.1113	0.6517
1	2 Hdac2	[illegible]	0.3706	0.8814	1.1622	0.93	0.9166	0.6323	0.5359	0.6269
1	2 Helz	0.0985	-0.0702	0.1907	0.3123	0.8304	0.7803	0.8986	0.9324	0.9506
1	2 Hes1	2.7384	1.9402	1.6295	1.337	1.4505	0.6719	1.2461	0.6711	-0.3999
1	2 Hes6	[illegible]	0.5096	1.2001	1.0245	0.9785	0.8547	0.5714	0.8029	0.1893
1	2 Hey1	3.7539	1.404	2.928	0.8798	0.5654	0.9973	1.3697	1.0605	0.7437
1	2 Hey2	1.2111	0.5477	1.6963	0.6254	0.4284	0.1919	0.2165	0.1498	[illegible]
1	2 Hhip	0.6341	0.5808	0.6718	0.5124	0.5058	0.5298	0.3985	0.6757	0.3381
1	2 Hiatl1	0.3585	0.387	0.5567	0.5748	0.6475	[illegible]	0.4936	0.5383	0.387
1	2 Hibadh	0.0772	0.1012	0.2583	0.473	0.414	0.4366	0.1184	0.3166	0.4471
1	2 Hipk2	0.5603	0.4558	0.8936	0.9048	0.8017	0.9778	0.2876	0.7515	0.1185
1	2 Hist1h2ae	0.4692	0.2509	0.3871	0.5056	0.7039	0.4891	0.8228	0.7614	0.8758
1	2 Hist1h2bb	0.1476	0.2349	0.4369	[illegible]	0.5947	0.6667	0.8405	0.6499	0.7193



1	2	Hist1h3f
1	2	Hist1h3g
1	2	Hist1h4b
1	2	Hist1h4c
1	2	Hist1h4d
1	2	Hist1h4f
1	2	Hist1h4i
1	2	Hist1h4k
1	2	Hist1h4m
1	2	Hist2h3c1
1	2	Hk1
1	2	Hmg20a
1	2	Hmgn2
1	2	Hmgxb4
1	2	Hnrnpab
1	2	Hnrnpc
1	2	Hnrnph1
1	2	Hnrnpk
1	2	Hnrnpl
1	2	Hnrnpm
1	2	Hnrnpu
1	2	Hnrnpul1
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1	2	Hnrpll
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1	2	Hoxc10
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1	2	Hpdl
1	2	Hprt
1	2	Hps3
1	2	Hras1
1	2	Hs6st1
1	2	Hspe1
1	2	Hsph1
1	2	Huwe1
1	2	Hyou1
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1	2	Ier2
1	2	Ifitm6
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1	2	Itfg2
1	2	Itgav
1	2	Itsn2
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1	2	Josd1
1	2	Jph1
1	2	Jund
1	2	Jup
1	2	Kat2a
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1	2	Lsm6
1	2	Lsm7
1	2	Lta4h
1	2	Ltbp1
1	2	Ltv1
1	2	Luc7l
1	2	Ly6d
1	2	Lypd4
1	2	Lypd6b
1	2	Mad1l1
1	2	Maea
1	2	Magi1

1	2	Magoh	0.3072	-0.1109	0.2637	0.0777	0.547	0.6252	0.9633	0.6461	0.7138
1	2	Magohb	0.2213	0.1742	0.4989	0.4671	0.701	0.2717	0.8518	0.638	0.5192
1	2	Mal	-1.6676	-0.4388	0.6161	1.2609	1.1298	1.6108	0.2943	0.7054	-2.1669
1	2	Malt1	0.376	[illegible]	0.7019	0.625	0.7305	0.3069	0.4885	0.453	[illegible]
1	2	Maml1	0.8256	0.3852	0.4076	0.1312	0.3812	[illegible]	0.7293	0.5052	[illegible]
1	2	Mansc1	-0.4092	-0.357	2.3006	0.7781	1.2649	0.197	0.3218	-0.4773	-0.9452
1	2	Map1lc3a	1.0302	1.1073	0.7607	0.7071	0.5637	0.4787	0.2959	0.2844	0.2825
1	2	Map2k1	0.1946	0.1523	0.4146	0.2317	0.5216	0.3222	0.7581	0.7113	0.9004
1	2	Map2k3	0.2694	0.2684	1.0344	0.3377	0.4782	0.6532	0.243	0.313	-0.6497
1	2	Map2k6	0.3614	0.3466	0.4843	0.2224	0.5073	0.3822	0.6875	0.4977	0.8686
1	2	Map3k7	0.7092	0.4716	0.3889	0.4337	0.6376	0.5464	0.4791	0.6039	0.212
1	2	Mapk1ip1	0.299	0.2932	0.5611	0.1833	0.4588	0.5008	0.1723	0.5707	0.3004
1	2	Mapk1ip1l	0.7836	0.4476	0.7824	0.5054	0.7144	0.7292	0.9465	0.8918	1.0814
1	2	Mapk3	0.3837	0.3113	0.1513	0.2998	0.4985	0.5283	0.3084	0.3479	[illegible]
1	2	Mapkapk3	0.1821	0.181	0.6131	0.3161	1.0056	1.1538	0.83	1.3607	0.3561
1	2	41338	0.5198	0.2244	0.92	0.5493	0.6386	0.3637	0.5272	0.2252	0.3101
1	2	41340	1.1204	0.5176	1.1613	0.4964	0.9548	0.6725	0.7808	0.8477	1.1525
1	2	Mark2	0.8938	0.529	1.2011	0.9987	1.3212	1.0941	0.9364	1.1853	-0.4026
1	2	Marveld3	-0.7182	-0.6307	[illegible]	0.1487	0.9441	0.6204	0.9133	0.8166	-0.2823
1	2	Mat2a	0.3099	0.3841	0.1936	0.9603	0.2632	1.0313	0.6105	[illegible]	1.3529
1	2	Max	0.2733	0.4171	0.5983	0.6299	0.5514	1.086	[illegible]	0.4311	0.6386
1	2	Mbip	0.318	[illegible]	0.7285	0.162	0.7089	[illegible]	0.7604	0.4741	0.8366
1	2	Mbp	-0.1746	-0.3071	1.9512	1.2288	2.0062	1.3184	1.2235	1.2256	-0.1495
1	2	Mbtd1	[illegible]	-0.3974	0.7191	0.4717	0.8612	0.4683	0.7644	0.5589	0.6119
1	2	Mcmbp	-0.2589	0.0673	0.3684	0.5284	0.401	0.546	0.1734	0.3552	0.3078
1	2	Mcoln3	0.4142	0.0978	0.1779	0.2428	0.4505	0.1779	0.2565	0.3128	0.5136
1	2	Mcph1	[illegible]	0.3637	0.4744	0.4708	0.5409	0.5926	0.7678	0.6604	0.848
1	2	Mcrs1	[illegible]	-0.0897	0.6073	0.4036	0.8593	0.5354	0.9128	0.8788	0.846
1	2	Mdh1b	[illegible]	0.2532	0.3119	0.1919	0.3612	0.5994	0.4205	0.4018	[illegible]
1	2	Mdm4	-0.0738	0.1783	0.4297	0.5729	0.3134	0.8022	[illegible]	[illegible]	0.526
1	2	Me2	[illegible]	0.6314	0.5168	0.6989	0.6526	0.7988	0.9577	1.1211	0.7054
1	2	Meaf6	0.1966	0.1375	0.3196	0.3629	0.4895	0.5499	0.5656	0.4751	0.433
1	2	Med1	0.4868	0.3548	0.9501	0.5175	0.5924	0.5885	0.2579	0.5506	0.3294
1	2	Med16	0.3823	0.4283	0.4027	[illegible]	0.5578	0.5257	0.6182	0.4698	[illegible]
1	2	Med19	-0.2708	-0.3265	0.5021	0.5066	0.9253	0.9767	0.8103	0.9914	0.8354
1	2	Med21	0.24	[illegible]	0.3996	0.672	0.6549	0.4308	0.5813	0.4857	0.3058
1	2	Med24	0.1016	0.2803	0.4583	0.5191	0.8564	0.7973	1.1002	0.9783	0.8133
1	2	Med25	0.6446	0.9027	0.5265	0.3896	0.4144	0.7293	0.655	0.5877	0.943
1	2	Med27	0.2216	0.2157	0.7241	0.4578	0.48	0.2666	0.3633	0.28	[illegible]
1	2	Memo1	0.4221	0.5192	0.6259	0.4678	0.6983	0.2984	0.6619	0.5634	0.272
1	2	Men1	0.4517	0.5898	[illegible]	0.2733	0.3741	0.3536	0.7074	0.5898	0.5916
1	2	Mest	1.4718	1.0651	-0.0883	-0.1293	[illegible]	[illegible]	1.2736	0.8213	0.7515
1	2	Metap1	0.2333	0.301	0.6181	0.6217	0.8896	0.6084	1.1093	0.9036	0.9327
1	2	Metap2	[illegible]	0.1531	0.4261	0.4116	0.4488	0.3819	0.467	0.5997	0.532
1	2	Mettl13	0.08	0.3587	0.2931	0.628	0.5024	0.6766	0.6556	0.5633	0.3402
1	2	Mettl9	0.7829	0.57	0.6696	0.2377	0.5784	0.0963	0.9924	0.3988	0.2543
1	2	Mex3a	0.273	0.1399	0.0812	0.1216	0.5259	0.273	0.2109	0.4859	0.3744
1	2	Mfap3l	0.6673	0.6058	0.7596	0.6256	0.4794	0.578	0.4179	0.5303	[illegible]
1	2	Mfsd10	0.4056	0.3971	0.5544	0.2628	0.5286	0.213	0.6013	0.6547	-0.601
1	2	Mgat3	0.3609	0.2363	0.2669	0.2541	0.737	0.4435	0.7324	0.3459	-0.7173
1	2	Mgat4b	0.1497	0.5102	0.5721	0.4342	0.7966	0.5705	0.2088	0.2193	-0.1705
1	2	Mid1	1.1607	0.8834	1.231	1.2795	1.193	1.1414	1.4724	1.5493	-0.3169
1	2	Mier1	0.4111	0.1694	0.2529	[illegible]	0.4054	[illegible]	0.6237	0.4526	0.1022
1	2	Miip	[illegible]	0.3488	0.2952	0.6046	0.6702	1.0015	0.5865	0.8124	0.5578
1	2	Minpp1	0.1996	0.5876	0.3209	0.3608	0.2309	0.5195	0.6501	0.515	0.5231
1	2	Spen	0.6149	0.2462	0.6802	0.4953	0.7171	0.6099	0.8214	0.6124	0.1132
1	2	Mixl1	0.1814	[illegible]	[illegible]	0.116	[illegible]	[illegible]	1.1965	0.7805	0.1318
1	2	Mllt3	0.3849	0.5116	1.3422	0.7351	0.5359	0.34	0.1622	0.455	-0.4421
1	2	Mmp15	0.1489	0.1378	0.2167	0.3673	0.5381	0.4709	1.0107	0.7413	0.6043
1	2	Mmp1a	0.5469	0.0752	0.3302	0.3467	0.349	0.4567	0.4239	0.3443	0.579
1	2	Mnt	0.3833	0.1745	0.7359	0.5621	0.3854	0.4184	0.2336	0.2498	0.5731
1	2	Mob3b	0.0929	0.1053	0.3351	[illegible]	0.5103	0.1685	0.5761	0.6263	0.4315
1	2	Mogs	-0.2636	0.1832	[illegible]	0.6253	0.4193	0.7847	0.5038	0.4831	0.1046
1	2	Morf4l1	0.7239	0.4234	0.5278	0.5336	0.287	0.5581	[illegible]	0.121	0.3261
1	2	Mospd3	0.4899	0.3897	0.5414	0.3569	0.5568	0.5188	0.3131	0.5049	[illegible]
1	2	Mpp5	0.28	0.2097	0.1455	0.3385	0.2281	0.5143	[illegible]	0.3427	0.4528
1	2	Mpp6	-0.4019	0.1952	0.5125	1.0489	0.957	1.0066	0.7273	0.8781	1.0131
1	2	Mpv17l2	0.3639	0.409	0.2535	0.2909	0.2914	0.4956	[illegible]	0.3719	0.6297
1	2	Mrp63	0.5557	0.5891	0.4829	0.49	0.6694	0.7906	0.4633	0.8344	0.2522
1	2	Mrpl15	[illegible]	0.5503	0.3227	0.6272	0.4823	0.6307	0.415	0.4584	0.6212
1	2	Mrpl18	[illegible]	0.2041	0.3803	0.5619	0.5773	[illegible]	0.5508	0.5991	0.2949
1	2	Mrpl3	[illegible]	0.1797	0.6298	0.7701	0.6073	0.8718	0.586	0.5967	0.5177
1	2	Mrpl35	0.1694	0.402	0.1982	0.3907	0.4722	0.5934	0.3701	0.4176	0.6081
1	2	Mrpl37	-0.0699	0.3407	0.5633	0.576	0.75	0.9159	1.082	1.0985	0.7035
1	2	Mrpl39	0.3614	0.5568	0.5482	0.5059	0.8063	0.7288	0.7258	0.5219	0.9071
1	2	Mrpl4	0.3882	0.393	0.355	0.5785	0.5005	0.7207	0.5073	0.5341	0.5846
1	2	Mrpl45	0.1329	-0.1186	[illegible]	[illegible]	0.3839	0.6038	0.7837	0.4221	0.2546
1	2	Mrpl48	0.3009	[illegible]	0.3474	0.1777	0.2718	0.2387	0.4487	0.4026	0.0921
1	2	Mrpl51	0.263	0.3465	0.207	0.6768	0.2458	0.56	0.3219	0.6269	0.0782
1	2	Mrpl53	-0.1196	[illegible]	[illegible]	0.5212	0.6392	0.6815	0.4231	0.7225	[illegible]
1	2	Mrpl54	0.406	0.3328	0.1398	0.4801	0.6357	0.523	0.6221	0.8141	[illegible]
1	2	Mrpl55	-0.0733	0.18	0.4815	0.3444	0.4445	0.4611	0.8093	0.8196	0.181
1	2	Mrpl9	0.4117	0.6889	0.4323	0.924	0.9545	1.2167	1.0206	1.0545	0.7583
1	2	Mrps10	-0.1466	0.264	0.2152	0.3441	0.674	0.8921	0.4289	0.8542	0.6112
1	2	Mrps15	0.3706	0.5463	0.688	0.6918	1.0046	0.9151	1.1333	0.7855	[illegible]
1	2	Mrps23	0.2456	0.5605	0.6109	0.5807	0.9219	0.6297	0.8452	1.02	0.2376
1	2	Mrps35	0.0703	0.3435	0.3786	0.7015	0.8095	0.8868	0.9316	0.7816	0.5551
1	2	Mrps6	0.7785	1.1102	0.378	0.733	0.6063	0.6451	0.9199	0.714	-0.2872
1	2	Mrto4	-0.4334	0.1908	0.3786	0.9028	0.7257	0.972	0.853	0.6846	1.1038
1	2	Msl3l2	0.489	0.5579	0.4487	0.6456	0.732	0.6691	0.6055	0.9188	0.3837
1	2	Msn	0.9031	1.2079	0.7392	1.1887	0.395	0.9417	0.2985	0.1387	-0.3323
1	2	Mta1	0.7829	0.8305	0.9087	0.9299	1.0096	0.9873	1.0597	1.2487	0.4694
1	2	Mta2	0.7648	0.6489	0.7523	0.4963	0.7429	0.565	1.0108	0.8068	[illegible]
1	2	Mtap1b	1.0121	1.0616	0.9138	0.9327	-0.2322	0.1034	0.493	0.1875	0.8924
1	2	Mtap1s	0.3025	0.4882	0.3697	0.3022	0.4839	0.471	0.8145	0.7104	0.4796
1	2	Mtch2	0.5667	0.4791	0.6508	0.6276	0.4481	0.2482	[illegible]	0.4358	-0.1669
1	2	Mterfd1	0.6814	0.3084	0.3783	0.4113	0.4826	0.2719	0.7259	0.6672	1.0698
1	2	Mtmr2	0.6244	0.5243	0.4255	0.5489	0.6286	0.5657	0.3402	0.4376	0.3814
1	2	Mtmr3	0.1947	0.624	0.7065	0.6041	0.5748	0.6309	0.2572	0.4478	1.0734
1	2	Mtmr9	0.1026	0.371	0.4057	0.2324	0.3775	0.2893	0.4571	0.6644	0.3994
1	2	Mtpap	0.4164	0.3095	0.4287	0.453	0.5679	0.474	0.6769	0.5073	0.5473
1	2	Mtrr	[illegible]	0.2574	0.4198	0.3583	0.4711	0.3942	0.1977	0.3764	[illegible]
1	2	Mtx1	-0.1984	0.254	0.3872	0.2446	0.618	0.7386	1.0029	0.5765	0.9553
1	2	Muc1	[illegible]	-0.2796	0.6752	0.2477	0.6881	0.5368	0.1017	0.5727	-0.2171
1	2	Myl12a	0.5574	0.4997	0.6192	0.1903	0.3712	0.1622	0.2587	0.4771	[illegible]
1	2	Myl12b	[illegible]	0.0819	0.5526	[illegible]	0.7482	0.3719	0.6785	0.702	0.145
1	2	Myl6b	0.7993	0.5883	0.4711	0.5228	0.7548	0.5616	0.6822	0.848	0.1269
1	2	Myo10	[illegible]	-0.1792	0.585	0.765	0.5408	0.6665	0.374	0.3723	0.6637
1	2	Myo1b	0.8925	0.9627	0.5521	0.4936	0.4392	0.2209	0.4579	0.3108	0.3549
1	2	Myo9a	0.3944	0.2011	0.4917	0.1381	0.5172	0.5073	0.3908	0.5139	0.4004
1	2	Mzt1	0.1897	0.4771	0.7446	0.7515	0.7773	0.845	1.0913	0.7074	0.4835
1	2	Naa15	-0.0828	[illegible]	0.7385	0.8278	0.8173	0.7658	1.5503	1.1368	0.6078
1	2	Naa16	-0.195	0.1921	0.309	0.7917	0.6942	0.7384	0.9792	0.9513	0.8977
1	2	Naa25	0.2292	0.2316	0.8817	0.5982	0.652	0.8167	0.5618	0.4398	1.4059
1	2	Naca	0.4919	0.1645	0.6876	0.4748	0.8598	0.3518	0.6628	0.3743	0.1616
1	2	Nampt	0.4143	[illegible]	0.4962	0.2906	0.4569	[illegible]	0.6819	0.6551	0.7877
1	2	Napa	0.4533	0.3999	0.4919	0.5983	0.2689	0.5659	0.5715	0.2479	0.2123
1	2	Naprt1	-0.2501	-0.4549	0.5741	0.4307	0.7951	0.8103	0.629	[illegible]	-0.2525
1	2	Napsa	0.1193	0.2441	0.4528	0.2611	0.4738	0.7667	0.249	0.8732	0.5955
1	2	Naa20	0.3725	0.115	0.4708	0.5007	0.3255	[illegible]	0.5669	0.4358	0.852
1	2	Ncapg2	-0.2718	[illegible]	0.4095	0.6878	0.8636	0.5522	0.7158	0.7263	[illegible]
1	2	Ncaph2	-0.0511	0.2527	0.5843	0.5024	0.8513	0.4705	1.0129	0.9222	0.3445
1	2	Ncdn	0.6293	0.5627	1.4287	1.0311	1.0206	0.4605	0.8218	0.4793	-0.4575
1	2	Nckap1	0.5222	0.2356	0.7236	0.6976	0.7273	0.4976	0.828	0.5196	0.374
1	2	Ncoa3	0.3948	0.3874	0.1813	0.0814	0.3525	0.3576	0.2748	0.3923	0.4166
1	2	Ncoa5	0.2068	0.4933	0.0933	0.3883	0.4772	0.3352	0.6322	0.7137	0.6224
1	2	Ncor1	0.144	[illegible]	0.2103	0.2284	0.4386	0.6363	0.2226	0.4892	0.4487
1	2	Ndufa4	-0.3036	0.2919	0.7931	0.9637	0.6055	0.6753	0.6416	0.5326	0.9353
1	2	Ndufa5	0.5177	0.5505	[illegible]	0.5264	0.2507	0.3801	0.279	0.2227	0.3213
1	2	Ndufa8	0.3002	0.2759	0.1989	0.3145	0.2273	0.4044	0.349	0.3509	0.1418
1	2	Ndufab1	0.1602	0.1923	0.2827	0.2382	0.5374	0.4319	0.6106	0.3974	0.2646
1	2	Ndufaf4	0.1248	0.1204	0.6314	0.9099	0.6963	0.7762	0.911	0.8836	0.4582
1	2	Ndufc2	0.2041	-0.254	[illegible]	0.5409	0.3579	0.4878	0.5553	0.3987	0.4188
1	2	Ndufs4	0.7087	0.2551	0.3265	[illegible]	0.4327	0.2311	0.7167	0.3715	0.5628
1	2	Necab1	-0.1364	0.4193	1.9185	1.8706	0.8527	0.2224	[illegible]	0.2957	-0.1552
1	2	Necab2	0.6398	0.3551	0.3257	0.2047	0.3811	0.6446	0.4537	0.5536	0.8632
1	2	Nek3	0.2933	0.281	0.4176	0.3568	0.3959	0.2199	0.335	0.4262	0.5566
1	2	Nes	-0.5238	0.4301	0.6594	0.7933	0.8314	1.3043	1.0444	1.6185	[illegible]
1	2	Nfatc3	0.1418	0.6956	0.5085	0.4905	0.5771	0.8351	0.5626	0.873	0.8051
1	2	Nfkbia	1.8448	0.2502	1.4629	0.2485	1.2117	0.8671	0.5592	0.3905	0.1892
1	2	Nfrkb	[illegible]	0.4329	0.3782	0.5823	0.4883	0.7153	[illegible]	0.3552	0.4392
1	2	Nfyc	-0.2749	[illegible]	0.5163	-0.1155	0.5747	0.2843	0.4071	0.4634	[illegible]
1	2	Nhej1	0.5113	0.2267	0.2892	0.2061	0.3014	0.3255	0.3632	0.2843	0.6532
1	2	Nhlrc2	-0.1064	-0.2241	0.3133	0.3525	0.2698	0.6044	0.355	0.48	[illegible]
1	2	Nhp2l1	[illegible]	0.2225	0.3398	0.7318	0.6598	0.8811	0.6186	0.8636	1.4029
1	2	Nlgn3	0.0989	[illegible]	1.1487	0.9369	1.2177	0.6565	0.8938	0.4927	-0.2104
1	2	Nmd3	0.5293	0.4746	1.0501	0.9869	1.0572	0.6363	0.6897	0.7838	0.6228
1	2	Nme5	0.2083	[illegible]	0.3753	[illegible]	0.7564	0.8679	1.0845	1.1692	-0.457
1	2	Nme7	0.2204	[illegible]	0.5781	0.5325	0.9277	0.5033	1.0766	0.928	1.0526
1	2	Nmu	0.2965	0.222	1.0439	0.5317	0.5591	0.4485	0.214	0.2034	0.4485
1	2	Nnat	0.1686	[illegible]	0.3219	0.1136	0.334	0.3146	0.675	0.8915	0.3122
1	2	Nob1	-0.134	0.2566	0.3839	0.7564	0.5872	0.8369	0.7768	1.0513	0.8815
1	2	Nol6	0.1875	0.4997	0.627	0.7982	1.0181	0.7188	1.2832	1.3176	0.7679
1	2	Nono	0.0874	0.1985	0.7103	0.4049	0.7151	0.2266	0.7825	0.2991	0.732
1	2	Nop10	-0.3035	0.2035	0.3157	0.7452	0.2759	0.6383	0.6203	0.5946	0.6607
1	2	Nop2	0.1247	0.6642	0.4477	1.0709	0.7448	0.6655	0.8924	0.9742	0.6799
1	2	Nop58	-0.0651	0.4397	0.6369	0.7709	0.9744	1.1092	1.3179	0.5891	0.7789
1	2	Notch3	0.5042	0.8891	-0.1406	-0.2695	0.2618	0.1064	0.9582	1.1614	0.3219
1	2	Npm1	-0.0622	0.433	0.4205	0.7814	0.699	0.6593	0.9884	1.0108	0.6019
1	2	Npm3	0.5354	0.6946	0.5774	0.8329	0.7314	1.3321	0.8421	0.9859	0.4659
1	2	Npm3-ps1	0.2336	0.701	0.6188	0.8816	0.6371	1.2046	0.8932	1.2176	0.7093
1	2	Nprl3	0.5349	1.0033	0.3434	0.7944	0.5166	0.6119	0.7868	0.7662	0.6877
1	2	Npy2r	0.0869	[illegible]	1.2581	0.4903	1.3287	0.7233	0.6186	[illegible]	[illegible]
1	2	Nr1d1	2.8405	1.3709	2.7494	1.4044	1.2818	0.787	0.6028	0.5688	-0.3595

1	2	Nr2f2
1	2	Nrarp
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1	2	Nsdhl
1	2	Nsmce2
1	2	Nsun5
1	2	Nt5c2
1	2	Nt5c3l
1	2	Nt5dc1
1	2	Ntn5
1	2	Nts
1	2	Nudcd2
1	2	Nudcd3
1	2	Nudc-ps1
1	2	Nudt14
1	2	Nudt4
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1	2	Nup98
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1	2	Olfr873
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1	2	Pik3r4
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1	2	Poc1b
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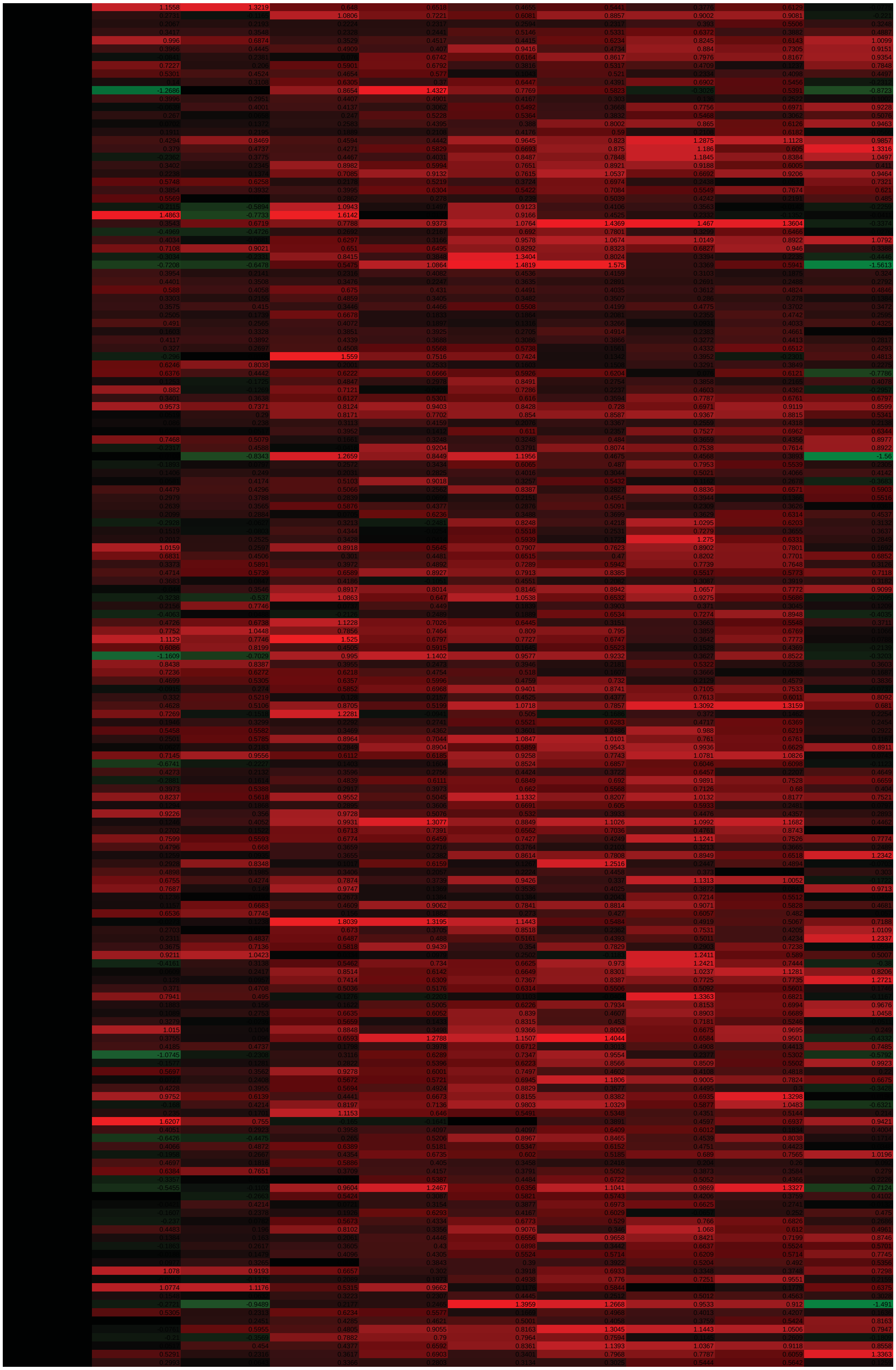
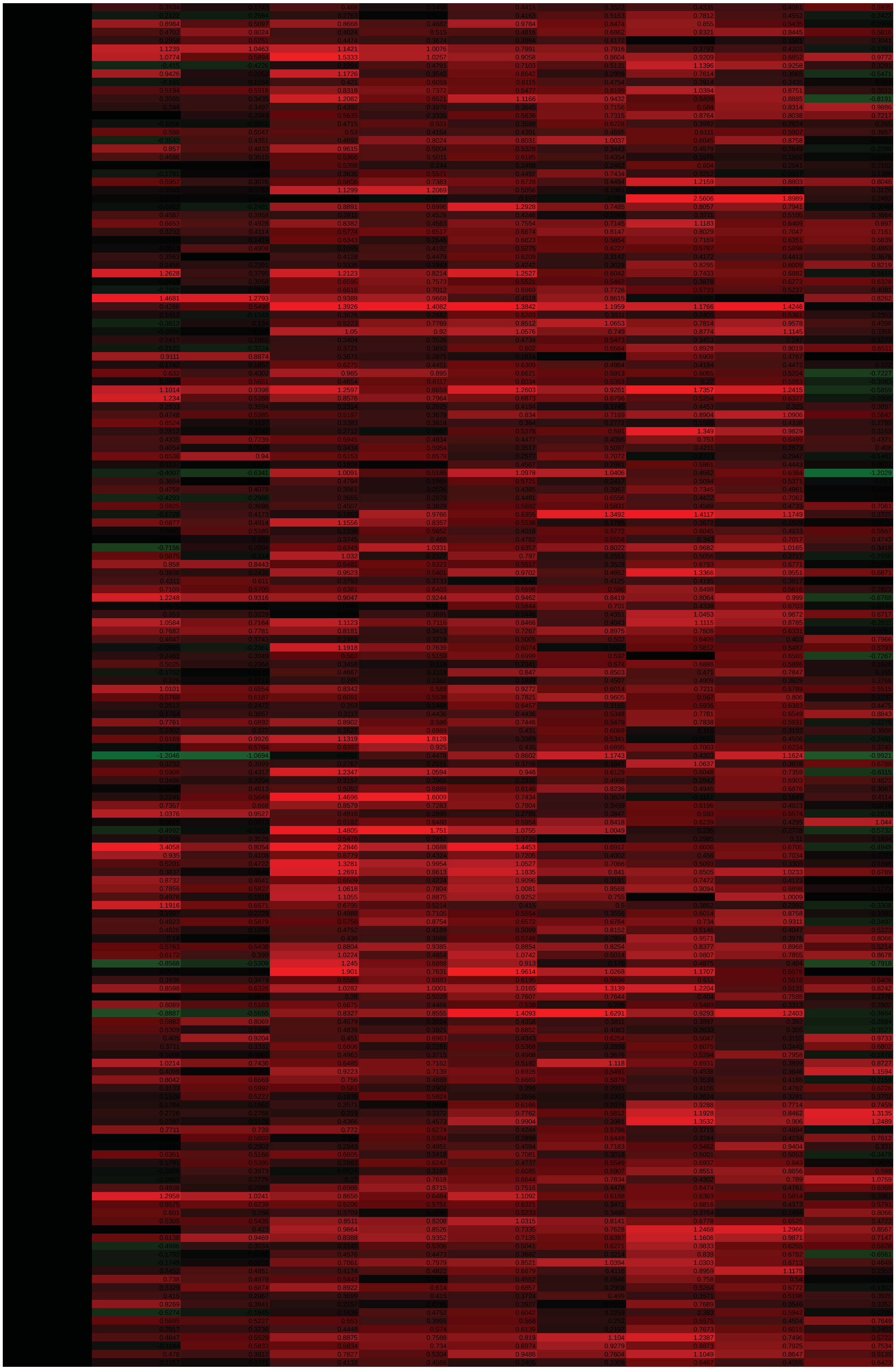
1	2	Poldip3
1	2	Pole3
1	2	Polh
1	2	Polr2d
1	2	Polr2k
1	2	Polr3a
1	2	Pop1
1	2	Pou2f1
1	2	Ppa2
1	2	Ppap2a
1	2	Ppfia3
1	2	Ppfibp1
1	2	Ppil2
1	2	Ppl
1	2	Ppm1a
1	2	Ppm1d
1	2	Ppm1g
1	2	Ppm1k
1	2	Ppp1ca
1	2	Ppp1cb
1	2	Ppp1r10



1	2 Ppp1r12c	0.2333	0.5166	0.3018	0.2874	0.1952	0.5001	0.1608	0.3113	0.5146
1	2 Ppp1r14d	0.1321	0.1691	0.9331	0.6626	0.9153	0.6767	0.6507	0.7068	0.8974
1	2 Ppp1r15a	2.438	1.1492	2.0277	1.0427	1.5139	0.8069	1.0252	0.9381	-0.6643
1	2 Ppp1r16a	0.5474	0.3632	0.2787	0.3544	0.5742	0.6423	0.7848	0.6662	0.5704
1	2 Ppp1r17	0.1882	0.1623	0.2818	0.303	0.3897	0.3316	0.4384	0.3135	[illegible]
1	2 Ppp1r1c	-0.8041	-0.4444	1.7054	1.5732	1.072	0.8714	-0.1454	0.4562	-1.9223
1	2 Ppp1r2	0.6127	[illegible]	0.3069	0.2466	0.3224	0.3397	0.914	0.6059	[illegible]
1	2 Ppp1r35	-0.2919	0.154	0.4588	0.7034	0.719	0.8168	0.7236	0.7842	0.6803
1	2 Ppp1r8	0.136	0.5637	0.6426	0.8348	0.8733	0.8718	1.2079	0.7725	1.0663
1	2 Ppp2cb	0.1036	-0.1792	0.9043	0.3723	0.5781	0.3589	0.7723	0.5055	0.2935
1	2 Ppp2r1a	-0.0894	[illegible]	0.6798	0.3461	0.9	0.9667	1.2125	0.7809	0.3535
1	2 Ppp2r1b	0.1659	0.5462	0.4496	0.3205	0.2407	0.4364	0.3713	[illegible]	0.6999
1	2 Ppp2r2c	0.5124	0.5443	0.219	0.3058	0.2563	0.2796	0.3599	0.2378	0.1646
1	2 Ppp2r5c	0.4043	0.1666	0.5985	0.2643	0.8358	0.5112	0.5151	0.7321	-0.2162
1	2 Ppp2r5d	0.4705	0.5528	0.4587	0.7651	0.7618	0.8325	0.3686	0.4901	0.7505
1	2 Ppp4r1	[illegible]	0.1649	0.2701	0.3846	0.5521	0.6651	0.452	0.2261	0.5588
1	2 Prdm4	0.3079	0.2937	0.4566	0.4367	0.4266	0.441	0.5269	0.7171	0.8173
1	2 Prdx2	0.3331	0.4694	0.6115	0.7085	0.4156	0.401	0.4211	0.3936	-0.2548
1	2 Prickle3	0.2381	0.362	0.2262	0.2332	0.681	0.7187	[illegible]	0.519	-0.2441
1	2 Prima1	-0.2073	-0.1511	0.61	0.43	0.7453	0.5666	0.2354	0.5771	-0.075
1	2 Prkaa2	-0.2691	-0.3339	0.5078	0.674	0.5305	0.8483	0.2245	1.0792	0.4318
1	2 Prkab1	[illegible]	0.2733	0.3209	0.1744	0.5592	0.4155	0.5992	0.6459	[illegible]
1	2 Prkdc	0.0957	0.2953	0.2791	0.355	0.3772	0.5433	0.7126	0.4626	0.6354
1	2 Prl8a9	0.1729	0.4473	0.4901	0.4494	0.4187	0.2768	0.2986	[illegible]	0.4451
1	2 Prmt5	-0.6195	0.2385	0.4227	0.6678	0.6837	0.8286	1.1171	0.8418	0.9344
1	2 Proca1	0.1229	0.2496	0.5324	0.3198	0.3155	0.2086	0.472	0.407	0.2917
1	2 Prosc	0.6004	0.5818	0.5017	0.796	0.3867	0.8985	0.7384	0.4272	0.7729
1	2 Prpf31	-0.1388	0.2517	0.1618	0.3405	0.3425	0.6359	0.4547	0.4241	[illegible]
1	2 Prpf38a	0.1862	0.1771	0.427	0.3157	0.7842	0.219	0.7842	0.4472	0.7397
1	2 Prpf40a	-0.1397	0.1583	0.2131	0.3009	0.6426	0.5547	0.4954	0.9163	0.3777
1	2 Prpf40b	0.2529	0.3634	0.244	0.2396	0.3135	0.3918	0.2639	0.2792	0.1711
1	2 Prr11	0.1433	0.2664	0.4788	0.2149	0.6399	0.608	0.5518	0.8049	0.4871
1	2 Prr18	-0.0843	[illegible]	0.8081	1.1361	0.4695	0.4903	[illegible]	0.3809	0.5127
1	2 Prr3	0.7583	0.8553	0.6399	0.5982	0.6109	0.6775	0.6056	0.5908	[illegible]
1	2 Prr7	0.317	0.4527	-0.1167	0.5998	[illegible]	0.9343	0.1817	0.7803	0.4808
1	2 Prrc2a	0.7407	0.2943	0.7975	0.601	0.6885	0.6271	0.6734	0.5783	[illegible]
1	2 Prrt3	0.0858	-0.0577	0.3416	0.0924	0.4097	[illegible]	0.49	0.6037	0.1057
1	2 Prss22	0.1186	0.0704	0.2429	[illegible]	0.5408	0.5986	0.7328	0.2602	0.2602
1	2 Prss8	-0.1581	[illegible]	0.1399	-0.1358	0.9942	0.4428	1.4534	0.9382	0.73
1	2 Prune	[illegible]	0.2529	0.5381	0.3208	0.4025	0.5646	0.3406	-0.1514	0.4917
1	2 Prx	-0.5409	-0.3548	1.0651	1.0766	1.1174	1.052	0.2213	0.9151	-1.0165
1	2 Psen1	0.0993	0.1009	0.8648	0.8012	0.6959	0.7875	0.2954	[illegible]	-0.4657
1	2 Psma3	0.0925	0.3163	0.6814	0.6648	0.4219	0.5608	0.4873	0.341	0.1244
1	2 Psmb10	0.3539	-0.2831	-0.128	0.3049	0.0852	0.3218	0.9101	0.7989	0.2185
1	2 Psmc1	[illegible]	0.0792	0.5	0.6904	0.7383	0.2962	0.9207	0.6203	0.5137
1	2 Psmd1	0.5453	0.6608	0.919	0.7395	1.0686	1.0711	1.2489	0.8988	0.785
1	2 Psmd11	0.1068	0.3721	0.6153	0.5047	0.5681	0.5018	0.5864	0.3881	1.2726
1	2 Psmd12	0.4278	[illegible]	0.6665	0.3746	0.7646	0.6716	0.93	0.6674	0.8853
1	2 Psmd6	0.6489	0.7347	1.0978	0.4831	1.29	0.5876	1.5114	0.996	0.3889
1	2 Psmd9	0.5953	0.5437	0.7237	0.4498	0.5953	0.5237	0.93	0.4783	0.4916
1	2 Psme3	0.2974	0.5384	0.996	0.9592	0.9863	0.8706	1.5514	1.3495	[illegible]
1	2 Psmg1	[illegible]	0.1651	0.2195	0.6136	0.6339	0.7478	1.1261	1.1171	1.1629
1	2 Psmg2	-0.273	-0.0422	0.2605	0.4921	0.5864	0.5319	0.734	0.6917	0.5321
1	2 Psors1c2	0.0604	-0.0454	0.3908	0.1309	1.219	0.7822	1.697	1.4142	0.0897
1	2 Psrc1	0.4189	0.4832	0.2669	0.7246	0.6089	0.617	0.5019	0.618	0.5532
1	2 Ptbp1	0.2477	0.3111	0.9152	0.6876	0.8035	0.9971	0.9477	1.1126	1.0885
1	2 Ptges3	-0.1436	-0.0945	0.7478	0.6036	0.8488	0.6315	0.7856	0.5086	1.192
1	2 Ptk2	0.4497	0.4571	0.1979	0.471	0.2239	0.3115	0.3463	0.5099	0.2115
1	2 Ptms	0.7754	0.6914	1.0143	0.6558	0.8698	0.5967	0.4107	0.4045	-0.766
1	2 Ptp4a2	0.8437	0.8318	0.4458	0.1876	0.3885	0.2356	0.6106	0.3891	-0.0644
1	2 Ptpn14	0.897	0.5937	1.1371	1.0469	0.897	0.8899	0.6099	0.9413	-0.3393
1	2 Ptpn21	1.7276	0.9593	0.8476	0.6758	0.6465	0.484	0.6716	0.927	0.0972
1	2 Ptprf	-0.5691	[illegible]	0.3681	0.5276	0.7427	0.9779	0.4471	0.6453	0.2788
1	2 Ptprk	-0.1978	-0.1419	1.025	0.6964	0.6821	0.5907	0.6337	0.7905	0.3435
1	2 Ptpru	-0.0667	-0.1442	[illegible]	0.2717	0.4452	0.8675	0.0562	0.6842	0.1058
1	2 Purb	0.5254	0.3402	0.88	0.6333	0.8257	0.7574	0.7826	0.6103	-0.1848
1	2 Pus10	-0.1193	0.0517	0.2954	0.802	0.5862	1.07	0.7937	0.9566	0.9522
1	2 Pus7	-0.2817	0.476	0.3179	0.4521	0.4336	0.7522	0.7304	0.4878	0.3537
1	2 Pvr	1.2531	1.0097	1.245	0.8974	0.9673	0.8799	0.5633	0.8129	0.1018
1	2 Pvrl2	1.5809	1.1143	-0.2693	-0.2693	0.567	0.4869	1.2867	0.9271	0.7798
1	2 Pvrl3	0.1946	0.0828	1.2141	1.1526	1.0965	0.8988	0.2135	0.2247	0.1338
1	2 Pwp1	0.137	0.2254	0.3298	0.4231	0.5408	0.4146	0.8307	0.4879	0.7587
1	2 Qars	-0.1977	0.0794	0.1393	0.2935	0.4066	0.6189	0.6049	0.704	0.4343
1	2 Qdpr	-0.0995	0.3289	0.4765	0.5107	0.9819	0.7062	0.6254	1.0243	0.9599
1	2 Rab1	0.5716	0.2669	0.4999	[illegible]	0.3969	0.2068	0.2678	0.2715	0.7806
1	2 Rab35	0.2183	0.1683	0.5155	0.4207	0.4504	0.4326	0.5083	0.3012	0.4871
1	2 Rab3gap2	0.2017	0.3377	0.4078	0.2401	0.202	0.424	[illegible]	0.4144	0.3157
1	2 Rab4a	0.7399	0.7921	0.7318	0.6501	0.6295	0.5271	0.7421	0.8439	1.3381
1	2 Rab5a	0.9203	0.317	0.7556	0.1263	0.3583	-0.0837	0.6113	0.2541	0.3158
1	2 Rab7	0.3409	0.2479	0.6612	0.7233	0.3165	0.6931	0.4193	0.116	1.081
1	2 Rab9	1.2093	0.6008	0.6055	0.0289	0.4241	-0.1238	0.5683	0.2158	0.7066
1	2 Rabif	0.2053	0.3845	0.3021	0.2854	0.2393	0.59	0.4738	0.1964	0.7798
1	2 Rabl3	-0.3119	0.1313	0.2342	0.2505	0.8117	0.5799	1.0884	0.8309	-0.124
1	2 Rabl5	0.4129	0.3965	0.0982	0.4482	0.5087	0.3206	0.3633	0.4996	0.2128
1	2 Rac3	-0.0376	-0.1565	0.1134	0.5159	0.9096	1.6017	0.6984	1.0267	0.2229
1	2 Rad17	0.3839	0.5053	0.4274	0.4114	0.6808	0.6318	1.0771	0.614	1.0112
1	2 Rad23a	0.4728	0.2662	0.8644	0.5801	0.6681	0.8389	0.7436	0.6589	0.8894
1	2 Rad23b	1.195	0.7745	1.3111	1.1427	1.3819	1.11	1.4249	1.2197	0.5677
1	2 Rad50	0.4045	0.2402	0.3121	0.249	0.585	0.2694	0.3726	0.4019	0.6816
1	2 Rad51l3	0.2525	0.368	0.3156	0.0433	0.4028	0.127	0.3351	0.4133	0.3544
1	2 Rad9	0.128	[illegible]	0.3568	0.4929	0.6654	0.4648	0.5295	0.4481	0.6817
1	2 Raet1b	0.6434	1.1163	-0.0726	[illegible]	0.2239	1.0284	0.6131	1.2276	-0.1365
1	2 Raf1	0.1895	[illegible]	0.7211	0.5867	0.7469	0.6458	0.8298	0.7132	0.6085
1	2 Rai14	0.9441	0.8719	0.9503	0.6769	0.6309	0.0711	0.172	0.2704	0.0556
1	2 Ralgapa2	0.0815	0.27	0.1987	0.5908	0.4874	0.3156	0.2758	0.4185	0.3761
1	2 Ralgps2	0.1858	0.1291	0.4797	0.3705	0.7564	0.494	0.6651	0.4315	0.9308
1	2 Raly	0.6267	0.4915	0.5729	0.6267	0.6448	1.3195	0.7606	0.2677	1.115
1	2 Ramp2	0.5202	0.4431	0.2736	0.5995	-0.0943	0.204	1.247	0.6815	0.4201
1	2 Ranbp10	0.1999	0.1169	0.5054	0.2392	0.5806	0.5251	0.2961	0.4714	-0.1775
1	2 Rap1gap2	-1.5947	-0.6804	1.8328	1.685	1.5223	1.3875	0.6892	0.9493	-2.4046
1	2 Rarg	1.06	1.0515	0.9805	0.8453	0.9666	0.9076	0.9723	0.9483	0.5595
1	2 Rars	[illegible]	0.5124	0.4955	0.5321	0.4803	0.4909	0.7953	0.2449	0.9866
1	2 Rb1	-0.518	0.0938	1.8031	1.5045	1.5894	1.235	0.5298	1.0656	-0.7118
1	2 Rbak	0.4578	0.3213	[illegible]	0.4467	0.3604	0.2268	0.4075	0.2632	0.2333
1	2 Rbbp7	0.0657	0.6069	0.2776	0.5608	0.47	0.8949	0.9277	0.3608	1.3239
1	2 Rbm12	[illegible]	0.3212	0.4934	0.4475	0.8047	0.4921	0.8819	0.5712	0.3301
1	2 Rbm14	0.1673	0.0267	0.9059	0.3451	0.5056	0.321	0.8117	0.9195	0.9321
1	2 Rbm15	0.6852	0.1963	1.3314	0.5525	0.9486	0.8076	1.0754	0.9384	0.8642
1	2 Rbm19	-0.0973	0.0642	0.4032	0.5746	0.6469	0.7525	0.8108	0.7152	0.5784
1	2 Rbm42	0.159	0.3807	0.3974	0.4154	0.4841	0.4384	0.6634	0.361	0.187
1	2 Rbm45	0.26	0.338	0.382	0.7143	0.2088	0.4182	0.1797	0.4049	0.764
1	2 Rbmx	0.4008	0.3098	0.831	0.6373	1.0883	0.9088	1.8692	1.4221	-1.4293
1	2 Rbmx2	0.2926	0.0707	0.2555	0.3288	0.4271	0.3933	0.3398	0.5191	0.4424
1	2 Rce1	0.0904	0.2401	0.352	0.4585	0.4553	0.6098	0.5903	0.7472	0.8579
1	2 Rchy1	0.1806	0.1986	0.2573	0.4582	0.1218	0.4355	0.24	0.663	0.1499
1	2 Rdbp	-0.1993	0.0916	0.3702	0.5877	0.6488	0.8144	0.6852	0.8782	0.6216
1	2 Recql5	0.2623	0.1555	0.446	0.2884	0.5401	0.2982	0.4349	0.4101	0.5556
1	2 Rev1	0.3174	0.2651	0.3903	0.3628	0.2945	0.3525	0.3159	0.5641	0.5981
1	2 Rexo1	0.2817	0.1665	0.349	0.4266	0.2091	0.2689	0.321	0.5079	0.3628
1	2 Rexo2	0.5158	0.7479	0.6808	0.8855	0.4827	0.3255	0.2773	0.1648	-0.1764
1	2 Rffl	-0.0592	-0.2307	0.4346	0.2641	0.5451	0.5732	0.7485	0.6726	0.5662
1	2 Rfng	[illegible]	[illegible]	0.3762	0.3892	0.4556	0.8347	0.3921	0.5812	-0.245
1	2 Rfx1	0.4074	0.3238	0.3583	0.5286	0.4661	0.6259	0.5949	0.9685	1.102
1	2 Rfx4	-0.2123	-0.7103	0.3752	0.6529	1.0056	1.6241	0.7667	1.5371	-0.4009
1	2 Rfxap	-0.1366	-0.2916	0.4534	0.4107	0.5241	0.4616	0.4398	0.4568	[illegible]
1	2 Rgl2	0.5537	0.4361	0.3204	0.2993	0.3282	0.3895	0.7265	0.4884	0.3378
1	2 Rgs12	0.4341	0.54	0.9094	0.9526	0.8751	0.8356	0.3761	0.6751	-0.5955
1	2 Rgs3	0.4839	0.3303	0.3632	0.2622	0.419	0.3652	0.2134	0.3468	0.3261
1	2 Rhbdd3	0.2961	0.3456	0.395	0.5672	0.278	0.3967	0.5371	0.497	0.849
1	2 Rhbdl1	0.4913	0.2893	0.1311	0.2289	0.1893	0.3089	0.4425	0.2207	0.5418
1	2 Rheb	0.2013	0.4268	0.4503	0.4171	0.7243	0.3837	0.6315	0.4873	0.3204
1	2 Rhot2	-0.1857	-0.112	0.3026	0.5556	0.5364	0.4888	0.6751	0.717	0.5107
1	2 Rhou	0.4509	0.2974	0.2376	-0.0724	0.4674	0.2637	0.5593	0.2755	0.1035
1	2 Rhox6	-0.1382	0.1837	0.5956	[illegible]	1.1552	0.619	1.3758	0.7874	0.9658
1	2 Ric8b	0.1046	-0.1432	0.583	0.1568	0.7202	0.5513	0.6704	0.7571	[illegible]
1	2 Rictor	1.403	0.7845	1.8391	1.1221	1.3219	1.116	1.1327	1.071	0.3533
1	2 Riok1	0.7812	0.6363	0.732	0.7842	0.5791	0.6137	0.6818	0.5153	0.6651
1	2 Rnase1	0.1354	0.9765	2.4518	1.9263	1.6418	0.7762	0.2459	0.4342	-1.0746
1	2 Rnd2	0.6887	0.3779	1.1791	0.8077	0.6704	0.9106	0.6854	0.4519	1.1103
1	2 Rnf10	-0.0936	0.2371	0.5198	0.559	0.5438	0.5015	0.2884	0.7361	0.1046
1	2 Rnf126	0.1274	0.5963	0.5373	0.9686	0.8189	0.9272	1.2148	0.7414	0.7642
1	2 Rnf138	0.8273	0.4635	0.4807	0.5698	0.544	0.3186	0.6837	0.6673	1.7552
1	2 Rnf141	0.309	0.1742	0.1969	0.345	0.1453	0.3124	0.4684	0.4946	0.3901
1	2 Rnf145	0.2608	-0.0666	0.0437	0.6115	0.5978	0.601	0.7485	0.746	0.1403
1	2 Rnf168	-0.1016	0.2096	0.4166	0.5951	0.6863	0.661	0.952	0.5927	0.8318
1	2 Rnf183	0.3343	0.2396	0.0722	0.2321	0.3437	0.4559	0.289	0.332	0.2015
1	2 Rnf185	0.7918	0.3594	0.8479	0.3289	0.4356	0.1506	0.2305	0.4375	0.1943
1	2 Pcgf3	0.8571	0.6984	0.7628	0.6944	0.5622	0.7589	0.4137	0.5183	0.6014
1	2 Rnf34	0.0428	0.0633	0.3291	0.5603	0.4747	0.2886	1.0049	0.4751	0.7871
1	2 Rnf4	0.6071	0.3581	0.9894	0.5712	0.3608	0.5244	0.7661	0.629	1.0979
1	2 Rnf40	0.4741	0.3609	0.6688	0.5377	0.4059	0.5165	0.5407	0.5243	0.1653
1	2 Rnf8	-0.0357	[illegible]	0.3405	0.5378	0.5084	0.5342	0.4203	0.2823	0.6283
1	2 Rngtt	-0.4413	0.0451	0.3327	0.6155	0.756	0.9306	0.5075	0.9152	0.1703
1	2 Rnu6	0.43	0.5566	0.9101	0.6126	1.0698	0.5301	1.126	0.7966	-0.0924
1	2 Rock2	1.0599	0.7929	1.2806	1.0546	0.8708	0.7288	0.6872	0.2851	0.4493
1	2 Ror2	0.7878	0.5575	0.3665	0.2614	0.5575	0.6262	0.5543	0.7622	-0.603
1	2 Rpa3	-0.2107	[illegible]	0.1124	0.3889	0.6618	0.5248	1.1241	0.9933	0.7055
1	2 Rpap1	-0.179	-0.06	0.2624	0.3844	0.2126	0.3371	0.5765	0.6255	0.2427
1	2 Rpl22l1	0.4383	0.2696	0.7067	0.2329	0.848	0.1673	0.5911	0.3937	1.1637
1	2 Rpl29	-0.0621	0.2348	0.9452	1.0318	1.3555	1.2578	1.1286	1.209	-2.5863
1	2 Rpl36al	-0.0578	0.1713	0.5305	0.646	0.5175	0.6916	0.5652	0.6779	0.5814
1	2 Rpl37a	0.6981	0.5854	0.7712	0.9239	0.6071	0.3203	0.6398	0.6905	[illegible]
1	2 Rpl41	0.4716	0.622	0.3477	0.5015	0.1881	0.4676	0.3585	0.6035	-0.2272
1	2 Rplp1	0.4108	0.6654	0.189	0.6066	0.2638	0.4405	0.2807	0.5189	-0.3221

1	2	Rps13	0.4188	0.2305	0.5708	0.6681	0.4519	0.5321	0.4804	0.4625	0.869
1	2	Rps6ka2	-0.3174	0.2988	0.6852	0.5176	0.7996	0.699	0.9247	0.7339	1.0635
1	2	Rps6ka5	[illegible]	0.2364	1.0821	1.0942	0.872	0.9361	0.5666	0.9974	[illegible]
1	2	Rps6kb2	0.3294	[illegible]	0.3186	0.3242	0.4571	0.3788	0.3503	0.3758	[illegible]
1	2	Rpusd1	[illegible]	0.4224	0.4083	0.2518	0.6108	0.4052	0.4719	0.495	[illegible]
1	2	Rqcd1	0.3273	0.2132	0.5786	0.4436	0.4654	0.4225	0.7713	0.61	0.5659
1	2	Rras2	0.2568	0.5612	0.2035	0.221	0.2075	0.1856	0.4248	0.4225	0.4147
1	2	Rreb1	[illegible]	0.1495	[illegible]	[illegible]	0.5256	0.5124	0.6686	0.53	0.2136
1	2	Rrm1	-0.4376	0.3619	0.614	0.5877	0.8003	0.7706	0.8301	0.7065	0.6037
1	2	Rrp36	[illegible]	0.3486	0.3230	0.4336	0.4342	0.3886	0.8521	0.528	0.405
1	2	Rtn4	0.8665	1.4501	0.3946	0.5907	0.3161	0.582	0.6994	0.3462	0.2823
1	2	Rtn4ip1	[illegible]	0.2713	0.4997	0.3737	0.4306	0.2742	0.6399	0.7648	0.5432
1	2	Rtp1	0.3332	0.42	0.3868	0.3795	0.3723	0.5663	0.415	0.3747	0.3137
1	2	Rufy4	0.2756	0.5726	0.5348	0.4053	0.3676	0.3567	0.2304	0.3317	0.5348
1	2	S100a3	-0.9939	-1.0393	1.2839	1.237	1.0881	2.0071	0.9533	1.2729	-1.8145
1	2	Sall2	0.591	0.5448	[illegible]	[illegible]	[illegible]	[illegible]	1.5358	1.007	[illegible]
1	2	Samd10	0.3675	[illegible]	0.7321	0.8813	0.7609	0.6315	0.5665	0.7212	-0.5237
1	2	Samd4b	1.1056	0.7382	0.8134	0.4762	0.5379	0.486	0.8387	0.6065	[illegible]
1	2	Sap130	0.2912	[illegible]	0.2435	0.1334	0.6246	0.3934	0.8164	0.6813	0.7425
1	2	Sarnp	0.3495	0.2358	0.3947	0.264	0.6714	0.3062	0.7331	0.7094	0.7792
1	2	Sars2	0.2902	0.3167	0.4811	0.588	0.8231	1.0886	0.9204	0.632	0.8958
1	2	Scaf1	0.8016	1.0192	0.844	0.7866	1.0213	0.7743	1.0144	0.9319	-0.5669
1	2	Scaf8	0.6051	[illegible]	0.9631	0.3054	0.5997	0.2943	0.5088	0.3881	-0.2856
1	2	Scamp4	0.5587	0.7938	0.4848	0.7237	0.7274	0.7636	0.5604	0.8059	-0.2872
1	2	Scly	0.1769	[illegible]	0.239	0.1779	0.3769	0.1743	0.8594	0.467	[illegible]
1	2	Scnn1a	-0.3142	-0.3147	0.3654	0.3315	1.0812	1.15	0.5474	1.159	-0.6054
1	2	Scrib	0.5136	0.631	0.6188	0.635	0.8577	0.8211	0.8611	0.563	0.643
1	2	Sct	0.3206	0.9101	0.9335	0.3504	0.643	0.7465	0.7546	0.9949	1.6008
1	2	Sctr	0.4789	0.5831	0.3776	0.4418	0.3534	0.2655	0.2134	0.3512	0.303
1	2	Scube3	0.1236	0.3378	0.5818	0.4032	0.6342	0.8227	0.3134	0.8438	[illegible]
1	2	Scyl1	0.9498	0.3783	0.4774	0.4606	0.5208	0.2563	0.5227	0.5348	0.2805
1	2	Sdccag3	0.4551	0.4171	0.1951	0.5354	0.3907	0.5067	0.4566	0.624	0.667
1	2	Sec61a2	0.2313	0.436	[illegible]	0.3129	0.3825	0.2962	0.6923	[illegible]	0.4712
1	2	Sehl1	[illegible]	0.2176	0.4733	0.4571	0.6961	0.9217	0.9243	0.8781	0.6838
1	2	Selp	0.4925	0.5927	0.5772	0.3874	0.6167	0.2276	0.4225	0.4925	0.2562
1	2	Sema4d	[illegible]	[illegible]	0.3765	0.2361	0.4467	0.6167	0.423	0.2173	[illegible]
1	2	Sema6b	0.178	0.4008	0.2964	0.3045	0.2778	0.3677	0.3259	0.3574	0.4038
1	2	Senp1	[illegible]	0.5096	0.3444	0.5869	0.6639	0.5296	0.9223	0.8706	1.048
1	2	Serbp1	-0.5881	[illegible]	0.4269	0.6573	0.6454	0.5419	0.949	0.7255	0.3132
1	2	Serpina3m	[illegible]	[illegible]	[illegible]	[illegible]	0.411	0.1474	0.8644	0.8698	[illegible]
1	2	Serpinb3a	-0.8846	-0.5426	1.7174	1.3954	1.6732	1.4518	0.8547	0.685	-1.076
1	2	Serpinb3d	-0.1635	[illegible]	1.2219	0.8181	0.8841	0.8484	0.2925	0.5681	[illegible]
1	2	Sesn2	0.503	0.7085	0.3341	0.6113	0.2633	0.5341	[illegible]	0.3788	1.0019
1	2	Sesn3	0.5908	0.3955	0.3765	0.4556	0.5438	0.5438	0.3325	0.4462	[illegible]
1	2	Setd1a	0.2878	0.4004	0.5945	0.3778	0.639	0.4216	0.9722	0.8436	0.472
1	2	Setd1b	0.9675	0.4639	0.6666	0.5382	0.8257	0.3565	0.7856	0.4627	[illegible]
1	2	Setd2	0.4879	0.1581	0.4564	0.4433	0.2198	0.2037	0.2767	[illegible]	0.3706
1	2	Setd7	[illegible]	[illegible]	0.3657	0.4399	0.5995	0.9077	0.616	0.8074	0.3737
1	2	Setd8	-0.308	[illegible]	0.2073	0.4071	0.7194	0.4466	0.6267	0.4745	[illegible]
1	2	Sf1	0.8776	0.3177	0.9872	0.5981	0.7003	0.6118	0.7398	0.4731	1.0093
1	2	Sf3a2	0.4098	0.1772	0.2545	0.4098	0.4688	0.4098	0.8137	0.6133	[illegible]
1	2	Sf3b4	0.431	0.1887	0.3981	0.3031	0.4863	0.2099	0.8960	0.2951	[illegible]
1	2	Sfn	-1.1974	-1.2196	0.4332	-0.1254	0.8568	1.1384	1.1309	1.2795	-0.5296
1	2	Sfpq	[illegible]	[illegible]	0.5589	0.5582	0.6094	0.4281	1.0824	0.576	0.6393
1	2	Sfr1	0.8678	0.395	0.621	[illegible]	0.6574	0.3698	0.853	0.5792	0.6154
1	2	Sfxn3	0.8756	0.6558	0.8293	0.7	0.5932	0.6126	[illegible]	0.5932	[illegible]
1	2	Sgk1	2.272	1.0566	0.7433	-0.9596	0.2819	-0.7624	1.59	0.4583	1.7548
1	2	Sgms1	[illegible]	[illegible]	0.2584	[illegible]	[illegible]	[illegible]	0.7423	0.5495	[illegible]
1	2	Sh3bp1	0.1982	0.3354	0.5319	0.5237	0.7334	0.5781	0.4842	0.8444	0.2465
1	2	Sh3rf2	0.1317	0.267	1.6164	0.6364	1.1555	0.64	0.4559	0.5647	[illegible]
1	2	She	[illegible]	[illegible]	0.8801	0.9177	0.7872	0.5868	0.3253	0.4269	0.2582
1	2	Shf	[illegible]	[illegible]	[illegible]	[illegible]	0.4892	0.6663	0.2965	0.3344	0.5607
1	2	Shisa2	0.2905	0.7136	1.3989	1.0196	0.6376	0.452	0.3466	0.2542	-0.2852
1	2	Shkbp1	0.1648	0.2816	0.4524	0.2606	0.5487	0.8474	0.6993	0.7063	1.1363
1	2	Shoc2	0.341	0.4126	0.3078	0.4054	0.2155	0.5258	0.5214	0.3378	0.6578
1	2	Shroom3	[illegible]	[illegible]	0.6322	0.4612	0.4134	0.399	0.9114	0.6376	[illegible]
1	2	Sik1	0.9434	0.2826	0.6554	0.2982	0.5475	0.5187	0.3288	0.5284	0.7475
1	2	Sirt6	0.1817	0.1637	0.453	0.3314	[illegible]	0.4462	0.2661	0.4507	0.5838
1	2	Siva1	0.4808	0.6726	[illegible]	0.5195	0.2843	0.257	0.3421	0.4773	0.5603
1	2	Skil	0.5399	[illegible]	0.8455	0.5876	0.7029	0.6728	0.8426	1.1219	1.1611
1	2	Skiv2l2	-0.4387	[illegible]	0.6985	0.6934	0.7747	1.0126	1.1695	1.1	0.8593
1	2	Slc12a2	0.6103	0.8678	0.3294	0.4802	0.3226	0.2047	0.616	0.4697	[illegible]
1	2	Slc12a3	[illegible]	0.4262	0.5984	0.4529	0.4209	0.6637	0.2323	0.4481	0.27
1	2	Slc16a13	0.3098	[illegible]	0.2191	0.2436	0.5918	0.4301	[illegible]	0.6423	[illegible]
1	2	Slc16a3	0.1894	0.315	0.4385	0.5345	0.9914	1.0227	1.476	1.5374	0.479
1	2	Slc18a2	[illegible]	[illegible]	0.7442	0.4208	1.0294	0.4404	0.1532	[illegible]	[illegible]
1	2	Slc1a4	0.7234	0.6287	0.619	0.5666	0.5404	0.4076	0.5306	0.6589	0.5365
1	2	Slc1a5	0.424	[illegible]	0.32	0.5904	0.32	0.8012	0.2714	0.4093	[illegible]
1	2	Slc20a1	0.439	0.272	0.4049	0.5007	0.7074	0.4968	0.8366	[illegible]	1.1641
1	2	Slc20a2	0.8359	0.8211	1.0591	1.0012	0.7023	0.36	1.0239	0.9197	1.0059
1	2	Slc22a12	0.3937	0.2627	0.3241	0.2679	0.36	0.2865	0.2587	0.3414	[illegible]
1	2	Slc25a1	0.1266	0.3726	0.3424	0.4203	0.4931	0.5234	0.5005	0.4782	0.8754
1	2	Slc25a11	0.5631	0.4685	0.4865	0.3603	0.5096	0.6614	0.6374	0.3947	0.8799
1	2	Slc25a16	0.4251	0.2997	0.2177	[illegible]	0.2779	0.3238	0.5202	0.3337	[illegible]
1	2	Slc25a20	0.4048	0.3828	0.3868	0.8039	0.3868	0.8512	0.3353	[illegible]	0.6642
1	2	Slc25a24	0.6164	0.7707	0.8567	0.6916	0.6566	0.2718	0.2789	0.2745	[illegible]
1	2	Slc25a3	0.1771	0.5082	0.3269	0.692	0.6056	0.4186	0.8831	0.5652	0.4876
1	2	Slc25a38	0.2089	-0.2918	0.4019	0.5579	0.6579	0.4025	0.3668	0.5179	0.3748
1	2	Slc25a39	0.4991	0.754	0.6509	0.9868	0.6007	0.8269	0.863	0.7603	[illegible]
1	2	Slc25a5	-0.3786	0.3213	0.5747	0.709	0.8492	0.5979	0.8753	0.8315	0.8102
1	2	Slc30a1	0.416	[illegible]	0.5154	[illegible]	0.3943	[illegible]	0.6843	0.1915	0.3633
1	2	Slc31a1	[illegible]	[illegible]	0.303	0.7602	0.4915	0.4349	0.3481	0.7853	[illegible]
1	2	Slc31a2	0.9193	0.2498	0.2847	0.1296	0.2777	0.3991	0.4844	0.2105	0.3258
1	2	Slc35b1	0.7949	0.8699	0.5476	0.2769	0.5504	0.4884	0.6122	[illegible]	0.335
1	2	Slc35e2	0.4973	0.1151	0.3618	0.2595	0.2453	[illegible]	0.5208	0.3487	0.4622
1	2	Slc38a2	0.7779	0.2771	0.7052	[illegible]	0.7533	0.3159	0.8416	0.4013	0.7182
1	2	Slc38a4	0.7175	0.6473	0.5362	0.4626	0.6614	0.4367	0.6133	0.3633	1.134
1	2	Slc38a7	1.0795	0.6132	0.7652	0.4027	0.5482	0.5004	0.7766	0.7211	0.8562
1	2	Slc39a1	0.5561	0.5518	0.43	0.6153	0.5212	0.216	0.43	0.4324	[illegible]
1	2	Slc39a10	[illegible]	[illegible]	0.521	0.5321	0.2136	0.4714	0.303	0.5531	0.3559
1	2	Slc39a14	[illegible]	0.2246	[illegible]	0.576	[illegible]	0.5163	0.2227	[illegible]	0.2756
1	2	Slc39a8	-0.2932	-0.3866	0.6367	0.61	1.3036	1.5363	1.1983	0.4336	-0.3560
1	2	Slc45a4	0.1904	0.1212	0.3312	0.4079	0.7492	1.0711	0.5917	0.7648	0.6726
1	2	Slc4a1ap	0.4701	0.4105	0.2429	0.3389	0.4792	0.4797	0.4255	0.429	0.4545
1	2	Slc5a8	[illegible]	0.4637	0.8866	0.8591	0.8775	0.4926	0.4292	0.5163	[illegible]
1	2	Slc7a6	[illegible]	0.1442	0.3686	0.5464	[illegible]	0.4356	0.5282	0.8578	0.2859
1	2	Slc9a8	0.3547	0.4859	0.3847	0.6095	0.4981	0.2461	0.4771	0.2222	0.2335
1	2	Slfn3	0.415	0.5231	0.5885	0.3354	0.3606	0.5006	0.526	0.3318	[illegible]
1	2	Smad5	1.3384	0.2767	1.6315	0.6729	0.9252	0.7035	0.5823	0.4983	[illegible]
1	2	Smap1	0.9421	0.347	0.4699	0.5556	0.4784	0.3868	0.2982	0.5512	0.2564
1	2	Smc1a	[illegible]	0.1804	0.493	0.43	0.5131	0.4703	0.7949	0.74	0.8997
1	2	Smc6	0.4814	0.7268	0.6651	0.7109	0.662	0.5931	0.7925	0.7532	1.1209
1	2	Smchd1	0.373	0.1985	0.3504	0.4384	0.7003	0.6672	0.7215	0.8305	[illegible]
1	2	Smek1	0.1408	[illegible]	0.6113	0.556	0.7595	0.7232	1.0711	0.795	0.6083
1	2	Smek2	[illegible]	0.1446	0.4657	0.2924	0.537	0.63	0.3374	[illegible]	[illegible]
1	2	Smg1	0.1808	[illegible]	0.5314	0.2955	0.6033	0.4268	0.7663	0.5028	[illegible]
1	2	Smpd3	[illegible]	0.1390	1.2525	1.1857	0.5085	[illegible]	[illegible]	[illegible]	[illegible]
1	2	Smpd4	[illegible]	[illegible]	0.1979	0.2458	0.5646	0.2776	0.9167	0.468	0.67
1	2	Smtn	1.4058	1.3284	0.1079	[illegible]	0.3883	0.4815	1.2425	0.7282	0.4804
1	2	Smug1	[illegible]	[illegible]	[illegible]	0.5601	0.3627	0.7148	[illegible]	0.4505	[illegible]
1	2	Smurf2	0.6003	0.5123	0.6379	0.4323	0.344	0.53	0.3826	0.4406	0.6424
1	2	Smyd5	[illegible]	[illegible]	0.4059	0.4889	0.626	0.6361	1.1311	0.7404	1.2985
1	2	Sncg	1.0345	1.3683	0.5961	0.6307	0.7908	0.821	0.6214	0.663	0.663
1	2	Snd1	0.632	0.8209	0.587	0.6295	0.4926	0.723	[illegible]	0.4803	[illegible]
1	2	Snrnp27	0.5680	0.2337	0.6231	0.4654	0.6608	0.358	0.859	0.781	0.5025
1	2	Snrpb	0.2613	[illegible]	0.4727	0.4483	0.5129	0.3408	0.6151	0.5581	[illegible]
1	2	Sntb2	1.245	1.0642	[illegible]	[illegible]	[illegible]	0.4172	[illegible]	[illegible]	1.1466
1	2	Snx12	[illegible]	[illegible]	0.5354	0.7481	0.9488	0.7198	0.4695	[illegible]	[illegible]
1	2	Snx16	0.3943	0.3102	0.6736	0.5688	0.4966	0.4436	0.3923	0.5692	0.8138
1	2	Snx3	0.5883	0.6051	0.3636	0.407	0.4745	[illegible]	0.3716	[illegible]	[illegible]
1	2	Socs6	[illegible]	0.4638	0.6798	0.5365	0.3776	0.302	0.477	0.3232	0.4887
1	2	Socs7	[illegible]	[illegible]	[illegible]	0.4952	[illegible]	0.6799	0.3793	[illegible]	[illegible]
1	2	Sox13	-0.2188	0.227	1.2179	1.1131	1.3565	1.1956	1.3183	1.0452	[illegible]
1	2	Sox17	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.7207	0.9865	[illegible]
1	2	Sp6	[illegible]	[illegible]	0.3959	0.337	0.8908	0.859	0.8444	0.9389	[illegible]
1	2	Spag16	0.1864	0.4074	0.4217	0.3219	[illegible]	[illegible]	0.2587	[illegible]	[illegible]
1	2	Spast	[illegible]	[illegible]	[illegible]	0.4244	0.5298	0.4146	0.4492	0.6006	0.5014
1	2	Spc24	-0.1446	0.4642	[illegible]	0.444	0.5865	0.6297	0.8334	0.6082	0.8752
1	2	Spg7	[illegible]	0.2998	[illegible]	0.3443	[illegible]	[illegible]	0.6003	0.4113	[illegible]
1	2	Sphk2	0.79	0.4666	0.6266	0.5326	1.1009	0.5365	0.8146	1.081	[illegible]
1	2	Spin1	[illegible]	[illegible]	[illegible]	[illegible]	0.5109	0.5106	0.4288	[illegible]	0.5365
1	2	Spnb1	-0.6466	-0.2352	0.7805	1.4121	0.5864	1.1608	[illegible]	1.245	[illegible]
1	2	Spock2	[illegible]	[illegible]	0.7471	0.9615	0.3857	[illegible]	0.3924	0.5615	[illegible]
1	2	Sprr2a1	0.6435	0.4643	0.5594	0.4978	0.7043	0.2742	0.8287	0.6425	0.5565
1	2	Spsb4	0.6754	0.6313	0.8056	0.7456	[illegible]	[illegible]	0.8157	0.4419	1.0048
1	2	Sptlc1	0.3903	0.5209	[illegible]	0.6148	0.6883	0.4260	0.6578	0.3034	[illegible]
1	2	Spty2d1	0.8217	0.3718	0.5195	0.4662	[illegible]	0.3121	0.492	0.1904	[illegible]
1	2	Sqle	0.537	0.5009	0.538	0.7952	0.4138	0.9979	1.1529	[illegible]	1.4758
1	2	Srebf1	0.4817	0.624	0.5762	0.7058	0.8174	0.3852	0.8236	0.8433	[illegible]
1	2	Srf	[illegible]	[illegible]	0.4053	[illegible]	0.5478	0.4059	0.3044	[illegible]	[illegible]
1	2	Srgn	-1.1916	-0.7715	0.6359	0.7776	1.0103	0.8624	0.2969	0.8321	-0.8074
1	2	Srp19	0.3496	0.3157	0.4996	0.6203	0.4806	0.3933	0.4628	0.3403	0.8069
1	2	Srp54a	0.2222	0.3098	0.8994	1.162	0.9684	1.2487	0.368	0.525	0.7314
1	2	Srp68	0.3233	0.2832	0.2742	[illegible]	0.4551	0.3013	[illegible]	0.5659	[illegible]
1	2	Srp9	0.5445	0.3693	[illegible]	[illegible]	0.3543	[illegible]	0.6851	[illegible]	0.4409
1	2	Srrm2	0.6128	0.3021	0.5792	0.2837	0.4601	0.4263	0.6717	0.6092	[illegible]
1	2	Srsf10	0.5934	0.4331	0.5787	0.4716	0.6604	0.918	1.0864	0.8321	1.2248
1	2	Srsf11	0.3782	[illegible]	0.4416	0.6345	0.4806	0.424	[illegible]	[illegible]	[illegible]
1	2	Srsf4	[illegible]	[illegible]	0.5451	0.5501	0.6428	0.8626	1.158	0.688	0.6344
1	2	Srsf6	0.3991	0.3166	0.942	0.3926	0.5775	[illegible]	0.7152	0.599	[illegible]
1	2	Ssbp1	0.2899	0.4251	[illegible]	0.2746	0.4536	0.2981	1.0385	0.5186	0.5936
1	2	Ssrp1	[illegible]	0.3106	[illegible]	0.2692	0.4248	0.4253	0.7066	0.6203	0.5309
1	2	Sssca1	-0.6001	[illegible]	[illegible]	0.7523	0.578	0.7002	0.8102	0.9613	[illegible]
1	2	St8sia2	[illegible]	[illegible]	1.5676	1.7358	1.7653	1.6344	0.6856	0.9989	-0.6033



1 2 Stag1
1 2 Stag2
1 2 Stard10
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1 2 Strap
1 2 Strn4
1 2 Stt3b
1 2 Sugp1
1 2 Sumo2
1 2 Sun1
1 2 Supt5h
1 2 Suv39h1
1 2 Suv420h1
1 2 Swap70
1 2 Syncrip
1 2 Syngr2
1 2 Syp
1 2 Sypl2
1 2 T
1 2 Tac2
1 2 Taf12
1 2 Taf1d
1 2 Taf3
1 2 Taf5l
1 2 Taf6
1 2 Taf6l
1 2 Tars
1 2 Tax1bp1
1 2 Tbc1d1
1 2 Tbc1d13
1 2 Tbc1d20
1 2 Tbc1d22b
1 2 Tbc1d24
1 2 Tbc1d25
1 2 Tbc1d8
1 2 Tbl1xr1
1 2 Tbrg4
1 2 Tceal8
1 2 Tceb2
1 2 Tcf12
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1 2 Tctn3
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1 2 Tecr
1 2 Terf2ip
1 2 Tes
1 2 Tex21
1 2 Tfap2a
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1 2 Tfpt
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1 2 Thop1
1 2 Thsd1
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1 2 Timm17a
1 2 Timm8a1
1 2 Tiparp
1 2 Tjap1
1 2 Tjp1
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1 2 Tmc7
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1 2 Tomm7
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1 2 Trip6
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1 2 Txnrd1
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1 2 Uba1
1 2 Ubap2l
1 2 Ube2dnl1

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1	2	Ube2m
1	2	Ube2o
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1	2	Ube2q2
1	2	Ube2z
1	2	Ubn2
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1	2	Ubtf
1	2	Uchl3
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1	2	Vmn2r-ps11
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1	2	Vsig4
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1	2	Ywhah
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1	3	Abi3bp
1	3	Adpgk
1	3	Ahcy
1	3	Arf4
1	3	Arpp19
1	3	Atg2a
1	3	Bag2
1	3	Baiap2
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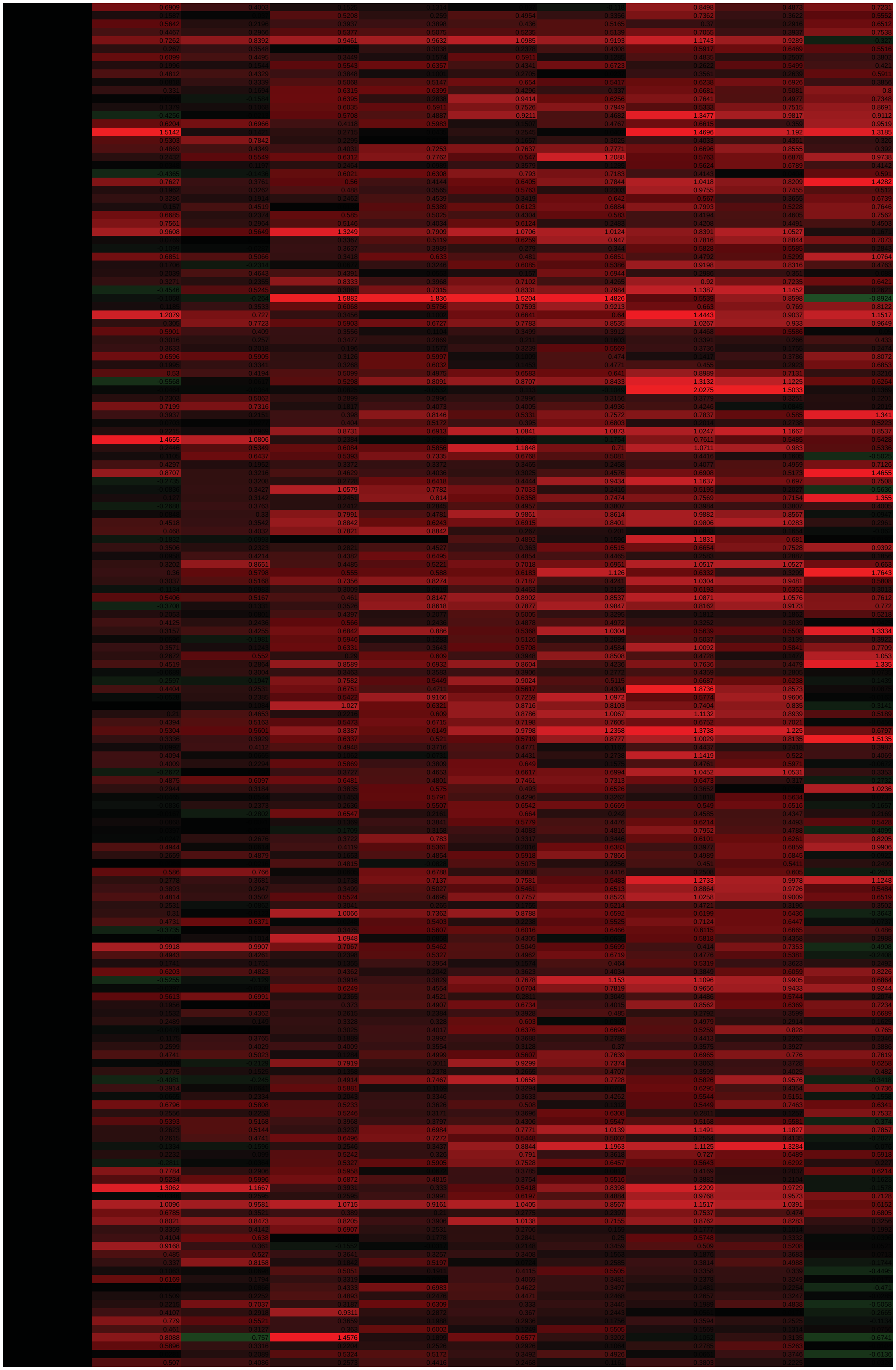
1	3	Capzb
1	3	Cbfb



1	3	Cbr2	-1.5169	-0.4376	-0.0906	0.2131	0.8181	1.5327	0.8099	1.2238	-2.4525
1	3	Cd200	0.2031	0.4059	0.8099	0.4411	0.5642	0.1872	0.1418	0.0915	-0.1059
1	3	Chi3l1	-0.7737	-1.163	0.5912	[illegible]	1.477	1.2371	0.3398	0.8984	-2.9746
1	3	Clptm1	0.2447	0.5023	0.6002	0.3888	0.5971	0.2106	0.3764	0.3292	-0.5095
1	3	Cnpy4	0.344	0.5237	0.3686	0.2583	0.2122	0.3796	0.2937	0.2725	[illegible]
1	3	Cux1	0.1904	0.3201	0.4811	0.3418	0.3298	0.4962	[illegible]	0.2503	0.1363
1	3	Dusp7	0.7703	0.778	[illegible]	0.229	0.192	0.5712	0.3868	0.3931	-0.1208
1	3	Eif2ak1	0.1152	0.2891	0.5037	0.4404	0.4399	0.2975	0.528	0.2265	-0.3876
1	3	Eno3	-0.0845	0.7144	0.3596	0.7402	[illegible]	0.1698	0.2347	0.1952	0.2072
1	3	Ero1lb	-1.2581	-0.0686	1.1371	0.8834	0.8924	0.3646	-0.0697	0.0663	-0.7083
1	3	Etfdh	0.1944	0.126	0.5529	0.5787	0.4042	0.4182	0.3439	0.0705	-0.1195
1	3	Foxj3	0.6487	0.1959	0.7886	0.2914	0.3191	0.1238	0.2731	0.1743	0.067
1	3	Fut8	0.3691	0.4054	0.4375	-0.0482	0.552	0.4165	0.3622	0.2865	-0.42
1	3	Galr2	0.3427	0.2067	0.1616	0.5364	0.1956	0.5379	0.2288	0.5685	-0.2955
1	3	Gga1	0.4592	0.062	0.398	0.1786	0.5253	0.3375	0.3358	0.2725	-0.0873
1	3	Gm136	0.3671	0.3744	0.5585	0.3695	0.2425	0.1292	0.2946	0.1717	0.1938
1	3	Gpsm2	0.7279	0.1472	0.2808	[illegible]	0.5208	0.4138	0.5601	0.308	-0.352
1	3	Hspb8	0.2369	-0.1687	0.988	0.7965	0.7541	0.7391	-0.1588	0.3509	-1.1832
1	3	Ifi44	0.5882	0.316	0.51	0.2238	0.246	0.2815	0.098	0.2238	0.2238
1	3	Igf1r	0.4191	0.141	0.8558	0.6366	0.6557	0.4631	-0.0739	0.2727	-0.5134
1	3	Ins1	0.3615	0.521	0.411	0.0695	0.3715	0.2998	0.238	0.3939	[illegible]
1	3	Itpkc	1.0389	[illegible]	1.3975	[illegible]	0.2358	0.5309	-0.1469	[illegible]	0.1946
1	3	Ivd	0.1242	0.3155	0.2061	0.3843	0.5022	0.4298	0.2761	0.5284	-0.3423
1	3	Klf13	0.1896	-0.2803	0.9711	0.1791	0.5645	0.4886	[illegible]	0.2162	-0.6259
1	3	Klf6	0.5308	-0.265	0.9301	0.0966	0.6689	0.2385	0.3146	[illegible]	-0.4947
1	3	Klhl9	0.7198	0.427	0.4752	0.6259	0.3297	0.431	0.2009	0.0746	-0.18
1	3	Klc1	-0.1062	-0.0751	0.6223	0.3228	0.5806	0.2131	0.5551	0.439	-0.9046
1	3	Ldoc1l	0.3086	0.2324	0.302	0.4401	0.2091	0.3036	0.394	0.6386	-0.6135
1	3	Lrrc14	0.3277	0.5082	0.4143	0.4357	0.3436	[illegible]	0.3115	0.2882	0.0787
1	3	Lysmd2	0.6184	0.4854	0.2506	0.3474	0.3151	0.2148	0.1369	0.4502	-0.1482
1	3	Macrod2	-0.0725	-0.0815	0.566	0.5925	0.361	0.3388	0.1478	0.2417	[illegible]
1	3	Map3k11	-0.5034	-0.6306	0.6731	0.5611	0.5373	0.4629	0.4233	0.5161	-0.8328
1	3	Mllt1	0.3926	0.2862	0.5312	0.5807	0.3801	0.2376	0.122	0.4091	-0.4193
1	3	Naalad2	-0.067	-0.0773	0.5169	0.2949	0.8116	0.1071	0.1342	0.2975	-0.0535
1	3	Nat15	0.2235	0.5952	0.417	0.4485	0.1008	0.3472	0.2771	0.3833	-0.0612
1	3	Nckap5l	0.6564	0.3414	0.4118	0.3903	0.3345	0.24	0.2418	0.3465	-0.3285
1	3	Nr1h2	0.4538	0.5375	0.215	0.2883	0.228	0.1115	0.6966	0.1359	-0.209
1	3	Nudt6	0.3972	0.4918	0.3944	0.8246	0.3613	0.357	0.1182	0.6297	-0.724
1	3	Olfr1477	0.5464	0.4079	0.1715	0.2305	0.4239	0.4052	0.1998	0.1133	0.2427
1	3	Orai1	-0.2815	-0.4264	0.5904	0.4234	0.4194	0.5755	0.2148	0.4017	-0.4006
1	3	P2rx7	0.1657	0.0804	0.366	0.2864	0.4389	0.4938	0.1189	0.2892	[illegible]
1	3	Papola	0.4674	0.2737	0.3179	0.4327	0.2368	0.1871	0.085	0.4723	0.1601
1	3	Pdxdc1	0.9481	0.674	0.3059	0.1944	0.2122	0.1638	0.3434	0.4063	0.0944
1	3	Phf13	0.4465	0.1514	0.5863	0.1052	0.4331	0.3766	0.1108	0.2967	[illegible]
1	3	Pitpnm3	-0.0321	0.2732	0.6689	0.6124	0.3916	0.4156	[illegible]	0.5586	-0.5041
1	3	Plaur	[illegible]	0.2128	0.8996	0.266	0.6514	0.3109	0.1436	0.228	-0.3738
1	3	Plce1	0.2583	0.1793	0.3637	[illegible]	0.2163	0.4671	0.4335	0.2934	[illegible]
1	3	Plekhg2	0.5933	0.361	0.6064	0.4831	0.4598	0.5448	0.1158	0.2321	-0.3233
1	3	Polm	0.4171	0.2212	0.258	[illegible]	0.3354	0.4905	0.4572	0.3181	-0.0763
1	3	Ppp2r5e	[illegible]	0.1347	0.3788	0.4196	0.5154	0.4228	0.1079	0.3911	-0.3061
1	3	Prkaca	0.7435	0.7913	0.4923	0.425	0.3824	0.2471	0.3311	0.3865	-0.3234
1	3	Psme2b-ps	0.6696	[illegible]	0.3699	[illegible]	0.5771	0.059	0.8036	0.4136	-0.3267
1	3	Ptk2b	0.6594	0.4805	0.252	0.4523	0.2983	0.2744	0.3297	0.4272	-0.1407
1	3	Ptp4a3	-0.6437	0.3522	0.5798	1.0215	0.6359	0.785	-0.2257	0.6092	-1.6535
1	3	Ranbp6	0.3849	0.2846	0.2424	0.2905	0.3682	0.2084	0.2021	0.3342	0.2239
1	3	Ranbp9	0.2221	-0.1351	0.5926	0.5123	0.297	0.4338	0.1815	0.169	-0.144
1	3	Rbfox1	0.619	0.7276	0.1636	0.1784	0.3915	0.1214	0.4802	0.1784	[illegible]
1	3	Riok3	0.3964	0.177	0.5837	0.1791	0.5476	0.1864	0.1869	0.4187	-0.6143
1	3	Rps3a	0.37	0.2025	0.5048	0.0305	0.765	-0.0748	0.7176	0.3946	-0.5337
1	3	41527	0.2041	0.5383	0.5383	0.5418	0.2795	0.269	0.1268	0.1151	-0.1223
1	3	Sertad2	0.9727	0.3681	0.4496	0.1831	0.1006	0.3914	0.0745	0.2231	0.2445
1	3	Sh2d1a	0.1879	0.2762	0.866	0.8641	0.2619	0.129	0.1195	0.1384	-0.0818
1	3	Sh3yl1	-0.1476	-0.0876	[illegible]	0.3947	0.7042	0.5634	0.1003	0.6377	-0.345
1	3	Slc25a25	0.8958	-0.2148	1.0801	-0.0565	0.4471	0.0544	0.3349	0.2213	[illegible]
1	3	Slc35c1	0.0561	0.4303	0.3155	0.5613	0.3963	0.4115	0.1766	0.589	-0.777
1	3	Slk	0.4346	0.422	0.5548	0.3646	0.4425	0.3914	0.1153	0.3638	-0.3792
1	3	Spata7	0.1732	0.3922	0.2999	0.559	0.2469	0.5626	0.2128	0.3697	-0.3448
1	3	Strn3	0.6514	0.3667	0.5409	0.3998	0.1766	0.3078	0.2754	[illegible]	[illegible]
1	3	Sypl	0.784	0.3503	0.1197	0.2478	0.3796	0.3078	0.5197	0.3448	-0.2384
1	3	Tagap	0.0811	0.1221	0.4818	0.4371	0.4759	0.5543	0.1867	0.4712	-0.4394
1	3	Tank	0.6606	0.3309	0.4389	0.5036	0.1635	0.4005	0.1031	0.394	-0.2981
1	3	Thbs3	0.7048	0.361	0.3163	0.1793	0.1793	0.1699	0.423	0.3472	0.1509
1	3	Ticam1	0.4121	0.2334	0.3781	0.2833	0.3267	0.1686	0.187	0.4076	0.0642
1	3	Traf3	0.5275	0.4007	0.6365	0.8195	0.4821	0.438	0.219	0.3196	-0.7285
1	3	Trpc4ap	0.6933	0.7387	0.5053	0.0556	0.4735	0.2506	0.2645	0.297	-0.2083
1	3	Tsen34	-0.1434	0.1895	0.3105	0.4658	0.5223	0.4973	0.4448	0.5714	-0.7435
1	3	Tspan12	-1.0194	-0.924	0.8113	0.8273	1.0932	0.533	0.2438	0.1942	-1.3122
1	3	Ubap1	0.4156	0.1704	0.9021	0.4049	0.308	-0.096	0.2387	0.196	-0.1933
1	3	Ube3b	0.2696	0.1282	0.4953	0.2594	0.4414	0.4826	0.1412	0.6031	-0.674
1	3	Ubl7	0.1629	0.2826	0.775	0.572	0.4905	0.5595	0.1432	0.2005	-0.4992
1	3	Zfp235	0.3291	0.5578	[illegible]	0.535	0.1403	0.2612	0.2495	0.6581	-0.1899
1	3	Zfp26	0.629	0.2807	0.5348	0.1069	0.629	0.2499	0.4408	0.2939	-0.4181
1	3	Zfp566	[illegible]	0.4914	0.3378	0.3679	0.5004	[illegible]	0.3429	0.2837	[illegible]
1	3	Zfpl1	0.7628	0.4266	0.6159	0.0659	0.414	[illegible]	0.2373	0.1816	0.0857
1	3	Zmpste24	0.3988	0.434	0.5675	0.5885	0.5869	0.49	0.2303	0.4423	-0.872
1	3	Zrsr1	0.3522	0.4813	0.177	0.0686	0.479	0.4277	0.2726	0.3721	-0.0558
1	4	0610009B22Rik	-0.022	0.0869	[illegible]	0.182	0.2925	0.1566	0.4983	0.4573	0.5007
1	4	0610010K14Rik	-0.2133	0.2311	[illegible]	-0.0852	0.1954	0.0649	0.7114	0.6092	0.9992
1	4	1110002N22Rik	-0.5775	-0.0312	-0.3403	0.2824	0.2111	0.6445	0.5628	0.433	1.517
1	4	1110017D15Rik	-0.3971	-0.4893	0.5755	0.4597	0.638	0.3323	1.2584	0.5847	0.9005
1	4	1110031I02Rik	-0.0553	-0.225	[illegible]	-0.07	0.14	0.3647	0.2951	0.34	0.7122
1	4	1110034A24Rik	0.0048	0.1274	0.0104	0.3021	0.282	0.3592	0.5657	0.4186	0.6954
1	4	1110054O05Rik	-0.0773	0.0626	0.2266	0.1783	0.415	0.1579	0.5904	0.316	0.2652
1	4	1200011M11Rik	0.1149	0.2364	0.197	0.2062	0.3373	0.4159	0.2834	0.1847	0.7193
1	4	1200014J11Rik	-0.7714	-0.2075	0.3448	0.3581	0.3411	0.7364	0.1725	0.1829	0.611
1	4	Swt1	-0.2104	-0.1019	-0.1223	0.0985	0.3312	0.2005	0.6029	0.6172	1.1175
1	4	1500001M20Rik	-0.3773	0.1098	-0.0309	0.4492	0.4403	0.6211	0.7747	0.6406	1.0437
1	4	Cklf	0.1187	0.1367	0.1311	0.0667	0.1833	0.2993	0.2582	0.3774	0.704
1	4	1700037H04Rik	-0.7076	-0.1596	0.1535	0.506	0.2415	0.4821	[illegible]	0.3552	0.5346
1	4	1700052N19Rik	-0.2419	0.0508	0.1453	0.3373	0.3927	0.4326	1.026	0.609	1.1123
1	4	1700071K01Rik	-0.3802	[illegible]	0.0724	0.3746	0.4809	0.5955	0.5005	0.7041	1.0639
1	4	2210409E12Rik	0.3504	0.1325	0.2909	0.1005	0.0234	-0.1323	0.9623	0.2786	1.1902
1	4	2310044G17Rik	-0.2435	-0.0556	0.0159	0.4485	0.4237	0.5769	0.0998	0.3383	0.3192
1	4	2310061C15Rik	-0.4706	0.049	0.3457	0.2297	0.3652	0.3579	0.4197	0.3309	0.5412
1	4	2410002I01Rik	0.2927	0.042	0.1312	0.2947	0.3552	0.5029	0.3644	0.5778	0.7384
1	4	Khdc3	[illegible]	-0.1307	-0.0803	[illegible]	0.4215	-0.1307	1.2328	0.6176	2.5975
1	4	2410022L05Rik	0.1827	0.1598	0.4146	0.4627	0.5472	0.4128	0.7931	0.7631	1.711
1	4	2610029G23Rik	-0.1446	0.0499	-0.0825	0.124	0.2258	0.6414	0.8211	0.6624	0.593
1	4	2610039C10Rik	-0.6074	-0.2664	-0.1754	0.1449	0.64	0.4226	0.954	0.6258	0.5467
1	4	U2surp	-0.4281	-0.3488	-0.2222	0.3719	0.5267	0.2842	0.5733	0.3068	0.9042
1	4	2610305D13Rik	-0.5425	-0.268	-0.5814	-0.5247	-0.3757	-0.5021	1.0904	0.0687	3.0916
1	4	2610528J11Rik	0.0475	-0.0422	[illegible]	0.0972	0.3656	0.1761	0.7651	0.477	0.4263
1	4	2700050L05Rik	-0.3179	-0.3637	-0.0245	-0.091	0.1658	0.1364	0.4395	0.3166	0.8912
1	4	2700094K13Rik	-0.8176	0.0126	0.4639	0.5061	0.6084	0.5085	0.459	0.6365	0.4006
1	4	2810004N23Rik	[illegible]	0.1794	0.2969	0.4528	0.7312	0.5098	0.9912	0.8078	1.2265
1	4	2810021B07Rik	-0.3633	-0.5001	-0.0511	0.0863	0.265	0.2977	0.6785	0.3263	0.5072
1	4	2900011O08Rik	0.1	-0.0694	0.2833	-0.0796	0.0631	0.0693	0.5446	0.1902	0.939
1	4	3010026O09Rik	-0.5296	-0.0844	[illegible]	0.2933	0.4453	0.7347	0.751	0.6338	1.2225
1	4	3110009E18Rik	-0.142	-0.1329	-0.0797	0.1455	0.3852	0.3011	0.3315	0.5728	0.2531
1	4	3632451O06Rik	0.3746	-0.5185	0.6043	0.0497	0.3696	0.3081	0.2548	0.4053	0.8289
1	4	Marf1	0.1359	0.1169	0.0454	0.1981	0.0906	0.4215	0.1359	0.0928	1.0409
1	4	4930427A07Rik	-0.5165	0.0782	0.1232	0.1669	0.3016	0.5727	0.725	0.7539	0.1607
1	4	4930452B06Rik	-0.0763	0.1494	0.5835	0.1513	0.3376	[illegible]	0.2392	0.3184	1.6294
1	4	4930539E08Rik	-0.0657	-0.0239	-0.0155	-0.2107	[illegible]	-0.1053	0.2901	-0.1381	1.9838
1	4	4930547N16Rik	-1.0322	-0.1946	-0.3359	0.3004	0.281	0.576	0.3409	0.4744	0.8105
1	4	4933403G14Rik	0.1152	-0.0238	-0.0634	0.3037	0.522	0.4548	0.8876	0.5915	1.3172
1	4	4933421E11Rik	0.3692	0.3129	-0.0792	0.2044	0.2262	0.0783	0.3074	0.3585	0.6952
1	4	5730419I09Rik	-0.4664	-0.3152	0.4209	0.3306	0.7903	0.6679	0.9117	1.1387	1.3614
1	4	5730469M10Rik	0.4455	0.2951	0.1634	-0.1301	0.1061	-0.2457	1.0961	0.2704	0.5061
1	4	5730528L13Rik	0.4314	0.4314	0.4854	0.1769	0.4335	0.5117	0.821	0.8745	1.5945
1	4	5930416I19Rik	-0.3749	-0.064	-0.215	0.2359	0.2911	0.2728	0.3892	0.4768	0.4365
1	4	6030458C11Rik	-0.2074	-0.1527	0.0717	[illegible]	0.3003	[illegible]	0.2376	0.38	0.8285
1	4	6330503K22Rik	-0.34	-0.1531	[illegible]	0.1028	0.5873	0.2011	0.6326	0.74	0.6635
1	4	6430590A10Rik	-0.0732	0.1065	0.0618	0.4586	0.1065	0.2219	0.2567	0.3928	0.4723
1	4	6430706D22Rik	-0.5223	-0.458	-0.0749	0.2333	0.2262	0.2333	0.8211	0.5074	0.6548
1	4	6720463M24Rik	-0.6109	-0.1213	[illegible]	0.4518	0.5381	0.7549	0.6764	0.6901	1.0141
1	4	8030462N17Rik	0.0636	0.2763	0.1716	0.3229	0.0425	0.634	0.0415	0.1892	0.9032
1	4	9130401M01Rik	0.3252	0.3405	-0.0361	0.323	0.1335	0.2442	0.3009	0.131	0.658
1	4	9630033F20Rik	-0.1326	0.2095	-0.0503	0.4042	0.2697	0.6044	0.1798	0.2976	0.9059
1	4	A430089I19Rik	0.084	0.4484	0.2503	0.206	0.084	0.2239	0.1478	0.4484	0.5976
1	4	A830080D01Rik	0.3231	0.0582	0.2822	0.1785	0.4217	0.0172	0.3652	0.342	1.1318
1	4	Aard	-0.1995	-0.5105	-0.1221	-0.4343	0.0125	-0.1831	0.8649	0.6427	3.6957
1	4	Aars	0.5228	0.4512	-0.1391	-0.0732	-0.169	[illegible]	0.4407	0.2088	1.67
1	4	Aars2	[illegible]	[illegible]	0.1801	0.1544	0.3932	0.4249	0.5928	0.5664	0.6986
1	4	Aarsd1	-0.3288	[illegible]	0.1617	0.3357	0.308	0.3029	0.5624	0.4539	0.6948
1	4	Abcf1	-0.1509	0.4877	0.3607	1.0007	0.1991	0.6868	0.2041	-0.1669	1.0583
1	4	Abcg1	[illegible]	0.048	[illegible]	-0.0709	0.598	0.2836	0.6215	0.2345	0.4288
1	4	Abhd1	0.3753	0.3753	0.0983	0.2947	0.2561	0.2259	0.0776	0.0776	1.3014
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1	4	Accsl	-0.203	-0.1487	0.0818	-0.0931	0.0502	0.1673	0.0445	0.2042	1.6592
1	4	Acly	[illegible]	0.1334	-0.1855	0.1489	0.241	0.1066	0.7165	0.5768	0.8779
1	4	Acot1	-1.2792	-0.5337	0.5671	0.3016	0.6436	0.162	0.0925	0.1284	0.6436
1	4	Acrbp	0.1006	-0.0166	-0.0845	0.1696	0.1668	0.0728	0.6717	0.1691	1.0573
1	4	Acsbg2	0.1178	-0.0828	0.1733	0.1052	0.397	0.2209	0.2297	0.2528	0.8127
1	4	Acsl1	-0.0331	-0.2108	0.3956	0.0927	0.3992	0.0522	0.2063	0.097	1.1869
1	4	Actn2	-0.2423	-0.2898	-0.239	0.2147	0.3449	0.9247	0.408	0.9157	0.8976
1	4	Actn3	0.0963	0.4013	0.2256	0.2501	0.2447	0.3136	0.4302	0.3594	1.5946
1	4	Actr5	-0.2923	[illegible]	-0.1248	0.0819	0.2061	0.4849	0.2463	0.2496	0.8329
1	4	Adam19	1.0372	0.9076	-0.9208	-0.7968	-0.2686	-0.6802	1.0454	0.4179	1.7866
1	4	Adh5	-0.0837	0.1649	0.177	0.8093	0.1988	0.7805	0.7243	0.3313	1.7868
1	4	Adsl	-0.8362	-0.2556	-0.2359	0.5278	0.1633	0.3574	0.28	0.485	0.6363
1	4	Adss	-0.288	0.0782	-0.228	0.0414	-0.1096	0.3196	0.3252	-0.0486	1.2493
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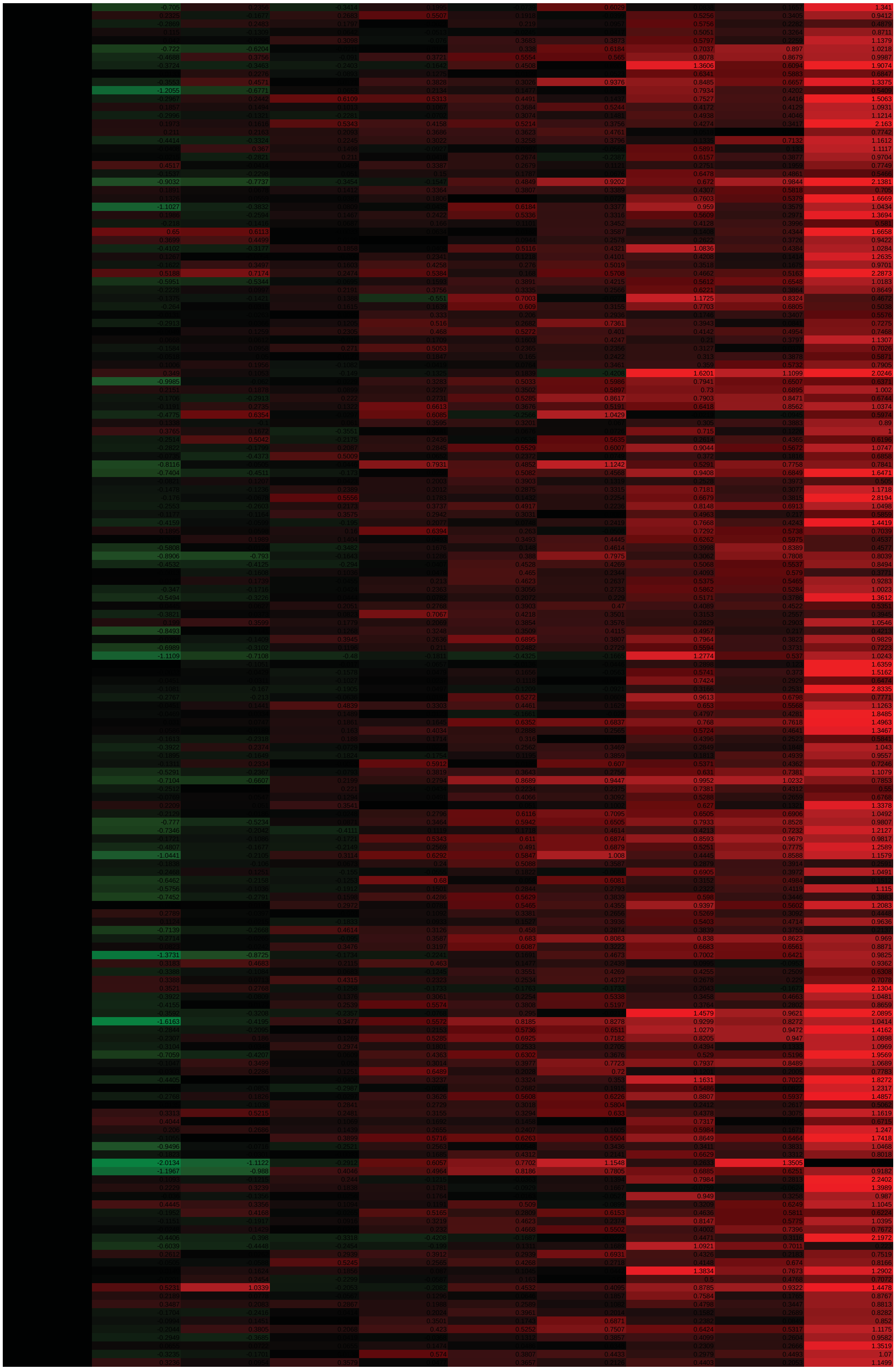

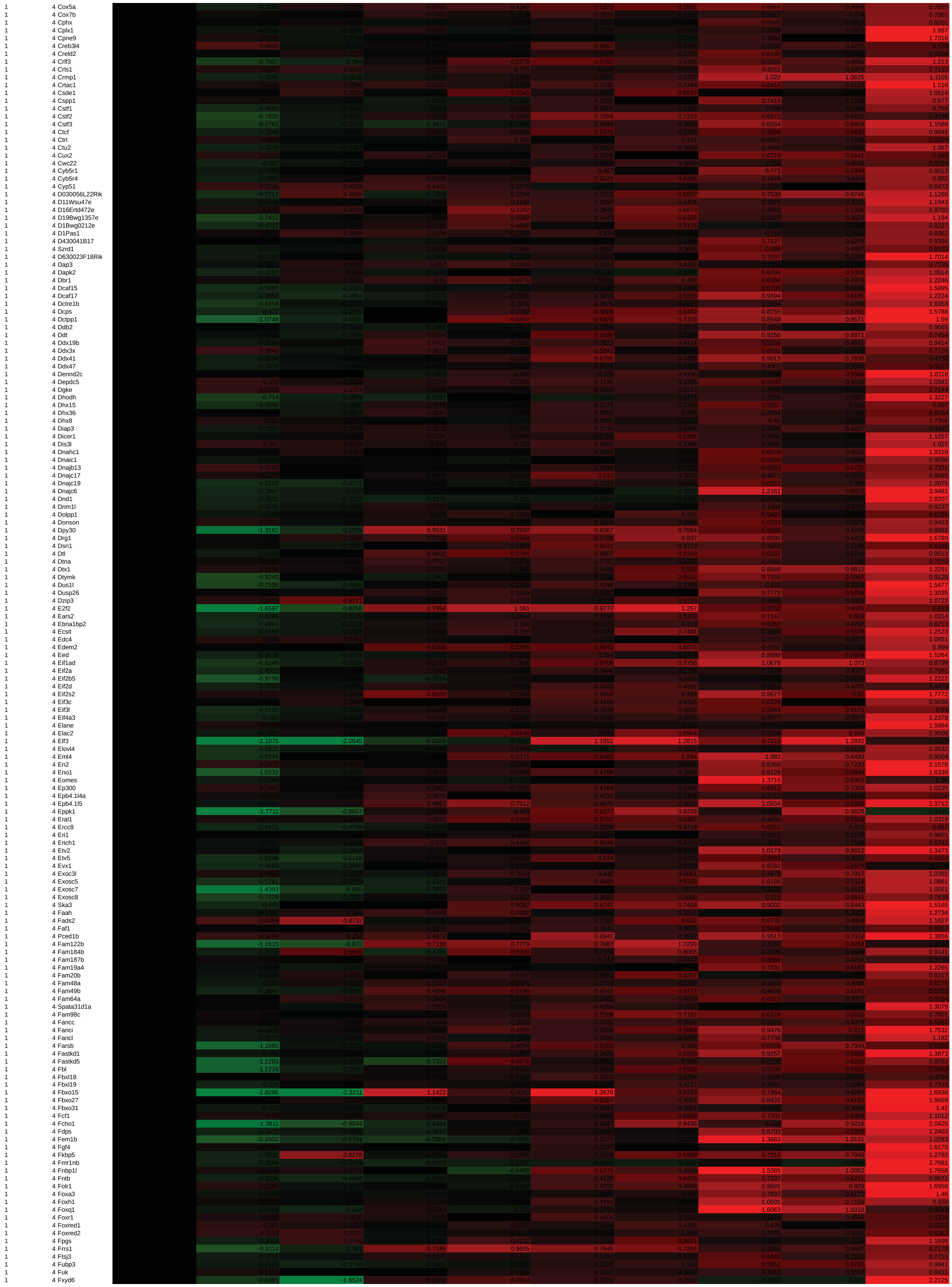

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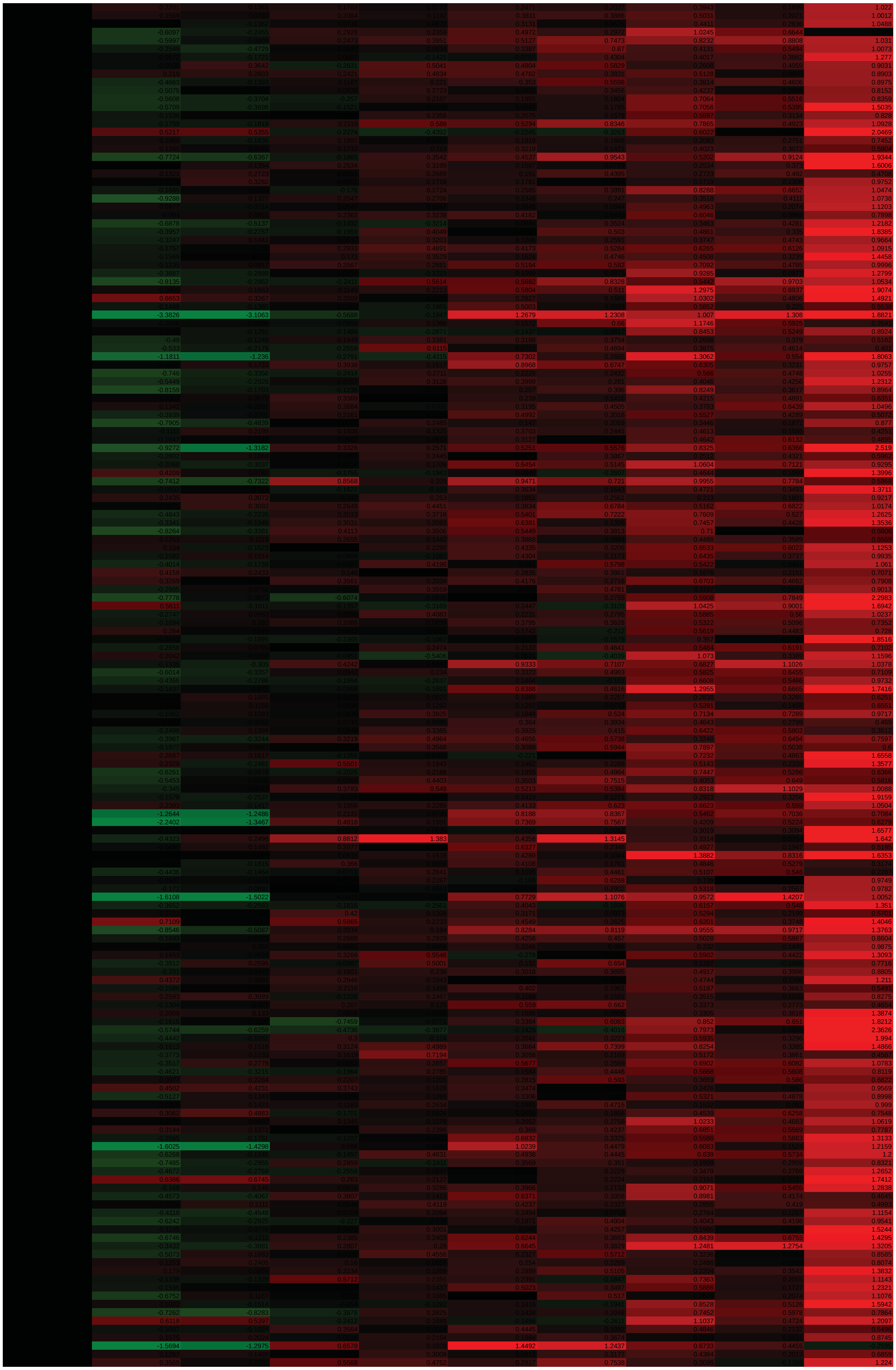

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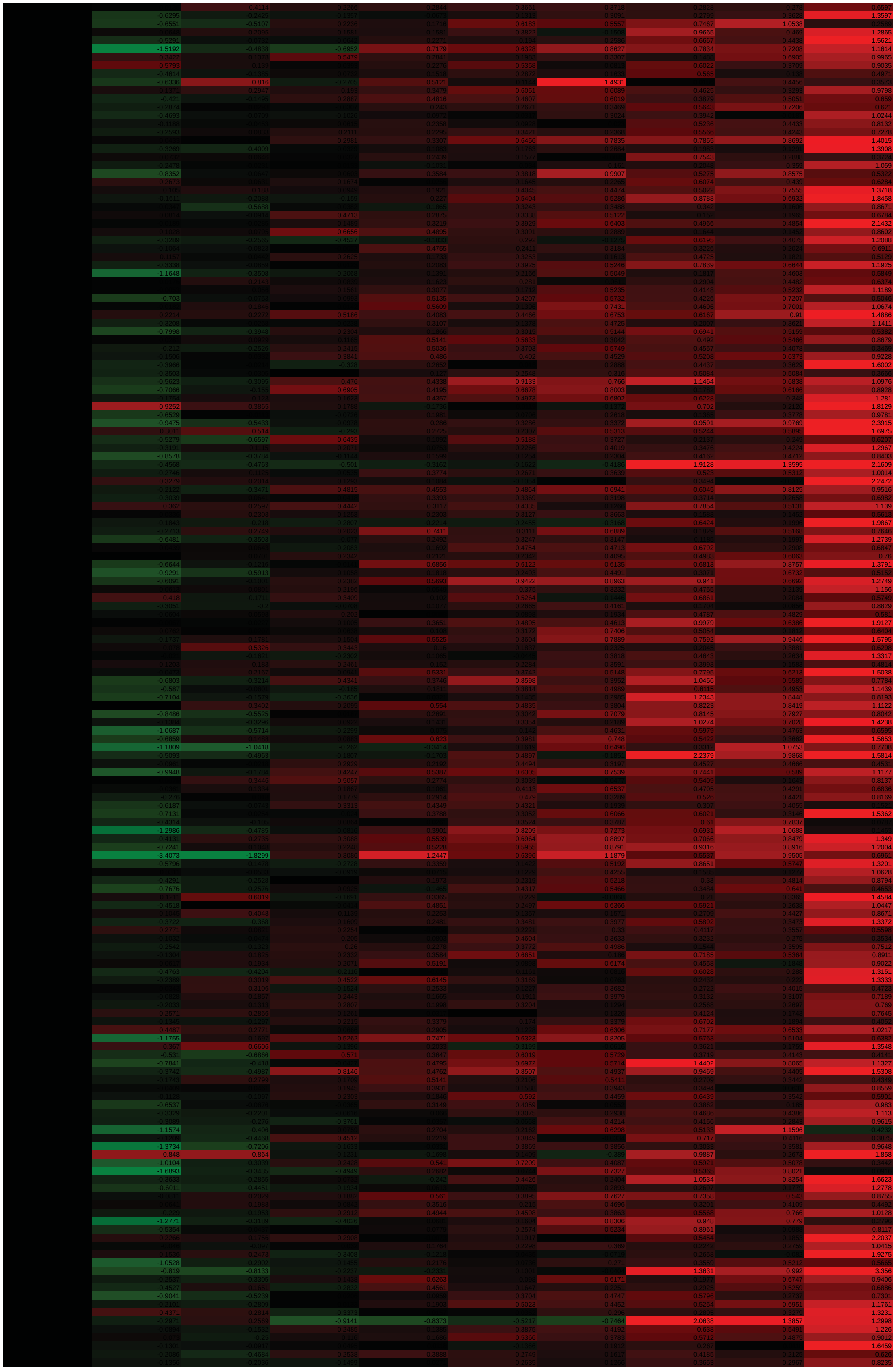

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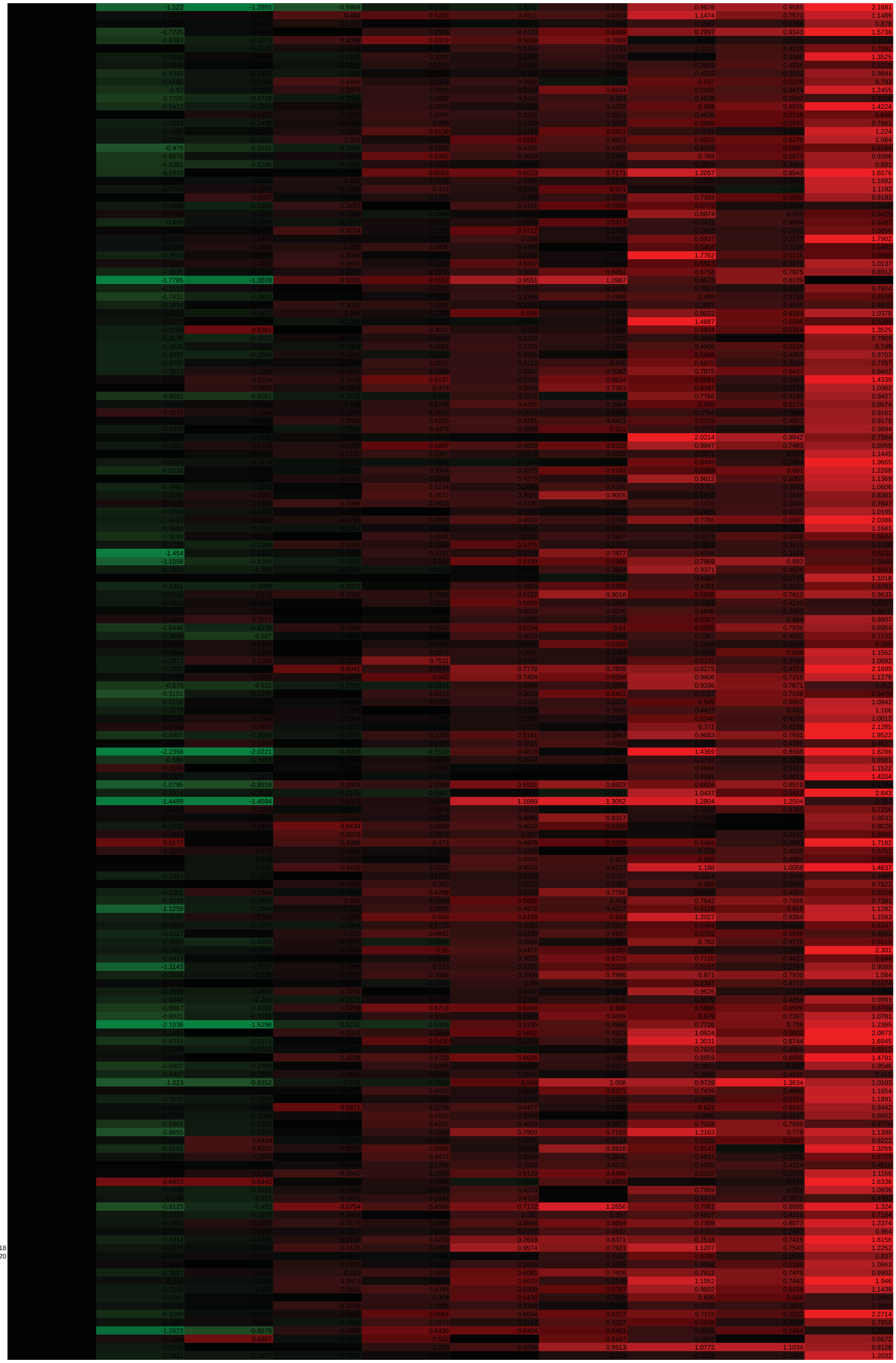

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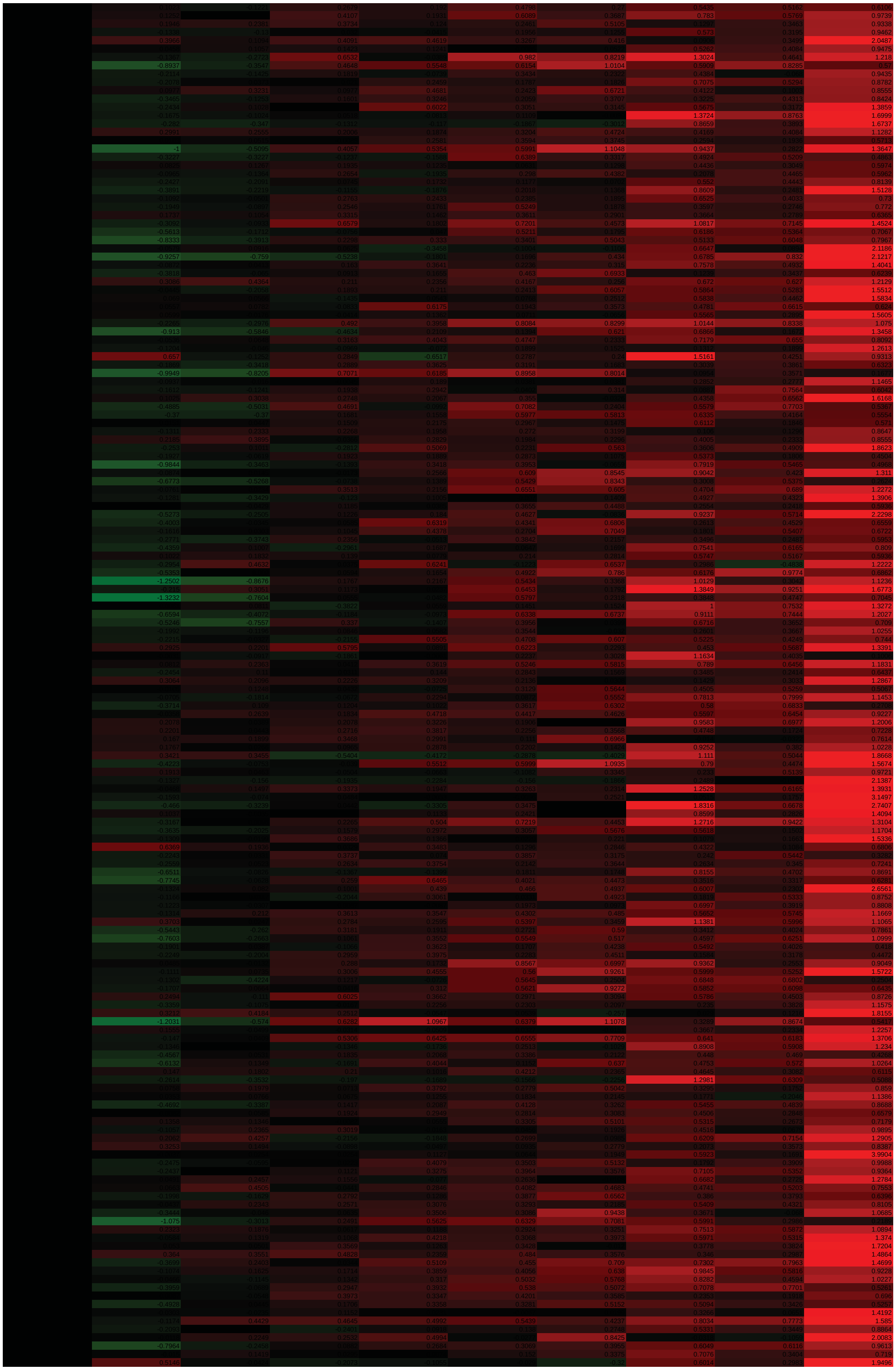

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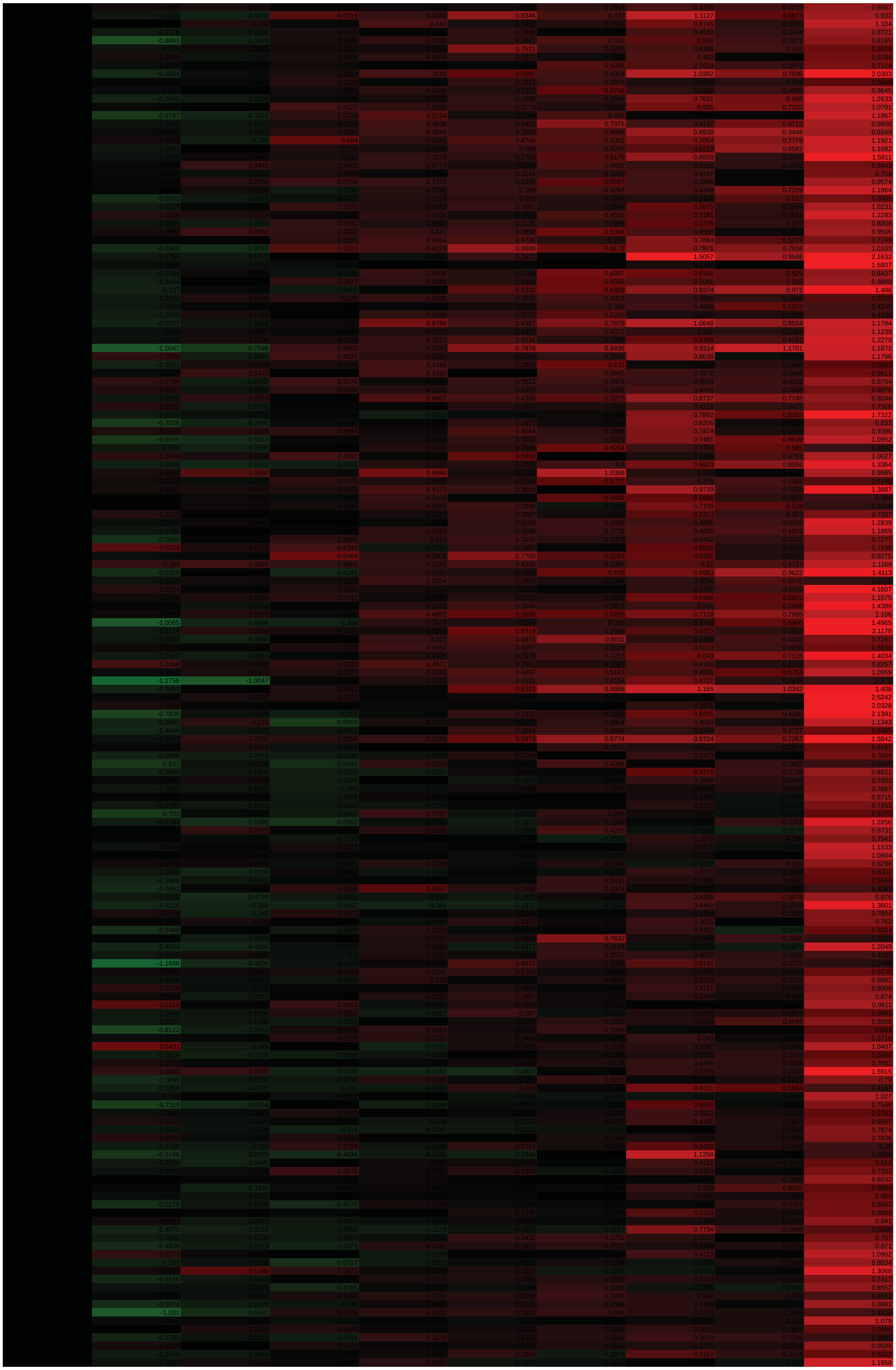

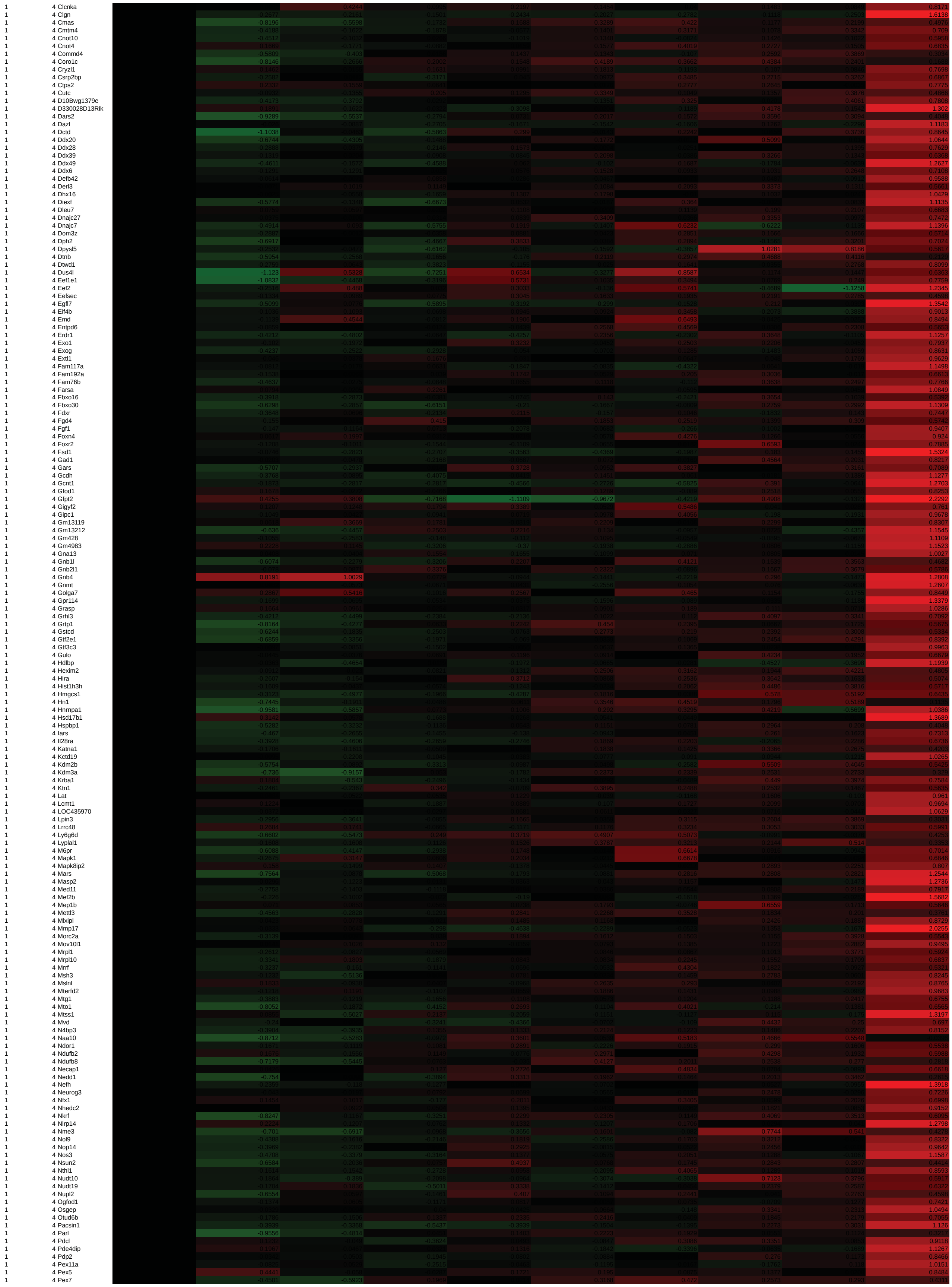
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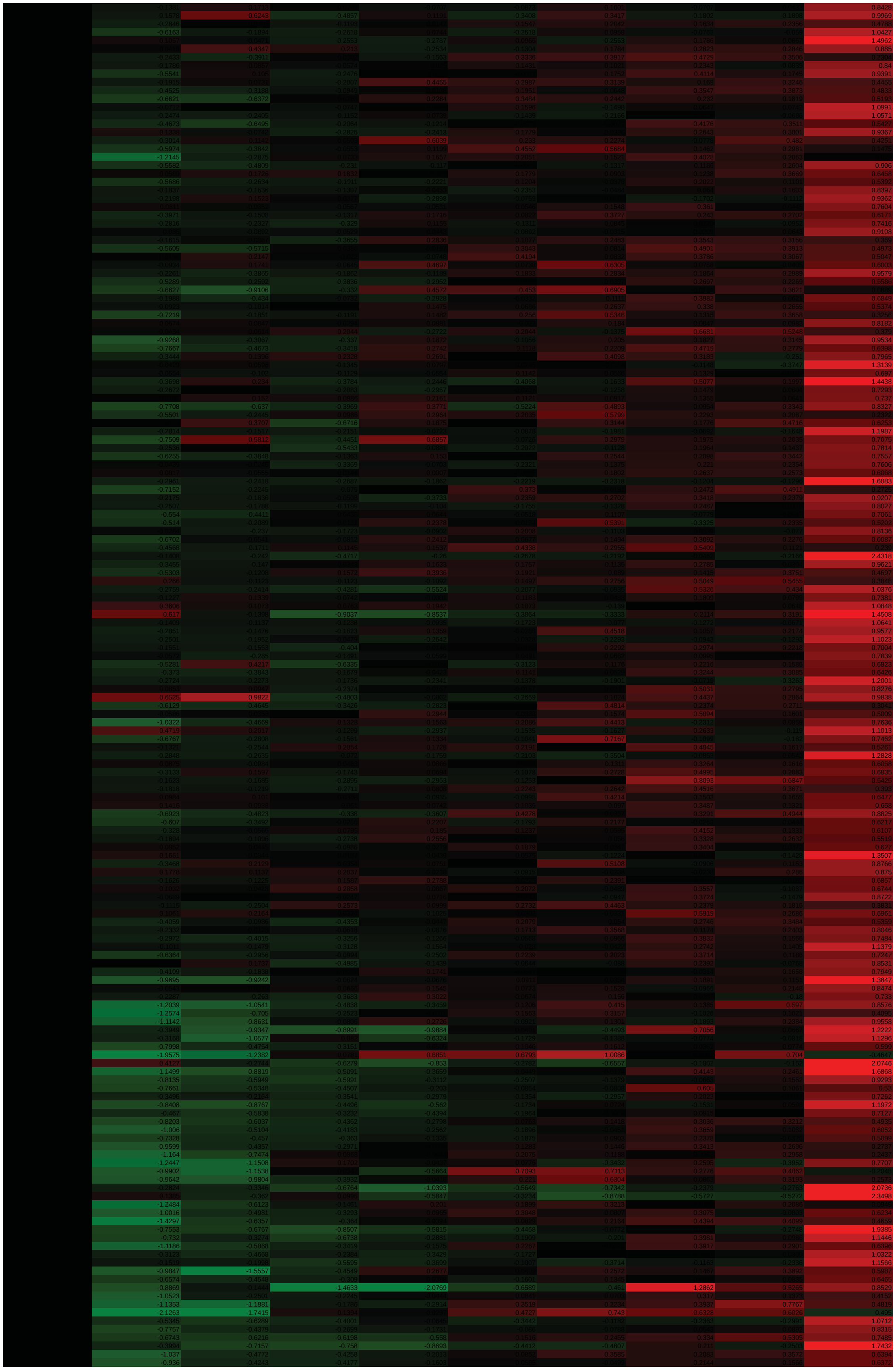

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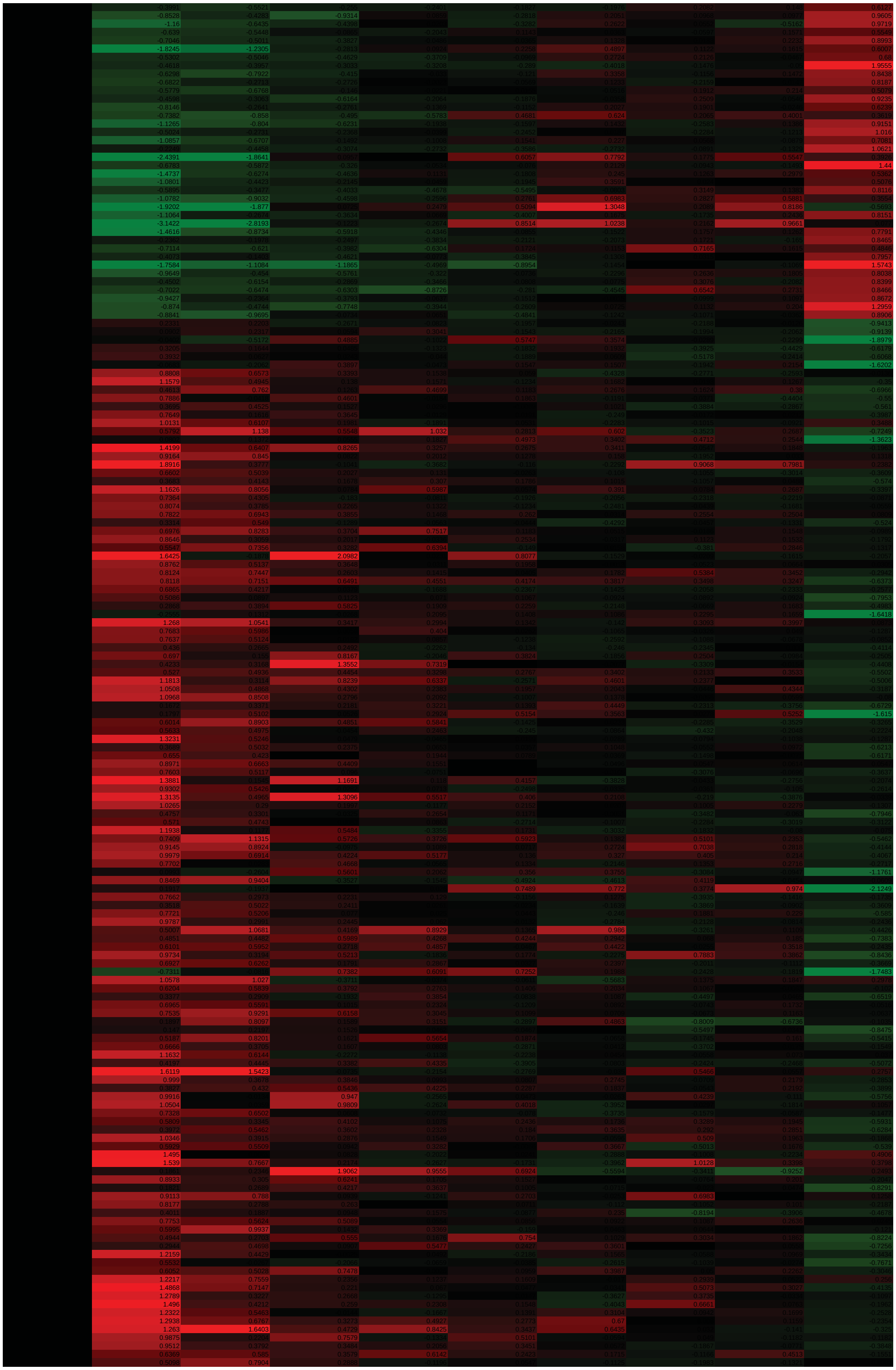

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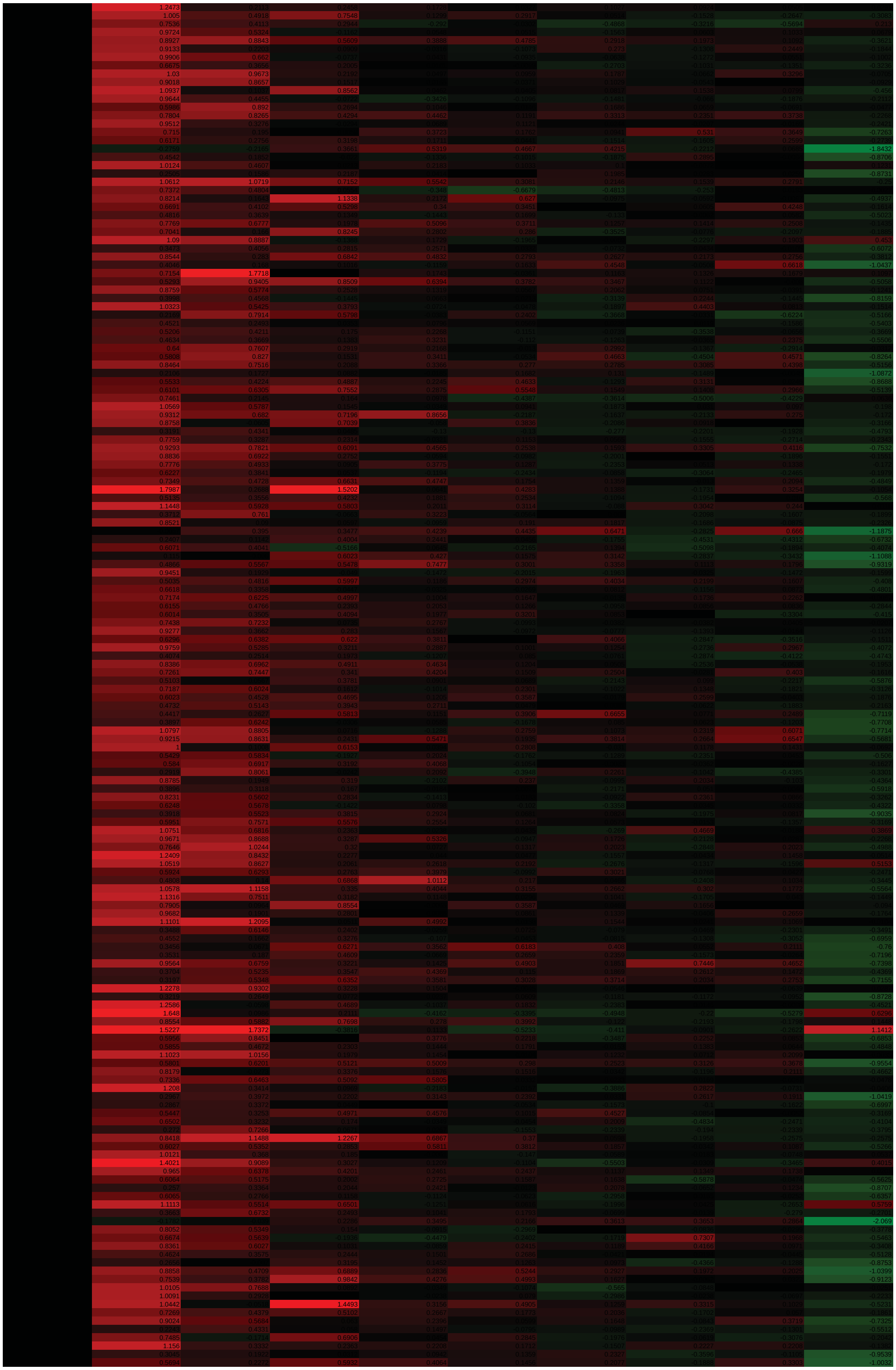

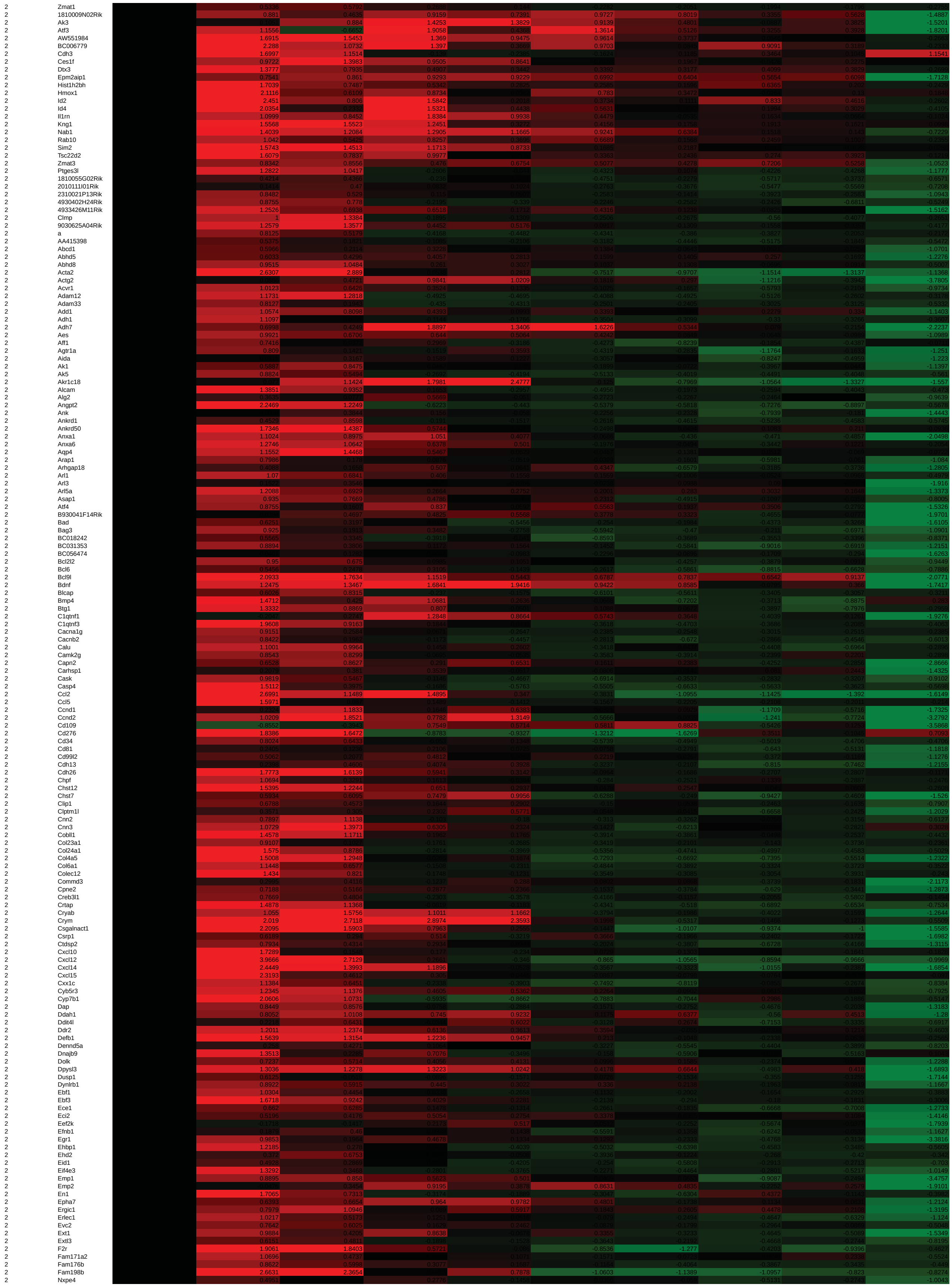
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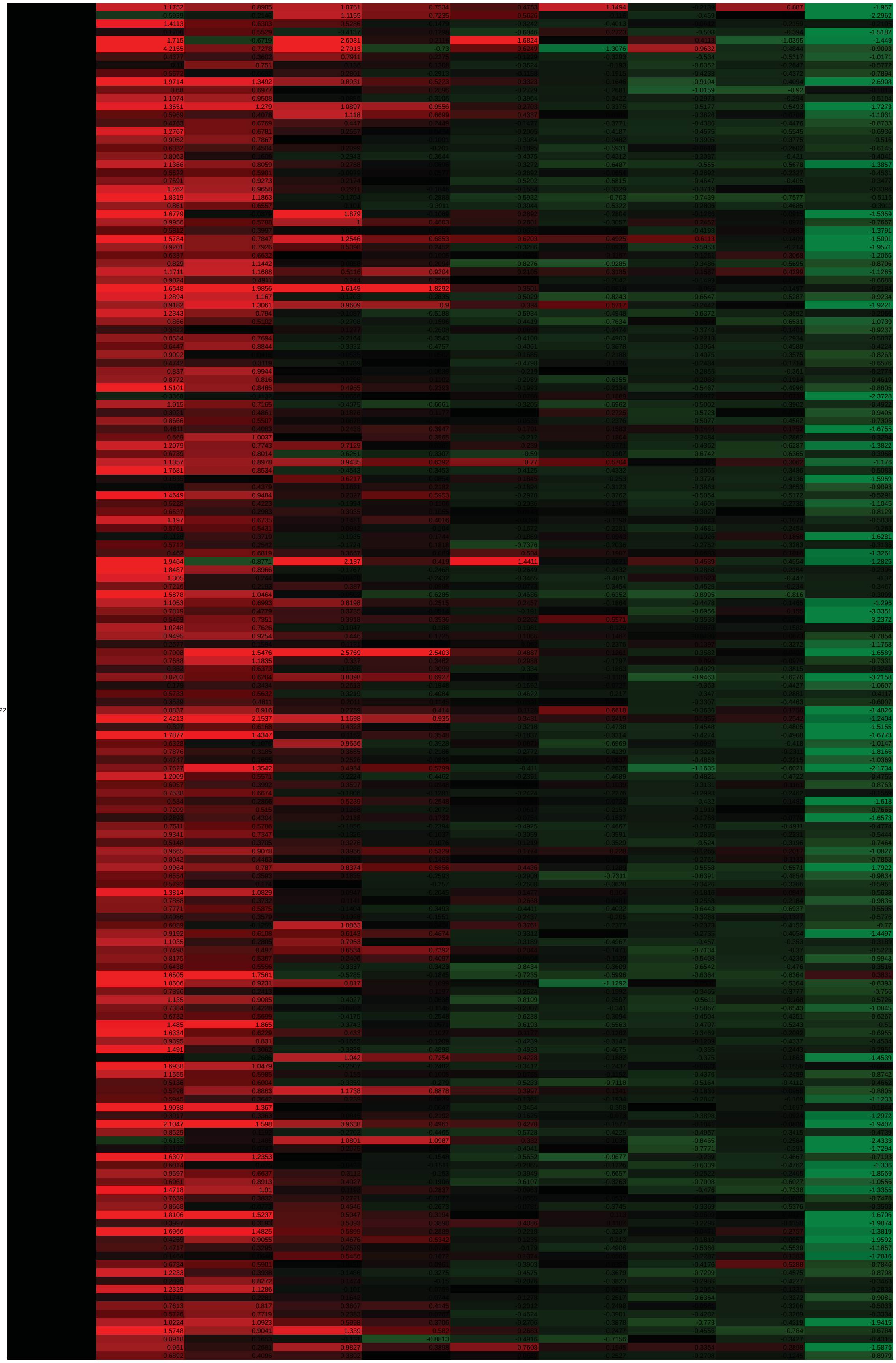
2	Fbln2	1.1415	0.7296	-0.4003	-0.3663	-0.3135	-0.3363	-0.3167	-0.4818	-0.5001
2	Fbxl3	0.3344	-0.5431	0.9676	-0.054	0.4766	-0.1539	0.1672	-0.2095	-2.1244
2	Fgl2	1.2285	0.4238	-0.2685	-0.3522	-0.2476	-0.3944	-0.3976	-0.431	-0.3238
2	Figf	3.399	2.2898	1.1398	1.3856	[illegible]	-0.2249	-0.641	-0.5117	-1.9656
2	Fkbp10	1.0662	1.4284	0.1267	0.2125	-0.2011	-0.101	-0.6144	-0.1155	-1.3172
2	Flna	0.411	0.9433	0.1318	0.0722	-0.134	-0.014	[illegible]	-0.2981	-0.8198
2	Flrt2	1.5694	1.0485	0.7249	0.5099	-0.1904	0.2062	-0.5554	0.1643	-1.4547
2	Fmo1	0.617	0.2899	1.6005	0.5225	0.4663	-0.6063	-0.8713	-1.4047	-2.2723
2	Fmod	0.5171	0.4854	[illegible]	-0.3597	-0.4384	-0.3188	-0.4452	-0.4051	-0.415
2	Fos	2.0365	1.128	1.348	1.0906	1.4085	1.2	0.8262	1.3217	-4.737
2	Fosl1	0.8159	0.8802	1.0384	[illegible]	-0.1996	[illegible]	-0.3369	-0.1386	-0.6554
2	Foxc1	1.3911	1.1849	0.6238	0.3611	0.3578	0.3419	[illegible]	0.3075	-1.2442
2	Frmd6	2.3911	1.4977	0.9619	0.3003	0.3745	-0.0828	-0.2117	-0.5552	-1.6271
2	Fyco1	0.8507	0.2338	0.128	-0.1919	-0.4245	-0.2192	-0.5965	-0.4255	-0.5287
2	Fzd2	1.4621	1.0398	-0.4398	-0.4306	-0.9445	-0.4422	0.3175	-0.1329	-0.6338
2	Gadd45b	2.2878	-0.1423	1.0531	0.1117	0.3231	0.2115	0.1419	0.1533	-0.5226
2	Galntl4	1.9995	1.6415	-0.2252	-0.1427	-0.7246	-0.7779	-0.7124	-0.8332	-0.8838
2	Gap43	1.9051	1.4125	-0.4108	-0.8172	-1.2139	-1.6027	0.2544	-0.3863	0.5623
2	Gbp4	3.6084	0.27	2.1862	-0.5942	0.3768	-0.763	0.5094	-0.2898	-0.6761
2	Gbp6	1.2777	-0.1553	0.199	-0.6594	-0.189	-0.4701	-0.3456	-0.4672	-0.5775
2	Gdnf	0.8321	0.41	0.176	[illegible]	-0.1008	-0.4234	-0.1891	-0.2266	-0.2892
2	Ggcx	1.5196	1.5088	0.2043	-0.0678	-0.2165	[illegible]	[illegible]	0.1277	-0.3767
2	Ggta1	0.7526	0.5459	-0.4111	-0.127	-0.0869	-0.0765	-0.3917	-0.3866	-0.969
2	Gldn	1.1164	0.5735	-0.2148	-0.1821	-0.1789	-0.2449	-0.166	-0.0973	-0.2483
2	Gm11818	0.5324	0.2012	0.0662	0.2245	[illegible]	0.1404	-0.577	0.2838	-1.0201
2	Gm15698	3.0443	1.3364	1.2619	0.2891	-0.4982	-0.4205	-0.2236	-0.1749	-0.1883
2	Gnaq	0.5696	0.1259	0.6652	0.2411	-0.0776	-0.2826	-0.4997	-0.4123	-1.3537
2	Gnas	0.976	0.778	0.2893	[illegible]	-0.1487	0.1054	0.2764	-0.2376	-1.1576
2	Gng7	0.5441	0.3849	-0.1939	-0.2951	-0.4725	-0.3644	-0.6935	-0.2584	-0.6565
2	Golim4	1.0746	1.1137	[illegible]	0.1502	-0.612	-0.3508	-0.7065	-0.7502	-0.9096
2	Gorab	0.9327	0.2357	0.3868	0.1052	-0.245	-0.4824	-0.3303	-0.2009	-0.116
2	Gosr2	0.6831	0.5217	0.1268	0.0822	-0.1831	-0.4507	-0.4356	-0.3684	-0.7844
2	Gpc3	1.8169	1.033	-0.8693	-1.2458	-1.4015	-2.1415	1.2786	0.2422	0.7006
2	Gpc4	1.4938	0.6526	[illegible]	-0.0829	-0.6393	-1.1895	-0.4352	-0.5072	-0.9543
2	Gpc6	0.9085	0.52	0.4868	0.0925	0.1672	-0.1573	-0.1999	-0.3577	-0.9319
2	Gpr108	0.3923	0.3955	[illegible]	0.1989	-0.0545	0.2148	-0.6491	-0.4693	-0.9677
2	Gpr153	1.2705	0.6054	-0.2732	-0.6569	-0.4952	-0.6047	-0.5991	-0.5489	-0.7079
2	Gpr64	1.121	0.7013	0.113	-0.0944	-0.2722	-0.5784	-0.4933	-0.3616	-0.3339
2	Gpx7	1.3767	0.7144	-0.4988	-0.6306	-0.3723	-0.3094	-0.3085	-0.159	0.3193
2	Grb10	0.7317	0.8774	0.6614	0.6559	0.7297	0.4292	0.4932	0.5751	-2.1091
2	Grb14	2.1289	2.0936	0.4712	0.4093	-0.3334	-0.2224	-0.1416	-0.2615	-0.3302
2	Grcc10	0.2598	0.2384	0.2417	0.1159	-0.2513	-0.5924	-0.2444	-0.3837	-0.879
2	Gria3	0.4906	0.3039	-0.2821	-0.0797	-0.0488	-0.0507	-0.3822	-0.1516	-1.0063
2	Grk5	0.8815	0.3064	0.5066	0.2299	-0.1679	-0.4623	-0.589	-0.7146	-0.762
2	Gsdmc2	0.2555	0.4263	0.2036	0.0876	-0.1849	-0.2318	-0.3942	-0.5771	-0.6566
2	Gsdmd	0.181	-0.4451	0.7321	0.3176	0.4962	[illegible]	-0.5485	-0.6143	-1.5929
2	Gsn	1.7776	1.4058	0.117	0.1334	-0.7887	-0.5895	-0.8913	-0.5287	-0.8913
2	Gsto1	0.5357	0.8224	0.5594	0.4693	0.7657	0.5975	0.4775	0.1775	-1.9018
2	Gstt1	1.4908	0.3512	0.1117	-0.581	-0.4705	-0.881	-0.2392	-0.3705	[illegible]
2	Gtf2ird2	0.4398	0.1404	0.1325	0.2125	0.0638	-0.1088	-0.214	-0.0508	-1.1077
2	Gvin1	2.4681	0.6689	1.3389	-0.2603	-0.7386	-1.0935	-0.749	-0.9742	-1.5077
2	Gypc	0.7558	0.7822	0.625	0.7718	0.2804	0.1664	-0.477	0.2157	-1.7827
2	H13	0.3712	0.3464	-0.1349	0.1469	[illegible]	-0.3367	-0.3615	-0.4613	-1.6223
2	H2-D1	0.8533	-0.2779	0.2118	-0.2715	-0.3015	-0.3058	-0.4446	-0.5797	-0.7346
2	H47	0.7377	0.2569	0.3499	-0.0939	-0.3033	-0.4471	-0.2312	-0.6537	-0.9521
2	Hbb-y	-0.3426	0.3193	0.7231	0.7303	0.3829	-0.2302	-0.9618	-1.0815	-1.8546
2	Hbegf	2.4156	1.1341	1.7499	0.2801	0.1946	-0.0689	-0.4361	-0.1423	0.3165
2	Hebp2	0.5705	0.6217	-0.3241	-0.1147	-0.6949	-0.5711	-0.2319	-0.2201	-0.3791
2	Hist1h2bm	1.2424	0.2127	0.0625	-0.1995	-0.0506	-0.3576	0.143	[illegible]	-0.5524
2	Hist1h4h	0.9027	0.1945	-0.2656	-0.081	-0.456	-0.6398	-0.6216	-0.8424	-0.1276
2	Hist2h2aa1	0.9396	0.3854	0.5046	0.5353	0.2498	-0.022	-0.142	-0.0697	-1.283
2	Hoxb6	1.1453	0.9109	[illegible]	0.3045	-0.1968	-0.0383	-0.3297	-0.4366	-0.5684
2	Hoxb7	1.426	1.6708	0.6942	1.0602	0.5345	0.8197	-0.2144	-0.7177	-1.2494
2	Hoxc6	2.0867	1.8984	0.45	1.4548	0.5122	0.8484	-1.1242	0.104	-3.0556
2	Hoxc9	1.8989	1.8083	0.2263	1.2824	0.038	0.4036	-1.0695	0.367	-1.252
2	Hoxd10	1.5511	0.4635	0.9866	[illegible]	0.3342	-0.5783	0.058	-0.5413	-1.0321
2	Hoxd3	0.8498	0.4218	[illegible]	0.2445	-0.1032	-0.4404	-0.1713	-0.1804	-0.2979
2	Hoxd4	0.9423	0.5253	0.3246	0.2232	0.1054	-0.1699	-0.5765	-0.2619	-0.6634
2	Hspa1a	1.6042	0.2886	0.5785	0.2603	0.6341	0.2378	[illegible]	0.3621	-1.1551
2	Hspb6	0.7589	1.1386	0.2018	0.2021	-0.5561	-0.2144	-1.3391	-0.7111	0.3054
2	Id1	1.2699	0.0032	1.4256	0.2094	0.7248	0.3111	-0.0299	0.1804	-1.8905
2	Id3	1.8689	0.8197	1.1176	0.1704	0.3599	-0.1674	0.473	0.2128	-1.2909
2	Ids	0.9159	0.5091	0.0637	-0.0554	-0.5485	-0.626	-0.4071	-0.4848	-0.7025
2	Ier5l	1.0418	1.2311	-0.3107	-0.415	-0.2494	-0.6049	[illegible]	0.1094	0.1227
2	Ifi35	1.079	0.2524	0.3265	-0.1594	-0.3612	-0.3599	-0.5119	-0.4986	-1.2668
2	Ifit2	1.8751	0.6846	0.023	-0.3313	-0.7822	-0.7085	-0.3899	-0.602	-0.5367
2	Ifit3	3.1396	0.3219	0.6617	-0.1299	-0.0556	-0.2224	-0.2224	-0.0556	-0.1386
2	Ifitm3	1.7029	1.5365	1.1704	0.6465	0.7025	0.222	0.4448	0.5225	-1.1965
2	Ifngr2	0.5075	0.3347	-0.0781	-0.3996	-0.3905	-0.1453	-0.5584	-0.4913	-0.7226
2	Igf2r	1.1191	1.1022	0.0662	0.0911	-0.3015	-0.5223	-0.5593	-0.5973	-0.4167
2	Igtp	2.3622	-0.0604	0.686	-0.7954	-0.2008	-1.0797	0.2449	-0.629	-1.045
2	Iigp1b	1.304	0.0061	-0.1286	-0.1387	-0.132	-0.1975	-0.173	-0.1765	-0.2773
2	Ikbke	0.46	[illegible]	-0.0849	0.1778	-0.1409	[illegible]	-0.5459	[illegible]	-0.8351
2	Il31ra	1.5496	0.8154	0.0321	-0.3858	-0.2582	-0.2907	-0.3072	-0.3409	-0.2907
2	Il33	1.0961	0.1424	-0.3018	-0.263	-0.3923	-0.5097	-0.1202	-0.1773	-0.4582
2	Il6	1.3635	0.585	0.7295	0.0992	-0.0701	-0.2619	-0.1205	-0.0018	-0.2791
2	Ilk	0.8789	0.6103	0.3129	0.0713	0.1069	-0.0638	-0.4295	-0.1978	-0.5584
2	Inf2	0.6729	1.1605	0.1646	0.3398	-0.358	-0.3802	-0.3597	-0.4966	-0.7286
2	Inhbb	1.1968	1.6608	-0.7016	-0.5265	-0.4365	-0.5681	-0.4346	-0.393	0.6456
2	Inpp5a	0.4338	0.6886	-0.1046	-0.7326	-0.4258	-0.3992	-0.3171	-0.2698	-0.4067
2	Irf7	2.0079	0.2417	0.8119	0.1139	0.2779	-0.108	0.1083	-0.2452	-0.2694
2	Irf9	1.2943	0.4215	0.2296	-0.497	-0.0255	-0.643	-0.3994	-0.4947	-0.3405
2	Irs2	0.9872	0.199	1.0856	0.1246	[illegible]	[illegible]	-0.2336	-0.2147	-0.6399
2	Irx3	0.8923	0.8145	-0.5317	-0.6033	-0.4671	-0.901	1.0004	[illegible]	-0.9907
2	Irx5	1.2489	0.9731	0.1098	0.2224	[illegible]	-0.1322	0.3485	-0.0766	-1.0814
2	Isg15	2.2999	0.2393	0.7496	-0.3354	-0.2147	-0.4772	-0.3201	-0.311	-0.305
2	Itgb1	0.4749	0.6625	0.1436	[illegible]	-0.2742	-0.2125	-0.5832	-0.2895	-0.5591
2	Itprip	1.1432	0.7505	0.4879	0.0554	-0.1746	-0.3798	-0.6544	-0.5143	-1.4638
2	Jak1	1.2199	1.0255	0.6067	0.1694	0.155	-0.0759	-0.0906	-0.0823	-0.3243
2	Jak2	1.2059	0.3776	0.5559	-0.1343	-0.1797	-0.3882	-0.5868	-0.478	-1.2093
2	Josd2	[illegible]	0.7421	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-2.0231
2	Junb	1.7301	0.8497	1.4225	0.7649	1.0139	0.6038	[illegible]	0.4244	-2.3206
2	Kank1	0.9611	0.3823	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.5489
2	Kcnab1	1.9241	1.1139	0.6927	[illegible]	-0.415	-0.3099	-0.4592	-0.7574	-0.5134
2	Kif26b	1.3795	0.8194	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	Klra18	0.9063	1.1962	[illegible]	0.5371	-0.2277	-0.3773	[illegible]	[illegible]	[illegible]
2	Klra4	[illegible]	0.915	-0.5036	[illegible]	-0.542	-0.4577	-0.4735	-0.4452	-0.4577
2	Lamb1	1.2875	0.9979	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	Large	1.1686	[illegible]	0.7188	[illegible]	[illegible]	[illegible]	-0.5553	[illegible]	[illegible]
2	Lbh	2.1942	2.2662	[illegible]	0.4185	-0.6481	-0.5006	-0.4921	-0.4362	-3.2492
2	Lgals9	1.9054	0.4105	0.8579	[illegible]	-0.5194	[illegible]	[illegible]	[illegible]	-1.7959
2	Lima1	1.5068	0.8209	[illegible]	-0.2656	-0.3821	-0.4172	-0.5877	-0.5653	0.8733
2	Lmna	0.7461	0.9272	0.5047	[illegible]	[illegible]	[illegible]	-0.4153	[illegible]	-1.9749
2	Loxl2	[illegible]	0.7733	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	Lpar4	1.5287	[illegible]	[illegible]	-0.7314	[illegible]	[illegible]	[illegible]	[illegible]	-1.0303
2	Lphn3	1.5406	0.5456	[illegible]	[illegible]	-0.6341	-0.522	-0.6374	-0.5785	[illegible]
2	Lrp12	0.7573	0.4103	[illegible]	[illegible]	[illegible]	-0.5084	[illegible]	-0.445	[illegible]
2	Lrrk2	[illegible]	0.7562	-0.5373	[illegible]	[illegible]	-0.6191	[illegible]	[illegible]	[illegible]
2	Ltbr	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.8723
2	Ly6e	1.019	0.5191	[illegible]	-0.5934	-0.6491	-0.5488	[illegible]	[illegible]	-0.8641
2	Man1a	0.8546	0.4551	[illegible]	[illegible]	-0.4067	-0.4749	[illegible]	-0.5103	-0.5538
2	Man2b2	0.7423	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.6135	-0.5816	-0.9693
2	Map3k8	0.854	[illegible]	0.6423	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-1.516
2	Mapre2	1.5084	0.9075	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.725
2	Mbd5	1.5725	0.7269	0.7303	[illegible]	[illegible]	[illegible]	-0.361	[illegible]	-0.8671
2	Mbnl2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.63	-0.4462	-1.5817
2	Mdfic	0.9977	0.4725	[illegible]	[illegible]	[illegible]	-0.6231	-0.51	[illegible]	-1.4783
2	Me1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.34	-0.5534	-1.4337
2	Meox1	0.8437	0.8544	-0.5173	-0.4702	[illegible]	-0.415	[illegible]	[illegible]	[illegible]
2	Meox2	1.2522	1.554	1.8328	1.8772	1.2294	0.7549	[illegible]	0.4926	-2.0951
2	Mgst1	1.9318	1.1349	1.8414	1.1013	0.6353	[illegible]	[illegible]	[illegible]	-1.5799
2	Mical2	[illegible]	0.7238	[illegible]	[illegible]	[illegible]	-0.341	[illegible]	[illegible]	[illegible]
2	Micall2	1.0331	1.0579	-0.3404	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	7-Mar	0.8583	[illegible]	[illegible]	[illegible]	[illegible]	-0.3461	[illegible]	[illegible]	-0.6492
2	Mme	1.2734	[illegible]	[illegible]	[illegible]	-0.4477	[illegible]	-0.3142	-0.7028	[illegible]
2	Mmp11	1.1889	1.0318	[illegible]	[illegible]	-0.7635	-1.1806	[illegible]	[illegible]	0.9762
2	Mmp16	0.7916	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	Mocs1	0.7294	0.6207	0.2469	[illegible]	[illegible]	-0.3719	-0.5789	-0.5027	-0.6465
2	Mocs2	0.7532	0.5869	[illegible]	[illegible]	[illegible]	[illegible]	-0.4282	-0.316	[illegible]
2	Meis2	[illegible]	[illegible]	0.7901	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-2.8962
2	Mrgprf	1.179	0.9056	1.0923	1.1934	0.9056	0.7504	-0.36	[illegible]	-3.0247
2	Prl2c3	2.014	2.3192	-0.6604	[illegible]	[illegible]	-0.7127	-0.6849	-0.8263	-0.86
2	Mrvi1	2.0644	1.2864	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	Mtap7d1	0.9249	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-1.3207
2	Mtpn	[illegible]	0.7392	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.9442
2	Mvp	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.3174	-0.5447	-1.203
2	Mx2	2.6419	[illegible]	0.8055	-0.3659	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	Myadm	0.6923	1.0115	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	Mycbp2	[illegible]	[illegible]	0.9489	[illegible]	[illegible]	[illegible]	-0.6171	[illegible]	-1.1662
2	Myh10	1.7405	1.5028	-0.6366	[illegible]	-1.3877	-0.8915	[illegible]	[illegible]	[illegible]
2	Myh9	0.7857	0.7738	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-1.075
2	Nacc2	[illegible]	0.584	0.4142	[illegible]	[illegible]	-0.8533	-0.9261	-0.4712	-1.5268
2	Ncald	0.9321	[illegible]	[illegible]	-0.4855	-0.4539	-0.6902	-0.3406	[illegible]	-0.8048
2	Ncstn	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-1.2534
2	Ndst1	0.4539	0.4539	0.6091	-0.3442	0.3516	0.2944	[illegible]	[illegible]	-1.3122
2	Nek9	[illegible]	0.5239	[illegible]	[illegible]	[illegible]	[illegible]	-0.3373	[illegible]	-1.301
2	Nelf	0.6024	0.9739	[illegible]	[illegible]	-0.632	-0.5772	[illegible]	-0.5049	-1.1158
2	Neo1	0.976	0.7765	[illegible]	[illegible]	[illegible]	-0.5542	[illegible]	-0.7267	[illegible]
2	Nfib	2.2697	0.7715	0.5275	[illegible]	[illegible]	[illegible]	-0.6	[illegible]	-1.9128
2	Nfic	1.7466	1.7813	0.6725	0.7952	[illegible]	0.52	-0.4435	[illegible]	-1.2878
2	Nlgn2	1.2564	0.4204	-0.4036	-0.8041	-0.3025	-0.3558	-0.3396	-0.312	-0.7527
2	Nptn	[illegible]	0.511	[illegible]	[illegible]	-0.2777	-0.343	-0.6398	-0.7795	-1.185
2	Nrg1	1.0406	0.5594	[illegible]	[illegible]	[illegible]	[illegible]	-0.6878	[illegible]	[illegible]

2	Nrn1
2	Nt5e
2	Nuak1
2	Nxn
2	Oas2
2	Oasl2
2	Ophn1
2	Osbpl6
2	Osgin1
2	Osmr
2	Oxct1
2	P4ha3
2	Pak3
2	Pam
2	Papss1
2	Parp3
2	Parp8
2	Pbx1
2	Pcdha6
2	Pcdhb22
2	Pcdhgc3
2	Pde1a
2	Pdgfc
2	Pdgfrb
2	Pear1
2	Per2
2	Pgrmc1
2	Phf2
2	Phlda1
2	Phlda3
2	Phldb1
2	Pik3r3
2	Pitpnm2
2	Pkd1
2	Pkig
2	Plau
2	Plec
2	Plekhf1
2	Pls3
2	Plxna2
2	Pofut2
2	Ppbp
2	Ppp3ca
2	Pqlc3
2	Prkca
2	Prkd1
2	Prrx1
2	Psmd8
2	Ptges
2	Ptk7
2	Ptpdc1
2	Pex2
2	Qsox1
2	Rbms1
2	Rbms2
2	Reep3
2	Reg3g
2	Rela
2	Rep15
2	Rgs4
2	Rhod
2	Rilpl2
2	Rnf11
2	Rnf215
2	Rpl22
2	Rprm
2	Rps6ka4
2	Rsad2
2	Rspo2
2	Rspo3
2	Rsu1
2	Runx1t1
2	S100a10
2	S100a11
2	S100a6
2	S1pr3
2	Sav1
2	Scand1
2	Scg5
2	Scmh1
2	Scoc
2	Sdc2
2	Sdc4
2	Sec16b
2	Sec63
2	41522
2	Sepw1
2	Serinc1
2	Serpinh1
2	Sertad1
2	Sh3bgrl
2	Sh3glb1
2	Sh3kbp1
2	Sh3rf3
2	Shc1
2	Shox2
2	Sidt2
2	Sirt2
2	Slc10a3
2	Slc35b4
2	Slc39a13
2	Slc41a2
2	Slc4a2
2	Slc50a1
2	Slco2a1
2	Smarcc2
2	Smpd1
2	Snai1
2	Snrk
2	Sod3
2	Sox5
2	Sqstm1
2	Ssbp2
2	Ssfa2
2	Stambpl1
2	Stard13
2	Stau2
2	Steap2
2	Sulf1
2	Svil
2	Svop
2	Syap1
2	Sytl2
2	Tagln
2	Tap1
2	Tbx1
2	Tbxa2r
2	Tek
2	Tgfbr3
2	Thra
2	Tle6
2	Tmbim1
2	Tmed10
2	Tmem100
2	Tmem109
2	Tmem176a
2	Tmem178
2	Tmem229b
2	Tmem43
2	Tmem98
2	Tmem9b
2	Tmsb4x
2	Tnfrsf12a
2	Tnfrsf1a
2	Tnks1bp1
2	Tor1aip1
2	Tpbg
2	Tpcn1
2	Tpm1
2	Tpm4
2	Tpp1
2	Tprgl
2	Trim47
2	Trnp1
2	Trpm6
2	Tspan11
2	Tspan17
2	Tspan3
2	Tubb6
2	Tulp4
2	Twist1
2	Twsg1
2	Ubc
2	Ube2j1



2	Ube2l6	1.1554	-0.166	-0.2044	-0.4166	-0.2439	-0.4263	-0.3022	-0.5765	-0.3785
2	Ugcg	1.3566	0.4874	0.1777	0.3394	0.3348	0.6036	[illegible]	0.1885	-0.8615
2	Unc5c	1.6829	0.9569	0.4168	0.2818	-0.1	[illegible]	-0.387	-0.162	-0.5814
2	Usp18	3.1616	0.5896	1.5025	-1.3	-0.0869	-1.3484	-0.3679	-1.112	-1.2367
2	Usp2	1.5276	0.4311	0.685	-0.7499	-0.2966	-0.2917	[illegible]	-0.1039	-0.1104
2	Vcl	1.6933	1.2889	1.1811	[illegible]	0.2502	-0.1775	0.2177	0.3171	-0.5421
2	Vdr	1.1676	1.2286	-0.3289	-0.4673	-0.5858	-0.477	-0.7265	-0.3691	-0.9117
2	Vip	1.1614	4.3869	0.154	0.5905	-0.1538	-0.061	-0.1067	[illegible]	-0.0472
2	Vkorc1	0.7643	0.687	[illegible]	[illegible]	-0.1454	-0.3384	-0.3881	-0.1226	-1.3358
2	Wisp1	0.9239	0.4602	-0.1491	-0.2692	-0.4661	-0.4691	-0.4939	-0.4939	-0.5317
2	Wsb2	0.5526	0.3105	0.3339	0.0887	-0.2424	-0.3261	-0.4784	-0.5019	-0.3352
2	Xkr8	0.63	0.7273	-0.3943	0.1053	-0.5034	-0.3176	-0.4262	-0.2719	-0.3093
2	Zeb1	1.0206	0.8185	0.1474	0.3854	-0.3858	-0.6472	-0.9018	-0.7353	-1.2363
2	Zfand2a	0.3408	-0.2949	1.1268	-0.1001	0.2322	-0.4915	-0.5451	-0.6304	-0.9534
2	Zfhx3	0.6565	0.4445	0.9832	0.6423	0.9894	0.6029	-0.1347	0.1122	-2.0097
2	Zfhx4	1.1209	0.2947	[illegible]	-0.0673	-0.3479	-0.3846	-0.5438	-0.671	-0.7919
2	Zfp36	1.9715	0.5428	0.5593	0.1188	0.586	-0.0769	-0.2919	0.0813	-2.6821
2	Zfp362	0.4973	0.1973	0.303	-0.1097	-0.2576	-0.1196	[illegible]	-0.1042	-1.7462
2	Zfp365	-0.3042	0.6251	0.058	0.5667	0.1052	0.098	-0.2576	0.2603	-1.9794
2	Zfp608	1.3203	0.7321	0.5925	0.5808	0.3815	0.371	0.7823	0.8934	-1.7336
2	Zfpm2	2.4563	1.4779	1.1966	0.5403	-0.8228	-0.848	-0.9751	-0.8823	-1.0512
2	Zhx3	0.1048	0.1932	0.5675	0.4647	[illegible]	-0.252	-0.5067	-0.4263	-1.1896
2	1190002H23Rik	0.5059	-0.2804	0.5146	-0.6602	-0.5478	-1.0373	-0.8089	-0.9788	-1.4723
2	2310047M10Rik	0.3807	-0.0664	-0.2888	-0.4018	-0.5114	-0.6086	-0.8041	-0.7031	-0.6966
2	4632417K02	0.3555	0.2209	-0.4072	-0.5401	-0.8739	-0.9832	-0.8514	-0.9052	-1.5093
2	6230427J02Rik	0.6983	0.5312	-0.4028	-0.3716	-0.5068	-0.7479	-0.5038	-0.5286	-0.6324
2	6430411K18Rik	1.0513	0.5163	-0.7815	-0.6851	-0.8016	-0.892	-0.6727	-0.6064	0.2235
2	6720456H20Rik	-0.1692	0.0858	-0.3784	-0.3775	-0.4284	-0.693	-0.7434	-0.4313	-2.0912
2	9530068E07Rik	0.6752	0.5382	-0.297	-0.3466	-0.5614	-0.4709	-1.4223	-0.469	-2.0268
2	Abat	0.606	0.3995	0.0819	-0.2616	-0.8784	-1.223	-1.1589	-1.082	-1.169
2	Abca3	0.1693	-0.1438	[illegible]	-0.2233	-0.4057	-0.2939	-0.9679	-0.4985	-1.5961
2	Abhd14b	0.3902	0.3884	-0.427	-0.1134	-1.1591	-0.6589	-1.3613	-0.8767	-0.6277
2	Acadsb	0.1131	[illegible]	-0.063	-0.4963	-0.5439	-1.4039	-0.8634	-0.8367	-0.6342
2	Acap3	0.4043	0.2205	-0.3421	-0.0946	-0.9336	-0.6695	-1.169	-0.9857	-1.9918
2	Actn1	1.2166	1.0925	-0.2723	-0.6297	-0.8477	-1.1502	-0.5191	-0.5931	-0.1485
2	Adam15	0.0779	0.4981	-0.3355	0.1284	-0.6419	-0.113	-1.4334	-0.8504	-2.7724
2	Adam9	1.1096	0.905	-0.1228	-0.5323	-0.465	-0.6109	-0.6329	-0.549	-1.4617
2	Adamts1	1.0743	0.6361	-0.6805	-0.4999	-1.2397	-0.8475	-1.277	-1.4015	-1.3857
2	Adamts2	1.3201	0.3726	-1.3021	-1.6643	-1.7412	-1.6246	-1.8224	-1.9188	-1.7812
2	Adamts4	0.5793	0.2633	-0.879	-0.9277	-0.8766	-0.9426	-0.6272	-0.7841	-0.8647
2	Adamts5	1.5442	0.5289	-0.687	-1.4215	-1.6888	-1.5624	-1.6033	-1.726	-1.6597
2	Adamtsl4	0.8877	0.559	[illegible]	-0.0824	-1.1323	-1.2548	-1.6802	-1.2467	-1.518
2	Adcy6	[illegible]	0.3033	-0.5546	-0.2235	-0.61	-0.3117	-0.6517	-0.5707	-1.5608
2	Ahnak	1.0322	0.3843	0.3879	-0.0604	-0.3942	-0.3979	-1.1774	-0.7569	-3.1379
2	Ahnak2	0.6127	0.2252	-0.1391	-0.1434	-0.7174	-0.4841	-1.5762	-0.8445	-3.2143
2	Akr1b8	1.2096	1.3985	-0.5237	-0.4704	-0.7879	-1.1029	-0.6981	-1.022	-0.3901
2	Amfr	0.1527	-0.147	-0.0891	-0.157	-0.432	-0.5369	-0.9811	-0.8103	-1.6917
2	Amotl2	1.3703	0.4908	0.2022	-0.613	-0.6054	-0.9191	-0.6175	-0.6282	-1.0159
2	Ang1	0.2107	0.0901	0.2407	0.3147	-0.3892	-0.3796	-1.1315	-0.6155	-1.5882
2	Angptl1	0.6498	[illegible]	-0.8448	-0.7738	-0.6388	-0.7091	-0.6609	-0.9773	-0.9228
2	Angptl2	1.3137	1.0548	-0.5603	-0.109	-0.8068	-0.425	-0.9257	-0.6898	-1.4981
2	Anpep	1.0776	0.5911	-0.6282	-1.0187	-0.9877	-0.6843	-0.8171	-0.4233	-0.3289
2	Antxr1	0.6982	[illegible]	-0.7898	-1.0952	-1.5651	-1.5821	-1.7886	-1.5778	-2.3515
2	Anxa2	-0.0607	0.1443	[illegible]	0.1878	-0.528	-0.3827	-1.2622	-0.8838	-3.6851
2	Anxa3	0.2759	0.4172	-0.143	-0.1349	-1.2376	-0.8788	-1.7346	-1.16	-2.4535
2	Anxa5	0.531	0.7793	0.3963	0.2187	-0.7222	-1.1384	-1.7147	-1.7086	-3.4801
2	Anxa8	0.1072	0.5813	0.0896	0.3881	-0.7592	-0.3449	-1.5868	-0.4704	-3.8898
2	Apbb1ip	1.0773	0.6917	-0.1359	-0.2704	-0.6399	-0.9462	-0.8575	-0.7992	-0.9287
2	Apbb2	1.1429	0.486	-0.6471	-0.8056	-0.9355	-0.8825	-0.6074	-0.9225	-0.1544
2	App	0.947	0.5604	0.1816	-0.151	-0.6953	-0.7784	-1.2156	-1.0698	-3.3568
2	Aqp1	0.5727	1.0558	-0.9035	-1.1987	-1.6312	-1.744	-1.5754	-1.8379	-1.8161
2	Areg	-0.129	-0.0613	0.8435	-0.9838	-0.1384	-0.5569	-0.9306	-0.9636	-2.0373
2	Arf2	0.5342	0.4563	[illegible]	-0.6931	-0.6859	-0.7912	-0.3527	-0.8457	-0.45
2	Arfgap3	0.2732	0.1081	-0.4437	-0.5299	-0.3635	-0.6064	-0.8113	-0.6637	-1.2578
2	Arhgap20	2.0081	0.3151	-0.262	-0.7587	-1.0433	-1.097	-1.5248	-1.3714	-1.6371
2	Arhgap24	1.0188	1.271	-0.5622	-0.513	-1.0497	-1.4904	-1.2204	-1.4517	-1.5159
2	Arhgap29	1.0608	0.5978	-0.6968	-1.066	-1.1522	-1.2882	-0.6353	-1.0647	-0.4467
2	Arhgef25	0.7588	0.5165	-0.6108	-0.3012	-1.1857	-0.9471	-1.2053	-0.9671	-0.8787
2	Arl6ip5	-0.2401	-0.2017	0.3504	[illegible]	-0.1587	0.2692	-1.3567	-0.597	-1.9872
2	Armcx3	1.1186	0.9768	[illegible]	-0.2772	-0.6763	-0.9206	-0.6622	-0.6571	-0.7975
2	Arpc1b	0.6408	0.5485	-0.1999	-0.1859	-0.4421	-0.553	-0.9856	-0.9211	-1.4731
2	Arsj	0.9572	0.4288	-0.4434	-0.393	-0.5894	-0.5499	-0.6543	-0.4254	-0.5827
2	Asah2	0.8152	0.3683	-0.3663	-0.5617	-0.7265	-0.9169	-1.0177	-0.971	-1.5041
2	Atp8b1	0.9225	0.1758	-0.5485	-0.6634	-0.2102	-0.5637	-0.6074	-0.4657	-0.9711
2	Avpr1a	1.1206	0.8928	-0.3024	-0.5326	-0.6683	-0.713	-0.7484	-0.7846	-0.6086
2	Axl	0.2549	0.4698	[illegible]	-0.2594	-1.1311	-1.4564	-2.0913	-1.7766	-3.9582
2	B3galnt1	0.2904	0.4068	[illegible]	0.1372	-0.4714	-0.5474	-1.0676	-0.7235	-0.5862
2	Bace1	0.7984	0.174	-0.1268	-0.065	0.0951	-0.3876	-0.9036	-0.8659	-1.8206
2	BC013529	0.761	0.3558	-0.1848	-0.3588	-0.3987	-0.7362	-0.8488	-0.9465	-1.0072
2	BC017158	[illegible]	0.0674	-0.4508	-0.1996	-0.5808	-0.5899	-0.7527	-0.7463	-1.2242
2	Bet1l	0.6439	0.1607	-0.3464	-0.6368	-1.0119	-0.9709	-0.9891	-0.8464	-1.3878
2	Bin1	0.2523	0.5294	-0.597	-0.1102	-0.8003	-0.5826	-1.1371	-0.8666	-2.0469
2	Bmp1	1.2178	1.0573	-0.5588	-0.9587	-1.4831	-1.7822	-1.4223	-1.6788	-1.8109
2	C1qtnf2	1.4489	-0.2162	-1.5132	-1.5432	-1.6423	-1.6236	-1.5609	-1.6669	-1.9021
2	C2	1.6136	-0.4923	-0.9648	-1.0857	-1.0983	-1.3447	-1.0288	-1.193	-0.2343
2	C4b	0.5115	-0.1752	-0.3598	-0.3772	-0.6121	-0.6062	-0.6966	-0.7376	-0.7537
2	Ccdc23	0.5149	0.1545	-0.6009	-0.7015	-0.6557	-0.7762	-0.8122	-0.4893	-0.4459
2	Ccdc3	1.5426	0.7232	0.2918	-0.3869	-0.5425	-1.2838	-1.1957	-1.3457	0.5002
2	Ccdc80	1.9853	0.8177	0.7813	0.0761	-0.8465	-1.5464	-1.9268	-1.6634	-3.561
2	Ccl7	2.5647	1.8866	2.2205	1.3785	-0.3312	-1.7426	-1.5324	-1.994	-3.6008
2	Cd248	1.5051	0.9976	-1.0137	-1.1827	-1.5202	-1.6922	-1.5772	-1.6953	-1.8103
2	Cd63	0.4236	0.5347	-0.4028	-0.8001	-1.2332	-1.7137	-1.91	-2.4933	-2.4592
2	Cd82	0.4334	0.1084	-0.7249	-1.3058	-1.8679	-1.6645	-1.8148	-1.7861	-2.4956
2	Cdc42ep2	0.2135	0.4592	-0.5697	-0.1552	-0.6653	[illegible]	-0.8508	-0.1162	-1.8673
2	Cdk14	1.4178	0.7575	-0.8713	-0.8428	-1.4188	-1.5705	-0.9493	-1.611	-1.594
2	Cdkn1a	0.138	0.1817	0.1903	-0.1107	-0.518	-0.1158	-1.3243	-0.716	-2.5663
2	Cdkn2a	0.6711	0.8107	-0.0845	0.1026	-0.5011	0.7623	-1.1338	-1.1962	-2.2061
2	Cdkn2b	1.0553	0.8716	-0.5173	-0.582	-1.1092	-0.9978	-1.6901	-1.1063	-3.5748
2	Cebpb	1.4847	0.5692	0.1744	-0.6181	-0.1956	-0.5789	-0.7285	-0.5259	-2.3961
2	Celf2	1.4912	0.5338	-0.4472	-0.5494	-1.3659	-1.3531	-1.509	-1.5541	-1.618
2	Cenpb	0.1781	0.1652	-0.2039	-0.1171	-0.5906	-0.5847	-0.98	-0.6764	-1.4136
2	Cgrrf1	0.491	0.2251	-0.2148	-0.234	-0.5146	-0.6409	-0.7456	-0.5828	-0.8291
2	Chst2	1.2629	1.3234	-0.3044	-0.1867	-0.7596	-0.8665	-1.1237	-0.908	-1.5796
2	Clec11a	0.8576	0.1572	-0.3825	-0.5759	-0.8853	-0.4878	-0.7746	-0.5778	-0.797
2	Clec3b	0.4966	[illegible]	-0.4105	-0.6027	-0.7567	-0.6451	-0.6636	-0.7468	-0.6087
2	Col1a2	1.4861	0.9578	-0.3591	-0.9954	-1.6165	-1.4975	-1.4748	-1.5205	-1.3053
2	Col28a1	1.2148	0.7687	-0.2474	-0.7267	-0.7904	-0.9595	-1.0137	-0.9662	-0.9696
2	Col3a1	1.9487	0.8135	-0.6454	-0.9298	-1.4928	-1.6265	-1.5927	-1.4773	-1.5532
2	Col4a1	1.4283	1.5673	0.7327	0.6291	-1.1797	-1.5656	-1.5728	-1.5903	-2.4772
2	Col5a2	0.9353	0.21	-0.723	-0.9132	-0.9849	-1.1399	-1.0153	-0.7711	-1.0995
2	Col7a1	0.1457	0.2912	-0.7478	-0.8826	-0.7652	-0.8162	-0.5798	-0.4018	-0.6872
2	Copz2	1.4593	1.1155	-0.8216	-0.8858	-1.4239	-1.6671	-1.3162	-1.6587	-1.1049
2	Cpne8	0.3533	0.375	-0.1142	-0.0713	-0.9902	-0.6923	-1.6092	-1.3536	-1.9255
2	Cpxm1	1.7888	1.6448	-1.3238	-1.209	-1.7295	-1.7609	-1.1685	-1.3121	-0.1929
2	Crabp1	1.2057	1.6846	-1.6822	-1.3712	-2.4103	-1.7942	-1.4027	-1.8815	-0.5483
2	Csf1	1.5768	0.9112	-0.2011	-0.5375	-1.0929	-1.2584	-1.104	-1.104	-1.3538
2	Cxcl1	3.4153	1.9817	1.0004	-0.5823	-0.9911	-1.6297	-1.6966	-1.7235	-3.2688
2	Cxcl5	1.4242	0.6087	-0.2541	-0.6273	-0.7958	-0.8264	-0.7266	-0.9042	-0.8299
2	Cyr61	1.0539	0.2187	0.1557	-0.328	-0.2828	-1.3618	-1.1306	-1.2028	-2.6733
2	Cyth3	1.259	0.8522	0.3732	-0.1973	-0.904	-0.6712	-0.8586	-0.8662	-1.6529
2	D4Bwg0951e	1.3206	0.5892	0.3743	-0.379	-1.042	-1.7514	-1.6866	-1.6337	-1.8786
2	Dbp	0.2119	-0.2285	0.2499	[illegible]	-0.3172	-0.2282	-1.4298	-0.6596	-1.2491
2	Dhx58	1.3034	-0.2893	0.4353	-0.9391	-0.5946	-1.0667	-0.6424	-0.733	-0.4622
2	Dpt	2.863	2.4184	-0.6652	-0.7818	-1.1619	-1.2362	-1.0358	-1.2121	-1.1851
2	Dusp23	0.5512	0.1517	-0.5644	-0.6855	-0.6029	-0.856	-0.5372	-0.7465	-1.1568
2	E130203B14Rik	0.8406	[illegible]	-0.8007	-0.8367	-0.848	-1.1213	-0.9087	-0.8998	-0.5921
2	Ecm1	0.6916	0.6669	-0.3944	-0.1092	-0.5982	-0.7866	-0.7392	-0.8152	-0.8652
2	Efemp2	1.3924	0.7523	-0.7321	-1.3022	-1.3311	-1.4151	-1.6314	-1.2111	-3.0314
2	Egfr	0.4526	-0.1106	-0.2809	-0.3396	-0.4232	-0.3236	-1.023	-0.8349	-1.5474
2	Eif2ak2	1.2224	0.1002	-0.1298	-0.7057	-0.6583	-0.8048	-1.107	-1.1015	-1.6297
2	Elk3	0.463	0.5539	-1.118	-1.088	-1.3379	-1.7039	-1.9465	-1.9377	-1.7764
2	Emilin1	0.6678	0.5797	-0.7664	-0.7451	-1.0635	-1.1472	-1.0287	-1.2411	-1.1994
2	Eml1	0.4619	0.8466	-0.7977	-0.5001	-1.0732	-0.9509	-0.2645	-0.2181	-1.0775
2	Emp3	0.5198	0.468	-0.1558	-0.2642	-1.1816	-0.6554	-2.3265	-1.1722	-3.9682
2	Endod1	0.8703	0.4144	-0.5051	-0.6949	-1.1798	-1.2981	-1.0156	-1.0329	-1.1654
2	Enpp2	0.5726	-0.119	-0.0558	-0.8934	-0.7091	-1.2815	-0.0757	-0.6802	-1.1864
2	Enpp5	0.4759	-0.3929	0.1531	-0.4447	-0.7038	-0.6577	-1.1362	-0.7015	-1.4055
2	Entpd2	0.6036	0.4657	-0.2435	-0.7586	-0.917	-0.9231	-0.8839	-0.7505	[illegible]
2	Epb4.1l3	1.8728	1.6515	-0.6357	-0.3732	-2.9827	-2.9209	-0.6529	-1.8085	-0.9097
2	Epdr1	0.6482	0.2615	0.3753	[illegible]	-0.7658	-0.9321	-1.2699	-1.1859	-1.9777
2	Ephb2	0.9943	0.6342	-1.0527	-1.0165	-1.153	-1.2102	-0.4171	-0.7706	-0.2714
2	Ephx1	0.5481	0.615	0.4194	0.3811	-0.2371	-0.2541	-1.2327	-0.1844	-3.4705
2	Ets1	0.7651	0.806	-0.3439	-0.4016	-1.3289	-1.2926	-1.0296	-1.0906	-1.486
2	Evi5l	0.2419	[illegible]	-0.4331	-0.3187	-0.6319	-0.6949	-0.9452	-0.6055	-1.121
2	Extl2	0.122	0.1096	-0.5336	-0.2453	-0.3686	-0.4605	-0.9838	-0.814	-2.0147
2	Fads3	0.4978	0.3806	-0.2084	-0.3804	-0.5819	-0.681	-0.4891	-0.728	-0.7178
2	Fam115c	0.9304	1.0671	-0.3301	0.1327	-1.1057	-1.0729	-0.8256	-1.1565	-0.2109
2	Fam171b	1.0696	0.4165	-0.6274	-0.7799	-1.0424	-1.0247	-0.336	-0.8718	[illegible]
2	Fam180a	0.9392	0.2192	[illegible]	-0.4267	-1.6442	-1.8464	-1.8579	-2.0817	-1.8265
2	Fam20a	0.6056	0.6436	-0.9277	-0.8616	-1.8575	-1.6807	-2.1222	-1.7867	-2.0621
2	Fam65c	0.6642	0.1163	-0.3809	-0.6206	-0.574	-0.5806	-0.6343	-0.6724	-0.5609
2	Farp1	0.6202	0.606	-0.1006	-1.0489	-0.9418	-1.6911	-1.0268	-1.8398	-2.4028
2	Fat4	1.3869	0.4849	-0.1625	-0.7944	-0.9343	-0.8838	-0.938	-0.7389	-0.8662
2	Fez2	0.655	0.3662	-0.5044	-0.4157	-0.9655	-0.9703	-0.6129	-0.8944	-0.5981
2	Fgf7	2.0848	1.6007	-0.8132	-0.9411	-1.7129	-1.7693	-1.6387	-1.6586	-1.7874
2	Fgfr1op2	-0.2584	-0.4168	0.1622	0.214	0.0902	-0.1505	-0.4072	-0.5427	-2.8764
2	Fgfrl1	0.9669	0.4101	-0.1872	-0.3049	-0.9924	-0.6954	-1.1217	-0.846	-0.5399
2	Fhl1	1.2878	1.2167	-0.8886	-0.905	-1.6093	-2.157	-0.2221	-0.7231	1.2378
2	Fhl2	1.7271	0.9131	-0.2505	-1.3365	-0.6832	-1.2885	-0.7348	-1.3594	-2.0986
2	Fkbp14	0.6236	0.3576	-0.4482	-0.3353	-0.3862	-0.9307	-0.718	-0.8695	-0.9307
2	Fkbp7	1.3265	0.7587	-0.2227	-0.6295	-0.8315	-1.1167	-1.2095	-0.9935	-1.622
2	Flt1	0.961	0.7305	-1.6505	-1.2806	-0.6973	-0.923	0.6935	-0.1335	-1.9544
2	Fmo3	0.5617	0.1766	-0.7077	-0.5195	-0.6729	-0.666	-0.4678	-0.7471	-0.6456
2	Fndc3b	0.9774	0.5144	-0.2561	-0.4567	-0.6189	-1.0131	-1.1034	-1.1459	-2.0059

2	Foxg1		0.5918	0.2945	-0.4809	-0.1676	-0.7308	-0.7411	-0.6288	-0.7308	-0.7172
2	Fst		1.6781	1.4544	-0.6099	-0.5151	-1.9762	-1.8905	-1.1184	-1.534	-1.7696
2	Fstl1		1.0637	0.689	0.2496	-0.2637	-0.4493	-0.9137	-1.1556	-0.89	-2.2973
2	Fzd1		1.0648	0.5228	-0.2789	-0.6458	-0.818	-0.8732	-0.704	-0.5869	-0.8627
2	Gabarap		0.5119	0.4199	0.143	-0.3442	-0.2891	-0.53	-0.7661	-0.6645	-1.4963
2	Gabarapl1		0.3477	0.2915	[illegible]	-0.214	-0.8479	-0.6082	-1.4209	-0.8146	-1.4594
2	Gadd45g		0.4968	-0.1417	0.1183	-0.2226	-0.1211	-0.7578	-0.6272	-0.8747	-3.5539
2	Galnt10		0.5517	0.1941	-0.6258	-0.883	-0.9758	-1.172	-0.7884	-0.9717	-1.2481
2	Gas7		0.6367	0.4755	-0.2002	-0.3345	-0.6978	-0.6439	-0.8843	-0.5074	-0.59
2	Gata2		0.273	0.3031	-0.1591	-0.7289	-0.8225	-1.301	-0.3995	-0.657	-0.8788
2	Glt8d1		0.5722	-0.0983	-0.4774	-0.6245	-0.6079	-0.7895	-0.6371	-0.7388	-0.7697
2	Gm1673		0.3004	[illegible]	0.3133	-0.0727	-0.4935	-0.6863	-0.7641	-0.8001	-1.5816
2	Gm8909		0.5171	-0.4277	-0.0992	-0.6815	-0.2768	-0.6355	-0.7009	-0.832	-0.7958
2	Gnb5		0.7482	0.3413	-0.422	-0.0988	-0.7742	-0.4571	-1.0299	-0.882	-0.7404
2	Gng10		0.4817	0.4718	-0.6674	-0.5464	-0.9663	-0.8289	-1.2541	-1.0857	-1.536
2	Gng8		1.3555	0.6895	-1.2103	-0.7782	-1.2623	-1.2164	-1.1748	-1.3161	-0.9478
2	Gns		1.299	0.6425	-0.2212	-0.5074	-0.8272	-1.0625	-0.8737	-0.9313	-1.6432
2	Gpr124		1.4041	1.1445	-0.1422	-0.6164	-1.118	-1.115	-0.9564	-0.9945	-1.0913
2	Gpr176		1.9884	1.7779	0.6885	-0.1813	-0.6566	-1.5842	-1.5271	-2.0854	-2.2147
2	Gpx3		1.4335	0.3872	-1.2332	-1.56	-1.7054	-1.8085	-1.348	-1.494	-1.3405
2	Gstm2		1.0489	0.6292	-0.5834	-0.7664	-0.6187	-0.776	-0.2935	-0.2547	-0.7857
2	Gxylt2		1.3171	0.6108	-1.1059	-1.3527	-1.5709	-1.6369	-1.5358	-1.5358	-1.3892
2	Gyg		0.6593	-0.0496	-0.4073	-0.7505	-0.9784	-0.8377	-1.0113	-0.8471	-1.2087
2	H2-T22		1.3052	0.1941	-0.3336	-0.8969	-0.8695	-1.3077	-0.9117	-0.9211	-1.5969
2	H2-T23		1.9175	-0.2485	0.4083	-0.8433	-0.5295	-1.0449	-1.1946	-1.1505	-1.7819
2	H6pd		0.7774	0.7829	-0.9907	-0.8432	-1.153	-1.0246	-1.2511	-0.8536	-1.19
2	Has2		0.9134	0.8015	-0.8621	-1.3332	-0.864	-0.6411	-0.3801	-0.3828	-1.2102
2	Hdac7		0.6304	0.5681	[illegible]	-0.757	-0.3638	-0.8556	-0.7627	-0.8207	-1.663
2	Herpud1		0.1621	-0.1604	0.2686	-0.1326	-0.7987	-0.9922	-1.3457	-0.9439	-0.5369
2	Hic1		2.1618	1.5419	-0.4649	-0.6661	-1.3803	-1.3084	-1.597	-1.3057	-1.4381
2	Hist1h1c		1.033	0.3671	0.903	0.3668	[illegible]	-0.6344	-0.7727	-0.8348	-3.4902
2	Hist1h2bc		1.1681	0.2636	[illegible]	-0.3875	-0.4676	-1.1046	-0.8	-1.3906	-2.279
2	Hist1h2bj		1.0454	[illegible]	-0.3645	-0.3919	-0.3516	-0.8543	-0.2181	-0.6697	-1.0542
2	Hmgn3		-0.2068	[illegible]	0.1946	0.1348	-0.288	-0.3066	-1.0661	-0.367	-3.4288
2	Hoxd8		1.5912	1.046	0.0907	-0.3203	-0.3041	-0.6435	-0.771	-0.9528	-1.6096
2	Hp		0.6439	1.2528	-0.6062	-0.7312	-0.9362	-0.803	-0.6239	-0.7997	-0.6689
2	Hs3st1		1.3446	0.3958	-0.757	-0.8528	-1.3643	-1.3735	-0.9858	-1.4496	-0.7251
2	Hspg2		0.3942	0.4574	-0.7185	-0.3873	-1.0119	-0.4999	-1.4524	-0.8522	-1.2205
2	Htra3		1.5128	1.152	-0.9427	-0.9935	-1.2501	-1.3654	-1.2999	-1.2761	-1.6212
2	Ier3		1.2474	0.1406	-0.1743	-0.4657	-0.6987	-0.4156	-1.1869	-0.7602	-1.1884
2	Ifi47		2.2397	-0.2017	0.6395	-0.9444	-0.6445	-0.9671	-0.5079	-0.8725	-1.0509
2	Igfbp3		2.2317	0.9488	-0.1117	-1.1043	-1.1831	-0.9657	-1.0149	-1.6039	-2.415
2	Ikbip		0.8628	0.5344	-0.2472	-0.5456	-0.5434	-0.6959	-0.9835	-0.6016	-0.446
2	Il13ra1		0.2966	0.6764	0.4898	-0.2156	-0.3067	-0.3641	-1.1479	-0.627	-1.8365
2	Il1rl1		2.4813	3.1087	-0.5561	-0.3405	-1.1748	-1.3587	-1.2654	-1.2747	-1.3889
2	Il6st		1.4383	0.3561	-0.3492	-0.8631	-0.9409	-1.506	-0.9309	-0.925	-0.7643
2	Ilvbl		0.0938	0.2386	-0.3552	-0.48	-0.7345	-0.5657	-0.9926	-0.9552	-0.9245
2	Inhba		1.5943	1.6043	-0.6093	0.0539	-1.5872	-1.5705	-1.443	-1.4832	-1.5408
2	Irgm2		1.6922	-0.0842	0.211	-1.0436	-0.27	-1.1811	-0.267	-1.0608	-1.5775
2	Irx2		0.8576	0.2742	-0.1499	-0.5125	-0.5648	-0.6854	-0.8152	-1.1038	-1.6424
2	Itga11		1.4763	0.8884	-0.5882	-1.0312	-1.1028	-1.0513	-1.242	-1.0412	-1.0751
2	Itm2b		0.1551	-0.5228	0.3789	-0.0989	0.1813	-0.4744	-0.7319	-0.8692	-3.379
2	Jdp2		1.5272	0.6917	-0.4573	-0.723	-1.2189	-1.789	-1.2383	-1.2815	-0.7813
2	Kazald1		0.6987	0.701	-0.1127	-0.1725	-0.8177	-0.747	-0.9236	-0.8544	-0.8144
2	Kctd12		1.1595	0.1718	0.3093	-0.9473	-1.5205	-1.3331	-1.4268	-1.7721	-1.8668
2	Kdelr3		0.9772	0.5349	-0.911	-1.103	-1.9631	-1.8559	-2.4806	-2.1034	-0.2322
2	Lamp2		0.8057	0.0398	-0.4149	-0.5716	-0.8508	-0.9463	-1.3098	-1.3551	-1.6361
2	Ldb2		1.263	0.2276	-1.0122	-1.2525	-1.2365	-1.3152	-1.051	-1.2786	-1.3842
2	Lgals1		0.9385	0.8351	-0.5689	-1.0452	-1.1818	-1.8874	-1.4942	-1.3891	-3.1909
2	Lgals3bp		2.8697	1.5736	1.3267	-1.2977	-0.7922	-2.0899	-0.9536	-2.2792	-3.1285
2	Lgals8		0.3428	0.1242	-0.0605	-0.3077	-0.531	-0.7001	-0.8684	-1.0791	-1.5554
2	Lgr5		2.1541	0.6865	-0.4183	-1.1251	-1.4331	-1.2947	-0.5917	-1.2359	-1.4733
2	Lhfp		0.9808	0.7945	0.1659	-0.2398	-0.6235	-1.0267	-1.1581	-0.9531	-4.3774
2	Lmcd1		0.3044	0.3997	-0.6956	-0.8925	-0.8119	-0.7255	-0.6989	-0.7733	-0.4486
2	Lmo4		1.345	1.0203	0.1789	-0.6005	-0.8906	-1.0695	-0.5801	-1.2448	-1.9324
2	Lpar1		1.2347	0.9603	0.1974	-0.3185	-0.9355	-1.197	-0.7882	-1.0762	-0.6439
2	Lrfn3		0.6028	0.4543	-0.739	-0.8044	-0.8361	-1.2547	-0.5928	-0.8065	0.15
2	Lrig3		1.139	0.4357	-0.9368	-0.6131	-1.2527	-1.0285	0.2826	-0.3481	[illegible]
2	Lrp1		0.6145	0.2044	-0.4051	-0.4242	-0.5882	-0.7623	-0.8415	-0.5831	-1.2722
2	Lrp10		[illegible]	[illegible]	[illegible]	-0.7964	-0.6112	-0.5777	-0.9029	-0.7238	-1.3317
2	Lrrc15		1.2861	0.9914	-1.121	-1.1046	-1.5831	-1.7427	-1.1567	-1.4866	-0.9222
2	Lrrfip1		0.4125	0.1773	-0.3958	-0.3693	-0.7309	-0.7574	-1.1065	-1.121	-2.0589
2	Lrrn3		0.8362	[illegible]	-0.4827	-0.9493	-1.0082	-1.0082	-1.0984	-1.1638	-1.2134
2	Ltbp3		0.765	0.8528	-0.4493	0.1166	-0.599	-0.5957	-0.9969	-0.84	-0.8905
2	Lxn		1.3997	1.0503	0.3004	0.14	-0.5106	-0.4448	-1.0691	-0.9205	-2.3007
2	Ly6a		[illegible]	[illegible]	0.344	0.6534	0.195	0.184	-0.4655	[illegible]	-5.9379
2	Ly6c1		0.4452	0.0596	0.5951	0.5934	-0.712	-0.6067	-1.2353	-0.9401	-4.2566
2	Lztr1		0.2892	0.1441	-0.3555	-0.4177	-0.5298	-0.5878	-0.8783	-0.691	-1.1897
2	Maged1		0.5298	0.2017	-0.3788	-0.7085	-0.796	-0.851	-0.8468	-0.6111	-1.4513
2	Magee1		1.0898	0.8553	-0.6113	-0.3161	-1.3411	-1.193	-1.686	-1.1224	-1.9954
2	Man2a1		0.8523	0.5497	-0.8763	-0.8981	-1.3778	-1.0526	-1.3571	-1.3432	-1.1159
2	Map3k14		0.4849	0.3948	-0.4328	-0.4727	-0.4576	-0.6675	-0.6163	-0.656	-0.8594
2	Mapkapk2		0.2585	[illegible]	0.2632	-0.201	-0.3375	-0.6356	-0.7356	-0.5644	-1.6234
2	Mbnl1		0.3434	0.1663	0.2318	[illegible]	-0.1369	-0.354	-1.1019	-0.5838	-3.2316
2	Mcfd2		0.4684	0.388	-0.3347	-0.3395	-0.5962	-0.6395	-0.5661	-0.5184	-1.0666
2	Mef2c		0.4408	0.0992	-0.4067	-0.6048	-0.6946	-0.8091	-0.9132	-0.7781	-0.8123
2	Meis1		0.6418	0.6542	-0.6153	-0.4954	-0.6078	-0.4662	-0.3774	-0.7322	-2.0663
2	Mfap2		1.6496	1.0538	-0.7972	-1.4635	-1.927	-1.7942	-0.9222	-1.6142	-1.7942
2	Mkx		0.3133	[illegible]	[illegible]	[illegible]	-0.7921	-0.5327	-1.0784	-0.8076	-0.9494
2	Mkl		1.3719	0.1963	-0.2726	-0.5527	-0.6227	-0.75	-1.0314	-0.9938	-0.6443
2	Mmp23		1.632	0.8509	-0.5239	-0.7217	-0.8152	-0.6573	-0.9777	-0.6951	-1.1976
2	Mpp1		1.0746	0.5069	-0.4639	-0.3841	-0.9949	-1.2312	-0.9808	-1.2707	-1.2257
2	Mtap6		0.6802	0.6994	-0.2189	-0.2626	-0.9296	-0.8814	-0.9005	-0.9037	-0.8941
2	Mxd4		0.1721	0.1437	-0.2038	-0.2277	-0.3376	-0.2811	-0.7109	-0.5676	-1.7257
2	Mxra7		1.4934	0.9567	-0.5827	-0.9106	-1.3682	-1.1633	-0.7278	-0.8409	-0.5057
2	Mxra8		1.6628	1.427	-0.6327	-0.2691	-1.238	-1.3746	-1.4921	-1.5564	-1.8278
2	Mylk		1.0367	0.4171	-0.6345	-0.695	-0.7678	-0.7776	-0.8208	-0.9512	-0.7427
2	Myo7a		0.3614	0.4916	-0.7456	-0.6581	-0.7693	-0.8117	-0.3911	-0.6507	-1.3178
2	Ncam1		0.8265	0.4099	-0.5674	-0.3739	-1.1524	-1.2502	-1.2853	-1.4219	-1.3582
2	Nedd9		1.5401	0.2697	-0.3786	-1.3079	-1.6588	-1.9628	-1.345	-1.5985	-1.6398
2	Nenf		1.0772	0.6311	-0.774	-0.9536	-1.3593	-1.5242	-1.4663	-1.2734	-1.4365
2	Nfatc4		1.0314	0.9214	-0.5407	-0.9024	-1.4715	-1.2578	-1.3395	-1.178	-0.816
2	Nfil3		1.6296	0.2802	0.9687	-1.0342	-1.1266	-1.6381	-1.6258	-1.3432	-1.6522
2	Nfix		0.9593	1.0289	0.6078	0.4856	-0.1795	-0.2963	-1.0769	-1.103	-4.2013
2	Nfkbiz		2.0977	0.7548	[illegible]	-0.3078	-0.6191	-1.0004	-0.9414	-0.6124	-2.2943
2	Nid1		1.701	1.1263	-0.4724	-0.6728	-0.5919	-0.7962	-0.8692	-0.8596	-0.7654
2	Nlrc5		1.003	0.4465	-0.5573	-0.6733	-0.7483	-0.8064	-0.745	-0.7416	-0.7719
2	Nnmt		1.8091	1.4426	-0.7315	-0.5893	-1.8712	-2.1144	-1.7494	-1.9173	-1.9617
2	Nox4		0.9956	0.1571	-0.1808	-0.4784	-0.7819	-0.8034	-0.7666	-0.6538	-0.2612
2	Npr2		1.2353	0.6163	-0.3502	-0.3647	-1.4323	-1.8796	-2.1269	-2.0162	-2.6606
2	Npy6r		0.5302	0.1748	-0.4534	-0.2777	-0.644	-0.8484	-0.6772	-0.6976	-0.6279
2	Nr2f1		0.5172	0.6062	0.665	0.6296	-0.7101	-0.8846	-1.1146	-0.5472	-2.9339
2	Nucb1		0.4192	0.289	-0.3363	-0.7697	-0.5856	-0.7074	-0.6712	-0.8	-1.5886
2	Odz3		0.5008	0.1894	-0.9189	-0.8123	-1.0769	-1.066	-0.6893	-0.7287	-0.4159
2	Ogn		1.796	0.5176	[illegible]	-0.3274	-0.6681	-0.8962	-0.7322	-0.694	-0.8249
2	Olfml1		1.2656	[illegible]	0.7362	0.4386	0.213	-0.9358	-0.875	-1.0597	-1.4513
2	Olfml2b		2.4417	2.0998	0.2767	-0.514	-1.4214	-1.4502	-1.2474	-1.2399	-0.9499
2	Os9		0.1211	[illegible]	-0.1831	[illegible]	-0.4579	-0.443	-1.3016	-0.9429	-1.8698
2	P4hb		0.3466	0.3163	-0.5883	-0.5809	-0.6606	-0.5804	-0.7975	-0.7101	-0.9015
2	Palld		1.1765	0.9983	-0.705	-0.6223	-1.5181	-1.3712	-1.0702	-1.2068	[illegible]
2	Parp14		0.9034	-0.8976	0.231	-1.0481	-0.3303	-1.0529	-0.4815	-0.903	-0.6441
2	Parva		0.6274	0.8493	-0.3033	-0.3801	-0.8922	-0.8091	-1.682	-1.2732	-3.6106
2	Pbxip1		1.0709	0.6412	-0.3383	-0.3278	-0.5649	-0.7849	-0.8143	-0.8167	-1.6413
2	Pcolce		0.7317	0.4922	0.3754	-0.1248	-0.5377	-0.6666	-1.4583	-0.9712	-2.5646
2	Pdgfrl		1.6425	0.6686	-0.3963	-1.2089	-1.6925	-1.8793	-1.4209	-1.4124	-1.0922
2	Pdia3		0.194	0.6193	-0.552	0.1881	-1.5454	-0.1901	-1.5208	-0.8475	-0.8236
2	Pdia5		0.3312	0.5949	-0.6152	-0.6163	-0.7273	-0.5496	-0.9501	-0.746	-0.6952
2	Pdlim2		1.2168	0.8501	-0.7543	-0.9354	-1.334	-1.3682	-1.0732	-1.2875	-0.944
2	Pdpn		0.9269	0.617	-0.8889	-1.2215	-1.9513	-2.7041	-1.256	-1.8386	-1.3184
2	Pea15a		0.44	1.1845	-1.0685	-0.7175	-1.2332	-1.0384	-0.3435	-0.8248	-1.4875
2	Pfn2		0.1896	0.2073	[illegible]	-0.3246	-0.6227	-0.3612	-0.767	-0.6074	-2.3606
2	Pgcp		1.0976	0.4502	0.1253	-0.2047	-0.6938	-0.6017	-1.1802	-0.9686	-2.0321
2	Picalm		[illegible]	0.1426	[illegible]	-0.1277	-0.2709	-0.3754	-0.5812	-0.9714	-2.379
2	Pik3r1		0.4043	[illegible]	-0.673	-1.1675	-1.8074	-1.7339	-2.3859	-2.2618	-1.7244
2	Pitpna		[illegible]	0.1158	0.2601	0.2869	-0.5055	-0.4304	-0.9734	-0.8459	-1.1712
2	Pja2		0.1177	0.1119	-0.3177	-0.2412	-0.6492	-0.5956	-0.6366	-0.5281	-1.2129
2	Pkd2		1.2594	0.9337	-0.5757	-0.5437	-0.8112	-1.0956	-0.5212	-1.0435	-0.5459
2	Pkia		0.9133	0.5879	-0.1956	-0.413	-0.8091	-0.7212	-0.6149	-0.8031	-1.0852
2	Plac8		2.2589	0.7949	-0.9836	-1.0107	-1.0654	-0.6297	-0.5139	-0.4596	-0.8174
2	Plac9		0.7625	0.2166	-0.4272	-0.6254	-0.8267	-0.7638	-0.7589	-0.5657	-1.0278
2	Pld1		0.6765	0.5443	-0.1615	-0.3942	-0.6198	-0.8046	-0.8535	-0.8387	-0.9354
2	Plekho2		0.8515	0.802	-0.1342	-0.2666	-0.6557	-0.6013	-1.1051	-0.6288	-1.8188
2	Pmp22		1.7723	0.9969	-0.1957	-0.4923	-1.6309	-1.3094	-1.8196	-1.6615	-2.0831
2	Podn		0.8329	0.1552	-1.5071	-1.6911	-1.6371	-1.769	-1.7085	-1.6571	-1.7473
2	Pold4		0.6068	0.3197	-0.6321	-0.4645	-0.8664	-0.4907	-0.9056	-0.6422	-1.3344
2	Ppap2b		1.2867	0.3219	-0.4728	-0.6117	-0.6248	-0.5514	-0.6085	-0.7194	-0.6054
2	Ppapdc1b		0.6677	0.3736	-0.4524	-0.4672	-0.6653	-0.5238	-0.6766	-0.5675	-0.6279
2	Pparg		0.7387	0.6999	-0.5609	-0.311	-0.6308	-0.5161	-0.3247	-0.6971	-0.69
2	Ppic		0.7496	0.6418	-0.1914	[illegible]	-0.604	-0.5508	-1.1844	-0.8272	-1.6844
2	Prdx5		[illegible]	[illegible]	-0.2169	-0.599	-0.5957	-0.6542	-0.4176	-0.7126	-1.4984
2	Prickle1		1.5549	0.5018	-0.8894	-1.1668	-0.9744	-1.4075	0.1223	-0.3176	-1.1554
2	Prkar1a		0.3387	0.1173	-0.3137	-0.3818	-0.5758	-0.8154	-0.7821	-0.8241	-1.1323
2	Prkcdbp		0.5923	0.5127	0.5408	0.2417	-0.6176	-0.7223	-1.648	-1.0793	-4.2603
2	Prss35		0.3591	-0.3468	-0.7269	-0.7499	-1.6974	-1.6911	-2.8583	-1.9293	-2.1673
2	Pter		-0.2729	0.3115	-0.2489	0.3011	-1.0334	-0.0502	-0.9979	-0.5898	-1.335
2	Ptgis		0.8108	1.5409	-0.9865	-0.997	-1.6418	-1.3512	0.1232	0.2442	0.4333
2	Ptpla		0.1673	0.3808	-0.8193	-0.5021	-0.9785	-0.4596	-0.3404	0.208	-1.5405
2	Ptprs		0.2711	0.1233	-0.1332	-0.4116	-0.6849	-0.8774	-0.7681	-0.6048	-0.9452
2	Ptprv		0.817	1.2292	0.4892	0.6756	-0.5595	0.0362	-1.6545	0.2025	-2.8466
2	Pttg1ip		0.3457	0.3364	-0.3694	-0.3239	-0.647	-0.8759	-1.0457	-1.1624	-1.116
2	Pygb		0.3078	0.1168	-0.3895	-0.6314	-0.668	-0.6709	-0.8956	-0.8291	-1.5449
2	Rab34		0.6539	0.4736	-0.7495	-0.8831	-1.3913	-1.0865	-0.9596	-0.7712	-0.5786
2	Rasl11a		1.9658	0.6653	-0.9035	-0.8766	-0.984	-0.7989	-0.4254	-0.4854	0.0266
2	Rcan2		0.85	0.3457	-0.4086	-0.4134	-0.8123	-0.8328	-0.9527	-0.9754	-0.795

2	Rcn3		1.0917	0.1748	-0.806	-1.2634	-1.0461	-1.2509	-0.8828	-0.7002	-0.9186
2	Reck		1.3801	0.614	-0.7357	-0.9356	-1.7944	-1.7389	-1.4288	-1.4411	-1.0538
2	Rerg		1.17	0.5128	-1.3463	-1.4008	-1.8599	-1.9918	-1.7209	-1.8046	-0.544
2	Rftn1		-0.0905	0.2627	-0.0703	-0.3814	-0.3983	-0.3232	-0.8237	-0.4854	-1.6992
2	Rgma		0.6616	0.8088	-0.3105	-0.6252	-0.4922	-0.4439	-0.3148	-0.5332	-1.9351
2	Rgs16		1.6507	0.5937	-0.4311	-0.8338	-1.5503	-1.4839	-1.2313	-0.7828	-1.6275
2	Rhbdd1		0.2578	0.1374	-0.4923	-0.5108	-0.7233	-0.8198	-0.9089	-0.8597	-0.611
2	Rhbdf1		0.5961	0.343	0.1517	-0.4185	-0.5915	-0.7289	-0.5142	-0.596	-0.9096
2	Rhob		0.1363	0.1219	0.128	-0.9497	-0.055	-0.6639	[illegible]	-0.5072	-1.9354
2	Rhobtb3		0.6182	0.3492	-0.2802	-0.228	-0.9008	-0.877	-0.3585	-0.5577	-0.9498
2	Rhoc		0.6883	0.7804	-0.8084	-0.8115	-0.8188	-0.4252	-0.9085	-0.5897	-0.8506
2	Rhog		0.3722	0.0789	-0.2486	-0.4626	-0.4839	-0.3037	-0.7422	-0.5756	-1.9416
2	Rin1		0.4934	0.8657	-0.1464	[illegible]	-0.834	-0.7055	-1.2537	-0.7182	-1.6051
2	Rin2		0.4368	-0.4923	-0.793	-1.2569	-1.6488	-1.8259	-1.9645	-1.88	-2.2478
2	Rnase4		1.0193	0.6866	0.067	-0.071	-1.2848	-1.5332	-2.3662	-2.0329	-3.4279
2	Rnd3		0.4203	0.2268	-0.1464	-0.5104	-0.7414	-1.0296	-1.3969	-1.1462	-2.512
2	Rnf103		-0.1714	-0.54	0.3968	[illegible]	-0.3083	-0.321	-0.9624	-0.7679	-2.0079
2	Rora		1.0989	0.172	0.4541	-0.0944	-0.6405	-0.8115	-0.6491	-0.9879	-1.1568
2	Rras		[illegible]	-0.2696	-0.308	-0.4524	-0.5071	-0.5912	-0.701	-0.2817	-1.386
2	Rusc2		0.2374	-0.1271	[illegible]	-0.2179	-0.3232	-0.373	-1.1923	-0.5891	-2.0652
2	S100a4		1.341	1.5262	-0.0941	0.0794	-1.0767	-1.0069	-1.5253	-1.1599	-2.3232
2	Samd9l		1.6057	-0.0637	0.6435	-1.433	-0.1724	-0.8931	-0.5736	-0.416	-2.5614
2	Atxn1		1.2021	0.4992	-0.1444	-0.6232	-0.7358	-0.4807	-0.5951	-0.7812	-0.9075
2	Sdk1		0.7239	0.2779	-0.7253	-1.2722	-0.7361	-1.235	-0.9477	-0.7756	-1.1576
2	Sdpr		1.917	1.5991	0.1811	-0.2653	-0.8764	-1.5638	-1.6317	-2.6993	-2.6705
2	Sec24d		1.0527	0.6208	-0.5178	-0.8429	-1.1224	-0.8898	-0.9717	-1.0674	[illegible]
2	Selk		0.5158	-0.3105	0.3779	-0.5271	-0.3078	-0.7712	-0.7354	-0.6857	-0.9808
2	Sema3f		1.1341	0.1298	-1.038	-1.2115	-1.3243	-1.376	-0.2819	-0.7058	-1.7616
2	Sepn1		0.6711	0.4985	-0.5265	-0.5483	-0.8549	-0.8878	-0.9026	-0.8822	-3.3052
2		41525	0.7638	0.5107	-0.5969	-0.9032	-1.0776	-1.1927	-0.7027	-1.0492	-1.0733
2	Serpina3h		0.1544	0.2127	-0.1531	-0.4161	-0.6569	-0.847	-0.9712	-0.7652	-0.8126
2	Serpinb1a		0.3773	0.1554	-0.2266	-0.3143	-0.4603	-0.6253	-0.569	-0.7308	-0.7477
2	Serpine2		1.3071	1.5279	-0.7524	-0.4667	-1.8167	-1.2656	-1.3039	-1.1609	-1.3308
2	Sfrp1		1.6684	0.7307	-0.2792	-1.0208	-0.6705	-1.1046	-0.7252	-0.9937	-0.8125
2	Sfrp2		2.2767	1.4647	-0.4353	-1.2524	-1.3319	-1.6561	-0.8966	-1.1192	-0.7636
2	Sgcb		0.8997	0.1808	-0.4935	-0.5349	-1.0723	-1.2406	-0.7467	-0.7382	[illegible]
2	Sh3pxd2b		0.89	0.722	-0.5675	-0.3635	-1.0945	-1.0525	-1.0243	-0.8654	-1.5767
2	Shisa5		0.8616	0.2419	[illegible]	-0.4156	-0.6102	-0.8421	-1.2563	-1.1342	-2.1224
2	Slc22a5		0.1349	-0.374	-0.2391	-0.6218	-0.4346	-0.6476	-0.4558	-0.6444	-1.2992
2	Slc24a3		1.3504	0.1449	-0.0635	-0.394	-0.6255	-0.777	-0.9208	-0.8181	-1.0558
2	Slc35a2		0.4866	0.3115	-0.0767	-0.1518	-0.7347	-0.9142	-0.8264	-0.5481	-1.5414
2	Slc39a6		0.1614	0.1776	-0.3491	-0.1488	-0.7501	-0.9581	-0.9876	-0.9709	-1.1601
2	Slc41a3		0.5956	0.1931	-0.5095	-0.4695	-0.6931	-0.7945	-0.81	-0.8132	-0.1265
2	Slc44a1		0.6491	0.3718	-0.454	-0.3514	-0.7756	-0.7483	-1.3851	-0.8485	-1.5781
2	Slc9a3r2		1.1033	0.8937	-0.7034	-0.4873	-1.0846	-1.095	-0.7253	-0.8603	-0.3856
2	Slit3		1.5131	0.8508	-0.7535	-0.6843	-0.823	-0.9444	-0.708	-0.9728	-0.7504
2	Smarca2		0.2959	-0.0704	0.5817	0.1494	0.4154	0.1362	-0.4981	-0.3156	-4.8499
2	Snx33		1.1232	0.7052	-0.0671	-0.1795	-0.502	-0.712	-0.6688	-0.4455	-1.6975
2	Snx7		0.4002	-0.3071	0.0705	-0.2203	-0.594	-0.5814	-0.9652	-0.8991	-1.4963
2	Socs5		0.7746	0.6975	-0.2162	-0.078	-0.8485	-0.8533	-1.1892	-1.0696	-2.2259
2	Sorcs2		1.1093	0.354	-0.8767	-0.8907	-1.0793	-0.8168	-0.9305	-0.9538	-1.1924
2	Sox9		0.3694	0.6505	-0.283	-0.9013	-0.7847	-0.9785	-0.3096	-0.8898	-0.9785
2	Sphk1		1.6726	1.2412	-0.1994	-0.8639	-1.1527	-1.3097	-1.2608	-1.4519	-0.6046
2	Sqrdl		0.755	0.2148	-0.7852	-0.4633	-1.2793	-1.2359	-1.2002	-1.3101	-1.197
2	Srpx		1.8927	1.05	-0.6298	-1.2493	-0.6603	-1.4906	-1.4848	-1.5286	-1.9018
2	Sspn		1.3077	1.216	0.2411	0.2743	-1.0188	-1.3795	-2.1681	-1.397	-3.6737
2	St3gal1		0.8524	0.3651	-0.7672	-0.7049	-0.9503	-0.7768	-0.9006	-0.7577	-0.9288
2	St5		0.7384	0.7146	-0.5634	-0.8278	-1.0354	-1.0027	-1.0771	-0.68	-0.7609
2	St7		0.2382	0.1851	0.5651	0.721	-0.5877	-0.7553	-1.193	-0.8898	-1.8658
2	Sun2		0.374	0.1958	-0.1556	-0.5251	-0.6375	-0.6151	-1.3426	-0.9465	-1.2537
2	Surf4		0.3861	0.285	-0.2446	-0.6606	-0.9683	-1.1229	-0.7039	-0.9877	-0.7397
2	Tax1bp3		0.7079	0.4171	[illegible]	-0.4632	-0.4621	-0.5679	-0.6523	-0.9216	-1.5829
2	Tbc1d9b		0.4701	0.2465	-0.3931	-0.4993	-0.5215	-0.6623	-0.6998	-0.646	-0.7912
2	Tcf4		0.8811	0.6007	[illegible]	-0.6375	-1.1424	-1.575	-1.3874	-1.3577	-1.1706
2	Tgfbr2		[illegible]	-0.2254	-0.5591	-0.6941	-0.4849	-1.2263	-1.851	-1.9572	-5.2814
2	Thbd		2.0097	1.2519	0.0889	-0.5396	-0.9318	-1.6644	-1.9871	-2.1108	-2.734
2	Thbs1		1.9864	1.4226	-0.0492	-0.1757	-1.8347	-1.6442	-1.6084	-1.7509	-1.6054
2	Timp1		-0.1034	0.2709	-0.6443	-0.6481	-1.4848	-1.4185	-2.3716	-1.6247	-2.8667
2	Timp3		1.1409	1.1483	-0.5785	-0.3219	-1.5915	-1.4908	-1.5371	-1.4284	-1.598
2	Tle2		0.8876	1.0123	-0.1734	-0.493	-0.8057	-0.8115	-0.6973	-0.663	-0.926
2	Tlr4		0.3402	-0.0294	-0.326	-0.6067	-0.7939	-0.8223	-0.9076	-0.8874	-0.8578
2	Tm2d2		0.1624	0.0516	-0.3381	-0.5633	-0.6751	-0.7652	-0.777	-0.835	-0.6997
2	Tmco3		0.2617	0.1604	-0.1087	-0.1728	-0.4359	-0.3996	-1.0039	-0.8387	-0.9263
2	Tmem119		1.157	0.8982	-0.8697	-0.7137	-1.478	-1.4243	-1.2274	-1.5106	-1.3081
2	Tmem127		0.5538	[illegible]	-0.3929	-0.4381	-0.6276	-0.6993	-0.5651	-0.6873	-1.2522
2	Tmem159		0.6452	0.6073	-0.0602	-0.5313	-0.7131	-0.6814	-0.6171	-0.6705	-1.0167
2	Tmem5		0.4638	0.3248	-0.5177	-0.1267	-0.4319	-0.1156	-0.5948	-0.4658	-1.3313
2	Tmem59		0.3754	0.3239	[illegible]	-0.095	-0.3402	-0.4724	-0.6985	-0.4591	-1.4926
2	Tmtc2		0.4502	-0.0459	-0.2478	-0.3666	-0.5867	-0.6246	-0.8244	-0.8562	-1.0306
2	Tnc		1.174	0.8941	-0.7191	-0.4067	-0.8978	-0.8209	-0.735	-0.9195	-0.8346
2	Tnfrsf11a		0.2013	0.0386	-0.3367	-0.5135	-0.6192	-0.9181	-0.7892	-0.8873	-0.8806
2	Tpm2		0.8674	0.9875	-1.124	-0.9201	-1.4235	-1.1461	-0.8697	-1.1269	-1.0652
2	Trib2		1.1795	1.0494	-0.0654	[illegible]	-0.7334	-0.6406	-1.1256	-0.4081	-1.7461
2	Trim16		0.1147	0.2117	0.4637	-0.2924	-0.3674	-0.6745	-0.8299	-0.6552	-1.1085
2	Trim3		0.5105	0.434	-0.5877	-0.2361	-0.8444	-0.6592	-0.7528	-0.7162	-0.3658
2	Trim30a		2.1623	-0.5801	0.477	-1	-0.7418	-1.1009	-0.8845	-1.0529	-1.0733
2	Tshz3		0.6233	0.62	-0.4143	-0.2773	-1.0437	-0.7063	-1.4659	-0.8755	-2.6456
2	Ttc17		0.1964	-0.0579	-0.286	-0.2205	-0.2568	-0.6385	-0.6872	-0.5659	-1.2116
2	Ttyh3		0.9162	0.4744	-0.4861	-0.789	-0.8495	-0.9872	0.0463	-0.3311	-0.9066
2	Txndc15		0.0724	-0.3112	[illegible]	-0.3899	-0.4948	-0.7408	-0.5784	-0.8795	-1.1747
2	Uap1		0.1235	-0.2917	-0.2074	-0.5608	-0.3115	-0.6346	-0.2887	-0.6793	-1.6616
2	Uba7		1.3679	-0.5751	-0.7733	-1.7534	-1.1914	-1.7917	-1.777	-1.9725	-2.4179
2	Ugt1a10		-0.2134	[illegible]	-0.0339	0.4322	-0.2727	0.4766	-1.2707	-0.5251	-3.0217
2	Ulk2		0.2402	[illegible]	-0.2586	-0.3484	-0.5075	-0.7267	-0.7452	-0.5794	-0.8817
2	Vim		1.0213	1.1735	0.2127	-0.0519	-1.6861	-1.7328	-2.2046	-1.6853	-2.6157
2	Vldlr		0.3761	0.5326	-1.1285	-0.6478	-0.9177	-1.1211	-0.8	-1.0234	-0.6467
2	Vopp1		0.6192	0.524	0.0802	0.1531	-0.8408	-0.751	-1.1047	-0.7759	-2.1571
2	Vwa5a		0.519	-0.219	[illegible]	-0.1914	[illegible]	-0.542	-0.5675	-0.3314	-2.043
2	Wdr1		0.0951	0.2547	-0.0862	-0.2816	-0.3952	-0.5567	-0.8433	-0.7177	-1.1632
2	Wipf1		0.9141	0.4422	-0.0934	-0.5921	-0.5984	-1.4687	-1.5709	-1.564	-1.6895
2	Wipi1		1.0666	0.691	-0.8345	-0.592	-1.0524	-0.9027	-1.5606	-1.2629	-1.191
2	Wls		1.0632	0.791	-0.1061	-0.0606	-1.0563	-1.0517	-1.1085	-1.1263	-1.953
2	Wnt5a		1.0355	0.945	-0.4009	-0.4118	-0.987	-0.8989	-0.8598	-0.7595	-0.7567
2	Xpnpep2		0.9339	0.3289	-0.2482	-0.4958	-0.8242	-0.9804	-0.9419	-0.8404	-0.8596
2	Zadh2		-0.3721	0.3154	-0.1385	0.2803	-0.2727	[illegible]	-1.1821	-0.698	-2.73
2	Zcchc5		1.9692	0.7563	-0.0682	-0.7944	-1.0262	-0.9364	-1.147	-1.0131	-1.2132
2	Zeb2		0.9395	0.4914	-0.5472	-0.7581	-1.2857	-1.428	-0.6703	-1.4252	-1.5153
2	Zfand3		0.0616	0.2018	0.1616	-0.1386	-0.297	-0.7382	-0.6246	-0.6444	-1.3181
2	Zfp521		1.5875	0.7437	0.198	-0.6663	-1.6303	-1.9028	-1.289	-1.5742	-2.352
2	Zfp637		0.1925	0.2642	-0.4353	-0.0865	-0.6119	-0.6986	-1.0114	-0.6955	-1.3555
2	Zfp68		-0.1457	-0.2385	-0.0914	-0.2771	-0.2745	-0.5576	-0.5668	-0.2348	-1.718
2	Zfpm1		0.6212	0.3691	-0.744	-1.1908	-0.9783	-0.8054	-0.5631	-0.7525	[illegible]
2	Ednrb		-0.8641	-1.1767	-2.3501	-2.186	-2.6152	-2.6832	-2.6505	-2.7304	-2.657
2	1500015O10Rik		[illegible]	-0.5307	-2.2402	-3.321	-4.5334	-4.524	-4.5429	-4.4536	-4.298
2	2510009E07Rik		0.2238	0.3167	-0.7276	-1.0005	-1.9289	-2.046	-1.8494	-1.9453	-2.6719
2	6330406I15Rik		1.4304	0.8143	-0.8502	-1.7897	-3.8572	-3.5548	-3.4955	-3.6359	-3.824
2	Aebp1		2.7844	2.3495	-0.9365	-1.0119	-1.9742	-2.2984	-2.0864	-2.1169	-2.4352
2	AL024069		-0.2929	-0.6894	-1.0961	-1.5647	-2.0177	-2.521	-2.0343	-2.3042	-2.8349
2	Aldh1l2		0.5417	0.6506	-1.8153	-1.8557	-2.2357	-2.233	-2.0839	-2.0625	-1.5703
2	Apod		1.1247	[illegible]	0.6456	-0.8962	-1.5638	-2.5981	-2.9342	-3.165	-3.0994
2	Arhgdib		0.6835	0.4957	-0.569	-1.4399	-1.2555	-1.8654	-2.37	-2.3647	-3.1775
2	Arsb		0.5017	[illegible]	-0.5005	-0.8777	-1.6502	-1.924	-2.6079	-2.096	-3.5517
2	B2m		1.6921	[illegible]	0.1271	-1.3562	-1.718	-2.3767	-2.1363	-2.4179	-3.1018
2	Bgn		0.3274	0.5679	-2.0717	-2.5251	-6.2268	-6.0344	-5.8455	-6.0402	-6.7208
2	Bicc1		1.7713	0.6249	-1.5481	-2.2703	-3.2322	-2.81	-2.4945	-2.8562	-2.6921
2	Capn6		1.1969	0.5931	-0.1808	-1.2509	-1.7597	-2.2479	-2.2076	-2.2431	-3.8754
2	Cav1		1.9003	1.7579	-0.5189	-0.4922	-2.5119	-2.002	-2.2949	-1.9224	-3.8429
2	Ccl8		-0.3993	-1.5212	0.1346	-2.077	-1.9149	-2.8411	-2.7658	-2.5786	-2.786
2	Cdkn1c		0.1814	-0.3927	-2.4285	-3.063	-2.7275	-3.3883	-2.3582	-2.6746	-2.8597
2	Cdo1		1.2863	0.6814	-1.164	-1.9905	-2.9046	-3.1765	-2.6245	-2.6407	-2.0875
2	Ch25h		1.0737	0.3862	-1.9159	-1.6182	-2.6687	-2.7228	-2.5297	-2.6955	-2.7541
2	Clu		-0.112	-0.6616	-0.9096	-2.0717	-1.7317	-2.2852	-2.3352	-2.067	-2.7838
2	Cmtm3		0.5333	-0.165	-1.8353	-1.7676	-2.1911	-2.3817	-2.2685	-2.2161	-2.0073
2	Col12a1		2.4962	1.6563	-0.663	-1.3269	-2.1127	-2.0742	-2.0299	-2.0434	-2.2943
2	Col16a1		1.1404	1.13	-2.0579	-2.1264	-3.4499	-3.547	-3.6877	-3.5139	-3.9772
2	Col1a1		2.39	1.9089	-0.6652	-1.3772	-4.2519	-4.4574	-3.7572	-4.2029	-4.6548
2	Col4a2		0.9363	0.9195	-0.0649	-0.6452	-2.3276	-2.9052	-2.7855	-3.0086	-3.6758
2	Col5a1		1.2152	0.8744	-2.3589	-2.2196	-4.7328	-4.8514	-4.7152	-4.368	-4.0468
2	Col6a2		2.4392	2.4654	-0.6779	-0.4915	-2.6435	-2.3342	-2.7246	-2.4223	-2.622
2	Ctgf		-0.4185	-0.7167	-0.8082	-1.4049	-1.6834	-2.635	-1.957	-2.4225	-3.4834
2	Ctsb		-0.1368	-0.6404	-1.1904	-1.592	-1.6706	-1.9689	-2.2215	-2.2549	-2.4902
2	Ctsk		1.3576	0.2347	-1.4076	-1.8365	-2.4797	-3.0277	-3.0329	-2.8653	-3.3966
2	Cyp1b1		2.2993	1.5814	-0.5621	-0.9617	-2.9494	-2.9686	-2.7047	-2.8394	-3.1413
2	Cyp2f2		3.012	2.2495	-0.5417	-1.2535	-1.8029	-1.9189	-1.9189	-1.7393	-1.8185
2	Dab2		-0.4096	-0.6756	-0.9296	-1.3334	-2.6521	-3.0567	-3.2903	-2.9828	-3.4943
2	Dcn		1.7556	0.7596	-1.9483	-2.4792	-4.7078	-4.5617	-4.0851	-4.3299	-5.2319
2	Dkk3		1.6845	1.2842	-1.4453	-1.2935	-3.131	-3.5614	-2.9946	-3.2628	-2.0288
2	Dlk1		2.4486	1.6566	-2.5387	-3.2364	-4.6708	-4.2423	-4.1977	-4.3358	-4.7449
2	Dram1		0.2971	0.4411	-1.5572	-1.5469	-2.3254	-2.54	-2.3823	-2.3884	-2.1673
2	Ednra		0.4362	-0.3556	-2.5941	-3.4027	-3.7407	-3.955	-3.276	-3.3756	-3.8831
2	Eln		0.798	0.6723	-1.7648	-2.4863	-3.665	-3.4546	-3.7272	-3.5831	-3.7672
2	Emilin2		[illegible]	0.4584	-1.9991	-2.1304	-2.4165	-2.6547	-2.5552	-2.5474	-2.4236
2	Errfi1		-0.2394	-0.5397	-1.0599	-2.6985	-1.5572	-2.314	-1.7449	-2.2412	-2.2402
2	Fam114a1		0.9997	0.3422	-1.5085	-1.9154	-2.5036	-2.6046	-2.4139	-2.5004	-2.3323
2	Fbn1		0.7489	0.3601	-0.9562	-1.4163	-2.1615	-2.7748	-2.7965	-2.9173	-3.5124
2	Fcgrt		-0.1992	-0.9512	-1.6866	-2.3816	-2.2974	-1.9998	-2.6208	-1.9641	-2.6669
2	Fxyd5		-1.1185	-0.4457	-2.4251	-1.7386	-3.5959	-3.3249	-3.5035	-3.4358	-2.7922
2	Gas6		0.3217	-0.5421	-2.1346	-1.9017	-2.3668	-1.925	-3.0574	-2.2403	-3.7199
2	Ghr		1.3972	0.5112	-0.4131	-1.0582	-2.268	-2.1463	-2.121	-1.8284	-3.1013
2	Wfdc17		0.8317	-0.972	-2.1667	-1.9606	-2.2164	-2.2819	-2.1896	-2.2367	-2.2265
2	Gpx8		1.0607	0.7041	-1.6437	-1.313	-2.9972	-3.0578	-2.6006	-2.4307	-2.7438
2	H19		1.862	0.7876	-0.7167	-2.7117	-1.2445	-2.1544	-0.2376	-1.089	-4.2474
2	Ifi27l1		0.5837	[illegible]	0.5174	-1.7143	[illegible]	-2.866	-1.0572	-2.9953	-4.7423
2	Ifi27l2a		2.2919	-1.4	1.1628	-3.14	-1.3742	-3.6551	-1.8518	-3.2125	-3.7936

2		Igf1	0.3848	-0.6441	-1.4092	-1.6646	-2.2429	-2.5859	-2.5887	-2.2921	-2.343
2		Igf2	0.6293	-0.2508	-1.6555	-3.2829	-2.7684	-3.8243	-2.0748	-2.9388	-4.8036
2		Igfbp4	[illegible]	-0.3718	-2.5608	-3.2387	-4.423	-4.0995	-3.5153	-3.7815	-3.8348
2		Igfbp5	1.7191	0.7697	-0.333	-1.3495	-2.8966	-2.9379	-1.6083	-2.3812	-4.5053
2		Igfbp6	[illegible]	-0.53	-2.2109	-2.0899	-3.291	-3.6498	-3.5248	-3.2109	-3.7496
2		Igfbp7	1.2109	0.9566	-2.4993	-1.4389	-4.2401	-4.6311	-3.9816	-3.9767	-4.3195
2		Il11ra1	0.3563	0.2962	-1.7113	-2.1929	-2.8127	-3.0672	-3.0028	-3.0574	-3.2653
2		Itgbl1	1.2458	0.1166	-0.8514	-1.8076	-3.6393	-3.8529	-3.7154	-3.9382	-3.9285
2		Itm2a	1.1421	[illegible]	-1.8387	-2.8771	-3.5599	-3.3026	-2.6449	-2.7673	-2.4873
2		Lhfpl2	[illegible]	[illegible]	-1.4145	-1.7483	-2.1178	-2.4993	-1.6811	-2.0084	-2.2747
2		Lox	1.2574	0.7126	-1.9098	-2.0993	-4.8802	-5.2536	-4.5427	-4.7513	-5.2294
2		Loxl1	1.5484	1.3445	-1.816	-2.1348	-3.9217	-3.8778	-3.9517	-3.6984	-3.629
2		Lpl	0.7926	-0.5468	-3.2897	-3.8005	-4.1206	-4.8205	-3.2427	-3.643	-2.5853
2		Lsp1	1.7156	1.4336	-1.4122	-1.7376	-2.2413	-2.0644	-2.0522	-1.889	-2.9292
2		Lum	1.5629	1.1029	-2.2674	-3.0954	-3.8619	-3.9356	-3.8307	-3.988	-4.062
2		Maged2	0.6937	0.4307	-1.6712	-2.3019	-2.2977	-2.3292	-1.5267	-1.8526	-2.1331
2		Mfap4	2.2227	0.7297	-1.4053	-2.2068	-2.2711	-2.245	-1.6334	-2.1635	-1.9804
2		Mfap5	1.0164	[illegible]	-1.3097	-1.585	-2.1689	-2.2249	-2.0185	-2.1114	-1.3003
2		Mgp	2.3503	2.1734	0.322	-1.2099	-3.6654	-4.9611	-4.7903	-5.7544	-6.2734
2		Mmp13	0.7024	0.5464	-1.4253	-1.5956	-2.3824	-2.0553	-2.2024	-2.4764	-2.3439
2		Mmp14	1.0921	0.3722	-1.0066	-1.6804	-1.9638	-2.3311	-2.2804	-2.442	-2.2641
2		Mmp2	1.3277	0.8535	-0.763	-1.4447	-3.1562	-3.5961	-2.918	-3.1694	-3.3971
2		Mmp3	1.8338	1.6559	-2.3726	-1.8652	-3.6284	-3.6854	-3.7181	-3.5825	-3.6693
2		Nbl1	0.1967	-0.1442	-1.0628	-1.6258	-2.2668	-2.3044	-2.7517	-2.4682	-3.562
2		Nrp	1.6103	1.1544	-1.4556	-1.7507	-3.122	-2.8673	-2.8597	-3.1566	-3.5647
2		Olfml3	2.6768	2.5018	[illegible]	[illegible]	-2.0971	-2.3413	-1.6192	-1.8229	-2.5855
2		Osr2	1.0446	[illegible]	-0.8673	-1.6088	-2.3136	-2.2231	-2.2087	-2.0428	-2.6694
2		Pamr1	[illegible]	-0.4956	-1.2882	-1.5761	-1.9896	-1.98	-1.9394	-2.1338	-2.0887
2		Pdgfra	1.977	1.2288	-1.6048	-2.4541	-2.9575	-3.0023	-2.8146	-2.5134	-2.5286
2		Prelp	[illegible]	[illegible]	-0.9898	-0.7286	-5.2153	-5.3577	-5.8888	-4.9323	-6.5507
2		Pros1	1.2422	1.0479	-0.2664	-0.7064	-1.7514	-2.3881	-1.9133	-2.6002	-1.9454
2		Ptn	3.1627	2.0939	-1.3009	-2.0756	-4.5165	-4.7115	-2.6748	-3.7034	-5.0035
2		Ptx3	1.7385	0.4164	-1.6852	-2.3	-3.4446	-3.3739	-3.5189	-3.5189	-3.7216
2		Rbms3	1.8301	1.2344	-1.0068	-1.158	-2.9729	-2.9799	-2.5613	-2.6017	-2.835
2		Reg1	2.7435	0.8229	-1.7547	-1.8648	-2.3477	-2.3812	-2.3326	-2.3237	-2.4444
2		Rgl1	0.9224	[illegible]	[illegible]	-0.8236	-1.6896	-2.3161	-1.965	-2.3135	-2.2644
2		Rhoj	1.1106	0.5613	-0.763	-0.9445	-2.1069	-2.3511	-2.1706	-2.2195	-2.2976
2		Saa3	0.4975	-1.5869	-1.0803	-1.8668	-2.1043	-2.9737	-2.2942	-2.8961	-2.9715
2		Scara3	1.0616	0.5825	[illegible]	-1.5703	-2.1536	-2.9977	-3.1615	-3.3294	-5.2405
2		Scara5	-0.7291	-1.0551	-1.4206	-2.3966	-1.7087	-2.0584	-2.6046	-2.4974	-3.7087
2		Scarf2	0.5308	[illegible]	-1.4706	-1.8532	-3.7947	-4.1309	-3.5513	-3.7688	-4.1175
2		Sdc3	0.6719	[illegible]	-1.8519	-1.84	-2.516	-2.5406	-2.2975	-2.6084	-2.4891
2		Sema5a	0.6039	[illegible]	-1.3053	-1.6553	-1.7318	-2.2008	-1.4777	-2.0837	-2.4971
2		Serpina3g	2.7213	2.2205	-1.0623	-0.9517	-1.8509	-1.8825	-1.7024	-1.8509	-1.8064
2		Serpina3n	1.2642	0.7458	-1.5459	-2.0314	-2.1434	-3.0695	-3.9815	-3.5702	-4.7241
2		Serpinf1	0.6616	0.3859	-2.6511	-3.2971	-6.3435	-6.4116	-5.7977	-6.047	-5.1892
2		Serping1	1.1793	[illegible]	[illegible]	-1.2751	-1.5637	-2.1587	-2.3856	-2.333	-3.1746
2		Sertad4	0.5237	0.7481	-1.2349	-1.1493	-2.3501	-2.5295	-1.315	-1.6921	-2.1477
2		Slit2	2.1794	1.4767	[illegible]	-0.9505	-1.3121	-3.4475	-2.5827	-3.1125	-2.997
2		Sostdc1	[illegible]	0.4701	[illegible]	-0.9116	-2.4346	-2.3819	-2.8022	-2.3977	-2.5237
2		Sparc	0.8151	0.7631	-1.4623	-1.4734	-3.1917	-2.6459	-2.7733	-3.1804	-2.5097
2		Spon2	1.2272	1.1887	[illegible]	-0.6331	-1.8623	-2.3687	-2.8146	-2.4814	-3.1116
2		Spp1	0.6996	1.1008	-2.823	-2.2397	-4.685	-5.3993	-2.9239	-4.2858	-0.7859
2		Srpx2	0.2281	-0.5856	-2.299	-2.3623	-2.9344	-2.7969	-2.7709	-2.9767	-2.6371
2		Svep1	2.0076	1.059	-0.8679	-1.541	-2.2731	-2.2943	-2.3219	-2.4148	-2.4826
2		Tgfb1i1	1.2505	1.2237	-1.374	-1.3812	-2.7978	-2.4746	-2.3788	-2.4003	-2.3228
2		Tgfb3	0.2439	-0.3675	-1.1801	-1.3179	-1.7508	-1.87	-2.2246	-2.1576	-2.4141
2		Tgfbi	[illegible]	[illegible]	-1.6863	-2.8402	-3.319	-3.8448	-3.7255	-3.8587	-2.7485
2		Thbs2	1.7477	1.408	-1.0391	-1.3714	-3.476	-3.9369	-3.9118	-3.5732	-5.3364
2		Thy1	2.1149	1.9572	-3.1033	-1.6802	-4.398	-4.2992	-3.7383	-3.6661	-3.7817
2		Timp2	1.5365	0.6945	-1.0476	-1.3886	-4.2178	-4.5271	-4.1414	-4.201	-5.4802
2		Tmem176b	-0.1962	-0.3442	-0.7589	-1.1135	-1.5645	-1.886	-2.5743	-2.0978	-5.5007
2		Tmem86a	0.3076	0.5932	-1.8091	-1.649	-2.4228	-2.3441	-2.3131	-2.2959	-1.6369
2		Tnfaip2	0.1721	0.1579	-1.8796	-1.6343	-2.311	-2.2839	-2.5161	-2.047	-2.4365
2		Tnfrsf11b	1.1185	0.7158	0.1871	-0.8963	-2.4463	-2.4287	-2.7456	-2.721	-2.8554
2		Tril	2.1461	1.6444	0.3922	-0.2472	-2.0306	-2.4659	-1.6378	-2.2987	-2.182
2		Twist2	1.6704	1.6387	-1.8154	-0.9781	-2.0983	-1.7836	-2.0161	-2.0346	-2.2171
2		Vasn	1.5922	0.9192	0.1885	-1.616	-2.0521	-2.4751	-1.8946	-1.9336	-2.513
2		Vcam1	2.2699	1.6592	[illegible]	0.0841	-1.9386	-2.6183	-2.5389	-2.6647	-2.638
2		Wisp2	1.3271	1.0719	-1.4691	-1.405	-2.7119	-2.6282	-2.9152	-2.6555	-2.7176
2		Zyx	0.162	0.3591	-0.7496	-1.001	-2.2623	-2.2729	-2.0827	-2.0928	-3.136
3	1	2010011I20Rik	0.2418	0.1315	[illegible]	-0.4832	-0.4297	-0.3845	-0.6997	-0.5335	-0.7056
3	1	3830406C13Rik	0.0225	-0.218	-0.1492	-0.127	-0.52	-0.2621	-0.7742	-0.7411	-1.1832
3	1	5033414D02Rik	0.0425	-0.0818	-0.3074	-0.0748	-0.26	-0.303	-0.6672	-0.4864	-1.1692
3	1	A830007P12Rik	[illegible]	0.0826	-0.2785	-0.2814	[illegible]	-0.0609	-0.5694	[illegible]	-1.4258
3	1	Acsl5	-0.934	-0.1439	0.2001	0.6047	0.1572	0.238	-0.8087	-0.2415	-2.4586
3	1	Alg5	0.117	0.2041	-0.0537	[illegible]	-0.3052	-0.2837	-0.7112	-0.2747	-0.8392
3	1	Anks6	0.4914	0.1488	-0.3473	-0.3073	-0.4573	-0.3164	-0.3103	-0.4607	-0.5297
3	1	Arl8a	0.2208	0.0901	-0.0532	-0.062	-0.1097	-0.1616	-0.8981	-0.5539	-0.823
3	1	BC029214	0.4343	-0.1883	-0.1025	-0.4962	-0.4191	-0.5267	-0.5657	-0.3106	-1.0503
3	1	Brdt	0.5443	0.3592	-0.3262	-0.5158	-0.2605	-0.3452	-0.5281	-0.4469	-0.5563
3	1	C85492	-0.2718	0.0883	-0.088	0.2209	-0.4886	[illegible]	-0.7272	-0.4924	-1.2984
3	1	Cbx8	[illegible]	0.176	-0.2328	-0.0975	-0.3514	[illegible]	-0.7441	-0.1451	-1.0777
3	1	Ccdc109b	-0.1351	0.1407	0.0605	[illegible]	-0.358	-0.2327	-0.9893	-0.3788	-1.2264
3	1	Cck	0.2816	0.3837	-0.5142	-0.179	-0.3988	-0.6073	-0.5583	-0.6181	-0.5209
3	1	Col2a1	0.2218	0.5159	-0.1235	-0.6191	-0.754	-0.6635	0.1761	-0.1432	-0.6283
3	1	Copg	0.4029	0.326	-0.1791	-0.3397	-0.5061	-0.4986	-0.4297	-0.1619	-0.6482
3	1	Csk	0.0574	0.1235	-0.24	0.1	-0.1034	-0.0756	-0.3735	-0.2652	-1.4181
3	1	Ctdspl	0.0686	0.2533	-0.5708	-0.5028	-0.3851	-0.6091	-0.2543	-0.4985	-1.1155
3	1	D19Wsu162e	0.1508	-0.0574	-0.1671	-0.3551	[illegible]	-0.3277	-0.383	-0.3296	-1.1574
3	1	Dnaja4	0.2347	[illegible]	[illegible]	-0.3207	-0.1718	-0.4955	-0.6212	-0.6289	-1.0317
3	1	Fam3a	0.1961	-0.1316	-0.1916	-0.2332	-0.3387	-0.1348	-0.7126	-0.3078	-1.2844
3	1	Fam65a	0.4049	0.4024	-0.1922	-0.3165	-0.6415	-0.9668	-0.4365	-0.6389	-0.1228
3	1	Fam89b	0.1403	[illegible]	-0.2238	-0.3437	-0.3626	-0.5228	-0.5603	-0.2206	-1.0279
3	1	Fbxw4	0.0574	0.1533	-0.2864	-0.1459	-0.3548	-0.3226	-0.5553	-0.6302	-1.0453
3	1	Fbxw8	0.0526	0.1523	-0.2057	-0.2382	-0.3948	-0.5555	-0.4218	-0.5524	-0.8593
3	1	Gstm5	0.2203	0.1784	-0.3488	-0.317	-0.3465	-0.6906	-0.2579	-0.293	-1.1738
3	1	Il15	[illegible]	-0.0535	[illegible]	[illegible]	-0.2102	-0.6385	-0.8328	-0.5686	-1.1449
3	1	Il15ra	0.1242	0.2797	-0.2808	-0.2077	-0.5166	-0.4365	-0.6491	-0.4962	-0.6785
3	1	Ip6k1	0.3937	-0.0375	0.0977	-0.1173	-0.1126	-0.5567	-0.4186	-0.3289	-0.6684
3	1	Itfg3	0.2061	-0.1549	-0.2939	-0.4868	-0.3219	-0.7462	-0.7744	-0.419	-0.9276
3	1	Kera	0.7166	0.2643	-0.3818	-0.405	-0.3112	-0.3917	-0.3461	-0.405	-0.3752
3	1	Kif1b	0.1959	-0.3497	0.1746	-0.2288	-0.2843	-0.5586	-0.3954	-0.3298	-1.1751
3	1	Macrod1	0.0631	0.2101	-0.2165	[illegible]	-0.5774	-0.3121	-0.9329	-0.4984	-0.7499
3	1	41335	0.3253	-0.1737	-0.2516	-0.3002	-0.3545	-0.6017	-0.7881	-0.7264	-0.7613
3	1	Mgat1	0.5485	-0.0812	-0.1673	-0.292	-0.422	-0.2531	-0.3711	-0.4351	-0.7103
3	1	Micu1	-0.8436	-0.6704	0.5536	0.362	0.4125	0.0951	-0.7969	-0.0532	-2.7717
3	1	Mmgt2	0.2827	0.1883	-0.1603	[illegible]	-0.253	-0.3444	-0.6281	-0.6171	-1.021
3	1	Nradd	0.2016	0.238	0.0578	0.1338	-0.4755	-0.1098	-1.2852	-0.4161	-0.5022
3	1	Nt5m	0.0966	0.109	[illegible]	[illegible]	-0.3137	-0.3682	-0.5803	-0.4921	-1.2779
3	1	Pcbd2	[illegible]	[illegible]	-0.055	-0.0309	-0.0766	-0.4152	-0.4916	-0.184	-1.3569
3	1	Pdlim7	0.5008	0.4378	-0.6434	-0.4286	-0.7561	-0.3571	-0.103	[illegible]	-0.767
3	1	Pdp1	0.8067	0.4606	-0.1347	-0.5632	-0.7034	-0.6784	-0.5758	-0.6671	[illegible]
3	1	Pik3ip1	[illegible]	-0.0676	-0.0414	-0.0569	-0.4135	-0.2703	-0.7742	-0.6042	-1.3539
3	1	Pld3	0.5992	0.2104	-0.1702	-0.3908	-0.5361	-0.5589	-0.3705	-0.609	-0.3476
3	1	Pou6f1	0.1238	-0.6747	0.1216	-0.3057	[illegible]	-0.3543	-0.8293	-0.8929	-1.3698
3	1	Prkacb	0.2825	0.0996	-0.7192	-0.1641	-0.5697	-0.7557	-0.2903	-0.5531	-0.7866
3	1	Ptpn11	0.1543	0.2395	-0.464	-0.2734	-0.5645	-0.4194	-0.5147	-0.4896	-0.7734
3	1	Rdh14	0.2837	0.1422	-0.5085	-0.3365	-0.4936	-0.6082	-0.5967	-0.7337	-0.671
3	1	Rgs17	0.3199	0.6759	-0.7573	-0.5507	-0.7994	-0.8637	-0.133	-0.4846	-0.4506
3	1	Rhbdl3	0.6993	-0.1621	-0.4134	-0.3352	-0.5174	-0.5799	-0.1934	-0.4749	-0.5139
3	1	Samd4	0.3083	0.1141	-0.3711	[illegible]	-0.4146	-0.1224	-0.7578	-0.3622	-1.1744
3	1	Scp2	0.1203	[illegible]	-0.0628	-0.174	-0.276	-0.6007	-0.37	-0.3742	-1.0276
3	1	Sema3c	0.4241	-0.0448	-0.1694	-0.3642	-0.5257	-0.4646	-0.5623	-0.5456	-0.6635
3	1	Slc10a6	0.7552	[illegible]	-0.5363	-0.4765	-0.4225	-0.4358	-0.4291	-0.3047	-0.4663
3	1	Slc2a10	0.4449	0.2575	-0.3799	-0.4591	-0.5779	-0.5156	-0.4429	-0.519	-0.4921
3	1	Slc30a7	0.1597	0.2649	-0.2237	-0.1555	-0.225	-0.1248	-0.3787	-0.4349	-1.0947
3	1	Slc35b3	0.2697	0.1399	-0.179	[illegible]	-0.0653	-0.5446	-0.5244	-0.4162	-0.8059
3	1	Snx24	-0.2042	-0.0649	-0.0361	0.1139	-0.2428	-0.1124	-0.6997	-0.5246	-1.5858
3	1	Spcs1	0.1784	0.0789	-0.1647	-0.0492	-0.4576	-0.2892	-0.3987	-0.745	-1.0948
3	1	St6galnac4	-0.1762	0.1668	0.0232	0.3015	-0.422	0.244	-0.8529	-0.2775	-1.2425
3	1	Stxbp1	0.3657	0.3404	-0.5877	-0.3449	-0.9203	-0.7253	-0.5325	-0.6212	-0.3774
3	1	Tbc1d5	-0.1543	[illegible]	-0.2364	-0.0736	-0.3703	-0.1643	-0.6755	-0.2977	-1.5064
3	1	Tcn2	0.3315	-0.0454	-0.3414	-0.4927	-0.4592	-0.263	-0.7542	-0.7806	-0.6536
3	1	Tmem106b	0.6142	0.1232	[illegible]	-0.7081	-0.4339	-0.845	-0.4509	-0.6738	-0.4543
3	1	Trex1	0.5711	-0.1079	[illegible]	-0.4162	-0.3113	-0.5956	-0.5379	-0.347	-0.7166
3	1	Trmt2b	-0.2626	[illegible]	-0.2859	0.101	-0.3041	[illegible]	-0.9514	-0.1905	-1.5302
3	1	Vamp5	0.3229	0.2055	-0.3734	-0.4483	-0.2791	-0.6437	-0.6327	-0.5308	-0.5513
3	1	Vezf1	0.0718	0.1189	-0.3939	-0.193	-0.5824	-0.6985	-0.4138	-0.5721	-0.8593
3	2	Spsb1	0.6583	0.1283	-0.9261	-1.0903	-1.2111	-1.3754	-1.0595	-1.1323	0.8988
3	2	0610007C21Rik	[illegible]	-0.426	-0.6854	-0.7874	-1.1651	-1.0792	-1.54	-1.1388	-1.6016
3	2	0610031J06Rik	-0.2283	-0.5939	-0.4321	-0.6855	-0.6799	-0.8552	-1.1553	-0.9917	-1.0385
3	2	1110003E01Rik	0.3154	-0.0679	-0.3752	-0.3992	-0.7502	-0.7571	-1.3481	-1.0807	-0.8661
3	2	1190007F08Rik	0.834	-0.1344	-0.9921	-1.3518	-1.2116	-0.9964	-1.2133	-0.7546	-1.2574
3	2	1600012H06Rik	0.146	-0.2268	-0.4966	-0.8484	-0.7523	-0.8963	-1.0298	-0.891	-0.9569
3	2	1700025G04Rik	-0.4118	[illegible]	-1.1012	-0.9141	-1.0827	-0.6936	-0.8417	-1.0201	-1.4386
3	2	2310022B05Rik	-0.368	-0.3783	-0.2101	-0.3483	-0.9583	-0.8721	-1.6933	-1.4079	-1.9891
3	2	Abcc5	[illegible]	-0.4277	-0.2178	-0.236	-0.5763	-0.5157	-0.9231	-1.0356	-1.3866
3	2	Abhd4	0.0627	-0.3906	-0.4466	-0.8436	-0.8094	-0.9571	-1.1243	-0.8757	-1.7053
3	2	Acadvl	-0.0966	0.2457	-0.6153	-0.2624	-0.7692	-0.714	-1.2887	-0.9664	-1.3555
3	2	Adm	0.5911	-0.299	-0.9434	-1.299	-0.9214	-1.0398	-0.9977	-0.9635	-1.6012
3	2	Adora2b	0.1606	0.7044	-0.3848	-0.5319	-1.6848	-1.4745	-1.4745	-1.3586	-0.507
3	2	Adra2a	0.2079	0.598	-1.3034	-1.28	-1.3652	-1.4354	-0.9653	-1.2569	-1.3956
3	2	AI316807	-0.076	-0.1562	-0.4656	-0.4232	-0.8264	-0.8691	-1.3093	-0.9363	-1.7575
3	2	Anapc16	-0.3737	-0.4233	-0.9227	-0.6058	-0.776	-0.9069	-0.8579	-0.927	-1.7263
3	2	Angptl7	0.2524	-0.108	-1.447	-1.5068	-1.5426	-1.6664	-1.5963	-1.5559	-1.6204
3	2	Ano10	0.0264	0.0582	-0.3033	-0.3703	-0.9589	-0.5521	-1.1201	-0.8314	-1.7783
3	2	Aoc3	0.6232	0.2847	-1.0467	-1.2373	-1.2373	-1.3125	-0.8464	-1.0551	0.2385
3	2	Appl2	0.1642	-0.4258	-0.4322	-0.6291	-0.5907	-0.5914	-1.0095	-0.5971	-0.8265
3	2	Aqp5	-0.2799	0.7023	-0.4318	-0.2561	-0.8695	-0.7826	-1.1208	-1.4003	-1.2404
3	2	Arsa	0.2973	-0.5469	-1.0495	-1.5114	-1.2971	-1.5151	-1.4524	-1.2782	-0.6219
3	2	Atf5	0.285	0.3324	-1.4556	-1.4147	-1.9031	-1.3356	-2.1208	-1.657	-1.4968
3	2	Atg10	0.0421	-0.6469	-0.5425	-1.2314	-0.8915	-1.0588	-1.0095	-0.9856	-0.7358
3	2	Atp6ap1	-0.1293	-0.2678	-0.752	-0.8348	-1.1712	-1.065	-1.1908	-1.1921	-1.8697

3	2 Atp6v0e		[illegible]	-0.2059	-0.3578	-0.4199	-0.6582	-0.7137	-0.6752	-0.6871	-1.16
3	2 BC028528		0.8069	[illegible]	-1.0767	-1.1043	-1.1686	-1.5603	-0.9946	-1.102	0.4312
3	2 Bcl11b		0.1259	-0.5724	-1.6972	-1.0642	-1.5242	-0.6787	-1.2502	-0.7763	-0.7375
3	2 Bloc1s1		0.2376	-0.3211	-0.6068	-0.8834	-0.7689	-0.7827	-0.8542	-0.8747	-0.9468
3	2 Cacna2d1		[illegible]	[illegible]	-0.9113	-0.7118	-1.4379	-1.0599	-1.2616	-1.3073	-1.2786
3	2 Camk1		0.4689	0.3402	-0.55	-0.7556	-1.0948	-1.2353	-1.391	-1.2724	-1.3179
3	2 Camk2n1		0.4661	-0.4072	-0.5625	-1.176	-0.7312	-0.7614	-1.2879	-0.8154	-0.6715
3	2 Camta2		-0.1628	[illegible]	-0.8206	-0.4345	-0.8037	-0.6805	-1.3406	-0.9633	-0.9078
3	2 Capg		-0.1646	0.2614	-0.7878	-0.7176	-0.9037	-0.8205	-1.2806	-0.7678	-1.4719
3	2 Casp6		-0.2196	-0.531	-0.9028	-1.1711	-0.918	-0.9673	-0.5476	-0.694	-0.9926
3	2 Cbr3		-0.2284	-0.1491	-1.3571	-0.8593	-1.4144	-0.661	-1.0049	-0.7832	[illegible]
3	2 Cd47		-0.1666	-0.4829	-0.7172	-0.6547	-0.7877	-0.8096	-1.7626	-1.151	-3.5087
3	2 Cd55		-0.317	[illegible]	-0.1841	-0.398	-0.9674	-1.127	-1.9382	-1.5114	-3.4711
3	2 Cdc42ep3		0.469	0.4124	0.342	-0.8907	-1.1572	-1.674	-1.5512	-2.0048	-1.5457
3	2 Cdipt		-0.2615	-0.2378	-0.3025	-0.1807	-0.7754	-0.536	-0.8618	-0.5634	-1.3377
3	2 Cdkn2c		-0.1978	-0.115	-0.6067	-0.6719	-0.8203	-0.8309	-1.1275	-1.1539	-1.0363
3	2 Cercam		0.4608	[illegible]	-0.9087	-0.9314	-1.3449	-1.2278	-1.3521	-1.1265	-0.8327
3	2 Ces2g		-0.7484	-0.1288	-0.4441	[illegible]	-1.2419	-0.9068	-1.4292	-1.0407	-1.8532
3	2 Cish		0.1854	-0.3213	-1.0265	-0.5166	-1.0659	-0.4651	-1.5994	-0.9102	-1.855
3	2 Clec2d		-0.2825	0.4602	-0.9848	-0.4684	-1.7347	-1.5296	-2.1669	-1.6689	-2.5173
3	2 Clic1		-0.1475	[illegible]	-0.4181	-0.4586	-0.8347	-0.4638	-0.8363	-0.6568	-1.1505
3	2 Clip4		0.6843	[illegible]	-0.6585	-0.8097	-0.9736	-1.2212	-1.0269	-1.2434	[illegible]
3	2 Col15a1		-0.1812	0.4802	-0.2228	-0.7293	-1.0469	-1.5559	-1.5164	-1.2217	-1.6916
3	2 Copa		[illegible]	-0.1626	-0.562	-0.5429	-0.9035	-0.6715	-0.861	-0.896	-0.593
3	2 Corin		-1.0339	-0.339	1.4555	-0.2927	[illegible]	-1.3814	-1.3056	-1.8691	-2.1279
3	2 Cpz		0.776	0.4471	-1.1	-0.9609	-1.0898	-1.1803	-1.0698	-1.166	-1.166
3	2 Crabp2		-0.7377	[illegible]	[illegible]	[illegible]	-0.5838	[illegible]	-0.9497	0.3444	-3.0941
3	2 Creb3		[illegible]	-0.2035	-0.4795	-0.5593	-1.0173	-0.9011	-1.3535	-1.0748	-1.4397
3	2 Cst3		0.4359	-0.2892	-0.6048	-0.955	-0.8882	-1.22	-0.9162	-1.1563	-2.4874
3	2 Cst9		[illegible]	-0.4787	-0.7965	-0.6521	-0.8138	-0.7456	-0.7256	-0.8138	-0.7029
3	2 Cstb		-0.311	-0.4768	-0.6973	-1.2131	-0.842	-1.2545	-0.865	-0.8944	-0.8117
3	2 Ctsa		[illegible]	-0.6614	-0.549	-0.5621	-0.5647	-0.5743	-1.0021	-1.0064	-0.8057
3	2 Ctsf		-0.2784	-0.4164	-0.194	-0.2651	-0.6286	-0.8981	-1.2353	-0.8878	-1.5924
3	2 Ctsz		-0.2435	-0.4473	-0.5737	-0.7269	-0.8662	-0.758	-0.879	-0.7114	-1.6877
3	2 Cx3cl1		-0.2477	-0.1489	-0.5438	-0.8107	-0.5288	-1.0629	-0.5247	-0.7502	-1.0356
3	2 Cygb		0.5649	-0.1748	-0.6755	-0.9484	-0.9345	-0.9696	-0.9449	-1.0201	-0.9242
3	2 Cyhr1		[illegible]	-0.4043	-1.0431	-0.9106	-0.8692	-0.8935	-1.0311	-0.8506	-0.5182
3	2 Cyp4v3		0.0885	-0.748	-0.586	-1.0542	-1.1585	-1.2852	-1.2823	-1.4956	-1.4627
3	2 D0H4S114		0.4271	[illegible]	-1.1146	-1.27	-1.8365	-1.444	-0.9737	-1.5038	-2.4912
3	2 Dbndd2		-0.4611	-0.5456	[illegible]	[illegible]	[illegible]	[illegible]	-1.5419	-0.7984	-2.6722
3	2 Dclk1		[illegible]	-0.4833	-0.7799	-0.6943	-0.628	-0.4119	-0.9038	-0.8016	-1.3162
3	2 Dctn1		[illegible]	-0.9766	-0.3744	-0.5672	-0.5757	-1.0514	-1.6625	-1.0182	-0.8754
3	2 Dctn6		[illegible]	-0.7544	-0.9662	-0.7397	-0.6592	-0.8648	-0.942	-0.798	-0.9727
3	2 Ddit3		0.5811	-0.5448	-0.317	-1.3601	-0.9856	-1.3901	-1.2202	-1.1051	[illegible]
3	2 Ddrgk1		-0.3888	-0.4337	-0.5696	-0.8271	-0.9129	-0.8488	-0.9607	-1.0147	-0.7905
3	2 Decr1		-0.2887	-0.0526	-0.7272	-0.5715	-0.8812	-0.7788	-1.0794	-0.7979	-0.9914
3	2 Dhrs1		-0.4169	-0.4279	-0.4729	-0.5689	-0.6451	-0.7703	-0.9965	-0.7736	-1.1228
3	2 Dhrs7		-0.2209	-0.4324	-0.5474	-0.8185	-0.4327	-0.7738	-0.777	-0.7127	-1.385
3	2 Dnajb2		-0.3109	-0.3934	-0.7348	-0.9097	-1.148	-1.0348	-1.2533	-1.0348	-0.922
3	2 Reep5		0.2163	0.2652	-0.27	-0.4481	-0.9158	-1.3454	-1.6801	-1.7413	-2.8128
3	2 Dpp7		0.2483	-0.3151	-0.2773	-0.6008	-0.82	-1.1053	-1.3396	-1.0715	[illegible]
3	2 Dtnbp1		-0.1609	-0.1919	-0.6734	-0.643	-1.012	-1.0321	-1.4993	-1.196	-1.2478
3	2 Dusp11		-0.2823	-0.3501	-0.3465	-0.3615	-0.5116	-0.7358	-1.3779	-1.0466	-1.3984
3	2 Dynlt3		0.1106	-0.1293	-0.4197	-0.4649	-0.8109	-1.0143	-1.442	-1.2558	-2.001
3	2 Efemp1		0.1787	-0.1657	-0.7833	-0.6812	-0.7765	-0.616	-0.8213	-0.8108	-0.6906
3	2 Efha1		-0.142	-0.3704	-0.4159	-0.4419	-0.3945	-0.4927	-0.9059	-0.8558	-2.5175
3	2 Efhd1		-0.056	-0.0678	-0.4784	-1.0546	-1.0429	-1.1862	-0.9666	-1.2121	-0.764
3	2 Ehbp1l1		-0.3057	0.1381	-0.4753	-0.235	-0.6345	-0.5772	-1.0427	-0.7581	-1.0866
3	2 Elmo2		[illegible]	0.1074	-0.7081	-0.7686	-1.0282	-1.1736	-1.4027	-1.2534	-1.3591
3	2 Entpd4		-0.5127	-0.491	-0.2672	-0.1928	-0.514	-0.6194	-1.092	-0.5216	-1.6021
3	2 Esrra		-0.481	-0.3821	-0.8263	-0.4982	-0.749	-0.4862	-1.191	-0.8084	-0.9666
3	2 Ext2		-0.2512	-0.334	-0.808	-1.084	-1.0455	-1.2671	-1.4947	-1.262	-1.2866
3	2 Fam132a		0.1029	0.3168	-0.5599	-0.9563	-0.8458	-1.0149	-0.6292	-0.8291	-1.9761
3	2 Fam63b		-0.1355	[illegible]	-0.5749	-0.5627	-0.8347	-0.9311	-1.3666	-0.9611	-1.5722
3	2 Fbxo4		-0.2748	-0.4035	-0.6386	-0.4752	-0.6609	-0.9832	-1.6283	-1.2122	-2.1507
3	2 Fchsd2		-0.2498	-0.2793	-0.4731	-0.6535	-1.0234	-1.1422	-0.9415	-0.8251	-0.8483
3	2 Fkbp9		0.742	0.2181	-0.9481	-0.9846	-1.3944	-1.2636	-1.0375	-0.9827	-0.8246
3	2 Fmnl3		0.6817	0.7672	-1.4505	-1.2261	-2.0826	-1.8686	-1.3705	-1.4259	-0.1026
3	2 Foxc2		-0.1472	[illegible]	-0.8026	-0.7167	-0.7965	-0.8585	-0.8428	-0.9003	-0.7814
3	2 Fth1		0.2233	0.1111	-0.5	-0.8224	-0.7114	-1.1972	-0.7645	-0.9143	-0.3776
3	2 Gaa		0.3584	-0.1931	-0.8665	-1.0717	-0.9838	-1.2959	-1.496	-1.2831	-1.3484
3	2 Ganc		-0.0272	-0.1845	-0.6189	-0.4638	-0.5576	-0.58	-1.044	-0.7426	-1.0754
3	2 Glis1		-0.0188	-0.1998	-1.0799	-0.5842	-0.8412	-0.9632	-0.9243	-0.438	-0.7892
3	2 Gnptg		-0.1081	-0.4026	-0.6163	-0.7813	-0.8316	-0.9258	-0.8684	-0.9878	-0.6824
3	2 Golga1		-0.3091	-0.368	-0.566	-0.6742	-0.6688	-0.4902	-1.0404	-0.685	-1.0757
3	2 Gpc1		-0.2048	0.1127	-1.2741	-1.5079	-2.0653	-1.9936	-1.1555	-1.5355	-1.323
3	2 Gpsm1		0.1564	-0.0302	-0.6778	-1.0971	-1.102	-1.2448	-0.6055	-1.0971	-0.9764
3	2 Grina		-0.2891	-0.658	-0.3084	-0.3504	-0.5699	-0.7321	-1.5843	-1.5929	-2.5844
3	2 Has1		0.137	-0.3615	-0.7038	-0.9419	-0.7636	-0.7758	-0.8387	-0.9419	-0.9663
3	2 Heg1		-0.0601	-0.5023	-0.4828	-0.643	-1.2384	-1.3673	-1.5108	-1.3286	-2.0457
3	2 Hexa		0.2268	-0.4787	-1.0576	-1.5531	-1.7549	-1.9641	-1.2686	-1.7531	-0.7995
3	2 Hp1bp3		-0.1529	-0.1084	-0.2231	-0.36	-0.4219	-0.352	-1.0361	-0.6412	-1.5884
3	2 Hsbp1		0.0464	-0.2204	-0.5568	-0.6189	-0.793	-1.0491	-1.1261	-1.0605	-1.1092
3	2 Hsd11b1		0.4338	-0.4812	-0.6968	-0.5879	-0.8215	-0.9062	-0.8422	-0.8597	-0.5392
3	2 Hsd17b7		-0.4722	-0.475	-0.1448	-0.6783	-0.483	-0.9263	-1.0617	-1.0954	-1.6479
3	2 Hsd3b7		-0.7794	-0.3595	0.0625	[illegible]	-0.4035	-0.3513	-1.1919	-0.5962	-1.9968
3	2 Hspa12b		0.0703	0.1368	-0.521	[illegible]	-0.9644	-0.7601	-1.5457	-1.3952	-2.3985
3	2 Igdcc4		0.8856	-0.0822	-1.4256	-2.1236	-1.8291	-1.8366	-0.9511	-0.9729	-1.6835
3	2 Il10rb		-0.0939	-0.4976	-0.5858	-0.572	-0.9406	-0.8651	-1.5435	-1.1451	-1.7573
3	2 Irf2		[illegible]	-0.3484	0.1148	-0.1998	-0.3786	-0.6169	-1.6065	-0.7381	-3.8794
3	2 Itga1		0.0822	0.1854	-0.7049	-0.906	-0.9332	-0.9367	-0.853	-0.8401	-1.0254
3	2 Itgb5		0.2007	[illegible]	-0.758	-0.9039	-1.1811	-1.23	-1.7249	-1.4057	-1.8217
3	2 Itpr2		-0.3388	-0.1563	0.0738	0.1668	-0.2556	-0.6817	-1.033	-0.9022	-1.6703
3	2 Izumo4		0.1374	-0.216	-0.4959	-0.512	-0.7961	-0.7266	-1.0271	-0.6897	-1.0071
3	2 Jazf1		0.2098	-0.1014	-0.6521	-0.8414	-0.8563	-0.9115	-0.8119	-0.6891	-0.8414
3	2 Jun		0.5729	-0.7829	-0.3928	-1.092	-0.6798	-0.8791	-0.7586	-1.1022	-2.8429
3	2 Kctd10		0.1688	0.1867	-0.4819	-0.6336	-0.9811	-0.9518	-1.0566	-1.0206	-1.1016
3	2 Keap1		-0.3972	-0.5555	-0.7057	-0.4016	-0.6163	-0.384	-0.9917	-0.676	-1.5262
3	2 Khk		-0.2629	-0.4311	-0.841	-1.089	-0.9578	-0.6564	-0.7586	-0.8364	-0.7076
3	2 Kif3c		0.0229	-0.2319	-1.0882	-1.2015	-1.4101	-1.4291	-1.1803	-1.079	-0.1317
3	2 Klhl26		-0.3494	0.0716	-1.2908	-0.6792	-1.1868	-1.0719	-1.1827	-1.0067	-0.6301
3	2 Lamb2		0.2918	0.1253	-0.5904	-0.8069	-1.204	-1.2101	-1.4797	-1.2346	-2.2093
3	2 Lamp1		-0.3265	-0.5158	-0.4188	-0.6951	-0.6233	-1.0287	-1.2972	-1.0563	-1.4293
3	2 Laptm4a		0.4973	0.1572	-0.4934	-0.6987	-1.3676	-1.4207	-1.665	-1.2249	-1.7524
3	2 Larp6		0.6535	0.5695	-1.0182	-1.2178	-1.2275	-1.2439	-1.2773	-1.2048	-1.1857
3	2 Lcn2		0.3139	-0.3712	-0.7976	-1.4918	-1.0166	-1.5939	-1.4918	-1.1583	-2.2567
3	2 Leprel2		0.8176	0.4797	-1.0649	-1.0932	-1.4193	-1.3729	-1.5934	-1.4653	-2.1531
3	2 Leprel4		-0.2902	[illegible]	-0.8377	-0.3137	-0.8135	-0.1186	-1.3712	-0.397	-1.7241
3	2 Leprot		0.1856	[illegible]	-0.6421	-0.5808	-0.7329	-1	-0.968	-1.051	-0.7023
3	2 Lgals3		-0.3734	-0.1106	0.4753	-0.2749	-0.1559	-0.4856	-1.1328	-0.8748	-2.6184
3	2 Lipa		0.5408	-0.0482	-0.9422	-0.9749	-1.0646	-1.1415	-1.1048	-1.2401	-1.2881
3	2 Litaf		-0.1196	-0.1499	0.1387	-0.5049	-0.439	-0.6339	-0.9166	-0.8958	-1.0527
3	2 Lman2		[illegible]	-0.192	-0.4726	-0.3574	-0.6825	-0.6429	-1.071	-0.8927	-1.1791
3	2 Lrrc57		-0.277	-0.3683	-0.3381	-0.3059	-0.5974	-0.5828	-0.7034	-0.5573	-1.7034
3	2 Lrrk1		0.0499	-0.1996	-0.7896	-1.1198	-1.126	-1.1205	-1.8092	-1.3416	-3.3942
3	2 Ly96		-0.035	-0.3918	-0.829	-1.0614	-1.0603	-1.3977	-1.4746	-0.9867	-2.4684
3	2 Lynx1		0.1416	-0.1278	-1.2255	-0.8934	-1.1017	-0.8395	-1.3471	-0.7915	-2.0933
3	2 Lyrm5		[illegible]	-0.1653	-0.6012	-0.6443	-0.7877	-0.5687	-0.9695	-0.4881	-0.9689
3	2 Marcks		0.6874	-0.0666	0.0521	-0.9725	-1.8093	-1.9478	-1.0409	-1.5406	-2.1277
3	2 Mfge8		0.3508	0.558	-1.2258	-1.2397	-1.5465	-1.7219	-0.8098	-1.3994	-0.4726
3	2 Mfn2		0.0689	[illegible]	-0.6033	-1.0931	-1.1014	-1.0212	-0.878	-1.1795	-1.5734
3	2 Mknk1		-0.3357	-0.5534	-0.5632	-0.4382	-1.0281	-0.9862	-1.6108	-1.3121	-0.6924
3	2 Mob3a		0.1665	0.1387	-0.6979	-0.7338	-0.9502	-0.4816	-0.9343	-0.7215	-1.0924
3	2 Mocos		0.1567	-0.5105	-0.7436	-0.8926	-0.3346	-0.8859	-0.614	-0.7138	-1.0036
3	2 Nagk		0.1737	-0.1162	-0.7557	-0.6781	-0.737	-1.0525	-1.0086	-0.9101	-0.37
3	2 Naglu		[illegible]	-0.1058	-0.2823	-0.6622	-0.3357	-0.8103	-0.717	-0.9002	-1.1765
3	2 Ndel1		-0.1165	-0.5206	-0.2402	-1.0357	-0.7515	-1.1302	-1.0243	-1.3453	-0.6461
3	2 Ndn		0.7155	0.3318	-1.1266	-0.8642	-1.693	-1.9639	-1.3751	-1.5929	-1.3388
3	2 Nfatc1		[illegible]	-0.1053	-0.6179	-0.4484	-0.6179	-0.9165	-0.9716	-0.9141	-0.9165
3	2 Nicn1		0.0708	-0.0606	-1.1871	-1.2645	-1.1944	-0.7765	-0.836	-0.9984	-0.5226
3	2 Nipa1		0.5244	0.2101	-0.8877	-0.7165	-1.3665	-1.3723	-1.3975	-1.1579	-0.8416
3	2 Npc2		0.2827	-0.0831	-0.5997	-0.9731	-0.9482	-1.1263	-0.9915	-1.1039	-0.9034
3	2 Nrap		0.2666	-0.8689	-1.0848	-1.1544	-1.297	-1.0092	-1.056	-1.2527	-1.0719
3	2 Nrbp2		0.4957	-0.2714	-0.6766	-1.3688	-1.4201	-1.4368	-1.3554	-1.3762	-0.8927
3	2 Nudt18		-0.2489	-0.2983	-0.5358	-0.5187	-0.7472	-0.6574	-1.3698	-0.9765	-1.3983
3	2 Nupr1		-0.1872	-0.5818	-0.0467	-0.5718	-0.6931	-0.5149	-1.247	-0.9528	-1.5777
3	2 Oaz2		[illegible]	0.1905	-0.6815	-0.6462	-0.8138	-0.6166	-0.8421	-0.9269	-0.7494
3	2 Omd		0.2028	-0.3835	-0.3281	-0.9131	-1	-1.1292	-0.9785	-1.2234	-0.9755
3	2 Ormdl3		0.1924	[illegible]	-0.6334	-0.8979	-0.8993	-0.8979	-0.8827	-0.8118	-1.1065
3	2 P4ha2		-0.0949	[illegible]	-1.0233	-1.1255	-1.1819	-1.0264	-1.2058	-0.8984	-1.449
3	2 Pcyox1		-0.1179	-0.4484	-1.1154	-1.1764	-1.3817	-1.1772	-1.4502	-1.165	-1.6229
3	2 Pde8a		0.1123	-0.126	-0.634	-0.734	-0.7193	-1.3849	-0.9476	-1.3264	-0.2205
3	2 Pdrg1		0.0677	[illegible]	-0.8053	-0.3421	-1.1511	-1.1403	-1.5299	-1.2118	-2.1216
3	2 Plin2		-0.2511	-0.2605	-0.2878	-0.674	-0.6897	-0.895	-0.7845	-1.1939	-1.4458
3	2 Plk2		-0.1958	-0.6223	0.5029	-0.7438	-0.1674	-0.6514	-0.8978	-1.1365	-2.0701
3	2 Plod3		-0.1572	0.185	-1.0671	-0.3605	-1.102	-0.5739	-1.3242	-0.9886	-1.0918
3	2 Plvap		0.4473	-0.2239	-0.8233	-1.4008	-1.2428	-1.5808	-1.0419	-1.1426	-0.64
3	2 Podxl2		0.5337	0.2272	-0.6502	-1.1742	-1.0942	-1.0105	-0.8849	-0.8516	-1.1194
3	2 Ppt1		0.303	-0.1699	-0.4847	-0.4868	-0.6915	-0.5493	-1.0781	-0.8385	-1.3929
3	2 Prmt2		-0.3297	-0.1815	-0.9574	-0.7311	-1.0874	-1.238	-0.9677	-1.0627	-1.0902
3	2 Prnp		0.4421	-0.1379	0.2985	-0.1355	-0.8427	-1.0607	-1.8919	-1.6232	-3.7028
3	2 Prosapip1		-0.0946	-0.0795	-1.0136	-0.7119	-1.1247	-1.144	-1.4155	-1.2242	[illegible]
3	2 Prss23		0.5528	-0.2364	-0.6755	-1.0446	-1.2198	-1.3519	-1.4159	-1.4472	-1.5047
3	2 Psap		0.1852	-0.3747	-0.7705	-1.3302	-1.0651	-1.3098	-1.2123	-1.3771	-1.9806
3	2 Psmb9		0.4249	-0.8604	-0.6011	-1.1795	-0.6583	-1.1221	-0.5862	-0.6937	-0.7991
3	2 Ptgs1		[illegible]	0.5342	-0.8207	-0.6846	-0.867	-0.8452	-0.7554	-0.8117	-0.8514
3	2 Ptprd		0.4428	-0.5315	-0.6182	-0.8915	-1.6068	-1.4599	-1.6863	-1.6392	-2.3065
3	2 Rab28		-0.2476	-0.4453	-0.8094	-0.6793	-0.7569	-0.9283	-0.9676	-0.8337	-0.8962
3	2 Rab32		-0.2355	-0.0301	-0.0525	-0.1934	-0.986	-1.3073	-1.7497	-1.1401	-3.2103
3	2 Rab33b		0.3827	-0.0471	-0.4997	-0.8754	-1.1683	-1.1973	-0.9215	-1.0712	-1.0088
3	2 Rab38		[illegible]	-0.1168	-0.2035	-0.7413	-0.7476	-1.1362	-0.5887	-0.4791	-1.512
3	2 Rab3d		-0.1896	-0.3487	-0.2134	-0.2739	-0.4893	-0.395	-1.2403	-0.9441	-1.8236
3	2 Rab7l1		-0.4772	-0.583	-0.1249	-0.163	-0.4814	-0.7485	-1.5751	-1.1645	-1.4323
3	2 Rap2a		[illegible]	0.1585	-0.6653	-0.5482	-1.1273	-1.0473	-1.2232	-0.7886	-1.0825

3	2 Rarres2	0.2798	[illegible]	-1.2839	-1.409	-1.5089	-1.5553	-1.5585	-1.68	-1.5212
3	2 Rbp1	[illegible]	0.3362	-0.7103	-0.4526	-1.3995	-1.4645	-1.2064	-1.1671	-1.9499
3	2 Rftn2	[illegible]	-0.1658	-0.6391	-0.7576	-0.8654	-0.8563	-0.899	-0.9462	-0.9021
3	2 Ring1	-0.2715	-0.4299	-0.6182	-0.3633	-0.7349	-0.4956	-0.774	-0.9276	-1.18
3	2 Ripk1	0.4504	0.1293	-0.3261	-0.604	-0.7896	-0.6991	-1.2964	-1.1001	-1.3807
3	2 Rit1	0.1551	-0.134	-0.1471	-0.6165	-0.7678	-0.9074	-1.0657	-1.1326	-1.6138
3	2 Rnf166	[illegible]	0.1192	-0.5951	-0.8481	-1.1742	-1.2483	-1.2499	-1.4022	-0.8306
3	2 Rps25	-0.811	[illegible]	-0.5274	-0.1994	-1.0364	[illegible]	-1.047	[illegible]	-1.6503
3	2 S100a13	-0.3166	-0.22	-0.272	-0.5661	-0.8026	-1.0489	-1.0329	-1.1172	-2.0016
3	2 Samd14	0.2693	0.1658	-1.1557	-1.1911	-1.6139	-1.3929	-1.3508	-1.5032	-1.9379
3	2 Sar1a	0.1443	0.1203	-0.2547	-0.6934	-1.1172	-0.9724	-1.119	-1.1994	-0.9684
3	2 Sat1	-0.249	-0.5993	[illegible]	[illegible]	[illegible]	-0.611	-1.048	-0.9618	-1.3366
3	2 Sdcbp	-0.0606	-0.2759	-0.6895	-0.7344	-1.2701	-1.0044	-1.5787	-1.535	-1.9683
3	2 Sdf2	-0.332	-0.5429	-0.6445	-0.8148	-0.7728	-0.9504	-1.0633	-0.8186	-1.2393
3	2 Sdf4	-0.2585	-0.1508	-0.4218	-0.5773	-0.7453	-0.922	-0.6434	-0.9623	-1.459
3	2 Sema3a	0.9909	0.2710	-1.0367	-1.0078	-1.058	-1.2881	-0.9948	-1.058	-1.1612
3	2 Serf1	0.3741	0.1434	-0.6784	-0.7187	-1.2639	-1.1942	-1.1736	-1.2867	-1.4814
3	2 Serf2	[illegible]	[illegible]	-0.8008	-0.8682	-0.9155	-1.0405	-0.9593	-0.7693	-0.4683
3	2 Serinc3	0.3305	-0.2859	-0.6433	-0.747	-1.1793	-1.428	-1.2439	-1.4148	-1.2822
3	2 Serpinb6a	[illegible]	0.2922	-0.9949	-0.7312	-1.4605	-1.3353	-1.4098	-1.2003	-1.6089
3	2 Sgpp1	0.1574	-0.2959	-0.8393	-0.5196	-0.8211	-0.8185	-1.328	-1.1218	-2.1374
3	2 Sh3bgrl3	0.2548	[illegible]	-1.396	-1.4402	-1.4154	-1.5369	-0.7889	-1.1132	-1.3927
3	2 Six1	0.1778	[illegible]	-0.9026	-1.0374	-1.1185	-1.0951	-0.2851	-1.0168	[illegible]
3	2 Slc22a18	[illegible]	-0.2543	-0.2416	-0.6896	-0.8861	-0.6081	-1.0522	-0.7878	-0.9277
3	2 Slc2a13	0.3723	0.452	-0.7459	-0.995	-1.0525	-0.9884	-1.0875	-0.905	-1.0184
3	2 Slc39a11	-0.1907	[illegible]	-0.5804	-0.5472	-0.771	-0.7801	-1.1105	-1.1236	-1.3781
3	2 Slc44a2	[illegible]	[illegible]	-0.8809	-1.3026	-0.7826	-0.9138	-1.3125	-1.2664	-1.8305
3	2 Slc8a1	0.2036	-0.4615	-0.8893	-1.2613	-1.3772	-1.3181	-1.2298	-1.519	-1.3572
3	2 Slco3a1	[illegible]	-0.3547	-0.509	-0.7443	-0.855	-0.9657	-1.1743	-1.3024	-1.3312
3	2 Smarca1	1.2227	[illegible]	-1.6498	-1.2868	-1.7074	-2.1925	[illegible]	-0.5906	[illegible]
3	2 Smpdl3a	[illegible]	[illegible]	[illegible]	[illegible]	-0.4299	-0.6433	-1.1205	-0.6629	-2.8267
3	2 Spop	-0.3576	-0.1338	-0.8086	-0.3804	-1.1513	-1.0035	-1.304	-1.0474	-1.3775
3	2 Sprr2k	0.2256	1.3743	-1.4349	-0.7976	-1.4835	-1.4221	-1.3572	-1.397	-1.3602
3	2 Ssr4	[illegible]	[illegible]	-0.4688	-0.4468	-0.7578	-0.7908	-0.9642	-0.9583	-1.3072
3	2 Stat5a	-0.3234	-0.287	-0.7553	-0.3872	-0.9584	[illegible]	-1.3403	-0.5463	-1.2761
3	2 Stx8	-0.1674	-0.3346	-0.5666	-0.6878	-0.9597	-1.0027	-1.0588	-0.976	-0.5455
3	2 Sucnr1	-0.1442	-0.5198	[illegible]	-0.7009	-0.585	-0.7752	-0.9797	-0.8569	-0.9471
3	2 Sybu	-1.081	-0.4613	0.5935	0.2225	[illegible]	-0.3422	-1.1042	-0.5032	-3.6687
3	2 Sytl1	0.2061	-0.2276	-0.8232	-0.3305	-1.2388	-0.7404	-1.0916	-1.0153	-1.1315
3	2 Tap2	0.3476	-0.1062	-0.6694	-0.7187	-0.875	-0.7747	-1.0117	-1.0532	[illegible]
3	2 Tbc1d2b	0.8229	0.3031	-0.9045	-1.2329	-1.6753	-1.6942	-1.2577	-1.3331	-1.348
3	2 Tcirg1	[illegible]	-0.126	-0.2897	-0.6653	-0.3427	-0.6111	-0.5935	-0.5751	-1.3419
3	2 Tdrd7	0.6081	[illegible]	[illegible]	-0.7342	-1.1226	-1.7179	-1.2488	-1.5605	-2.3015
3	2 Tgfb1	[illegible]	-0.1007	-0.6819	-0.949	-1.1734	-1.1936	-1.0902	-0.9912	-0.7106
3	2 Tgfb2	[illegible]	-0.5276	-0.4495	-0.4815	-0.7358	-0.5751	-0.9079	-0.5769	-1.2255
3	2 Tmed3	0.8114	0.5742	-0.7477	-0.6811	-1.3633	-1.0447	-1.8827	-1.3614	-1.9175
3	2 Tmed9	[illegible]	[illegible]	-0.4782	-0.1978	-0.7259	-0.2452	-0.7709	-0.828	-1.0993
3	2 Tmem106c	-0.2812	[illegible]	-0.5907	-0.5962	-0.7466	-0.5122	-0.7929	-1.0771	-0.9851
3	2 Tmem111	0.1108	-0.1626	-0.3780	-0.331	-0.7337	-0.512	-1.1147	-0.9064	-0.9685
3	2 Tmem167b	0.1626	-0.3190	-0.4569	-0.5963	-0.7778	-0.8256	-0.9824	-0.6946	-1.0778
3	2 Tmem204	-0.1352	-0.152	-0.7154	-0.9899	-1.1416	-1.197	-1.2375	-1.3147	-1.1805
3	2 Tmem50a	[illegible]	[illegible]	-0.5883	-0.9438	-0.5969	-0.7498	-1.0256	-0.8959	-0.7625
3	2 Tmem53	0.4714	0.3395	-0.562	-0.7469	-1.0906	-1.0406	-1.6142	-1.19	-2.0438
3	2 Tmx4	-0.0602	-0.1158	-0.4583	-0.6775	-0.8716	-0.908	-0.6997	-0.7057	-0.841
3	2 Tnfaip8	-0.2764	[illegible]	-0.6926	-0.9037	-0.704	-1.1244	-0.6314	-1.0304	-1.3577
3	2 Tnxb	0.4095	[illegible]	-1.2412	-1.1302	-1.1819	-1.4224	-1.4029	-1.3584	-1.2941
3	2 Trp53inp2	0.2072	[illegible]	[illegible]	-0.9244	-0.7256	-0.9663	-1.2201	-1.2493	-0.6909
3	2 Tsc22d3	0.1730	-0.3973	-0.6963	-1.0511	-1.0356	-0.9378	-0.7181	-0.8252	-1.0476
3	2 Tspo	[illegible]	0.2538	-0.8717	-0.6759	-1.1995	-1.142	-1.7904	-1.4325	-2.0801
3	2 Ttpal	-0.3632	[illegible]	-0.69	-0.749	-0.9209	-1.1741	-0.8976	-0.8373	-0.8546
3	2 Txndc5	0.3012	0.2942	-0.8278	-0.8683	-1.3292	-1.18	-1.4114	-1.1686	-1.2365
3	2 Vamp4	[illegible]	-0.5397	-0.2984	[illegible]	-1.1093	-1.305	-2.3054	-1.5195	-2.8904
3	2 Vsnl1	-0.6893	0.2765	[illegible]	[illegible]	-1.1193	-1.3901	-1.6228	-1.5449	-1.7211
3	2 Wnt2	-0.1422	-0.4237	-0.8861	-0.9398	-1.6302	-1.8185	-1.7874	-1.9228	-1.9604
3	2 Zcchc6	-0.1570	-0.5738	-0.5302	-0.757	-0.7392	-0.834	-0.8102	-0.8005	-0.8601
3	2 Zfp46	0.2270	[illegible]	-0.7325	-0.4654	-1.0138	-0.7664	-1.4076	-1.1058	-1.2646
3	2 Zfp672	[illegible]	-0.2255	-0.9085	-0.4222	-0.807	-0.7741	-1.2971	-0.6636	-2.1974
3	3 Alox12b	-2.0564	-2.2653	-1.1584	-0.7562	0.5792	1.2539	[illegible]	1.1078	-1.9245
3	3 Cldn3	-2.4182	-2.071	-0.173	-0.5242	0.7854	0.3484	[illegible]	[illegible]	-1.8206
3	3 Dsp	-2.604	-1.9344	[illegible]	[illegible]	0.5090	[illegible]	[illegible]	0.4067	-2.082
3	3 1190003J15Rik	-3.724	-3.2867	-0.7631	-1.2771	-0.4667	-0.6164	-0.9001	-0.9332	-1.9466
3	3 1300014I06Rik	-0.741	-1.1285	-0.7387	-0.6599	-0.4534	-0.4252	-1.1285	-0.9367	-2.416
3	3 1700057K13Rik	-1.5161	-1.6239	0.4318	[illegible]	[illegible]	-0.5415	-0.6143	-0.9959	-1.6994
3	3 2310057N15Rik	-0.9687	-0.8916	-0.47	-0.3757	-0.5221	-0.7847	-0.8851	-1.0392	-1.0685
3	3 2410002F23Rik	-1.2161	-1.2614	-0.7502	-0.659	-0.9949	-1.1212	-0.9695	-0.7882	-0.9864
3	3 2810405K02Rik	-1.1085	-1.1033	-1.5783	-1.3137	-1.4818	-1.1824	-1.3977	-1.2972	-1.1007
3	3 3110056O03Rik	-0.6217	-0.2802	-0.9201	-0.4090	-1.0569	-0.7578	-1.063	-0.8438	-1.4271
3	3 Mgarp	-3.0606	-2.5442	-2.0551	-2.1974	-1.6818	-1.3617	-1.1689	-1.1053	[illegible]
3	3 5330417C22Rik	-0.8222	-1.0036	-0.8509	-0.7364	-1.0108	-0.7909	-0.8736	-0.8253	-0.9509
3	3 5430435G22Rik	-0.3884	-0.5213	-0.8014	-0.6899	-1.2414	-1.3772	-1.8333	-1.6777	-2.436
3	3 Aatk	-2.1331	-1.7202	-2.2213	-1.6426	-1.8188	-1.589	-1.9609	-1.6321	-1.0611
3	3 Abca9	-0.6505	-1.0047	-0.8844	-0.9706	-1.1121	-1.0525	-1.1121	-0.9554	-0.9798
3	3 Abcc3	-0.3633	-0.429	-0.995	-1.0456	-1.0117	-1.0769	-1.0769	-1.0456	-0.9302
3	3 Acaa1a	-0.7885	-0.7798	-1.1689	-1.2825	-1.3088	-1.4441	-1.0489	-1.4258	-1.1844
3	3 Adcy2	-0.3749	-0.8178	-1.3308	-1.2964	-1.402	-1.3719	-1.8314	-1.1805	-2.0878
3	3 Adrb2	-0.9762	-1.3425	[illegible]	-0.7536	-0.9728	-0.9912	-1.6795	-1.1	-2.0294
3	3 Adssl1	-1.1498	-0.7847	-1.3714	-1.0744	-1.2233	-1.0326	-0.7513	-0.873	[illegible]
3	3 Aifm2	-0.2895	-0.4001	-1.2577	-0.8339	-1.2139	-1.0114	-1.7189	-1.1104	-0.5344
3	3 Aim1	-2.0503	-2.0304	-1.2123	-1.248	-0.8534	-1.0442	-2.0787	-1.3724	-2.9564
3	3 Akr7a5	-1.2116	-0.5024	-0.9658	-0.5467	-1.0639	-0.485	-0.8066	-0.6893	-0.493
3	3 Aldh1a3	-1.1994	-1.2295	-0.9109	-1.309	-0.5552	-1.249	-1.283	-1.4859	-1.4565
3	3 Aldh3a1	-2.4792	-0.3346	0.8582	1.2275	[illegible]	[illegible]	-1.0342	-0.6011	-4.7432
3	3 Aldh3b1	-1.4449	-1.3006	-1.3388	-1.4279	-1.24	-1.1984	-1.9766	-1.306	-1.1429
3	3 Als2	-1.5886	-1.7327	-1.0073	-1.0686	-0.6493	-0.7985	[illegible]	-0.5544	0.6321
3	3 Ap1b1	-1.0744	-1.0997	-1.3246	-1.1854	-1.2969	-1.2545	-1.2652	-1.1569	-0.8495
3	3 Ap2s1	-0.8473	-0.6927	-0.7472	-0.7215	-0.6004	-0.9465	-0.584	-0.7314	-1.305
3	3 Apcdd1	-1.675	-1.0735	[illegible]	[illegible]	[illegible]	-0.5397	[illegible]	[illegible]	-2.9361
3	3 Apobr	[illegible]	-0.7327	-1.6702	-1.4826	-1.2794	-1.379	-1.1627	-1.1863	-0.6835
3	3 Apoc1	-2.0353	-2.4883	-1.8674	-2.3625	-0.9151	-1.9533	[illegible]	-0.8821	0.4532
3	3 Apoc2	-0.9148	-1.0063	-0.7984	-0.6681	-0.774	-0.8568	-0.8855	-0.9386	-0.6831
3	3 Aqp3	-2.5678	-2.2155	[illegible]	[illegible]	[illegible]	[illegible]	-1.2487	[illegible]	-1.421
3	3 Arap3	-1.5934	-1.5221	-1.5404	-1.5776	-1.3246	-1.4059	[illegible]	[illegible]	[illegible]
3	3 Arc	-0.8553	-1.756	-0.4444	-1.2116	-0.7925	-1.1688	-1.2802	-0.7415	-1.9249
3	3 Arg1	-2.3889	-1.7459	[illegible]	-0.8973	-0.5573	-1.3071	-1.171	-2.0368	-2.5295
3	3 Arhgap25	-0.7109	-0.8501	-0.777	-0.7245	-0.728	-0.7349	-0.777	-0.6806	-0.7985
3	3 Arhgap30	-1.3887	-1.3492	-1.5651	-1.4677	-1.2621	-1.3825	-1.1667	-1.282	-0.5511
3	3 Arhgap4	-1.5474	-1.3957	-1.062	-1.3018	[illegible]	-1.082	-0.6241	-0.7932	[illegible]
3	3 Arhgap9	-1.362	-1.4004	-1.3046	-1.4253	-1.1215	-1.0339	-1.0013	-1.1186	[illegible]
3	3 Arhgef6	-0.5541	-0.9737	-1.0619	-1.3281	-1.4264	-1.3092	-1.5596	-1.4087	-1.6253
3	3 Arl11	-1.9005	-1.8051	-1.461	-1.5017	-1.1507	-1.2512	-1.6889	-1.4992	-1.9039
3	3 Arpc3	-0.9577	-0.5459	-0.9051	[illegible]	-1.0799	-0.5577	-1.1166	-0.9471	-0.5946
3	3 Arpc5	-1.2019	-1.0279	-0.4807	-0.4865	-0.6011	-0.8524	-1.3554	-0.9673	-2.1222
3	3 Artn	-0.6339	-0.7947	-0.8223	-0.9965	-0.7543	-0.7751	-1.2456	-0.9895	-1.1319
3	3 Atp1b3	-2.0297	-1.4786	-0.5855	-0.7364	-0.6446	-0.8684	-1.162	-1.437	-1.6567
3	3 Atp2a3	-3.8904	-2.9206	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-3.3312
3	3 Atp5o	-1.1578	-0.8988	-1.207	-0.9392	-0.8039	-0.7123	-1.1764	-0.4692	[illegible]
3	3 Atp6v1g1	-0.8667	-0.884	-0.9098	-0.7384	-0.8072	-0.7405	-0.9554	-0.793	[illegible]
3	3 Avil	-1.6489	-1.9198	0.5517	0.4674	0.6517	0.3194	-0.614	-0.6726	-2.3683
3	3 Avpi1	-1.6595	-1.371	[illegible]	-0.5835	[illegible]	[illegible]	-0.7186	-0.6709	-1.1548
3	3 B3gat1	-0.6364	-0.6899	-1.0976	-1.1177	-1.2569	-1.2474	-1.138	-1.2474	-1.2349
3	3 B3gnt6	-0.2887	-0.5358	-1.1501	-1.0355	-1.2962	-1.0775	-1.2695	-1.1166	-1.4604
3	3 BC013712	-0.7779	-0.853	-0.9771	-0.9221	-0.9053	-0.9736	-0.853	-0.8987	-0.4961
3	3 BC026590	-0.8567	[illegible]	-0.7478	-0.461	-0.8143	-0.6789	-1.1224	-0.7395	-1.1591
3	3 BC037034	-1.319	-0.8079	-1.0749	[illegible]	-0.5852	-0.5406	-0.9127	-0.8326	[illegible]
3	3 Blvrb	-0.9011	-1.036	-2.3055	-2.6321	-1.8594	-2.2919	-1.23	-1.2835	-1.2947
3	3 Bmp3	-1.2029	-1.5531	-0.5652	-1.7058	-1.5795	-2.1471	-2.129	-2.3524	-2.3736
3	3 Bmper	-0.506	-0.6724	-0.4304	-0.5613	-1.0012	-1.0336	-1.2045	-1.1904	-1.4783
3	3 Brox	-0.6251	-0.4938	-0.798	[illegible]	-0.6034	-0.6182	-1.1774	-0.963	-1.4044
3	3 C130026I21Rik	-0.927	-0.9655	-1.056	-1.0117	-1.0491	-0.995	-0.9618	-1.0629	-0.9785
3	3 C1ql2	-1.7438	-1.8724	-1.7054	-1.7803	-1.7289	-1.5957	-1.4964	-1.4034	-1.8336
3	3 Cacna2d3	-1.1608	-0.4908	[illegible]	[illegible]	-0.563	-0.786	-0.9494	-1.0423	-1.1043
3	3 Calcb	-0.9492	-0.5945	-0.8329	-0.5396	-0.8166	-0.5025	-0.8329	-0.7813	-1.0412
3	3 Car12	-1.7427	-1.3134	-1.0247	-0.7207	-0.6921	-0.5095	-0.9164	-0.7718	-1.2536
3	3 Ccdc28b	-2.0822	-1.8852	-0.9005	-0.5033	-0.2279	-0.3916	-1.057	-0.4613	-2.901
3	3 Ccdc53	-1.0055	-0.9336	-0.7321	-0.692	-0.8452	-0.8093	-1.11	-0.8696	[illegible]
3	3 Ccl27a	-0.6198	-0.7261	-0.812	-0.7726	-0.6878	-0.718	-0.6902	-0.5166	-2.6927
3	3 Ccl4	-1.7674	-1.944	-1.8447	-1.8647	-1.8282	-1.8185	-1.712	-1.825	-1.7959
3	3 Ccng2	-0.7149	-0.8199	-1.016	-1.2285	-0.885	-1.056	-1.0778	-1.0384	-1.4796
3	3 Ccpg1	[illegible]	-0.609	-1.0616	-1.0057	-1.8661	-1.4528	-1.8255	-1.7648	-1.0434
3	3 Ccr5	-1.8827	-1.5213	-1.664	-1.8682	-1.5442	-1.6671	-1.7575	-1.781	-1.7083
3	3 Cd151	-1.5034	-0.4469	[illegible]	[illegible]	-0.4316	[illegible]	-0.5616	-0.4160	-1.639
3	3 Cd180	-0.8058	-0.6034	-0.7534	-0.8201	-0.8201	-0.7499	-0.8419	-0.8826	-0.7458
3	3 Cd28	-0.6283	-0.717	-0.7411	-0.7764	-0.6176	-0.7551	-0.6999	-0.798	-0.8459
3	3 Cd300lh	-1.4241	-1.1427	-1.1297	-1.2794	-1.3897	-1.341	-1.3202	-1.1664	-1.3026
3	3 Cd33	-0.7832	-1.1718	-1.0961	-1.0738	-1.1058	-1.0613	-1.0334	-1.1318	-1.2095
3	3 Cd74	-1.5579	-1.5182	-1.2373	-1.4234	-0.9819	-0.9137	-1.0893	-0.9485	-1.3669
3	3 Cd83	-1.7758	-1.7257	-1.7434	-1.8127	-1.6403	-1.7186	-1.5882	-1.7117	-1.6909
3	3 Cd84	-1.671	-1.4652	-1.6268	-1.5511	-1.4876	-1.6145	-1.5365	-1.6807	-1.3947
3	3 Cd86	-1.6338	-1.5781	-1.4921	-1.4953	-1.4509	-1.5311	-1.6057	-1.3808	-1.5679
3	3 Cdhr1	-2.4443	-2.3096	-1.0681	-1.0385	-0.5005	[illegible]	-0.9511	[illegible]	-1.4309
3	3 Ceacam10	-0.8527	-0.8288	-0.7736	-0.7707	-0.7937	-0.8587	-0.9524	-0.9719	-0.6111
3	3 Cela1	-1.0626	-0.6844	-1.1905	-1.1178	-1.362	-1.2541	-1.3377	-1.1967	-0.4692
3	3 Cerk	-1.0962	-0.9928	-1.5229	-1.2084	-1.0899	-1.08	-1.5112	-1.378	-2.7934
3	3 Chodl	[illegible]	-1.7119	-2.0311	-1.9136	-2.0621	-2.1224	-2.0517	-2.0937	-1.9975
3	3 Chst15	-1.0882	-0.7246	-0.5356	[illegible]	-0.9228	-0.6488	-1.1436	-0.5663	-2.1387
3	3 Clec4a1	-2.0984	-1.9772	-1.1285	-1.4282	-0.9886	-1.3933	-1.1833	-1.8185	-2.0399
3	3 Clec4a3	-1.5963	-1.8442	-1.5781	-1.5989	-1.5524	-1.8349	-1.628	-1.6965	-1.5806
3	3 Clec4b1	-1.5457	-1.336	-1.6338	-1.4057	-1.5908	-1.2981	-1.6122	-1.4307	-1.556
3	3 Clec4n	-1.9305	-1.8711	-1.9147	-1.8348	-1.9052	-1.9052	-1.9401	-1.7311	-1.6474
3	3 Clec7a	-0.9807	-0.9677	-0.9087	-1.033	-0.8293	-0.7943	-0.8985	-0.9189	-1.0293
3	3 Cln3	-1.4694	-1.6031	-1.0084	-1.3524	-1.0564	-1.0042	-1.691	-1.3175	[illegible]
3	3 Cln5	-0.3717	-0.7887	-0.6896	-0.764	-0.7283	-1.1038	-0.9095	-1.0991	-0.502
3	3 Clrn3	-0.9514	-0.9848	-0.9547	-0.9449	-0.9589	-0.6548	-0.6574	-0.8103	-0.9514
3	3 Cmc1	-0.771	-0.792	-0.554	-0.6375	-0.655	-0.5986	-1.2734	-1.0987	-1.0124

3	3 Cnfn	-0.9059	-0.8156	-0.8662	-0.7667	-0.699	-0.7082	-0.908	-0.8417	-0.9955
3	3 Coch	-1.7485	-2.0465	-2.0465	-1.9935	-1.8304	-1.779	-1.6248	-1.8658	-1.7132
3	3 Col14a1	-1.0478	-0.8989	-1.0015	-1.0168	-1.1518	-0.9596	-1.1552	-1.051	-1.0384
3	3 Cops8	-0.9815	-0.9541	-0.9851	-1.2792	-1.2149	-1.38	-0.9308	-0.9541	-1.2545
3	3 Coro1a	-1.3387	-1.3557	-1.3421	-1.2695	-1.3489	-1.2792	-1.0517	-1.2955	-1.1255
3	3 Cotl1	-2.1411	-1.9311	-2.7469	-2.67	-2.1024	-2.4006	-0.7938	-1.3801	[illegible]
3	3 Cox6a2	-0.52	-1.0091	-0.7794	-0.8206	-0.767	-0.9552	-0.9482	-0.9204	-0.5096
3	3 Cpped1	-0.5078	-0.5178	-0.6211	-0.4592	-0.5382	-0.4762	-1.161	-1.0258	-1.7905
3	3 Crp	-0.7673	-0.7214	-0.7976	-0.8425	-0.6247	-0.8531	-0.8637	-0.7606	-0.7606
3	3 Csf1r	-1.4997	-1.493	-1.6005	-1.5826	-1.5579	-1.4699	-1.5544	-1.415	-1.4831
3	3 Csf2rb2	-0.9754	-0.9641	-0.9165	-0.9346	-0.9679	-0.9419	-0.9867	-0.931	-0.895
3	3 Csprs	-0.8112	-2.0412	[illegible]	-0.8177	-0.5924	-1.3427	-1.6549	-2.2447	-2.2016
3	3 Ctnnal1	-1.9647	-2.2794	-0.7399	-0.9285	-0.4123	-0.1136	-0.1002	-0.4183	-0.2418
3	3 Ctsc	-1.2076	-1.6758	-1.9357	-1.9046	-2.5686	-2.2646	-2.0795	-2.3336	-2.7948
3	3 Ctse	-1.7478	-1.6176	-1.7759	-1.7759	-1.5868	-1.6148	-1.7727	-1.6578	-1.7982
3	3 Ctss	-0.9019	-0.7535	-1.0673	-0.53	-0.7995	-0.9501	-0.866	-0.8688	-0.8311
3	3 Cx3cr1	-0.6554	-0.8869	-0.8802	-0.9345	-0.8669	-0.9311	-0.7619	-0.897	-0.6669
3	3 Cxcl13	-0.7108	-0.7914	-1.1185	-1.158	-1.2405	-1.2547	-1.244	-1.112	-1.2476
3	3 Cxcl16	-0.9295	-0.9844	-0.5409	-1.0808	-1.0841	-1.3994	-1.3788	-1.2897	-1.1629
3	3 Cyba	-0.6868	-0.6992	-1.8655	-1.5805	-1.6492	-1.5529	-2.0333	-1.6486	-2.1785
3	3 Cyp27a1	-1.2005	-1.4603	-1.4829	-1.3584	-1.4959	-1.3289	-1.0727	-1.4038	-0.8076
3	3 Cyp4f13	-0.9823	-0.9325	-1.123	-0.984	-0.8369	-0.8191	-1.1968	-0.785	-0.3692
3	3 Cyp4f18	-0.8841	-0.9223	-0.9126	-0.9814	-1.0396	-0.8108	-0.9417	-0.8562	-0.8623
3	3 Cyp4f39	-2.4334	-2.1564	-1.1955	-0.4133	-0.3687	0.3328	-1.1719	-0.2562	-2.185
3	3 Cysltr1	-1.2854	-1.1155	-1.1217	-1.064	-1.1753	-1.0551	-0.969	-0.8386	-1.1372
3	3 Cytip	-1.1138	-1.2073	-1.3256	-1.2158	-1.3854	-1.0564	-1.4114	-1.2653	-1.2981
3	3 Daglb	-0.938	-1.105	-0.6911	-0.7571	-0.9619	-0.9347	-1.3676	-1.1555	-1.9066
3	3 Darc	-1.386	-1.3366	-1.5065	-1.3928	-1.5777	-1.8299	-2.1266	-2.2548	-2.7755
3	3 Dbi	-1.1315	-1.4694	-1.2236	-1.2535	-1.2257	-1.3938	-1.5256	-1.2884	-0.3761
3	3 Dgat2	-2.1232	-1.371	-1.1969	-1.1496	-1.6112	-1.3454	-0.995	-1.0973	-1.3569
3	3 Dmkn	-2.9995	-2.2985	-0.8803	-1.0775	-0.0407	-0.2889	-0.803	-0.2381	-3.3079
3	3 Dnajc5b	-1.2683	-1.1526	-0.2891	-0.1079	-0.4186	-0.3448	-1.0482	-1.2843	-1.1822
3	3 Dok3	-1.3302	-0.9269	-1.3253	-0.9759	-1.2309	-1.2377	-1.3401	-1.2309	-0.6543
3	3 Dpep2	-1.0631	-0.9144	-0.9481	-1.1035	-1.129	-0.8129	-1.1615	-1.0508	-0.934
3	3 Dram2	-0.8827	-1.2107	-1.0044	-0.9429	-0.7867	-1.0569	-1.3113	-1.0336	-0.6526
3	3 Drp2	-1.633	-1.84	-0.0901	-0.256	0.2777	-0.1845	-0.3929	-1.1036	-1.982
3	3 Dtx4	-0.4119	-0.7277	-1.1325	-1.2291	-0.8811	-1.0557	-0.7014	-0.9438	-0.8424
3	3 Edn2	-2.4015	-2.2273	-1.502	-1.2937	-0.786	-0.4211	-0.9865	-0.4877	-2.15
3	3 Efcab1	-0.8824	-1.0963	-0.8263	-0.7976	-0.7229	-0.4757	-0.5768	-0.3983	-1.0181
3	3 Ehd4	-1.5712	-1.5573	-0.5909	-0.7513	-0.7179	-0.6199	-1.057	-1.0128	-1.4919
3	3 Espn	-1.7923	-1.9992	-1.6305	-1.754	-0.4388	-0.5475	-0.1408	-0.4137	-1.4898
3	3 Ethe1	-0.7606	-0.7199	-1.0627	-0.8296	-0.6462	-0.6558	-0.8564	-0.6733	-0.6964
3	3 Fah	-1.4734	-1.4045	-1.4338	-0.9204	-1.0261	-0.8216	-1.8995	-0.9632	-1.5299
3	3 Fam110c	-1.8426	-1.3122	0.266	-0.0988	-1.7435	-1.4991	-2.6282	-1.7253	-3.8434
3	3 Fam126a	-0.7866	-1.1483	-0.5122	-0.3481	-0.792	-0.7141	-1.2417	-1.0624	-1.6261
3	3 Fam165b	-0.4172	-0.3879	-1.1976	-0.6328	-1.4204	-1.1526	-1.3044	-0.8894	-1.1094
3	3 Fam78a	-1.6582	-1.5315	-1.5782	-1.6124	-1.3674	-1.4643	-1.0137	-1.133	1.1191
3	3 Fau	-0.9981	-1.0678	-0.6807	-0.8308	-0.7096	-0.7132	-1.1231	-0.9039	-0.8555
3	3 Fcgr1	-0.8118	-0.7567	-0.7537	-1.0161	-0.8498	-1.0342	-0.7718	-0.7477	-0.7932
3	3 Fcgr2b	-1.8034	-1.476	-1.3678	-1.3232	-1.05	-1.3365	-1.7029	-1.5823	-1.8188
3	3 Fcna	-1.101	-1.1202	-1.1527	-1.0915	-1.1759	-1.0329	-1.1428	-1.1202	-1.1363
3	3 Fermt3	-1.6755	-1.6996	-1.5232	-1.6417	-1.6152	-1.7709	-1.7636	-1.7101	-1.6451
3	3 Fes	-1.0692	-1.584	-1.5562	-1.5154	-1.3271	-1.4498	-1.5812	-1.375	-1.5479
3	3 Flcn	-0.8244	-1.215	-0.7	-1.1364	-0.8077	-1.0387	-0.7569	-0.946	-0.3175
3	3 Fyb	-2.0262	-2.1226	-1.9358	-2.1193	-1.9387	-2.2224	-2.1326	-2.0387	-1.9594
3	3 Gamt	-0.5217	-0.2842	-1.0831	-1.2405	-1.5998	-1.8091	-1.5532	-1.6894	-1.7263
3	3 Gbf1	-0.7872	-0.8956	-0.8992	-0.8188	-0.9187	-0.7838	-1.101	-1.1765	-0.6752
3	3 Gchfr	-0.8614	-0.5024	-0.8699	-0.5225	-0.8277	-0.6332	-0.9117	-0.6715	-1.3332
3	3 Gm2a	-0.547	-0.9158	-0.8526	-1.2074	-1.2084	-1.1575	-1.3017	-1.1299	-0.3793
3	3 Gmfg	-2.8351	-2.4607	-1.7627	-1.3263	-1.0075	-0.7121	-0.784	-0.8628	-0.3976
3	3 Gmip	-0.8887	-0.6221	-0.9352	-0.7604	-1.2262	-1.0115	-1.1226	-0.966	-1.1497
3	3 Gna14	-2.2488	-1.3445	0.5723	0.5883	0.3713	[illegible]	-0.3531	-0.7191	-3.3179
3	3 Gngt2	-1.177	-1.0298	-0.4449	-0.5006	-0.4131	-0.4497	-0.7342	-0.5023	-1.1905
3	3 Gpnmb	-0.6914	-1.4214	-0.7653	-1.8597	-0.4807	-1.9964	-1.5521	-2.6475	-3.0288
3	3 Gpr146	-0.8258	-1.3129	-1.1954	-1.2981	-1.0341	-1.3523	-1.3189	-1.3554	-1.415
3	3 Gpr183	-1.6413	-1.585	-1.5241	-1.5746	-1.5781	-1.5678	-1.4818	-1.4563	-1.4626
3	3 Gpr20	-1.4232	-1.5454	-0.7569	-0.8393	-0.2558	[illegible]	-0.3579	-0.185	-1.2399
3	3 Gpr30	-0.7847	-0.5997	-0.633	-0.8898	-1.025	-0.7847	-0.9573	-0.8008	-1.116
3	3 Gpr34	-0.9878	-0.9843	-0.8611	-0.933	-0.9567	-0.5138	-0.9499	-0.9636	-0.967
3	3 Gpr65	-1.6275	-1.6841	-1.6777	-1.7396	-1.6183	-1.5612	-1.7396	-1.573	-1.7768
3	3 Gramd4	-0.7826	-0.7383	-0.2595	-0.469	-0.3755	-0.3932	-0.8232	-0.6968	-1.7447
3	3 Grn	-0.8062	-1.2537	-0.9612	-1.6805	-1.1816	-1.4309	-1.5778	-1.5408	-1.7263
3	3 Gtpbp2	-0.6352	-0.6757	-0.9822	-0.9261	-0.9669	-1.0487	-1.039	-0.9148	-0.9313
3	3 Gusb	-0.9821	-0.5815	-1.3429	-0.9699	-1.3226	-1.0799	-1.2676	-1.4008	-0.9445
3	3 H2-Ab1	-0.8796	-1.1759	-0.6781	-0.8994	-0.4133	-0.8821	-0.6318	-0.7594	-0.9788
3	3 H2-Q7	[illegible]	-1.0321	-0.651	-0.8794	-0.707	-0.691	-0.8495	-0.9537	-0.9432
3	3 Hcls1	-1.364	-1.4216	-1.1871	-1.1246	-1.5911	-1.4884	-1.4714	-1.4413	-1.4747
3	3 Hebp1	-0.88	-1.3339	-2.2434	-2.1601	-2.3085	-1.7908	-2.3085	-1.6776	-0.2634
3	3 Hgfac	-1.076	-0.9657	-0.9164	-0.5265	-0.7244	[illegible]	-0.7987	-0.1697	-1.3106
3	3 Hgsnat	-0.9116	-0.9118	-1.3957	-1.4163	-1.6794	-1.8803	-1.4038	-1.75	-2.4217
3	3 Hk3	-1.6287	-1.5197	-1.4681	-1.5477	-1.5135	-1.6556	-1.6221	-1.3535	-1.5668
3	3 Hlx	-0.5804	-0.8603	-1.2292	-1.5428	-1.5192	-1.531	-1.5339	-1.5577	-1.585
3	3 Hmgcl	-0.9568	-0.8935	-0.9392	-0.9162	-0.6723	-0.8411	-0.6603	-0.7593	-0.1855
3	3 Hmha1	-1.8955	-1.84	-1.3386	-1.5557	-0.5583	-0.557	-0.6053	-0.5505	-0.7469
3	3 Hpgd	-1.0206	-1.5798	-1.0458	-1.7247	-1.5199	-1.5346	-1.3379	-1.7247	-1.3199
3	3 Hpgds	-0.7056	-0.7654	-0.873	-0.8697	-0.8245	-0.8599	-0.7745	-0.6426	-0.6624
3	3 Hr	-0.9658	-1.0924	-0.5287	-0.9487	-0.8704	-1.0283	-1.1595	-1.0877	-1.4796
3	3 Hs3st3a1	-1.9076	-1.1934	-0.4937	0.4323	-0.4448	0.4311	-1.2225	0.3074	-4.1107
3	3 Htatip2	-0.6878	-0.6851	-1.0494	-0.8817	-1.039	-1.08	-1.5735	-1.4978	-1.3674
3	3 Htra1	-0.3675	-0.6827	-1.0541	-1.6914	-1.165	-1.0578	-1.2783	-1.3252	-2.827
3	3 Hyi	-0.6002	-0.8479	-0.8029	-1.3222	-1.027	-1.1862	-1.6192	-1.4588	-2.2968
3	3 Ica1	-1.3587	-0.8052	-0.6576	-0.2916	-0.6262	-0.5059	-1.2053	-0.6396	-0.911
3	3 Ifi30	-0.882	-0.8864	-1.2173	-0.7846	-0.7695	-0.7	-0.6905	-0.5021	-0.4562
3	3 Ifngr1	-0.7377	-0.9146	-1.0668	-1.0267	-1.0322	-0.978	-1.4476	-1.1809	-2.0691
3	3 Il10ra	-1.1891	-1.1534	-1.3054	-1.2393	-1.1891	-1.2393	-1.2393	-1.3126	-1.3019
3	3 Il16	-0.4318	-0.4188	-0.8953	-0.9944	-1.306	-1.2553	-1.4738	-1.2753	-1.4394
3	3 Il18	-0.9773	-1.1925	-0.4745	-0.99	-0.8205	-1.0418	-1.1904	-0.7588	-1.8188
3	3 Il19	-0.6763	-1.0088	-0.8582	-0.5788	-0.7219	-0.7393	-0.8487	-0.5073	-0.8487
3	3 Il1b	-0.8841	-0.8159	-0.9732	-0.7784	-0.8512	-0.928	-0.7815	-0.9557	-0.8223
3	3 Insig2	-0.6881	-0.719	-0.8188	-0.9359	-0.7724	-0.8495	-1.0069	-0.8052	-0.5914
3	3 Insm1	-1.841	-1.2347	-0.282	[illegible]	-0.4171	-0.8186	-1.0355	-0.7221	-1.2432
3	3 Iqsec3	-1.0468	-0.8268	-1.0366	-1.1597	-1.0811	-1.0673	-1.0299	-1.0232	-1.1597
3	3 Irf5	-0.8537	-0.9243	-1.0979	-1.1193	-1.2884	-1.1949	-1.2144	-1.2543	-1.0739
3	3 Irf8	-0.9468	-0.9691	-0.928	-0.891	-1.0248	-0.9627	-0.846	-0.7244	-0.6764
3	3 Itga7	-1.7446	-1.9143	-1.4591	-1.2982	-0.8964	-1.1925	-1.6848	-1.9385	-2.8424
3	3 Itgb4	-2.3818	-0.8353	-0.2823	-0.1186	-0.2849	-0.1132	-1.2249	-0.1671	-4.3112
3	3 Kcnab2	-1.6189	-1.3432	-2.1294	-2.0269	-2.4833	-2.4577	-2.0316	-2.1757	-1.8898
3	3 Klhl6	-2.1296	-1.8724	-2.0289	-1.9409	-2.1648	-2.1296	-1.8637	-1.6642	-1.7713
3	3 Klk1b24	-1.9119	-1.0461	-0.7225	-0.59	-1.2651	-1.516	-1.8931	-1.4433	-1.8806
3	3 Klk1b27	-2.8466	-2.3111	-1.5321	-0.8331	-1.6006	-1.3229	-2.4332	-1.5253	-2.8164
3	3 Klk1b4	-4.4967	-2.7077	-0.6671	-0.5462	-0.8083	-0.4694	-2.2711	-0.6701	-4.4136
3	3 Klk5	-4.4836	-2.5654	-0.4508	-0.1628	-0.3363	-0.1682	-1.7882	-0.2066	-4.7904
3	3 Klk6	-4.6412	-2.378	-0.5643	-0.2213	-0.5239	-0.1217	-1.9537	-0.4473	-4.6064
3	3 Krt16	-2.2539	-2.0022	[illegible]	-1.0082	-0.3438	-0.9689	-1.0282	-1.1048	-2.6371
3	3 Krt79	-1.1611	-0.8843	-1	-0.9581	-0.8941	-1.0214	-1.0952	-0.9684	-0.8519
3	3 Krtdap	-2.5502	-1.5255	-0.7532	-0.6963	-0.3483	0.3513	-0.7315	-0.1366	-3.2196
3	3 Kynu	-1.4495	-1.4744	-1.3441	-1.2612	-1.302	-1.4708	-1.2925	-1.2006	-1.3539
3	3 Lat2	-0.5864	-0.7379	-0.4725	-0.4804	-0.9447	-0.8915	-0.7784	-1.0841	-0.8351
3	3 Lcp1	-1.8545	-1.7969	-1.7869	-1.5726	-1.7129	-1.7869	-1.4896	-1.7446	-1.8339
3	3 Lcp2	-0.9092	-0.8883	-1.0265	-0.9341	-1.077	-0.9377	-0.8439	-0.8676	-0.9163
3	3 Leprotl1	-0.8331	-0.4697	-0.5758	-0.3148	-0.68	-0.4077	-0.9114	-0.7676	-1.2407
3	3 Lgals7	-2.819	-2.3413	0.3695	[illegible]	[illegible]	0.2482	-0.7046	[illegible]	-3.2795
3	3 Lgmn	-1.5048	-1.7785	-1.5708	-2.0929	-1.8596	-2.0059	-2.1082	-1.8309	-2.3286
3	3 Lilrb4	-1.0556	-1.0951	-1.122	-1.072	-1.1633	-1.0851	-1.1703	-1.1703	-1.0173
3	3 Lpar3	-1.8369	-1.6873	-1.6904	-1.4513	-1.7765	-1.6935	-1.6628	-1.5434	-1.6209
3	3 Lpar6	-2.2636	-1.3478	-1.5266	-1.0454	-0.8998	-1.0129	-0.2787	-0.5041	-2.106
3	3 Lpxn	-1.5738	-1.3581	-1.5248	-1.1382	-1.3214	-1.2061	-1.3439	-1.512	-1.512
3	3 Lrmp	-3.5547	-3.1081	-1.6474	-1.2152	-1.1598	-0.7697	-1.9476	-1.1003	-2.1685
3	3 Lst1	-1.4386	-1.7798	-1.9612	-1.8583	-1.7798	-1.725	-1.9479	-1.6723	-1.6533
3	3 Ltc4s	-1.2072	-0.8763	-1.338	-1.2462	-1.3033	-1.2233	-1.1881	-1.0639	-1.0962
3	3 Lyl1	-1.4906	-1.5932	-1.151	-1.3917	-1.2314	-1.2934	-1.237	-1.3642	-1.3856
3	3 Lypd2	-3.3597	-2.028	-1.9878	-1.5141	-1.8873	-1.3565	-2.1782	-0.82	-3.8101
3	3 Lypd3	-3.6158	-3.4666	-1.4427	-1.7804	-0.7673	-1.0345	-1.316	-1.4989	-3.3549
3	3 Man2b1	-0.3702	-0.778	-1.0631	-0.9905	-1.2127	-1.0035	-1.3152	-1.0496	-1.3248
3	3 Mapk13	-2.3188	-2.4129	-1.212	-1.2447	-0.1492	-0.091	-0.7674	-0.5263	-2.2486
3	3 Matn4	0.0848	-0.6896	-1.2017	-1.5891	-1.5829	-1.4126	-1.608	-1.6336	-1.4749
3	3 Mboat1	-1.585	-0.964	-0.4261	-0.1631	[illegible]	-0.1613	-0.8467	-0.3021	-1.7919
3	3 Mertk	-0.7167	-0.9061	-1.2437	-1.3316	-1.0598	-1.3852	-1.2962	-1.53	-1.0951
3	3 Mfsd1	-0.6369	-0.6038	-0.6006	-0.7904	-0.6968	-1.0402	-0.7978	-1.009	-0.9785
3	3 Mgl2	-1.2444	-1.2819	-1.1689	-0.9524	-1.1721	-0.8109	-1.1466	-1.1721	-1.1721
3	3 Mgst3	-0.9926	-0.7344	-0.7132	-0.8106	-0.4841	-0.3958	-0.8785	-0.5658	-1.62
3	3 Mmp9	-1.6494	-1.0977	-1.7517	-1.7578	-1.5724	-1.8751	-1.3612	-1.3635	-1.3635
3	3 Msln	-2.5845	-0.7586	0.405	0.9334	[illegible]	0.4782	-1.0515	0.1047	-3.491
3	3 Mtap2	-0.2504	-0.6935	-1.0704	-1.0308	-0.8692	-0.5757	-1.0276	-0.4101	-1.629
3	3 Mtus1	-0.2529	-0.4436	-1.2411	-0.8868	-1.3316	-0.9107	-1.4224	-0.826	-0.3451
3	3 Mustn1	-0.8743	-0.2216	-0.999	-0.9658	-1.4738	-1.5909	-1.6332	-1.4016	-1.5498
3	3 Myd88	-0.2231	-0.7712	-1.0608	-1.2017	-1.6172	-1.7016	-1.9251	-1.9477	-1.8572
3	3 Myo1f	-2.2042	-2.3417	-2.096	-2.328	-2.2105	-2.3011	-1.8961	-2.1047	[illegible]
3	3 Myo1g	-1.9383	-1.6893	-1.6448	-0.7841	-1.1847	-0.3455	-1.7323	-0.6781	-0.5128
3	3 Myzap	-0.761	-0.8279	-0.8918	-1.1027	-0.7592	-0.6005	-0.9652	-0.4727	-1.3219
3	3 Nat1	-1.3474	-1.2693	-1.2157	-1.1167	-0.8734	-0.756	-1.204	-1.0552	-1.2573
3	3 Nccrp1	-4.2543	-2.025	-0.4928	0.844	0.4569	1.3442	[illegible]	0.8824	-4.6293
3	3 Ndrg1	-1.1763	-2.1728	-0.7564	-1.1636	0.2847	[illegible]	0.2159	0.2933	-2.4331
3	3 Neu1	-1.3974	-1.8418	-1.0617	-1.3806	-0.8796	-1.0633	-1.3081	-1.1225	-0.8928
3	3 Nlrc3	-0.6558	-0.667	-1.0323	-1.2426	-1.1905	-1.3835	-1.1427	-1.1611	-1.0468
3	3 Nod1	-1.3389	-1.5082	-0.808	-0.6544	-0.1384	[illegible]	-0.8366	[illegible]	-2.8662
3	3 Nrcam	-1.2071	-1.1466	-1.2614	-1.1589	-1.6764	-1.8189	-0.6749	-0.7788	-1.7397
3	3 Nt5c3	-1.765	-1.5303	-0.8295	-0.8937	-0.747	-0.7025	-1.1709	-0.9022	-2.0518
3	3 Ntrk3	-0.8699	-0.7169	-0.5459	-0.7692	-0.8106	-0.7913	-0.684	-0.7913	-0.6432
3	3 Nudt11	-1.822	-1.8145	-1.4214	-1.2113	-1.1853	-0.6879	0.2739	-0.1942	-0.1179
3	3 Nudt16	-0.8321	-0.8186	-0.5968	-0.9323	-0.9559	-0.9393	-1.5921	-0.9775	-1.5212
3	3 Oat	-0.1616	-0.3483	-1.5848	-1.4415	-1.51	-1.4278	-1.4203	-1.3156	-1.584
3	3 Odz4	-1.3538	-1.2612	-0.739	-0.663	-1.022	-0.9181	-1.507	-1.3556	-1.8986
3	3 Osbpl3	-1.4218	-1.0185	-0.7181	-0.2695	-0.7502	-0.8826	-1.4521	-1.0881	-2.3733

3	3 Osm		-1.917	-1.9555	-1.9265	-1.7331	-1.787	-1.9329	-1.6466	-1.9201	-1.1333
3	3 Ostf1		-0.9103	-0.8123	-0.8561	-0.7178	-0.7183	-0.5582	-1.2707	-1.0287	-1.8952
3	3 Otx1		-2.1135	-2.1488	-1.8664	-1.6532	-2.0214	-1.8505	-1.5107	-1.5191	-2.2018
3	3 P2rx4		-0.5432	-0.5275	-1.0212	-0.8201	-1.0645	-0.8068	-1.5104	-1.3381	-1.7865
3	3 P2ry13		-1.0431	-1.023	-1.0098	-0.955	-1.0464	-0.7851	-1.0944	-0.9206	-0.9741
3	3 Palmd		-0.5492	-0.7694	-0.4637	-0.8134	-1.6195	-1.3852	-2.0375	-1.9544	-2.422
3	3 Parm1		-1.4247	-1.7068	-0.7378	-1.6548	-1.287	-2.0185	-1.7446	-1.8616	-2.8259
3	3 Pcdh20		-1.0831	-0.848	-1.3775	-1.3976	-1.5137	-1.4991	-1.3544	-1.2653	-1.2439
3	3 Pfkfb4		-0.7137	-0.4436	-0.8931	-0.7369	-0.785	-0.784	-0.837	-0.7052	-1.0323
3	3 Pfkp		-2.7612	-1.7971	-1.2785	-0.5224	-0.4943	[illegible]	-0.8899	-0.6604	0.6131
3	3 Pik3cd		-0.8036	-1.0778	-0.8006	-0.9294	-0.7263	-1.0152	-0.696	-0.9684	-0.3655
3	3 Pik3cg		-1.0754	-1.2589	-0.9821	-1.2068	-1.3199	-1.2359	-1.2293	-1.3164	-1.2328
3	3 Pip4k2a		-0.3294	-0.8545	-0.8377	-0.918	-0.7893	-1.004	-1.0332	-1.4637	-1.3313
3	3 Pira4		-0.6799	-0.8886	-0.9231	-0.6624	-0.7586	-0.7648	-0.7555	-0.7555	-0.7097
3	3 Pkp1		-2.3076	-1.3405	[illegible]	[illegible]	[illegible]	[illegible]	-0.9837	[illegible]	-2.8794
3	3 Pla2g15		[illegible]	[illegible]	-1.5121	-1.2052	-1.7889	-1.5524	-1.1428	-1.5019	[illegible]
3	3 Plcg2		-2.2005	-2.0485	-1.7973	-1.7719	-1.2937	-1.1769	[illegible]	-0.9027	[illegible]
3	3 Plek		-1.6417	-2	-2.1666	-2.2029	-2.1633	-2.0699	-2.214	-2.027	-2.1699
3	3 Plek2		-1.4878	-1.2916	-0.8666	-0.4942	-0.6206	-0.3915	-1.1756	-0.7059	-1.2939
3	3 Pmch		-2.0351	-1.76	-1.3535	-1.7863	-1.9054	-2.1297	-2.15	-2.2345	-2.1776
3	3 Pon2		-0.7563	-0.6416	-0.8119	-1.0823	-1.2242	-1.6823	-1.2796	-1.6971	-1.9032
3	3 Popdc3		-0.9526	-0.5256	-0.419	[illegible]	-0.7009	-0.7815	-1.0013	-0.8884	-1.0039
3	3 Ppp1r3c		-0.4999	-0.7275	-1.3746	-1.4212	-1.5687	-1.5172	-1.3294	-1.2512	-0.5569
3	3 Pqlc1		-0.5094	-1.1213	-0.6211	-0.4395	-0.6587	-0.7398	-1.5797	-1.1336	-1.7552
3	3 Prkch		-1.827	-1.5567	-0.9394	-0.9176	-0.6008	-0.8647	-0.8577	-1.0067	-1.7969
3	3 Prokr1		-0.4563	-0.8578	-0.9156	-0.9519	-0.6862	-1.0082	-1.0413	-1.1337	-1.2678
3	3 Prom2		-1.7329	-1.767	-0.8321	-0.8303	0.4293	[illegible]	[illegible]	[illegible]	-1.7963
3	3 Psca		-1.16	-1.0138	-0.9301	-0.989	-0.8215	-1.0909	-0.9407	-1.0391	-0.9863
3	3 Psmd4		-1.558	-0.9503	-0.8526	-0.3411	-0.7542	[illegible]	-1.1797	-0.824	[illegible]
3	3 Ptpn18		-1.9009	-1.9898	-2.1138	-1.9463	-1.7239	-1.7324	-1.7582	-1.6685	-1.9629
3	3 Ptpn6		-2.4343	-2.6357	-1.2188	-1.7543	[illegible]	-0.7253	[illegible]	[illegible]	-0.6343
3	3 Ptpre		-1.0217	-0.9258	-0.3187	-0.5604	-0.3563	[illegible]	-0.8078	-0.4011	-2.1997
3	3 Ptpro		-1.0412	-1.1618	-0.9449	-0.9005	-1.1204	-1.1723	-1.263	-1.2043	-1.0476
3	3 Pwwp2b		-0.5173	-0.8957	-0.9027	-0.8556	-0.8764	-0.4718	-1.1269	-0.7869	-1.1438
3	3 Pygl		-1.3713	-1.6343	-0.8389	-1.1016	[illegible]	-0.4737	-0.3694	-0.6052	-1.5995
3	3 Rab11fip5		-1.016	-0.7006	-0.8393	-0.7985	-1.7334	-1.7276	-2.6024	-2.0389	-2.5021
3	3 Rab31		-1.0399	-1.208	-1.3102	-1.064	-1.2536	-1.3784	-1.5812	-1.6169	-1.5032
3	3 Rab3il1		[illegible]	-0.4928	-1.2199	-1.5903	-1.4677	-1.6031	-1.5493	-1.3988	-0.9478
3	3 Rab8b		-1.2254	-1.1762	[illegible]	[illegible]	[illegible]	[illegible]	-0.907	-0.4882	-2.0771
3	3 Rabac1		-0.5165	-0.5109	-0.7333	-1.1587	-0.9613	-1.0584	-1.1796	-1.239	-1.456
3	3 Rac2		-1.0139	-1.007	-0.9522	-0.9522	-0.9896	-0.8487	-1.0458	-0.9828	-0.8899
3	3 Ramp3		-2.0197	-1.4599	[illegible]	-0.3077	-0.6445	-0.594	-1.1562	-0.7899	-1.4642
3	3 Rasl11b		[illegible]	-1.0495	-1.254	-1.481	-1.7045	-1.839	-0.977	-1.2904	[illegible]
3	3 Rassf1		-0.688	[illegible]	-0.7166	-0.7886	-1.3183	-0.9425	-1.7919	-1.6292	-2.5865
3	3 Rassf2		-0.4715	-0.7371	-1.4172	-1.2997	-1.8044	-1.6402	-1.7095	-1.6855	-1.934
3	3 Rassf4		-1.285	-1.3935	-1.4628	-1.4393	-1.1002	-1.4494	-1.3367	-1.4032	-1.1702
3	3 Rassf5		[illegible]	-0.6166	-1.399	-1.1844	-1.088	-1.4485	-1.3659	-1.0831	-0.8933
3	3 Rcan1		-0.804	-1.0267	-0.4481	-0.3613	-0.5869	-0.4124	-0.8702	-0.7528	-0.9944
3	3 Rcan3		-0.808	-0.9339	-1.1011	-0.7936	-0.8002	-0.7089	-0.951	-0.9479	[illegible]
3	3 Rcsd1		-1.0792	-1.1422	-1.0841	-1.2913	-1.1577	-0.9495	-0.8856	-0.9723	-1.2243
3	3 Reep1		-2.7114	-1.922	[illegible]	[illegible]	[illegible]	-0.7446	-1.1995	-1.2419	-2.5088
3	3 Reln		-2.4538	-2.2608	-1.7948	-1.5543	-2.2908	-1.9622	-1.991	-1.9666	-2.0296
3	3 Ret		-1.8469	-1.3023	-1.4005	-0.9159	-0.9444	-0.8393	-1.2556	-0.6562	-1.5807
3	3 Retsat		-1.0933	-0.5727	-1.0677	-0.489	-0.9802	-0.623	-1.5359	-1.0664	[illegible]
3	3 Rnf135		-0.5706	-0.3836	-0.8315	-0.6566	-1.0453	-0.8463	-1.0655	-1.1951	-0.4253
3	3 Rnpep		-1.1644	-0.8278	-1.0879	-0.8761	-0.9885	-0.8233	-0.9259	-0.885	-0.9447
3	3 Rpl24		-1.6254	-1.5498	-1.2991	-1.3233	-1.4774	-1.3886	-1.5917	-1.5072	-0.9785
3	3 Rpl7a		-2.764	-1.9632	-1.8309	-1.6892	-1.7009	-1.5919	-2.3962	-1.6975	-1.1449
3	3 Rps9		-1.0918	-0.7015	-0.7403	-0.8048	-0.6149	-0.6573	-0.7597	-0.7415	-0.9901
3	3 Ryr3		-1.415	-1.5983	-1.0437	-1.2721	-1.426	-1.5707	-1.5798	-1.6046	-1.0887
3	3 S100a1		-0.6746	-0.8893	-0.668	-0.3131	-0.989	-0.4932	-1.5745	-0.9089	-2.6095
3	3 S100a16		-0.7522	-0.872	-0.6625	-0.6584	-0.4532	-0.5428	-0.9193	-0.8506	-1.1763
3	3 Samsn1		-0.9596	-0.9323	-0.6298	-0.8477	-0.7177	-0.9906	-1.0877	-0.8392	-1.0063
3	3 Sash3		-1.3769	-1.4413	-1.4413	-1.4709	-1.4561	-1.4268	-1.3492	-1.3526	-1.4304
3	3 Sbsn		-1.0501	-0.5136	-1.3072	-0.939	-1.1055	-0.9058	-1.2334	-1.1804	-1.2488
3	3 Scamp5		-0.6707	-0.8055	-0.9524	-0.8696	-1.226	-1.1419	-1.0648	-1.0464	[illegible]
3	3 Scin		-1.3745	-1.2889	-1.2576	-1.4178	-1.0859	-1.0859	-1.3237	-1.1972	-1.3414
3	3 Sdcbp2		-1.3219	-1.8326	-0.818	-1.0368	-0.5925	-0.4369	-0.6624	-1.157	-0.7565
3	3 Sele		-0.7558	-0.9763	-0.5421	-0.7189	-0.4601	-0.5901	-0.8916	-0.8511	-0.9107
3	3 Selenbp1		-1.7199	-1.3391	-0.6002	-1.2398	-0.419	-0.5341	-1.0504	-0.7109	-1.6236
3	3 Selplg		-1.1561	-0.9938	-1.2301	-1.1155	-0.9816	-1.241	-1.1055	-1.0438	-1.1357
3	3 Serhl		-0.7477	-0.7685	-0.935	-0.779	-0.6192	-0.7727	-0.8933	-1.2999	-0.9951
3	3 Serp1		-0.6537	-0.4848	-0.7578	-0.5746	-0.8436	-0.9658	-1.2431	-1.1204	-1.4886
3	3 Serpinb6c		-0.8967	-0.7255	-1.3914	-1.3667	-1.3759	-1.246	-0.9394	-1.1478	1.162
3	3 Sesn1		-1.4791	-1.5592	-1.417	-1.804	-1.5888	-1.7718	-1.4667	-1.6319	-1.9777
3	3 Sh3bp2		-0.9279	-0.9527	-0.2576	-0.3512	-0.7926	-0.5696	-1.3512	-0.8682	-1.4336
3	3 Sla		-1.69	-1.5104	-1.5796	-1.6155	-1.7323	-1.7576	-1.7833	-1.7467	-1.6693
3	3 Slc15a3		-2.0345	-1.9734	-1.4729	-1.5522	-1.8136	-1.9524	-1.8487	-1.667	-1.942
3	3 Slc25a45		-2.5867	-2.4947	-1.6111	-1.3542	-1.4492	-1.0308	-2.048	-1.3454	-3.2235
3	3 Slc2a6		-3.0314	-2.2597	-1.292	-0.5003	-1.3291	-1.1941	-2.5216	-1.7268	-2.8931
3	3 Slc35d3		-1.7213	-1.5709	-0.8702	-0.659	-0.3493	-0.2317	-0.9229	-0.2021	-1.8823
3	3 Slc38a5		-5.6064	-4.8942	-0.0301	-0.1618	0.4332	0.6579	-0.6815	0.6691	-5.3905
3	3 Slc40a1		-1.357	-2.0884	-2.2625	-2.6086	-1.4097	-2.018	-0.9215	-1.4005	-2.4995
3	3 Slc46a3		-1.4236	-1.6399	-0.419	-1.098	-0.2362	-0.5616	-0.7041	-0.9362	-0.9082
3	3 Slc48a1		-0.5196	-0.7167	-1.2067	-1.1867	-1.3681	-1.6263	-1.7415	-1.6447	-1.5611
3	3 Slc6a9		-0.3198	-0.5718	-1.4235	-1.0991	-1.9523	-1.6295	-1.8303	-1.6047	-0.772
3	3 Slc7a8		-1.3608	-1.6577	-1.4083	-1.6821	-1.6699	-1.6072	-1.4575	-1.6337	-1.584
3	3 Slurp1		-1.6769	0.1573	-0.6429	0.0706	-1.5719	-1.0573	-2.0474	-1.2859	-2.4624
3	3 Smap2		-0.5423	-0.5611	-0.893	-0.8232	-1.0243	-0.9489	-0.9521	-1.0037	-0.716
3	3 Snrpg		-1.629	-1.143	-1.0856	-0.9568	-0.7561	-0.6633	-0.5229	-0.7592	-0.172
3	3 Snx21		-0.6909	-0.912	-0.7117	-0.8594	-0.9792	-0.7815	-1.4357	-0.9954	-1.7471
3	3 Soat1		-0.4704	-0.3199	-1.2717	-1.0408	-1.0052	-1.0031	-0.6338	-0.7945	-0.9623
3	3 Sort1		-1.8214	-1.818	-1.6107	-1.8587	-1.4274	-1.9083	-0.6867	-1.1703	-1.7358
3	3 Sprr2d		-2.3159	-2.1021	-1.4642	-1.6891	-0.3473	-1.4001	-1.0073	-2.0508	-2.5312
3	3 St3gal3		-0.4724	-0.6585	-0.9583	-0.9091	-0.901	-0.9358	-1.2195	-1.1564	-0.5729
3	3 St3gal6		-1.891	-0.9366	-0.0571	0.1471	-0.4061	-0.5413	-1.7875	-1.0332	-5.3912
3	3 St6gal1		-2.1662	-1.5104	-1.9504	-1.2304	-2.177	-2.2547	-0.7106	-1.1193	-0.918
3	3 St8sia4		-0.6699	-0.5949	-0.9889	-1.0062	-0.8776	-0.6195	-0.8708	-0.6233	-1.0062
3	3 Stambp		-0.574	-0.6282	-0.4246	-0.4813	-0.4289	-0.6394	-1.3085	-0.7835	-1.7953
3	3 Stard8		-1.8444	-1.9821	-2.3412	-2.3242	-2.2078	-2.1172	-1.8607	-1.7928	-0.46
3	3 Sult1a1		-0.6699	-1.2925	-0.8966	-1.1886	-0.7914	-1.4739	-1.596	-1.5767	-1.8398
3	3 Sumo1		-1.091	-1.2018	-1.0459	-0.9138	-1.3538	-0.787	-1.0289	-0.8571	[illegible]
3	3 Syt16		-1.6387	-1.6208	0.1913	-0.2677	-0.3354	-0.935	-1.175	-1.4121	-2.056
3	3 Sytl1		-1.744	-1.3378	-0.8134	-0.3605	[illegible]	0.23	-0.3266	[illegible]	-1.7937
3	3 Tacstd2		-2.3955	-1.913	-0.2151	-0.9665	0.9166	[illegible]	0.3938	[illegible]	-1.9796
3	3 Tbxas1		-0.8618	-0.681	-0.6022	-0.7288	-0.6449	-0.6474	-0.8382	-0.8151	-0.6784
3	3 Tfap2b		-0.4497	-0.9147	-1.0397	-1.4468	-1.4126	-1.3067	-1.1388	-1.6214	-1.533
3	3 Tgfbrap1		-0.5472	-0.6253	-0.7201	-0.8413	-1.1245	-1.2918	-1.5944	-1.3434	-1.8092
3	3 Tha1		-1.235	-0.7572	-0.8735	-0.4703	-0.6433	-0.6579	-0.9316	-0.7706	-1.5368
3	3 Tlr13		-1.2029	-1.3316	-1.284	-1.1624	-1.1966	-1.3212	-1.3212	-1.0876	-1.284
3	3 Tlr2		-0.8094	-1.1043	-0.5729	-0.9107	-1.0215	-1.4333	-1.5786	-1.5396	-1.6371
3	3 Tlr6		-0.279	-0.7649	-0.9225	-0.9069	-0.6934	-1.0506	-0.8078	-0.7734	-0.9162
3	3 Tlr7		-1.9588	-1.6991	-1.7277	-1.5437	-1.8355	-1.8958	-1.8417	-1.8669	-1.7306
3	3 Tm6sf1		-1.083	-1.1502	-1.1338	-1.2324	-1.1752	-1.1015	-1.3381	-1.3164	-0.9405
3	3 Tmem106a		-0.3297	-0.9368	-0.6084	-0.8691	-0.6006	-0.7254	-1.0104	-0.7084	-0.9795
3	3 Tmem184a		-1.3517	-0.8521	-0.3866	-0.3194	-0.5426	-0.2646	-0.5561	-0.3168	-1.5415
3	3 Tmem205		-0.4234	-0.5031	-0.8988	-1.0693	-1.0214	-1.1385	-1.2677	-0.9655	-1.021
3	3 Tmem51		-1.5396	-1.5982	-1.7306	-1.868	-1.117	-1.1034	-0.7854	-0.458	0.3086
3	3 Tmem8		-1.1606	-0.9272	-1.074	-1.1209	-1.1434	-1.0876	-0.8416	-0.8119	0.5493
3	3 Tnfaip8l2		-1.3063	-1.1651	-1.2805	-1.1651	-1.2199	-1.2989	-1.3249	-1.2375	-1.1684
3	3 Tnfrsf25		-1.1682	-1.1998	-1.2753	-1.0453	-0.9347	-1.0626	-0.932	-1.2619	-0.6439
3	3 Tnn		-0.117	-0.4641	-1.4299	-1.5437	-1.469	-1.5195	-1.5648	-1.5368	-1.5093
3	3 Tnni2		-0.8562	-0.8037	-0.5957	-0.7951	-0.3023	-0.6722	-0.5565	-0.8592	-0.9902
3	3 Trappc6a		-0.6876	-0.723	-1.0333	-0.7502	-0.9667	-0.6037	-1.2215	-0.9533	-0.8862
3	3 Trp63		-0.7657	-0.505	-0.4701	-0.9206	-1.1299	-1.306	-1.1145	-1.1017	-1.5615
3	3 Trpc4		-1.2902	-1.3812	-0.3401	-0.3605	-0.2644	-0.6666	-0.8445	-1.0782	-1.3847
3	3 Tspan32		-1.5775	-1.264	-0.9071	-0.716	-1.2888	-0.9861	-1.7053	-1.0009	-1.8027
3	3 Tspan7		-1.5512	-2.057	-0.2102	-0.523	-0.4	-0.1334	-0.451	-0.4012	-1.9241
3	3 Tspan8		-2.2221	-1.7376	-0.5129	-0.4508	-0.4419	-0.6056	-1.6117	-1.1003	-2.5186
3	3 Tuft1		-2.1891	-1.8394	-0.1548	-0.456	-0.0672	0.0786	-0.7199	-0.6042	-1.8113
3	3 Txnip		-1.1644	-1.2318	-1.8722	-1.3013	-1.2314	-0.9218	-1.5002	-0.6865	0.2927
3	3 Unc93b1		-0.9853	-1.1609	-1.2542	-1.1281	-1.173	-1.0961	-1.3574	-1.3032	-1.2319
3	3 Upk1b		-0.9387	-1.3304	-0.2946	-1.2812	-1.2082	-1.3032	-1.2174	-1.2716	-1.8163
3	3 Upk3b		-0.7047	-0.9299	0.144	-0.9703	-0.9077	-0.7391	-1.2395	-0.9424	-0.8106
3	3 Ush1c		-2.871	-2.6904	-1.2553	-0.3124	-0.6166	0.1883	-1.1849	-0.4162	-1.7132
3	3 Vamp8		-0.5746	-0.9204	-0.7272	-0.8901	-1.0996	-1.0283	-1.6377	-1.376	-2.614
3	3 Was		-1.5743	-1.5364	-1.733	-1.5871	-1.6297	-1.6873	-1.5839	-1.6066	-0.9318
3	3 Xpa		-0.4875	-0.5973	-0.6335	-0.7272	-0.8532	-0.7712	-0.8248	-0.9731	-1.2197
3	3 Ydjc		-2.2348	-0.9817	-1.4799	-0.2391	-0.8003	-0.308	-0.976	-0.4572	-0.6418
3	3 Ypel3		-0.5728	-0.7819	-0.2934	-0.495	-0.6927	-0.7899	-1.2608	-0.9925	-2.0914
3	3 Zc3h12d		-0.7007	-0.7742	-0.7204	-0.8159	-0.7984	-0.7914	-0.7708	-0.7204	-0.7605
3	3 Zdhhc14		-0.6496	-1.1428	-0.9222	-0.9825	-1.3372	-1.2245	-1.4951	-1.562	-1.4161
3	3 Zer1		-0.4551	-0.5584	-0.5315	-0.8002	-0.8256	-0.7555	-0.76	-0.9276	-0.9716
3	3 Msx1		0.426	-1.2791	-1.372	-2.1951	-1.9441	-2.3609	-1.0278	-1.6762	-2.5456
3	3 Sepp1		-0.4497	-1.8375	-0.9375	-2.2263	-1.863	-2.3026	-2.0217	-2.2296	-3.0419
3	3 4732456N10Rik		-5.3298	-3.8625	-4.4889	-3.8129	-5.4236	-5.4914	-5.5265	-5.7875	-5.9081
3	3 Aif1		-2.6135	-2.6448	-2.5114	-2.6849	-2.5905	-2.3981	-2.8006	-2.5778	-2.6581
3	3 Alox5ap		-3.1739	-3.3657	-3.8142	-3.5277	-3.5843	-3.6736	-3.1937	-3.274	-2.4326
3	3 Angptl4		-1.8451	-1.4122	-3.1326	-2.8223	-2.7986	-2.8733	-2.9429	-2.9918	-2.1208
3	3 Apoc4		-2.3126	-2.2573	-2.3736	-2.2994	-2.3736	-2.4445	-2.4015	-2.5001	-2.2071
3	3 Bglap		-3.1076	-2.9518	-3.0663	-3.0322	-3.1941	-3.1569	-3.2044	-3.2253	-3.2044
3	3 Bglap2		-4.4347	-4.5626	-4.7172	-4.94	-5.0446	-5.0506	-5.0843	-5.103	-5.0446
3	3 Bglap-rs1		-3.1394	-3.0281	-3.1326	-3.1949	-3.2599	-3.2234	-3.1057	-3.0925	-3.2126
3	3 Btk		-2.4453	-2.4809	-2.4666	-2.2887	-2.4918	-2.3336	-2.273	-2.3732	-2.414
3	3 C1qa		-2.3253	-2.3356	-2.4239	-2.3598	-2.3152	-2.4166	-2.2917	-2.3118	-2.3424
3	3 C1qb		-6.0898	-6.0135	-6.0202	-5.7714	-6.1332	-6.0304	-6.1332	-6.1041	-6.0407
3	3 C1qc		-5.0684	-4.9382	-5.1691	-4.9442	-5.0651	-5.1691	-5.1246	-5.0716	-5.1045
3	3 C3		-0.9349	-1.5737	-1.6413	-2.4334	-3.1941	-3.2929	-3.4202	-3.2649	-3.6105
3	3 Casp1		-3.0078	-3.1692	-3.1657	-3.1553	-3.0747	-3.1553	-3.2044	-3.0489	-3.2333
3	3 Ccl12		-2.8729	-3.0673	-3.0313	-2.8507	-2.972	-3.0783	-3.0384	-2.9583	-3.0783
3	3 Ccl3		-2.1518	-2.2381	-2.3391	-2.3452	-2.5868	-2.4744	-2.4983	-2.5051	-2.3116
3	3 Ccl9		-2.0758	-2.2908	-2.9191	-3.0242	-3.6142	-3.4216	-3.2487	-3.452	-3.4384
3	3 Cd14		-2.3502	-2.5534	-2.981	-2.6457	-2.7926	-2.3128	-2.8811	-2.4765	-3.1004
3	3 Cd52		-3.668	-3.5298	-3.5488	-3.2029	-3.533	-3.3753	-3.4866	-3.4066	-3.272

3	3 Cd53		-2.0504	-1.7734	-2.3283	-2.2118	-2.4104	-2.3737	-2.3836	-2.3283	-2.4274
3	3 Cd68		-3.315	-3.1073	-2.4463	-2.7	-2.0148	-1.9566	-2.2836	-2.0373	-2.5891
3	3 Cfp		-3.2672	-2.9085	-3.2512	-2.7096	-3.1518	-3.2456	-2.8688	-2.8737	-2.1861
3	3 Cldn11		-5.0184	-4.027	-0.9029	-1.0862	-0.7875	-0.5406	-1.7313	-1.2439	-6.9658
3	3 Clec4d		-2.2405	-2.2736	-2.0536	-2.2018	-2.2537	-2.3777	-2.2307	-2.3958	-2.3109
3	3 Ctsh		-1.5934	-1.7401	-2.4106	-2.6895	-2.1747	-2.4754	-2.2721	-2.4106	-2.0771
3	3 Egr2		-1.2421	-1.9073	-1.6065	-2.3791	-1.8476	-2.5174	-2.5733	-2.531	-4.6783
3	3 Emr1		-4.0323	-4.2562	-4.1743	-4.0144	-4.171	-4.2668	-4.171	-4.1063	-4.2457
3	3 Evi2a		-2.4144	-2.4005	-2.4249	-2.4109	-2.2687	-2.4858	-2.2437	-2.4005	-2.307
3	3 F13a1		-4.7816	-4.6696	-4.7262	-4.7571	-4.7194	-4.6278	-4.7745	-4.7026	-4.9339
3	3 Fcer1g		-4.7785	-4.7439	-4.5657	-4.4675	-4.898	-4.8042	-4.8604	-4.6303	-4.8437
3	3 Fcgr3		-4.1646	-4.0184	-4.1241	-4.0655	-3.9344	-3.7772	-3.8661	-3.7642	-4.0184
3	3 Fcgr4		-3.2646	-3.203	-3.3462	-3.3817	-3.2547	-3.2514	-3.3781	-3.3533	-3.2879
3	3 Fcrls		-3.9822	-4.1583	-4.1159	-4.1583	-4.1924	-4.2967	-4.2502	-4.1041	-4.1583
3	3 Fgd2		-2.7853	-2.7189	-2.5336	-2.57	-2.5366	-2.4018	-1.9199	-1.9637	-2.2487
3	3 Gdf10		-0.3651	-1.4218	-3.3459	-3.5271	-3.2534	-3.4577	-3.4289	-3.5823	-3.367
3	3 Gkn1		-3.1547	-3.0958	-3.2462	-2.9242	-3.1611	-3.2462	-3.3366	-3.2529	-3.2495
3	3 Krt14		-5.07	-3.3278	-1.903	-1.7961	-2.6164	-1.4355	-3.091	-1.1748	-5.286
3	3 Laptm5		-5.6177	-3.8837	-2.3997	-1.3754	-2.1698	-1.1093	-2.8517	-1.74	-1.7919
3	3 Lbp		-2.6215	-2.3489	-2.8693	-2.9941	-3.5892	-3.7914	-4.2673	-4.1853	-4.7946
3	3 Lmo2		-2.9695	-2.3335	-3.0571	-3.0596	-3.3724	-3.2062	-2.5294	-2.5935	-2.9604
3	3 Lrrc33		-3.0514	-2.8919	-2.5248	-2.8183	-2.5332	-2.6653	-2.2882	-2.6043	-2.2776
3	3 Ltf		-3.213	-3.1276	-0.6412	-1.1614	-1.5627	-2.0611	-2.7737	-2.8477	-3.656
3	3 Luzp2		-2.6837	-2.04	-2.5168	-2.2565	-2.5442	-2.536	-2.7145	-2.6269	-2.6357
3	3 Ly6g6c		-4.0191	-3.9145	-2.5448	-1.6607	-1.0506	-0.9733	-1.7817	-1.2972	-3.633
3	3 Ly86		-2.2829	-2.2396	-2.331	-2.331	-2.1818	-2.1383	-2.2663	-2.2528	-2.2495
3	3 Lypd1		-2.1072	-3.0049	-2.3268	-2.797	-2.7593	-3.0632	-3.0578	-3.1325	-3.4139
3	3 Lyz1		-7.2503	-6.7799	-8.0865	-6.0834	-8.0645	-8.3919	-8.4102	-8.4164	-8.3738
3	3 Lyz2		-5.9046	-5.6013	-6.4742	-5.2106	-6.3787	-6.4359	-6.4848	-6.3173	-6.3492
3	3 Clec10a		-3.6228	-3.5261	-3.5418	-3.4356	-3.6195	-3.6161	-3.6328	-3.5168	-3.5898
3	3 Mrc1		-5.2823	-5.184	-4.9374	-5.1774	-5.2239	-5.0766	-5.0736	-4.8181	-4.5881
3	3 Ms4a6d		-3.2318	-3.1441	-2.9721	-3.0885	-3.2152	-3.16	-3.2554	-3.252	-3.0379
3	3 Ms4a7		-2.6322	-2.5477	-2.7727	-2.6288	-2.6972	-2.6056	-2.6422	-2.7113	-2.6729
3	3 Ncf4		-2.3495	-2.3594	-2.3762	-2.4207	-2.4	-2.3661	-2.4207	-2.3007	-2.4
3	3 Nckap1l		-2.9148	-2.6941	-2.7199	-2.7356	-2.9945	-2.6916	-2.8737	-2.8085	-2.2394
3	3 Nrip3		-2.0449	-2.2399	-2.167	-1.9475	-2.3101	-2.2492	-2.1318	-2.48	-1.585
3	3 Otop1		-2.4854	-2.6547	-2.4126	-2.431	-2.3204	-2.3299	-2.4663	-2.3786	-2.9606
3	3 P2ry6		-1.5012	-2.1975	-3.4647	-3.6977	-3.4371	-3.5162	-3.3621	-3.4076	-3.262
3	3 Pf4		-4.325	-4.0969	-4.4919	-3.9853	-4.527	-4.4678	-4.4953	-4.4712	-4.3499
3	3 Pi16		-1.4732	-1.6815	-2.8896	-2.4893	-3.2441	-3.1986	-3.3997	-2.8583	-3.0346
3	3 Pld4		-3.2103	-3.2724	-3.1572	-2.9913	-3.1475	-3.2759	-3.0385	-3.0535	-3
3	3 Ppp1r1b		-2.486	-2.3596	-2.1062	-2.046	-2.1304	-2.0667	-2.1662	-2.1496	-1.8015
3	3 Rgs10		-1.3163	-1.5736	-3.1251	-2.8129	-3.1012	-3.1413	-2.5837	-2.7893	-2.1495
3	3 Sirpa		-1.2081	-1.61	-3.2627	-3.3436	-3.8132	-4.0586	-3.2991	-3.3189	-3.6781
3	3 Slc6a12		-4.3255	-4.2595	-4.3011	-3.4076	-4.0446	-3.5331	-4.3659	-3.8555	-4.0396
3	3 Slco2b1		-1.8714	-2.287	-2.9185	-2.8826	-2.5946	-2.7652	-2.6212	-2.9054	-2.9251
3	3 Slpi		-2.7518	-2.0622	-2.5716	-3.2859	-2.7604	-3.1747	-3.0109	-3.2398	-3.3563
3	3 Stab1		-2.8375	-2.6828	-2.7597	-2.7755	-2.7628	-2.7284	-2.7948	-2.6014	-2.7346
3	3 Trem2		-2.9884	-2.8112	-2.9052	-2.9412	-2.9052	-3.0056	-2.9918	-3.0196	-3.0301
3	3 Trf		-2.4956	-2.4537	-2.7943	-2.5243	-2.5835	-2.5804	-2.6546	-2.617	-1.3333
3	3 Tyrobp		-2.7126	-2.7594	-2.6929	-2.8399	-2.8079	-2.7662	-2.7594	-2.7158	-2.8507
3	3 Vav1		-2.4568	-2.3219	-2.5448	-2.4597	-2.4276	-2.3822	-2.3517	-2.4479	-2.1384
3	3 1700025K23Rik		-0.2592	-0.5938	-0.4751	-0.305	-0.5473	-0.6117	-0.6573	-0.5962	-1.143
3	3 1700088E04Rik		-0.3814	-0.3542	-0.851	-0.6148	-0.4779	-0.4986	-0.5439	-0.2764	-1.254
3	3 1700123O20Rik		-0.3881	-0.3939	-0.6859	-0.3777	-0.537	-0.4221	-0.4461	-0.4127	-1.63
3	3 1810020D17Rik		-0.0697	-0.4314	-0.6355	-0.6779	-0.6125	-0.7948	-0.8719	-0.6201	-0.6169
3	3 1810027O10Rik		-0.7603	-0.6016	-0.9875	-1.0848	-0.6717	-0.6549	-0.9967	-0.7361	-0.1313
3	3 1810046J19Rik		-1.0776	-1.1297	-0.779	-0.7605	-0.4015	-0.4749	-0.6847	-0.0984	-0.4847
3	3 2210418O10Rik		-0.1879	-0.4077	-0.652	-0.6454	-0.8794	-0.9787	-0.8423	-0.8529	-0.1522
3	3 2310002J15Rik		-1.1035	-0.8434	-0.6131	-0.5833	[illegible]	-0.2265	-0.6955	-0.4211	-1.0722
3	3 Emc10		-0.3009	-0.3039	-0.4152	-0.4794	-0.441	-0.5831	-0.6617	-0.4597	-1.2395
3	3 2410001C21Rik		-0.4969	-0.6852	-0.5338	-0.6521	-0.6358	-0.6967	-0.8466	-0.5651	-0.8605
3	3 6330416G13Rik		-0.5453	-0.585	-0.8464	-0.6195	-0.5571	-0.5453	-0.9129	-0.6011	-0.3846
3	3 6720456B07Rik		-0.6597	-0.5354	-0.5014	-0.4923	-0.7212	-0.605	-0.9798	-0.7486	-0.8763
3	3 Akr1b10		-0.6039	-0.5114	-0.8277	-0.392	-0.4017	-0.3802	-0.6642	-0.5437	-1.4276
3	3 Akr1c12		-0.6351	-0.6061	-0.7086	-0.5683	-0.7052	-0.5965	-0.3256	-0.5902	-0.7645
3	3 Anks1		-0.9286	-0.5645	-0.5659	-0.2548	-0.5007	-0.5507	-0.6769	-0.552	-0.794
3	3 Anks3		-0.2362	-0.4348	-0.8925	-0.7845	-0.7863	-0.766	-0.7244	-0.8618	-0.2173
3	3 Aox3		-1.1697	-1.3249	[illegible]	-0.7577	0.6697	[illegible]	[illegible]	-0.1194	-2.41
3	3 Ap2m1		-0.2607	-0.3455	-0.5565	-0.8156	-0.5697	-0.6817	-0.6404	-0.7414	-0.9391
3	3 Atp13a2		-0.627	-0.8369	-0.5335	-0.5257	-0.5897	-0.6291	-0.5257	-0.5375	-0.8763
3	3 Atp6v1e1		-1.0697	-1.0136	-0.2621	-0.3445	-0.3008	-0.3802	-0.7717	-0.7745	-0.7788
3	3 Atp6v1f		-0.513	-0.8961	-0.4942	-0.5091	-0.6109	-0.606	-0.8033	-0.416	-0.707
3	3 AU040320		-0.6343	-0.7564	-0.0832	-0.2321	-0.1662	-0.2222	-0.6895	-0.5592	-1.8646
3	3 BC089491		-0.8934	-0.8127	-0.3723	-0.5889	-0.5121	-0.3648	-0.6333	-0.823	-0.8437
3	3 Bcap29		-1.2291	-0.5711	-0.3495	-0.2313	-0.3233	-0.1844	-0.8821	-0.1901	-1.2518
3	3 Blvra		-1.0467	-1.0325	-0.1852	0.0885	-0.1964	-0.2314	-1.0925	-0.3145	-1.5393
3	3 Bmx		-0.6898	-0.7007	-0.5549	-0.585	-0.5616	-0.5159	-0.6971	-0.5353	-0.5582
3	3 Calcrl		-0.7818	-0.6739	-0.6739	-0.5517	-0.5987	-0.7891	-0.7891	-0.6572	-0.8371
3	3 Calm3		-0.2101	-0.3217	-0.8326	-0.9102	-0.7741	-0.3963	-0.8789	-0.7293	-0.7383
3	3 Calm4		-0.639	-0.6994	-0.7356	-0.8356	-0.7224	-0.7457	-0.3646	-0.6021	-0.7027
3	3 Casp7		-0.4823	-0.569	-0.7045	-0.6944	-0.6743	-0.4437	-0.9712	-0.6207	-0.6562
3	3 Cbfa2t3		-0.3485	-0.3335	-0.3638	-0.2083	-0.609	-0.7364	-0.7364	-0.6458	-1.0733
3	3 Ccdc88b		-0.7963	-0.7963	-0.6781	-0.646	-0.5992	-0.584	-0.5042	-0.6556	-0.4814
3	3 Cdk20		-0.401	-0.3187	-1.1645	-0.9881	-0.8155	-0.9881	-0.7319	-0.9145	-0.3052
3	3 Chst8		-0.5609	-0.6777	-0.7092	-0.9727	-0.9632	-0.7853	-0.4841	-0.8277	-0.2256
3	3 Clca6		-0.7621	-0.81	-0.569	-0.7018	-0.7299	-0.6983	-0.7299	-0.773	-0.6439
3	3 Col17a1		-1.0313	-1.0761	0.2561	-0.439	-0.4537	-0.2949	-0.8192	-1.0591	-0.7338
3	3 Cox7a2l		-0.6607	-0.7047	-0.6837	-0.7983	-0.4993	-0.8404	-0.7627	-1.0165	-0.1985
3	3 Cpn1		-0.7019	-0.5261	-0.9445	-0.2221	-0.9022	-0.7019	-0.8242	-0.9412	-0.1106
3	3 Crip2		-1.1974	-0.3309	[illegible]	0.3333	-0.2268	-0.0712	-0.5207	-0.3797	-2.0435
3	3 Csf2ra		-0.3482	-0.6038	-0.5268	-0.6119	-0.2371	-0.6078	-0.6139	-0.8104	-0.7066
3	3 Ctns		-0.2305	-0.8339	-0.4451	-0.8056	-0.3642	-0.6626	-0.9317	-0.7163	-0.2979
3	3 Dmrta2		-0.8417	-0.7289	-0.628	-0.6206	-0.5657	-0.3479	-0.6507	-0.8858	-0.9594
3	3 Dusp14		-0.8755	-0.6907	0.9805	0.3501	0.1346	-0.1341	-0.681	-0.9261	-2.3488
3	3 Ebi3		-1.0528	-0.7226	-0.8859	-0.6552	-0.8952	-0.6395	-0.8645	-0.6035	-0.2634
3	3 Elfn1		-0.3435	-0.4695	-0.7351	-0.6333	-0.7824	-0.7413	-0.6773	-0.4669	-0.8247
3	3 Erlin1		-1.0157	-0.4438	-0.7563	-0.4643	-0.7819	-0.4569	-1.1775	-0.8399	-0.3581
3	3 Erp29		-0.5547	-0.2846	-0.9379	-0.7103	-0.8625	-0.5569	-0.7569	-0.6027	-0.2044
3	3 Fahd2a		-0.5977	-0.4485	-0.3566	-0.5218	-0.628	-0.7748	-0.7856	-0.6576	-0.5063
3	3 Fam173a		-0.5591	-0.5939	-0.7412	-0.4601	-0.4232	-0.2114	-0.7739	-0.4461	-1.2145
3	3 Fam3b		-1.0169	-0.7193	-0.6244	-0.7783	-0.2188	-0.1682	-0.7994	-0.4537	-1.0736
3	3 Fbxl13		-0.7335	-0.6785	-0.6094	-0.6617	-0.7126	-0.5282	-0.7092	-0.6191	-0.5434
3	3 Fert2		-0.6913	-0.1843	-0.6825	-0.4359	-0.4114	-0.2169	-0.7197	-0.5399	-1.0985
3	3 Fgf13		-0.6542	-0.8356	-0.4306	-0.2207	-0.5831	-0.6615	-0.5488	-0.8489	-0.76
3	3 Gdpd1		-0.9149	-0.6127	-0.3132	[illegible]	-0.3999	-0.3005	-1.0167	-0.4582	-1.1019
3	3 Glb1		-0.6547	-0.5523	-0.4748	-0.7113	-0.6737	-0.4599	-1.0651	-0.8574	[illegible]
3	3 Glg1		-0.6139	-0.7414	-0.9872	-0.8667	-0.7882	-0.7404	-0.5867	-0.9237	-0.2112
3	3 Glycam1		-0.6284	-0.7183	-0.4986	-0.4639	-0.6389	-0.6354	-0.646	-0.6215	-0.5571
3	3 Gm4937		-0.642	-0.7501	-0.6482	-0.6117	-0.6207	-0.5415	-0.5703	-0.5443	-0.5188
3	3 Gm962		-0.7025	-0.4948	-0.8774	-0.4997	-0.5363	-0.2846	-0.4181	-0.5363	-0.9296
3	3 Gng2		-0.4918	-0.7403	-1.0034	-0.9933	-0.9604	-1.1077	-0.3874	-0.6197	0.2257
3	3 Gpha2		-0.3612	[illegible]	-0.5635	-0.6309	-0.737	-0.9445	-0.7711	-0.5958	-0.6668
3	3 H2-DMb1		-0.4814	-0.2764	-0.7589	-0.6567	-0.6915	-0.5614	-0.9932	-0.5795	-0.6937
3	3 H2-Eb1		-0.5727	-0.5832	-0.7964	-0.5753	-0.7131	-0.7781	-0.6816	-0.4812	-0.5648
3	3 H2-Ke6		-0.6282	-0.8298	-0.5771	-0.3083	-0.8869	-0.5581	-1.0149	-0.7823	-0.4441
3	3 Hcst		-0.6357	-0.4085	-0.6357	-0.6479	-0.7009	-0.6664	-0.682	-0.5997	-0.4163
3	3 Hfe		-0.776	-0.7351	-0.8247	-0.7633	-0.5794	-0.6478	-0.7538	-0.7258	-0.642
3	3 Hmox2		-0.6345	-0.2755	-0.7865	-0.9689	-0.8712	-0.778	-0.5215	-0.6794	-0.3689
3	3 Hpse		-0.585	-0.8151	-0.4552	-0.3311	-0.3396	-0.2925	-0.6556	-0.3075	-1.3092
3	3 Idua		-0.2078	-0.515	-0.6172	-0.653	-0.7748	-0.6415	-0.9577	-0.811	-0.6497
3	3 Ikbkg		-0.6241	-0.4894	-0.4139	-0.4185	-0.5927	-0.6356	-0.883	-0.7291	-1.1622
3	3 Ing4		-0.6074	-0.7127	-0.9476	-0.759	-0.7127	-0.6982	-0.8775	-0.8283	-0.3197
3	3 Irf3		-0.7314	-0.4241	-0.9472	-0.4154	-0.6961	-0.3751	-0.9916	-0.4706	-0.9595
3	3 Jmjd8		-0.4647	-0.195	-0.3953	-0.2557	-0.6349	-0.3559	-0.8769	-0.5416	-1.2717
3	3 Lemd2		-0.4309	-0.6237	-0.6063	-0.5939	-0.734	-0.7263	-0.9832	-1.0723	-0.6673
3	3 Lgals4		-0.4248	-0.4838	-0.7013	-0.8869	-0.675	-0.6713	-0.9262	-0.7514	-0.7891
3	3 Lrg1		-0.5992	-0.6263	-0.6208	-0.7758	-0.64	-0.5595	-0.7608	-0.9124	-0.8959
3	3 Lrp4		-0.4455	-0.6407	-0.6822	-0.4435	-0.8428	-1.0809	-0.5697	-0.659	-0.5063
3	3 Lyrm2		-0.2253	-0.4109	-0.6087	-0.5756	-0.5296	-0.6079	-0.5296	-0.5771	-0.854
3	3	41337	-0.7095	-0.6159	-0.3783	-0.4815	-0.5408	-0.4393	-0.7095	-0.7275	-0.7131
3	3 Mllt11		-0.6629	-0.2515	-1.1682	-0.1197	-0.7519	-0.1802	-1.2485	-0.4165	-0.6258
3	3 Muted		-0.5115	-0.7036	-0.6527	-0.4867	-0.7537	-0.6165	-0.983	-0.7934	-0.6838
3	3 Mycbpap		-0.5687	-0.3477	-0.6724	-0.6759	-0.618	-0.7111	-0.4841	-0.5431	-0.585
3	3 Myo9b		-0.258	-0.3558	-0.7189	-0.8417	-0.9293	-0.7909	-0.9846	-0.6663	-0.3388
3	3 N4bp2l1		-0.2331	-0.8293	-0.6201	-0.7356	-0.6264	-0.8245	-0.8149	-0.4673	-0.5952
3	3 Napg		-0.6262	-0.5993	-0.64	-0.4565	-0.5976	-0.6136	-1.0122	-0.6651	-0.4817
3	3 Nat2		-0.6456	-0.5781	-0.8636	-0.2916	-0.4709	-0.411	-0.5736	-0.4171	-1.0622
3	3 Nat9		-0.4505	-0.2344	-0.7373	-0.3757	-0.6272	-0.4952	-0.9742	-0.8011	-0.6176
3	3 Ncf1		-0.642	-0.6232	-0.6157	-0.6307	-0.6382	-0.4704	-0.5898	-0.6269	-0.5219
3	3 Ndfip1		-0.7497	-0.8034	-0.599	-0.2135	-0.4472	-0.0764	-0.3349	-0.9295	-1.257
3	3 Ndufa3		-0.2025	-0.3513	-0.7315	-0.7152	-0.5931	-0.6789	-0.7643	-0.562	-0.9765
3	3 Ndufv3		-0.613	-0.6581	-0.9848	-0.9022	-0.7084	-0.5441	-0.316	-0.3444	-0.697
3	3 Necap2		-0.4207	-0.6416	-0.3455	-0.6284	-0.4887	-0.6832	-0.7942	-0.5315	-1.0571
3	3 Nisch		-0.6786	-0.4341	-0.5958	-0.5556	-0.5014	-0.5372	-0.6314	-0.4907	-0.9018
3	3 Nme2		-1.0397	-0.5718	-0.8391	-0.3736	-0.7335	-0.4866	-1.0961	-0.6531	-0.472
3	3 Nme4		-0.4098	-0.0529	-1.3758	-0.8317	-1.2592	-0.892	-0.7349	-0.642	-0.3748
3	3 Nsmce1		-0.9774	-0.8425	-0.8117	-0.5228	-0.507	-0.5563	-0.964	-0.6076	-0.362
3	3 Nudt7		-0.5702	-0.5157	-0.6295	-0.1898	-0.4833	-0.1187	-1.0448	-0.4695	-1.4921
3	3 Ogt		-0.7306	-1.0461	-0.219	-0.4698	-0.1937	-0.6778	-0.8178	-0.8971	-0.914
3	3 Otub2		-0.722	-0.7555	-1.1146	-0.7914	-0.9527	-0.848	-1.0698	-0.576	0.2335
3	3 P2ry14		-0.393	-0.5305	-0.6531	-0.613	-0.5014	-0.6736	-0.7431	-0.7872	-0.9635
3	3 Paqr7		-0.1512	-0.3288	-0.4567	-0.7015	-0.8202	-0.7874	-0.8631	-0.7015	-0.5412
3	3 Parvg		-0.6626	-0.5778	-0.5962	-0.7053	-0.7086	-0.777	-0.7562	-0.712	-0.8089
3	3 Pepd		-0.4885	-0.6674	-0.8131	-0.8246	-0.9371	-0.8559	-0.543	-0.9539	-0.1638
3	3 Pfdn2		-1.5872	-0.9222	-1.2995	-0.3773	-1.2672	0.0886	-0.8957	-0.6662	0.2786
3	3 Pink1		-0.3132	-0.8643	0.4766	-0.0999	-0.0777	-0.5825	-0.5348	-0.433	-2.0656
3	3 Pira11		-0.6793	-0.6233	-0.7203	-0.6659	-0.6265	-0.6659	-0.7272	-0.6298	-0.6593
3	3 Plekhg5		-0.9002	-1.011	-0.4663	-1.0172	-0.4771	-0.6199	-0.2268	-0.4059	-0.7182
3	3 Plk1		-1.0107	-0.8188	-0.8323	-0.6663	-0.5933	-0.7456	-0.5729	-0.5683	-0.4515
3	3 Ppil3		-0.7203	-0.3536	-0.9549	-0.8361	-0.6899	-0.6377	-0.6684	-0.6174	-0.4871
3	3 Ppp3cc		-0.4247	-0.5184	-0.4247	-0.2585	-0.5428	-0.3697	-1.003	-0.4448	-1.2668
3	3 Prcp		-0.4906	-0.0535	-0.8784	-0.7572	-0.9733	-0.4091	-0.811	-0.571	-0.3104
3	3 Pstpip1		-0.541	-0.716	-0.6206	-0.5237	-0.5637	-0.7764	-0.6936	-0.9022	-0.5311

3	3 Ptrh1		-0.5073	[illegible]	-0.9427	-0.5634	-0.7448	-0.6685	-0.9527	-0.6218	-0.5845
3	3 Rab14		-0.3268	-0.5715	-0.3435	-0.4303	-0.3996	-0.7766	-1.0504	-0.9347	-0.938
3	3 Rap1b		-0.3405	-0.6148	-0.1947	-0.6491	-0.4569	-0.6945	-0.5278	-0.6982	-0.8534
3	3 Rap1gds1		-0.567	-0.4933	-0.6046	-0.3078	-0.6161	-0.5156	-0.9973	-0.6385	-1.0687
3	3 Rarb		-0.5709	-0.5474	-0.6362	-0.75	-0.6661	-0.8437	-0.5293	-0.6465	-0.7601
3	3 Repin1		-0.4443	[illegible]	-0.4113	-0.1726	-0.8271	-0.9312	-0.9813	-1.0395	-0.4363
3	3 Rgs1		-0.7251	-0.6083	-0.5829	-0.7356	-0.6672	-0.7078	-0.7964	-0.7147	-0.6772
3	3 Rnf25		-0.4984	-0.3796	-0.7937	-0.6793	-0.9079	-0.5392	-1.2014	-0.8252	-0.4495
3	3 Rnpepl1		-1.0667	-0.9441	-0.4653	-0.3196	-0.3208	-0.1824	-0.671	-0.313	-1.3702
3	3 Rpn2		-0.4445	-0.406	-0.7676	-0.5872	-0.6512	-0.587	-0.679	-0.6942	-0.6558
3	3 Rps19		-0.8586	-0.5103	-0.8442	-0.4531	-0.6936	-0.8899	-0.6112	-0.5447	-0.5743
3	3 Rps3		-1.0495	-0.63	-0.4984	-0.4804	-0.416	-0.5993	-0.7281	-0.9771	-0.4033
3	3 Sar1b		-0.3929	-0.4501	-0.6376	-0.718	-0.7109	-0.7144	-0.7278	-0.6872	-0.7205
3	3 Sbf1		-0.7679	-0.7428	-0.7768	-0.4433	-0.6359	-0.2315	-0.8913	-0.7295	-0.7142
3	3 Scamp2		-0.2679	-0.4579	-0.4112	-0.4999	-0.6827	-0.6748	-0.6857	-0.5353	-0.713
3	3 Sdhc		-0.7755	-0.7067	-0.9898	-0.7999	-0.7908	-0.4308	-1.0709	-0.4454	[illegible]
3	3 Sec61b		-0.4004	-0.6973	-0.8799	-0.8805	-0.7824	-0.9155	-0.6948	-0.7405	[illegible]
3	3 Sema6d		-0.7776	-0.3852	0.8038	0.2261	-0.3488	-0.7633	-0.73	-1.0554	-1.6393
3	3 41519		-0.4623	-0.2492	-0.506	-0.4144	-0.3782	-0.3863	-1.0383	-0.8742	-0.9385
3	3 Sepx1		-0.8212	-0.6868	-0.6199	-0.7153	-0.5932	-0.7633	-0.9104	-0.8128	-0.4571
3	3 Sh3tc2		-0.5418	-0.6374	-0.7894	-0.5696	-0.8134	-0.567	-0.6671	-0.8439	-0.3642
3	3 Slc23a3		-0.2945	-0.6601	-0.67	-0.6454	-0.524	-0.7179	-0.6799	-0.7102	-1.067
3	3 Slc39a12		-0.4118	-0.8559	-0.5205	-0.5064	-0.6878	-0.7298	-0.7897	-0.5752	-0.733
3	3 Snap29		-0.1209	-0.4226	-0.6719	-0.5419	-0.5244	-0.6283	-0.7324	-0.5611	-0.7597
3	3 Snta1		[illegible]	[illegible]	-0.9322	-0.8648	-1.3835	-0.983	-1.0274	-0.8814	0.2419
3	3 Snx15		-0.8184	-0.5002	-0.859	-0.5379	-0.6068	-0.6823	-0.7247	-0.6335	-0.5839
3	3 Snx2		-0.6673	-0.73	-0.5127	-0.7848	-0.5489	-0.538	-0.8235	-0.8154	-0.6145
3	3 Snx20		-0.9291	-0.9548	-0.7351	-0.4736	-0.495	-0.3637	-0.6396	-0.241	-0.8035
3	3 Sorbs1		-0.3874	-0.4452	-0.7798	-0.2186	-0.6337	-0.7303	-0.8477	-0.7719	-0.9725
3	3 Specc1l		-0.4338	-0.5198	-0.7166	-0.7945	-0.7984	-0.72	-0.8134	-0.5363	-0.6171
3	3 Srp14		-0.515	-0.5052	-0.2635	-0.4264	-0.6475	-0.7897	-0.914	-0.8524	-0.4489
3	3 Stbd1		-0.7948	-0.2932	-0.8875	-0.6426	-0.5263	-0.6152	-0.5088	-0.4555	-1.1221
3	3 Supt3h		-1.0035	-1.0877	-0.6083	-0.5648	-0.3006	-0.207	-0.6814	-0.4537	-0.6825
3	3 Tbc1d2		-0.215	-0.9841	-0.9132	-0.44	-0.8205	-0.2656	-0.9364	-0.5362	-0.955
3	3 Tbc1d22a		-0.4632	-0.9848	-0.5226	-0.6755	-0.5745	-0.7403	-0.6306	-0.7947	-0.6565
3	3 Tbca		-0.6911	-0.3856	-0.5762	-0.4211	-0.6366	-0.6662	-0.7384	-0.5593	-0.7465
3	3 Ticam2		-0.7229	-0.6291	-0.664	-0.7195	-0.8195	-0.7567	-0.7162	-0.6291	-0.6449
3	3 Tk2		-0.3059	-0.6757	-0.6183	-0.7893	-0.6561	-0.9166	-0.7182	-0.8623	[illegible]
3	3 Tmbim4		-0.3048	-0.2344	-0.3485	[illegible]	-0.4967	-0.6073	-0.9755	-0.5444	-1.1506
3	3 Tmem141		-0.2722	-0.4664	-0.7824	-0.9451	-0.8913	-0.6362	-0.753	-0.534	-0.3746
3	3 Tmem160		-0.7193	-0.4715	-0.7572	-0.7286	-0.9764	-0.8619	-0.9119	-0.9871	-0.182
3	3 Tmem203		-0.1208	-0.28	-0.4325	-0.7618	-0.4376	-0.6509	-0.9581	-0.7044	-0.5683
3	3 Tmem30a		-0.5722	-0.4246	-0.7334	-0.4581	-0.7154	-0.7783	-0.837	-1.1996	-0.5309
3	3 Tmem42		-0.5142	-0.2833	-0.3155	-0.4926	-0.4459	-0.8754	-0.4441	-0.5839	-1.1267
3	3 Trappc1		-0.7876	-0.5874	-0.3473	-0.503	-0.4534	-0.4868	-0.6605	-0.4774	-1.0158
3	3 Treml1		-0.7285	-0.7497	-0.725	-0.7391	-0.7076	-0.7076	-0.66	-0.7641	-0.5818
3	3 Ttc3		-0.3045	-0.3059	-1.2974	-0.8765	-0.7514	-0.699	-0.4172	-0.5871	-0.8994
3	3 Ubxn6		-0.6438	-0.6591	-0.7583	-0.7414	-0.7557	-0.6863	-1.2083	-0.6747	-0.4629
3	3 Use1		-0.461	-0.8263	-0.5046	-0.5835	-0.6416	-0.6046	-0.8209	-0.718	-0.7206
3	3 Usp47		-0.1905	-0.2501	-0.5407	-0.6049	-0.5222	-0.5562	-0.5701	-0.6396	-0.935
3	3 Vav3		-0.4702	-0.8402	-0.4779	-0.7219	-0.7329	-0.621	-0.7	-0.92	-0.776
3	3 Vegfa		-0.2862	-0.3759	-1.0586	-1.0011	-0.668	-0.5739	-0.7948	-0.8368	-0.9349
3	3 Wtip		-0.4971	-0.3674	-0.9171	-1.1832	-1.1677	-0.8507	-1.3348	-1.0266	0.5828
3	3 Xbp1		-0.27	-0.4976	-0.5612	-1.0348	-0.6203	-1.329	-0.8464	-1.1956	[illegible]
3	3 Xpr1		-0.3227	-0.2001	-0.5103	-0.5311	-0.4977	-0.6514	-0.6796	-0.279	-1.0876
3	3 Zbtb7c		-1.5397	-0.8676	-0.5388	0.2537	[illegible]	0.701	-0.917	0.3222	-2.1855
3	3 Zfp420		-0.6399	-0.811	-0.2502	[illegible]	-0.4972	-0.4768	-0.613	-0.5291	-1.5564
3	3 Zfp597		-0.3431	-0.6036	-0.8928	-0.8746	-0.8343	-1.0503	-0.7582	-0.806	[illegible]
4	6.33E+19		-0.1348	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.7582	[illegible]	-0.1846
4	0610007P22Rik		-0.4723	-0.3256	-0.4937	-0.4489	-0.5153	-0.3499	-0.2294	-0.3627	0.271
4	0610012G03Rik		-0.1614	-0.218	-0.5031	-0.5304	-0.374	-0.4406	-0.3035	-0.4378	-0.3199
4	0610037L13Rik		[illegible]	[illegible]	[illegible]	-0.3965	-0.3321	-0.5829	-0.3364	-0.3808	[illegible]
4	0610040J01Rik		-0.3275	-0.3102	-0.124	-0.3769	-0.2764	[illegible]	-0.324	-0.2764	[illegible]
4	1110002B05Rik		[illegible]	-0.3068	[illegible]	[illegible]	-0.1917	-0.4119	-0.3213	[illegible]	-0.6791
4	1110005A03Rik		[illegible]	-0.2175	-0.3126	-0.2774	-0.3026	-0.1304	[illegible]	-0.263	[illegible]
4	1110007C09Rik		-0.2377	[illegible]	-0.1964	[illegible]	-0.2126	-0.1174	-0.2671	[illegible]	[illegible]
4	1110012L19Rik		[illegible]	-0.1812	-0.4552	[illegible]	-0.4443	[illegible]	-0.3106	-0.3415	[illegible]
4	1110018G07Rik		-0.2272	-0.53	-0.3384	-0.3662	-0.2135	-0.2626	-0.2124	[illegible]	-0.2135
4	1110038D17Rik		[illegible]	[illegible]	-0.3382	-0.2081	[illegible]	[illegible]	[illegible]	[illegible]	-0.3205
4	Pithd1		-1.0806	-0.5707	-0.3081	[illegible]	[illegible]	[illegible]	-0.3607	[illegible]	-0.5045
4	1110058L19Rik		[illegible]	[illegible]	-0.3863	[illegible]	[illegible]	[illegible]	-0.3584	[illegible]	[illegible]
4	1110059G10Rik		-0.2674	[illegible]	-0.1311	[illegible]	-0.3758	[illegible]	[illegible]	-0.2609	[illegible]
4	1300001I01Rik		-0.3481	-0.2101	-0.1284	[illegible]	[illegible]	-0.2507	[illegible]	-0.273	[illegible]
4	1300018J18Rik		[illegible]	[illegible]	-0.1824	-0.2183	-0.2426	-0.2954	-0.6714	-0.4362	-0.8698
4	1500003O03Rik		-0.259	-0.1268	[illegible]	-0.4964	-0.583	-0.4972	-0.6953	-0.6256	-0.945
4	1520401A03Rik		-0.2524	-0.2876	-0.3116	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	1600002K03Rik		-0.2083	[illegible]	-0.1354	[illegible]	[illegible]	[illegible]	-0.623	[illegible]	-0.4394
4	1600014C10Rik		-0.3426	[illegible]	-0.3538	[illegible]	-0.3415	[illegible]	-0.56	-0.342	-0.5904
4	1700003F12Rik		-0.2873	[illegible]	-0.121	-0.1266	[illegible]	-0.3417	[illegible]	-0.1716	[illegible]
4	1700010M22Rik		[illegible]	-0.2416	[illegible]	[illegible]	-0.1535	[illegible]	-0.1416	-0.136	-0.2348
4	1700016D06Rik		-0.4016	-0.258	-0.3019	-0.1978	-0.256	-0.3333	-0.1959	[illegible]	0.4136
4	1700019E19Rik		[illegible]	[illegible]	-0.3089	-0.137	-0.2704	-0.271	-0.315	[illegible]	-0.607
4	1700021F05Rik		-0.3198	-0.2972	-0.4442	-0.3234	-0.2075	-0.5092	-0.2899	-0.3726	[illegible]
4	1700027D21Rik		-0.2524	-0.2665	-0.2463	-0.2273	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	1700028K03Rik		[illegible]	[illegible]	-0.1568	-0.2618	-0.1326	-0.2619	-0.2106	-0.3386	[illegible]
4	1700029J07Rik		[illegible]	[illegible]	-0.1299	-0.2572	-0.3085	[illegible]	-0.188	[illegible]	-0.662
4	1700030K09Rik		-0.3134	-0.2267	-0.6767	-0.3848	-0.3148	-0.3314	-0.6115	-0.5795	0.7348
4	1700034H14Rik		-0.4178	-0.186	-0.74	[illegible]	-0.6556	[illegible]	-0.3634	[illegible]	[illegible]
4	1700037C18Rik		[illegible]	-0.2649	[illegible]	[illegible]	[illegible]	[illegible]	-0.148	-0.2513	[illegible]
4	1700049E17Rik1		-0.3605	-0.2912	-0.1396	-0.1538	-0.1512	[illegible]	-0.2065	[illegible]	-0.3534
4	Samt3		-0.3174	-0.2771	-0.2755	-0.1318	[illegible]	-0.2219	-0.2218	-0.2755	-0.1549
4	1700084C01Rik		-0.2867	-0.3132	[illegible]	[illegible]	[illegible]	-0.1678	-0.1946	-0.4678	-0.2299
4	1700123K08Rik		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.1728	[illegible]	[illegible]	[illegible]
4	1810008A18Rik		-0.612	-0.247	-0.6161	-0.2657	-0.1855	[illegible]	[illegible]	[illegible]	[illegible]
4	1810009J06Rik		[illegible]	-0.2524	-0.1668	-0.1729	-0.2148	[illegible]	[illegible]	-0.2078	-0.2423
4	1810026J23Rik		[illegible]	[illegible]	[illegible]	-0.142	-0.3299	-0.197	-0.336	-0.3043	-0.3807
4	1810030N24Rik		[illegible]	-0.451	[illegible]	[illegible]	[illegible]	-0.1724	-0.4286	[illegible]	-0.3187
4	1810049H13Rik		-0.7228	-0.3558	-0.7431	-0.1799	-0.6095	-0.3768	-0.7128	-0.448	-0.6881
4	1810074P20Rik		-0.265	-0.2972	-0.4421	-0.3804	-0.5464	-0.2034	-0.3703	-0.5055	0.4511
4	2010106E10Rik		-0.271	-0.1361	-0.1382	-0.2433	-0.24	-0.1483	-0.227	-0.3137	-0.2387
4	2010106G01Rik		[illegible]	[illegible]	-0.2337	-0.2377	-0.26	-0.2878	-0.4316	-0.2967	-0.3439
4	2310001A20Rik		-0.6597	-0.5702	-0.352	-0.3906	-0.4506	-0.4973	-0.7049	-0.3253	-0.2738
4	2310003H01Rik		-0.9069	-0.4037	-0.529	-0.1326	-0.3664	[illegible]	-0.4895	[illegible]	0.8919
4	2310011J03Rik		[illegible]	[illegible]	-0.2602	-0.2268	[illegible]	-0.2982	-0.2379	[illegible]	-0.5274
4	2310016M24Rik		-0.3226	-0.3074	[illegible]	-0.3384	-0.2848	-0.4004	-0.6246	-0.3618	-1.1904
4	2310033E01Rik		-0.2329	-0.1523	-0.2719	-0.3675	-0.2219	-0.2869	-0.281	-0.2625	[illegible]
4	2310034C09Rik		-0.5472	-0.408	-0.4665	-0.4509	-0.3366	-0.5134	-0.5946	-0.5225	-0.5754
4	2310035K24Rik		[illegible]	[illegible]	-0.2403	-0.1664	-0.5799	-0.4182	-0.7279	-0.3302	-0.329
4	2310036O22Rik		-0.7025	-0.3204	-0.4085	-0.3222	[illegible]	[illegible]	-0.2254	[illegible]	[illegible]
4	2310039H08Rik		-0.6326	-0.5229	[illegible]	[illegible]	[illegible]	0.2119	-0.2657	-0.5228	-1.0544
4	2400003C14Rik		-0.1863	-0.6522	0.3245	-0.3657	[illegible]	-0.2067	[illegible]	-0.3948	-0.463
4	2410015M20Rik		-0.1656	-0.3146	-0.2979	-0.4208	-0.3549	-0.4217	-0.5453	-0.4624	-0.3914
4	2410066E13Rik		[illegible]	-0.1791	-0.2514	-0.2601	-0.1869	-0.3196	-0.4134	-0.3165	[illegible]
4	2410091C18Rik		-0.4105	-0.3347	-0.405	-0.1974	-0.4317	-0.3183	-0.2836	-0.396	[illegible]
4	2610042L04Rik		-0.1657	-0.213	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	2810006K23Rik		-0.1488	[illegible]	[illegible]	-0.1807	-0.2026	-0.1238	-0.1316	-0.1994	[illegible]
4	2810403A07Rik		-0.1595	[illegible]	-0.4728	-0.2603	-0.2937	-0.2611	[illegible]	[illegible]	0.456
4	2900026A02Rik		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	3110001D03Rik		-0.8781	-0.642	-1.1223	-0.4441	-0.5548	-0.2987	[illegible]	[illegible]	[illegible]
4	3110002H16Rik		-0.8172	-0.4738	[illegible]	[illegible]	[illegible]	[illegible]	-0.2318	[illegible]	[illegible]
4	3110035E14Rik		[illegible]	[illegible]	-0.2039	[illegible]	-0.153	-0.1363	-0.2148	-0.1322	-0.183
4	3110040N11Rik		-0.2013	-0.2742	-0.503	-0.1888	-0.3108	-0.1939	-0.4322	[illegible]	-0.1753
4	3110057O12Rik		-0.6214	-0.594	-0.6493	-0.2917	-0.4133	-0.237	-0.3318	-0.4954	-0.2825
4	3110082I17Rik		-0.7526	-0.2998	-0.2568	-0.2735	[illegible]	0.3118	-0.2256	-0.3042	[illegible]
4	3300002I08Rik		[illegible]	-0.1415	[illegible]	-0.3498	-0.3192	-0.2437	-0.2341	-0.3276	-0.2901
4	4632404H12Rik		-0.4052	-0.1368	-0.3457	-0.3926	-0.262	-0.2337	-0.3981	-0.1806	0.5046
4	4632434I11Rik		-0.1115	-0.2248	[illegible]	[illegible]	-0.1863	-0.1565	-0.1875	[illegible]	[illegible]
4	4833427G06Rik		[illegible]	[illegible]	-0.1856	-0.2667	-0.2139	-0.1989	-0.2892	-0.2593	-0.3526
4	Rbm4b		-0.3956	-0.2721	-0.2284	-0.6879	-0.3987	-0.6426	[illegible]	-0.3649	[illegible]
4	4921509C19Rik		-0.2372	-0.1575	-0.2423	-0.2022	[illegible]	-0.1983	[illegible]	-0.249	-0.229
4	4921517D21Rik		-0.1913	[illegible]	-0.2852	-0.2443	[illegible]	[illegible]	-0.1025	-0.2097	[illegible]
4	4930451I11Rik		-0.3206	-0.1858	-0.3277	-0.3837	-0.4314	-0.3937	-0.277	[illegible]	-0.4132
4	4930473A06Rik		-0.2512	-0.3187	-0.3447	-0.4127	-0.3019	-0.2798	-0.3001	-0.521	[illegible]
4	4930486L24Rik		[illegible]	[illegible]	-0.304	-0.1865	-0.2562	-0.3372	-0.1452	-0.2313	[illegible]
4	4930524B15Rik		[illegible]	-0.2291	-0.2709	-0.2957	-0.182	-0.16	-0.2112	-0.2312	[illegible]
4	Ube2dnl2		-0.2952	-0.1947	-0.3405	-0.1758	[illegible]	-0.4098	-0.1341	-0.2169	-0.1957
4	Samt4		-0.2865	[illegible]	[illegible]	-0.2207	[illegible]	[illegible]	-0.3248	-0.1982	-0.1529
4	4930544G11Rik		[illegible]	-0.3005	-0.1726	-0.1388	-0.3482	-0.4075	-0.4415	-0.2177	-0.1576
4	4932438H23Rik		-0.1361	-0.1347	[illegible]	[illegible]	-0.1451	-0.2784	[illegible]	-0.2125	-0.1344
4	4932441K18		-0.231	-0.1102	[illegible]	-0.1048	-0.2632	-0.272	-0.1251	-0.2248	[illegible]
4	4933403F05Rik		-0.1858	[illegible]	[illegible]	-0.1658	-0.108	-0.2198	-0.155	[illegible]	-0.1669
4	4933407P14Rik		[illegible]	-0.1862	-0.2223	-0.1954	[illegible]	-0.2065	-0.1798	[illegible]	-0.2526
4	4933411G06Rik		[illegible]	-0.2854	-0.1483	-0.1879	-0.182	-0.2086	[illegible]	-0.1573	[illegible]
4	4933411G11		-0.1897	[illegible]	-0.1384	-0.1102	-0.1778	-0.1564	-0.2112	[illegible]	-0.2702
4	4933434E20Rik		-0.3318	-0.3142	-0.1313	[illegible]	[illegible]	-0.3189	-0.4107	-0.3136	-0.2099
4	5031410I06Rik		-0.2496	-0.2708	[illegible]	-0.2625	-0.1969	[illegible]	-0.284	-0.3414	[illegible]
4	5031414D18Rik		-0.182	-0.2312	-0.3253	[illegible]	-0.3423	-0.3188	-0.2436	-0.3086	-0.2398
4	Idnk		-0.3269	-0.768	-0.4345	-0.7974	-0.8444	-0.9396	-0.3717	-0.4934	-0.3729
4	Tmem242		-0.4009	-0.1866	-0.3812	-0.3427	-0.7173	-0.4063	[illegible]	-0.5484	-0.3729
4	Cacfd1		-0.1826	-0.1777	-0.2054	[illegible]	-0.2994	[illegible]	-0.713	-0.4687	-0.7201
4	6030408B16Rik		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.2756	[illegible]	-0.1942	[illegible]
4	6230409E13Rik		-0.2441	-0.1685	[illegible]	[illegible]	-0.108	-0.3184	-0.1808	-0.241	[illegible]
4	6330407J23Rik		-0.5828	-0.4743	-0.41	-0.2784	-0.5014	-0.3817	-0.2226	[illegible]	[illegible]
4	6330439K17Rik		-0.2825	-0.3098	-0.3442	-0.1966	-0.2825	-0.3407	-0.2087	-0.3722	-0.2767
4	6430571L13Rik		-0.2353	-0.2298	-0.2688	-0.3076	-0.2847	[illegible]	-0.3535	[illegible]	-0.3123
4	6430598A04Rik		-0.2095	-0.1605	-0.2844	-0.1789	-0.2567	-0.2602	-0.3006	-0.3278	[illegible]
4	8430410K20Rik		-0.4933	-0.4117	-0.8934	-0.7165	-0.7082	-0.6202	-0.4158	-0.6045	-0.5613
4	8430427H17Rik		-0.4773	-0.212	-0.6826	-0.341	-0.6662	-0.676	-0.4859	-0.4518	-0.5095
4	9130011J15Rik		[illegible]	-0.1586	[illegible]	-0.184	[illegible]	[illegible]	-0.7423	-0.3918	-0.5232
4	9130221H12Rik		[illegible]	-0.1312	-0.4282	[illegible]	-0.4212	-0.1404	-0.5408	-0.2365	[illegible]
4	9330182L06Rik		-0.4243	-0.3697	-0.3004	-0.3484	-0.2808	-0.3	-0.2683	-0.3	-0.2965
4	9530009G21Rik		-0.2164	-0.109	-0.1718	-0.1269	-0.1756	-0.1792	-0.1762	-0.1288	-0.1545
4	9630028B13Rik		-0.2709	-0.4064	-0.4764	-0.2396	-0.1988	-0.265	-0.3727	-0.4744	[illegible]
4	9930021D14Rik		-0.1905	[illegible]	[illegible]	[illegible]	-0.208	-0.1663	[illegible]	[illegible]	[illegible]

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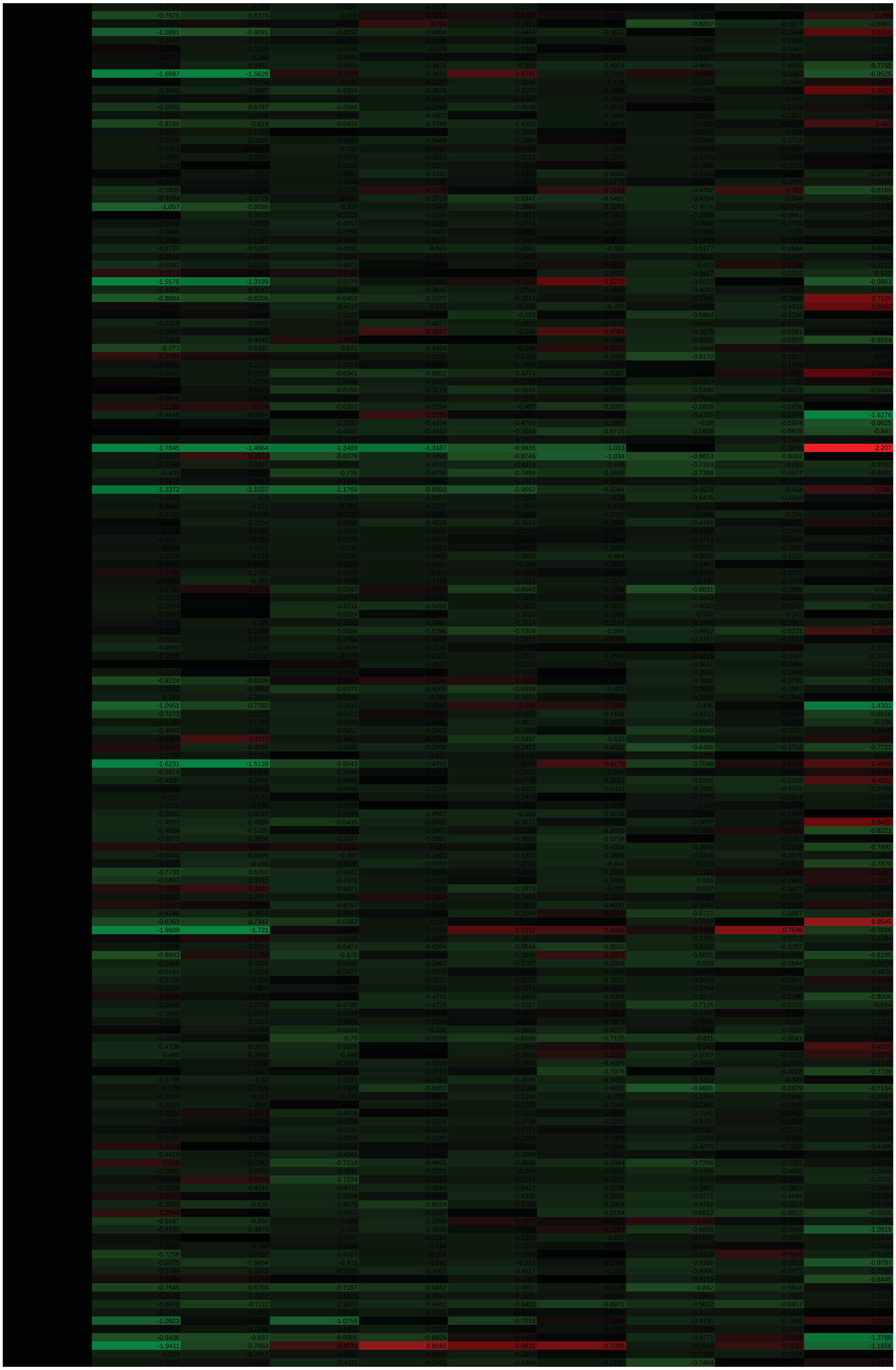

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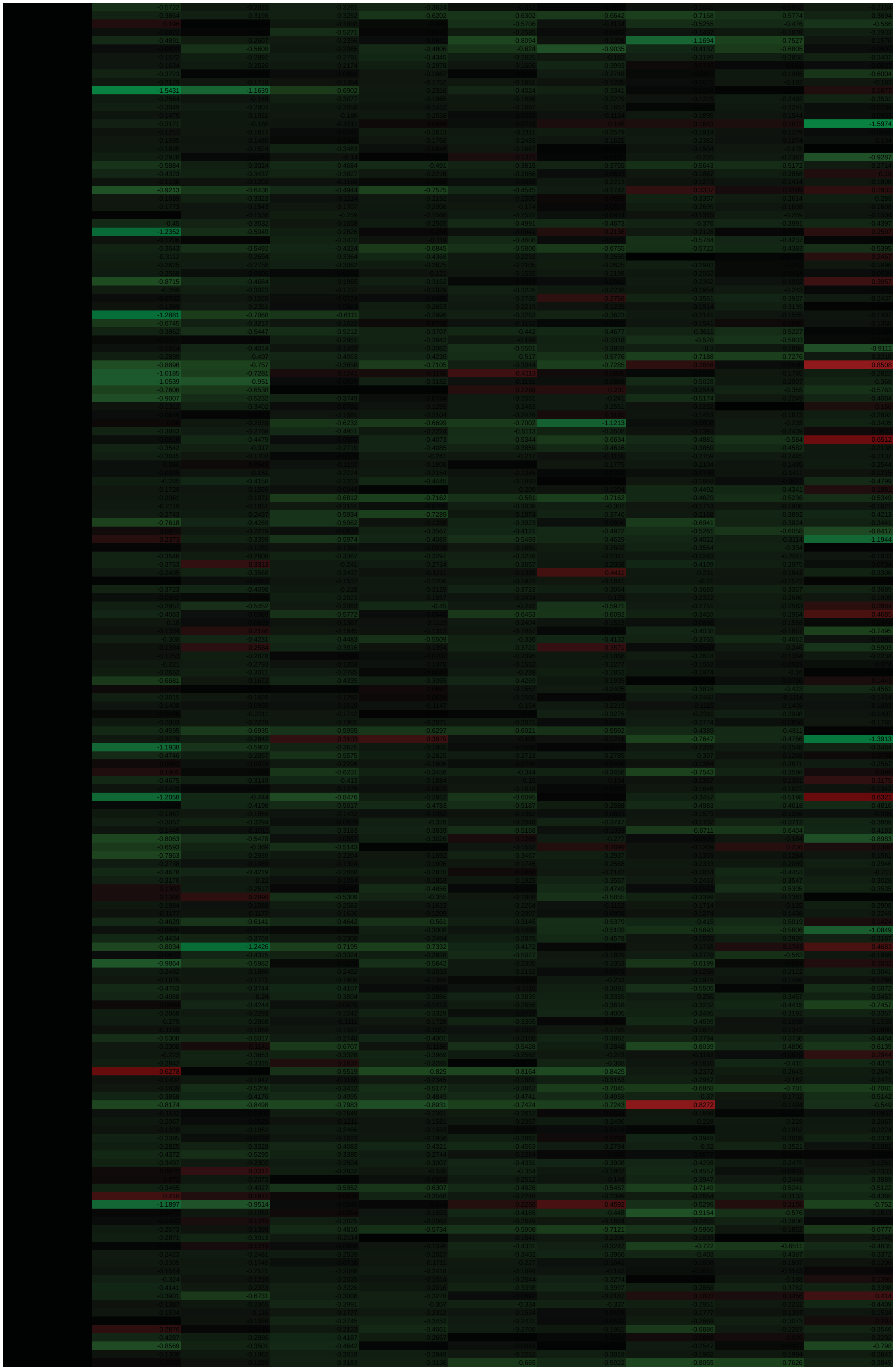

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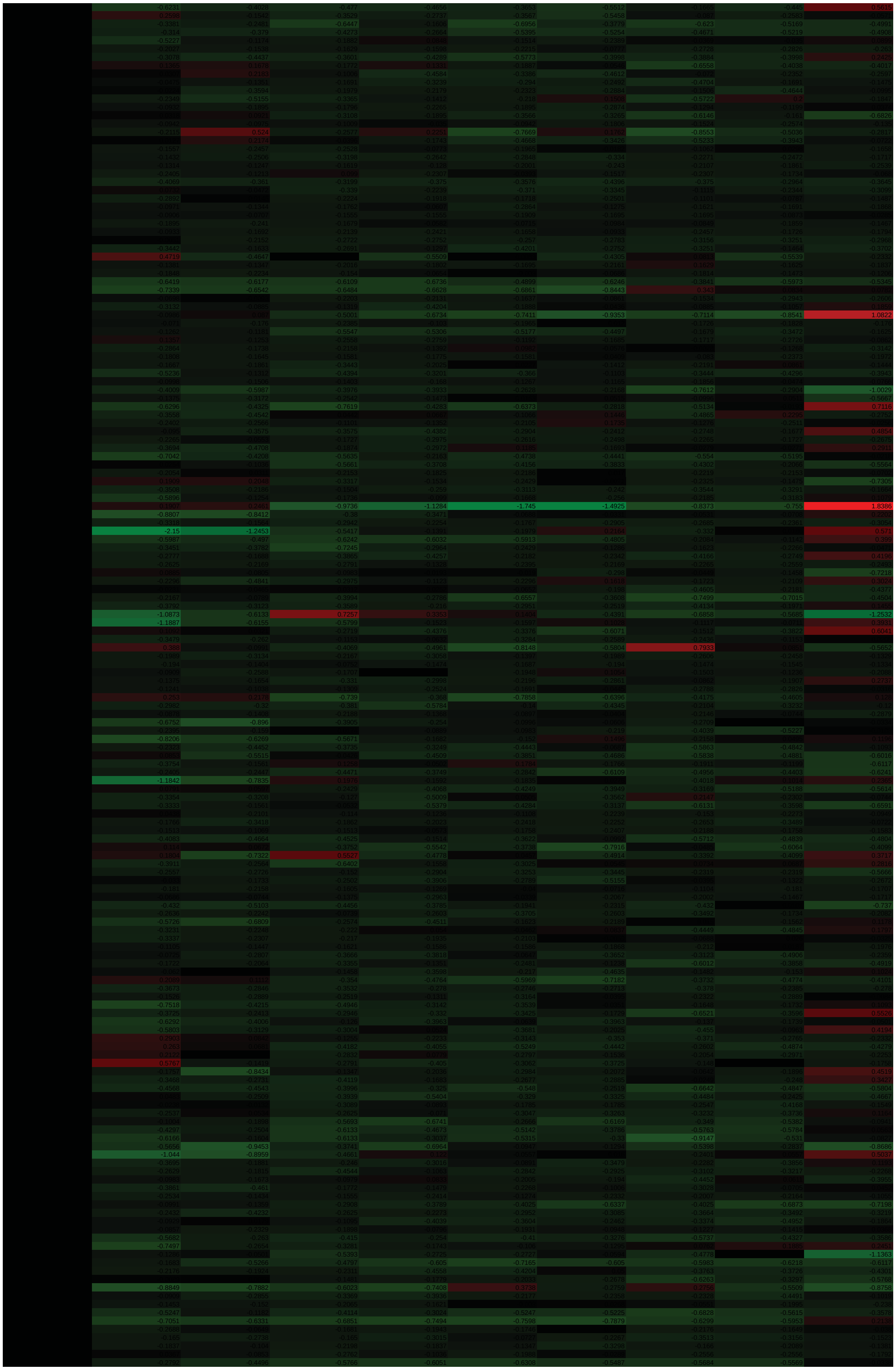

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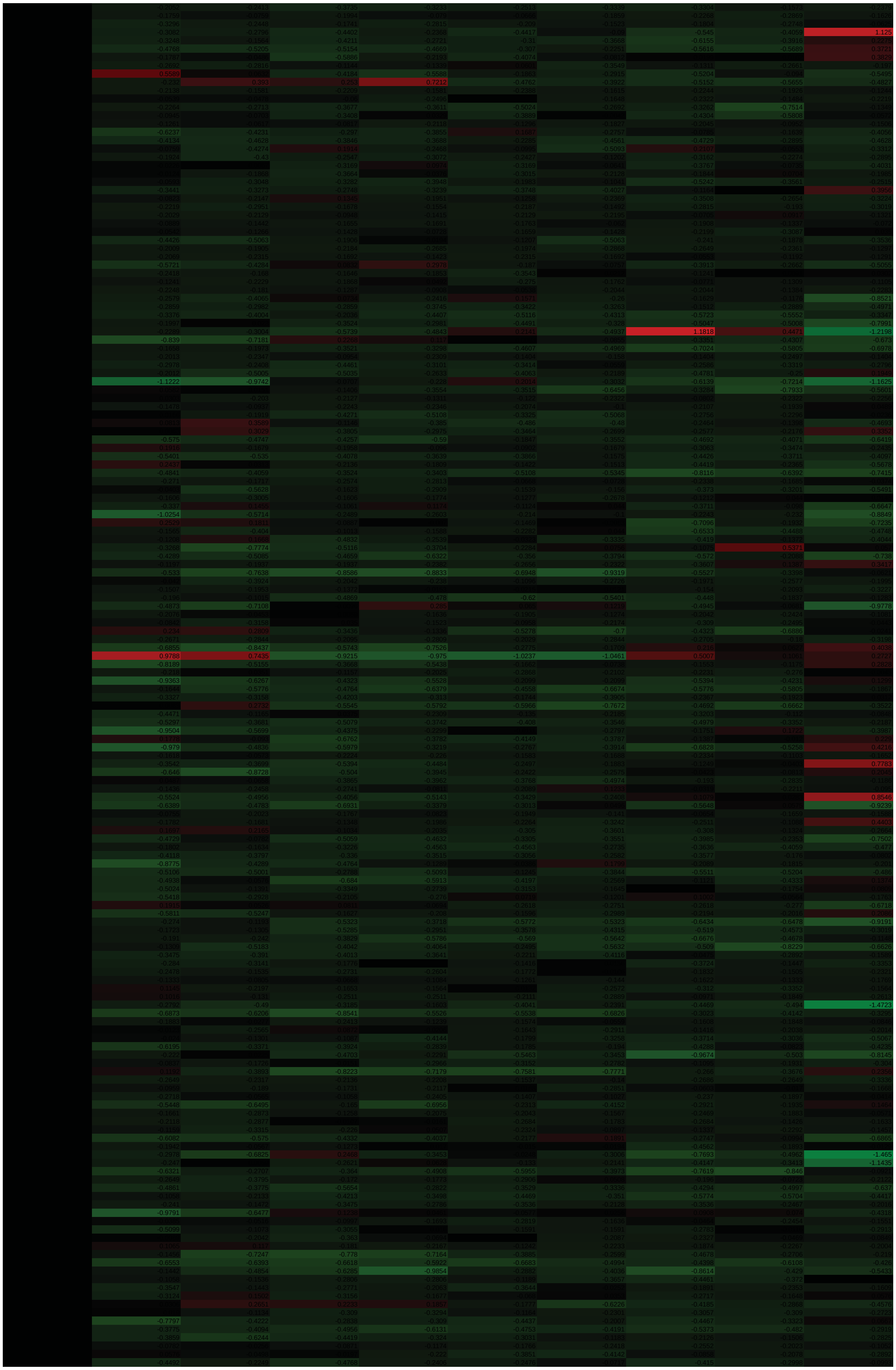

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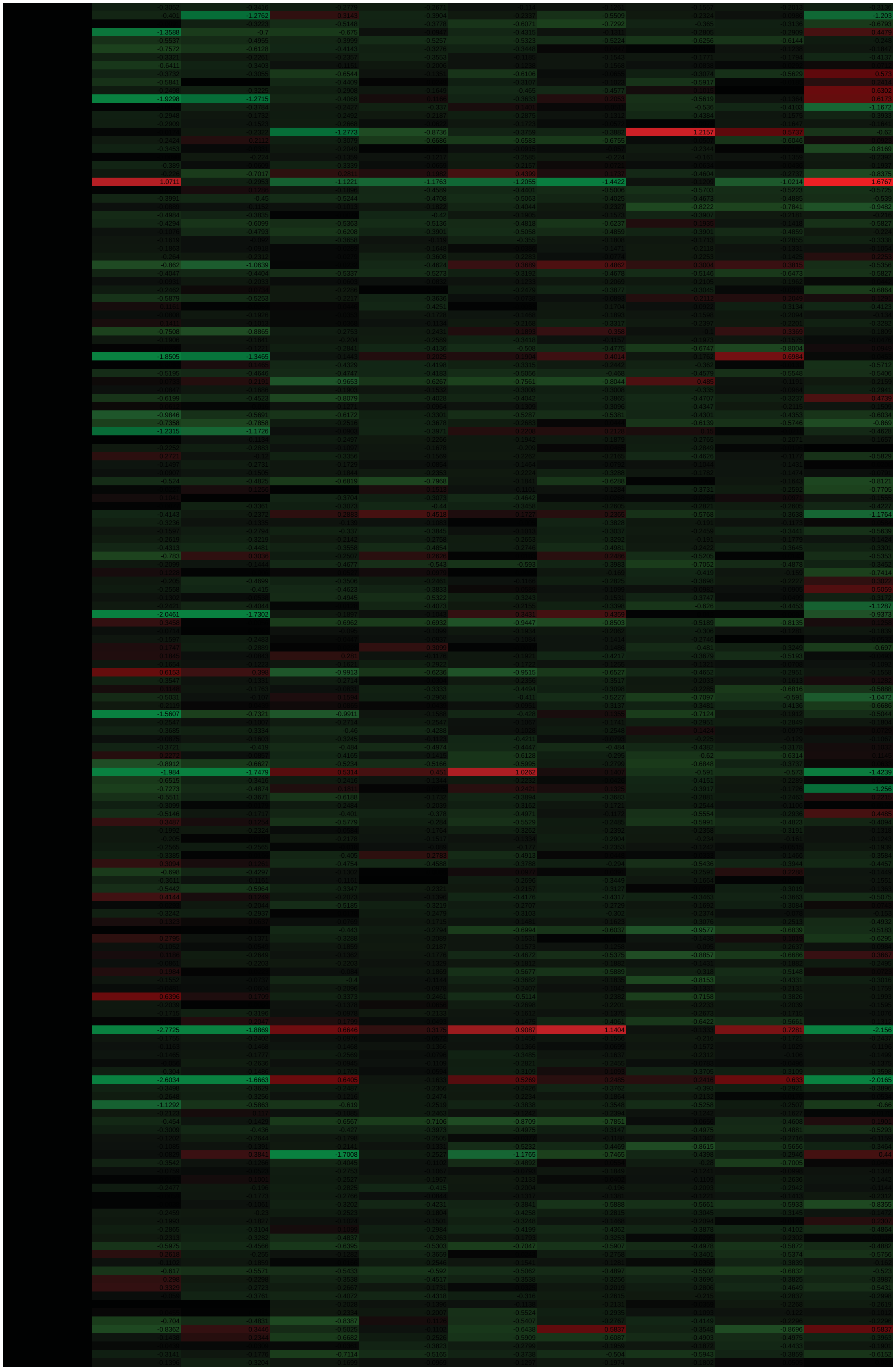

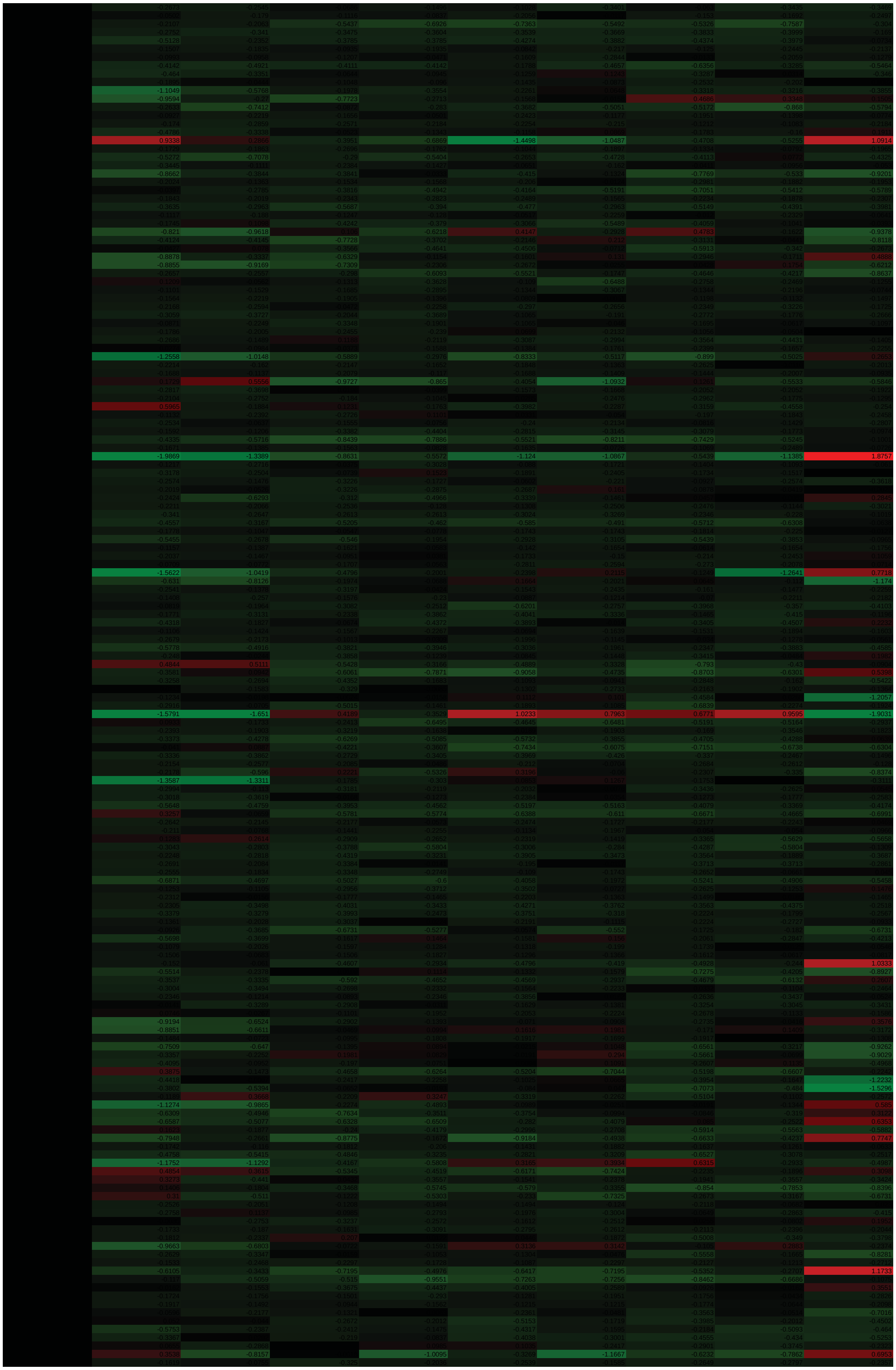

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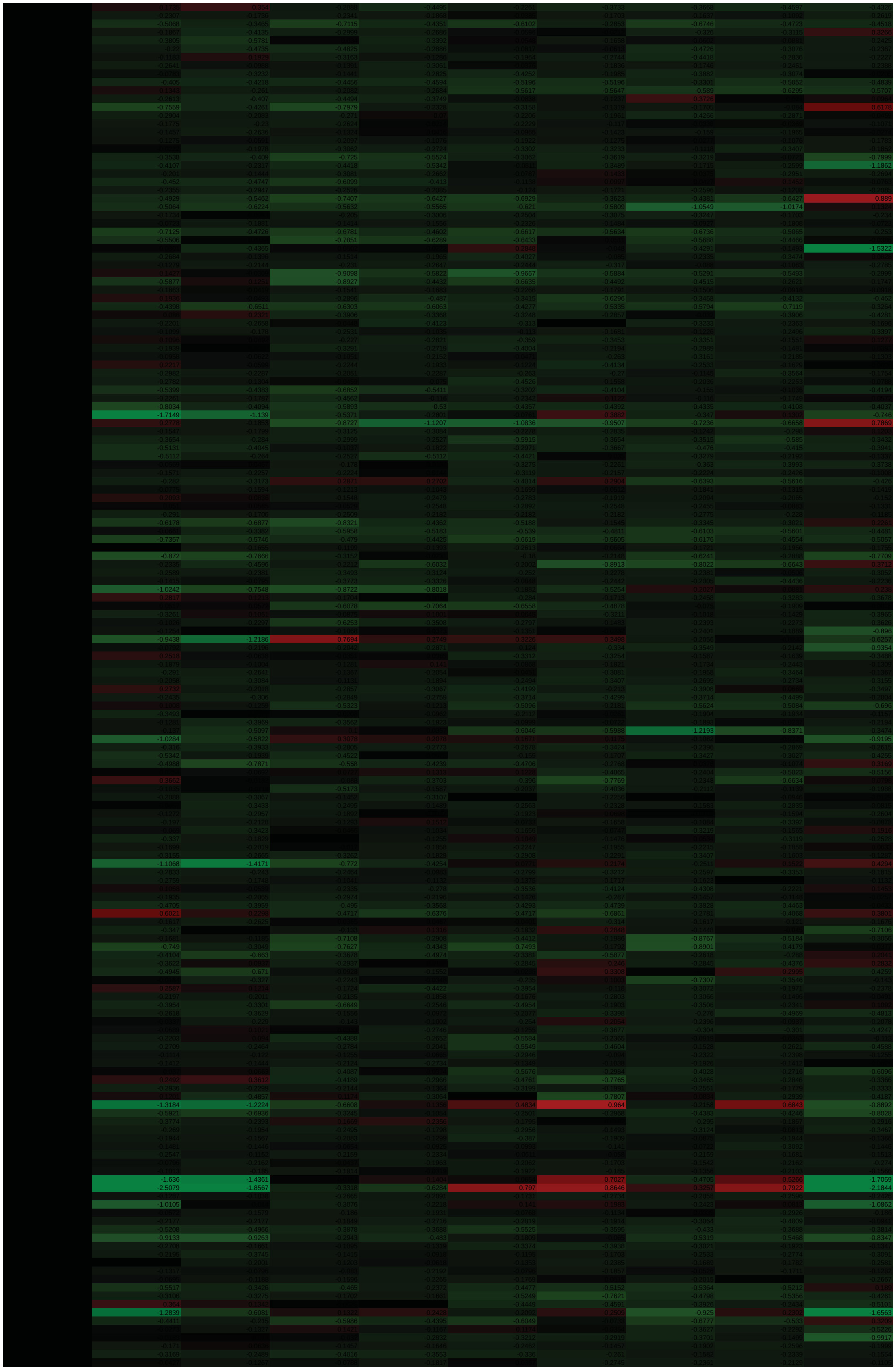

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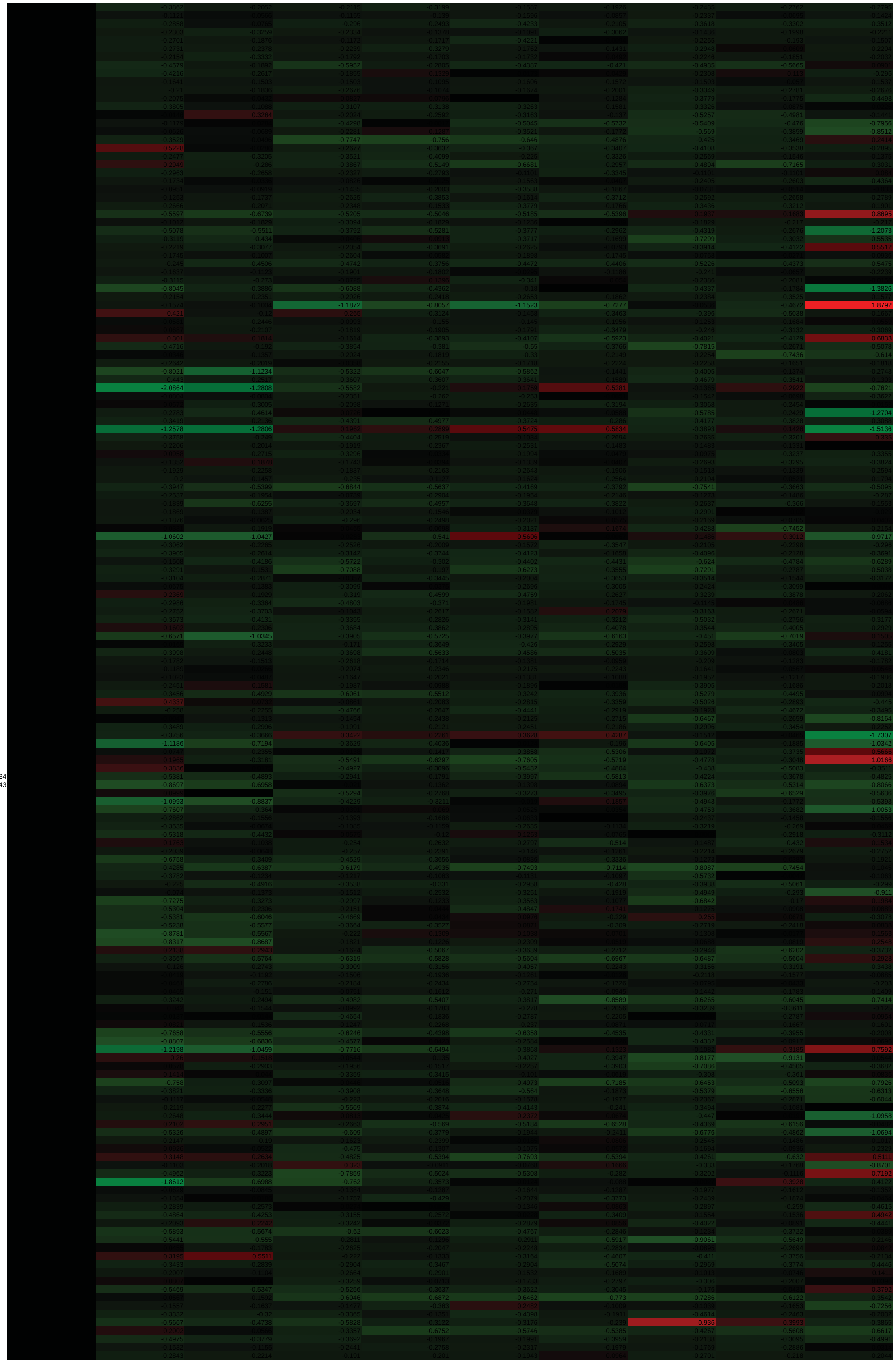

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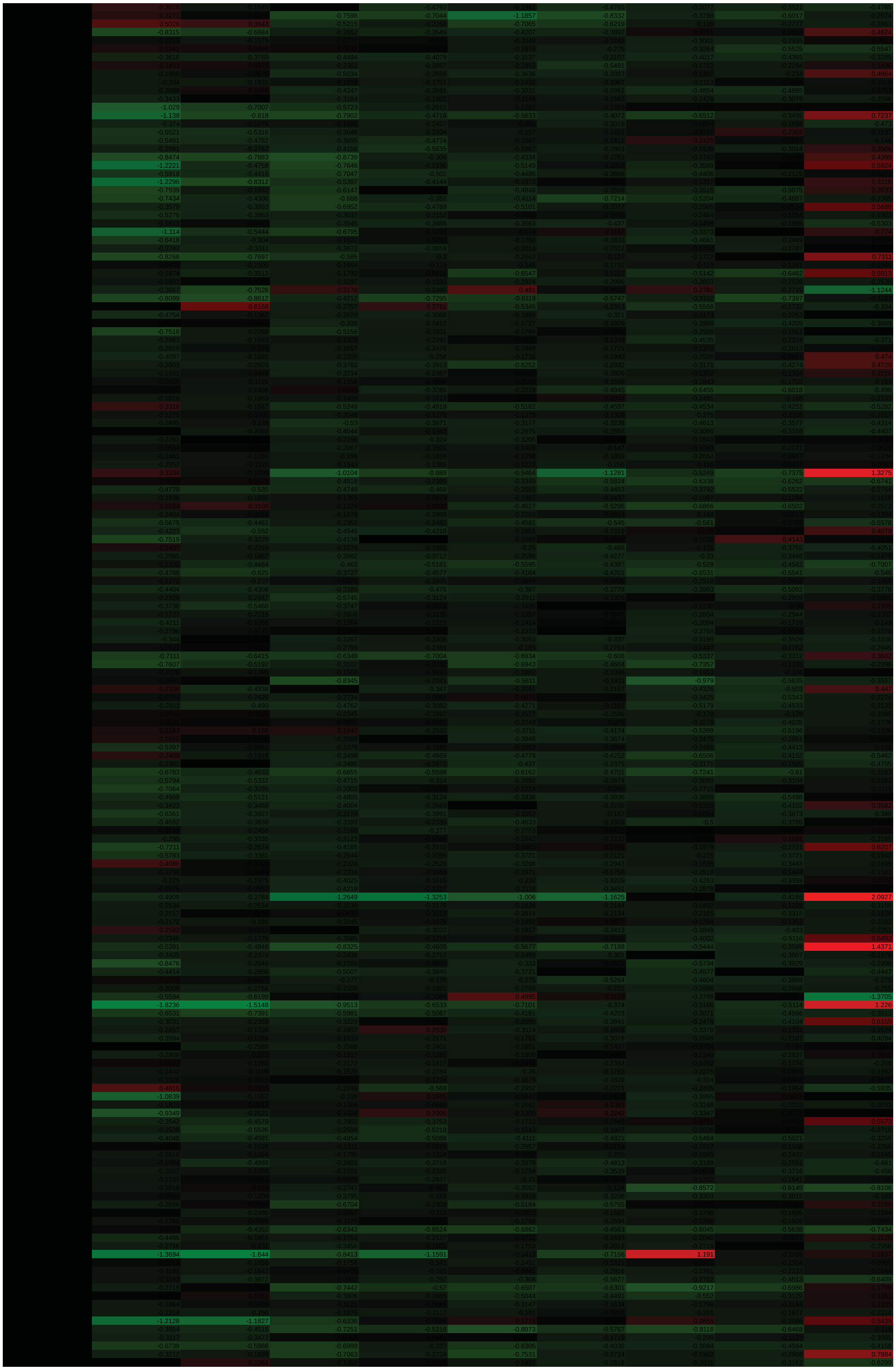

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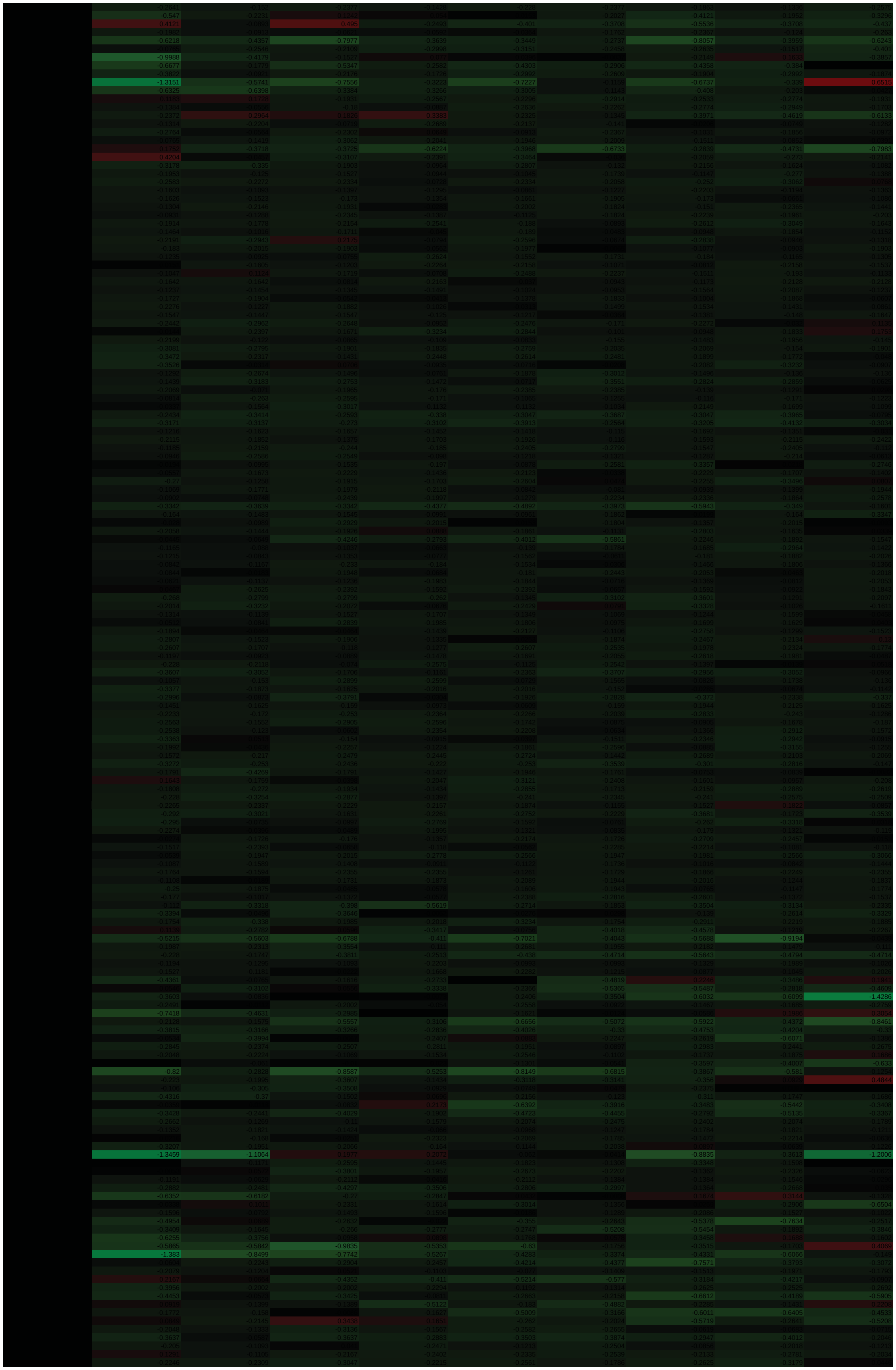
4	Ovgp1
4	Oxt
4	P2rx2
4	P2ry1
4	P2ry12
4	Pabpc2
4	Pabpc5
4	Pabpn1l
4	Pacrgl
4	Pacs1
4	Pacsin2
4	Pacsin3
4	Padi1
4	Paf1
4	Pafah1b3
4	Pak1
4	Palm2
4	Panx1
4	Panx3
4	Papln
4	Pard6a
4	Park7
4	Parp6
4	Pax7
4	Pbld2
4	Pcbd1
4	Pcca
4	Pccb
4	Pcdh10
4	Pcdh17
4	Pcdh8
4	Pcdhb1
4	Pcdhb10
4	Pcdhb3
4	Pcdhb4

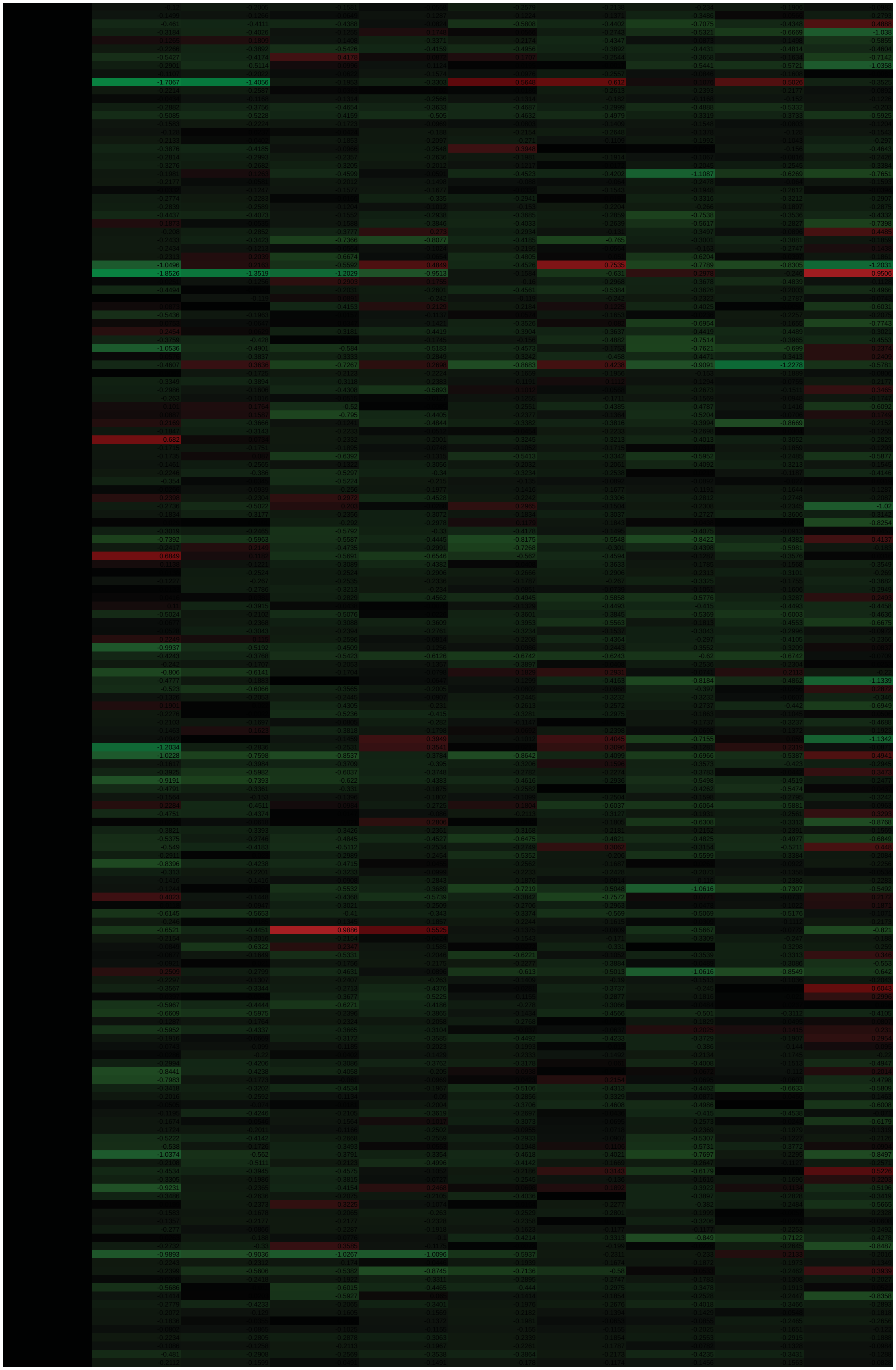


4	Pcdhb5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pcdhga5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pcgf1	[illegible]	[illegible]	-0.5688	[illegible]	-0.3697	[illegible]	-0.4062	-0.3705	[illegible]
4	Pck1	-0.2606	[illegible]	-0.2445	[illegible]	-0.3247	[illegible]	-0.3576	-0.4028	[illegible]
4	Pcmtd2	-0.2358	-0.536	[illegible]	[illegible]	[illegible]	-0.16	-0.5283	-0.292	-0.3955
4	Pcnx	[illegible]	[illegible]	-0.3885	-0.3398	-0.8546	-0.7555	-0.5755	-0.5685	[illegible]
4	Pcolce2	-0.8078	[illegible]	0.3443	[illegible]	[illegible]	[illegible]	-0.8504	-0.7796	-0.3685
4	Pcsk2	-0.6895	-0.5102	-0.5676	-0.5482	-0.5102	-0.5971	-0.4371	-0.4762	-0.6305
4	Pdcd5	-0.692	-0.5282	-0.5774	-0.7156	-0.2768	[illegible]	-0.3257	-0.4153	-0.3378
4	Pdcl3	-0.4956	-0.2258	-0.5351	-0.4135	-0.3042	[illegible]	[illegible]	-0.4135	-0.5155
4	Pde6c	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pde6d	[illegible]	[illegible]	-0.5126	-0.3217	-0.5177	-0.2742	-0.582	-0.3535	[illegible]
4	Pdlim4	-0.5387	0.4209	-0.7527	-0.9444	-0.7481	-0.5277	-0.3631	[illegible]	-0.8269
4	Pdyn	[illegible]	[illegible]	[illegible]	-0.4124	[illegible]	-0.3133	-0.3266	-0.3166	-0.3323
4	Pdzd11	-0.2819	-0.2592	-0.2819	-0.2768	-0.3018	[illegible]	[illegible]	-0.23	-0.4952
4	Peli3	[illegible]	[illegible]	[illegible]	-0.4092	[illegible]	[illegible]	-0.284	[illegible]	[illegible]
4	Pelo	[illegible]	[illegible]	-0.8577	-0.4751	-0.8712	-0.5734	-0.3956	-0.6767	[illegible]
4	Pex11b	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.516	[illegible]	[illegible]
4	Pex11c	-0.3791	-0.396	-0.4068	-0.282	[illegible]	[illegible]	-0.6832	-0.3223	-0.3045
4	Pex14	-0.2727	-0.2451	[illegible]	-0.2129	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pex26	-0.6276	-0.3418	-0.6668	-0.3977	-0.4402	-0.3903	-0.6668	-0.3163	-0.5643
4	Pex3	[illegible]	[illegible]	-0.2622	-0.3662	-0.3144	-0.5344	-0.3542	-0.5664	[illegible]
4	Pex6	-0.2614	-0.4685	-0.516	-0.7301	-0.1602	-0.361	-0.3788	-0.516	[illegible]
4	Pfdn5	[illegible]	-0.2478	-0.4916	-0.2564	-0.3143	-0.3632	-0.405	-0.4281	-0.7336
4	Pfkfb1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pfkfb2	[illegible]	[illegible]	[illegible]	-0.3829	-0.3896	-0.5107	-0.616	-0.5604	-0.2975
4	Pfkm	-0.2137	[illegible]	-0.2743	-0.2415	-0.2198	[illegible]	-0.4145	-0.3855	[illegible]
4	Pgam5	-0.684	-0.3172	-0.4677	[illegible]	-0.7437	-0.19	-0.9571	-0.6205	[illegible]
4	Pgap2	[illegible]	-0.232	-0.5377	-0.45	-0.403	[illegible]	-0.3692	-0.433	[illegible]
4	Pgls	[illegible]	[illegible]	-0.6817	-0.446	-0.6894	-0.6755	-0.8898	-0.5909	[illegible]
4	Pglyrp1	-1.747	-1.7691	0.2125	0.3948	0.6029	0.7108	[illegible]	0.5825	-1.8342
4	Pglyrp3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pglyrp4	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pgm2	-0.7818	-0.7221	-0.3773	-0.3897	-0.2551	-0.3172	[illegible]	[illegible]	-0.7493
4	Pgr	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phactr1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phc2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.7557
4	Phf11	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phgr1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phka1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phka2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phkg2	[illegible]	[illegible]	[illegible]	[illegible]	-0.313	[illegible]	[illegible]	[illegible]	[illegible]
4	Phospho2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phox2b	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Phtf2	-1.3012	-0.8735	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pias1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pigc	[illegible]	[illegible]	-0.5889	-0.6066	-0.6518	-0.557	-0.6095	-0.7176	-0.5036
4	Pigz	-0.48	-0.5155	-0.4976	-0.406	-0.48	-0.5955	[illegible]	[illegible]	-0.7595
4	Pih1d1	-0.4073	-0.4004	-0.5354	-0.4705	-0.3315	[illegible]	[illegible]	[illegible]	[illegible]
4	Pik3ap1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pik3r6	-0.5259	-0.3493	-0.484	-0.4874	-0.5083	-0.5654	-0.5618	-0.4266	[illegible]
4	Pir	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.4083	[illegible]	[illegible]
4	Pisd-ps3	[illegible]	[illegible]	[illegible]	[illegible]	-0.4453	-0.503	-0.3874	-0.3845	[illegible]
4	Pkhd1l1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pkib	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pklr	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pla1a	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pla2g12a	-0.8298	-0.5346	-0.8691	[illegible]	-1.1917	-0.5341	-1.0464	-0.5544	[illegible]
4	Pla2g4d	-0.684	-0.6605	[illegible]	[illegible]	-0.4322	-0.4563	-0.6772	-0.4448	-0.6941
4	Pla2g4e	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.4448	[illegible]	[illegible]
4	Pla2g4f	[illegible]	-0.6645	-0.4965	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Plcb3	-0.4273	-0.5058	-0.4878	-0.482	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Plcl2	-0.8101	-0.6053	[illegible]	[illegible]	-0.3545	-0.3612	-0.5855	[illegible]	-1.2238
4	Pld2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.5741
4	Plekha2	[illegible]	[illegible]	-1.6608	-1.4042	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Plekha6	-1.2204	-0.5682	[illegible]	[illegible]	0.506	[illegible]	[illegible]	[illegible]	-2.4725
4	Plekhg1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Plekhm1	-0.5067	-0.388	-0.406	[illegible]	[illegible]	-0.5237	-0.4288	[illegible]	[illegible]
4	Plin3	[illegible]	-0.698	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Plin4	0.4017	[illegible]	[illegible]	-0.3718	-0.3819	-0.4367	-0.4472	[illegible]	[illegible]
4	Plscr3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pmepa1	[illegible]	[illegible]	-0.6305	-0.4158	-0.3705	-0.6234	-0.4468	-0.422	[illegible]
4	Pnck	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pnkp	-0.3987	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pnliprp2	-0.4102	[illegible]	-0.4835	-0.5041	-0.4938	-0.4597	-0.3644	-0.5216	[illegible]
4	Pnma3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pnpla1	[illegible]	-0.4424	[illegible]	-0.4048	[illegible]	[illegible]	[illegible]	-0.3967	-0.5178
4	Pnpla2	-1.1622	-1.0064	[illegible]	[illegible]	[illegible]	[illegible]	-0.812	-0.5492	-0.5486
4	Pnpla7	[illegible]	-0.4208	-0.768	-0.5044	-0.5251	-0.6626	-0.6334	-0.6318	-0.6127
4	Pnpla8	[illegible]	-0.5265	[illegible]	-0.4085	-0.4067	-0.8222	[illegible]	[illegible]	[illegible]
4	Pnpo	-0.8828	-0.6178	[illegible]	[illegible]	[illegible]	0.4921	[illegible]	[illegible]	0.493
4	Pnrc2	[illegible]	[illegible]	-0.4091	[illegible]	-0.4362	-0.4285	[illegible]	[illegible]	-0.6663
4	Pofut1	0.4448	[illegible]	[illegible]	[illegible]	-0.3989	[illegible]	[illegible]	[illegible]	[illegible]
4	Poglut1	[illegible]	[illegible]	-0.7234	[illegible]	[illegible]	[illegible]	-0.4048	[illegible]	[illegible]
4	Poll	-1.085	-0.4927	-0.718	[illegible]	-0.4991	[illegible]	[illegible]	[illegible]	[illegible]
4	Poln	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Polr1e	-1.2072	-0.5046	-0.5452	[illegible]	[illegible]	[illegible]	-0.4148	[illegible]	[illegible]
4	Polr2j	[illegible]	[illegible]	-0.59	[illegible]	-0.411	[illegible]	[illegible]	[illegible]	[illegible]
4	Polr3b	-0.8061	-0.722	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.6976
4	Polr3h	-0.9612	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Polr3k	-0.4683	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pomgnt1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pomp	-0.7055	-0.5996	-0.7229	-0.4446	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pomt1	-0.4182	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.4503	[illegible]
4	Pon3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Por	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Postn	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pou2f2	-0.4141	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pou3f3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pou4f1	-0.4321	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppapdc2	[illegible]	[illegible]	0.4215	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-1.0963
4	Ppargc1a	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppcdc	-0.6439	-0.5105	[illegible]	-0.4183	[illegible]	-0.4755	[illegible]	[illegible]	[illegible]
4	Ppef2	-0.4516	[illegible]	[illegible]	[illegible]	-0.4971	[illegible]	[illegible]	[illegible]	0.5641
4	Ppm1f	[illegible]	[illegible]	[illegible]	[illegible]	-0.5156	-0.4325	-0.7171	-0.6025	[illegible]
4	Ppme1	-0.7156	-0.5141	-0.5338	[illegible]	-0.421	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppnr	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.3401	-0.4107	-1.4747
4	Ppox	[illegible]	[illegible]	[illegible]	-0.4283	[illegible]	-0.244	-0.4321	[illegible]	-0.7893
4	Ppp1r13b	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.5166	-0.6823	-0.7894	-1.0458
4	Ppp1r26	-0.6283	-0.4021	-0.8308	-0.6304	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppp1r3a	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppp1r3b	-0.5114	[illegible]	-0.4261	-0.5256	[illegible]	-0.4459	-0.4974	-0.5544	-0.4291
4	Ppp1r9a	-1.5149	-1.1349	-0.4025	[illegible]	[illegible]	-0.6075	[illegible]	-0.4524	0.4569
4	Ppp2ca	-0.6162	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.5595	[illegible]	[illegible]
4	Ppp2r3c	-0.7416	-0.721	-0.6667	[illegible]	-0.536	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppp3cb	[illegible]	[illegible]	-0.4716	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppp3r1	-0.5164	0.4117	-0.4246	[illegible]	-0.6892	0.7176	-0.7597	[illegible]	[illegible]
4	Ppp6r2	[illegible]	-0.5148	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Ppwd1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Pqlc2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.4569	[illegible]	[illegible]	[illegible]
4	Prdx3	-0.6622	-0.4186	-0.6047	[illegible]	-0.4432	[illegible]	-0.8439	-0.5655	[illegible]
4	Prdx4	[illegible]	[illegible]	[illegible]	[illegible]	-0.4862	-0.5666	[illegible]	[illegible]	[illegible]
4	Prdx6	[illegible]	-0.4546	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prdx6b	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Preb	-0.551	-0.4473	-0.517	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prep	-0.9054	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.4414
4	Prepl	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.7799
4	Prex1	-1.193	-1.3513	-0.8118	-0.7929	[illegible]	[illegible]	[illegible]	[illegible]	-0.5695
4	Prkcd	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.5035
4	Prkd2	[illegible]	-0.4316	-0.5786	[illegible]	[illegible]	[illegible]	-0.6824	[illegible]	-1.0599
4	Prkd3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prkg2	[illegible]	[illegible]	[illegible]	-0.5699	[illegible]	[illegible]	-0.5782	-0.6822	[illegible]
4	Prkra	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.6305
4	Prkrip1	-0.6718	-0.6472	-0.4735	-0.4402	[illegible]	[illegible]	[illegible]	-0.4244	[illegible]
4	Prkrir	[illegible]	[illegible]	-0.4087	-0.4643	-0.4902	[illegible]	[illegible]	-0.7185	[illegible]
4	Prkx	[illegible]	-0.9333	[illegible]	[illegible]	[illegible]	-0.4369	[illegible]	-0.4511	[illegible]
4	Prlr	[illegible]	[illegible]	-0.5866	-0.7566	-0.4348	[illegible]	[illegible]	[illegible]	[illegible]
4	Prm1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prmt3	-1.0141	-0.6401	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.4707
4	Prok2	-0.4827	-0.4854	[illegible]	[illegible]	0.5211	[illegible]	[illegible]	-0.4307	-0.4371
4	Prokr2	-0.4057	[illegible]	[illegible]	-0.4125	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prorsd1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.4558	[illegible]	[illegible]
4	Prox2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Proz	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prpmp5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prr13	-0.9346	-0.5095	0.4078	0.5971	[illegible]	[illegible]	-1.0638	[illegible]	-1.7588
4	Prr14	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prr15	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.7232	[illegible]	-0.9175
4	Prrc1	0.5924	[illegible]	[illegible]	-0.5257	-0.6699	-0.4323	-0.6879	-0.6456	1.2073
4	Prrc2b	[illegible]	[illegible]	-0.7574	-0.4658	-0.6963	-0.6378	-0.6986	-0.581	[illegible]
4	Prrt1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prss29	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prss34	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Prss41	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Psd3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Psen2	[illegible]	[illegible]	[illegible]	-0.4133	-0.3727	-0.5091	-0.6314	-0.4445	-0.6077
4	Psenen	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-0.718
4	Psg18	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Psg27	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Psma4	-0.4506	[illegible]	-0.4611	-0.4238	-0.394	-0.5885	[illegible]	[illegible]	[illegible]
4	Psma5	-1.0896	-0.8481	-0.4692	-0.5077	-0.5311	[illegible]	-0.5863	-0.4084	[illegible]
4	Psma7	-0.8999	-0.5288	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Psmb2	-0.5833	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Psmb8	[illegible]	-0.5729	-0.5598	-0.5117	-0.4172	-0.5729	-0.4657	-0.4992	-0.4009

4	Psmd10	-0.3001	-0.0316	-0.4027	-0.1928	-0.5805	-0.0805	-0.4274	-0.1185	0.1578
4	Psmd13	-0.8828	-0.2932	-0.2268	-0.1166	-0.1534	0.1879	-0.2066	-0.1999	0.5208
4	Psme2	-0.2726	-0.505	-0.0991	-0.3573	-0.159	-0.2384	-0.2465	-0.2018	[illegible]
4	Psmf1	-0.6912	-0.5049	-0.6049	-0.3857	-0.3238	-0.1587	-0.4063	-0.2424	-0.0801
4	Psmg3	-1.0608	-0.3012	-0.5254	0.1731	-0.1935	0.2343	-0.4074	[illegible]	[illegible]
4	Ptdss1	-0.2491	-0.2143	-0.3553	-0.1413	-0.2913	-0.0521	-0.2749	-0.1773	-0.2491
4	Ptgfrn	[illegible]	-0.2289	[illegible]	-0.1165	-0.1343	-0.1842	-0.1819	-0.2075	-0.3585
4	Pth1r	-0.1869	-0.0373	-0.1327	-0.2054	-0.3734	-0.2368	-0.3321	-0.4413	-0.2179
4	Ptplad1	-0.1903	0.1416	-0.455	0.374	-0.4452	0.0713	-0.4449	-0.4056	-0.5558
4	Ptplad2	0.1182	0.0739	-0.4348	-0.2703	-0.2386	-0.1371	-0.445	-0.3003	-0.1164
4	Ptpmt1	-0.261	-0.5805	-0.0898	-0.0276	0.1197	-0.0252	-0.1975	-0.2375	-0.5934
4	Ptpn1	-0.4008	-0.899	-0.5803	-0.6566	-0.6432	-0.6206	-0.6206	-0.4811	[illegible]
4	Ptpn22	-0.1848	-0.2114	-0.1491	-0.108	-0.1491	-0.1652	-0.294	-0.1947	[illegible]
4	Ptpra	0.2658	-0.0617	[illegible]	-0.2913	-0.0843	-0.3724	-0.224	-0.4336	-0.7002
4	Ptprc	-0.4294	-0.2662	-0.3286	-0.2219	-0.3153	-0.263	-0.3153	-0.3938	-0.3053
4	Ptprg	-0.152	-0.1325	-0.2607	[illegible]	-0.1884	-0.2892	-0.1784	-0.2362	-0.2293
4	Ptprr	0.0673	-0.4406	-0.1872	-0.332	-0.3962	-0.3291	-0.3531	-0.3683	-0.2173
4	Ptprt	-0.1129	-0.21	-0.1781	-0.2172	-0.1887	-0.1641	-0.0962	-0.1958	-0.1503
4	Ptrf	-0.0358	0.2775	-0.2252	0.3064	-0.4525	0.4075	-0.9311	-0.6707	-0.7965
4	Ptrh2	-0.2295	0.1071	-0.2924	0.0844	-0.2107	-0.3817	-0.2319	-0.4742	-0.1178
4	Pts	0.1859	0.1336	-0.1817	-0.0725	-0.2404	-0.2063	-0.2296	-0.2368	-0.4919
4	Pus1	-0.4013	-0.2484	-0.0757	0.0653	[illegible]	-0.3214	[illegible]	-0.0903	-0.1973
4	Pxmp4	-0.2216	-0.4022	-0.3337	-0.4244	-0.1037	-0.0771	-0.6052	0.0746	0.0626
4	Pxn	-0.158	[illegible]	-0.5876	-0.2503	-0.3718	-0.1168	-0.3534	-0.4186	-0.1187
4	Pxt1	-0.4655	-0.073	-0.365	-0.4947	-0.5006	-0.2262	-0.4088	-0.3409	-0.1292
4	Pygo2	-0.1098	-0.0237	-0.3051	-0.2539	-0.1743	0.1279	-0.06	-0.1844	-0.2091
4	Qk	-0.3064	-0.1248	[illegible]	-0.1404	-0.1721	-0.2045	-0.1753	-0.2144	[illegible]
4	Qpct	-1.3314	-1.4974	0.2343	-0.1929	0.3266	0.5071	-0.3613	-0.2812	-1.3314
4	Qrfpr	[illegible]	-0.1604	-0.1712	-0.2118	-0.2739	[illegible]	-0.2118	[illegible]	[illegible]
4	Qtrt1	-0.5657	-0.4975	[illegible]	[illegible]	-0.5029	[illegible]	-0.1694	[illegible]	0.527
4	R3hdm1	[illegible]	[illegible]	-0.4743	[illegible]	[illegible]	[illegible]	-0.3507	-0.4615	[illegible]
4	Rab11fip3	-0.4639	-0.4493	-0.4324	-0.5784	-0.6894	-0.7955	-0.7227	-0.6683	-0.2985
4	Rab13	-0.1544	[illegible]	-0.2825	[illegible]	-0.4999	-0.1257	-0.517	-0.3426	-0.4271
4	Rab18	0.3909	[illegible]	-0.2923	-0.0944	-0.4181	-0.6053	-0.1462	-0.473	-0.4712
4	Rab1b	-0.2272	-0.1655	-0.2236	-0.2694	-0.2223	-0.313	-0.2497	-0.4947	-0.3339
4	Rab24	-0.1859	[illegible]	-0.3274	-0.2267	-0.2535	-0.1776	-0.3146	-0.2075	[illegible]
4	Rab25	-1.9416	-1.6707	-0.3063	-0.4186	0.9451	0.8955	0.4977	1.0848	-1.5752
4	Rab2a	-0.3767	-0.2611	-0.305	-0.212	-0.3407	-0.3832	-0.4606	-0.6405	-1.2077
4	Rab3a	-0.2361	[illegible]	-0.4735	-0.1386	-0.4073	-0.1388	-0.8074	-0.6214	-0.5572
4	Rab3gap1	[illegible]	-0.3048	-0.3724	-0.4807	-0.4278	-0.5209	-0.6897	-0.4102	[illegible]
4	Rab40c	-0.3994	-0.2456	-0.565	-0.15	-0.2526	[illegible]	-0.2474	-0.1107	-0.2585
4	Rab42-ps	-0.1625	-0.3752	-0.3785	-0.2863	-0.253	-0.212	-0.3461	-0.4218	-0.1893
4	Rab43	0.116	-0.1164	[illegible]	[illegible]	[illegible]	-0.6472	-0.3113	-0.2401	-0.6377
4	Rab5b	-0.2587	-0.2704	-0.2485	-0.173	-0.1402	-0.1952	-0.2137	-0.1514	0.3003
4	Rab8a	-0.1974	[illegible]	-0.1962	[illegible]	-0.6888	-0.297	-0.3678	-0.7096	0.4455
4	Rabep2	-0.1092	-0.1971	-0.3027	-0.3579	-0.3711	-0.3675	-0.5733	-0.1795	[illegible]
4	Rabgap1	-0.3119	-0.238	-0.1392	-0.3334	-0.2191	-0.2191	-0.2525	-0.1567	-0.3359
4	Rabgap1l	[illegible]	[illegible]	[illegible]	-0.2807	-0.2201	-0.3493	-0.2277	-0.1532	[illegible]
4	Rabgef1	-0.4896	-0.446	-0.1255	[illegible]	-0.2922	[illegible]	-0.8535	-0.3604	-0.9818
4	Rabl2	-0.3975	-0.7081	-0.4113	[illegible]	-0.3882	-0.1766	-0.1559	-0.3906	-0.8417
4	Rac1	-0.1866	[illegible]	-0.1054	[illegible]	-0.22	-0.1402	-0.2866	-0.5305	-0.7478
4	Rad52	-0.3523	[illegible]	-0.4109	-0.1324	-0.1952	[illegible]	-0.182	-0.2232	[illegible]
4	Rala	-0.2587	-0.2451	-0.3342	[illegible]	[illegible]	-0.3142	-0.1255	-0.2182	-0.3137
4	Ralb	-0.1634	-0.1325	-0.7235	-0.6844	-0.6755	-0.5511	-0.8403	-0.7617	[illegible]
4	Ralgapb	-0.5476	-0.4241	-0.3114	-0.3057	-0.238	-0.3049	-0.3096	-0.3663	-0.283
4	Ramp1	[illegible]	[illegible]	-0.2383	-0.3355	-0.1763	-0.3152	-0.5066	-0.61	-0.3088
4	Rapgef1	-0.1224	-0.1525	-0.3656	-0.3992	-0.3472	-0.3592	-0.2388	-0.4254	[illegible]
4	Rapgef4	-0.2774	[illegible]	-0.3169	-0.1673	[illegible]	-0.2465	[illegible]	-0.1426	-0.2226
4	Rapgefl1	-0.3258	-0.3699	-0.425	[illegible]	-0.1316	0.4641	-0.1177	0.2946	-1.3213
4	Rapsn	-0.288	-0.6555	-0.4453	-0.665	-0.5035	-0.1392	-0.2496	-0.2241	0.2909
4	Rasgef1b	[illegible]	-0.1962	-0.2743	-0.2374	-0.323	-0.3261	-0.2759	-0.3063	-0.2172
4	Rasgef1c	[illegible]	-0.2044	-0.3099	-0.2412	-0.2203	-0.3751	-0.1213	-0.3183	-0.1151
4	Rasgrf1	-0.3615	-0.3747	-0.3461	-0.4391	-0.3881	-0.4253	-0.203	[illegible]	-0.2813
4	Rasl12	-0.3216	-0.3974	-0.5712	-0.779	-0.4969	-0.4858	-0.3915	-0.3358	[illegible]
4	Rasl2-9	-0.1786	-0.2813	-0.3407	-0.282	-0.3101	-0.3762	[illegible]	[illegible]	[illegible]
4	Rassf3	-0.9812	-0.62	-0.2403	-0.2457	[illegible]	-0.2222	-0.152	[illegible]	-0.2338
4	Rbbp9	[illegible]	[illegible]	-0.7473	-0.2633	-0.5406	-0.5488	-0.3118	-0.2986	-0.512
4	Rbfa	-0.4326	-0.1921	-0.3552	[illegible]	-0.3826	-0.1637	-0.7254	-0.3115	0.2572
4	Rbks	-0.2835	-0.6035	[illegible]	-0.2041	[illegible]	-0.1473	[illegible]	-0.177	-0.4449
4	Rbm12b	-0.1919	-0.3226	-0.2393	-0.1577	-0.3326	-0.2184	-0.2952	-0.2421	-0.2441
4	Rbm18	[illegible]	[illegible]	-0.2427	-0.1671	-0.507	-0.2508	-0.4883	-0.2091	[illegible]
4	Rbm4	[illegible]	[illegible]	-0.5119	-0.4138	-0.293	-0.3788	[illegible]	[illegible]	-0.3844
4	Rbm5	-0.5173	-0.3526	-0.8491	-0.4646	-0.4624	-0.5624	-0.5889	-0.4842	-0.5086
4	Rbmy1a1	[illegible]	-0.3966	[illegible]	-0.4579	-0.2463	[illegible]	-0.1908	-0.3186	[illegible]
4	Rbx1	-0.594	-0.4207	-0.4719	-0.3712	-0.3525	-0.4031	-0.3875	-0.352	-0.5032
4	Rdh11	-0.3365	-0.4189	-0.3049	-0.3717	-0.2957	[illegible]	[illegible]	[illegible]	0.6042
4	Rdh12	-0.303	-0.2228	-0.6256	-0.2362	-0.209	0.3105	-0.2145	-0.086	[illegible]
4	Rdh16	-0.3153	-0.1678	-0.1794	[illegible]	[illegible]	[illegible]	-0.1327	[illegible]	-0.2775
4	Rdh18-ps	-0.2597	-0.1919	-0.2045	-0.0942	-0.1483	-0.0592	-0.2335	-0.1392	-0.227
4	Rdh8	-0.1503	-0.2053	-0.1913	0.0837	-0.1673	-0.2158	-0.1203	-0.1336	-0.181
4	Rdh9	0.0982	-0.1401	-0.2671	-0.2601	-0.1956	-0.1989	-0.2532	-0.1401	[illegible]
4	Relb	0.5126	-0.1501	-0.1107	-0.3649	-0.1471	-0.2815	-0.1951	-0.3683	-0.1442
4	Rell1	-0.4301	-0.6779	0.2914	-0.25	-0.2712	[illegible]	-0.3878	[illegible]	-0.2819
4	Renbp	-0.2892	-0.9891	-0.5015	-1.2118	-0.4913	-1.1244	-0.2353	-0.8394	0.7979
4	Reps1	-0.5287	-0.4201	-0.273	-0.2329	-0.1111	-0.0587	0.0945	-0.0634	0.116
4	Rer1	-0.1284	0.0764	-0.412	-0.3083	-0.1148	-0.2423	-0.4426	-0.3895	-0.5975
4	Retn	-0.068	0.1271	-0.2182	-0.2555	-0.3015	-0.3653	-0.2442	-0.0515	-0.105
4	Rgnef	0.2672	0.0555	-0.3256	-0.195	-0.3335	-0.5683	-0.475	-0.5997	-0.3873
4	Rgs13	-0.1786	-0.2219	-0.1819	-0.1366	-0.1526	-0.1366	-0.277	-0.2876	-0.0896
4	Rgs7bp	0.2583	0.1762	-0.077	0.4841	-0.6403	-0.4986	-0.4933	-0.7	-0.2489
4	Rgs9	-0.1905	-0.2565	-0.3071	-0.2214	-0.2424	-0.2816	-0.1603	-0.0826	0.1603
4	Rhbdd2	-0.2046	-0.1404	-0.2198	-0.3067	-0.065	-0.0288	-0.0952	-0.0748	-0.1549
4	Rhbdl2	-0.1882	-0.4285	[illegible]	-0.2533	-0.1799	-0.1455	0.1808	-0.5811	0.2279
4	Rhof	-0.8559	-0.4168	-0.5153	-0.2741	-0.2337	[illegible]	0.1425	-0.2741	-0.2443
4	Rhoq	-0.105	[illegible]	-0.1605	-0.0747	-0.2256	-0.263	-0.1325	-0.0747	-0.1325
4	Riiad1	[illegible]	-0.163	-0.1161	-0.1779	-0.31	-0.271	0.0675	-0.1809	-0.0876
4	Rltpr	-0.2031	-0.1922	-0.1672	-0.1994	-0.1287	-0.1047	0.1326	-0.2399	-0.115
4	Rmnd1	-0.6559	-0.3678	-0.7129	-0.4272	-0.4897	-0.2425	-0.6081	-0.4832	[illegible]
4	Rnase6	-0.2352	-0.1046	-0.2352	-0.2138	-0.1926	-0.1718	-0.1178	-0.1412	-0.1926
4	Rnaseh1	-0.4072	-0.4456	-0.5115	-0.1703	-0.3246	-0.2176	-0.117	[illegible]	0.0664
4	Rnasek	-0.2208	0.0636	-0.1701	-0.1073	-0.5536	-0.3918	-0.4776	-0.5011	[illegible]
4	Rnaset2	-1.097	-1.1475	0.2578	0.0754	0.3742	[illegible]	-0.476	-0.124	-1.8759
4	Rnf121	-0.1433	-0.1413	-0.1333	-0.226	-0.4488	-0.1779	-0.4364	-0.6828	-0.2714
4	Rnf181	-0.0908	-0.1476	-0.6126	-0.4328	-0.4578	-0.6946	-0.4772	-0.2712	0.1063
4	Rnf182	-0.1522	-0.4776	-0.3485	-0.338	-0.495	-0.492	-0.5363	-0.5819	-0.2107
4	Rnf214	-0.1666	-0.1353	-0.0872	-0.1184	-0.2049	-0.0556	-0.3469	-0.1666	[illegible]
4	Rnf219	-0.3838	0.2277	-0.6257	0.3167	0.2461	0.4107	[illegible]	0.1758	-1.7045
4	Rnf38	-0.1966	-0.2224	-0.1129	-0.1588	-0.2354	0.1481	-0.0714	-0.2486	[illegible]
4	Rnf6	-0.1397	[illegible]	-0.2375	-0.239	-0.2907	-0.0872	-0.4815	-0.5983	-0.6564
4	Rnft2	-0.7478	-0.6719	-0.4506	-0.4708	-0.6682	-0.5997	-0.3956	-0.4442	0.0987
4	Rnls	-0.05	-0.2538	-0.1101	-0.1963	-0.1018	-0.3428	-0.2786	-0.1612	[illegible]
4	Robo1	0.2218	-0.209	-0.0765	[illegible]	-0.3717	-0.4064	-0.5415	-0.4259	-0.2998
4	Rorb	-0.419	-0.366	-0.3845	-0.4414	-0.3538	-0.369	-0.4511	-0.4414	-0.4511
4	Rp9	-0.2151	-0.0478	[illegible]	-0.0398	-0.1735	0.1285	-0.2737	-0.3981	-0.3997
4	Rpain	-0.3438	-0.6682	-0.7144	-0.6583	-0.2431	-0.2223	-0.1787	-0.1863	0.4161
4	Rpia	-0.1999	-0.1964	-0.4023	-0.1976	-0.3707	-0.2834	-0.4678	-0.4539	-1.2221
4	Rpl13a	-0.7188	-0.4659	-0.1053	-0.1075	0.0801	-0.0733	-0.4623	-0.7561	0.126
4	Rpl18	-0.5678	-0.5695	-0.3012	-0.5339	[illegible]	-0.3551	-0.1817	-0.2375	[illegible]
4	Rpl23	-0.8458	-0.1881	-0.5848	-0.2571	-0.2246	-0.1668	0.3994	-0.2691	0.1268
4	Rpl23a	-0.3223	[illegible]	-0.1743	-0.2541	[illegible]	-0.2346	-0.3936	-0.2431	[illegible]
4	Rpl27	-1.066	-0.5921	-0.4312	-0.3473	-0.4501	-0.5922	-0.7159	-0.7349	0.2157
4	Rpl31	-0.745	-0.5281	-0.3024	0.3393	-0.1802	0.0688	-0.3069	-0.3757	-0.0844
4	Rpl35	-0.3055	-0.1918	-0.3002	-0.1859	-0.156	-0.2694	[illegible]	[illegible]	-0.2648
4	Rpl37	-0.1795	[illegible]	-0.288	-0.1558	[illegible]	-0.2688	-0.051	-0.073	-0.1647
4	Rpl38	-1.3476	-0.8137	-0.6111	-0.287	-0.1311	0.1099	-0.1365	-0.1356	0.6077
4	Rpl9	-0.5751	-0.5434	-0.4497	-0.2679	-0.2672	-0.4523	-0.3107	-0.0792	-0.1776
4	Rplp0	-0.5047	-0.0826	-0.0944	-0.1677	-0.2317	-0.237	-0.1404	-0.2058	-0.6131
4	Rpp14	-0.7235	-0.4145	-0.3095	0.293	-0.1255	0.1956	-0.1609	-0.1116	-0.5319
4	Rpp38	-1.0852	-0.8601	-0.9363	-0.3519	-0.3669	-0.5119	-0.4642	-0.4954	-0.3067
4	Rps10	-0.4339	-0.337	-0.148	-0.1237	-0.0647	-0.1982	-0.2016	-0.1652	-0.7487
4	Rps12	-0.1529	-0.0286	-0.3739	-0.0467	-0.1135	-0.234	-0.168	-0.03	-0.2415
4	Rps2	-0.4122	-0.1117	-0.4924	[illegible]	-0.0474	-0.0386	0.0877	0.1387	-0.4218
4	Rps26	-0.4099	-0.2755	-0.5385	-0.1588	-0.4505	-0.2954	-0.3893	-0.1436	-0.8462
4	Rps4x	-0.3453	-0.1323	-0.2713	[illegible]	-0.1222	-0.3327	[illegible]	[illegible]	-0.3327
4	Rps5	-0.5349	-0.5898	-0.3786	-0.7484	-0.4909	-0.6704	-0.3526	-0.5564	-0.3547
4	Rps6	-0.5663	-0.1988	-0.1339	-0.1607	-0.1739	-0.1988	-0.4416	-0.1318	0.5316
4	Rps6kb1	-0.3426	-0.218	-0.1644	[illegible]	-0.2421	-0.249	0.0687	-0.249	-0.0939
4	Rps7	-0.7105	-0.6334	-0.4945	-0.4448	-0.6448	-0.6118	-0.9689	-0.8359	-0.0821
4	Rragc	0.1396	-0.1516	0.1807	-0.278	-0.2582	-0.2817	-0.6346	-0.6301	-0.7829
4	Rrm2b	-0.6353	-0.6633	-0.286	-0.1392	0.0809	-0.0815	-0.4346	-0.1734	-1.1294
4	Rsad1	-0.4234	-0.1565	-0.6389	-0.0997	-0.3369	-0.417	-0.5531	-0.228	-1.359
4	Rtn4r	-0.2771	-0.1319	-0.2075	[illegible]	-0.3045	0.3225	-0.416	-0.1258	-0.1166
4	Rufy1	-0.2894	-0.2894	[illegible]	-0.2375	-0.2107	-0.6215	-0.528	-0.4367	-0.4763
4	Rufy3	-0.1017	-0.2459	-0.089	-0.2249	[illegible]	-0.2318	-0.0826	-0.1471	-0.1405
4	Rundc1	-0.1021	-0.0377	-0.235	-0.4338	-0.1906	-0.0974	-0.1487	-0.1222	-0.2571
4	Runx1	-0.2476	-0.1055	[illegible]	-0.3031	-0.0821	-0.1941	-0.3506	-0.1536	-0.6777
4	Rusc1	-0.13	-0.2907	-0.3855	-0.1934	-0.1768	[illegible]	-0.183	-0.0925	-0.2423
4	Rxrb	-0.7084	-0.5851	-0.5665	-0.3379	-0.546	-0.4782	-0.5058	-0.3633	0.5176
4	S100a14	-0.5999	-0.5555	-0.3877	-0.43	[illegible]	0.0624	-0.2224	-0.2806	-0.5555
4	S100a8	-0.3732	-0.3426	-0.1304	-0.3326	-0.2737	-0.2514	-0.4293	-0.3061	-0.4257
4	S100a9	-0.4753	-0.444	-0.444	-0.3442	-0.2065	-0.189	-0.3933	-0.341	-0.4966
4	S1pr2	0.3632	0.4453	-0.3294	-0.2974	-0.3671	-0.4646	-0.362	-0.3269	-0.3047
4	S1pr5	-0.1121	-0.2508	-0.2439	-0.416	-0.0964	-0.1931	-0.1569	-0.2789	-0.1439
4	Sacm1l	-0.1716	[illegible]	[illegible]	-0.1119	-0.1944	-0.4626	-0.4259	-0.2468	-0.61
4	Samd5	0.2352	[illegible]	[illegible]	-0.2474	-0.2275	-0.3654	-0.2541	-0.1601	-0.2112
4	Samhd1	-0.403	-0.9658	-0.5329	-0.775	-0.3115	-0.5914	-0.1999	-0.5758	-0.4633
4	Sap30l	-0.3828	-0.344	-0.431	-0.1132	-0.5798	-0.3909	-0.7512	-0.7294	0.8159
4	Sars	-0.0988	0.1028	-0.5204	-0.1537	-0.3862	-0.0552	-0.2573	-0.1419	0.4692
4	Sat2	[illegible]	-0.077	-0.6628	-0.456	-0.4279	-0.4322	-0.4937	-0.4129	-0.0899
4	Sbds	-0.5853	-0.1993	-0.5487	-0.0346	-0.5456	[illegible]	-0.6395	-0.4615	0.1961
4	Sc5d	0.099	0.2548	-0.0353	-0.1063	-0.124	-0.5829	-0.0997	-0.142	-0.5023
4	Scamp1	-0.4841	-0.6364	0.1504	-0.0532	0.1011	0.2398	[illegible]	-0.1043	-1.1484
4	Scarb2	-0.7468	-0.8159	0.0826	-0.0272	0.4944	0.1759	-0.5386	[illegible]	-1.0276
4	Sccpdh	0.5683	0.5919	-0.4532	-0.5435	-0.8358	-1.0828	-0.214	-0.69	0.2749

4	Scd1	-0.7297	-0.5802	[illegible]	-0.4344	[illegible]	[illegible]	[illegible]	[illegible]	-0.46
4	Scd2	-0.9449	-0.3538	-0.5503	-0.6157	-0.6038	[illegible]	-0.263	[illegible]	[illegible]
4	Scel	-0.5872	-0.2905	-0.1549	-0.2812	-0.1901	-0.4922	-0.216	-0.4031	-0.534
4	Scg2	[illegible]	-0.3128	-0.3968	-0.4577	-0.3933	-0.366	-0.3956	-0.3717	-0.3459
4	Scgb1a1	-0.3253	-0.1356	-0.2593	-0.2136	-0.4413	-0.2625	-0.2464	-0.3789	-0.258
4	scl0003251.1_21	[illegible]	[illegible]	-0.0858	-0.1602	-0.3047	[illegible]	-0.1326	-0.3931	-0.3453
4	scl000510.1_2	-0.2872	-0.5324	-0.2557	-0.342	-0.2172	-0.4526	-0.2897	[illegible]	-0.3172
4	Scml4	[illegible]	-0.3759	[illegible]	[illegible]	-0.3646	[illegible]	[illegible]	-0.1474	[illegible]
4	Scnm1	-0.6084	-0.5826	-0.5826	-0.2856	-0.3876	-0.2519	-0.5235	-0.4795	[illegible]
4	Scrn1	-0.3043	-0.3586	[illegible]	[illegible]	[illegible]	-0.2702	-0.3468	-0.4736	-0.3521
4	Scyl3	-0.6899	-0.616	-0.4869	-0.3458	-0.4	-0.3136	-0.2271	[illegible]	[illegible]
4	Sdccag8	[illegible]	[illegible]	[illegible]	-0.2345	[illegible]	[illegible]	[illegible]	[illegible]	-0.2509
4	Sdhaf2	[illegible]	[illegible]	-0.3831	-0.3239	-0.4565	-0.3581	-0.2898	-0.6679	-0.4114
4	Sdr42e1	-0.3033	-0.2893	-0.3145	-0.1622	[illegible]	[illegible]	-0.2527	-0.1673	[illegible]
4	Sdr9c7	-0.1463	-0.2797	-0.2073	-0.3214	[illegible]	[illegible]	-0.1517	-0.3321	[illegible]
4	Sdsl	-0.5301	-0.3464	-0.2563	-0.3723	-0.3443	-0.5786	-0.4623	-0.5951	-0.872
4	Sec11a	[illegible]	[illegible]	-0.4019	-0.2022	-0.4529	-0.2097	[illegible]	-0.6711	-0.4723
4	Sec11c	[illegible]	-0.1568	-0.3895	-0.2597	-0.2516	-0.3221	-0.3249	-0.3723	-0.3149
4	Sec22a	[illegible]	-0.3251	-0.3021	-0.2196	[illegible]	-0.1549	[illegible]	[illegible]	-0.2766
4	Sectm1a	-0.1281	[illegible]	-0.2249	-0.1686	-0.1858	-0.301	-0.2488	-0.1682	-0.145
4	Selenbp2	-0.4148	-0.2534	-0.3584	-0.1506	-0.2411	-0.3337	-0.2171	[illegible]	-0.3102
4	Sell	-0.4906	-0.6598	[illegible]	[illegible]	[illegible]	-0.3284	-0.3693	-0.5179	-0.6362
4	Selm	-0.5694	[illegible]	-0.5468	-0.6115	-0.6306	-0.6044	-0.5811	-0.3604	-0.3284
4	Sema3b	[illegible]	-0.1736	-0.4806	-0.1885	-0.2549	[illegible]	-0.493	-0.5023	-0.3296
4	Sema3d	[illegible]	[illegible]	[illegible]	-0.2057	-0.2596	-0.2455	-0.3409	-0.3787	-0.2123
4	Sema4a	-1.2895	-1.2895	-0.9103	-0.7045	-0.5595	-0.2998	-0.6117	-0.4789	1.33
4	Senp5	[illegible]	[illegible]	-0.4052	[illegible]	[illegible]	-0.1463	-0.3965	[illegible]	[illegible]
4	Senp6	-0.2636	-0.2659	[illegible]	-0.1264	[illegible]	-0.3768	-0.1702	-0.1629	-0.262
4	41529	[illegible]	-0.2072	-0.3193	-0.3241	-0.3231	-0.1685	-0.1572	-0.1943	[illegible]
4	41523	-0.6493	-0.2882	[illegible]	[illegible]	-0.2831	[illegible]	[illegible]	-0.3067	-0.457
4	Sergef	-0.7395	-0.3159	-0.3434	-0.2316	-0.2105	-0.1654	-0.5959	-0.4305	-0.6412
4	Serinc4	-0.1847	-0.212	-0.2294	-0.1643	-0.3116	-0.2829	-0.161	-0.1802	-0.1443
4	Serpina12	-0.1271	[illegible]	-0.1473	-0.1673	-0.212	-0.1865	-0.1457	-0.2131	-0.2139
4	Serpina1b	-0.7981	-0.7885	-0.5943	-0.4817	-0.7917	-0.2812	-0.6747	[illegible]	-0.7917
4	Serpina1d	-0.7633	-0.5078	-0.3421	-0.4853	[illegible]	-0.1151	-0.5049	-0.3749	-0.6788
4	Serpina1e	-1.0952	-1.0045	-0.804	-0.4985	-0.581	[illegible]	-0.6279	0.3217	-1.0952
4	Serpina3k	-0.1471	[illegible]	-0.2657	-0.1609	-0.2637	[illegible]	-0.1173	-0.154	-0.1804
4	Serpina9	-0.1946	-0.3369	-0.5667	-0.3941	-0.4327	-0.5093	-0.3677	-0.3332	-0.487
4	Serpinb11	-0.4203	-0.4228	-0.3856	-0.3417	-0.1992	-0.4133	-0.3024	-0.3024	-0.5071
4	Serpinb2	-0.2444	-0.1619	-0.1981	-0.1273	-0.1841	-0.1489	-0.1645	-0.1143	-0.1776
4	Serpinb3b	-0.1229	-0.1683	-0.3167	-0.1026	-0.3101	-0.2525	[illegible]	-0.1872	-0.2086
4	Serpinb6b	-0.1239	-0.1152	-0.3482	-0.2557	-0.2853	-0.24	-0.2054	-0.2825	-0.3201
4	Serpine1	-0.2569	-0.2024	-0.2149	-0.2617	-0.1107	-0.2138	-0.2605	[illegible]	[illegible]
4	Serpini1	-0.1706	-0.3825	-0.2422	-0.3177	[illegible]	-0.3454	-0.2744	-0.1929	-0.3121
4	Sertad3	-0.1729	-0.3058	-0.318	-0.3034	-0.3637	-0.273	-0.1526	-0.5494	-0.5343
4	Setd5	-0.2619	-0.3255	-0.4607	-0.4111	[illegible]	-0.3319	[illegible]	[illegible]	-0.3032
4	Sfpi1	-0.683	-0.5465	-0.6303	-0.3805	-0.5561	-0.4673	-0.3251	-0.5238	-0.4423
4	Sft2d2	-0.5954	-0.4608	-0.3836	-0.4885	[illegible]	[illegible]	[illegible]	-0.1174	[illegible]
4	Sfxn1	-1.4329	-0.5756	-0.5203	[illegible]	-0.285	[illegible]	-0.6994	-0.3803	-0.2939
4	Sfxn4	-0.2221	-0.6968	-0.634	-0.5736	-0.4844	-0.661	-0.4487	-0.5919	-0.4025
4	Sfxn5	-0.2048	[illegible]	-0.6398	-0.6365	-0.4993	-0.6669	-0.5488	-0.3112	-0.1665
4	Sgca	-0.2337	-0.3189	-0.1777	-0.4377	-0.363	-0.2496	-0.2789	-0.1287	-0.1905
4	Sgip1	-0.2075	-0.1813	-0.1351	-0.2472	-0.2006	-0.2542	-0.3022	-0.2771	-0.3064
4	Sgk3	-0.3073	-0.1233	[illegible]	-0.1919	-0.1886	-0.3367	-0.3305	-0.3045	-0.2891
4	Sgsm1	-0.742	-0.7146	-0.1878	-0.1223	-0.1387	-0.1604	[illegible]	[illegible]	-0.1626
4	Sgta	-0.3191	-0.1866	-0.1271	[illegible]	[illegible]	-0.1154	-0.1371	-0.24	-0.1175
4	Sgtb	-0.6999	-0.5081	[illegible]	-0.3051	[illegible]	[illegible]	-0.2687	-0.2303	[illegible]
4	Sh2d1b2	-0.2332	-0.3372	-0.2586	-0.2787	-0.2224	-0.2059	-0.3226	-0.3164	-0.2133
4	Sh2d2a	-0.2462	-0.136	-0.1	-0.2179	-0.1137	[illegible]	[illegible]	-0.2249	[illegible]
4	Sh3gl1	[illegible]	[illegible]	-0.2617	-0.5488	-0.6575	-0.6838	-0.5363	-0.5175	[illegible]
4	Sh3glb2	-0.738	-0.1753	-0.435	-0.2179	[illegible]	[illegible]	-0.5551	-0.1764	-0.5247
4	Sh3rf1	[illegible]	-0.346	-0.4142	-0.435	-0.1802	-0.43	[illegible]	-0.1643	[illegible]
4	Shank3	-0.547	-0.2464	[illegible]	-0.1626	-0.2109	-0.3197	-0.3201	-0.1871	-0.3273
4	Shpk	[illegible]	-0.112	[illegible]	-0.1011	-0.1945	-0.2082	-0.2123	-0.1821	-0.1752
4	Shprh	-1.089	-0.3556	-0.6045	-0.3201	-0.5446	-0.2406	-0.1776	-0.235	-0.2429
4	Shroom1	[illegible]	[illegible]	-0.5792	-0.5879	-0.5198	-0.3551	-0.5365	-0.4958	-0.8009
4	Siah1a	[illegible]	-0.3761	[illegible]	-0.3577	[illegible]	-0.4507	[illegible]	-0.1895	[illegible]
4	Siglec1	-0.4169	-0.4242	-0.363	-0.3594	-0.4132	-0.3987	-0.438	-0.4427	-0.4502
4	Sil1	[illegible]	-0.3165	-0.375	-0.2833	-0.5807	-0.2156	-0.9225	-0.4218	-0.8671
4	Sirpb1a	-0.4779	-0.2791	-0.2591	-0.1904	-0.3256	-0.3219	-0.2985	-0.2545	-0.2664
4	Sirt3	-0.3994	-0.8127	-0.5196	-0.6674	-0.4895	-0.3053	-0.4203	-0.4939	-0.5745
4	Sirt5	-0.3846	-0.4141	-0.2444	-0.3737	-0.336	-0.4177	-0.5272	-0.4411	-0.3726
4	Sirt7	-0.3799	-0.3926	-0.1967	-0.2289	-0.2938	-0.2734	-0.7896	-0.4142	-0.7348
4	Sit1	-0.2577	-0.3292	-0.3525	[illegible]	-0.2609	-0.3494	-0.2836	-0.2821	-0.1066
4	Six3	-0.1243	-0.1407	[illegible]	-0.1576	-0.1264	-0.1282	-0.1757	-0.1236	-0.1178
4	Skap2	-0.5901	-0.7098	[illegible]	-0.2444	-0.2502	-0.1169	-0.1464	[illegible]	[illegible]
4	Skint2	-0.3482	-0.3515	-0.1709	-0.2677	-0.2306	-0.2306	-0.2215	-0.2337	[illegible]
4	Skint7	-0.2256	-0.219	-0.1455	[illegible]	-0.1751	-0.1835	-0.1586	-0.1598	-0.1247
4	Skint9	-0.1707	-0.1461	-0.1916	[illegible]	-0.1844	-0.1436	-0.1077	-0.1648	-0.1479
4	Skiv2l	-0.33	-0.3993	[illegible]	-0.1866	-0.1575	-0.2761	-0.2714	-0.2296	-0.2228
4	Slamf9	-0.1598	-0.3666	-0.4167	-0.4547	-0.156	-0.4442	[illegible]	-0.1997	[illegible]
4	Slc10a1	-0.1608	-0.2012	-0.2359	-0.154	-0.1606	-0.1875	-0.1786	-0.1966	[illegible]
4	Slc11a2	-0.4298	-0.2608	-0.203	-0.3212	-0.3637	-0.5147	-0.4613	-0.506	-0.649
4	Slc12a9	-0.3872	-0.5507	-0.477	-0.4379	-0.5789	-0.4387	-0.6034	-0.6662	-0.527
4	Slc16a10	-0.3523	-0.3096	-0.2808	-0.3632	-0.182	-0.1429	-0.3466	-0.1626	-0.1526
4	Slc16a12	-0.1295	-0.1841	-0.1369	-0.1879	-0.1298	[illegible]	-0.177	-0.1177	-0.1341
4	Slc16a6	-0.8697	-0.9109	-0.6927	-0.5101	-0.3902	-0.3682	-0.2964	-0.3258	-0.2632
4	Slc16a9	-0.1646	-0.3469	-0.2451	-0.4847	-0.402	-0.5487	-0.5778	-0.613	-0.2844
4	Slc17a5	-0.4609	-0.5946	-0.6416	-0.6149	-0.5688	-0.5185	-0.8126	-0.3529	-0.6105
4	Slc17a8	-0.1229	[illegible]	-0.1226	[illegible]	[illegible]	-0.1642	-0.3279	-0.1513	-0.1176
4	Slc19a1	-1.2308	-0.1306	-0.8033	-0.2424	-0.8422	-0.2154	-1.0426	-0.3564	-0.7328
4	Slc1a2	[illegible]	-0.1712	-0.1646	[illegible]	-0.1726	-0.1725	[illegible]	-0.1745	-0.1726
4	Slc1a3	0.8426	0.616	-1.5792	-1.7907	-1.4501	-1.7951	0.6454	0.1806	1.1668
4	Slc22a13b	-0.3788	-0.3228	-0.2428	-0.1811	-0.4326	-0.3019	-0.3447	-0.3645	-0.2469
4	Slc22a19	-0.1842	-0.3242	-0.2153	-0.2866	-0.3255	-0.2234	-0.1571	[illegible]	-0.1735
4	Slc22a9	-0.1648	[illegible]	-0.1999	-0.5015	-0.5044	-0.3647	-0.5456	-0.382	-0.5278
4	Slc24a2	-0.1807	-0.1542	-0.1701	-0.3247	-0.1615	-0.1611	-0.1867	-0.2254	-0.1929
4	Slc24a6	-0.9538	-1.036	-0.3767	[illegible]	-0.4731	-0.1764	[illegible]	-0.373	-0.5512
4	Slc25a12	-0.3521	-0.1869	-0.7274	-0.3706	-0.7289	-0.9302	-0.846	-0.7197	-0.4135
4	Slc25a18	-0.5682	-0.4715	-0.3551	-0.1159	-0.5718	-0.4837	-0.5021	-0.3384	-0.2502
4	Slc25a27	-0.2417	[illegible]	-0.1705	-0.1723	-0.2746	-0.2379	-0.1545	-0.167	-0.1474
4	Slc25a28	-0.7266	-0.4238	-0.6608	-0.5079	-0.4169	-0.5074	-0.6561	-0.4002	-0.2005
4	Slc25a37	[illegible]	-0.1638	-0.2989	[illegible]	-0.2358	-0.304	-0.5368	[illegible]	-0.4605
4	Slc25a47	-0.1793	-0.2707	-0.3848	-0.2487	-0.1562	-0.2527	-0.2898	-0.3443	-0.2779
4	Slc25a48	-0.3809	-0.2787	-0.1918	-0.1241	[illegible]	[illegible]	-0.1406	[illegible]	-0.1954
4	Slc26a1	-0.2163	-0.3549	-0.2476	-0.324	-0.2404	-0.2971	-0.3289	-0.2631	-0.3195
4	Slc26a4	-0.1092	-0.3115	-0.3341	-0.3633	-0.3888	-0.3568	-0.3405	-0.3786	-0.3162
4	Slc26a6	-0.1064	-0.1543	-0.288	-0.3675	-0.2024	-0.1218	-0.1393	-0.1371	-0.1364
4	Slc26a9	-0.1582	-0.2545	-0.2179	-0.2343	-0.3458	[illegible]	-0.1678	-0.3028	-0.1965
4	Slc27a4	-0.1967	-0.2758	-0.2344	-0.1777	-0.2629	-0.2109	-0.4535	-0.2406	-0.4467
4	Slc27a6	-0.2883	-0.4193	-0.1864	-0.3472	-0.3263	-0.3124	-0.3883	-0.3867	-0.1804
4	Slc29a3	-0.2045	[illegible]	-0.3884	-0.3981	-0.5395	-0.3236	-0.7789	-0.6661	-0.6065
4	Slc2a9	-0.1022	-0.1166	-0.2501	-0.1931	-0.1121	-0.2507	[illegible]	-0.3107	-0.1616
4	Slc30a4	-0.4976	-0.1182	-0.1776	-0.1839	[illegible]	[illegible]	-0.4119	-0.3529	-0.2386
4	Slc35a1	-0.1529	[illegible]	-0.4378	-0.4472	-0.5037	-0.4924	-0.4373	-0.4657	-0.2966
4	Slc35e3	-0.5066	-0.3496	-0.6746	-0.3991	-1.1768	-0.4145	-1.1481	-0.9838	-0.2609
4	Slc35f5	-0.1926	-0.1453	[illegible]	-0.4354	-0.1461	-0.3934	-0.2124	-0.1424	-0.3462
4	Slc38a10	-0.1566	-0.3006	-0.1662	-0.283	-0.4456	-0.562	-0.4219	-0.6482	[illegible]
4	Slc38a3	-0.3959	-0.3185	-0.2352	-0.3123	-0.3416	-0.3417	-0.3436	-0.1536	[illegible]
4	Slc38a9	-0.2663	-0.4577	-0.2568	-0.4745	-0.4535	-0.6789	-0.5277	-0.42	-0.3168
4	Slc39a3	-0.2279	-0.1683	-0.3779	-0.2605	-0.4763	-0.4583	-0.4192	-0.4025	-0.5818
4	Slc39a7	-0.1755	-0.2585	-0.4789	-0.6031	-0.7336	-0.7451	-0.5828	-0.6329	-0.7049
4	Slc4a3	[illegible]	[illegible]	-0.4957	-0.4693	-0.8308	-0.8649	-0.7048	-0.771	-0.6718
4	Slc4a8	-1.2318	-0.6528	-0.5399	-0.4041	-0.6412	-0.6459	-0.6441	-0.6034	-0.3562
4	Slc5a10	-0.3115	-0.2536	-0.2384	-0.3019	-0.1626	-0.4386	-0.131	-0.3106	-0.2336
4	Slc6a13	-0.2751	-0.3261	-0.2735	-0.2427	[illegible]	-0.2121	-0.1667	-0.1771	-0.2364
4	Slc6a6	-0.5195	-0.4208	-0.1747	[illegible]	-0.2784	-0.2656	-0.642	-0.4571	-0.7904
4	Slc7a11	-0.6568	-0.4228	-0.2728	-0.2877	-0.3243	-0.4143	-0.6026	-0.3729	-1.0056
4	Slc7a14	-0.4479	-0.5106	-0.2448	-0.3878	-0.3389	-0.3119	-0.3715	-0.1985	-0.3132
4	Slc8a3	-0.2577	-0.2588	-0.2044	-0.3412	-0.3116	-0.2507	-0.3007	-0.2719	-0.3134
4	Slc9a1	-0.1081	-0.1813	-0.5807	-0.6399	-0.6741	-0.8444	-0.6541	-0.7121	-0.3211
4	Slc9a6	-0.1965	-0.2254	-0.1817	-0.2617	[illegible]	-0.2711	[illegible]	-0.2431	-0.2144
4	Slc9a9	-0.4433	-0.3372	-0.4092	-0.4639	-0.3925	-0.3278	-0.4294	-0.4431	-0.4639
4	Slco1c1	-0.6071	-0.4688	-0.4421	-0.5346	-0.5279	-0.517	-0.4159	-0.5031	-0.6488
4	Slfn2	-0.2551	-0.1091	-0.1069	-0.2768	-0.246	-0.1095	-0.2257	-0.1694	-0.2224
4	Slitrk1	[illegible]	[illegible]	[illegible]	-0.1057	[illegible]	-0.1198	-0.1461	-0.1117	[illegible]
4	Slitrk5	-0.3485	-0.3066	-0.9958	-0.6054	-0.8629	-0.2847	-0.4751	-0.4731	-1.0878
4	Slitrk6	-0.3465	-0.1659	-0.3288	-0.2216	-0.1791	-0.1264	-0.2904	-0.1968	-0.2216
4	Slmo1	-0.389	-0.2923	-0.1525	[illegible]	-0.193	-0.1062	-0.1313	-0.1106	-0.1439
4	Slu7	-0.3374	-0.2055	-0.3079	-0.3047	-0.2577	-0.3546	-0.3368	-0.3208	-0.2144
4	Smad1	[illegible]	-0.1868	-0.1447	-0.1502	-0.1955	-0.4165	-0.3892	-0.6394	-0.2283
4	Smad7	-0.3029	-0.1742	-0.1662	-0.2664	-0.2325	-0.3717	-0.3299	-0.2866	-0.2295
4	Smarcd2	-0.9118	-0.5737	-0.488	-0.3491	-0.3201	[illegible]	-0.5302	-0.5	-0.1815
4	Smarce1	-0.2058	-0.1772	-0.4369	-0.1481	-0.5124	[illegible]	-0.3187	[illegible]	-0.304
4	Smg6	-0.2265	-0.2041	-0.2584	-0.521	-0.369	[illegible]	-0.4751	[illegible]	-0.3993
4	Smox	-0.3311	-0.2788	-0.3597	-0.3696	-0.3729	-0.2461	-0.3476	[illegible]	-0.647
4	Smtnl1	-0.1877	-0.1071	-0.2934	-0.2664	-0.3379	-0.2833	-0.2071	-0.1669	-0.2959
4	Smyd2	-0.3749	-0.1863	-0.1027	-0.1195	[illegible]	-0.1183	-0.4963	-0.3412	-1.3356
4	Snap23	-0.2726	-0.6058	-0.5356	-0.4294	-0.4416	-0.7708	-0.2251	-0.5062	-0.2906
4	Snap47	-0.1988	-0.2517	-0.2168	-0.1148	-0.2668	-0.1961	-0.4786	-0.3443	-0.2221
4	Snapc5	-0.1806	-0.2354	-0.1963	-0.1842	-0.2722	[illegible]	-0.1232	-0.2001	[illegible]
4	Snapin	-0.1976	-0.3908	-0.3348	-0.6859	-0.6356	-0.8069	-0.7494	-0.8439	-0.4772
4	Snn	-0.1166	-0.3009	-0.9962	-0.8682	-1.0461	-0.9578	-0.4228	-0.2083	-0.2405
4	Snora65	-0.7753	-0.7497	-0.7943	-0.6856	-0.4207	-0.5871	-0.1847	-0.3773	-0.4526
4	Snrnp48	-0.4197	-0.1411	-0.2466	-0.343	-0.1617	-0.1692	-0.2817	-0.3116	-0.1623
4	Snrnp70	-0.7598	[illegible]	-0.2518	[illegible]	-0.4422	-0.1662	-0.5283	-0.9081	0.9687
4	Snrpd3	-1.1497	-0.3459	-0.6086	[illegible]	-0.7256	-0.7042	-0.8335	-0.5479	0.6635
4	Sntn	-0.3404	-0.1668	-0.1366	-0.1978	-0.2321	-0.232	-0.3748	-0.2776	-0.1985
4	Snx13	-0.338	-0.3236	-0.2454	-0.2373	-0.1641	-0.3273	-0.3374	-0.3328	-0.7382
4	Snx14	-0.3636	-0.5802	-0.3562	-0.3403	-0.3308	-0.2073	-0.8467	-0.6355	-0.4824
4	Snx17	-0.2064	-0.1842	-0.1081	-0.2085	-0.2396	-0.34	-0.3886	-0.3171	-0.3794
4	Snx25	-0.681	-0.5773	-0.1742	-0.1565	[illegible]	-0.1426	-0.6487	-0.1869	-0.4825
4	Snx4	-0.1661	-0.1453	-0.1781	-0.2341	-0.4253	-0.2505	-0.2029	-0.2961	-0.3469
4	Snx6	-0.6187	-0.4329	-0.5327	-0.4324	-0.3212	-0.4565	-0.4802	-0.3065	-0.683

4	Snx8	-0.132	-0.6092	-0.9154	-0.6058	-0.6772	-0.8395	-0.2126	-0.7392	0.2018
4	Son	-0.2641	-0.207	-0.2515	-0.2252	-0.2206	-0.1418	-0.207	-0.0496	[illegible]
4	Sord	-0.083	-0.1929	-0.3678	-0.5754	-0.4004	-0.6762	-0.4785	-0.6072	0.2434
4	Sorl1	-1.293	-1.5094	-0.9711	-1.0573	-0.4841	-0.1378	-0.2889	-0.1741	1.4724
4	Sowahb	-0.398	-0.4048	-0.1549	-0.4358	0.0805	-0.3349	0.1653	0.1067	0.1994
4	Sp110	-0.2117	-0.1452	-0.2322	-0.2288	-0.188	-0.2636	-0.1847	-0.2357	-0.1387
4	Sp140	-0.4906	-0.4375	-0.3862	-0.3795	-0.3142	-0.3239	-0.3079	-0.2858	-0.3079
4	Spag4	-0.304	-0.1621		-0.2313	-0.1186	-0.2533	-0.111	-0.2926	-0.1211
4	Spata17	-0.1727	-0.224	-0.1945	-0.0566	-0.2315	-0.0889	-0.1407	-0.1337	-0.2018
4	Spata24	-0.4225	-0.1811	-0.6857	-0.5205	-0.4837	-0.4158	[illegible]	-0.0828	0.5123
4	Spata2l	0.2868	0.0472	-0.2091	-0.2625	-0.1224	-0.0965	-0.3146	-0.2371	-0.3347
4	Spats2	-0.0514	-0.1304	-0.1337	-0.0731	-0.2037	-0.0637	-0.1272	-0.1833	-0.1566
4	Spcs3	-0.7272	-0.2836	-0.5196	-0.2243	-0.3462	-0.1118	-0.2387	-0.1927	0.4348
4	Speer2	-0.1176	-0.0641	-0.166	-0.104	-0.104	-0.1944	-0.1485	-0.1074	-0.152
4	Spef1	0.1829	-0.0714	-0.2224	-0.1839	-0.2224	-0.1808	-0.1682	-0.122	-0.2957
4	Spg21	-0.2812	-0.4835	-0.2152	-0.2781	-0.1114	-0.0795	-0.2216	-0.1572	0.4
4	Spink12	-0.3857	-0.4085	-0.4619	-0.3889	-0.4551	-0.4019	-0.289	-0.4859	-0.2097
4	Spire1	-0.3539	-0.5698	-0.485	-0.2912	-0.4911	-0.2543	-0.4136	-0.5959	-0.0488
4	Spock1	-0.3494	-0.2563	-0.3039	-0.3674	-0.4225	-0.4225	-0.2765	-0.2497	-0.4605
4	Spock3	0.3156	0.1032	-0.319	-0.2418	-0.1685	-0.2384	-0.4045	-0.1685	-0.1881
4	Sppl3	-0.0386	-0.3054	-0.3537	-0.6621	-0.3927	-0.4639	-0.2567	-0.4213	-0.1293
4	Sprr1a	-0.655	-0.3941	-0.446	-0.0884	0.2641	0.2122	-0.0123	0.1231	-0.5497
4	Sprr1b	-0.3852	-0.3393	-0.1216	-0.3484	[illegible]	-0.1557	-0.1191	-0.2404	-0.5255
4	Sprr2f	-0.2338	-0.1401	-0.1214	-0.1152	-0.1878	-0.2848	-0.3163	-0.1495	-0.1717
4	Sprr2g	-0.452	-0.3128	-0.3655	-0.2809	-0.0597	-0.4133	-0.1365	-0.2558	-0.3926
4	Spry3	-0.2061	0.1257	-0.3925	-0.334	-0.3056	-0.3629	0.0567	-0.2839	-0.3245
4	Sra1	0.2395	0.0944	-0.2684	-0.4412	-0.3559	-0.2807	-0.4923	-0.4317	-0.0706
4	Srd5a3	-0.0254	-0.0386	0.1169	-0.3543	-0.1033	-0.2925	[illegible]	-0.2669	-0.4214
4	Srr	0.0846	[illegible]	-0.3702	-0.4971	-0.6204	-0.3969	-0.7963	-0.8324	-0.6658
4	Srrm4	-0.3474	-0.3405	-0.337	-0.3131	-0.2729	-0.4707	-0.1648	-0.3405	-0.3336
4	Srsf5	-0.402	-0.2815	0.1277	[illegible]	-0.2424	0.1414	-0.0944	-0.7793	-0.2993
4	Srxn1	0.1736	0.3483	-0.335	-0.6604	-0.7152	-0.8202	-0.9086	-0.8338	0.1712
4	Ss18l1	-0.1032	-0.0344	-0.2228	-0.159	-0.2543	-0.3563	-0.1402	-0.2925	-0.0722
4	Ssh3	[illegible]	-0.0411	0.1248	-0.2035	0.1352	[illegible]	-0.3491	-0.1633	-1.0515
4	Ssr2	-0.266	-0.3293	-0.3698	-0.3305	-0.1998	-0.3562	-0.5012	-0.3363	0.0613
4	Ssu72	-0.7095	-0.5404	[illegible]	0.1093	0.0742	0.0627	-0.1208	[illegible]	-0.7669
4	St3gal5	0.151	0.2983	-0.4281	-0.9615	-0.75	-0.8905	-0.5584	-0.5512	[illegible]
4	St6gal2	-0.2747	-0.1442	-0.2747	0.0371	-0.088	-0.1544	-0.2027	[illegible]	-0.1241
4	Stab2	-0.1308	-0.1808	-0.0622	-0.1168	-0.0689	-0.2746	-0.1917	-0.1238	[illegible]
4	Stac	-0.737	-0.7396	0.1446	0.2179	-0.24	-0.4726	-0.724	-0.4234	-0.9598
4	Stap1	-0.4389	-0.3279	-0.4615	-0.4812	-0.4583	-0.5078	-0.4421	-0.3823	-0.4009
4	Stard5	-0.0428	0.1525	0.0688	-0.059	-0.2173	-0.4119	-0.6047	-0.3708	[illegible]
4	Steap4	-0.0591	-0.2747	-0.2204	-0.2491	-0.2636	-0.3235	-0.26	-0.1308	-0.1853
4	Stim1	0.4882	-0.1531	-0.2244	-0.4423	-0.5694	-0.5915	-0.1358	-0.2583	-0.1706
4	Stk17b	0.8704	-0.2512	-0.906	-0.8709	-0.4142	-0.6282	-0.2335	-0.3717	[illegible]
4	Stk19	-0.3878	-0.1291	-0.2963	0.0346	-0.1847	-0.1974	-0.5428	-0.2224	-0.788
4	Stmn2	-1.8212	-0.9278	-0.415	0.4501	-0.4108	0.4448	-0.7167	[illegible]	-0.6965
4	Stmn4	-0.2666	-0.2558	-0.203	-0.238	-0.3107	-0.2487	-0.1858	-0.119	-0.263
4	Stx12	-0.4419	-0.2647	-0.5927	-0.3479	-0.609	-0.5909	-0.6384	-0.7461	-0.249
4	Stx18	-0.3318	-0.4199	-0.5726	-0.5808	-0.4712	-0.4249	-0.2325	-0.4348	-0.374
4	Stx2	[illegible]	0.2007	-0.3145	[illegible]	-0.1442	-0.1119	-0.1988	-0.1532	-0.3112
4	Stx7	-0.3846	-0.4725	0.4689	0.4352	0.2385	-0.0803	-0.5003	-0.4255	-1.404
4	Stxbp2	-1.8837	-1.4032	-0.3083	-0.2971	-0.0871	0.0887	0.3798	0.3909	-0.2955
4	Stxbp4	0.5037	[illegible]	-0.4154	-0.4254	-0.3857	-0.4832	-0.2817	-0.1837	-0.1933
4	Stxbp5l	-0.0356	-0.1189	-0.204	-0.1349	-0.2006	-0.266	-0.2209	-0.2624	-0.1413
4	Sub1	-0.6924	-0.4923	-0.2144	-0.1003	0.0961	[illegible]	0.5241	-0.1289	-0.2567
4	Suclg1	-0.675	-0.6446	-0.5328	-0.4461	-0.3282	-0.2887	[illegible]	-0.2	0.3568
4	Sult1d1	-0.4052	-0.2213	-0.2837	-0.2976	-0.2319	[illegible]	-0.4082	-0.3345	-0.2054
4	Sult2b1	-0.1258	-0.1752	-0.2263	-0.3678	-0.0486	0.2384	-0.1752	-0.0538	-0.2921
4	Sumf2	-0.4445	-0.4175	-0.4076	-0.3586	-0.3269	-0.5071	-0.4513	-0.3238	-0.1335
4	Sun5	-0.0954	-0.2013	-0.0853	-0.1369	-0.1545	-0.1264	-0.1977	-0.1652	-0.1474
4	Surf1	0.163	-0.3261	-0.4891	-0.3776	-0.3657	-0.4943	-0.5309	-0.3586	-0.1921
4	Susd3	-0.4513	-0.3917	-0.2573	-0.3444	-0.3985	-0.318	-0.351	-0.341	-0.273
4	Suv39h2	-0.0944	-0.1155	-0.2105	-0.2105	-0.2067	-0.1477	-0.1297	-0.2029	-0.0632
4	Suv420h2	-1.2263	-0.8089	-0.9739	-0.5997	-0.4919	0.111	-0.3388	0.0759	0.91
4	Svs2	-0.1738	-0.2224	-0.0724	-0.2323	-0.177	-0.2323	-0.133	-0.0724	-0.0659
4	Syce1l	-0.2281	-0.3206	-0.0028	-0.2281	-0.1765	-0.0954	-0.1976	-0.301	-0.2688
4	Syf2	-0.2595	-0.4758	-0.1628	-0.4936	-0.4445	-0.4161	-0.3574	-0.4471	-0.0665
4	Syn2	-0.1186	-0.2035	-0.2383	-0.1334	-0.2067	-0.3274	-0.2161	-0.3308	-0.1069
4	Synj2bp	-0.1352	-0.1072	-0.1821	-0.1106	-0.0261	-0.0796	-0.1748	-0.2229	-0.1495
4	Synpo2l	-0.4662	-0.434	-0.3061	-0.3747	-0.5227	-0.2406	-0.4662	-0.476	-0.3208
4	Syt1	-0.3752	-0.2228	0.2613	0.3651	-0.3618	-0.193	-0.2907	[illegible]	-0.3226
4	Syt2	-0.3992	-0.3698	-0.2681	-0.2313	-0.359	-0.2019	-0.3808	-0.2149	-0.2749
4	Syt8	-0.3917	-0.3892	-0.3992	-0.4873	[illegible]	-0.567	-0.1191	-0.3867	-0.567
4	Sytl4	[illegible]	[illegible]	-0.4194	[illegible]	-0.5488	-0.4962	-0.4811	-0.5269	-0.7623
4	Syvn1	-0.1529	-0.1954	-0.2363	-0.2073	-0.4656	-0.5138	-0.5748	-0.6056	-0.3831
4	Tab1	-0.4688	-0.0921	-0.4124	-0.3433	-0.2503	-0.1244	-0.2575	-0.0569	-0.6516
4	Tab2	0.0866	-0.2557	-0.1869	-0.2521	-0.7244	-0.5012	-0.5845	-0.5761	-0.4131
4	Tacc1	0.4476	-0.1639	-0.3139	-0.5439	-0.4243	-0.5106	-0.0177	-0.4684	0.2105
4	Tacr1	-0.2219	-0.0365	-0.2283	-0.2029	-0.238	-0.3144	-0.3076	-0.1593	[illegible]
4	Tal1	-0.1434	-0.2029	-0.1781	-0.1851	-0.1851	-0.2427	-0.123	-0.2029	-0.0687
4	Tapt1	-0.0438	-0.0749	-0.0498	-0.0264	-0.3373	-0.2096	-0.9037	-0.4344	-1.0253
4	Tarsl2	-0.5704	-0.3892	-0.2055	0.0907	-0.3247	-0.0887	-0.4857	-0.2103	0.4265
4	Tas2r136	-0.2308	-0.0987	-0.2474	-0.3087	-0.2811	-0.2408	-0.0868	-0.2275	-0.2675
4	Tatdn2	-0.4198	0.0929	-0.0949	-0.0435	[illegible]	0.511	-0.428	-0.277	-0.4294
4	Taz	-0.0358	-0.1443	-0.4515	0.0474	-0.2247	-0.2781	-0.295	-0.3589	-0.1683
4	Tbc1d10c	-0.4557	-0.2166	-0.2128	-0.2753	-0.0762	-0.0469	-0.3385	-0.2773	0.5146
4	Tbc1d14	-0.1935	-0.2163	-0.2733	-0.1742	-0.2835	-0.1935	-0.152	-0.1583	[illegible]
4	Tbc1d16	-0.1554	-0.2655	[illegible]	-0.2112	-0.0789	-0.115	-0.3181	-0.1554	-0.1452
4	Tbc1d19	0.2242	-0.1476	-0.2377	-0.5536	-0.2116	-0.5058	[illegible]	-0.0863	-0.3763
4	Tbc1d9	-0.2389	-0.4438	-0.8763	-0.5813	-0.6425	-0.62	-0.5227	-0.6916	0.5487
4	Tbcel	-0.1402	-0.2996	-0.5316	-0.3195	-0.8427	-0.55	-1.1094	-0.5826	-0.2968
4	Tbrg1	-0.276	-0.5463	-0.4948	-0.4433	-0.0948	-0.392	[illegible]	-0.288	0.2074
4	Tbx22	-0.0322	-0.1746	-0.0988	-0.3094	-0.2171	[illegible]	-0.2451	-0.2295	-0.1217
4	Tbx6	-0.1935	-0.1688	-0.0737	-0.0541	-0.1583	-0.1375	-0.2115	[illegible]	-0.1341
4	Tcea2	-0.5639	-0.5205	-0.6483	-0.1098	-0.6272	-0.2372	-0.8179	-0.4416	-0.2533
4	Tceb3	-0.1073	-0.4207	0.2297	-0.404	-0.0657	-0.4011	-0.3297	-0.404	-0.6647
4	Hnf1a	[illegible]	-0.2135	-0.2585	-0.0946	-0.3302	-0.2892	-0.2799	-0.1843	-0.1248
4	Tcf25	-0.3654	-0.3106	-0.3222	-0.5316	-0.4008	-0.1841	-0.4575	-0.2878	-0.4765
4	Tcl1b1	-0.24	-0.2094	-0.1372	-0.2263	-0.1728	-0.0716	-0.2365	-0.1761	-0.1213
4	Tdpoz1	-0.366	-0.2824	-0.158	0.2132	-0.1699	-0.0938	-0.1372	-0.06	-0.091
4	Tdpoz5	-0.1222	-0.1988	-0.16	-0.1222	-0.2253	-0.1006	-0.1536	-0.0944	-0.176
4	Tdrd6	-0.1706	-0.2125	-0.1866	-0.0576	-0.0843	[illegible]	-0.2898	-0.0195	-0.2323
4	Tdrkh	-0.3205	[illegible]	-0.6078	-0.3034	-0.265	-0.1912	0.2051	0.1897	0.128
4	Tec	-0.6339	-0.7176	-0.6536	-0.6668	-0.4597	-0.5923	-0.4312	-0.5829	-0.5673
4	Tecpr2	-0.9517	-0.5318	-0.828	-0.5875	-0.4976	-0.3314	-0.3188	-0.3538	-0.091
4	Tep1	-0.2009	-0.1617	-0.0631	-0.2793	-0.2413	-0.2447	-0.2142	-0.2898	-0.0659
4	Terf2	-0.2005	-0.0346	-0.3	-0.4058	-0.3348	-0.1769	-0.1871	-0.7158	0.7808
4	Tesc	-0.6385	-0.6326	-0.609	-0.3509	-0.4835	-0.2588	-0.3779	-0.2183	-0.7855
4	Tex13a	-0.2514	-0.1572	-0.1835	-0.2069	-0.2689	-0.0873	-0.1868	-0.2689	-0.1378
4	Tfb2m	[illegible]	-0.1339	-0.1401	0.1695	-0.1228	-0.196	-0.3738	-0.3107	-0.1552
4	Tfr2	-0.2925	[illegible]	0.025	-0.2636	-0.1636	-0.0732	-0.1438	-0.2672	-0.1081
4	Tgfbr1	0.5135	0.2591	-0.0486	-0.4323	-0.552	-0.728	0.0951	-0.1222	-0.3309
4	Tgm3	-0.9329	-0.9177	0.1414	0.2529	-0.0454	-0.0372	-0.4922	-0.0786	-1.0805
4	Tgm5	-0.2418	-0.2088	-0.2687	0.0795	-0.0388	-0.2252	-0.1959	-0.2351	-0.1991
4	Thap4	-0.5285	-0.519	-0.5165	-0.5165	-0.3673	-0.5182	-0.5802	-0.4953	[illegible]
4	Thap7	-0.0167	-0.0547	-0.2036	-0.0344	-0.1649	-0.1993	-0.5299	-0.4022	-0.7209
4	Theg	-0.3089	-0.2515	-0.4063	-0.0507	-0.2115	-0.1375	-0.2609	-0.3252	[illegible]
4	Them4	-0.2736	-0.5125	-0.3207	-0.436	-0.1173	-0.2563	-0.3088	[illegible]	-0.4754
4	Themis	-0.3205	-0.2002	[illegible]	-0.2759	-0.3032	-0.3522	-0.156	-0.331	-0.1685
4	Thnsl2	0.3936	[illegible]	-0.6348	-0.6003	-0.73	-0.3405	-0.4768	-0.5176	-0.049
4	Thsd7b	-0.2229	-0.1598	-0.1663	[illegible]	[illegible]	-0.206	-0.186	-0.1436	-0.1794
4	Thtpa	-0.1708	-0.0611	-0.1497	0.1048	-0.1109	-0.0593	-0.6938	-0.455	-1.0578
4	Tifa	-0.2505	-0.2693	-0.2725	-0.2016	-0.4081	-0.429	-0.3437	-0.3503	-0.3044
4	Tigd2	[illegible]	0.0655	-0.4694	-0.599	-0.3273	-0.4186	-0.4337	-0.2697	-0.2826
4	Timm22	-0.0784	0.0811	-0.1964	-0.046	-0.1349	-0.2924	-0.3551	-0.3612	-0.3953
4	Timm44	-1.0731	-0.5578	-0.3005	-0.4209	-0.3911	-0.0591	-0.4929	-0.159	0.2227
4	Timm50	-1.0813	-0.598	-0.6047	[illegible]	-0.2601	0.0651	-0.2835	-0.0981	0.4459
4	Tirap	-0.7533	-0.3199	-0.5457	-0.037	-0.3199	-0.1247	-0.8249	-0.4944	-0.9294
4	Tle3	-0.272	-0.0954	-0.1039	-0.0367	-0.2128	-0.2128	-0.3338	-0.3539	0.1737
4	Tlk1	-0.521	-0.5868	-0.1622	-0.4297	0.1722	-0.0295	0.0824	0.0981	[illegible]
4	Tln1	-0.2388	0.1112	-0.4935	-0.3169	-0.3308	[illegible]	-0.4748	-0.5219	-0.276
4	Tlr1	-0.2864	-0.2895	-0.2321	-0.5088	-0.5232	-0.395	-0.0804	-0.4594	-0.4117
4	Tlr3	0.0881	-0.1942	-0.1942	-0.333	-0.333	0.0447	-0.2261	-0.2752	-0.2553
4	Tlr8	-0.2587	-0.3494	-0.1826	-0.1888	-0.3669	-0.3529	-0.3287	-0.2652	-0.3845
4	Tm2d3	-0.3036	-0.3528	[illegible]	0.0881	-0.0924	-0.1572	-0.2844	-0.2725	0.1477
4	Tm6sf2	-0.1169	-0.1808	-0.2476	[illegible]	-0.2442	-0.184	-0.1136	[illegible]	-0.0558
4	Tmbim6	0.2358	-0.1366	-0.3139	-0.6029	-0.3765	-0.4567	-0.2976	-0.3558	-0.6614
4	Tmc6	-1.1379	-0.7386	0.2677	0.3144	-0.0893	[illegible]	-0.5335	-0.2321	-0.3608
4	Tmco4	-0.2319	-0.2739	-0.1069	-0.363	-0.3422	-0.333	-0.8737	-0.5661	-0.2849
4	Tmem101	-0.9144	-0.477	-0.2348	-0.1191	-0.2258	0.0989	-0.1203	-0.0246	0.4178
4	Tmem11	-0.5587	-0.4741	-0.3348	-0.0712	-0.1777	-0.1876	-0.0757	-0.2337	0.291
4	Tmem110	-0.29	-0.1955	0.1527	-0.0758	-0.1431	-0.416	-0.5956	-0.693	-0.6459
4	Tmem120a	0.2763	0.4701	-0.1293	-0.4269	-0.6076	-0.5107	-0.2282	-0.3042	-0.1447
4	Tmem128	-0.5403	-0.6034	-0.1398	-0.0842	-0.185	-0.2148	-0.1564	[illegible]	-0.7978
4	Tmem132c	-0.1815	-0.1848	-0.259	-0.162	-0.3299	-0.2555	-0.1122	-0.2418	[illegible]
4	Tmem132d	-0.509	-0.0648	-0.2787	[illegible]	-0.1542	-0.2758	-0.2846	-0.1515	[illegible]
4	Tmem132e	-0.5386	-0.5073	-0.5177	-0.5813	-0.4468	-0.3824	-0.4971	-0.5351	-0.437
4	Tmem135	-0.2559	-0.3596	-0.26	-0.2076	-0.101	-0.188	-0.2973	-0.09	0.0928
4	Tmem136	-0.425	-0.3052	-0.4572	-0.433	-0.3651	-0.6241	-0.0503	-0.1347	0.7825
4	Tmem144	-0.252	-0.3016	-0.2243	-0.151	-0.1445	-0.1381	-0.1707	-0.2872	-0.0968
4	Tmem147	-0.5537	-0.2841	-0.1646	-0.051	-0.4607	-0.1293	-0.7147	-0.096	-0.5912
4	Tmem14c	-0.5448	-0.4061	-0.6776	-0.6486	-0.6926	-0.3706	-0.4504	-0.662	-0.3292
4	Tmem154	-0.3677	-0.1161	-0.2039	-0.2696	-0.1836	-0.0569	-0.1636	-0.097	-0.3449
4	Tmem161a	-0.0827	-0.2665	-0.0943	-0.3978	-0.4622	-0.1559	-0.2177	-0.1705	0.2796
4	Tmem164	-0.0893	0.2467	0.2057	-0.1071	-0.3023	-0.0698	-0.423	-0.2575	-0.3391
4	Tmem169	-0.0905	-0.0607	-0.1783	-0.297	-0.3033	-0.275	-0.238	-0.2875	0.1377
4	Tmem177	-0.5968	-0.3209	-0.7878	-0.3296	-0.2396	0.1617	0.0561	0.1496	-0.1255
4	Tmem179b	-0.1645	-0.2075	-0.1924	-0.3092	-0.1429	-0.2733	-0.2002	-0.125	-0.1388
4	Tmem185b	-0.5688	-0.159	-0.5031	-0.2193	-0.3306	-0.3081	-0.3867	-0.4129	-0.6332
4	Tmem198	-0.5012	-0.5858	0.2715	-0.1875	-0.2634	-0.6921	-0.6621	-0.6977	-0.831
4	Tmem202	-0.14	-0.1264	-0.0332	-0.0896	-0.0896	-0.239	-0.1537	-0.1537	-0.1434
4	Tmem208	-0.1738	-0.0688	-0.491	-0.0953	-0.3598	-0.4987	-0.4449	-0.3075	[illegible]
4	Tmem218	-0.3635	-0.4309	-0.0819	-0.1309	[illegible]	[illegible]	-0.6664	-0.4502	-0.8507

4	Tmem232	
4	Tmem38a	
4	Tmem38b	
4	Tmem45a	
4	Tmem50b	
4	Tmem56	
4	Tmem62	
4	Tmem65	
4	Tmem74	
4	Tmem79	
4	Tmem85	
4	Tmem86b	
4	Tmie	
4	Tmod1	
4	Tmod2	
4	Tmprss11a	
4	Tmprss11e	
4	Tmprss4	
4	Tmsb15b2	
4	Tnf	
4	Tnfaip1	
4	Tnfaip6	
4	Tnfrsf1b	
4	Tnfsf13b	
4	Tnfsf14	
4	Tnip2	
4	Tnnc1	
4	Tnpo2	
4	Tnrc6c	
4	Tomm20	
4	Top1mt	
4	Tpcn2	
4	Tpd52	
4	Tpd52l2	
4	Tph2	
4	Tprkb	
4	Tpst2	
4	Trabd	
4	Traf2	
4	Traf5	
4	Trak2	
4	Trap1	
4	Trappc2l	
4	Trappc3	
4	Trat1	
4	Triap1	
4	Trib3	
4	Trim10	
4	Trim11	
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4	Trim29	
4	Trim30d	
4	Trim30e-ps1	
4	Trim32	
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4	Trim66	
4	Trim72	
4	Trim8	
4	Trim9	
4	Triobp	
4	Trip10	
4	Trit1	
4	Trove2	
4	Trp53i13	
4	Trp53inp1	
4	Trpt1	
4	Trpv1	
4	Trpv2	
4	Tsc2	
4	Tslp	
4	Tsnax	
4	Tspan31	
4	Tspyl2	
4	Tsr2	
4	Tsta3	
4	Ttc19	
4	Ttc33	
4	Ttc39a	
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4	Ttc5	
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4	Ttll1	
4	Ttyh2	
4	Tuba8	
4	Tubg2	
4	Tufm	
4	Tut1	
4	Txk	
4	Txnl4b	
4	Txnrd2	
4	Tyk2	
4	Tyr	
4	Uap1l1	
4	Uba3	
4	Ube2b	
4	Ube2d1	
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4	Ube2n	
4	Ubqln3	
4	Ubr3	
4	Ubtd1	
4	Ubtd2	
4	Ubxn11	
4	Uck1	
4	Ucma	
4	Ucn3	
4	Ucp3	
4	Ufc1	
4	Ufsp2	
4	Uggt1	
4	Ugp2	
4	Ugt2b38	
4	Uhrf1bp1	
4	Unc119	
4	Unc119b	
4	Unc13d	
4	Unc5a	
4	Upf2	
4	Upf3a	
4	Upp2	
4	Uprt	
4	Uqcc	
4	Uqcrc1	
4	Uqcrc2	
4	Uqcrh	
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4	Urgcp	
4	Uroc1	
4	Uros	
4	Ush1g	
4	Uso1	
4	Usp12	
4	Usp20	
4	Usp3	
4	Usp45	
4	Usp5	
4	Utp11l	
4	Uts2	
4	Uvrag	
4	Vmn1r51	
4	Vmn1r45	
4	V1ra8	
4	Vamp2	
4	Vamp3	
4	Vangl2	
4	Vav2	
4	Vdac3	
4	Veph1	
4	Vezt	
4	Vgll4	
4	Vhl	
4	Vipr1	
4	Vmn1r192	
4	Vmn1r198	
4	Vmn1r202	
4	Vmn1r210	
4	Vmn1r36	
4	Vmn1r56	

4	Vmn1r78	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Vmn2r89	-0.0873	-0.1695	[illegible]	-0.2161	-0.0806	-0.1451	-0.166	-0.2568	[illegible]
4	Vnn3	-0.9091	-0.8592	0.1666	0.4407	0.2016	-0.1685	-0.7164	-0.6727	-1.0208
4	Vpreb1	-0.3328	-0.114	-0.2447	-0.3219	-0.4305	-0.2969	-0.3585	-0.2345	-0.2105
4	Vps11	-0.1118	-0.5404	-0.2125	-0.2445	-0.1736	-0.3628	-0.2456	-0.237	[illegible]
4	Vps26b	-0.2627	-0.3336	-0.2173	-0.5346	-0.3986	-0.3797	-0.6355	-0.4644	-0.0746
4	Vps28	-0.6017	-0.5533	-0.4885	-0.0629	-0.1188	-0.1244	-0.491	-0.2058	-0.6877
4	Vps29	[illegible]	-0.1081	-0.3688	-0.1782	-0.4312	-0.3622	-0.3466	-0.2755	0.5289
4	Vps33b	-0.3914	-0.4621	-0.3409	-0.2025	-0.2403	-0.2371	-0.1358	[illegible]	0.4025
4	Vps35	-0.3294	-0.6936	-0.5883	-0.6164	-0.3321	-0.2327	-0.0606	-0.1859	0.6688
4	Vps39	-0.2938	-0.1815	-0.2174	-0.2475	-0.2441	[illegible]	-0.5694	-0.4598	-0.0654
4	Vps41	-0.3837	-0.5598	-0.4155	-0.4137	-0.5856	-0.3123	-0.7004	-1.004	0.2226
4	Vps4a	[illegible]	[illegible]	-0.4655	-0.0824	-0.275	-0.2334	-0.5688	-0.3855	0.1239
4	Vps53	-0.4534	-0.5045	-0.2318	-0.1592	-0.248	-0.1884	-0.6467	-0.4281	-0.9372
4	Vrk3	-0.6966	-0.6378	-0.3918	-0.4156	0.154	[illegible]	-0.0475	-0.1185	0.2497
4	Vstm2a	0.199	-0.2177	-0.1689	[illegible]	-0.2276	-0.2012	-0.1721	-0.1914	-0.1248
4	Vti1a	-0.1099	-0.3472	-0.0526	-0.0516	-0.1686	0.1904	-0.2384	-0.1695	-0.445
4	Vwa3a	-0.203	-0.1321	-0.1926	-0.1722	-0.1354	-0.119	-0.1255	-0.1824	-0.152
4	Vwc2l	-0.2661	-0.2661	-0.4219	-0.2723	-0.3549	-0.2	-0.2909	-0.2147	-0.1311
4	Wasf3	-0.2056	-0.1369	-0.2394	-0.0472	-0.1054	-0.1594	-0.2394	-0.1401	0.0985
4	Wbp2	-0.3479	-0.4076	-0.1282	-0.2372	-0.0775	0.1305	-0.3323	-0.0694	[illegible]
4	Wbp4	-0.1184	[illegible]	-0.1566	-0.1821	-0.1814	-0.2228	-0.4174	-0.5378	0.7731
4	Wdpcp	-0.2837	-0.1445	-0.2908	-0.3612	-0.2192	-0.5496	-0.2237	-0.3964	-0.5439
4	Wdr13	-0.0868	-0.0362	-0.1591	-0.1792	-0.1478	[illegible]	-0.2748	-0.2503	-0.1032
4	Wdr27	-0.1966	[illegible]	-0.1502	-0.0532	-0.1716	-0.3665	-0.2316	[illegible]	-0.2641
4	Wdr44	-0.2943	-0.2912	-0.1024	-0.2514	0.2228	-0.2666	-0.1836	-0.1467	[illegible]
4	Wdr45	[illegible]	-0.5992	0.0737	-0.1836	[illegible]	-0.2777	-0.1364	-0.1506	-0.7933
4	Wdr54	-0.2165	-0.4306	-0.3862	[illegible]	-0.3103	-0.2582	-0.4231	-0.2014	-0.3959
4	Wdr55	-0.8827	-0.3044	-0.2322	0.1705	-0.0953	0.163	-0.1251	-0.2722	0.2279
4	Wdr5b	-0.1487	-0.1422	-0.1751	[illegible]	-0.3073	-0.2536	-0.1851	-0.1784	-0.2258
4	Wdr61	-0.2965	-0.1375	-0.6402	-0.1984	-0.2093	-0.21	-0.141	[illegible]	0.1003
4	Wdr65	-0.2304	-0.2975	-0.3508	-0.2556	-0.2877	-0.334	-0.2118	-0.2942	-0.2211
4	Wdr78	-0.0479	-0.0668	-0.5841	-0.4296	-0.4996	-0.3035	-0.2508	-0.0763	-0.7029
4	Wdr8	-0.0286	-0.3013	-0.3319	-0.2111	-0.1894	[illegible]	-0.12	-0.0756	-0.6497
4	Wfdc1	-0.3915	-0.0729	-0.2763	-0.3618	-0.4184	-0.4951	-0.3684	-0.4321	-0.3849
4	Wfdc15b	-0.2346	-0.0691	-0.0632	-0.2379	-0.1355	-0.0721	[illegible]	[illegible]	-0.3093
4	Wfdc6b	-0.2137	-0.2724	-0.1155	-0.167	[illegible]	-0.0596	-0.1769	-0.217	0.1549
4	Wfs1	-0.1949	-0.1382	-0.0778	-0.585	-0.1932	-0.4621	-0.5558	-0.5558	[illegible]
4	Whrn	0.2118	0.263	-0.847	-0.5168	-1.0825	-0.765	0.1707	-0.0969	0.6676
4	Wipi2	-0.6699	-0.199	-0.5835	-0.3193	-0.4465	-0.1297	-0.6374	-0.5709	-0.6466
4	Wnt16	-0.0352	-0.0435	[illegible]	0.0832	-0.2732	-0.2287	-0.2476	-0.2508	-0.3737
4	Wnt5b	-0.1693	-0.4791	-0.2842	-0.6461	-0.5215	-0.1215	-0.8233	-0.4653	-0.7019
4	Wnt7a	-0.4999	-0.0605	-0.2134	0.1281	-0.2194	-0.1153	-0.3123	0.1281	-0.3155
4	Wnt7b	-0.4271	-0.6844	-0.3283	-0.5423	-0.0893	-0.3796	[illegible]	[illegible]	0.2985
4	Wtap	-0.1761	-0.2745	-0.1669	-0.2614	[illegible]	-0.0526	-0.1013	-0.1946	-0.0667
4	Wwox	-0.1798	-0.2277	-0.0832	0.113	-0.1993	-0.1687	-0.4045	-0.1387	-0.3225
4	Xdh	0.205	-0.2337	[illegible]	-0.318	[illegible]	-0.3264	-0.4377	-0.532	-0.5063
4	Xist	-0.4546	-0.2398	-0.3814	-0.4423	-0.417	-0.1206	-0.2151	0.2301	-1.8957
4	Xkr9	-0.1987	-0.2128	-0.1953	-0.2022	[illegible]	-0.1987	-0.0943	-0.1107	-0.1239
4	Xkrx	-0.1901	-0.2249	-0.1759	-0.2308	-0.3763	-0.1646	-0.3063	-0.1702	-0.1674
4	Xlr	-0.1384	-0.2733	-0.1922	-0.0457	-0.1617	-0.1187	-0.2129	-0.2553	-0.1786
4	Xlr4c	-0.1183	-0.1183	-0.2076	-0.1865	-0.2183	-0.19	-0.0984	-0.1351	-0.2255
4	Xylt1	-0.2985	-0.1327	-0.2148	-0.1005	-0.1005	-0.0776	[illegible]	-0.3287	-0.2305
4	Xylt2	-0.0793	0.1149	-0.2408	-0.367	-0.2825	-0.1546	-0.2182	-0.1164	0.1895
4	Yaf2	[illegible]	0.0684	0.087	0.2353	-0.161	-0.3659	-0.347	-0.2085	-0.5354
4	Yeats2	-0.386	-0.2999	-0.6262	-0.4954	-0.5485	-0.458	-0.1068	-0.3746	-0.1197
4	Yif1b	-0.5933	-0.7496	-0.7192	-0.6598	-0.2942	-0.5088	-0.3227	-0.5925	-0.1093
4	Yipf1	0.2493	-0.1076	-0.1062	-0.1623	-0.2382	-0.5397	-0.5954	-0.4924	-0.7126
4	Yipf4	-0.2123	-0.2669	-0.4347	-0.2817	-0.2906	[illegible]	-0.4248	-0.4918	-0.3671
4	Yipf6	-0.4389	-0.571	-0.3819	-0.2815	-0.4229	-0.4249	-0.4795	-0.2148	-0.2743
4	Yod1	[illegible]	-0.5841	0.5583	-0.2489	[illegible]	-0.1845	-0.4017	-0.2776	-0.4888
4	Ypel1	-0.2812	-0.2274	-0.1829	-0.5036	-0.2786	-0.1046	0.215	[illegible]	-0.1349
4	Ypel4	-0.0937	-0.36	-0.2692	-0.3347	-0.4448	-0.2586	-0.4753	-0.1466	-0.4939
4	Zbtb40	[illegible]	-0.2592	-0.2505	-0.2305	-0.3365	-0.239	-0.2248	-0.3926	-0.2944
4	Zbtb41	-0.0963	-0.2164	-0.1697	-0.1976	-0.2706	-0.2725	-0.1938	-0.2374	-0.5768
4	Zbtb46	-0.0728	-0.0543	-0.2245	[illegible]	-0.3808	-0.4041	-0.2215	-0.2881	0.4916
4	Zbtb5	-0.4805	-0.2383	-0.2947	-0.1048	-0.1479	[illegible]	-0.2488	0.1368	[illegible]
4	Zbtb9	-0.8822	-0.3981	-0.5672	-0.1757	-0.3736	[illegible]	-0.2227	-0.378	[illegible]
4	Zc3h6	[illegible]	-0.2755	-0.6082	-0.6341	-0.6563	-0.4449	-0.9841	-0.3357	-0.6465
4	Zc3h7a	[illegible]	-0.2268	-0.0542	-0.3887	[illegible]	-0.4736	-0.4007	-0.4457	-0.3841
4	Zcchc13	-0.15	-0.2728	-0.1669	-0.2474	-0.1466	-0.1806	-0.2366	-0.1102	[illegible]
4	Zcchc14	-0.2952	-0.1375	-0.4477	-0.1252	-0.4486	-0.2203	-0.2134	-0.2687	0.2427
4	Zcchc18	-0.3376	-0.2787	-0.9854	-0.7389	-0.8692	-0.6581	0.813	0.2517	0.7005
4	Zdhhc1	0.1693	0.1605	-0.297	-0.2729	-0.5194	-0.2214	-0.6098	-0.1828	-0.7522
4	Zdhhc12	-1.012	-0.795	-0.381	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
4	Zdhhc15	-0.5954	-0.6631	-0.5307	-0.5766	-0.1492	-0.4892	[illegible]	-0.1492	[illegible]
4	Zdhhc24	-0.2193	-0.4181	-0.3785	[illegible]	-0.4181	-0.0759	-0.3139	-0.2193	[illegible]
4	Zdhhc3	-0.1209	-0.1585	-0.1265	-0.2207	-0.5322	-0.3847	-0.3236	-0.4695	-0.2733
4	Zdhhc4	-0.121	[illegible]	[illegible]	0.1542	[illegible]	-0.2457	-0.4537	-0.5121	-1.0942
4	Zdhhc9	0.0658	0.1302	0.1477	0.1081	-0.304	-0.179	-0.7316	-0.2439	-0.6068
4	Zfand2b	-0.3372	-0.35	-0.3539	-0.2371	-0.078	-0.0759	-0.2808	[illegible]	-0.2771
4	Zfc3h1	-0.1555	-0.2171	0.337	-0.1275	-0.3464	-0.4122	-0.4064	-0.2334	0.0961
4	Zfhx2	-1.1984	-0.5359	-0.4588	-0.165	-0.2301	0.1172	-0.3587	-0.1089	0.2752
4	Zfp119a	-0.6576	-0.3098	-0.3487	-0.4398	[illegible]	[illegible]	-0.0541	-0.154	-0.3714
4	Zfp120	-0.1723	-0.1264	-0.0853	-0.1904	-0.1652	-0.1091	-0.1723	-0.1334	-0.2087
4	Zfp128	-0.2883	-0.0862	-0.2568	-0.1057	-0.1399	-0.3337	-0.2198	-0.3304	0.1009
4	Zfp148	-0.1712	0.0613	-0.064	0.2261	-0.4956	0.1416	-0.8836	-0.2579	-0.6858
4	Zfp157	-0.0787	-0.1487	-0.1422	-0.2053	[illegible]	-0.1553	-0.1165	-0.1133	-0.1784
4	Zfp187	-0.1204	[illegible]	-0.2391	[illegible]	-0.2907	[illegible]	-0.3239	-0.2202	[illegible]
4	Zfp202	-0.1586	[illegible]	-0.2663	[illegible]	-0.2684	-0.3943	-0.2513	-0.2093	-0.8653
4	Zfp238	-0.7622	-0.486	-0.0997	[illegible]	-0.1517	-0.361	-0.215	-0.115	0.4531
4	Zfp259	-1.024	-0.5321	-0.4039	-0.0858	-0.1506	0.1379	-0.1357	[illegible]	0.6229
4	Zfp263	-0.3209	-0.5631	0.0983	-0.1028	-0.1919	[illegible]	-0.3295	-0.3474	[illegible]
4	Zfp27	[illegible]	-0.209	-0.2317	0.0871	[illegible]	-0.0768	-0.1816	-0.185	-0.4514
4	Zfp273	-0.1474	-0.2184	-0.0923	-0.1774	-0.0797	-0.131	-0.2394	-0.1147	-0.1342
4	Zfp276	[illegible]	-0.0517	-0.477	-0.293	-0.4536	-0.2639	-0.5913	-0.3404	-0.5786
4	Zfp277	-0.6137	-0.6149	-0.3406	-0.4059	[illegible]	-0.2496	-0.2633	-0.2486	0.8909
4	Zfp282	-0.4253	-0.1798	-0.2586	[illegible]	-0.2926	[illegible]	-0.4836	-0.1387	-1.0489
4	Zfp295	-0.1542	-0.1325	[illegible]	-0.1355	-0.0574	-0.1386	-0.1987	-0.1826	-0.1666
4	Zfp30	[illegible]	[illegible]	-0.9579	-0.5585	-1.0258	-0.7267	-0.9435	-0.8637	0.3456
4	Zfp316	[illegible]	-0.0677	-0.0995	0.1077	-0.1834	-0.0501	-0.4024	-0.2142	-0.3906
4	Zfp346	-0.2985	-0.2224	-0.4082	-0.2569	-0.2692	-0.1674	-0.2548	-0.5594	0.7297
4	Zfp369	-0.1438	-0.286	-0.286	[illegible]	-0.3248	-0.0761	-0.2148	-0.1344	0.2482
4	Zfp384	-0.197	-0.2692	-0.3035	-0.1767	-0.3098	-0.3947	-0.4742	-0.3484	0.1597
4	Zfp385b	-0.2835	-0.2274	-0.3356	-0.2775	-0.3263	-0.2745	-0.2478	-0.1402	-0.1294
4	Zfp39	-0.3578	-0.1902	-0.6112	-0.0497	-0.3721	-0.0728	-0.0812	[illegible]	0.1875
4	Zfp397	-0.3515	-0.2493	-0.3119	-0.0604	-0.3709	-0.175	-0.4477	0.1078	-0.7799
4	Zfp422	-0.4004	-0.0854	-0.2792	-0.397	-0.2886	-0.2177	-0.1471	[illegible]	[illegible]
4	Zfp455	-0.1971	-0.2946	-0.3191	-0.2876	-0.3622	-0.2004	-0.2568	-0.3658	-0.2946
4	Zfp467	0.392	0.1019	-0.0477	-0.4252	-0.3396	-0.4765	-0.1559	-0.3546	-0.3941
4	Zfp523	-0.557	-0.2635	-0.2037	-0.2871	-0.3932	-0.1253	-0.1988	-0.3733	-0.4723
4	Zfp579	0.1278	0.1248	-0.0492	-0.2412	-0.4605	-0.4224	-0.1055	-0.4092	-0.6887
4	Zfp60	-0.8293	-0.2076	-0.7234	0.1409	[illegible]	0.1319	[illegible]	0.1064	0.3188
4	Zfp655	0.1457	-0.7763	0.3562	-0.7197	-0.4169	-0.7471	-0.3009	-0.6072	0.8736
4	Zfp697	-0.2636	-0.2636	-0.3171	-0.2636	-0.3309	-0.2935	-0.4718	-0.244	-0.2702
4	Zfp709	-0.3057	-0.1615	-0.3119	-0.3594	-0.2481	[illegible]	-0.2099	-0.2128	-0.1984
4	Zfp711	-0.2851	-0.1883	-0.1608	-0.3	-0.2022	-0.1676	-0.2926	-0.1008	-0.1574
4	Zfp715	-0.1762	-0.1457	-0.3725	-0.3122	-0.444	-0.6233	-0.3698	-0.3035	-0.1442
4	Zfp738	[illegible]	-0.2253	-0.2118	-0.1721	-0.277	-0.1303	-0.1852	-0.1688	-0.3343
4	Zfp747	-0.459	-0.2942	-0.3427	[illegible]	-0.3404	[illegible]	-0.5716	-0.3205	[illegible]
4	Zfp760	-0.5074	-0.121	-0.1713	-0.151	-0.1868	-0.0819	-0.1586	-0.4754	-0.0606
4	Zfp768	-0.5554	-0.3795	-0.2408	-0.4462	-0.5639	-0.2546	-0.5696	-0.5668	-0.7525
4	Zfp770	-0.6265	-0.2144	-0.5251	-0.256	-0.2425	-0.1389	0.1278	0.0653	0.4813
4	Zfp787	-0.4841	-0.2116	-0.4215	-0.0794	-0.3619	-0.2684	-0.4403	-0.404	-0.6148
4	Zfp790	-0.2086	-0.1108	-0.4827	0.1181	-0.3016	0.1319	-0.4543	[illegible]	-0.0917
4	Zfp808	-0.0766	-0.168	-0.182	-0.2996	-0.2214	-0.1506	-0.247	[illegible]	-0.2214
4	Zfp87	-0.7102	-0.3172	-0.7329	0.116	-0.2853	-0.089	0.0935	-0.2418	0.5082
4	Zfp90	0.3449	0.0594	-0.4357	-0.4064	-0.5276	-0.2566	[illegible]	-0.1039	[illegible]
4	Zfp94	-0.716	-0.1548	-1.0673	-0.2134	-0.5228	-0.0472	-0.5667	-0.0583	[illegible]
4	Zfp943	0.0995	[illegible]	-0.1682	-0.2876	[illegible]	-0.0847	-0.1363	-0.1664	-1.2734
4	Zfp954	-0.3355	-0.4142	-0.574	-0.2533	-0.3735	[illegible]	-0.5607	[illegible]	-0.3785
4	Zfx	-0.3148	-0.1709	-0.1142	0.1423	[illegible]	[illegible]	-0.414	-0.2138	[illegible]
4	Zfyve20	0.1984	-0.0974	-0.1392	-0.0749	-0.3541	-0.2893	-0.2618	-0.2375	-0.4072
4	Zfyve21	-0.0655	[illegible]	-1.1365	-0.7128	-0.8705	-0.7811	-0.5434	-0.6259	0.2838
4	Zg16	-0.3541	-0.3255	-0.2295	-0.3326	-0.2262	-0.263	-0.2462	-0.1426	-0.387
4	Zgpat	-0.1596	-0.1326	-0.0905	[illegible]	-0.1815	-0.1596	-0.1678	-0.3146	-0.1596
4	Zkscan14	-0.5037	-0.2947	0.1537	0.0622	-0.402	-0.0733	-0.4776	-0.1561	[illegible]
4	Zkscan4	-0.2664	[illegible]	-0.7222	-0.0665	-0.3094	0.1447	-0.242	0.2136	-0.3256
4	Zkscan6	-0.132	-0.1958	-0.0823	0.119	-0.2225	-0.1551	-0.5091	-0.3101	-0.7103
4	Zmiz1	0.0968	0.1128	-0.3749	-0.3408	-0.1499	-0.0656	[illegible]	-0.0804	-0.4057
4	Znhit2	-0.4732	-0.4282	-0.3098	-0.182	-0.465	-0.3206	-0.3526	-0.2029	-0.3267
4	Zranb1	0.218	-0.137	[illegible]	-0.1334	-0.3292	-0.1782	-0.3973	-0.378	-0.2268
4	Zranb2	-0.6908	-0.2223	-0.4324	-0.2373	[illegible]	[illegible]	0.1102	[illegible]	0.3144
4	Zscan12	-1.0973	-0.3082	-0.7153	-0.1151	-0.1603	0.3077	-0.1549	-0.1196	0.2659
4	Zscan21	-0.4782	-0.5723	-0.1398	[illegible]	[illegible]	[illegible]	-0.0493	-0.2917	0.169
4	Zzz3	-0.225	-0.2128	-0.2097	-0.2312	-0.3539	0.0795	-0.087	-0.3372	0.1761
5	4.93E+23	-0.2007	[illegible]	[illegible]	-0.1209	-0.1603	[illegible]	-0.1703	-0.067	-0.0764
5	0610009O20Rik	-0.2907	-0.368	-0.1501	-0.1895	-0.0842	[illegible]	0.1015	-0.1614	0.126
5	0910001L09Rik	0.1472	-0.2274	-0.1024	0.0578	-0.0712	-0.0935	-0.2472	-0.1055	-0.3734
5	1110018J18Rik	-0.0538	-0.1366	-0.2476	0.1873	-0.1179	-0.0823	-0.2819	-0.1404	[illegible]
5	Kansl1l	0.2141	-0.074	[illegible]	-0.2413	-0.1424	-0.2619	-0.0619	-0.2277	-0.1297
5	Exoc3l4	-0.0604	0.0984	[illegible]	-0.1671	-0.1782	-0.0604	-0.0707	-0.2044	-0.1021
5	1200011I18Rik	-0.1006	-0.2196	-0.0482	-0.273	[illegible]	0.1028	[illegible]	-0.3314	-0.2475
5	Mb21d2	-0.2138	-0.2607	[illegible]	[illegible]	-0.3208	0.0774	-0.0475	-0.3957	0.1613
5	1700008P20Rik	-0.3665	-0.4204	-0.208	-0.1336	0.1202	[illegible]	[illegible]	0.1717	0.0984
5	1700009P17Rik	-0.418	-0.6305	-0.3422	-0.0671	0.0669	0.2332	-0.0549	0.4021	-0.4544
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5	1700029H14Rik	-0.0979	-0.0979	[illegible]	-0.1839	-0.1069	-0.0655	-0.1713	[illegible]	-0.1495
5	1700049G17Rik	[illegible]	-0.0892	-0.2692	-0.1843	[illegible]	-0.054	-0.1101	-0.2327	0.2806
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5	1700065D16Rik	-0.1499	[illegible]	[illegible]	-0.106	-0.0796	-0.1812	-0.1989	-0.1603	-0.1128
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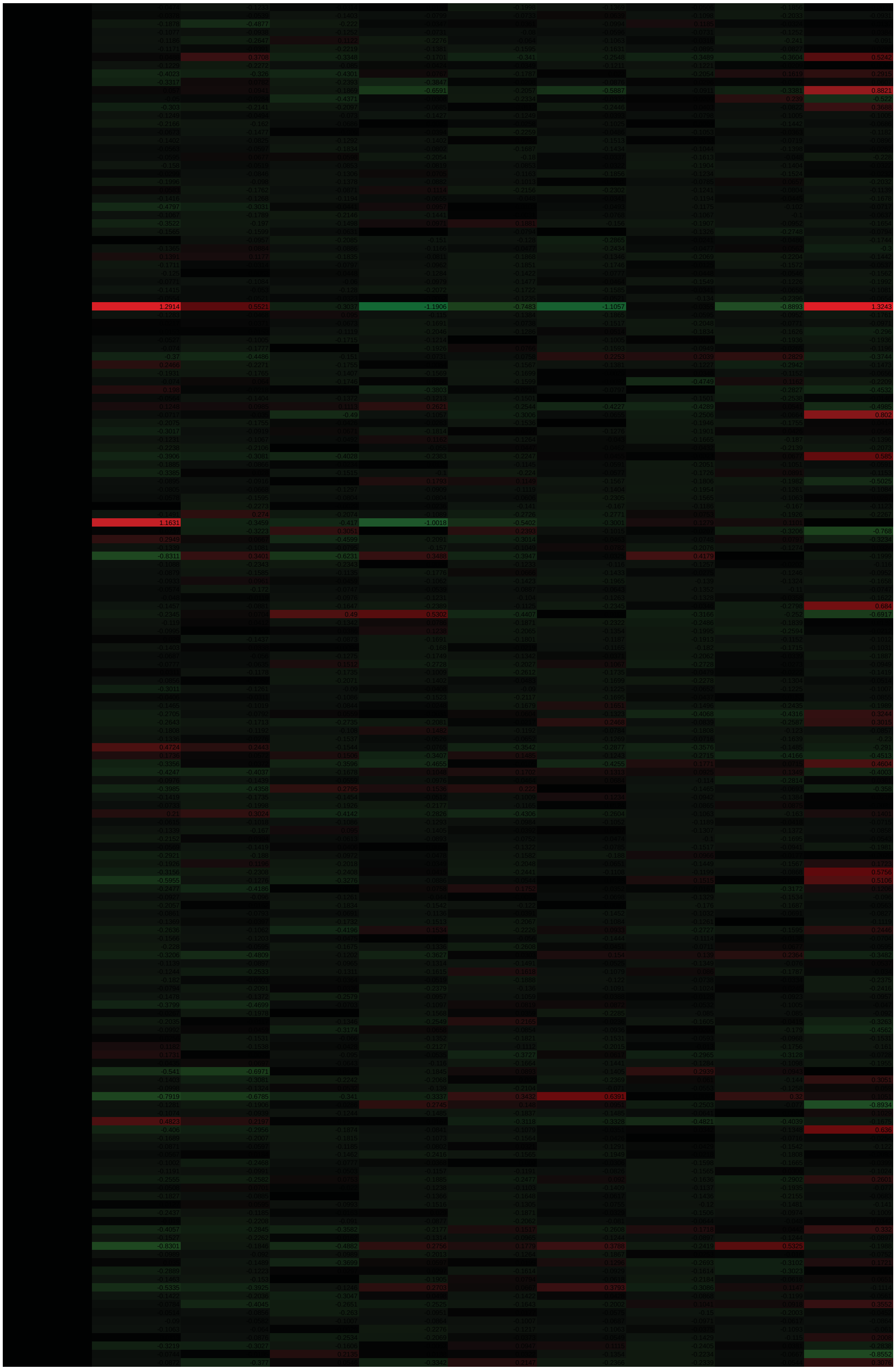

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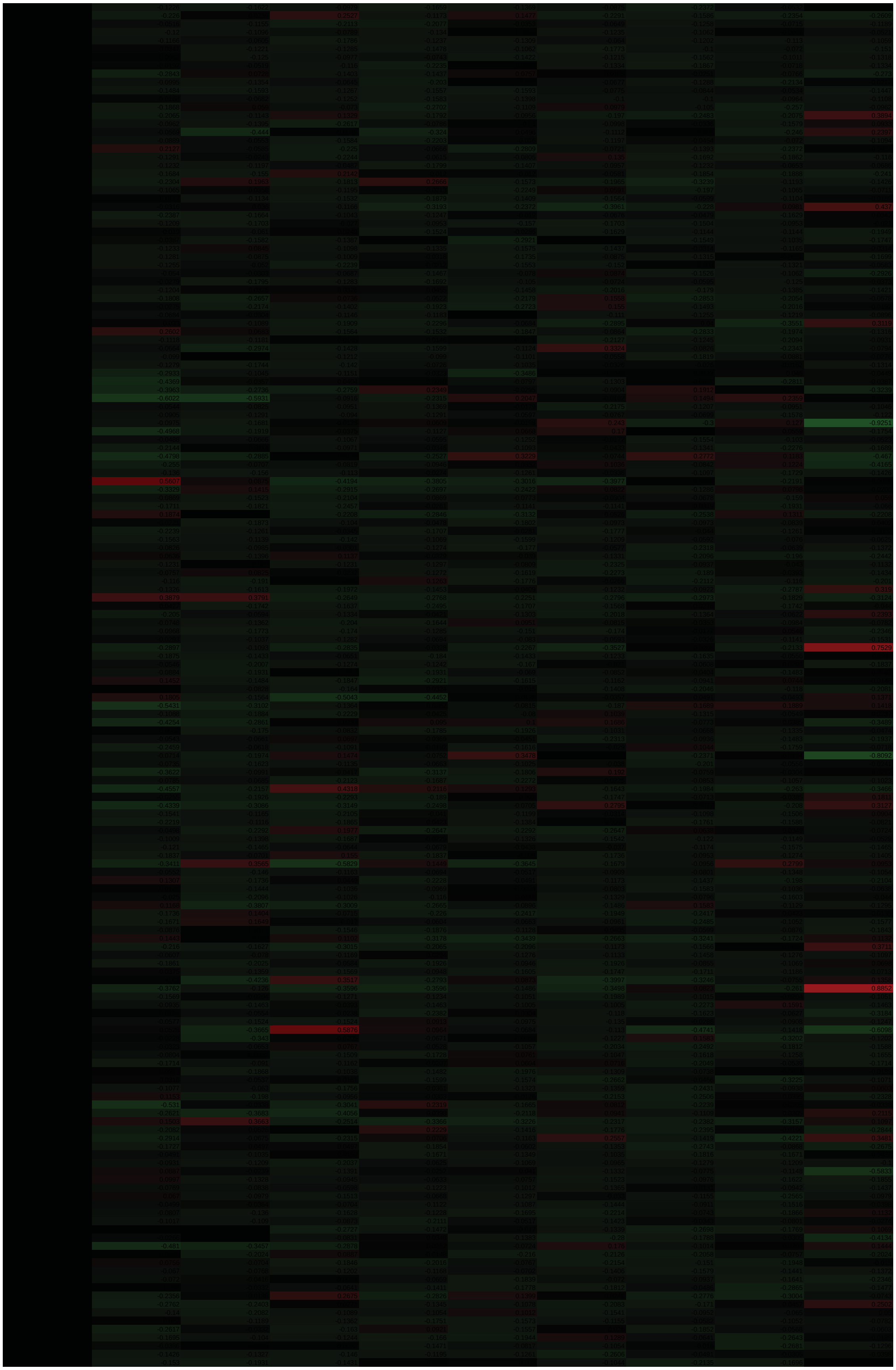

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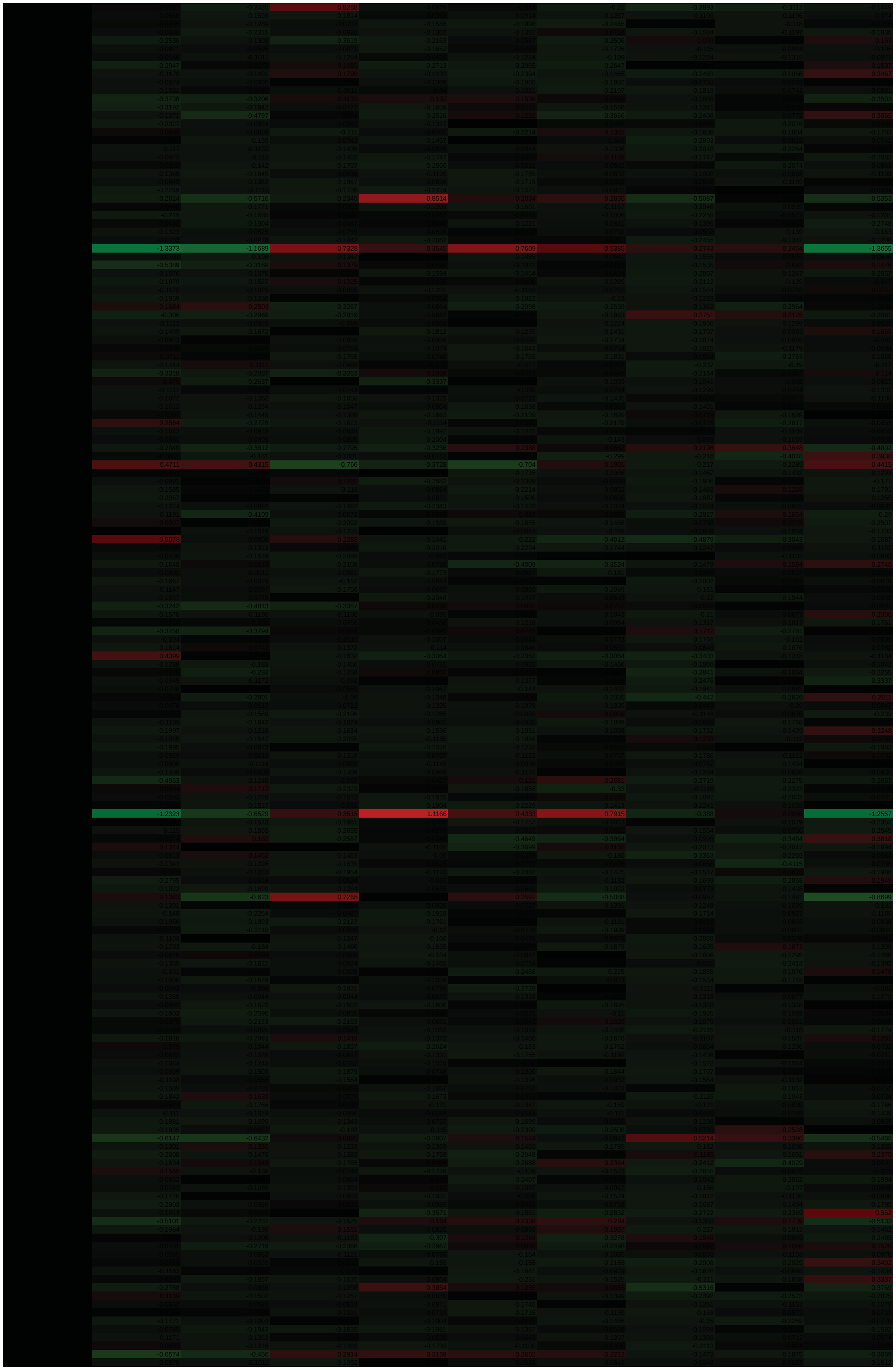

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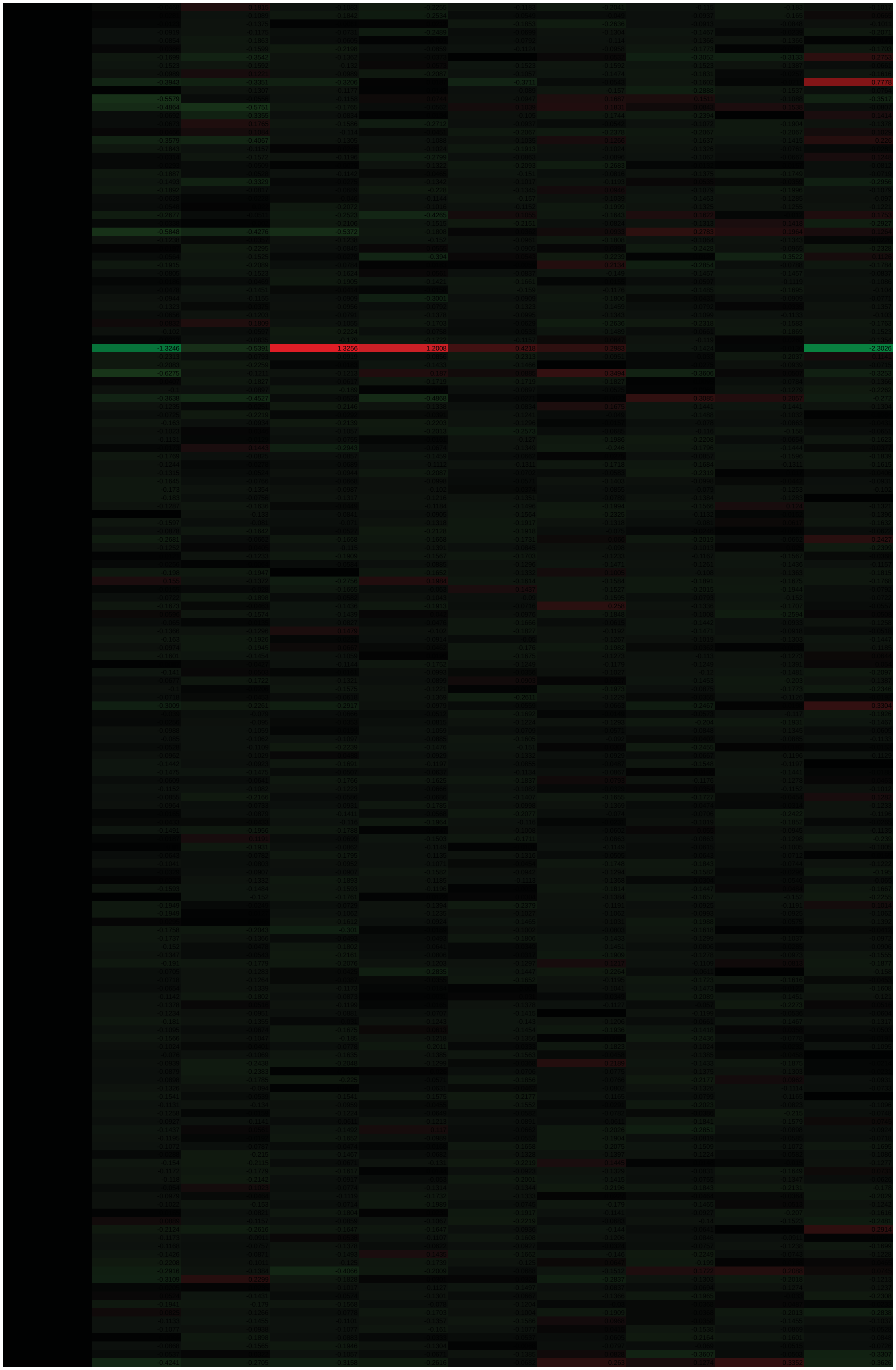

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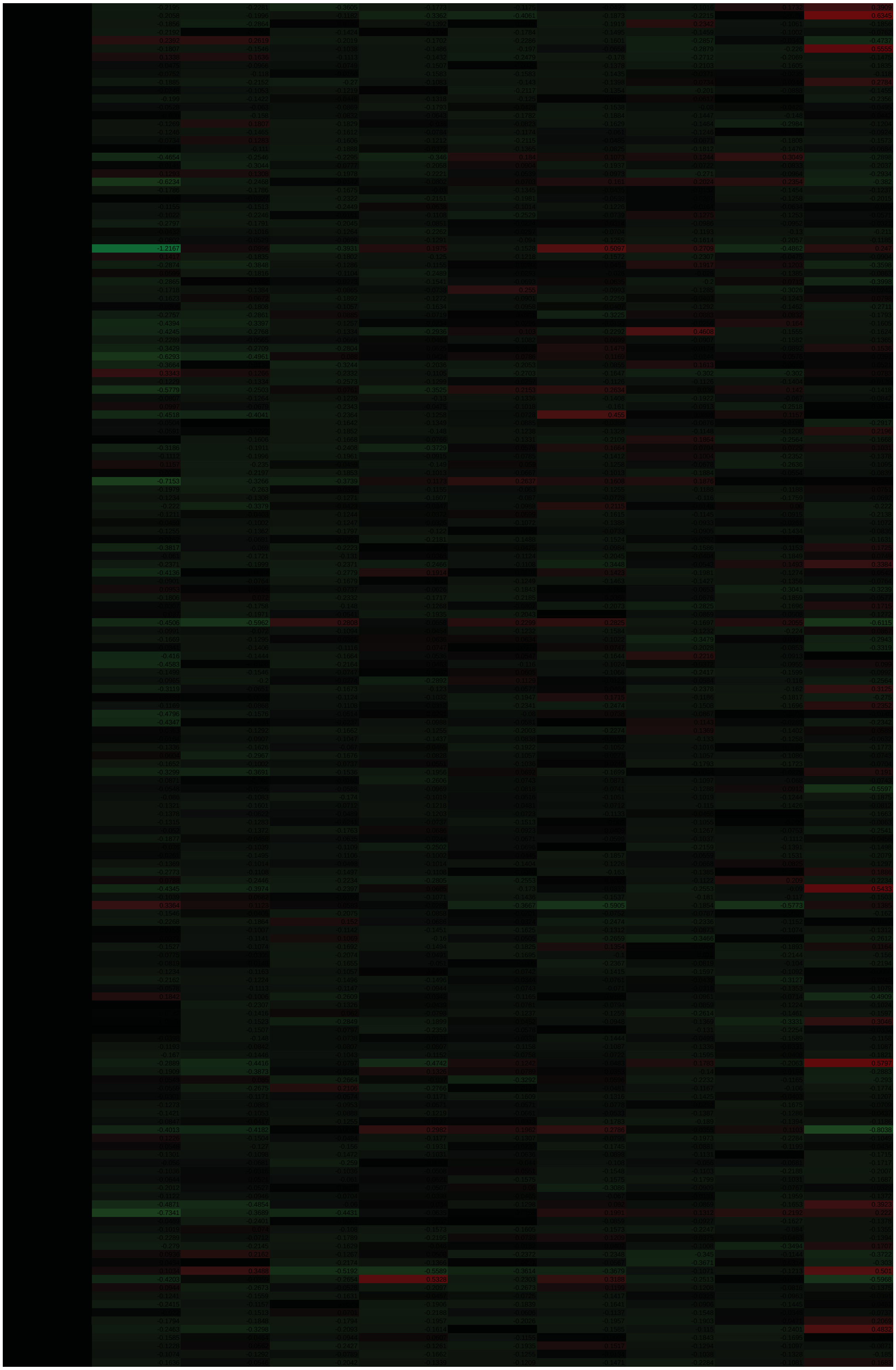

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5	Zfp33b		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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5	Zfp423		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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5	Zfp438		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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5	Zfp593		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Zfp622		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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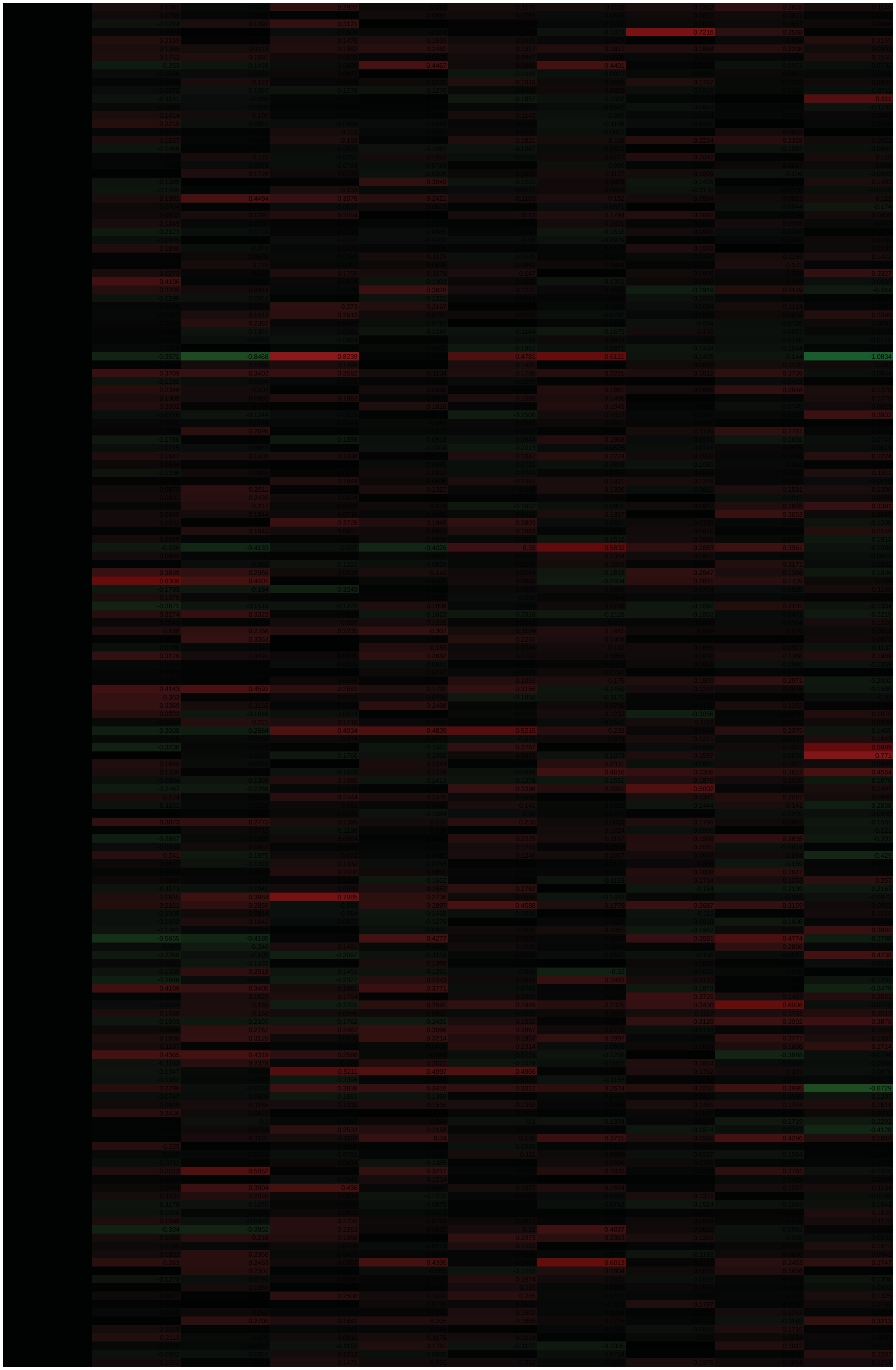

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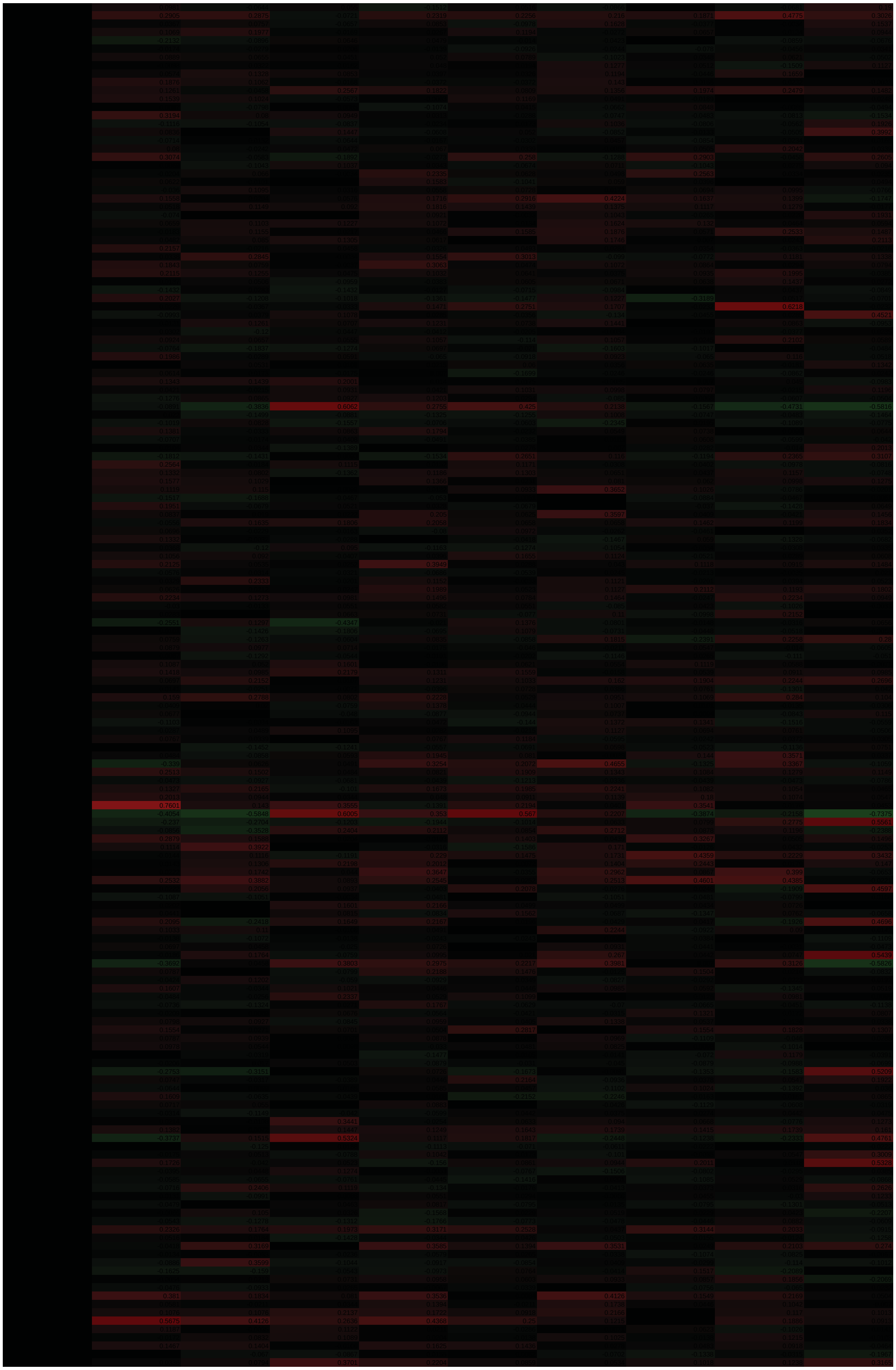

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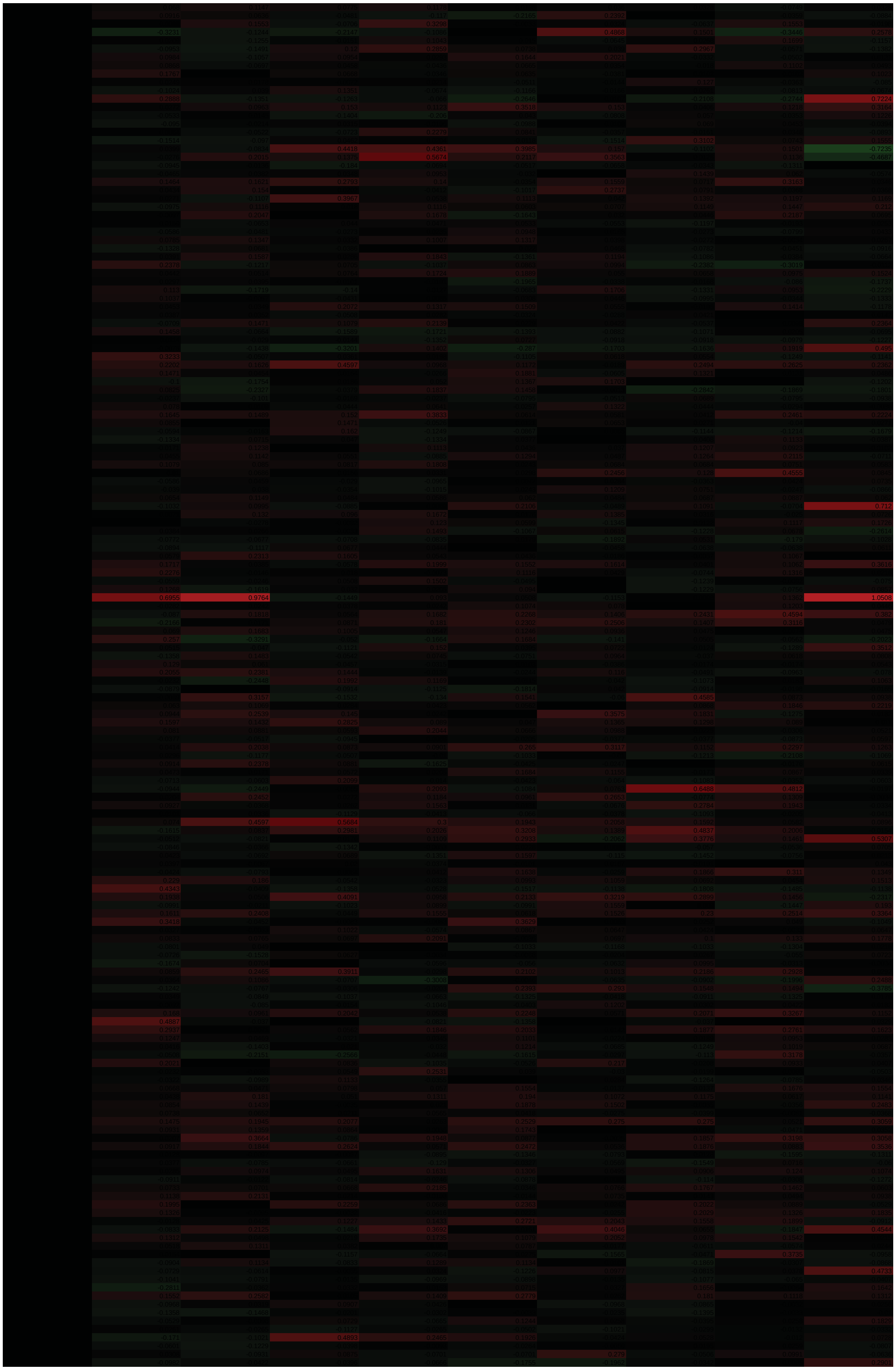

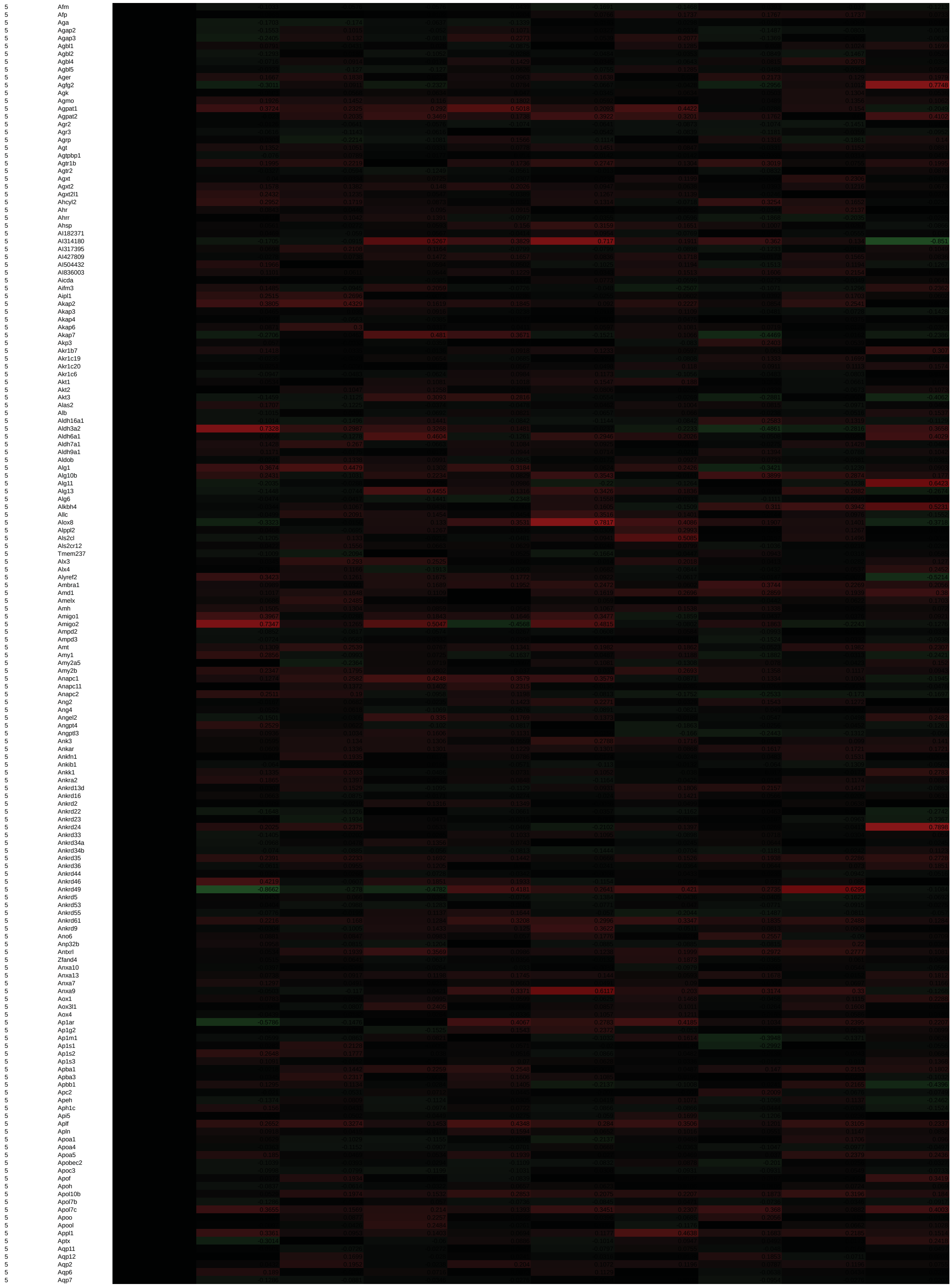
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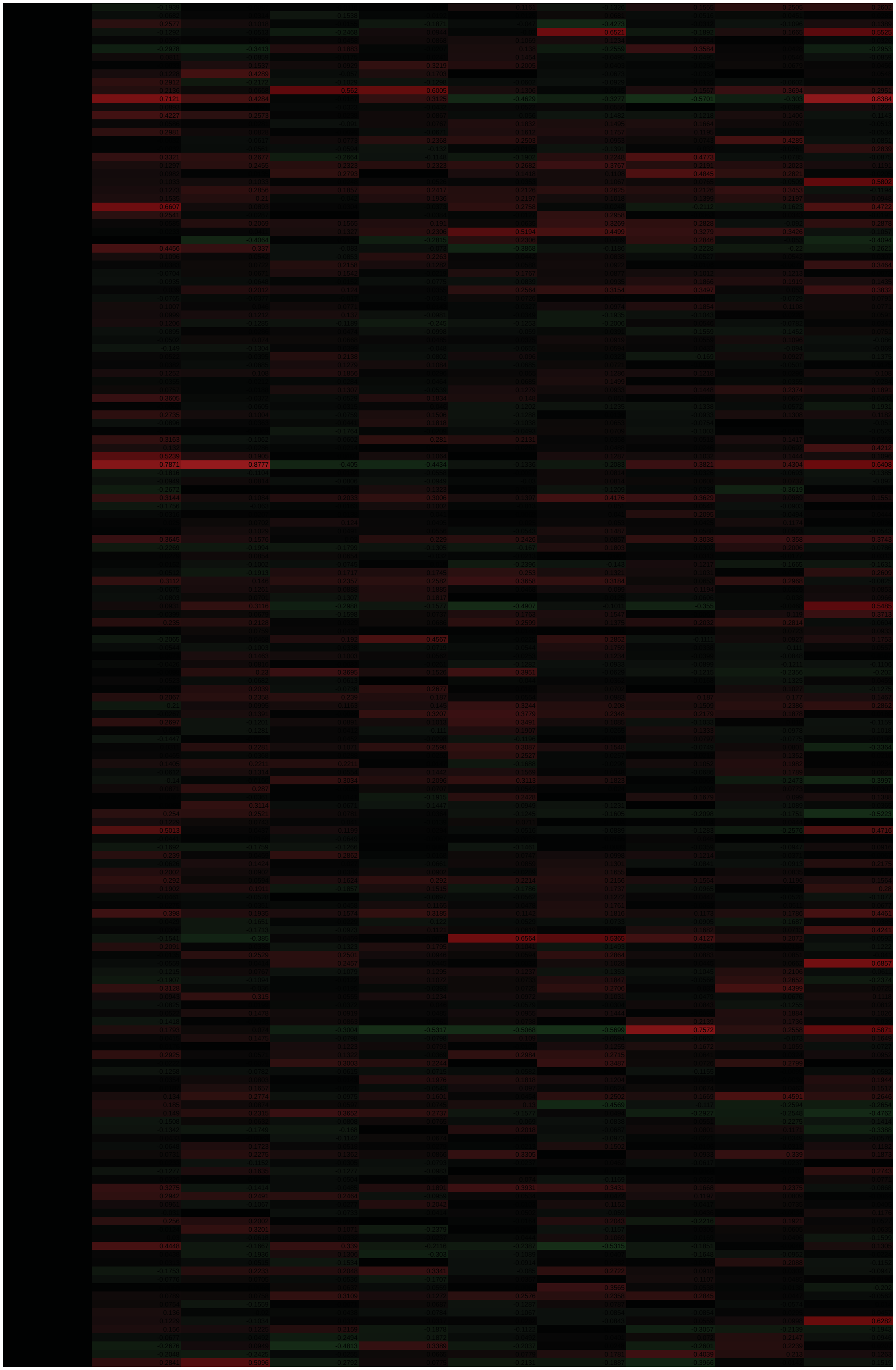

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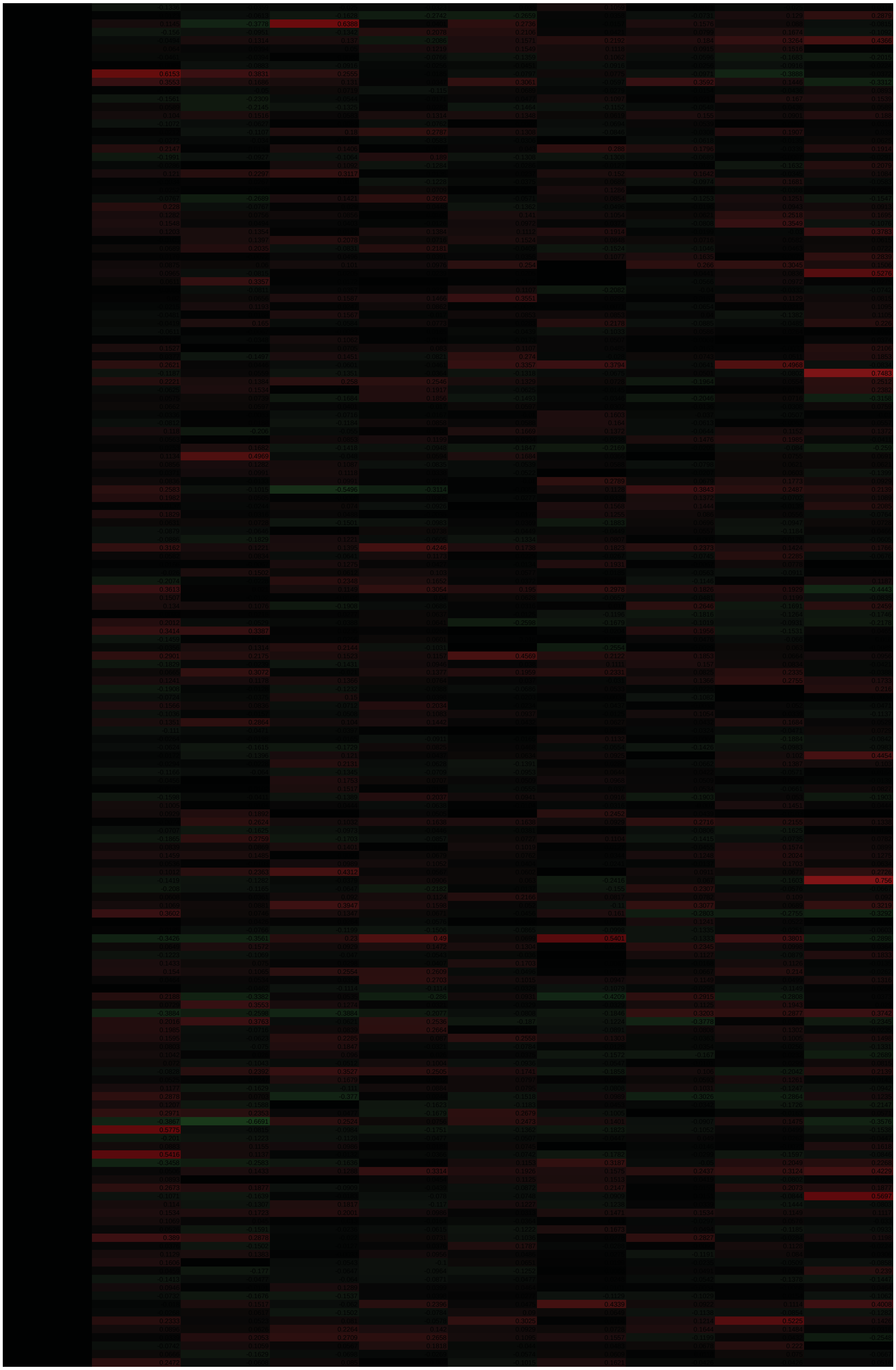

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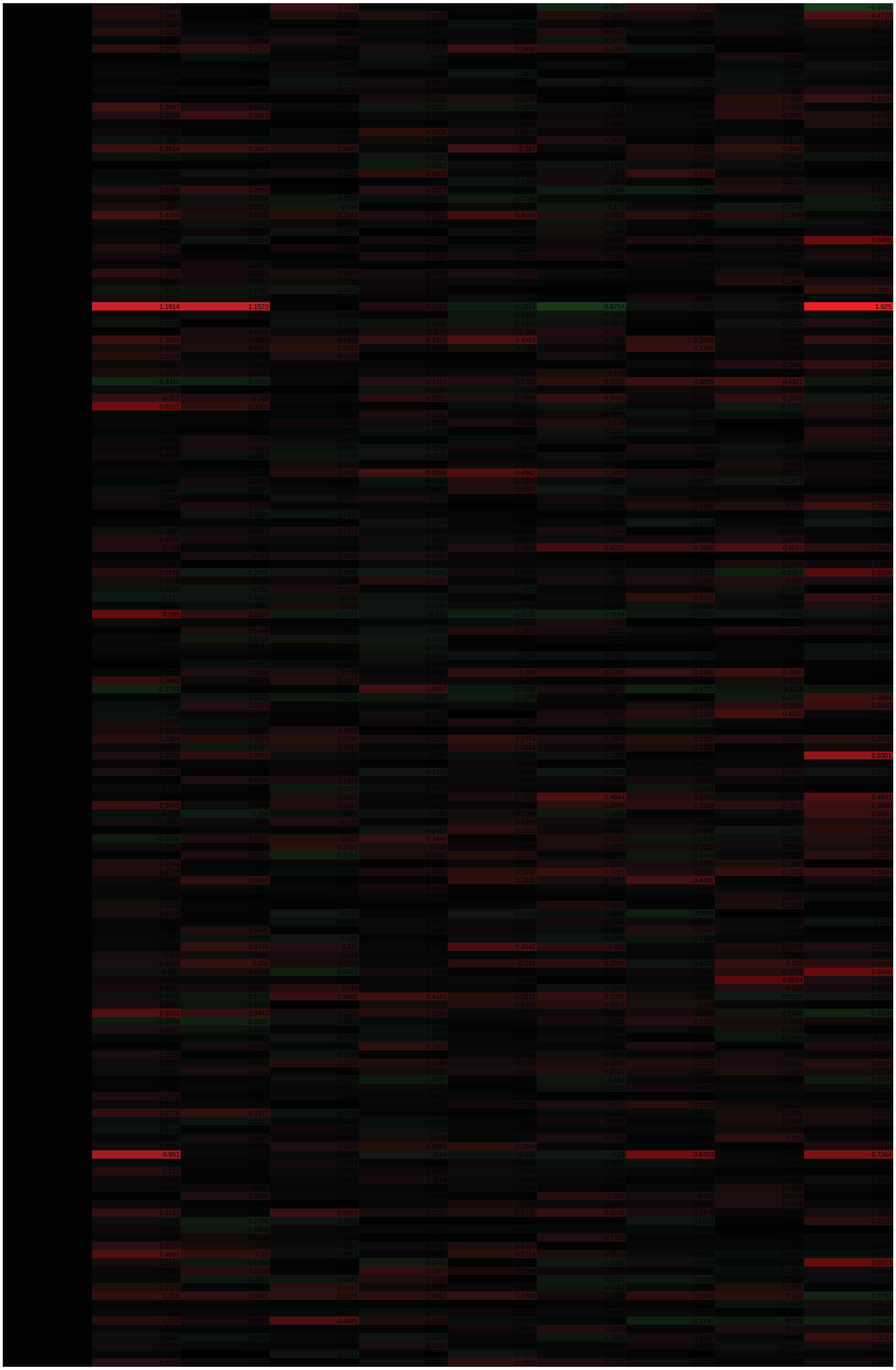

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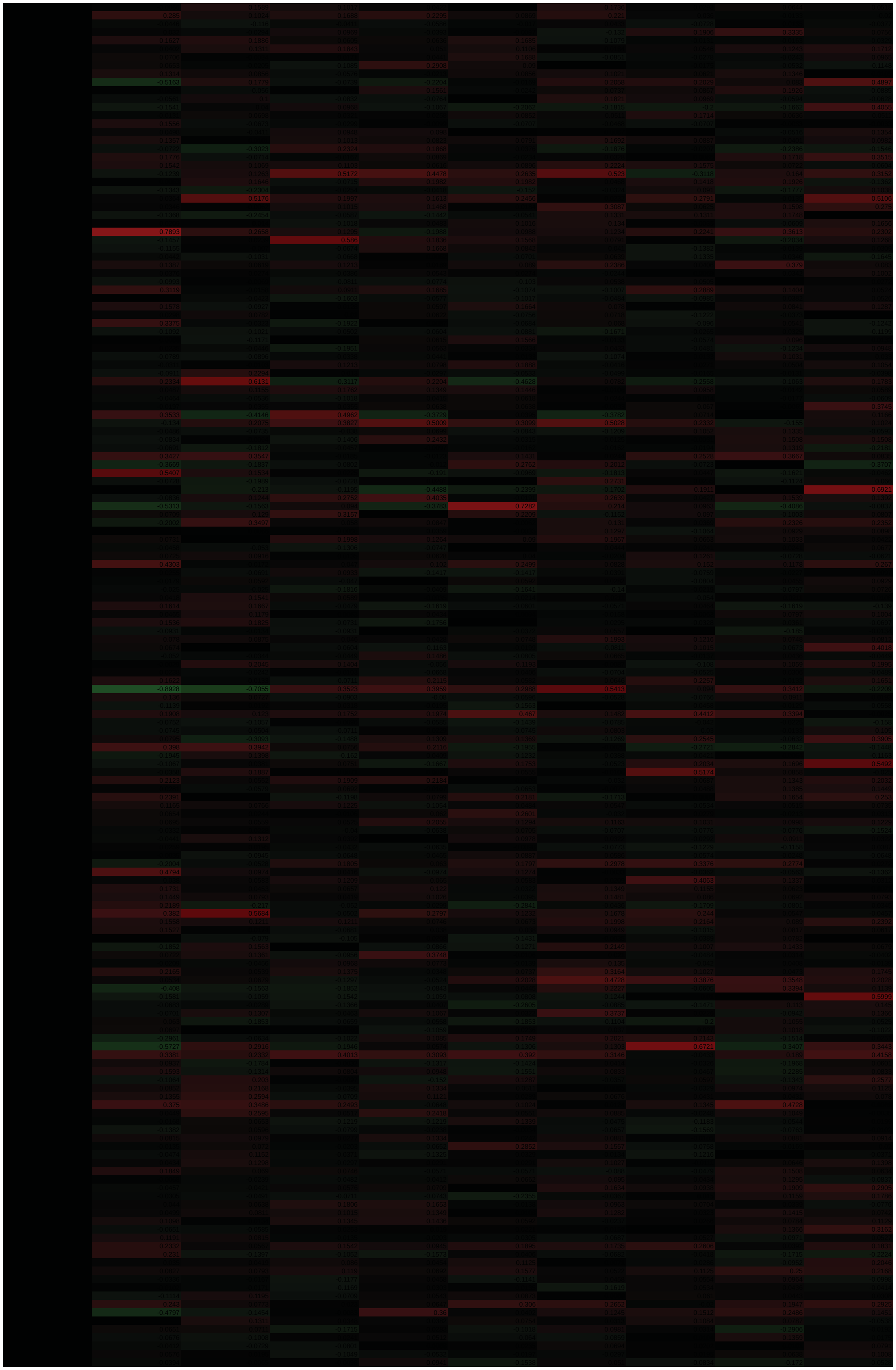

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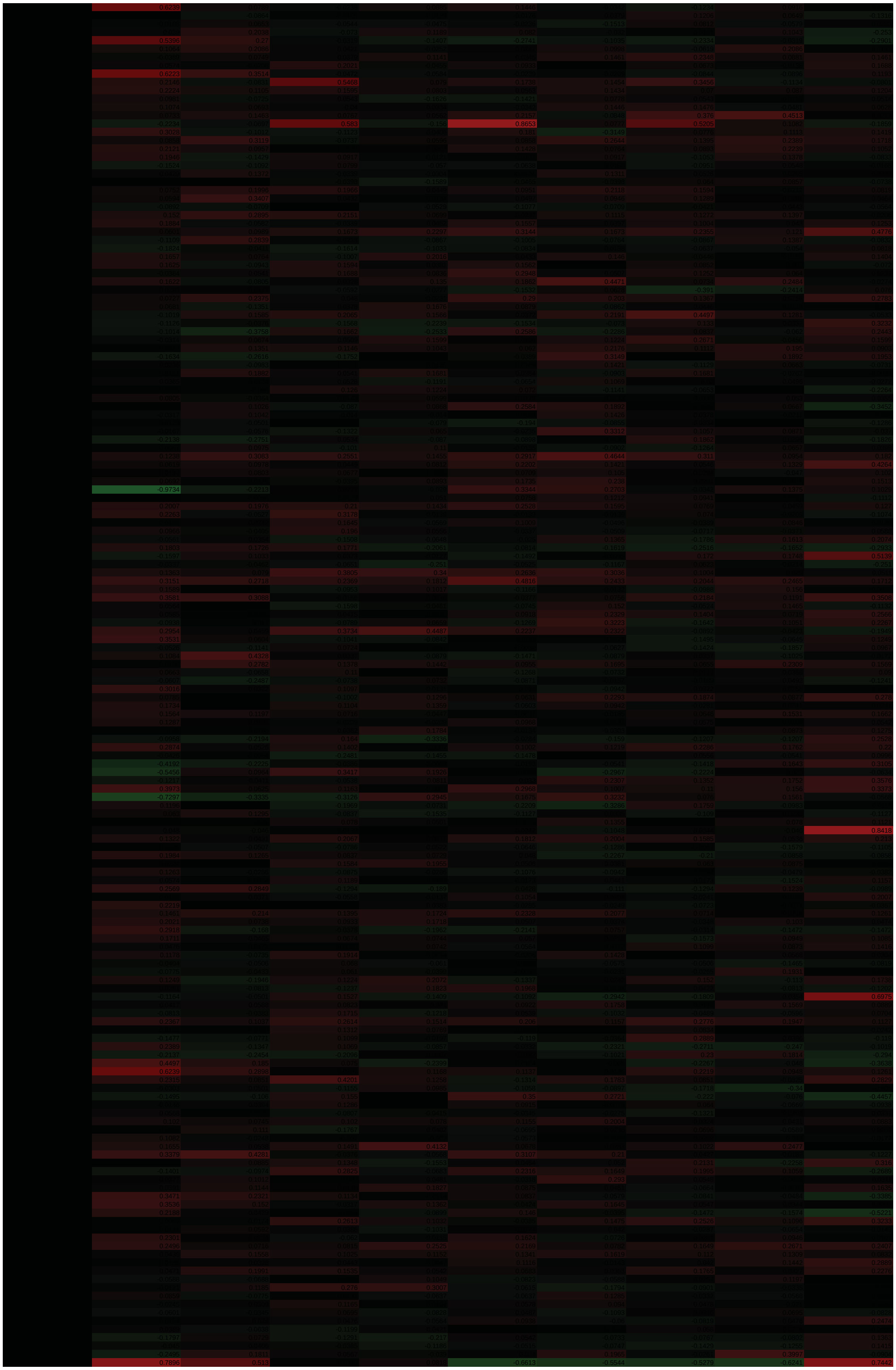
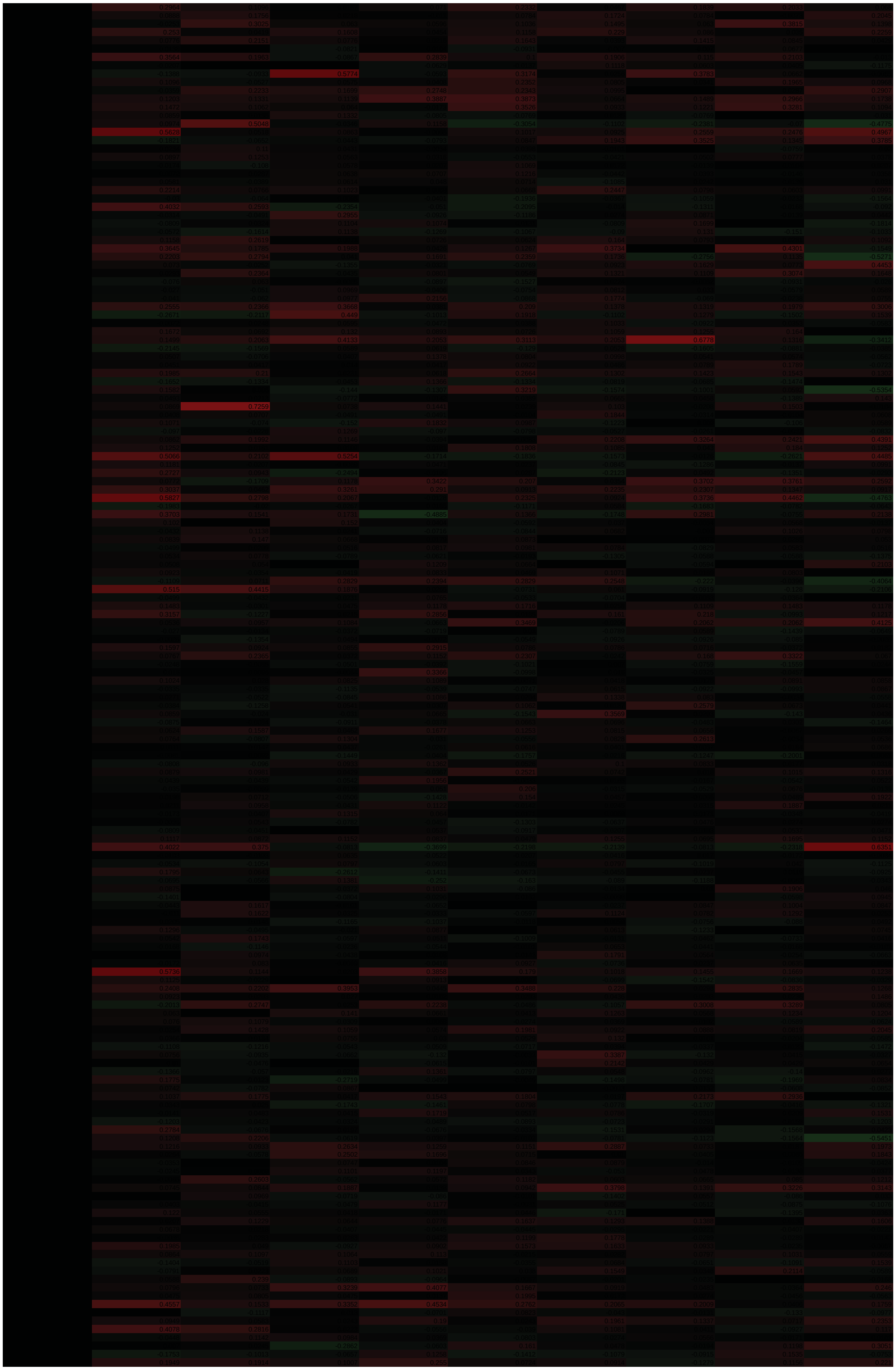


5	Csdc2	
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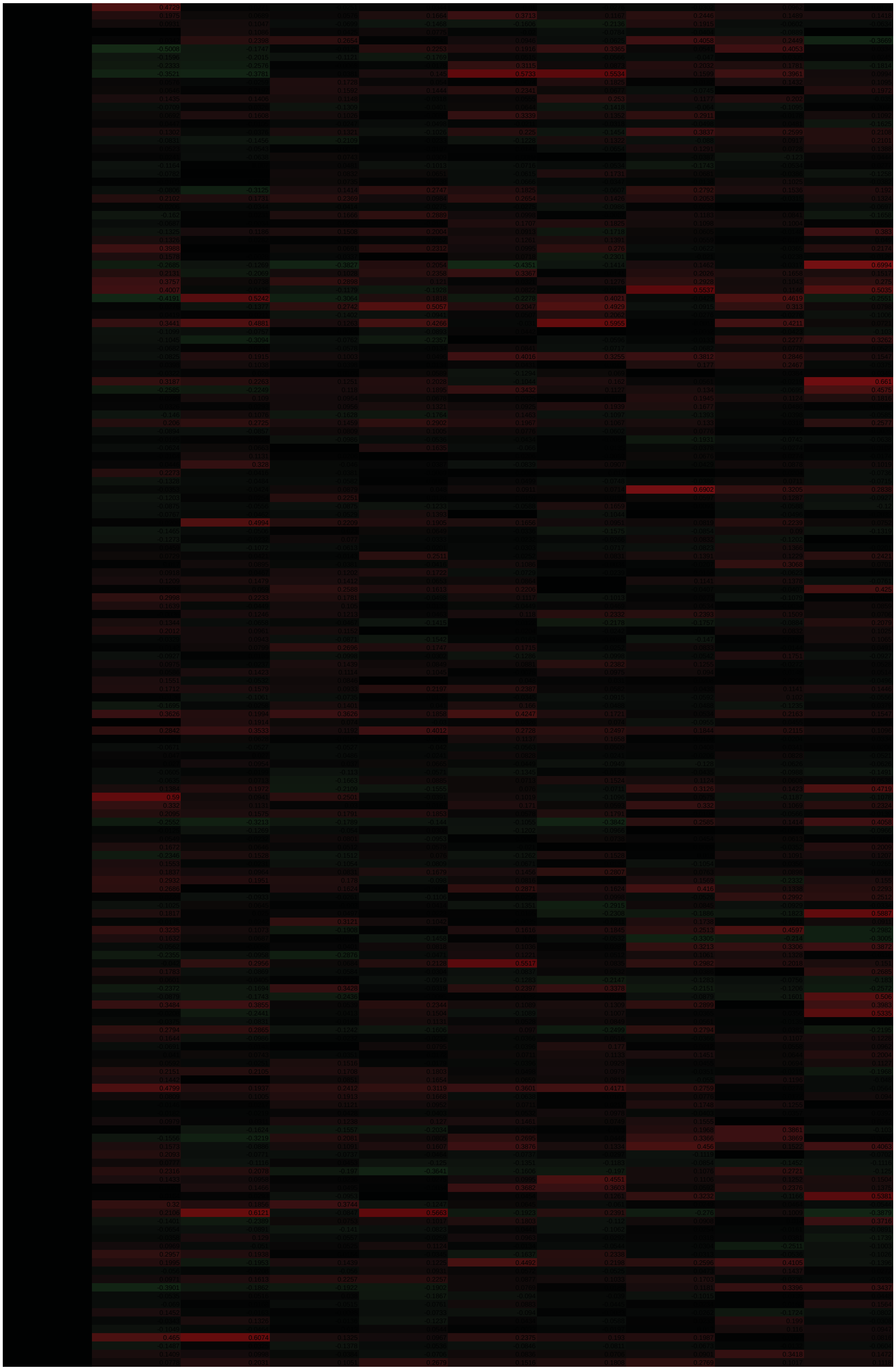

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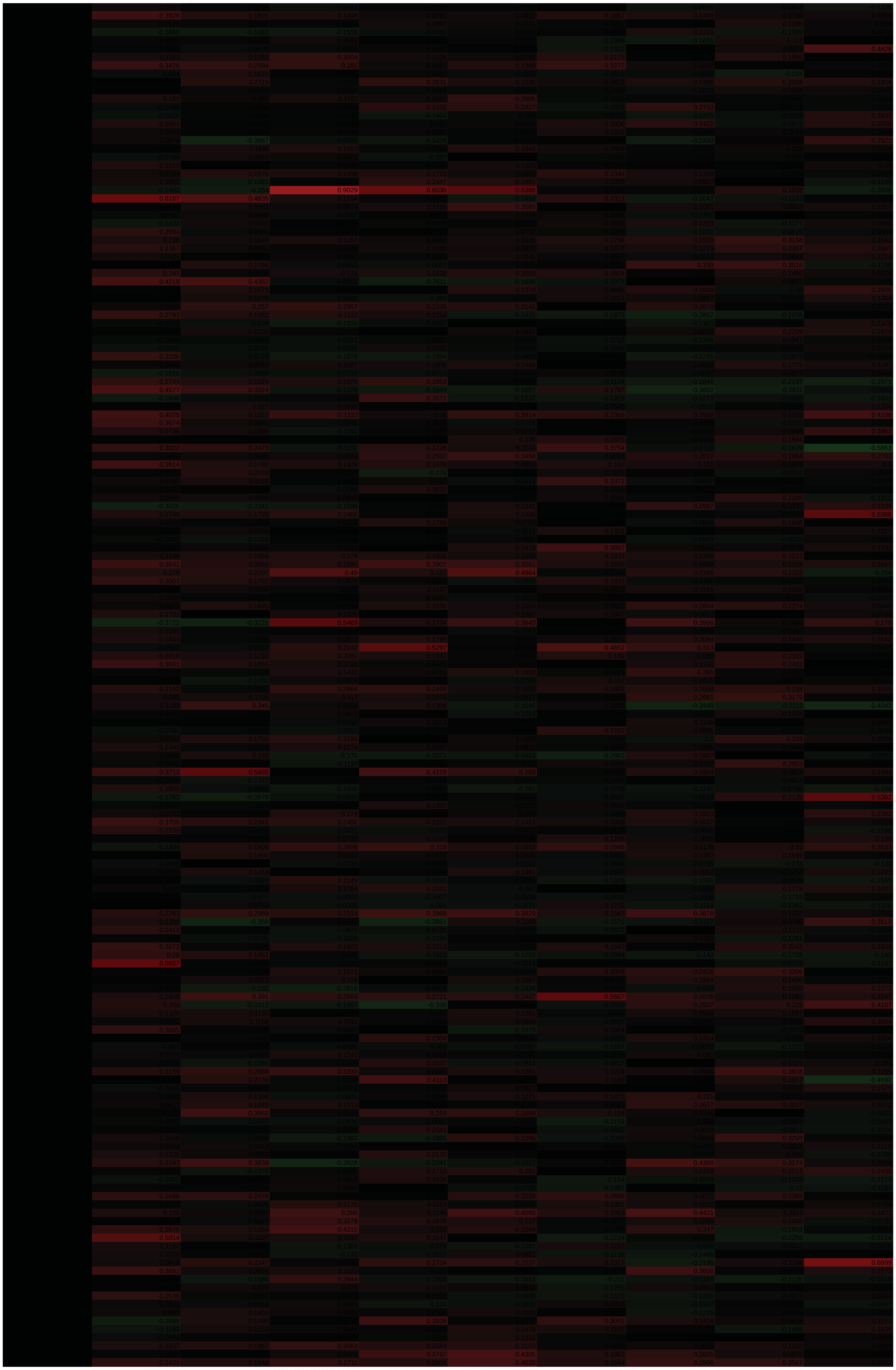

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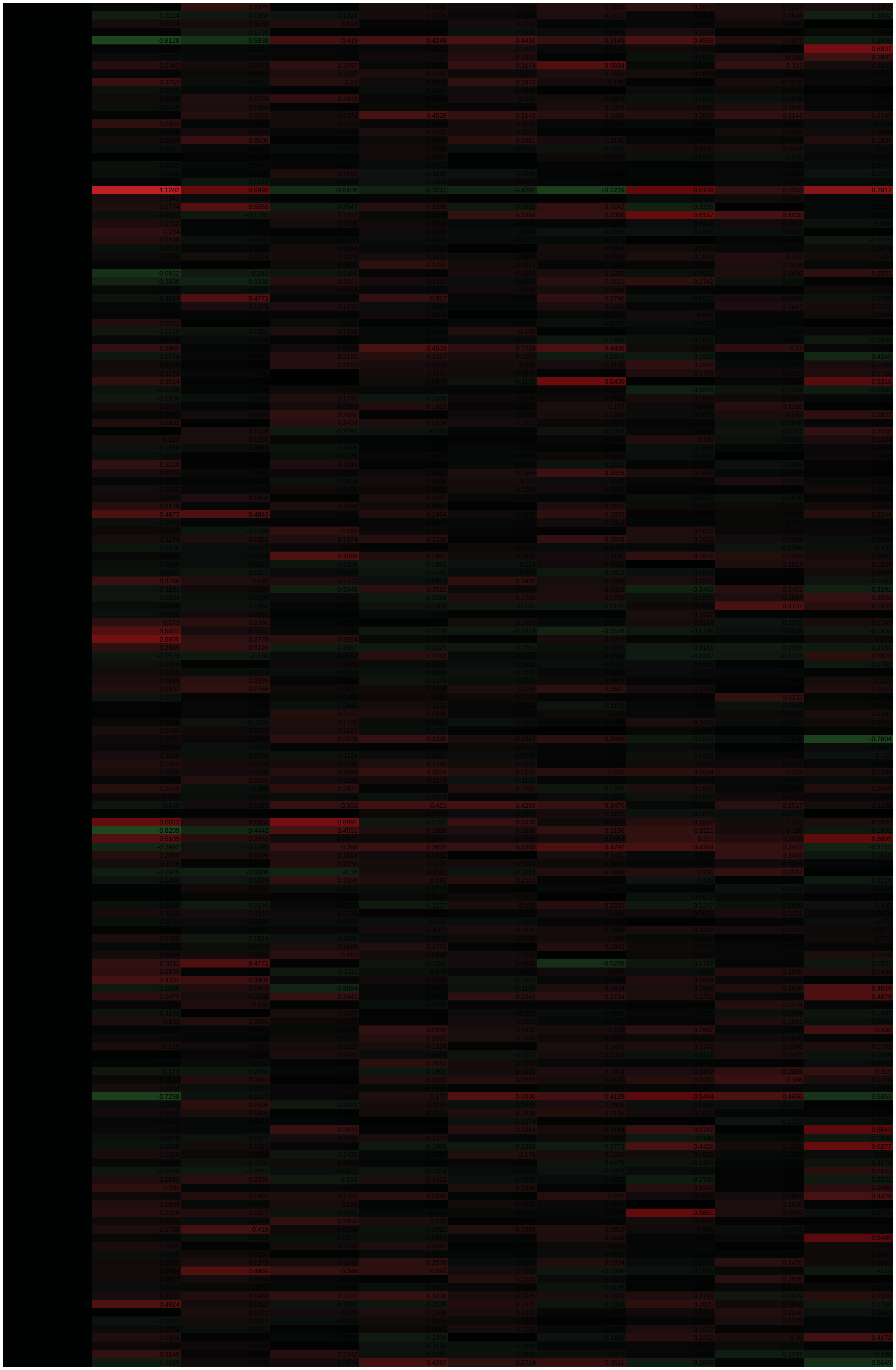

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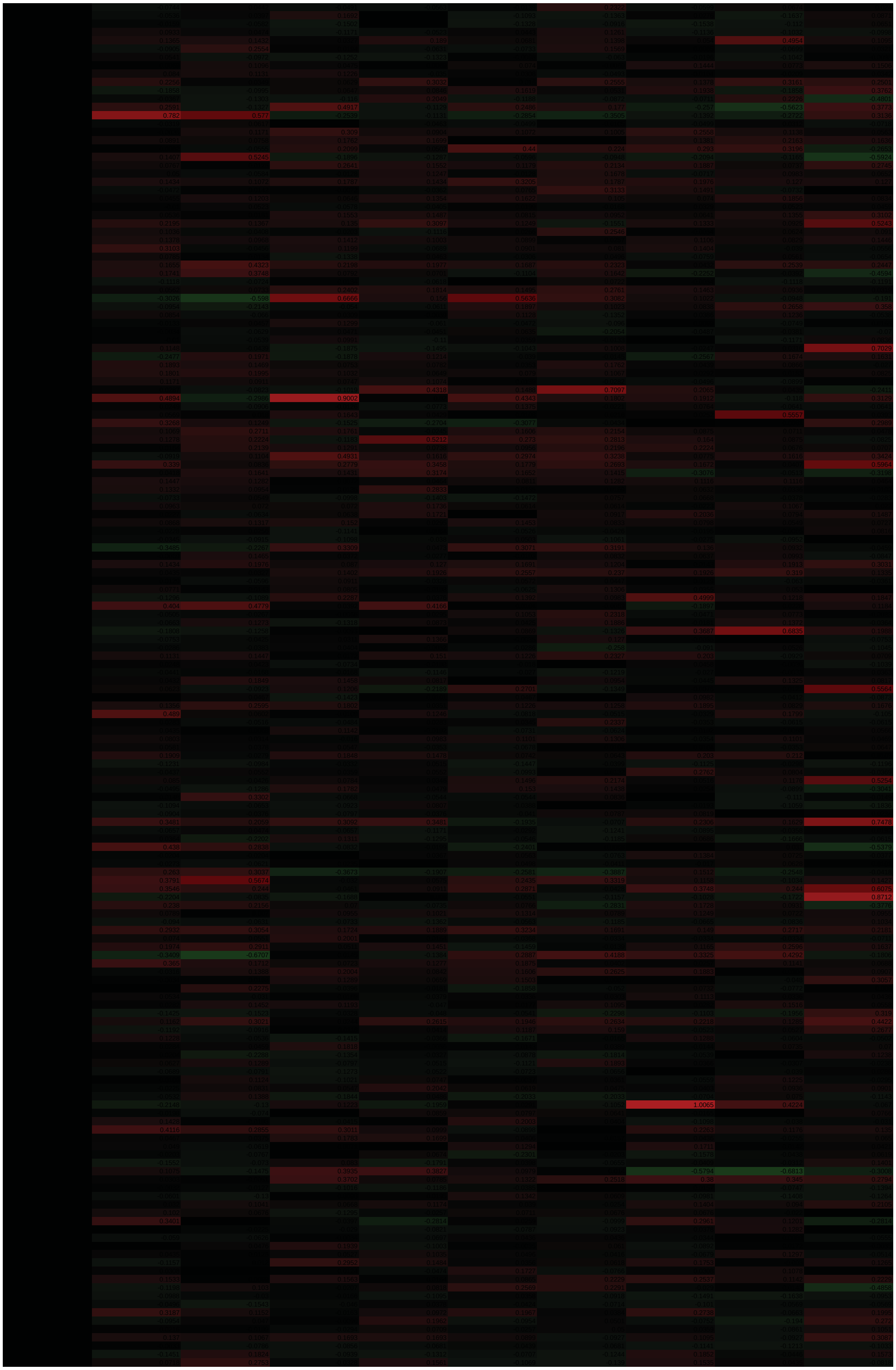

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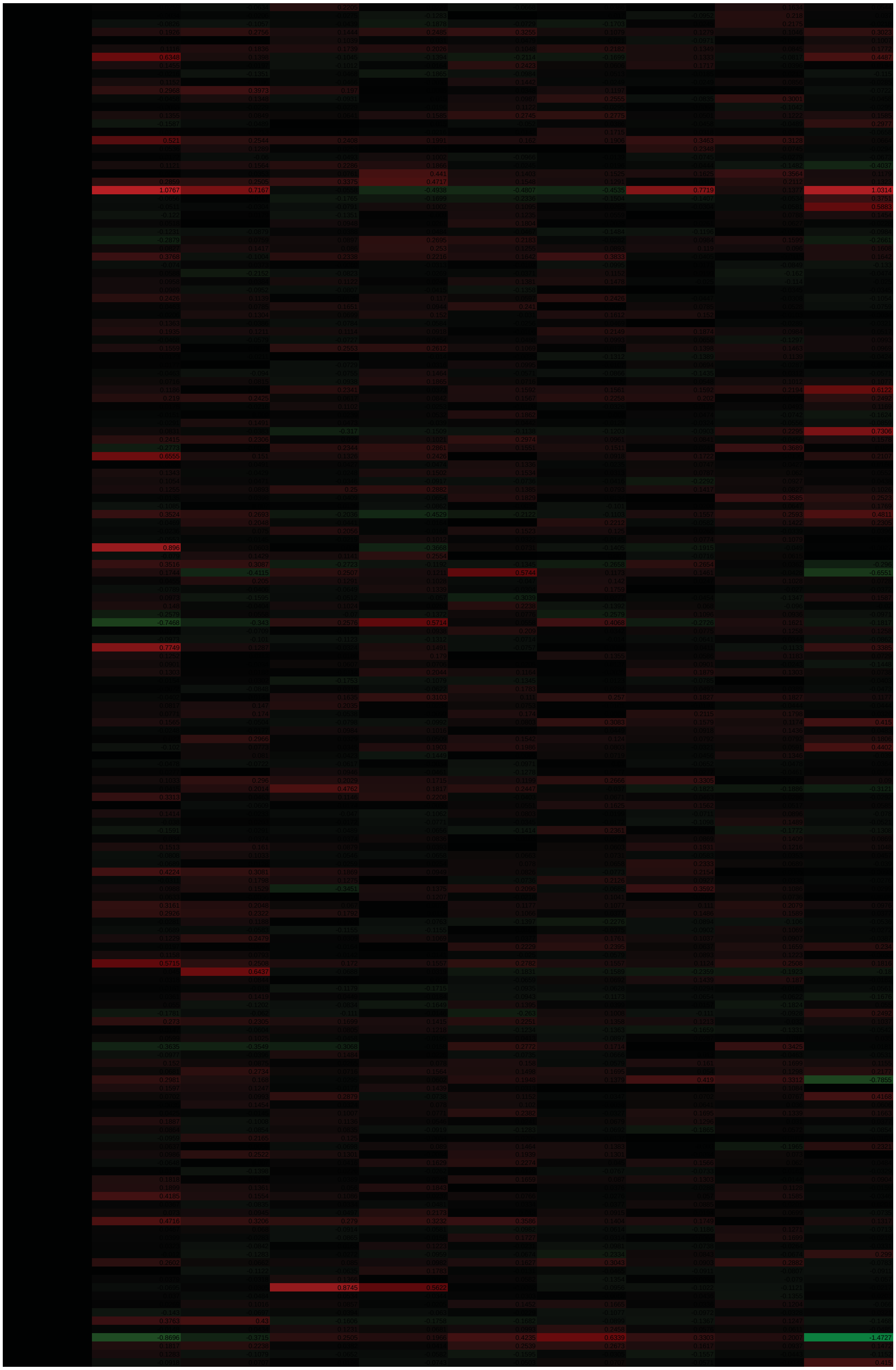

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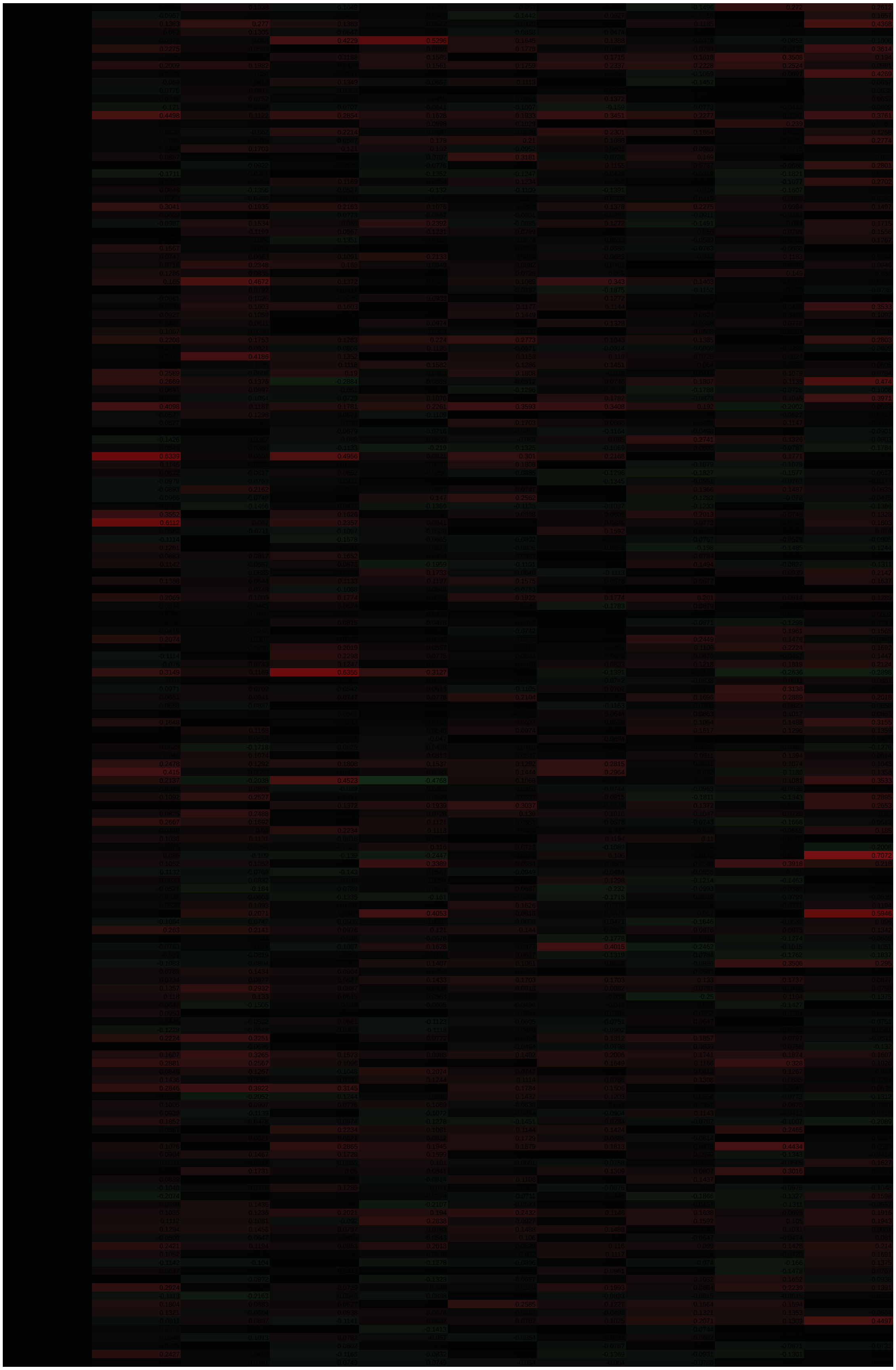

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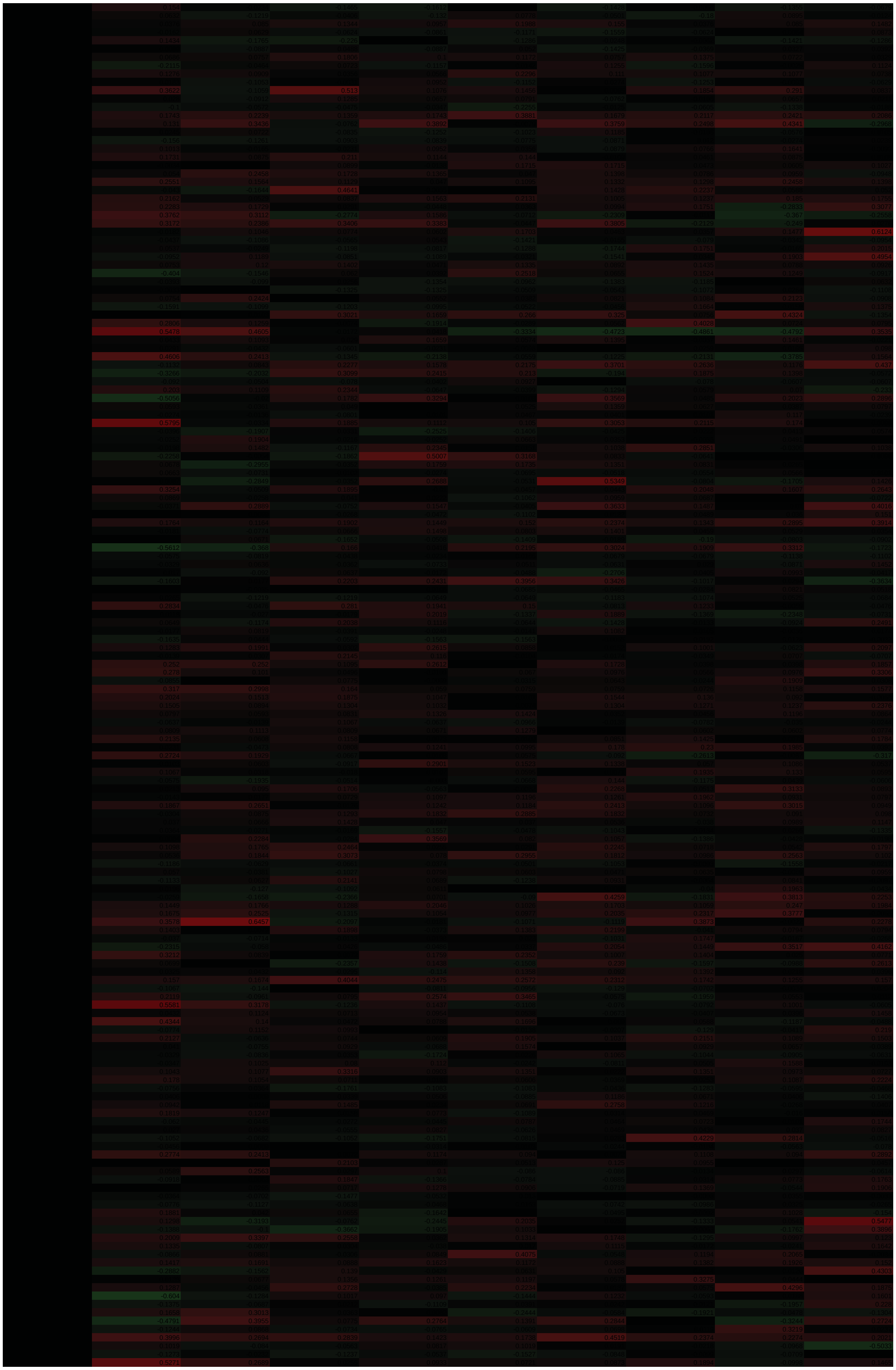

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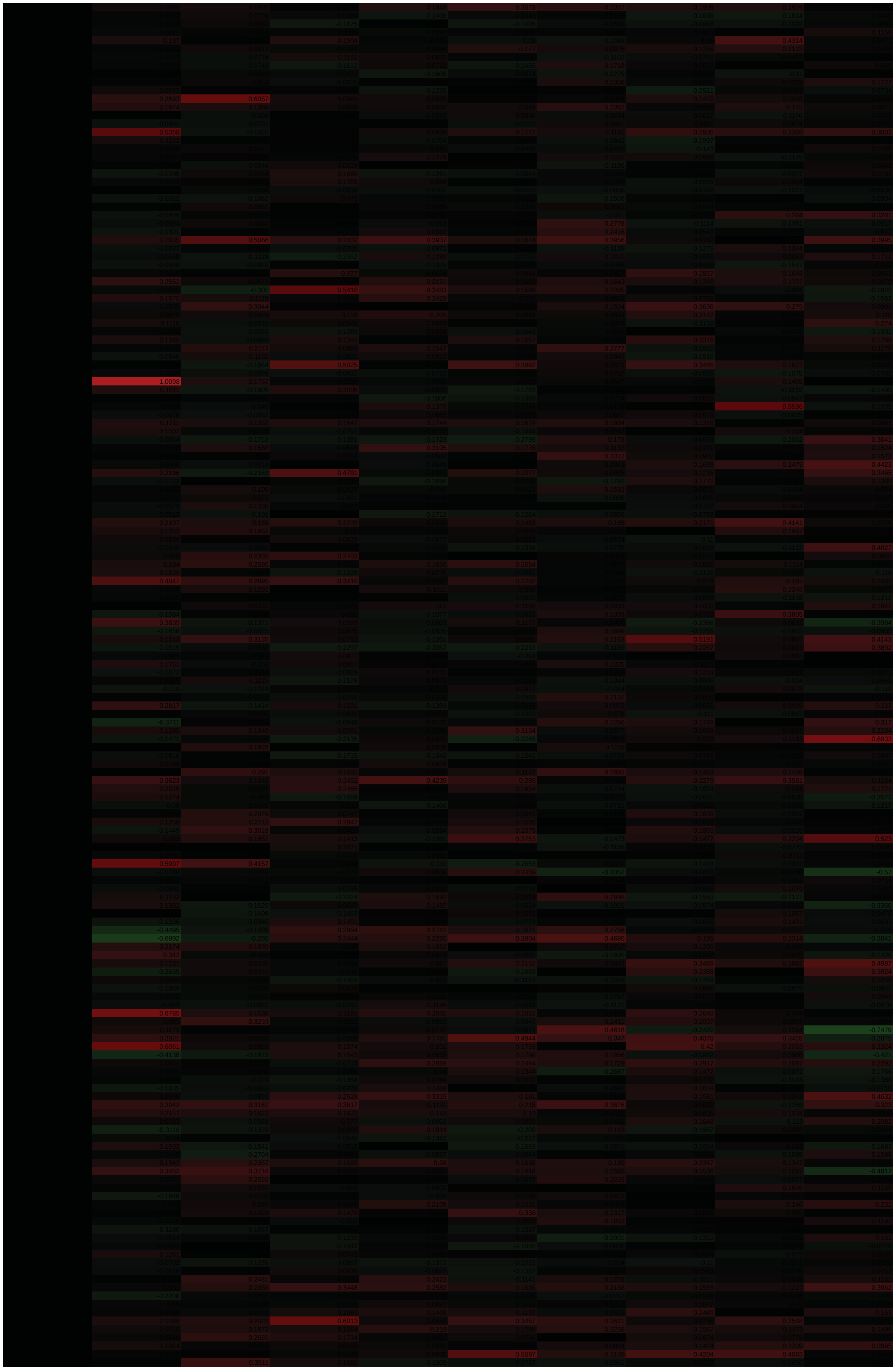

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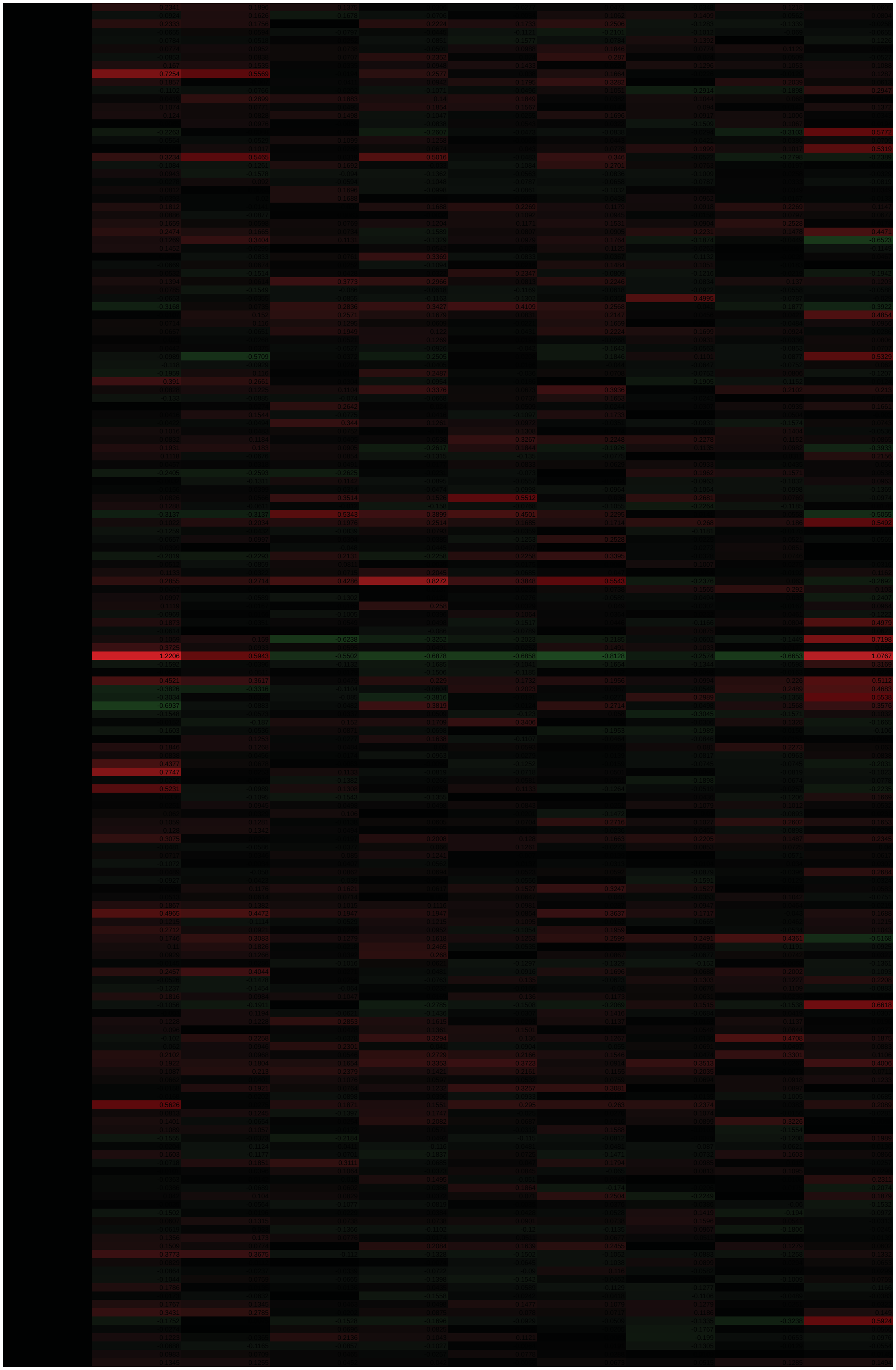

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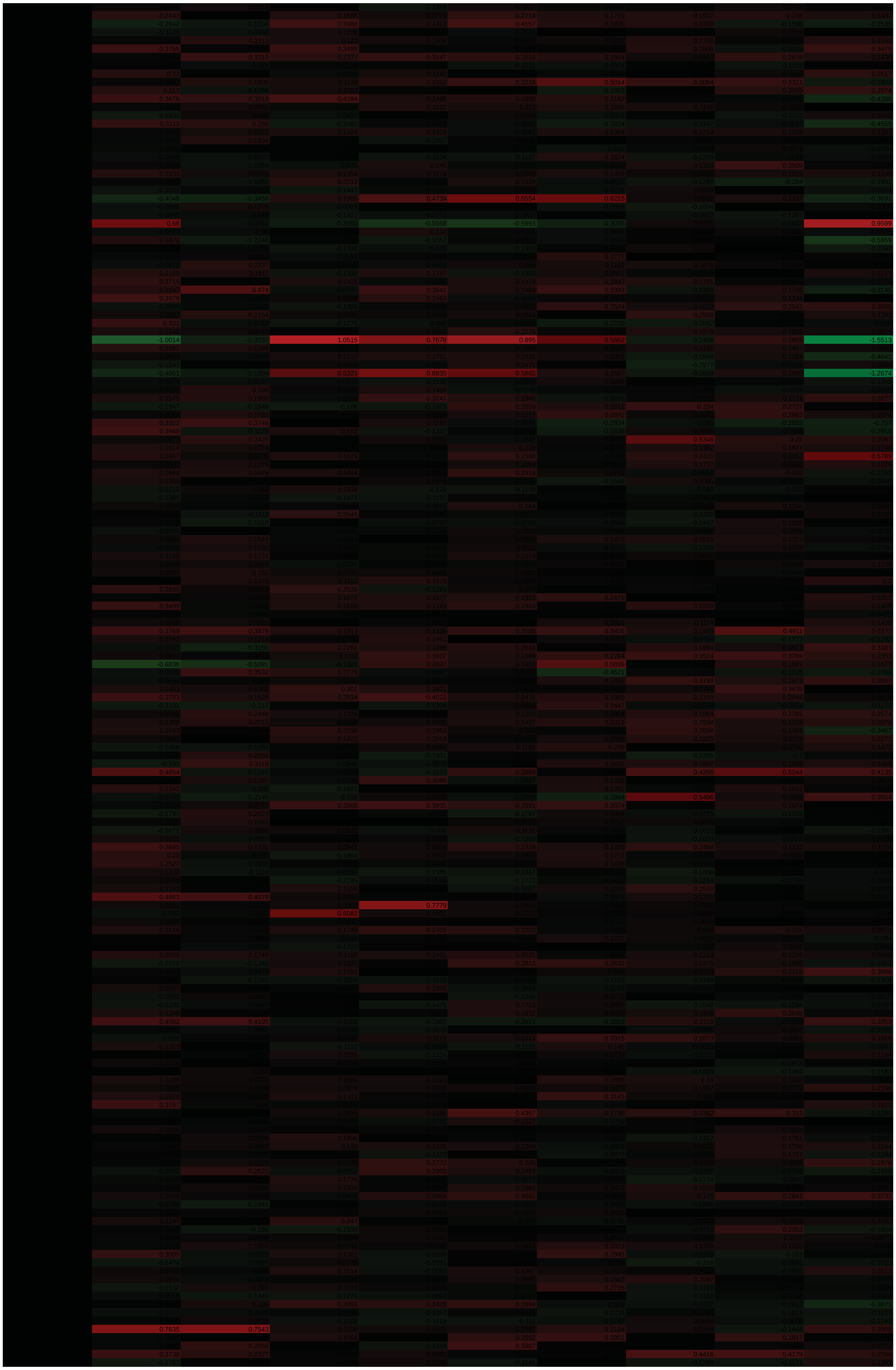

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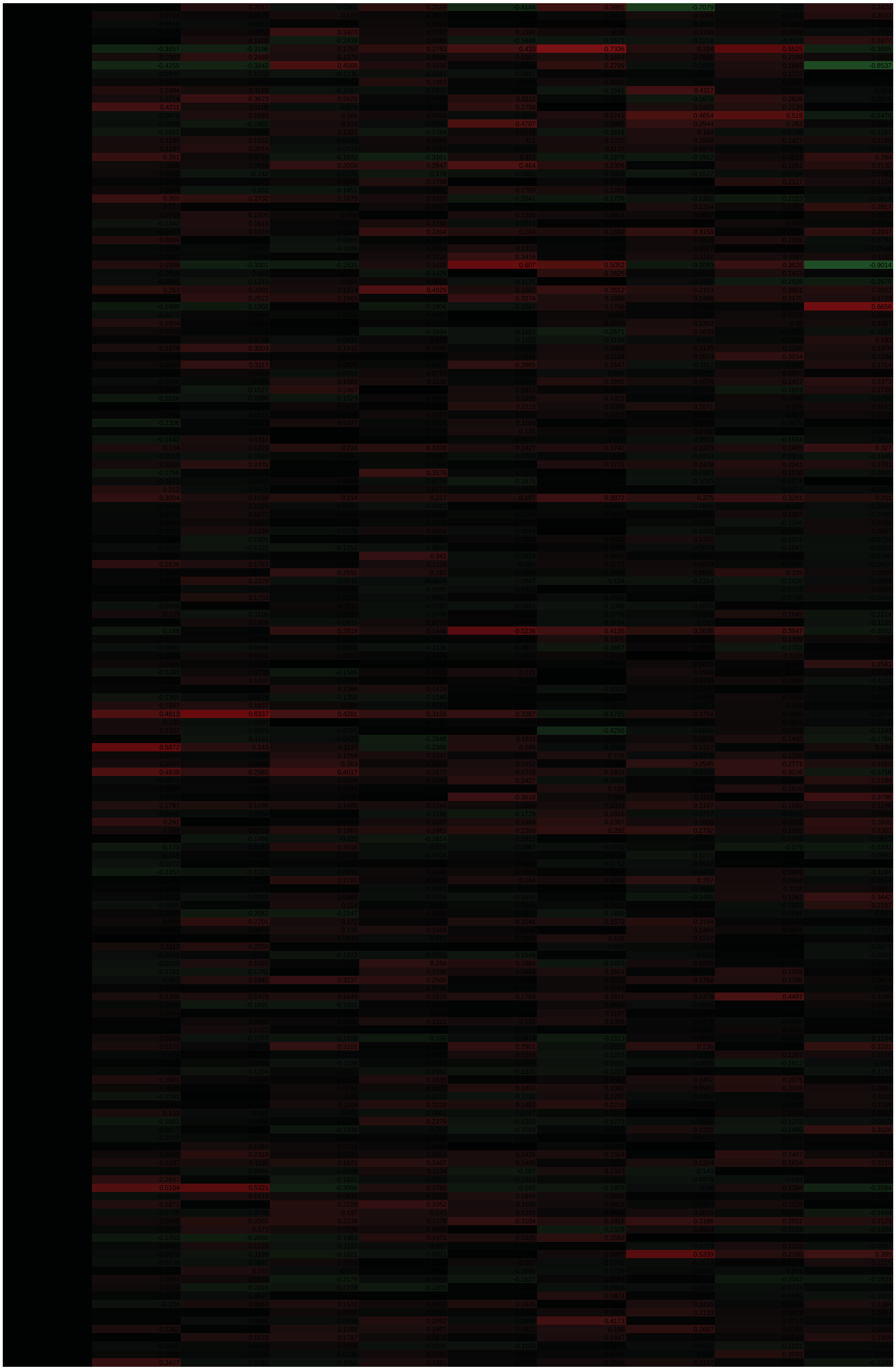

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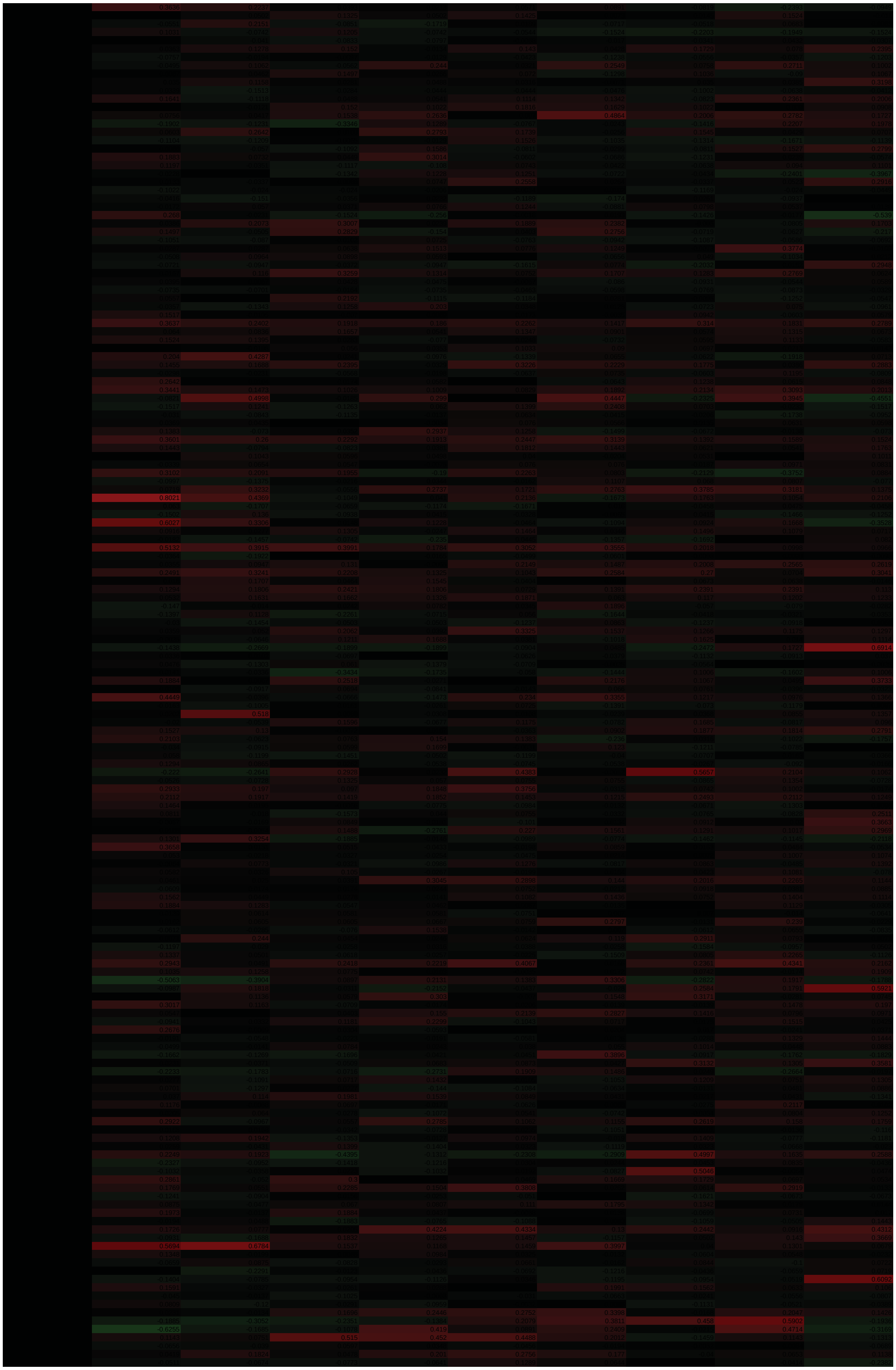

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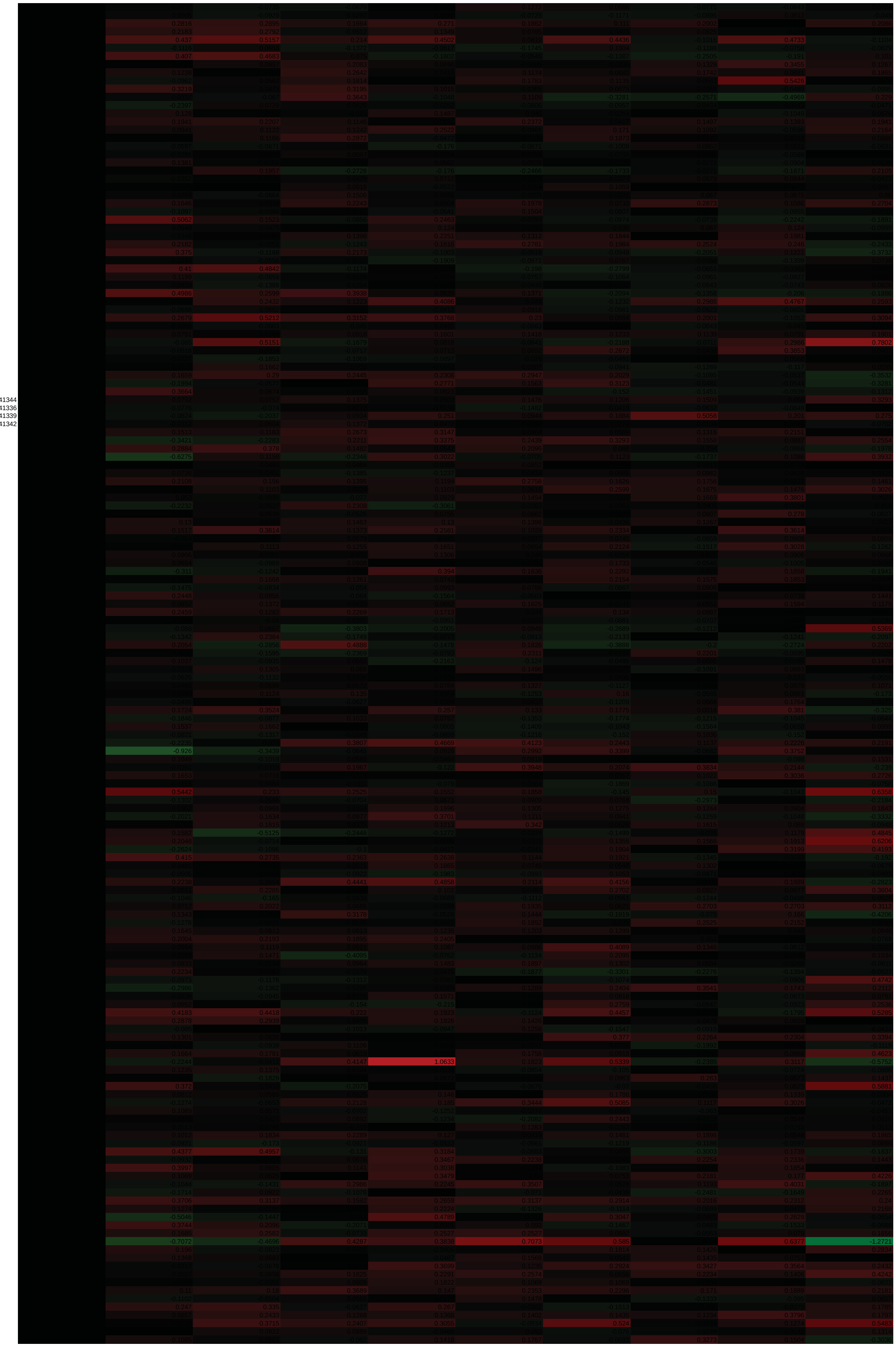

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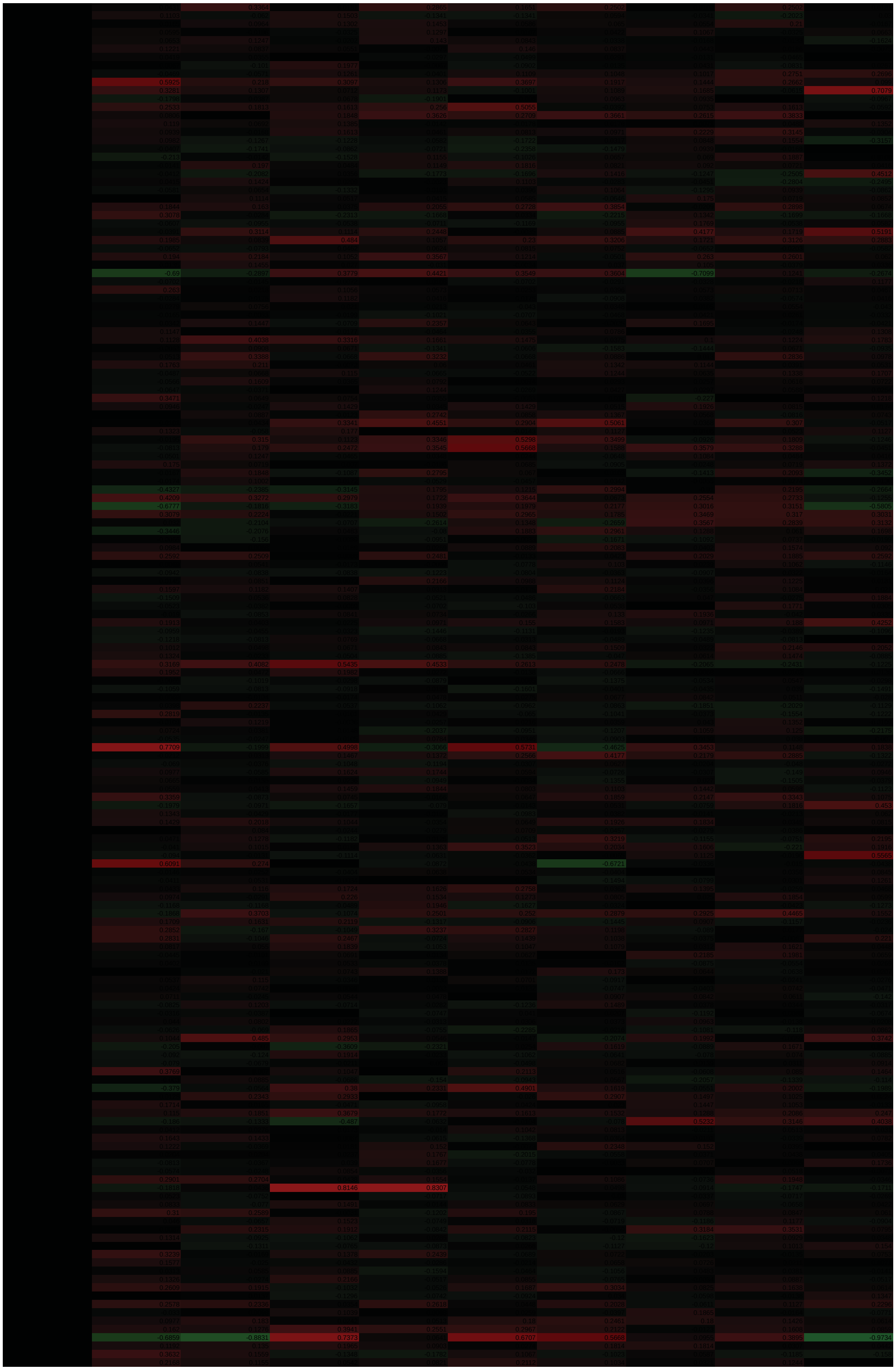

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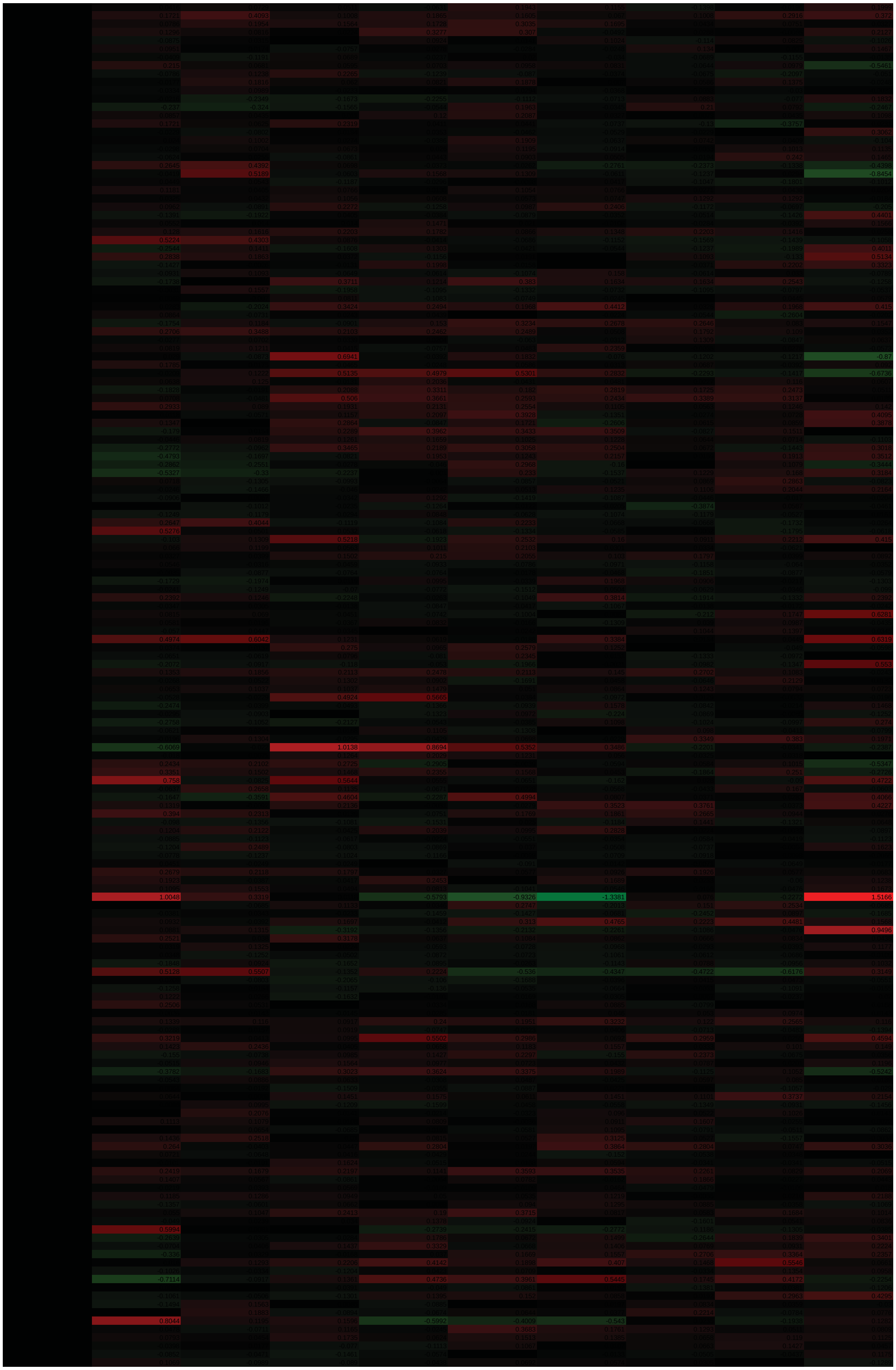

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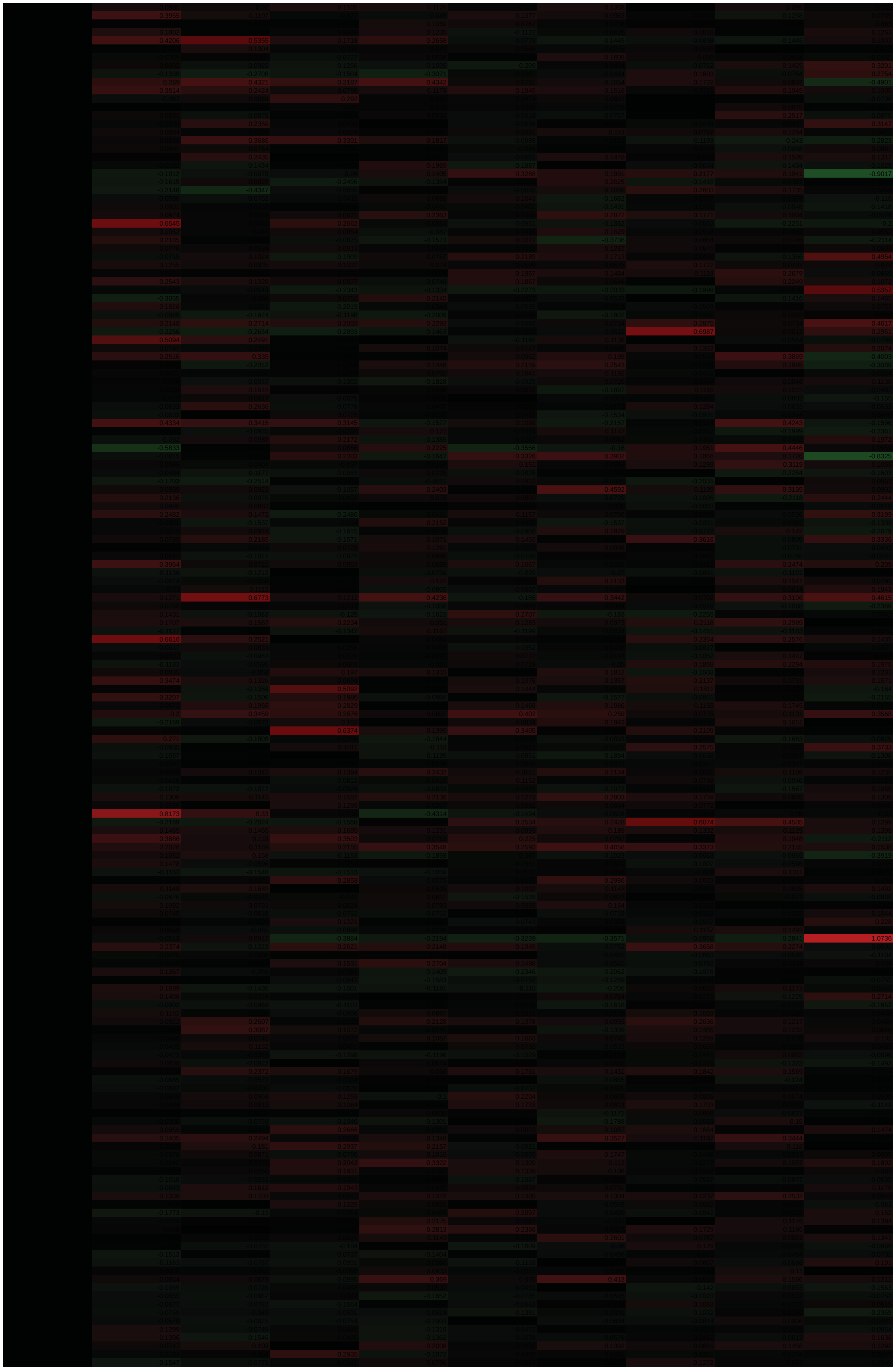

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5	Olfr1087	-0.0864	[illegible]	0.0621	0.0443	[illegible]	0.0784	0.1375	[illegible]	[illegible]
5	Olfr1089	0.127	-0.2126	-0.0913	0.0719	-0.0851	0.0914	-0.1788	[illegible]	[illegible]
5	Olfr109	-0.1235	-0.1614	-0.09	-0.0834	0.1022	[illegible]	[illegible]	[illegible]	-0.1033
5	Olfr1093	0.1605	0.0631	0.2141	0.2993	0.111	0.2258	[illegible]	0.2287	0.111
5	Olfr1094	0.1517	0.1872	0.4463	0.2446	0.3292	[illegible]	0.2807	0.2971	0.2133
5	Olfr1097	0.0931	0.1359	0.0864	[illegible]	[illegible]	0.0695	0.1326	0.0864	0.2178
5	Olfr1098	0.0538	[illegible]	[illegible]	-0.0347	-0.0604	0.0538	0.112	-0.0242	[illegible]
5	Olfr11	[illegible]	0.0494	[illegible]	-0.0330	[illegible]	0.0494	0.0622	-0.0627	[illegible]
5	Olfr110	-0.0431	[illegible]	0.0491	-0.1513	0.0611	0.0641	-0.2444	-0.0704	-0.2407
5	Olfr1101	0.0465	[illegible]	0.0350	[illegible]	[illegible]	0.0813	[illegible]	0.1744	0.0905
5	Olfr1102	-0.0588	0.0989	-0.0588	-0.1235	-0.0789	-0.1588	-0.1804	[illegible]	-0.1552
5	Olfr1104	[illegible]	0.103	0.2317	-0.1639	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1105	0.2873	0.0901	[illegible]	0.3546	0.0441	0.2675	-0.1187	0.1535	[illegible]
5	Olfr1106	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1107	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1109	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr111	0.4738	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1113	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.4005
5	Olfr1116-ps	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1118	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr112	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1120	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1122	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1123	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1126	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1128	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1129	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr113	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1131	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1133	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1134	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1135	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1136	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1138	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1140	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1143	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1148	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr115	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1151	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1152	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1153	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1155	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1156	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1157	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr116	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1160	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1162	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1165-ps	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1166	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1167	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1168	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1170	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1173	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1176	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1178	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1179	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr118	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1181	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1182	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1184	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1186	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1188	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1189	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr119	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1193	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1195	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1196	-0.0574	[illegible]	[illegible]	0.062	[illegible]	-0.0833	[illegible]	0.1019	[illegible]
5	Olfr1197	-0.056	0.0973	0.2306	-0.0591	0.1530	0.2018	0.0997	-0.1011	[illegible]
5	Olfr1199	0.0561	-0.0816	-0.1829	-0.0737	-0.1478	[illegible]	-0.0541	-0.0803	[illegible]
5	Olfr12	-0.0815	[illegible]	-0.0706	-0.0884	0.0574	-0.0851	[illegible]	-0.0334	[illegible]
5	Olfr120	0.0751	[illegible]	-0.0695	0.1381	-0.0534	-0.0566	0.047	[illegible]	[illegible]
5	Olfr1200	[illegible]	0.0883	[illegible]	0.1464	-0.0464	[illegible]	0.1112	[illegible]	-0.0467
5	Olfr1201	-0.0611	0.0777	-0.1105	-0.0611	-0.1395	-0.027	-0.0578	-0.0430	[illegible]
5	Olfr1202	-0.0993	-0.0735	-0.0595	-0.0847	-0.1141	-0.0730	-0.0499	-0.0312	[illegible]
5	Olfr1204	0.2966	[illegible]	-0.0767	[illegible]	0.1329	-0.0554	0.122	-0.0483	-0.0412
5	Olfr1205	-0.0633	-0.0888	0.0673	[illegible]	-0.0455	-0.0455	0.0836	-0.0836	0.1223
5	Olfr1208	0.2764	0.0883	0.1464	0.3219	0.159	0.055	0.2144	0.1777	0.1305
5	Olfr1209	-0.1169	-0.0955	[illegible]	-0.0885	[illegible]	[illegible]	[illegible]	-0.1133	-0.1133
5	Olfr121	0.1249	0.1513	0.0673	0.0638	0.1249	0.0742	0.1836	0.2673	0.1149
5	Olfr1211	-0.1177	[illegible]	-0.1213	-0.0962	-0.0295	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1212	-0.0390	-0.1531	-0.1531	[illegible]	-0.0307	[illegible]	-0.1234	-0.1494	-0.0557
5	Olfr1213	0.065	-0.0516	[illegible]	-0.0319	0.1112	0.1176	-0.094	[illegible]	0.1369
5	Olfr1214	0.0468	0.1463	[illegible]	-0.0452	[illegible]	-0.0456	[illegible]	0.0660	-0.0630
5	Olfr1217	[illegible]	0.0986	0.0887	0.0754	[illegible]	[illegible]	0.0552	0.1311	[illegible]
5	Olfr1218	0.0786	0.0993	0.1662	0.1857	0.0578	0.2764	0.1061	0.2271	0.1825
5	Olfr1219	[illegible]	-0.0361	0.1253	[illegible]	0.1253	-0.0795	0.064	-0.1177	0.1971
5	Olfr1220	[illegible]	0.1335	-0.0717	-0.1157	0.0419	0.2715	[illegible]	-0.0784	-0.0485
5	Olfr1222	0.0875	0.1753	-0.1288	0.0987	-0.1587	-0.052	-0.0489	0.2605	0.2198
5	Olfr1223	[illegible]	0.1572	0.1866	0.0685	0.1101	0.1135	0.0929	0.1271	-0.045
5	Olfr1225	[illegible]	-0.0619	-0.2546	0.071	0.091	[illegible]	-0.0715	0.0681	[illegible]
5	Olfr1226	-0.1146	-0.0649	-0.0789	0.143	-0.0719	-0.0896	-0.0579	[illegible]	-0.0614
5	Olfr1229	[illegible]	-0.0321	0.0417	-0.0249	-0.0502	[illegible]	0.048	0.0823	[illegible]
5	Olfr123	0.1544	0.1016	0.0825	[illegible]	0.1726	-0.043	0.2517	0.1329	-0.0524
5	Olfr1230	[illegible]	-0.0388	0.09	0.1199	-0.11	0.1199	0.0595	0.0933	0.1588
5	Olfr1231	[illegible]	0.0482	0.0896	[illegible]	0.2019	0.0929	[illegible]	-0.058	[illegible]
5	Olfr1232	0.3601	0.0935	0.2721	0.1145	0.0935	[illegible]	0.1955	0.4215	-0.0332
5	Olfr1233	-0.0744	0.0871	-0.0314	0.074	-0.1	[illegible]	[illegible]	0.0707	[illegible]
5	Olfr1234	0.1224	[illegible]	-0.0314	0.0707	0.1875	-0.0635	0.1128	-0.0475	0.0674
5	Olfr1238	-0.0684	0.152	[illegible]	[illegible]	-0.0441	-0.1292	-0.0406	0.1124	0.1847
5	Olfr1239	0.0737	[illegible]	0.0516	[illegible]	-0.0356	-0.1342	-0.0332	-0.0916	[illegible]
5	Olfr124	-0.0554	-0.0839	-0.0448	-0.066	-0.0839	-0.0767	-0.0413	[illegible]	0.0825
5	Olfr1240	0.1305	-0.0606	[illegible]	-0.0951	0.0555	-0.1566	0.0667	-0.027	-0.1014
5	Olfr1241	0.1453	-0.1505	-0.0507	-0.0891	[illegible]	-0.1141	[illegible]	-0.0389	-0.1395
5	Olfr1242	0.0659	0.041	[illegible]	0.1564	-0.094	0.1289	[illegible]	-0.0437	[illegible]
5	Olfr1243	0.0809	0.1079	0.0809	0.0978	0.1444	0.2993	[illegible]	0.1279	0.1509
5	Olfr1245	[illegible]	-0.0889	0.0957	-0.1267	-0.0787	-0.072	[illegible]	-0.1302	-0.0487
5	Olfr1246	0.0463	0.2088	-0.0391	0.0951	[illegible]	0.3	0.0788	[illegible]	[illegible]
5	Olfr1248	[illegible]	[illegible]	[illegible]	0.2402	0.1551	0.2284	[illegible]	0.1645	[illegible]
5	Olfr1249	0.1157	0.1618	0.4206	[illegible]	0.1069	0.1361	0.1186	-0.0451	0.3552
5	Olfr125	[illegible]	-0.0521	-0.0279	-0.0843	[illegible]	-0.0735	-0.0663	[illegible]	[illegible]
5	Olfr1250	-0.0373	[illegible]	[illegible]	[illegible]	0.1553	[illegible]	-0.0615	0.1095	0.0906
5	Olfr1251	-0.0742	-0.0705	[illegible]	0.0984	[illegible]	[illegible]	-0.0502	-0.0484	0.0954
5	Olfr1252	[illegible]	[illegible]	0.0944	[illegible]	[illegible]	0.0526	-0.0479	[illegible]	[illegible]
5	Olfr1254	0.0656	[illegible]	0.0687	[illegible]	0.1152	0.1695	0.1048	[illegible]	[illegible]
5	Olfr1255	0.0843	0.0748	[illegible]	[illegible]	-0.027	[illegible]	0.0906	[illegible]	[illegible]
5	Olfr1257	0.1134	[illegible]	0.1103	0.2387	0.1654	0.0946	0.1258	0.2501	[illegible]
5	Olfr126	[illegible]	-0.1524	0.0611	0.1107	-0.0986	-0.1597	-0.1057	[illegible]	-0.1819
5	Olfr1260	0.0718	[illegible]	0.1703	0.1033	0.0813	[illegible]	[illegible]	0.1762	[illegible]
5	Olfr1261	0.4769	0.1539	0.0908	[illegible]	0.1198	-0.0541	[illegible]	[illegible]	[illegible]
5	Olfr1262	0.0775	[illegible]	0.0742	[illegible]	0.061	0.3045	0.1163	[illegible]	0.0675
5	Olfr1263	0.0817	[illegible]	0.0616	[illegible]	[illegible]	0.0583	-0.0426	0.1144	0.0461
5	Olfr1264	-0.0521	0.0957	[illegible]	[illegible]	0.0957	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1265	-0.0537	[illegible]	-0.1095	-0.1166	-0.0571	0.1079	-0.0537	-0.1675	-0.1095
5	Olfr1269	[illegible]	[illegible]	[illegible]	[illegible]	-0.1098	[illegible]	0.1272	0.1973	[illegible]
5	Olfr1270	0.2108	0.0539	0.0714	[illegible]	0.0714	0.1527	0.0644	0.0853	0.0885
5	Olfr1271	[illegible]	[illegible]	0.0982	0.1315	0.1345	[illegible]	0.1043	[illegible]	-0.0534
5	Olfr1272	0.0989	[illegible]	-0.1305	[illegible]	-0.0488	0.0809	-0.1552	-0.1165	[illegible]
5	Olfr1274-ps	0.0948	0.1567	[illegible]	-0.066	0.1567	0.0948	[illegible]	[illegible]	0.1956
5	Olfr1275	-0.0804	-0.0729	-0.0691	0.0929	-0.0993	-0.0804	-0.0617	-0.0841	[illegible]
5	Olfr1276	[illegible]	0.1112	0.1112	-0.1319	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
5	Olfr1277	0.3527	0.0686	0.1838	[illegible]	0.2256	0.0931	0.1341	0.1675	0.0966
5	Olfr1278	[illegible]	[illegible]	0.0927	[illegible]	0.1086	-0.0451	[illegible]	-0.0603	-0.099
5	Olfr1279	0.0539	0.0922	[illegible]	[illegible]	0.0679	0.0922	[illegible]	0.1059	0.1093
5	Olfr128	0.1284	0.1631	0.1665	0.1459	0.0857	0.1835	0.0929	0.0638	0.2003
5	Olfr1280	0.0624	[illegible]	0.1417	0.1513	[illegible]	[illegible]	[illegible]	[illegible]	0.096
5	Olfr1281	[illegible]	[illegible]	[illegible]	-0.0787	[illegible]	-0.0964	[illegible]	[illegible]	[illegible]
5	Olfr1282	0.0929	[illegible]	-0.0523	[illegible]	[illegible]	[illegible]	-0.0702	0.0929	-0.1327
5	Olfr1283	[illegible]	[illegible]	[illegible]	-0.0756	-0.0511	[illegible]	-0.0756	-0.0476	[illegible]
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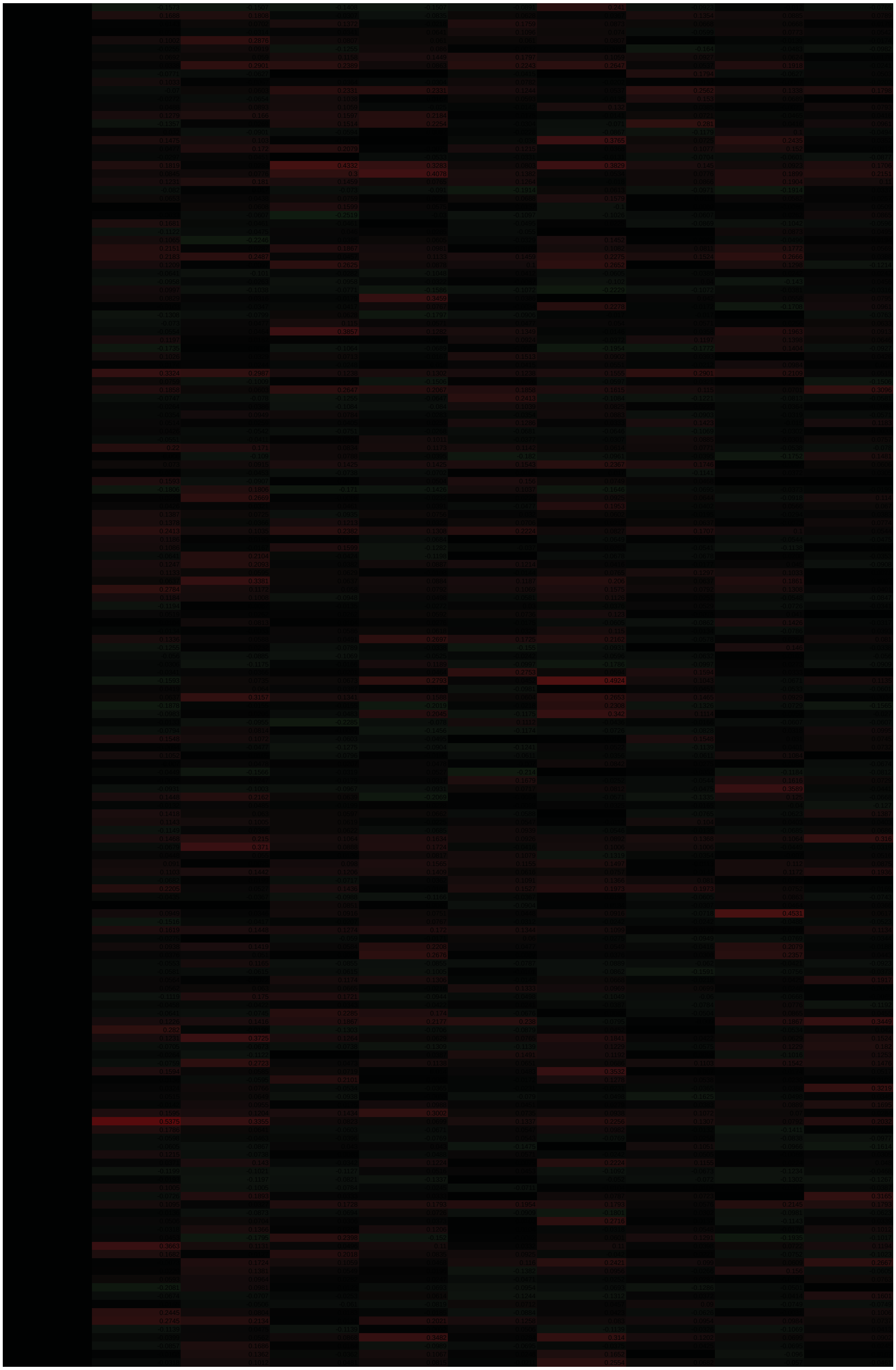

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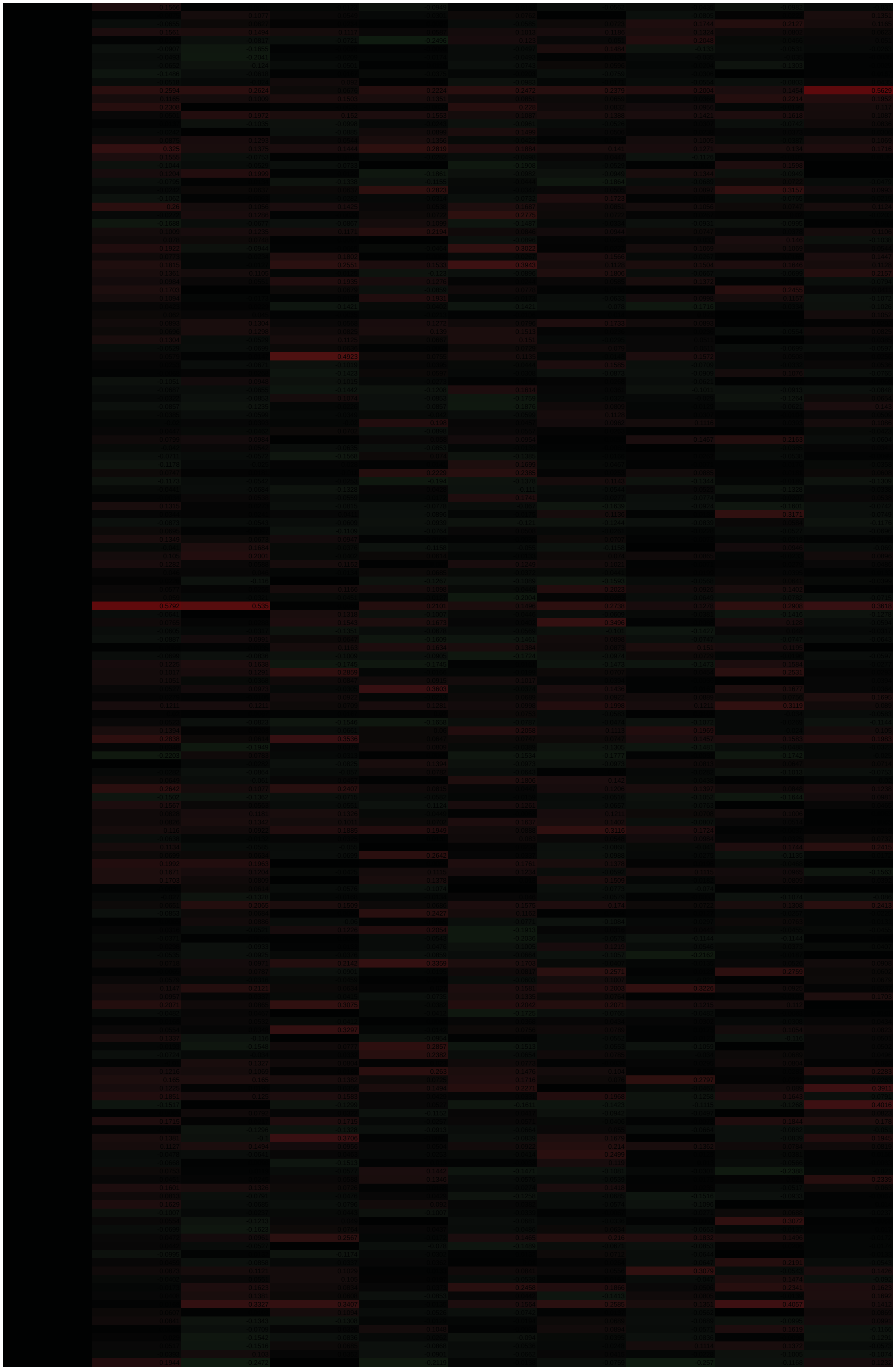

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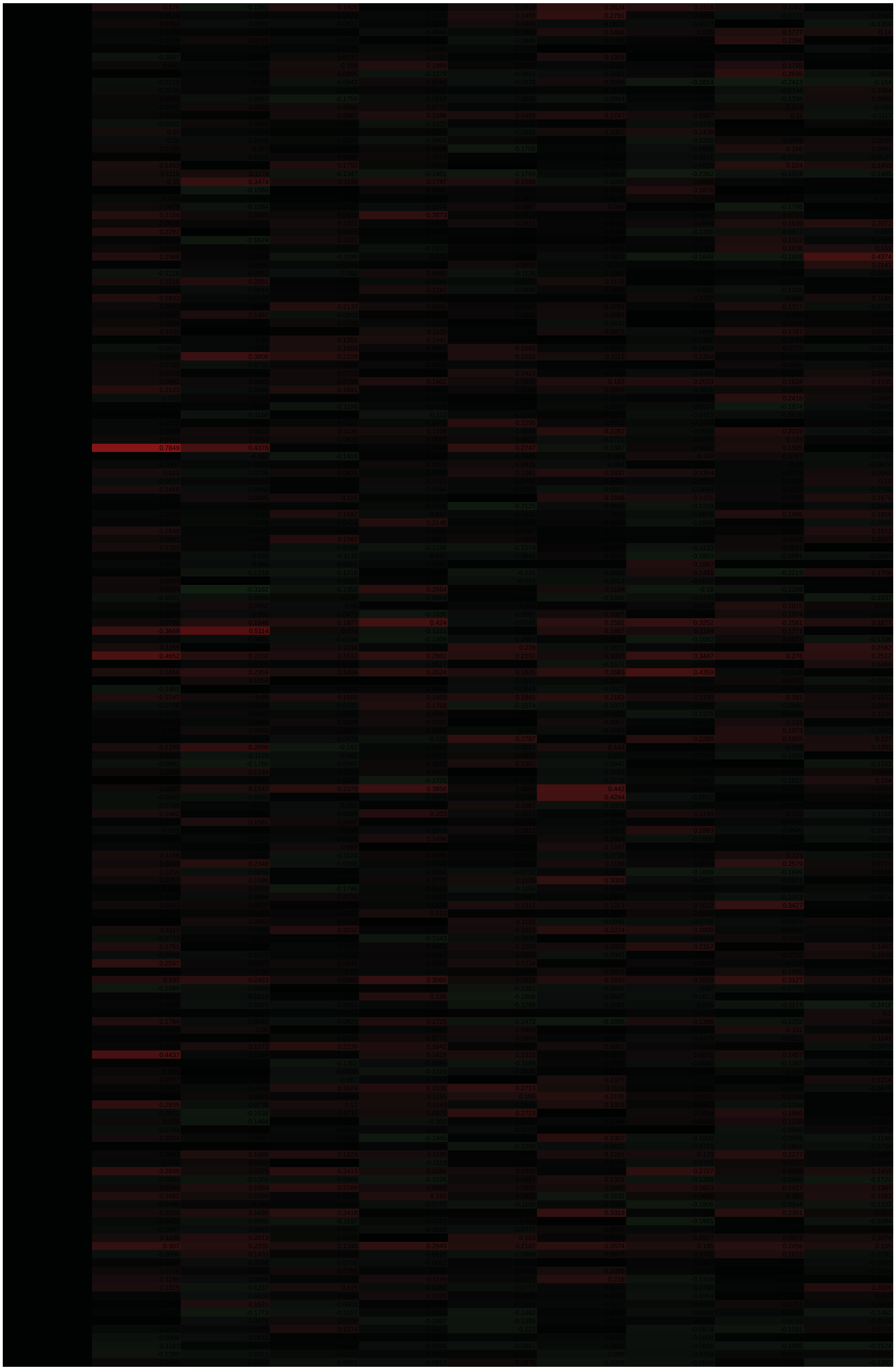

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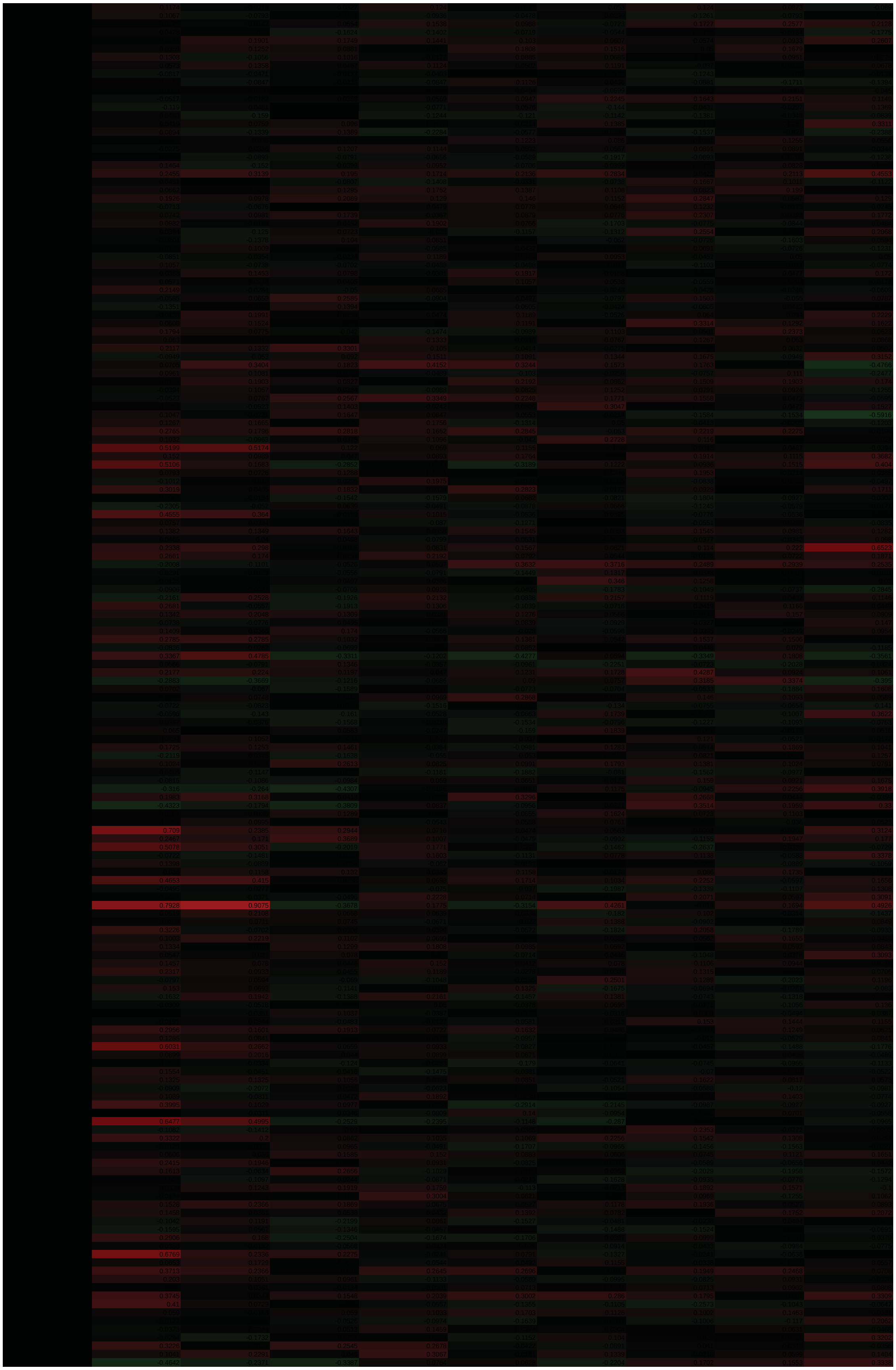

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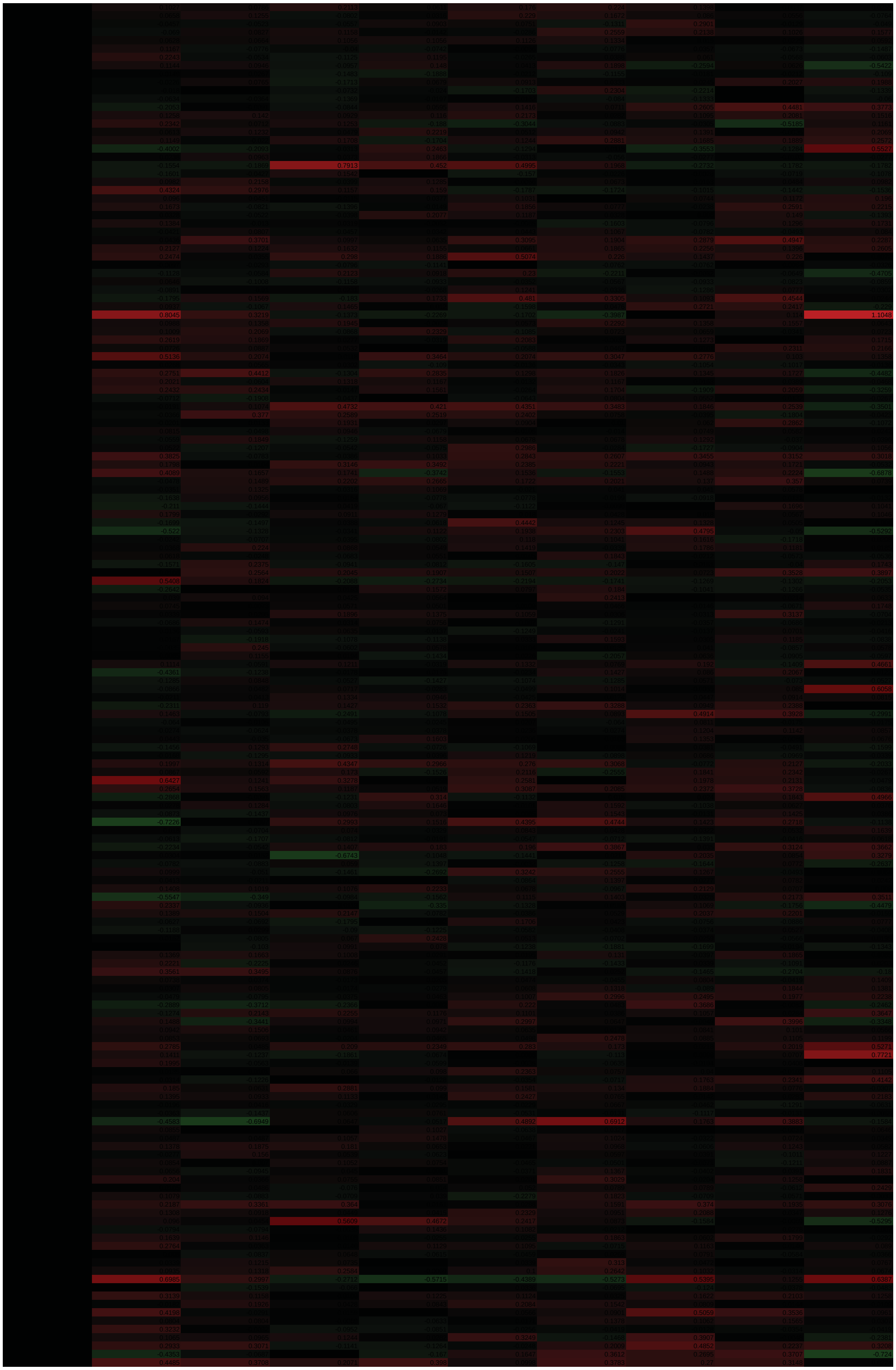

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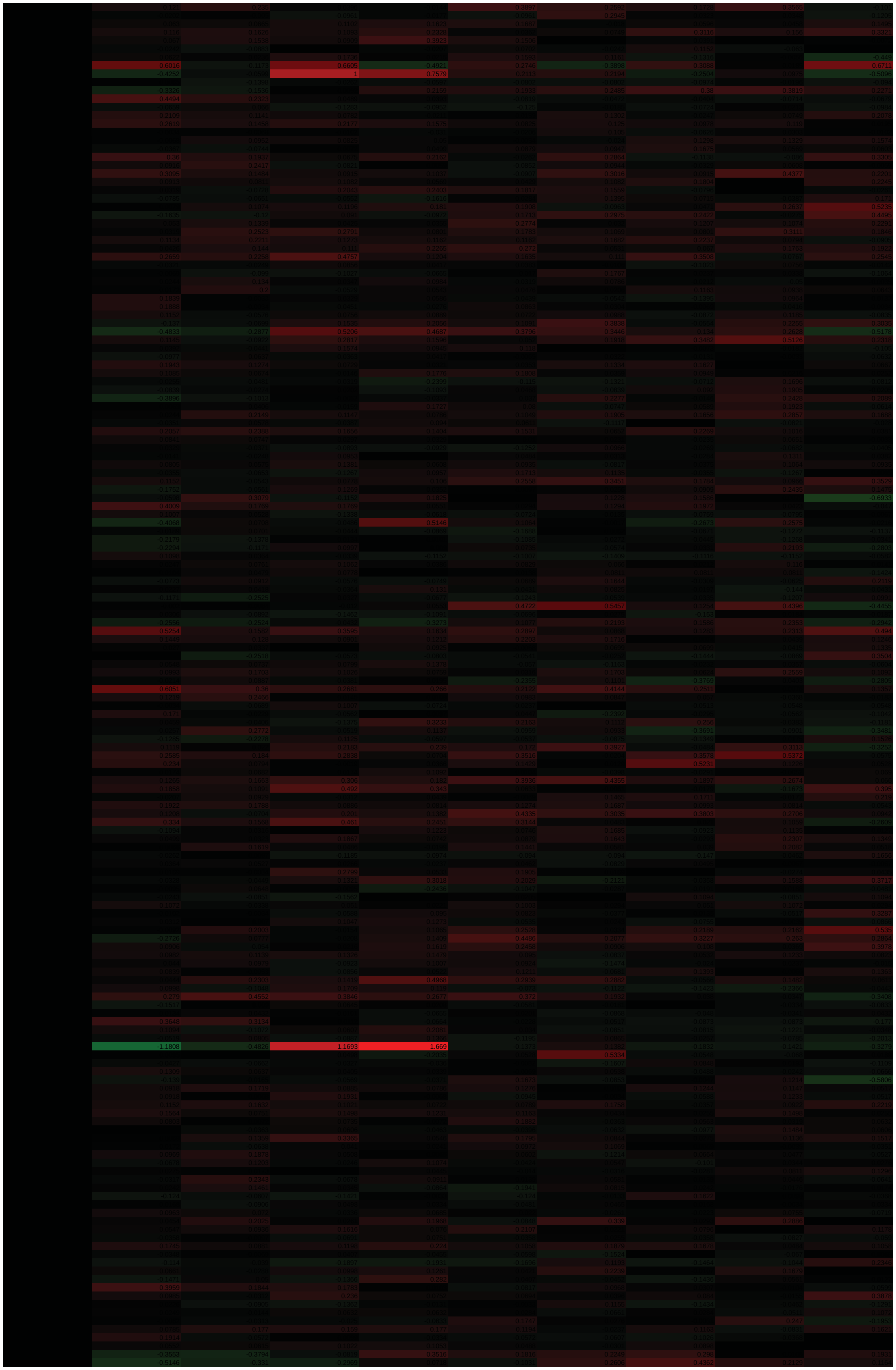

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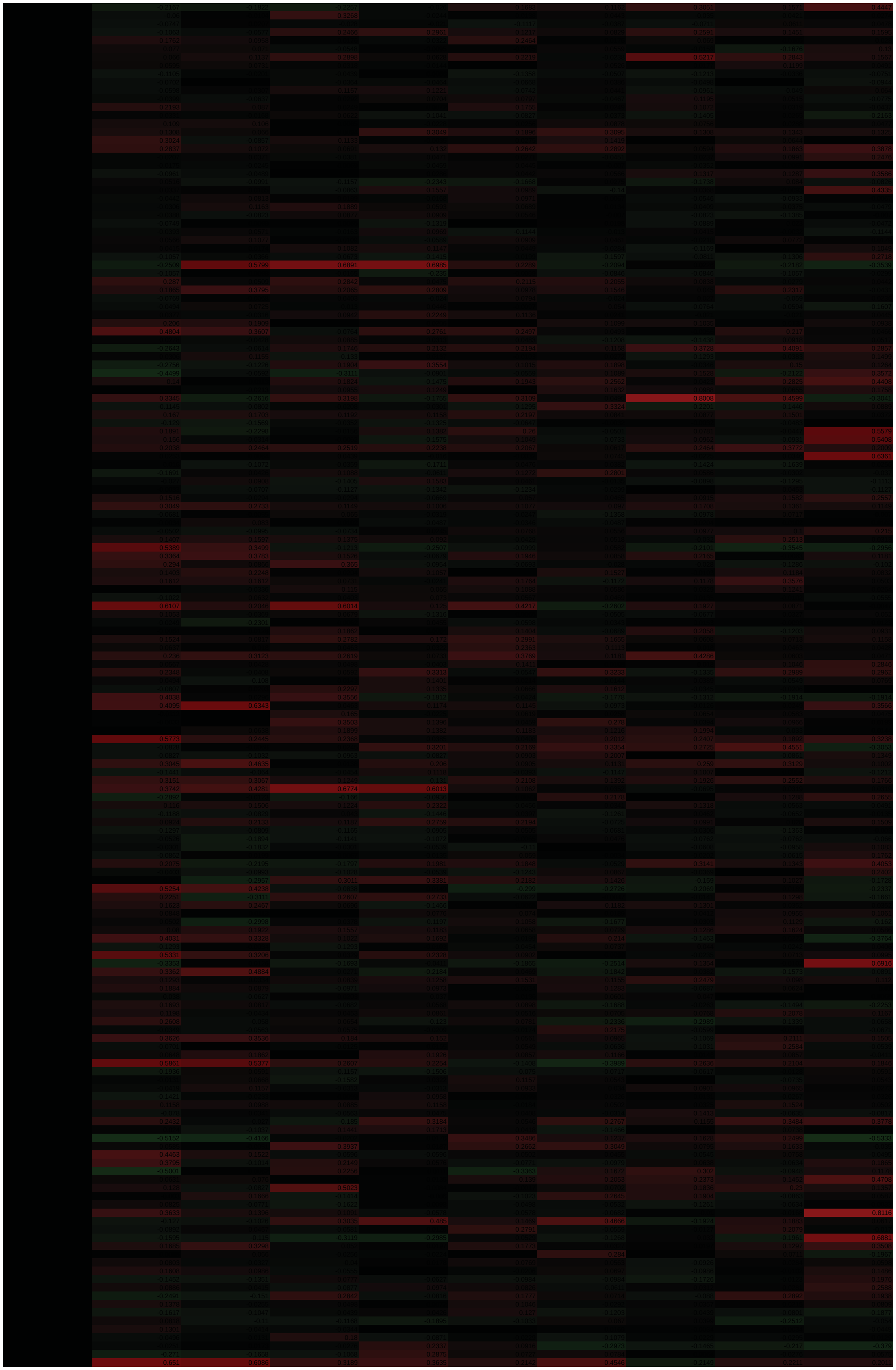

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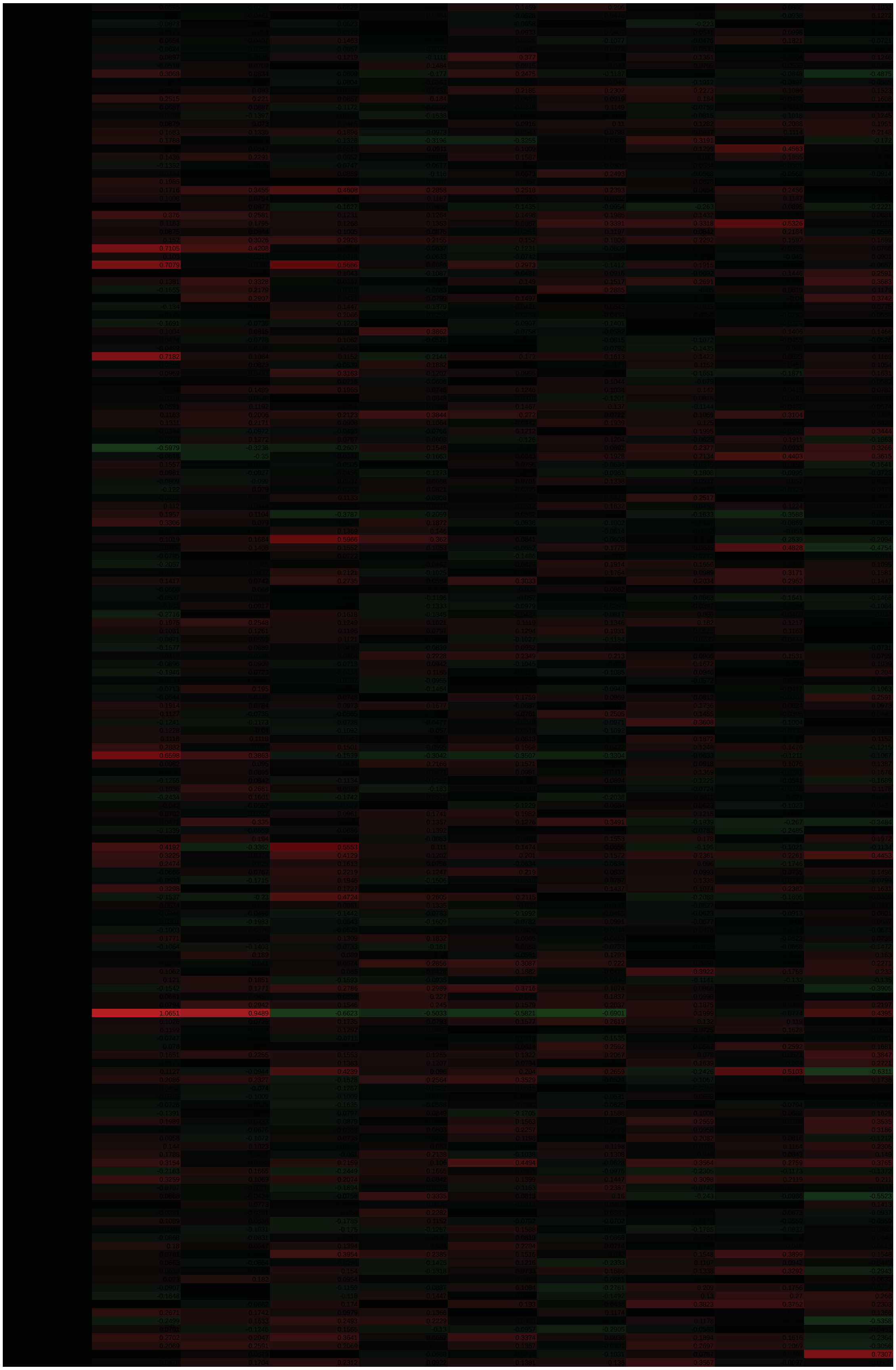

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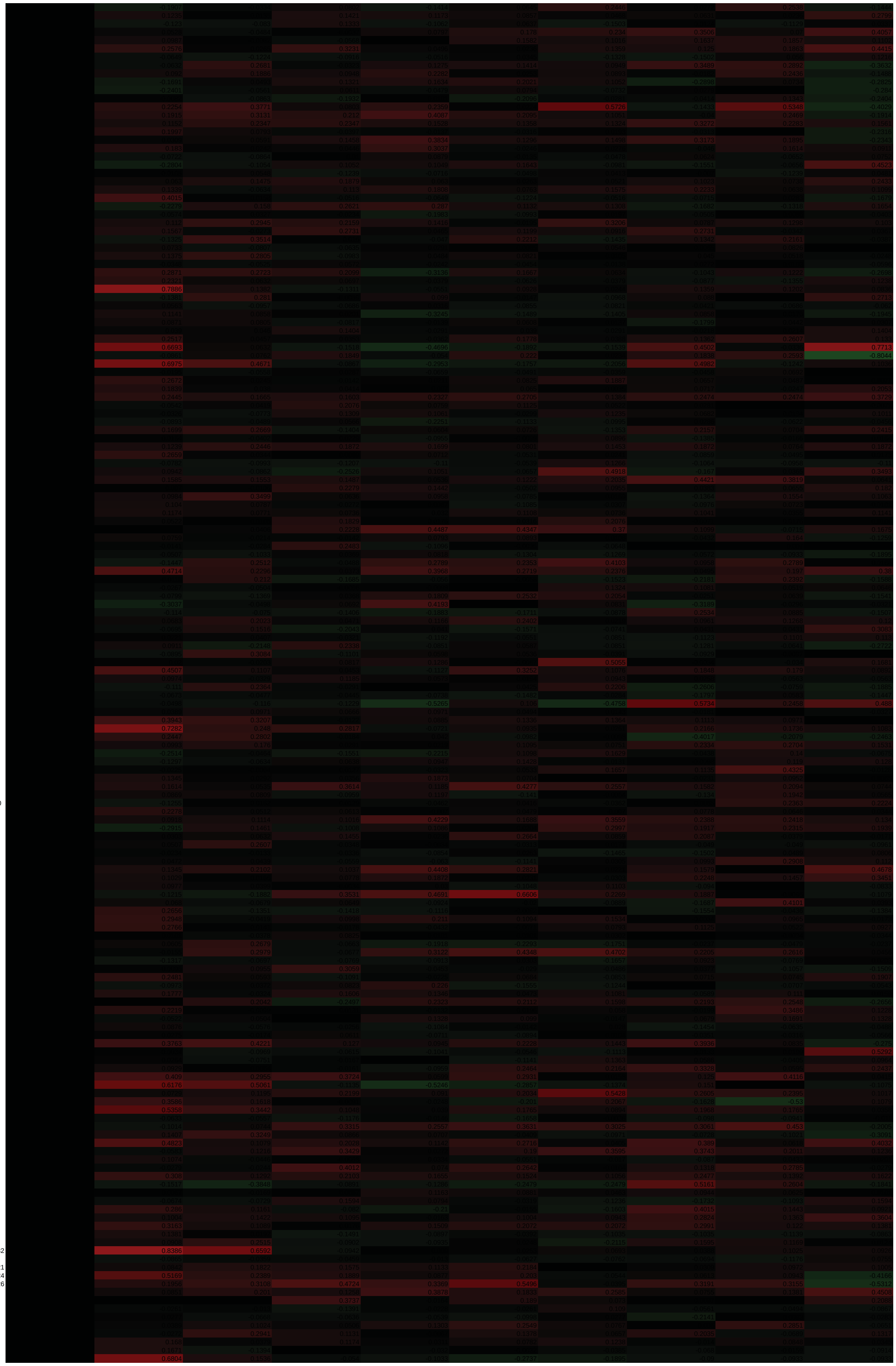

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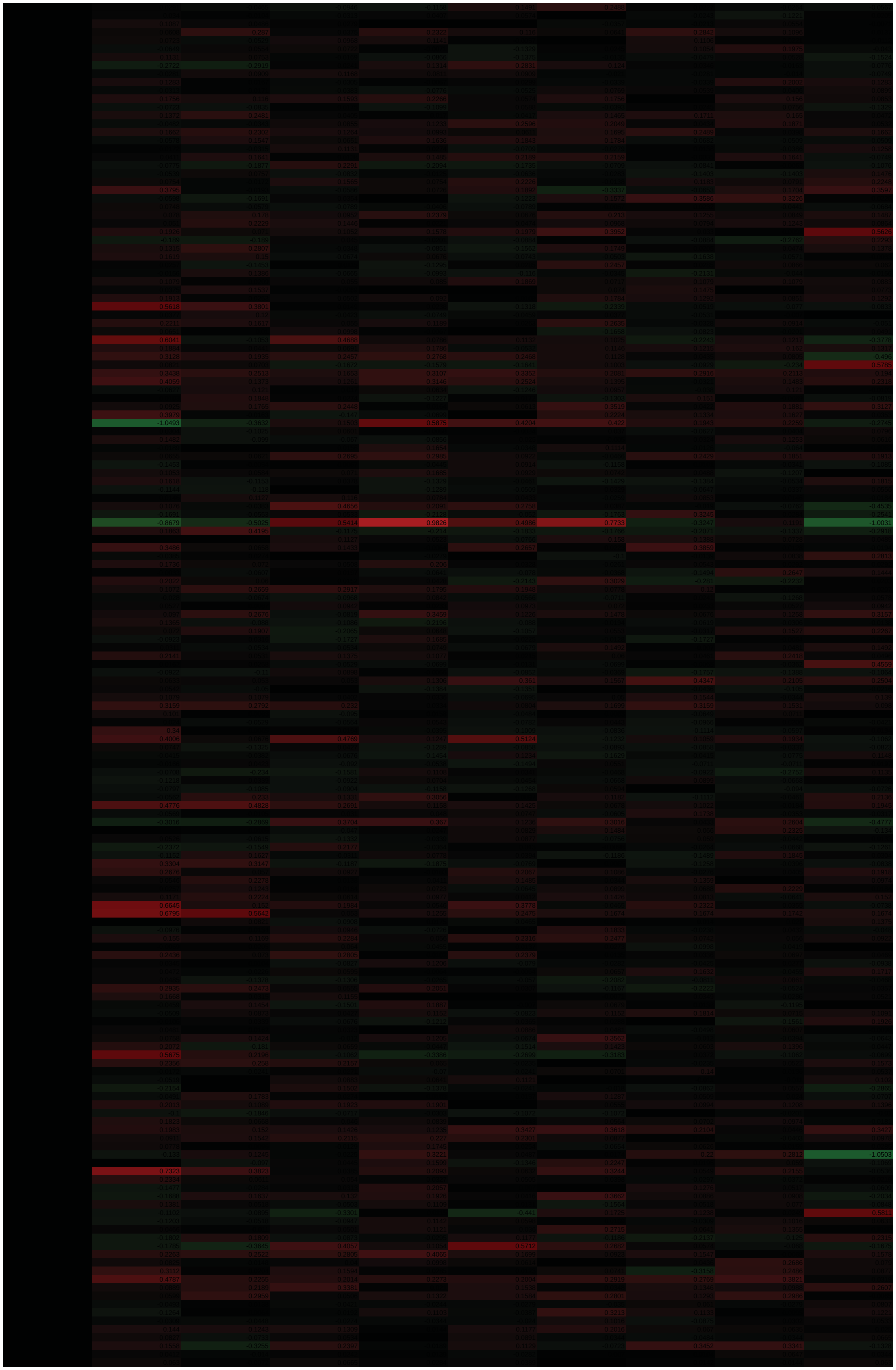

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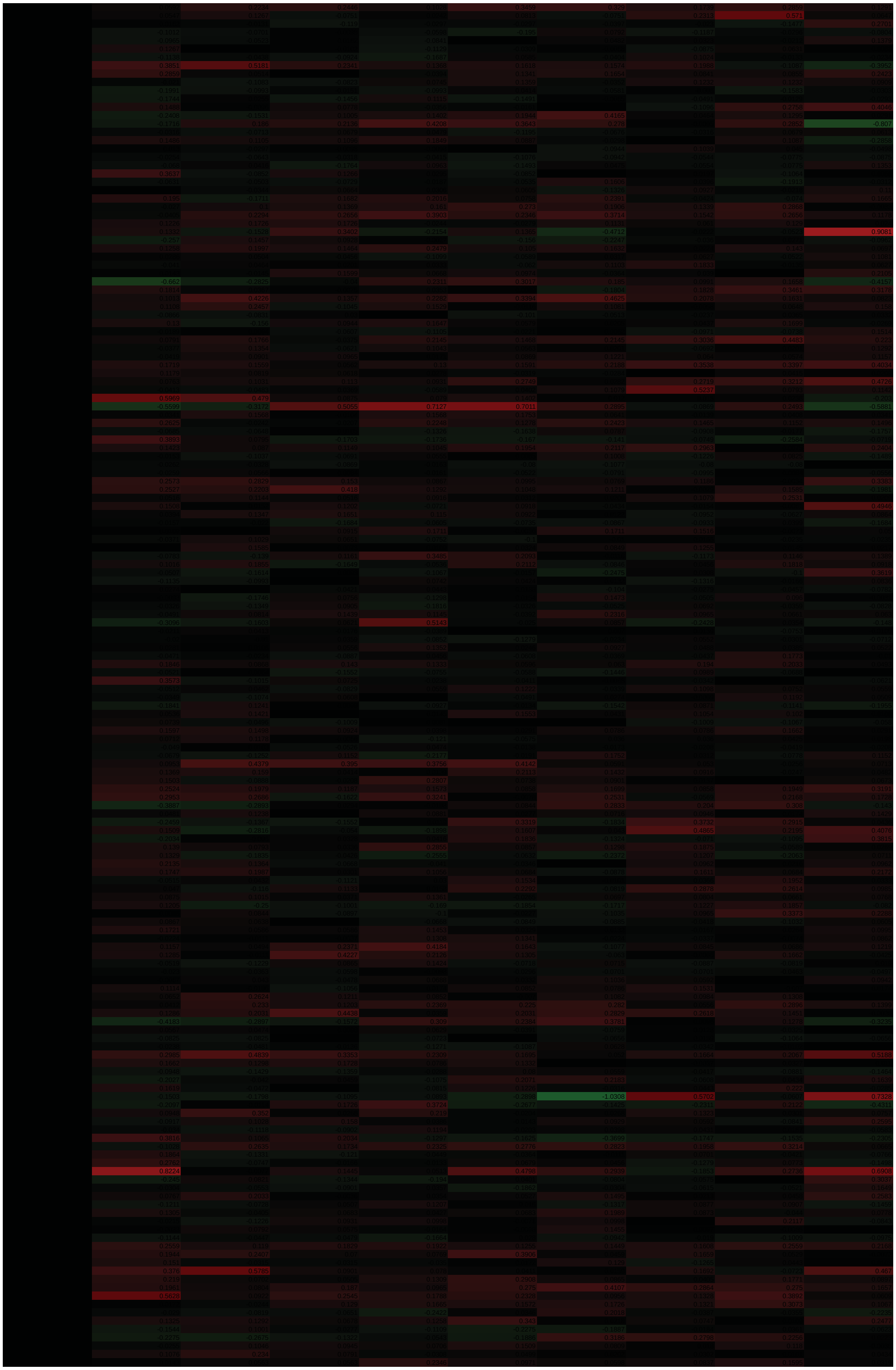

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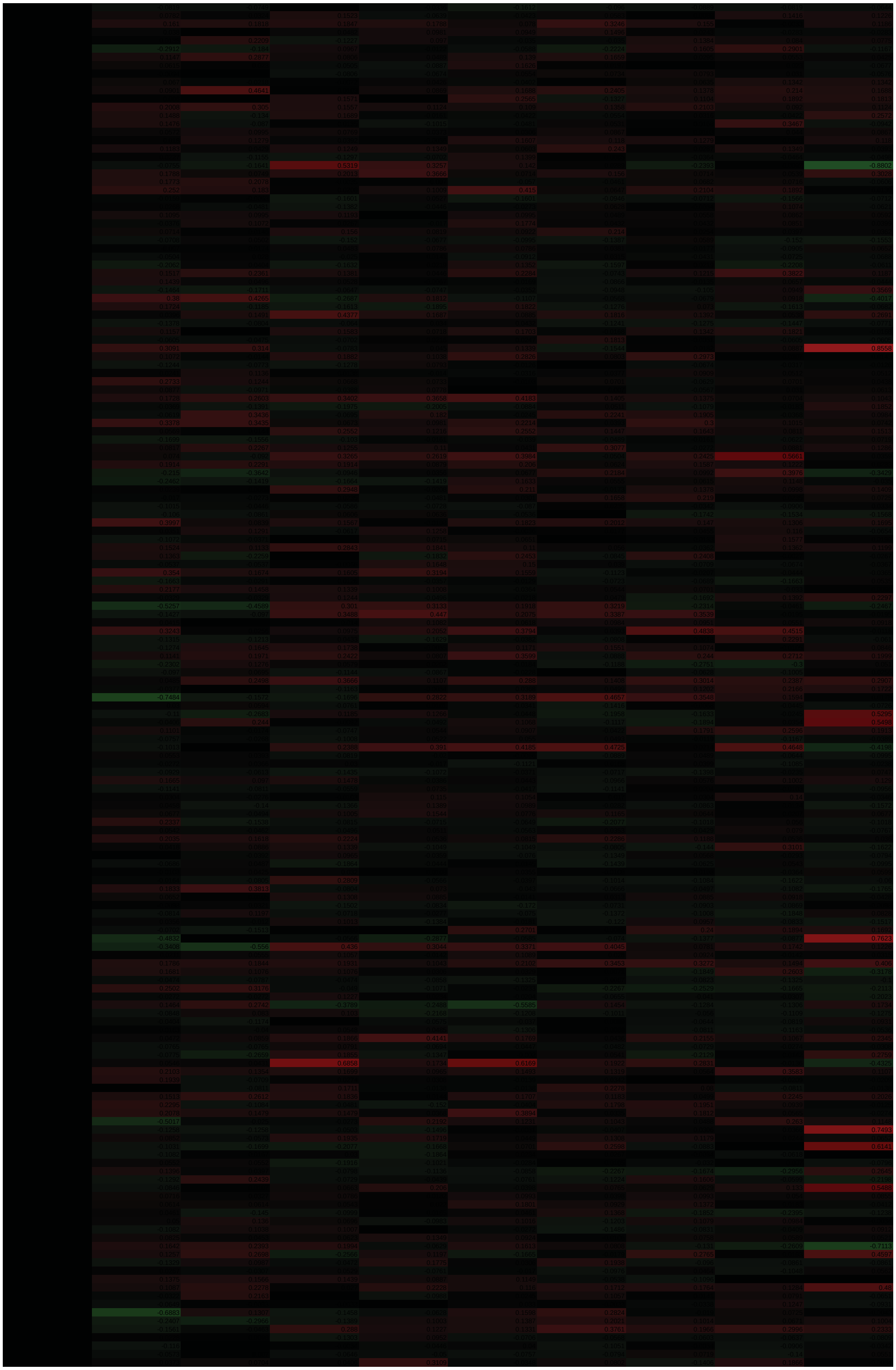

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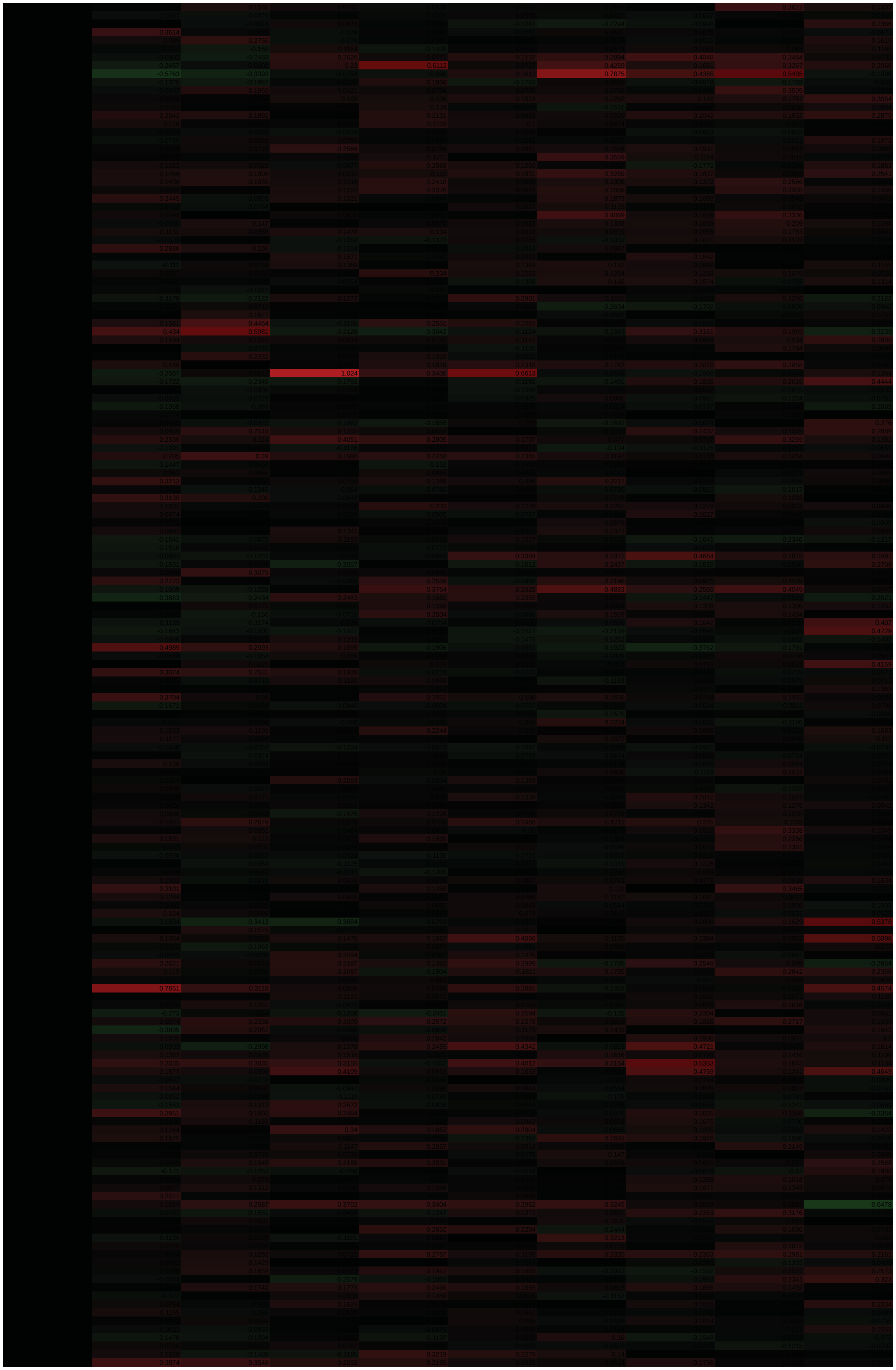

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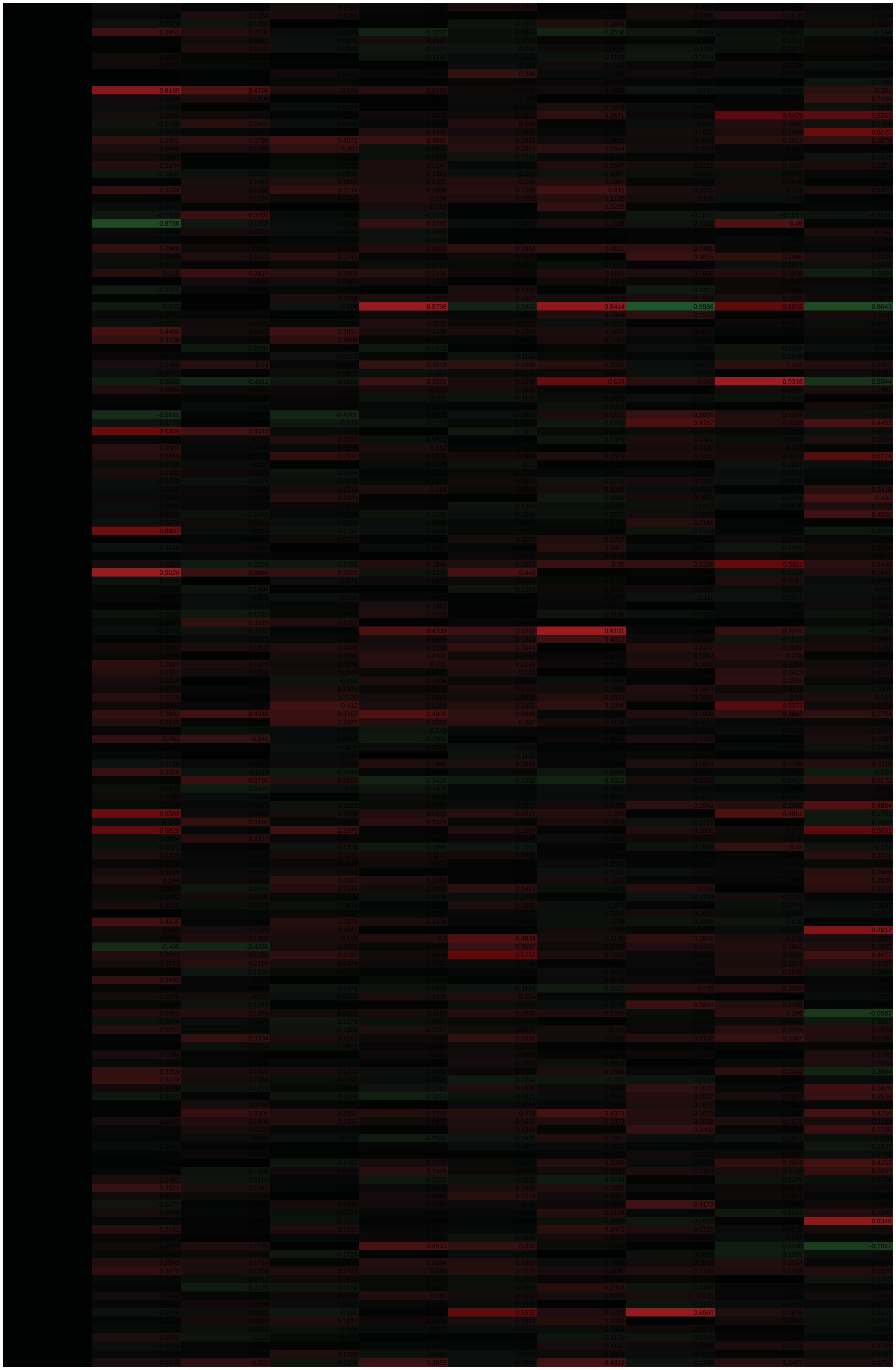

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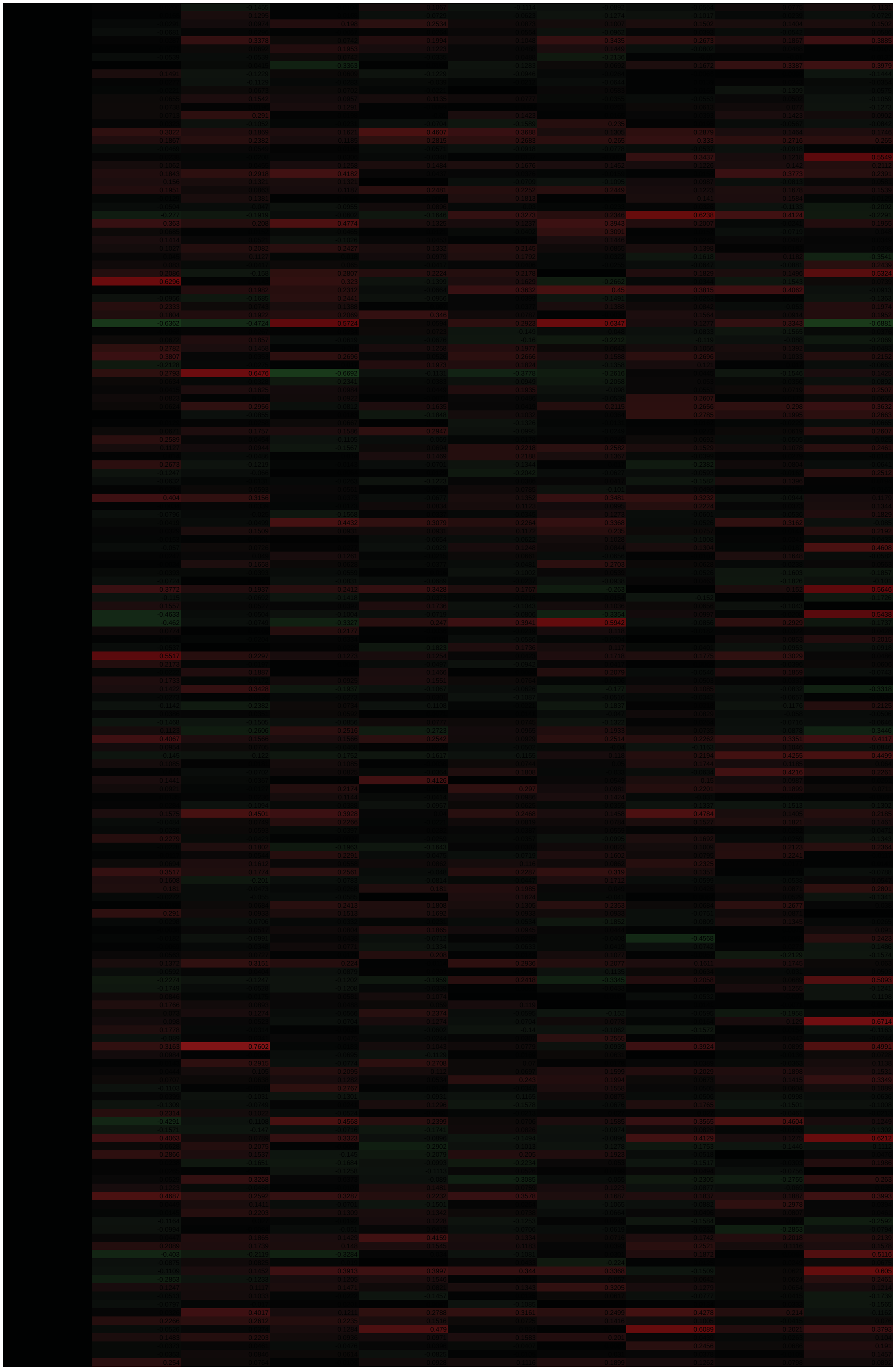

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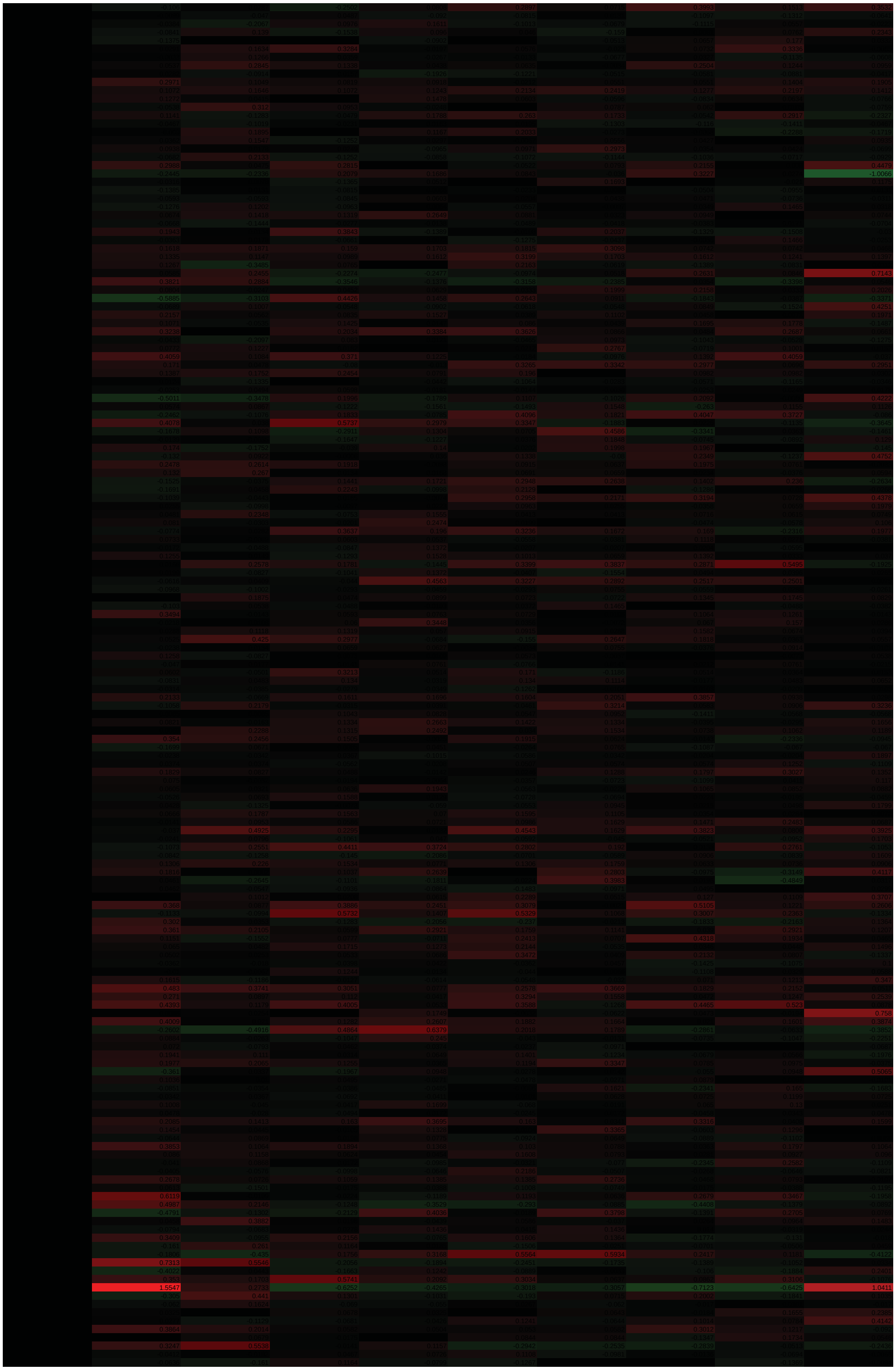

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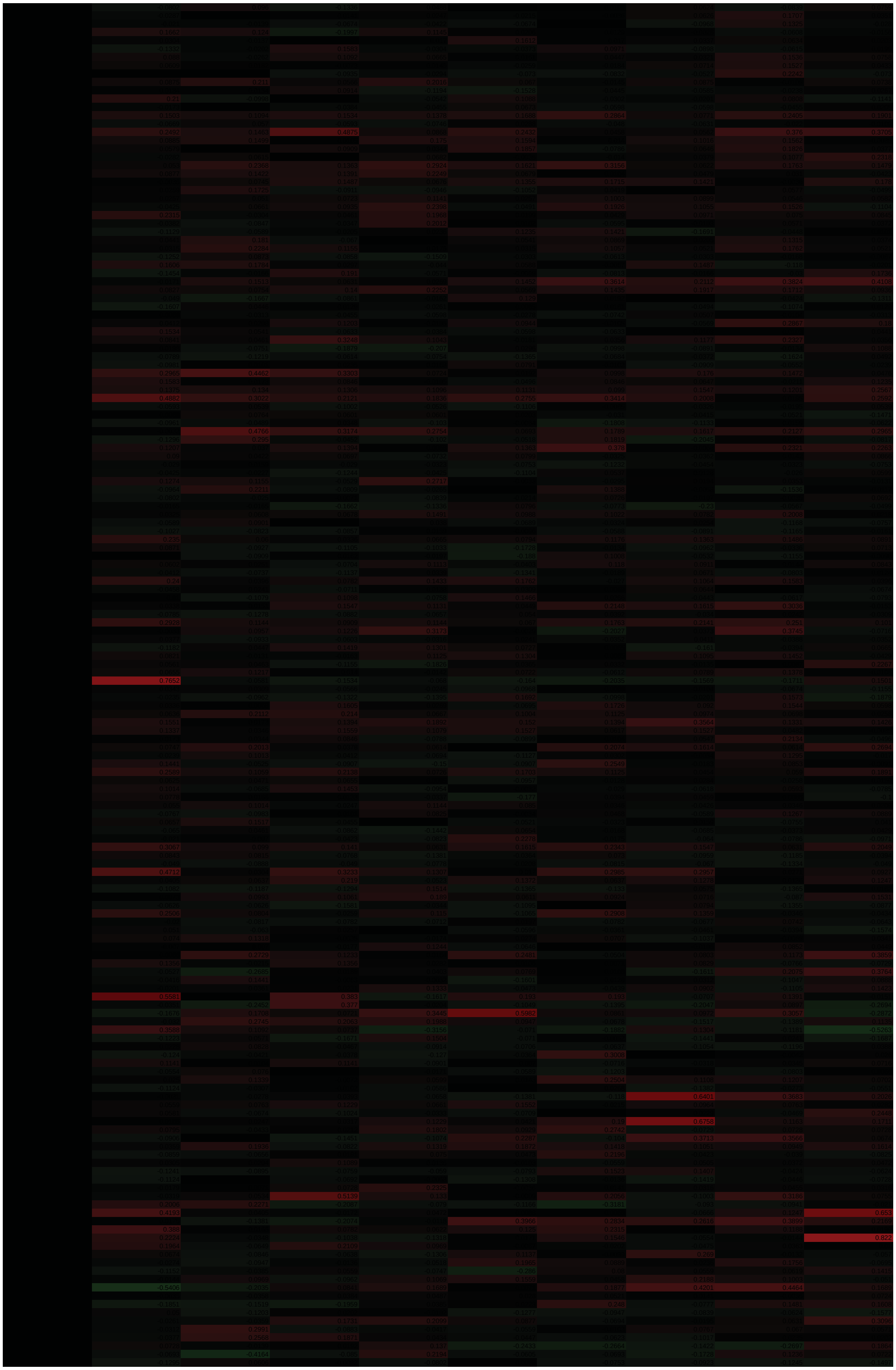

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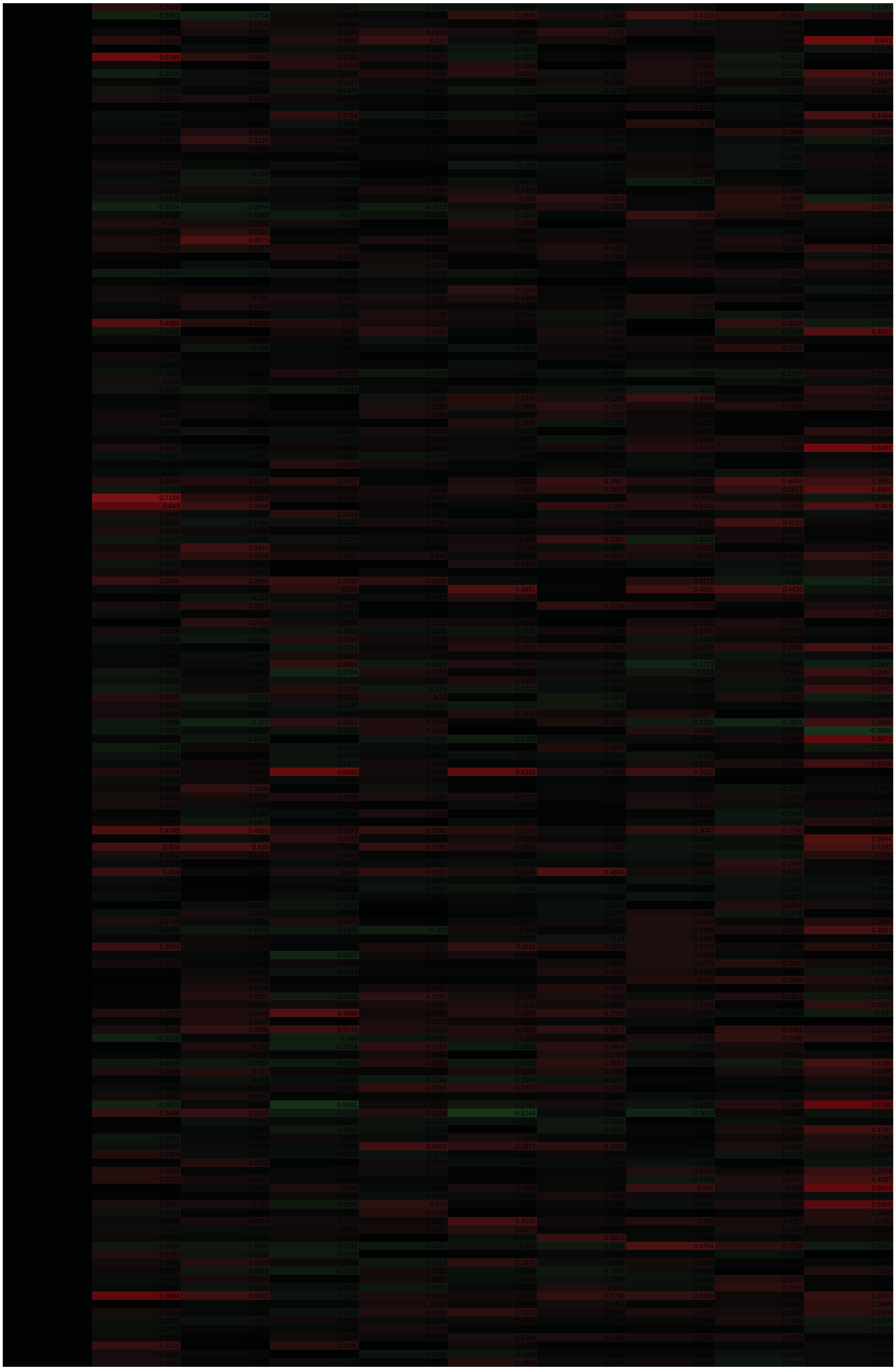

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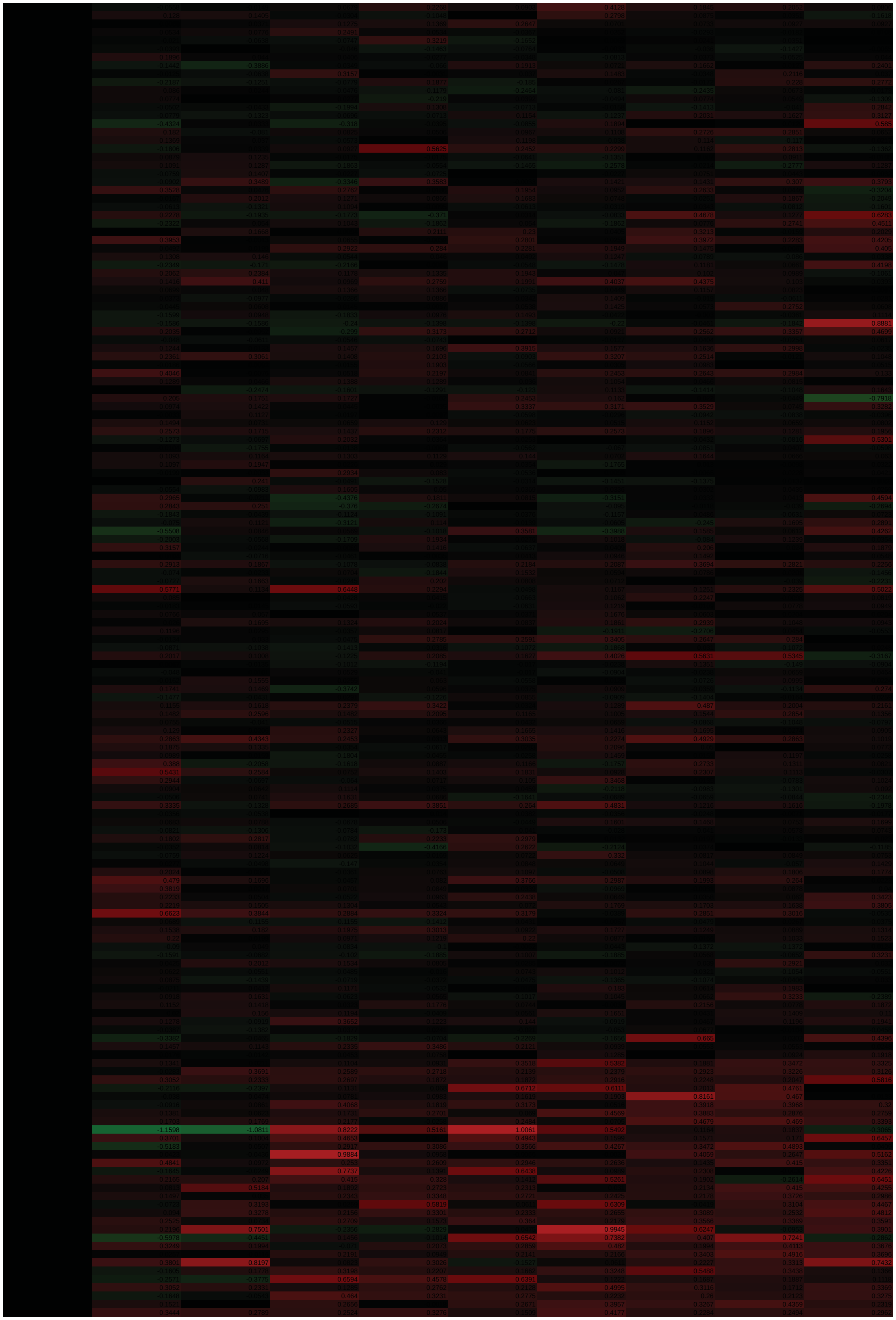

Appendix 3. Top Biological Functions of mRNA group I to V

Group# I			
Name	p-value*	score = -log10(p-value)	# Molecules
Diseases and Disorders			
Cancer	8.23E-19	18.08460016	256
Gastrointestinal Disease	5.63E-14	13.24949161	127
Reproductive System Disease	2.97E-08	7.527243551	102
Hematological Disease	2.20E-07	6.657577319	70
Respiratory Disease	2.00E-05	4.698970004	41
Molecular and Cellular Functions			
DNA Replication, Recombination, and Repa	5.42E-11	10.26600071	114
Cell Cycle	8.04E-09	8.094743951	123
Cellular Assembly and Organization	1.07E-07	6.970616222	113
Cellular Growth and Proliferation	3.26E-07	6.4867824	192
Gene Expression	1.71E-06	5.76700389	143
Physiological System Development and Function			
Embryonic Development	1.20E-06	5.920818754	111
Connective Tissue Development and Functi	1.30E-06	5.886056648	57
Tissue Morphology	2.66E-06	5.575118363	78
Organismal Development	1.26E-05	4.899629455	97
Organismal Survival	9.32E-05	4.030584088	95

Group# II			
Name	p-value*	score = -log10(p-value)	# Molecules
Diseases and Disorders			
Cancer	6.10E-37	36.21467016	275
Gastrointestinal Disease	6.48E-24	23.18842499	140
Reproductive System Disease	2.10E-20	19.67778071	156
Dermatological Diseases and Conditions	7.99E-17	16.09745322	74
Inflammatory Response	3.73E-16	15.42829117	123
Molecular and Cellular Functions			
Cellular Movement	7.38E-34	33.13194364	188
Cellular Growth and Proliferation	1.45E-24	23.838632	239
Cellular Development	9.17E-21	20.03763066	225
Cell Death and Survival	4.13E-18	17.38404995	198
Cell-To-Cell Signaling and Interaction	1.56E-15	14.8068754	144
Physiological System Development and Function			
Cardiovascular System Development and F	2.55E-37	36.59345982	153
Organismal Development	2.55E-37	36.59345982	213
Organismal Survival	5.99E-19	18.22257318	145
Immune Cell Trafficking	3.29E-18	17.4828041	100
Connective Tissue Development and Functi	1.93E-17	16.71444269	157

Group# III			
Name	**p-value***	**score = -log10(p-value)**	**# Molecules**
Diseases and Disorders			
Inflammatory Response	1.04E-14	13.98296666	143
Infectious Disease	2.44E-11	10.61261017	60
Connective Tissue Disorders	3.09E-10	9.510041521	78
Immunological Disease	3.09E-10	9.510041521	87
Inflammatory Disease	3.09E-10	9.510041521	1.11E+02
Molecular and Cellular Functions			
Cellular Function and Maintenance	4.85E-17	16.31425826	115
Cellular Movement	5.46E-15	14.26280736	126
Cell-To-Cell Signaling and Interaction	9.54E-13	12.02045163	121
Cellular Development	1.41E-09	8.850780887	129
Cellular Growth and Proliferation	1.41E-09	8.850780887	170
Physiological System Development and Function			
Immune Cell Trafficking	5.46E-15	14.26280736	104
Hematological System Development and Functior	4.18E-14	13.37882372	141
Tissue Development	9.54E-13	12.02045163	79
Tissue Morphology	7.79E-12	11.10846254	103
Connective Tissue Development and Function	1.92E-07	6.716698771	32

Group# IV			
Name	**p-value***	**score = -log10(p-value)**	**# Molecules**
Diseases and Disorders			
Gastrointestinal Disease	2.78E-04	3.555955204	44
Hepatic System Disease	2.78E-04	3.555955204	22
Inflammatory Disease	2.78E-04	3.555955204	23
Neurological Disease	4.18E-04	3.378823718	45
Organismal Injury and Abnormalities	4.18E-04	3.378823718	60
Molecular and Cellular Functions			
Cellular Assembly and Organization	5.99E-05	4.222573178	87
Cellular Function and Maintenance	5.99E-05	4.222573178	166
Cellular Movement	5.99E-05	4.222573178	51
Molecular Transport	5.99E-05	4.222573178	229
Small Molecule Biochemistry	1.58E-04	3.801342913	238
Physiological System Development and Function			
Nervous System Development and Function	5.99E-05	4.222573178	147
Hematological System Development and Functior	4.18E-04	3.378823718	118
Immune Cell Trafficking	4.18E-04	3.378823718	47
Hematopoiesis	5.58E-04	3.253365801	59
Humoral Immune Response	5.58E-04	3.253365801	57

Group# V			
Name	**p-value***	**score = -log10(p-value)**	**# Molecules**
Diseases and Disorders			
Hereditary Disorder	1.97E-08	7.705533774	187
Neurological Disease	1.97E-08	7.705533774	489
Psychological Disorders	1.97E-08	7.705533774	274
Cardiovascular Disease	1.38E-06	5.860120914	303
Organismal Injury and Abnormalities	1.80E-06	5.744727495	204
Molecular and Cellular Functions			
Cell Signaling	4.05E-07	6.392544977	202
Molecular Transport	2.30E-06	5.638272164	970
Nucleic Acid Metabolism	1.48E-04	3.829738285	171
Small Molecule Biochemistry	1.48E-04	3.829738285	728
Lipid Metabolism	5.46E-04	3.262807357	452
Physiological System Development and Function			
Nervous System Development and Function	4.29E-236	235.3675427	1225
Behavior	3.61E-04	3.442492798	213
Embryonic Development	1.02E-03	2.991399828	208
Organ Development	1.02E-03	2.991399828	157
Organismal Development	1.02E-03	2.991399828	201

*The most significant value is shown here.

Appendix 4. Transcriptome changes in each transition step during reprogramming.

***Expression changes of genes log2 >1 are highlighted in Red and <1 in Green.**

Gene	MEF to Thy1+	Gene	Thy1+ to Thy1-	Gene	Thy1- to SSEA1+	Gene	DsRed+ to DsRed-
Ifit3	4.60087553	Slc38a5	5.576252823	Dppa5	2.372302205	Car4	3.535718391
Oasl2	4.215472665	Cldn11	4.115449761	Dnmt3b	2.139249635	Spink3	3.475134577
Cxcl12	3.966645338	Cldn4	4.082141292	Krt1-17	1.877030802	Fgf8	2.86847761
Fosb	3.834763644	Klk6	4.076882713	Grb7	1.836717754	Gpc3	2.771341943
Usp18	3.768288073	Klk5	4.032781113	Esrrb	1.792448715	Dnmt3l	2.764510157
Hey1	3.753932125	Slc7a3	3.972972082	Elf3	1.787887621	Fgf5	2.749079103
Gbp4	3.608386846	Fbxo15	3.97177617	Slc2a3	1.779248023	Sp5	2.741234944
Cxcl1	3.415339596	Atp2a3	3.949286967	Tcfap2c	1.755056051	Lefty2	2.732882217
Tnfaip3	3.405770736	Klk1b27	3.853710558	Alox12b	1.737651775	Gldc	2.655727188
Figf	3.398967219	Ngfa	3.829616104	Nanog	1.700779056	Dppa4	2.63089641
LOC217066	3.29484073	Trh	3.771456256	Gpx2	1.641000188	Otx2	2.588972521
Irgm	3.284597817	LOC233038	3.76157962	Sall4	1.560096407	Pitx2	2.585427961
Ptn	3.16273614	Krt2-8	3.733036601	Mdk	1.549185456	Dgkk	2.458843364
BC099439	3.044322799	Nup210	3.715904908	Rbm35a	1.510582932	Cldn6	2.373803579
Cyp2f2	3.012038635	Msc	3.653750408	Ly6g6c	1.49421988	T	2.363638347
Cxcl14	3.009999817	1600023A02Rik	3.643498822	Olig1	1.489832798	Epb4.1l3	2.32983194
Acta2	2.949465136	Upp1	3.624418253	Col18a1	1.478029639	Dnmt3b	2.323044498
Axud1	2.947951056	L1td1	3.480851484	Otx2	1.452512205	Lin28	2.297187187
Lgals3bp	2.869655138	Fetub	3.437078874	2410146L05Rik	1.416764432	Esrrb	2.265173317
Dpt	2.863048422	Garnl4	3.427568572	Zscan10	1.39340123	Trh	2.259166024
Nr1d1	2.840512602	Tdh	3.414693304	Plekha2	1.393359388	Nanog	2.21432369
Aebp1	2.784363008	Aldh3a1	3.337408162	2010001M09Rik	1.374338893	Mest	2.206405077
Reg1	2.743532588	Dmrtc2	3.304874368	Dnmt3l	1.369980224	Dppa5	2.112289321
Hes1	2.738401047	Acsbg1	3.245589271	Lefty2	1.353996576	Slc1a3	2.095532437
Serpina3g	2.721268173	Fgfbp1	3.243909292	2410116G06Rik	1.330420805	Smarca1	2.075597619
Ccl2	2.69912319	Laptm5	3.217989393	Med18	1.328036103	Lmyc1	2.07498704
Olfml3	2.676776953	Lgals7	3.18848082	Rab15	1.308880376	Bex4	2.039343712
1110032E23Rik	2.663095866	Krt1-17	3.179245629	Dppa4	1.286731135	Bex2	2.035465477
Mx2	2.641934686	Npy	3.174528033	Prom2	1.261232163	Mdk	1.998026436
Gcnt2	2.586388794	Krt1-14	3.167007518	Rab25	1.251377225	Pla2g1b	1.98622888
Ccl7	2.564685197	Atp12a	3.082655047	Igsf9	1.236427151	Igdcc3	1.981711081
D930038M13Rik	2.560683565	BC004728	3.019899557	Klk7	1.226284317	Igfbp2	1.945173307
Col12a1	2.496155407	2200001I15Rik	2.994815465	Igfbp2	1.205860697	7420416P09Rik	1.914516488
Il1rl1	2.481300799	Msln	2.989420894	Espn	1.191760803	Utf1	1.90988758
Il1rn	2.471992328	Cth	2.975752454	Spnb3	1.179852876	Pou3f1	1.902460751
Lbh	2.469776035	Slc17a6	2.966553517	Ppl	1.178267883	Ptn	1.841679183
Gvin1	2.468089052	1190003J15Rik	2.960880903	Ap1m2	1.178228305	Lefty1	1.802542135
Zfpm2	2.456285063	1700019D03Rik	2.943416472	Gldc	1.172292016	Spp1	1.761162538
Id2	2.450966221	5730453H04Rik	2.912480896	Egln3	1.163298088	Nr6a1	1.748171049
Dlk1	2.448576878	Reep1	2.878262456	BC013481	1.148183222	Gsc	1.734799927
Olfml2b	2.441746309	Ramp3	2.82483058	Klk11	1.144229387	Sall4	1.732041201
Col6a2	2.439210311	Gna14	2.821060171	Tacstd2	1.131747057	Zscan10	1.722633151
Myd116	2.438000863	Grb7	2.813765815	Krt1-19	1.128779019	Chst1	1.721628271
Sepw1	2.421310814	Acpp	2.812609175	Abp1	1.125130671	Gbx2	1.714719873
Dtr	2.415597443	Itpk1	2.731947519	Sprr2d	1.116897638	Igsf4a	1.709844251
Frmd6	2.391126315	Mal	2.718587065	Cdc20	1.108550153	1500031H04Rik	1.682199791
Col1a1	2.390014448	Mansc1	2.709785281	Rbpms2	1.089267338	Rbpms2	1.681931101
Itga11	2.388076278	Arg1	2.690578798	Prss19	1.084375163	6030411F23Rik	1.672283184
Igtp	2.362185186	E130012A19Rik	2.675395967	H2-Bl	1.078387899	Fabp3	1.659588167
Mglap	2.350282641	Nppb	2.650162484	Chst1	1.076038492	Sox17	1.658211483
Epha3	2.329562973	Serpinb3a	2.602071746	Rbpms	1.0706856	Car14	1.648330516
Cxcl15	2.319337977	Ltf	2.571861888	L1td1	1.068136569	LOC620807	1.610248135
C1qtnf3	2.301117908	Tfrc	2.555205999	Gbx2	1.062887706	Chrd	1.608074561
G1p2	2.299864359	1110061N23Rik	2.534863889	Mapk13	1.062871885	Glipr2	1.598400623
Cyp1b1	2.299268427	Egln3	2.525852444	Ckmt1	1.061400545	Emb	1.591626231
2310061N23Rik	2.291929726	Dppa5	2.522600846	Zfp473	1.051225323	A230098A12Rik	1.574341385
BC006779	2.28802221	D12Ertd553e	2.515395876	3110043J09Rik	1.046891717	Ppp1r1a	1.57422112
Gadd45b	2.287823509	Ppp1r1c	2.509539283	Tpd52	1.04450255	Ptgis	1.57395551
Sfrp2	2.276711468	Ngfr	2.506797404	Rps6ka1	1.042629853	Cadps2	1.569663364
Sgk	2.272046468	Foxd1	2.491155974	Ndrg1	1.04116331	Prf1	1.551593233
Vcam1	2.269862254	Corin	2.489364403	Phc1	1.025132697	Tro	1.548255279
Nfib	2.269701707	F2rl1	2.488242257	E130306D19Rik	1.013313183	Fhl1	1.535752579
Tnc	2.266936608	Uhrf1	2.474161717	Gstp2	1.009271851	Lrig3	1.535554182
Mdk	2.265318746	Dmkn	2.46276926	Kif22	1.008214798	1700012H05Rik	1.528632531
Plac8	2.258893226	E2f2	2.455543533	Bcl2l11	1.00288507	Defcr-rs2	1.526367847
Spnb2	2.25281801	Krt1-12	2.454992152	Car4	1.001021377	B930096L08Rik	1.524453518
Gbp2	2.252271928	Tle4	2.453054141	Prelp	-4.225504517	Tm4sf6	1.50701078
Agpt2	2.246853003	Cxadr	2.39998924	Bgn	-4.155118567	1700029P11Rik	1.503734845
Ifi47	2.239661913	1300013B24Rik	2.395235163	Mglap	-3.993321071	Tex19	1.484093673
Mmp3	2.236234346	Snrpn	2.37884073	Serpinf1	-3.69241559	Stx3	1.477505032
Igfbp3	2.231669554	Prkcb	2.350112323	Col1a1	-3.586710163	Snn	1.468924813
Mfap4	2.2227328	9330186A19Rik	2.349769764	Dcn	-3.392261157	Gap43	1.468285694
4732435N03Rik	2.209453366	Arhgef3	2.344171887	Igfbp5	-3.229591263	Irx3	1.467499691
Cdh3	2.182671992	Acp6	2.341433746	Ptn	-3.215573899	St6gal1	1.466390047
Slit2	2.179411523	Cobl	2.333730078	Timp2	-3.170181321	2610305D13Rik	1.466057095
Trim30	2.162323279	Rb1	2.321074177	Col6a1	-3.103528212	BC030476	1.460260259
Hic1	2.161796437	Rnase1	2.316332632	Ogn	-3.026296744	Nudt11	1.459138179
Gpr49	2.154080057	Aqp3	2.313307612	6330406I15Rik	-3.006990944	Gfpt2	1.457996656
1200009O22Rik	2.146064541	Itgb4	2.29812039	Lox	-2.970372034	Fgf15	1.457547795
Nrp	2.132389142	Slc2a3	2.296696058	Slit2	-2.914118871	Tnfrsf19	1.454690036
Grb14	2.12891948	AU040576	2.296162627	Timp3	-2.893656727	Egfl7	1.442729233
Ifit2	2.122791894	Lmnb1	2.295696553	Tnc	-2.832773371	B3gnt5	1.436194151
Thy1	2.114904064	Dpp4	2.293452926	Itgbl1	-2.787938493	Sall2	1.427349439
Hmox1	2.1115804	Prkcz	2.281925297	Crym	-2.697586305	Arid3b	1.419720733
Tmem176a	2.104747583	Akp2	2.278653406	Ifit3	-2.646496227	Armcx2	1.413841887
Plf2	2.102076647	S100a3	2.277775251	Tnfrsf11b	-2.633408815	6530401D17Rik	1.413296866
Nfkbiz	2.097686292	2810410M20Rik	2.269355138	Ccl7	-2.551737387	Lhx1	1.406952769
Bcl9l	2.093259266	H2afz	2.269094274	Col3a1	-2.538915133	Tcfl5	1.398821694
Hoxc6	2.086690076	Krt1-16	2.267132974	2310061N23Rik	-2.537008218	Fgf10	1.398667538
Fgf7	2.084790895	Itga3	2.265657406	Sostdc1	-2.481335731	Flt1	1.390789953
Fbln1	2.078852239	Cldn5	2.255500733	Thbs2	-2.436880472	Rbpms	1.388988428
Mrvi1	2.064403033	Mcm10	2.252155831	1200009O22Rik	-2.422741114	Foxq1	1.380803435
Cyp7b1	2.060600011	Mcm5	2.247325077	Mmp2	-2.393241115	E030006K04Rik	1.36812735
Kcnab1	2.056472769	Cldn3	2.245237172	Cyp1b1	-2.387383352	Slc2a3	1.359019744
B230104P22Rik	2.053381676	Ccnb1	2.241524757	Cxcl14	-2.381921224	Igsf9	1.345915329
Fgf10	2.04647443	Mapt	2.227133454	Col5a1	-2.373880175	Ramp2	1.34129342
Ssbp3	2.038917874	Avil	2.200525506	Hey1	-2.362621032	Eomes	1.340306624
Fos	2.036512069	6030405A18Rik	2.193479729	Epb4.1l3	-2.346972103	Nptx2	1.332250187
Idb4	2.035425842	Tacstd2	2.180366748	Il1rn	-2.326179494	2410146L05Rik	1.329907883
Crym	2.018954326	Krt1-19	2.176111146	Scarf2	-2.324055251	2810046M22Rik	1.322408113
Prl2c3	2.014033695	Rasgrp1	2.173563579	Nedd9	-2.323480215	Adam19	1.313947643
Thbd	2.009688389	2310061G07Rik	2.173064709	1500015O10Rik	-2.293232662	Zbtb2	1.311851022
Arhgap20	2.008077583	Cdca7	2.169256534	Col4a2	-2.262712771	Foxa2	1.31045531
Irf7	2.007928896	Tjp2	2.166039916	Slitl2	-2.240567345	Cotl1	1.308618798
Polydom	2.007581342	Rbm35a	2.161385024	Apod	-2.209461911	Sgk	1.308115708
Galntl4	1.999534539	Rpp25	2.161369051	Oasl2	-2.166403163	Tdgf1	1.306954766
D14Ertd668e	1.997761528	Sox21	2.159608479	Scara3	-2.156997776	Acvr2b	1.303430127
Gm1012	1.988372861	Pdgfb	2.155898375	Spon2	-2.144092855	Igfbp5	1.288331305
Thbs1	1.986389568	Pkp1	2.154239673	Dlk1	-2.132054147	Cntnap2	1.278880442
2610001E17Rik	1.985265368	Tcfap2c	2.145108681	Lgals3bp	-2.11886813	Pnma2	1.271679119
Nedd9	1.981532595	Aoah	2.140186481	Loxl1	-2.105632041	Mfap2	1.27064759
Ccl11	1.980157728	Mybl2	2.135633132	Nfil3	-2.095222681	Axin2	1.264061601
Pdgfra	1.977027726	Gm484	2.134007669	Sgne1	-2.088199323	Phlda2	1.263034406
Zfp36	1.97145943	Wasf1	2.132819445	Usp18	-2.087462841	Fzd2	1.261933532
Osmr	1.971386642	Mbp	2.125823797	B230104P22Rik	-2.080965534	Slc27a2	1.261508552
Zcchc5	1.969211485	Mcm6	2.122453802	Gvin1	-2.077566685	Mogat2	1.25358293
Col3a1	1.966355604	AK129128	2.120477357	Ccl8	-2.049479054	Whrn	1.253258387
Rasl11a	1.965784285	9030611O19Rik	2.108649381	Olfml3	-2.049075992	Fzd7	1.252622863
Actb	1.950139485	Tnrc9	2.101860726	Zfpm2	-2.019328261	Mapk12	1.249317527
2510004L01Rik	1.946406794	Bex4	2.10150612	Acta2	-2.014301448	Ddx25	1.244903953
Fas	1.946105002	Tcfap2a	2.096786891	9030611O19Rik	-2.009479456	Dnajc6	1.24320682
Irf1	1.938549032	Dgka	2.086508993	Cav1	-1.993093327	Evl	1.241138348
Stx3	1.935204877	Slc2a1	2.071188786	Cxcl1	-1.99143375	Socs2	1.237366445
Mgst1	1.931808228	EG638695	2.070055795	Rbms3	-1.96609466	Mlp	1.234962569
H2-T23	1.917477351	Sh3rf2	2.058998418	Col6a2	-1.965632128	2410004F06Rik	1.231281092
Sdpr	1.917026319	Efcbp1	2.054908341	Vcam1	-1.951828001	Pknox2	1.226015216
Per1	1.916427897	Iqgap2	2.052947266	Akr1c18	-1.923143495	Igf2bp1	1.219989031
Drpla	1.9083589	Nos3as	2.03562391	Col4a1	-1.912379418	Cmya4	1.215056668
F2r	1.90605794	Slc9a3r1	2.034700322	Eln	-1.90010143	Prickle1	1.197735268
Lgals9	1.905359773	Tuft1	2.03435483	Vim	-1.898794774	Lrp11	1.189503547
Gap43	1.90512655	Apcdd1	2.031520743	Ccl2	-1.872574929	Col18a1	1.188157494
1810057C19Rik	1.903784685	Aldoc	2.030856249	Dab2	-1.870119717	Dpysl5	1.187290562
Cav1	1.900271834	Nt5e	2.008358439	Igfbp4	-1.862177043	Gata6	1.185911971
Hoxc9	1.898948094	Gng13	1.997974217	Spp1	-1.862046618	Fgf17	1.181718606
Srpx	1.892650303	Zic3	1.996560916	Ghr	-1.854910794	Myh10	1.180651408
6330403K07Rik	1.891634973	2310046K01Rik	1.992684616	B2m	-1.845135275	Dppa3	1.171045541
Epb4.1l3	1.872830364	Dhx32	1.982054801	Mfap2	-1.831505534	Celsr3	1.162920068
Idb3	1.868891097	Tmprss5	1.979743963	Nrp	-1.831292977	Stard8	1.145548071
H19	1.862027314	Cenpa	1.963962227	Kctd12	-1.829800069	Fuom	1.143653822
Sulf1	1.850574708	Porcn	1.961843858	Zfp521	-1.828329873	Gm691	1.143443168
Rspo2	1.848668865	BC065123	1.961157524	Gbp4	-1.809378054	Pla2g10	1.139765815
Nfkbia	1.844811936	Pglyrp1	1.959447621	Thbs1	-1.785495488	Mixl1	1.139010255
6030411F23Rik	1.838617698	Ndg2	1.951231123	Sparc	-1.763908016	Slc39a4	1.1294263
Dkk3	1.835555602	1700057K13Rik	1.947862377	BC099439	-1.760049207	2810004A10Rik	1.12500877
Pdgfrb	1.831877241	Iap	1.944790913	Ptx3	-1.759386889	Olig1	1.124901767
Rbms3	1.830089039	Tmem16d	1.91268844	Marcks	-1.757177981	Rragb	1.120658342
Gpc3	1.816917318	Eppk1	1.911399021	Igfbp7	-1.740766538	Ndg2	1.118857397
Tpbg	1.81064243	Cdh1	1.909397451	Cdo1	-1.740641252	Actb	1.10679149
Nnmt	1.809125462	Dok2	1.909108421	0610041G09Rik	-1.737292504	LOC545007	1.09867314
Slc39a13	1.803660438	Lrmp	1.90729636	Itm2a	-1.721185011	2410116G06Rik	1.092249141
Ogn	1.796031535	Krt2-6b	1.902364997	LOC217066	-1.692807456	1110025F24Rik	1.090810288
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Cpxm1	1.788791317	Sgne1	1.876040735	Dkk3	-1.685685089	Cyp7b1	1.08684326
Serpinh1	1.787718895	4632404H22Rik	1.875235897	Bicc1	-1.684100354	D230005D02Rik	1.084573405
Gbp1	1.779637778	Ddc	1.869320675	Tgfbi	-1.632680915	Robo4	1.058645995
Gsn	1.777607579	Plekhf2	1.869162058	2610001E17Rik	-1.627834308	Slc29a4	1.052573653
Gm1010	1.777264692	Notch4	1.864629727	2810022L02Rik	-1.604862058	Gprasp1	1.048083505
Pmp22	1.772317759	Parp1	1.860159035	Rgl1	-1.597977684	Sema3f	1.042378602
Bicc1	1.771260178	1810015C04Rik	1.85634655	Per2	-1.596644306	Fem1b	1.040631483
Reg3g	1.76811329	Dusp14	1.856010057	Lum	-1.594510484	Neurl	1.036206094
Dcn	1.755555046	Optn	1.855000294	Serping1	-1.587608324	Sertad4	1.035166854
Casp4	1.752822695	Cd109	1.85488374	Wisp1	-1.582459994	Cd40	1.029087579
Thbs2	1.747695683	Tph1	1.847815561	Adamts2	-1.578927915	Mnd1	1.022857716
1110019L22Rik	1.746616998	Cte1	1.846325029	Capn6	-1.578927082	6330403K07Rik	1.022786532
Klf2	1.743611552	Siat10	1.833926301	Dtr	-1.555296719	Nudt10	1.019701914
Myh10	1.740510112	Tmem20	1.831292977	C3	-1.55277191	Sqle	1.018018389
Ptx3	1.738454883	Pip5k1a	1.831223184	Cxcl12	-1.548090299	Greb1	1.017417053

Ankrd50	1.73456092	Tm4sf12	1.830652886	Fas	-1.548043873	Nid2	1.008638918
Junb	1.730084273	Syt14l	1.830004663	Pmp22	-1.528638894	Crabp1	1.007688534
Cxcl10	1.728912805	AI427138	1.829015584	Mxra8	-1.524943501	Enc1	1.006993203
Ptpn21	1.727558035	Hist1h2ak	1.827792869	Zyx	-1.512759054	H19	1.006848359
Fhl2	1.727142512	Anln	1.827678235	Cdc42ep3	-1.497764059	Atp1b1	1.001921032
Adar	1.723376529	Prg	1.827532804	Cryab	-1.480582438	C130076O07Rik	1.001474395
Igfbp5	1.719080497	Clic3	1.819903385	2310016C16Rik	-1.474642656	Zcchc3	1
Lsp1	1.715582043	Nsbp1	1.815390252	Corin	-1.4708348	Serpina3n	-1.838122321
Oas2	1.71494963	4930538D17Rik	1.815111366	Nr1d1	-1.467658135	Hoxc6	-1.636376112
Col6a1	1.707103399	Chn2	1.813022362	Aqp1	-1.461744248	D12Ertd553e	-1.617159856
En1	1.706531332	Mtap7	1.811202111	Col12a1	-1.449707733	Il1rn	-1.59317365
Hist1h2bh	1.703901535	Sftpd	1.801066551	Osr2	-1.446286471	Adh7	-1.543595683
Tnfrsf1a	1.703018262	Enpp1	1.798516568	F2r	-1.425634973	Pcolce	-1.521864523
Ifitm3	1.70292122	Rab8b	1.798000104	Tgfb1i1	-1.423749931	Ngfa	-1.462827451
Nid1	1.700999326	Krtdap	1.797041729	D4Bwg0951e	-1.416322886	Klk5	-1.451857971
Efs	1.69780546	Avpi1	1.77710551	Vsnl1	-1.405526405	Sftpd	-1.445447389
Tpm1	1.696637651	Centa1	1.772161068	Polydom	-1.405256478	Klk6	-1.429847658
Tgfbr3	1.69384323	4930429A22Rik	1.766596558	Pik3r1	-1.396744825	Meox2	-1.407018849
Vcl	1.693329741	Hist1h2ah	1.764520823	Col16a1	-1.391944412	Rnase1	-1.395871197
AI481100	1.692153107	Gdf3	1.747979612	Pros1	-1.385004019	Cd109	-1.392317423
B2m	1.692139847	Mthfd1	1.742204562	Chst7	-1.376745715	Siat10	-1.381437654
Hoxc10	1.691551148	Hmga1	1.739949184	Nr2f1	-1.375190279	Apod	-1.37031447
Unc5c	1.682925754	Slc2a6	1.739447569	Itga11	-1.374620989	Tgfbr2	-1.36607612
Fst	1.678071905	Pem	1.736436068	Mgst1	-1.369515346	Aldh3a1	-1.350634327
Per2	1.677933391	Hist1h2ao	1.736087405	Fst	-1.366285321	Hbb-y	-1.34471546
Sphk1	1.672556502	Lamc2	1.725130458	Epha3	-1.360402243	Fmo1	-1.337581359
Ebf3	1.671845767	Ckmt1	1.722164489	Pdgfra	-1.352742418	D2Bwg0891e	-1.336985327
Twist2	1.670351078	C430004E15Rik	1.721485466	Bmp15	-1.352640962	Actg2	-1.303262632
Sfrp1	1.668432065	Akr1c18	1.721134721	Rnase4	-1.351758171	Corin	-1.29024325
Mxra8	1.662810232	Sall4	1.720298188	Gm1012	-1.345060311	Oas2	-1.271099808
Mest	1.659278789	Gch1	1.720145127	Ccnd2	-1.344872532	Avil	-1.265742496
Pkig	1.654823642	1810043M15Rik	1.71316257	Rhoj	-1.343954401	Mrgprf	-1.265531139
Ddx58	1.651036516	Tm4sf3	1.709197975	Mme	-1.3382803	Acsbg1	-1.264505087
Rgs16	1.650729978	D9Ertd280e	1.706228258	Pcdh7	-1.325305455	Msc	-1.257695627
Steap2	1.650466546	Sod2	1.701972576	Ly6c	-1.307140774	Slc17a6	-1.254939948
Mfap2	1.649561234	Pbk	1.701773596	Chst3	-1.306832493	Osmr	-1.242750134
Stat2	1.648002895	Liph	1.700439718	Prkcb	-1.306610684	Irf2	-1.227926537
Eps8	1.645403079	Cdca2	1.699632064	Pdgfrl	-1.302214587	Egfr	-1.22659241
Pdgfrl	1.642516492	Sap30	1.696570414	Adora2b	-1.300044977	Aim1	-1.223288227
2310016F22Rik	1.6425087	2010004A03Rik	1.694251832	Thy1	-1.294644012	Foxd1	-1.219132526
Zfp36l1	1.641345721	AI427515	1.693991908	2310016F22Rik	-1.290515142	Ppp1r1c	-1.217396324
Tap1	1.63343121	6330442E10Rik	1.693279317	Herpud1	-1.286865482	Ltf	-1.211012193
Mmp23	1.632026646	Ranbp1	1.686405899	D14Ertd668e	-1.285940317	Cbara1	-1.209470151
Tmem98	1.630747311	2610019F03Rik	1.68442396	Sox21	-1.284876551	Nfix	-1.205780896
Nfil3	1.629629832	5730410E15Rik	1.674514086	Ifi47	-1.283932467	Acpp	-1.203070987
Avpr1a	1.623868408	Fuom	1.662163981	Pscd3	-1.277171517	Ccnd1	-1.203002267
Mapk6	1.620861718	Dutp	1.660789624	Anxa3	-1.272825472	Ccl7	-1.201258208
Pltp	1.620712526	Cyp2s1	1.659869468	Hey2	-1.267913325	Cmtm7	-1.200861983
C2	1.613593789	2410137M14Rik	1.657686665	Pkig	-1.264812949	Nt5e	-1.198438483
1810043J12Rik	1.607946441	Dpp6	1.656347134	Cyp2f2	-1.261227326	Arl6ip5	-1.197930289
AA175286	1.60568041	Krt1-13	1.654732779	Cdh13	-1.260112087	Vamp4	-1.196117141
Hspa1a	1.604149521	Ripk4	1.650160767	Sspn	-1.259883092	Slc2a6	-1.192561198
Atp1b1	1.599477701	Limk2	1.646844269	Col1a2	-1.257411011	Cldn5	-1.182864057
Ccl5	1.597050896	Nusap1	1.646780116	Mmp3	-1.255761171	6330442E10Rik	-1.178424271
Inhba	1.594281065	Ucn3	1.640664994	Per1	-1.252517163	0610041G09Rik	-1.175830716
Ldb2	1.59331085	Hist1h2ad	1.63648872	Wisp2	-1.242775567	Tm4sf3	-1.169755362
Slitl2	1.592152026	Rab25	1.63530015	Fosl1	-1.238046754	1700047I17Rik	-1.16116883
Hoxd8	1.59118744	Sfn	1.630535983	Cd248	-1.235840231	Prss35	-1.16083999
Cbfa2t1h	1.587820031	Frrs1	1.629865137	C1qtnf3	-1.235080344	D12Ertd647e	-1.156428675
Zfp521	1.587514217	Gngt2	1.627893895	Ppap2b	-1.231233855	Sspn	-1.149368819
Bteb1	1.586355886	Plekha6	1.626126995	Ccrn4l	-1.224356136	Olfm1	-1.145042879
LOC381480	1.585773231	Nfe2l3	1.620733632	Wnt5a	-1.220675949	Emp3	-1.14486161
Bmp1	1.581033984	Phc1	1.619887009	Trim30	-1.218894977	Dmrtc2	-1.13904207
Pvrl2	1.580935034	4930572J05Rik	1.618864246	Gch1	-1.213815137	Chi3l1	-1.137208876
Phlda1	1.578378686	Hal	1.617514616	Id2	-1.21079386	Mal	-1.136547273
Csf1	1.576795875	Ush1c	1.61562555	Fbn1	-1.205296837	Iqgap2	-1.135541223
Col24a1	1.575036536	Spink3	1.609730406	Nbl1	-1.203974421	Aqp3	-1.12860328
Twist1	1.57477097	Ncaph	1.608387986	2510009E07Rik	-1.201239305	Npy	-1.128252589
Sim2	1.574283732	Chchd4	1.608265445	Bmp1	-1.191179504	Mglap	-1.124869117
Mbd5	1.572530756	2810417H13Rik	1.607284169	Fxyd5	-1.170719656	Atbf1	-1.124055708
Flrt2	1.569365646	Prx	1.605993413	Spink3	-1.170144273	1110020C13Rik	-1.119444118
Defb1	1.563860703	Llglh2	1.605050264	Jak2	-1.169599814	Prok2	-1.118585359
Lum	1.56292099	A230091H23	1.603136743	Itpkc	-1.161709176	Slc38a5	-1.114624137
Pcdh7	1.562758621	Clcn3	1.601275834	Prkcdbp	-1.158300027	Arhgdib	-1.11449068
Hoxa5	1.562706833	Hdac6	1.597982399	Palmd	-1.155822687	Dbp	-1.112630444
Kng1	1.556833128	9130210N20Rik	1.593491503	St7	-1.1527537	5730410E15Rik	-1.106776316
Prickle1	1.554944356	Pga5	1.593039191	1110007C02Rik	-1.14972194	Rbms1	-1.101674386
Vegfc	1.554740886	Sema4b	1.587708997	Ednra	-1.146655222	Ptprv	-1.095013115
Fez1	1.55442232	Pik3cb	1.587143446	Mtap1b	-1.146028496	Rab7l1	-1.09366475
Hoxd10	1.551134572	Hist1h2an	1.584495324	Tcf4	-1.145387123	Emp2	-1.08822036
Il31ra	1.549607224	Kcnk13	1.583856563	Olfml2b	-1.144728626	Olfml1	-1.087929909
Loxl1	1.548440117	Sema6d	1.581373705	Kai1	-1.142957954	Dctn1	-1.086772722
9330196J05Rik	1.548340288	Rps6ka1	1.580493643	Prnp	-1.141281665	Cdh13	-1.084599403
Adamts5	1.54415784	Stk6	1.579334576	AU040950	-1.141162926	Rnase4	-1.081394622
Ccdc3	1.542593528	Stxbp2	1.5753338	Nnmt	-1.139701498	2610001E17Rik	-1.080297871
Lphn3	1.540635469	Kcnk1	1.570433727	Antxr1	-1.139162748	Siat8b	-1.079621864
Adamts2	1.54023569	Qpct	1.569736026	Figf	-1.138433395	Gm484	-1.079489327
Chst12	1.539496675	D11Ertd636e	1.566569327	Bmp4	-1.134852884	Axud1	-1.073899627
Gata6	1.539020825	Insm1	1.558967292	Fmo1	-1.134135618	Gpnmb	-1.071384633
Timp2	1.5365331	Usp1	1.548828715	Edg2	-1.132957338	Mras	-1.06480033
Gpr23	1.528717215	Dnmt3b	1.546029871	Ucn3	-1.126091821	Gngt2	-1.064722416
Usp2	1.527571181	Slc28a1	1.544418422	Anxa1	-1.119599552	Csprs	-1.06252973
Jundm2	1.527154895	Pacs1	1.543598513	Rgs16	-1.119253036	Rb1	-1.059657418
Steap	1.522678222	Pak4	1.543263209	Anxa5	-1.118520718	Atp2a3	-1.058972743
Ggcx	1.519552611	Drp2	1.542855107	Sertad4	-1.115188938	Thbd	-1.055252716
Calr	1.515762771	Sh3gl2	1.53723946	Ssfa2	-1.114228671	Msln	-1.052287649
Thbs3	1.515075329	Prc1	1.528627803	Ssb4	-1.11388119	Prnp	-1.049199364
Cmya4	1.514233675	2310006J04Rik	1.528219989	Axl	-1.112991686	Gsdmdc1	-1.044669049
Slit3	1.513109622	Elavl2	1.52300478	Igf2	-1.112876107	Fetub	-1.041953961
Htra3	1.512784943	Hist1h2af	1.521071947	Lxn	-1.110991746	Hoxc9	-1.040611062
Tbxa2r	1.511725141	Tk1	1.520363261	Kcnab1	-1.107713817	Atf3	-1.035871109
Prrx1	1.510084708	2310010M24Rik	1.512812715	Il11ra1	-1.101361726	Gch1	-1.033510304
Mapre2	1.508428653	AI256711	1.511859923	Tsrc1	-1.094662057	Scarb2	-1.032937139
D15Ertd366e	1.506783825	2310042N02Rik	1.511439396	Rora	-1.094609644	Prkcdbp	-1.030510412
Cd248	1.50513561	Podxl	1.505852662	1110032E23Rik	-1.088606113	Enpp1	-1.023773631
Col4a5	1.500774792	Hmgb2l1	1.505829924	Lbh	-1.087240083	Rab8b	-1.023545204
Hist1h2bn	1.49596618	Elf3	1.504702929	Adrb2	-1.085952701	Bdnf	-1.021719722
Galnt9	1.494961044	Syngr1	1.503432615	Npr2	-1.082091621	Lamp2	-1.019822882
Gpc4	1.493794813	Abp1	1.493988841	Bst2	-1.081019351	Grina	-1.01436922
1810057P16Rik	1.493388695	Sox13	1.493539473	Igfbp6	-1.080170349	Efna5	-1.012771643
Cugbp2	1.491167118	C1qtnf1	1.489449214	Ctsc	-1.079551299	Cdkn1a	-1.011774605
Gstt1	1.490759234	8430408G22Rik	1.4836456	Armcx1	-1.078677372	1810009M01Rik	-1.009775258
Mme	1.489999557	Pfkp	1.482712442	Ctsk	-1.072084622	Scara3	-1.007900869
Crtap	1.487818159	9930023K05Rik	1.47955982	Igfbp3	-1.071326447	Ak3	-1.002577623
Hist1h2bf	1.486816867	Itgb7	1.477478074	Axud1	-1.071109739	Oit1	-1.001049614
Oas1g	1.486330488	Tmc6	1.475320084	Twist1	-1.070779011	Rims2	0.993486693
Col1a2	1.486087251	Ly6g6c	1.474283022	A230091H23	-1.069645862	Calca	0.993476876
Mlf1	1.485595475	Rims2	1.473931188	Lmo4	-1.06944204	Sirt1	0.993388187
Tagln	1.484998579	Lig1	1.46555146	Ecm1	-1.068261118	Acas2l	0.991769071
Cebpb	1.484707059	8430410A17Rik	1.460680165	Efcbp1	-1.06583199	Cxcl12	0.991165343
Fblim1	1.482133001	Msh6	1.459356657	Serpine2	-1.064280751	AW548124	0.990938629
Plekha4	1.479845795	Cltb	1.458747967	Gp38	-1.062416923	E2f5	0.990227813
Ppap2a	1.476160698	Nasp	1.456252474	1190002H23Rik	-1.062389922	5730469M10Rik	0.990002073
Ltbp1	1.471787151	BC004853	1.454031631	Irgm	-1.061263295	Grip1	0.988991676
Bmp4	1.471247263	Gpx2	1.446831582	Reck	-1.058712776	Ung	0.98231513
2810442O16Rik	1.468049831	Atp1b3	1.444219369	Irs2	-1.058137758	Garnl3	0.978958863
Wbp5	1.46545565	Tcfcp2l2	1.442046233	Sdpr	-1.057533764	Plcd1	0.978382331
Rgs4	1.464878238	Blm	1.437484863	Garnl3	-1.054654075	Foxa1	0.97819563
Fzd2	1.462080339	Adam23	1.435127465	Kdelr3	-1.052112989	Foxd4	0.977381697
Copz2	1.459270288	Olig1	1.430055138	Upk3b	-1.051723661	2210409E12Rik	0.974777416
Cobll1	1.457761081	BC085271	1.428375996	Aebp1	-1.03766562	H2-Bl	0.97375255
Armcx1	1.457259254	Chst3	1.427010141	Copz2	-1.036568609	D14Ertd449e	0.967745801
Rabl4	1.455679484	Suz12	1.426868322	Mansc1	-1.035666253	Clic6	0.965234582
Epb4.1l2	1.455530683	Cbr2	1.426264755	Tnfsf9	-1.032914622	Cmtm8	0.961088904
C1qtnf2	1.448929482	Rbm38	1.425968395	D11Lgp2e	-1.02988428	Pdlim3	0.96069835
Ccrn4l	1.438620981	Tm4sf11	1.425238812	Emp3	-1.025797081	Gababrbp	0.959209735
Il6st	1.438269806	Myo6	1.423174053	Saa3	-1.023962672	Pem	0.955039859
Colec12	1.433960363	Vil2	1.421443626	Thbd	-1.020772146	Agtrl1	0.945273073
Gpx3	1.433545988	Dusp4	1.42103624	Gpr49	-1.014780158	6820449I09Rik	0.944212222
6330406I15Rik	1.430397233	Nrn	1.419426994	Bmp3	-1.014274131	2410012C07Rik	0.940128544
Col4a1	1.428250216	Incenp	1.419232603	Tnfrsf12a	-1.013370763	Tal2	0.939739475
Hoxb7	1.425993914	Ppat	1.418263419	Gm129	-1.012299265	Blm	0.936559872
Cxcl5	1.424231294	Lamb3	1.416164165	Defb1	-1.010569242	Ttyh3	0.935825768
4933428G20Rik	1.419892633	Elmo1	1.414828519	Sim2	-1.002837159	Tnnt1	0.935187197
Pftk1	1.417839394	Hs3st3a1	1.413971963	Adamts5	-1.001834323	Eras	0.934671577
Gprc5a	1.41565076	Gsta3	1.413294061	Tcfcp2l3	0.993724675	Trp53i11	0.934623991
Adcy4	1.411462045	Pcsk1n	1.410072561	Pou3f1	0.993510133	Col2a1	0.930115906
Nuak1	1.411287615	D830007B15Rik	1.409289703	Ly6d	0.991917654	Rragd	0.928446739
Ltbp3	1.411110924	4930504E06Rik	1.40706932	Utf1	0.986824611	Car2	0.92833112
Peg3	1.407973321	Spnb1	1.407009596	Kif2c	0.985123072	Tex10	0.926530985
Smtn	1.40582115	Stmn2	1.406139947	Pem	0.981208916	Epb4.9	0.924538461
Gpr124	1.40411385	Slc35f2	1.405656263	2300002G24Rik	0.976132494	Ssb4	0.923971079
Nab1	1.403863694	Cova1	1.401410403	Sgol1	0.975363731	Slc7a7	0.923330232
4921505C17Rik	1.402992473	Cdc20	1.3991674	BC004728	0.97364542	Heatr1	0.921581714
Tmem150	1.402147122	Cbara1	1.39728798	Acvr2b	0.97256677	Mylpf	0.920997542
Lxn	1.399725373	Msi2h	1.397140295	Ripk4	0.965623231	Etsrp71	0.918975503
Ghr	1.397242235	2410146L05Rik	1.396722602	BC022765	0.963128361	Msx1	0.916246549
Efemp2	1.392418929	Foxm1	1.393501415	Cldn3	0.958338219	1110012J17Rik	0.916095748
Foxc1	1.391082767	Frat2	1.389927108	Flt1	0.95322931	Rasl11b	0.915085861
Ccnl1	1.390229141	Plcd3	1.386170438	Apoc1	0.952312018	Itm2a	0.915050128
1700012H17Rik	1.389085791	Serpinb3d	1.384439777	LOC233038	0.949623711	Slc29a1	0.914427325
Tyki	1.388129626	Krt1-18	1.383981564	Pvrl2	0.949198562	Bmp7	0.913548899
6030410K14Rik	1.386910117	Ckb	1.381829871	Fgf5	0.94079642	2610318I01Rik	0.910986733
Alcam	1.385056073	Hbb-y	1.37830965	Apoe	0.939187758	Gpc1	0.909756359
Snai1	1.381403763	Pcdh21	1.376213728	Cldn6	0.938167989	Aire	0.90974214
Reck	1.380065361	4930432K21Rik	1.375356713	2300003P22Rik	0.936689143	Acat2	0.908818412
Kif26b	1.379515586	Rangap1	1.372095473	BC018222	0.936285126	Siah1b	0.908347128
Dtx3	1.377734526	0610005K03Rik	1.371920201	Olfm1	0.934454727	1810008K03Rik	0.907699838
Gpx7	1.376711489	Ppp2r2d	1.370151076	Zic3	0.930522828	Igfbp4	0.907676591
Mlkl	1.37193352	Pald	1.369996535	Bex4	0.930184879	Dbn1	0.904326633
Tcf7l2	1.370568448	3110004L20Rik	1.368793315	Il17re	0.929258409	Tmc7	0.900464326
Amotl2	1.370256273	Prps1	1.368633391	Pla2g10	0.928848484	Sult4a1	0.895411099
Ube1l	1.36792518	Golph2	1.368412997	Orc5l	0.928837593	Zxda	0.89182445
Il6	1.363520158	Rfx2	1.368273032	Kcnk5	0.9272574	Fbln1	0.891323586
Gstm2	1.362507479	Lad1	1.36670981	Bex2	0.927039199	Pea15	0.889726804
2810410P22Rik	1.360475675	Chi3l1	1.364873072	Fem1b	0.926301902	LOC634428	0.887994974
Gm129	1.359005309	Mcm2	1.3640161	Liph	0.92589871	Upp1	0.887973382
Ctsk	1.357629886	Fcgr2b	1.362040358	Sh3gl2	0.923613953		

Ugcg	1.356559296	Ung	1.359821887	Lad1	0.922150583	Cdca7	0.885992078
Gng8	1.355495554	1700019H03Rik	1.35856473	Birc5	0.921352042	Aard	0.881700687
Pak3	1.355061839	E430034L04Rik	1.357010984	Cyp2s1	0.919642723	2410081M15Rik	0.880642405
Dnajb9	1.351342824	Jam2	1.3568238	Cbr2	0.908781978	Rapgef5	0.88038855
Slc24a3	1.350352172	D5Bwg0834e	1.355480655	E130016E03Rik	0.908560629	Zfp41	0.880260756
Lmo4	1.345009602	Rnaset2	1.354743944	Lefty1	0.905784658	Mfge8	0.879607292
Hs3st1	1.344640719	Cd59a	1.351361971	Lrrc34	0.904624608	Nope	0.877972864
S100a4	1.341020389	Timm8a1	1.350091774	Krt7	0.903104208	Lpl	0.877923404
Smad5	1.338389342	Hist1h2ag	1.349095413	Nudt5	0.902492526	Gcnt1	0.87731748
Jund1	1.335703474	Card10	1.34533795	Emb	0.901415291	Apoc1	0.875741897
Btg1	1.333233252	1110020C13Rik	1.34188583	Slco4a1	0.892494375	Dusp6	0.869048225
Stat1	1.33009872	Mta3	1.341291805	Tcf15	0.890999223	Kif5c	0.86818946
1300018P11Rik	1.329183911	Tspan7	1.341036918	Rangnrf	0.890586622	Gadd45a	0.866361938
Mmp2	1.327669787	Itpr3	1.336243376	Nup43	0.889927481	Plcg2	0.864361862
Wisp2	1.327094813	2700097O09Rik	1.336235013	Atad4	0.888900794	Sbk	0.864316402
Fkbp7	1.326469976	Dedd2	1.335073471	Mns1	0.888372669	D0H4S114	0.862804383
Cd44	1.325130527	Mboat2	1.333578455	Marveld3	0.88655905	Lck	0.861703569
D4Bwg0951e	1.320575577	Hist2h2ac	1.331915597	Krt42	0.886398605	Snx10	0.859956471
Zfp608	1.320333075	Slc24a6	1.330548203	Cstf3	0.886373156	Hist1h3d	0.857935256
Apg3l	1.318230318	Top2a	1.324073766	Depdc1b	0.886064947	Fst	0.857771072
BC049816	1.317140145	Tst	1.324063839	Chi3l1	0.885788943	Syngr3	0.854931973
Dusp6	1.31390992	St14	1.323251062	Cdca7	0.884713805	Smtn	0.854222884
Angptl2	1.313724013	Hmgb2	1.321594485	Tdgf1	0.883462211	Hist1h3a	0.850585822
Coq10b	1.313519627	Ak3	1.320182693	Ndrl	0.882388781	Nasp	0.850072464
Bnc2	1.312169128	Tead4	1.317464998	Smarcad1	0.881904153	Ybx2	0.849294294
Sspn	1.307708556	Cdca3	1.313899721	Stx3	0.881897768	Pdlim1	0.847808084
Serpine2	1.307120968	Ivns1abp	1.313548429	Cdh1	0.881011964	Hnrph1	0.846189976
3632413B07Rik	1.306193626	Pkp2	1.312656906	LOC620807	0.877399299	Ly6g6e	0.84295629
H2-T17	1.305207932	Birc5	1.311245812	Slc7a3	0.87729025	Lmo2	0.842925917
Thsd2	1.304979941	Oas1d	1.305831488	Psmc3ip	0.876496596	Gpr49	0.841379028
LOC435565	1.303975425	Uble1b	1.305079938	2610206B13Rik	0.871805563	Ubtd2	0.837855945
Mylc2b	1.303824783	Cipp	1.304569255	Nusap1	0.870834144	En2	0.836761189
Dpysl3	1.303567558	Hat1	1.302454855	Trib3	0.866270478	Clcnkb	0.834662268
D11Lgp2e	1.303443219	Rad52b	1.301806499	Ncapd2	0.863050428	Six1	0.833414345
Gns	1.299004461	Hus1	1.296166328	Klf3	0.860076324	Acsl3	0.83298073
Tsku	1.295756039	Ddef2	1.293379316	Blm	0.859146402	Spc25	0.831728517
Isgf3g	1.294341007	Pmm1	1.291359416	C78212	0.858273847	5730599I05Rik	0.830760664
Hoxb4	1.293766487	C130036G08	1.291296476	Prss8	0.854371549	Gja7	0.82663764
A230050P20Rik	1.291372638	BC037006	1.289969985	Hcph	0.853334387	Psmb10	0.824895384
Plau	1.289432096	Csda	1.288531889	Slc40a1	0.852820117	Tcf15	0.822751658
Fhl1	1.287767898	Gm1698	1.288244969	Kcnk6	0.849167925	Xab1	0.818553129
Lamb1-1	1.287500685	Rab27a	1.287834896	Kif11	0.845331665	Ldhc	0.818068053
Ppap2b	1.286707235	Col17a1	1.287377547	Dcxr	0.843753683	C86987	0.816288047
Cdo1	1.286300909	Pold2	1.287031462	Hmgb2l1	0.841713049	Anxa11	0.815734361
Lrrc15	1.28608529	2700094K13Rik	1.281529501	Msh6	0.839464772	Hn1l	0.813723822
Ptges3l	1.282170386	Syt4	1.2807894	Mylpf	0.838215886	Ube2e3	0.81283859
Hist1h2bk	1.278859373	Arl6ip1	1.279160389	Hist2h2ab	0.837527002	2810003C17Rik	0.812610181
Itga5	1.278206717	Pa2g4	1.276856586	Arhgef19	0.836887997	Nap1l1	0.811939276
Gbp6	1.277720703	2210412D01Rik	1.27594478	Calmbp1	0.833374646	Khdc3	0.811238357
Parp3	1.276735316	Atp2c1	1.271587328	Fignl1	0.830866098	Tead2	0.811224131
2310016C16Rik	1.275474146	Ak4	1.27085391	Dmkn	0.830636686	Wbp5	0.810964511
Anxa6	1.274560837	2010001M09Rik	1.269389901	5430425C04Rik	0.830349041	8430415E04Rik	0.810052389
6530401D17Rik	1.272354528	Olfm1	1.268303649	Psors1c2	0.828113482	Eml1	0.808733366
Gpr153	1.270499856	Cdc2a	1.26787708	4732474A20Rik	0.826851098	Moxd1	0.8069385
Idb1	1.269914476	Abr	1.264517897	Slc2a1	0.825569995	Asphd2	0.80560726
B4galt1	1.268042108	G3bp	1.264079334	Exosc5	0.820958785	Fhod1	0.805292456
Olfml1	1.265558176	Hspd1	1.262012399	2610039C10Rik	0.815388617	Dhcr24	0.805131114
Serpina3n	1.264204876	Hap1	1.260005884	5830411K18Rik	0.814606138	Hey1	0.80433824
Pvr	1.263791925	Heatr1	1.258622136	H2afx	0.813794145	Trim28	0.804230257
Hoxb5	1.263034406	Cct3	1.257784912	Kntc1	0.813629035	Chka	0.802685404
Chst2	1.262856416	Ncapd2	1.256756846	Kcnk1	0.813184001	Folr1	0.800826288
Tax1bp1	1.262778994	Cdc6	1.255908441	Gyltl1b	0.810273768	0610039P13Rik	0.79783012
Pdgfc	1.262038643	Zc3hdc1	1.255020838	D5Ertd708e	0.80934165	Actl6a	0.794014114
2210404D11Rik	1.259748445	Celsr2	1.253598289	Eras	0.805360321	Crmp1	0.79329221
Pkd2	1.259410192	Pdss1	1.253238829	Nras	0.805116071	AA408556	0.788485827
Pscd3	1.259000195	C86302	1.252096559	Espl1	0.804180674	A530050D06Rik	0.78823672
9030625A04Rik	1.257943639	Eif4a1	1.250785317	Lin54	0.803910912	Pfkl	0.787583373
Lox	1.25736151	Gphn	1.249801144	Ndg2	0.798432098	Gjb3	0.783342194
Nlgn2	1.256357628	H2afx	1.249545076	Rac3	0.796183308	Rnf144	0.781937832
4933426M11Rik	1.252613667	Acvr2b	1.248776953	Spire2	0.795271332	C130034I18Rik	0.781718995
Meox2	1.252230824	Fen1	1.248239954	Mapt	0.791444933	Dapk2	0.781493766
Tgfb1i1	1.250450738	9630015D15Rik	1.245531146	D14Ertd449e	0.787968779	Ezh2	0.781090248
Lmna	1.249000256	Celsr1	1.245163729	Satb1	0.784927542	Rbmx	0.780911449
Irx5	1.248888349	1500016H10Rik	1.244132073	Pfkp	0.784271309	Vegfb	0.780248258
Bdnf	1.247516126	Cd151	1.238517138	Sytl1	0.783995907	2310016C16Rik	0.779951519
Ier3	1.247369771	4732474A20Rik	1.237888758	Zswim3	0.783309448	2900011O08Rik	0.779821073
Ifi203	1.247347769	Hhex	1.237747008	C530028I08Rik	0.783116999	Acsl6	0.779801792
Itgbl1	1.245812723	Zfp296	1.233291351	Il28ra	0.783107376	Foxh1	0.77940086
Sntb2	1.245044083	Pde1b	1.233273272	Cldn4	0.781837542	2900093B09Rik	0.778169266
Hist1h2bm	1.24239285	Itgb4bp	1.231747683	2200001I15Rik	0.781265277	Heph	0.776522111
Pros1	1.242150763	Klk10	1.231384006	6330406L22Rik	0.780247461	Manba	0.776474364
Smad6	1.240858729	Thoc4	1.230870637	Wdr31	0.779663188	Thop1	0.776181991
Npr2	1.235278419	Cct6a	1.22883935	Cdc25c	0.777997233	Mreg	0.771677618
Edg2	1.234705683	Rpa1	1.226870287	Skp2	0.773213134	Maged2	0.771019127
0610041G09Rik	1.234502307	Pcyt1b	1.225369648	Cdca8	0.772613425	Marcks	0.768352261
Cyb5r3	1.234463021	Catnal1	1.224737314	Sftpd	0.772021849	Tceal5	0.767735138
Plekhf1	1.234280145	E130016E03Rik	1.224725936	Krtcap3	0.771438553	Vdac3	0.766927832
Ier2	1.23300561	Ptp4a3	1.223555041	2410081M15Rik	0.767918522	Smoc1	0.765087237
Cyr61	1.232943919	Ptprk	1.222793895	Swt1	0.766360728	2310045A20Rik	0.764070824
Tspan11	1.232912338	Cmtm7	1.221460827	Ptk9l	0.765773397	Evx1	0.763404914
Hoxb2	1.232173442	D6Ertd365e	1.219965684	Scrib	0.764187063	Zfp37	0.761927506
Fgl2	1.228451928	Dbf4	1.219684723	Sox15	0.763880596	Qprt	0.760512929
Siat5	1.227805918	Rad54l	1.218819181	Gdf15	0.763585012	Ap3b2	0.760286668
Spon2	1.227170801	3000004C01Rik	1.218064803	Mcm2	0.762834334	Josd3	0.759324741
Cyp2j9	1.225846325	Nudt5	1.21702085	Slc37a1	0.762567	Actc1	0.757231443
Kifap3	1.224831952	Cd59b	1.216220455	Tsga2	0.762010724	Cbx2	0.754824712
Tm9sf4	1.224759436	Ebp	1.215736564	Peg3	0.761685583	Lbr	0.750326451
2300002D11Rik	1.223334928	Hcph	1.21548173	Lig1	0.760435959	Zic3	0.749269644
Adh1	1.222673183	Eno1	1.211040867	2310042N02Rik	0.760076487	Bcat1	0.748999343
Smarca1	1.222658675	Anp32e	1.210334649	Ruvbl2	0.758896234	Slitrk5	0.748098337
Prkr	1.222392421	Pdk1	1.210016024	Gmfg	0.755201166	Rnf134	0.742977796
Hif1a	1.221702384	2700055K07Rik	1.208586622	Ccnb1	0.754415721	En1	0.741983669
Icam1	1.220560893	Chrnb1	1.208399149	Tmprss2	0.754243586	Sort1	0.740720734
Jak1	1.219868421	Smpd3	1.200791657	1700028N11Rik	0.752400096	Syn1	0.740289231
Igf2r	1.21926632	Sh3bgrl2	1.199596499	Syt9	0.752205472	1700013H19Rik	0.739631258
Ehbp1	1.218540953	Crip2	1.197825846	Mif	0.749589814	4930403C10Rik	0.738684111
Calm2	1.218504156	Pdxp	1.194444052	U2surp	0.748914327	Rnu3ip2	0.73768377
Pdlim2	1.216769865	Tpi1	1.190762883	Fcho1	0.747075205	Bicc1	0.737681394
Actn1	1.21658927	Aox3	1.190057829	Biklk	0.746775713	Fkbp11	0.736611949
Gulp1	1.215937399	Adh7	1.189944168	G22p1	0.74620617	Rnf44	0.736156001
Col5a1	1.215214972	Klk24	1.189477799	Morc3	0.744765205	Ephb2	0.735842437
Col28a1	1.214802494	Fbl	1.189285023	Fen1	0.744568255	Csrp2	0.735819922
Hey2	1.211073557	Pcna	1.188789764	Gbif	0.742310662	Psip1	0.73336159
Igfbp7	1.210918937	Vnn3	1.185836689	Dp1l1	0.74229586	Narg1	0.732977816
Akr1b8	1.209560777	G3bp2	1.184234801	1110012J17Rik	0.741138854	Lrrn1	0.730473603
Rab9	1.209309831	Apitd1	1.183583411	Rnf134	0.739903717	Lss	0.726389388
Tceal1	1.208008503	Nfatc2ip	1.183446141	Pop5	0.737374521	B3gnt7	0.725970587
Vegfb	1.207894848	Nes	1.183238815	Sh3tc1	0.73586388	Krt1-18	0.725565263
Rbms1	1.207867227	Dnmt1	1.181777918	2310006J04Rik	0.734069031	Pvrl2	0.725391292
Dusp10	1.206019127	1810010N17Rik	1.181663838	H2afy	0.733242508	Mtap1b	0.725160893
Jak2	1.205916447	Mapk13	1.181451255	Hps3	0.728173569	Tcf7	0.725035384
Crabp1	1.205663437	1700029G01Rik	1.18104495	Trim40	0.72678332	EG436240	0.72478547
Armcx2	1.203752769	Tnfsf9	1.180813318	Impa2	0.72555582	Appbp1	0.724641545
Atxn1	1.202143737	Gpd2	1.180185039	C79407	0.723913899	Nup37	0.722861609
Ddr2	1.201123805	Gsta4	1.178351169	2400009B11Rik	0.722946362	Nup43	0.722472011
Sh3md4	1.200912694	Igfals	1.177822738	Cdc5l	0.721903807	B230104P22Rik	0.722364822
Rnf11	1.196969824	Map3k11	1.176454817	Gls2	0.720450507	Mcm3	0.721941912
Capn6	1.196897116	Kif11	1.176169405	Pygl	0.720057004	Bing4	0.719258336
Inhbb	1.196800707	Siat8b	1.175821713	Mterf	0.719381282	Hnrpdl	0.719238064
Rad23b	1.194958252	Cdc14b	1.175286613	Bxdc1	0.719032303	Elavl1	0.718979026
Cry2	1.193823269	Fignl1	1.174764305	Krt2-8	0.717864035	Rps15a	0.71791217
Flot1	1.191743112	Prok2	1.172720536	Edn2	0.715998165	Gpr19	0.717142937
Tob2	1.19161376	Pip3ap	1.171337885	Fmn2	0.715881993	Efs	0.716165076
Car13	1.191386365	Npy2r	1.17121716	Cdc7	0.714339839	2600005C20Rik	0.715116839
Mmp11	1.188927474	0710001E13Rik	1.170601212	Csrp2	0.713874592	Nsfl1c	0.714953291
Hist2h3b	1.183664841	Espl1	1.169925001	Gtse1	0.713290957	Ngfrap1	0.713812985
Bst2	1.181311762	Gnptab	1.168457463	Pold1	0.71236441	A230050P20Rik	0.7128428
Apbb1ip	1.181158501	Rrm2	1.167944637	Phactr4	0.712134903	Llgl1	0.712168372
Trib2	1.179480456	Bub1b	1.165549625	Igf2bp1	0.71183114	Fmnl3	0.712066292
Serping1	1.179314181	AI316787	1.165071918	B4galt3	0.711097906	Fdps	0.712023387
Mrgprf	1.179044314	Hes6	1.164555465	Sprr1a	0.710030015	Gm50	0.711128344
Lamc1	1.178763369	Eif2b5	1.160941517	5730466H23Rik	0.708731466	2410008J05Rik	0.709633612
Wnt5a	1.177459997	Oact1	1.158814887	Ngfr	0.707314788	D430039N05Rik	0.706364552
Palld	1.176487104	BC022224	1.158487127	6330516O17Rik	0.706739401	Tbx3	0.705929555
Nrn1	1.175179601	Phtf2	1.156860302	2700091N06Rik	0.705914848	Fscn1	0.705749472
Adam12	1.173064709	Pcolce2	1.152109798	Gstk1	0.705894352	AK122525	0.703460687
Pitpnm2	1.171077774	Lrrc34	1.150855038	Rad54l	0.70586481	1700007G11Rik	0.701703134
Rerg	1.170026517	Cryz	1.148660185	Esco2	0.704826262	Rbbp7	0.701473749
Large	1.168612466	Tbc1d8	1.148596492	Ndc80	0.703987182	Pold3	0.698571041
Hist1h2bc	1.168054965	Tssc1	1.146802745	Ddx41	0.703276768	Sox21	0.697647443
Vdr	1.167588653	Cdca8	1.145371001	Spag5	0.700439718	Tgif	0.697507741
Lhfp	1.165466124	Oit1	1.144936281	Nptx2	0.699966056	Skb1	0.697444724
Mcam	1.163932691	Mad2l1	1.144101226	Mkrn3	0.69945729	H1fx	0.69637421
Pdzrn3	1.163453186	Dyrk3	1.143909411	C86302	0.698693216	Notch3	0.696372722
Agrn	1.163131961	Atp6v1c1	1.142559703	Ppp1r10	0.698384361	Ncbp2	0.695501948
Thsd6	1.162583026	Nola2	1.141757749	5330431N19Rik	0.694854758	Gp38	0.695359452
Hist1h3f	1.162136199	Wdr6	1.141479504	Scnn1a	0.694794696	Gbp2	0.695239188
Vip	1.161424404	F11r	1.141137518	Kif18a	0.694244719	Tbl2	0.694084223
Mid1	1.160663432	Cacna2d3	1.140990101	D130058I21Rik	0.693338662	Col9a2	0.693775988
Kctd12	1.159496041	Hspb1	1.140356234	Abi3	0.692252042	Igf2	0.693568751
1190002N15Rik	1.157906578	2610528A15Rik	1.137230053	Fgf8	0.691714513	Nodal	0.691993551
Tmsb10	1.157443633	Mknk2	1.135903558	Sh3yl1	0.691463791	Bccip	0.691975984
Tmem119	1.157022974	Capn5	1.135159583	Aire	0.691161905	6720485C15Rik	0.690440101
2700033K02Rik	1.155770907	Acsl5	1.134106891	Mthfd1	0.690644214	4933424A10Rik	0.690190835
Atf3	1.155623807	Ncl	1.133609087	Timeless	0.688751604	Psx2	0.689849073
Thra	1.155451976	EG433923	1.133536505	Pkp2	0.687770876	6430510M02Rik	0.689309603
Ube2l6	1.155376693	5830411K18Rik	1.130917117	Sp5	0.686371228	3632413B07Rik	0.688572765
Aqp4	1.155215713	BC018222	1.128556035	Taf15	0.686218485	Zfp473	0.68822126
Cxxc1	1.151303556	AI663987	1.128258338	Hspb1	0.685303474	Tmem47	0.688140453
Rgs3	1.147368144	Cdc45l	1.125757418	D11Ertd636e	0.685140772	Xlr4a	0.687447698
Vldlr	1.147199058	OTTMUSG00000(	1.123757775	Bspry	0.684224132	Dek	0.686106709
Hoxb6	1.145339363	Kntc1	1.121091817	Inpp5d	0.683940503	Lisch7	0.682760551
Dscr5	1.144836633	Dst	1.120508149	Narg2	0.683696454	Pcbp3	0.681958827
BC063749	1.14319059	BC036313	1.12040585	2810417H13Rik	0.683108353	2010005A06Rik	0.681049605
Apbb2	1.142941799	Gltp	1.120081722	AI449441	0.682337912	Ly6e	0.679903124
Itm2a	1.14213363	Selenbp1	1.119739244	BC055324	0.681193629	Tex9	0.678964877
Fbln2	1.141529762	Sfrs1	1.116796641	AU067695	0.680893212	Zc3hc1	0.678670244
Timp3	1.140937929	1200014J11Rik	1.116231071	Klf2	0.679864405	Insl6	0.677772311

Col16a1	1.140445755
Eif5	1.139924208
Lrig3	1.138966886
Cxx1c	1.138408792
2810022L02Rik	1.137462422
Pcdhb22	1.136604928
Bbc3	1.136375003
Tgfb1i4	1.13606155
D10Ucla1	1.135720033
1110030H18Rik	1.134957341
Sema3f	1.134092896
Ecm1	1.132848204
Arf5	1.131691867
Sh3d4	1.131644006
Enc1	1.128196701
Apod	1.124710733
Stk3	1.123864216
E130307J07Rik	1.123170797
Gpr64	1.120990389
Zfh4	1.12093371
Axot	1.120398868
Armcx3	1.118644496
Tnfrsf11b	1.118540795
Colm	1.116354236
Mbd1	1.114025083
1110019C08Rik	1.113827292
Pde4d	1.112911122
Eif2s3y	1.112266232
Tmem66	1.111284661
Rhoj	1.110635629
EG433180	1.110131917
Adam9	1.109636116
Sorcs2	1.109292145
P4ha3	1.107394871
BC042901	1.105565756
S100a10	1.105261053
Arih1	1.104150598
Ssfa2	1.103498804
Slc9a3r2	1.103275044
Anxa1	1.102392645
Tac1	1.102314095
Tcf3	1.101360146
Calu	1.100094749
Rora	1.09887525
Pgcp	1.097574648
Cald1	1.096753233
9230117N10Rik	1.09609659
Jag1	1.093659107
Cacna1g	1.092141013
Mmp14	1.092074345
Rcn3	1.091664023
Map3k12	1.089958402
Magee1	1.089784153
Itgav	1.0890433
Rrbp1	1.079656742
BC031853	1.079503969
Ifi35	1.078988296
Anpep	1.077595098
Ppfibp1	1.077416374
Stk35	1.077385769
Nenf	1.077197443
Sparc	1.07712703
Fzd7	1.076734513
BC060615	1.0751122
Slc6a8	1.075080112
Golph4	1.074572268
Mpp1	1.074559132
Adamts1	1.074270611
Gdi1	1.073899925
Ch25h	1.073713683
Cnn3	1.072873035
D230005D02Rik	1.071098443
Pbxip1	1.070910764
Pml	1.070604672
Arl1	1.069974334
D430039N05Rik	1.069634188
BC025575	1.069568576
D1Bwg1363e	1.069395954
Gcap14	1.068750395
Cdr2	1.067946152
Ifitm1	1.067763327
Trim21	1.067337991
Wipi1	1.066554795
Fkbp10	1.066163491
Rnf144	1.06513763
Fzd1	1.064798368
Plscr1	1.064745166
Fstl1	1.063747997
Gpr177	1.063188493
Scara3	1.061618193
E430036I04Rik	1.061206119
B130017I01Rik	1.060785716
Rarg	1.059989399
Rock2	1.059871456
4930403O06Rik	1.058382517
Snx9	1.057816074
Epb4.1l1	1.057767244
Bat1a	1.05751711
Add1	1.057442204
Ngfb	1.056885064
Mylk	1.056034035
Cdkn2b	1.055286491
Cryab	1.054991405
Sec24d	1.052697423
Smarcd3	1.051927792
6430411K18Rik	1.051292784
1810009B06Rik	1.050772527
Fnip1	1.050408341
Idh1	1.049884462
Hist1h2bj	1.04539733
Osr2	1.044615137
Wsb1	1.044162719
Fgfr2	1.043068722
Rab10	1.04198428
Ier5l	1.04176865
Nrg1	1.040574743
Asah1	1.039403785
Itpkc	1.038902483
Tmem9	1.037642034
Adam19	1.037159509
Fzd8	1.034626343
Sncg	1.03445051
Mospd3	1.034306122
A930021H16Rik	1.033065505
Hist1h1c	1.032971939
Ahnak	1.032154443
Nfatc4	1.031436804
Ebf1	1.030373649
Map1lc3a	1.030178149
Hoxa7	1.0283856
Cpeb2	1.026526295
Edg3	1.024761653
Tulp4	1.022349575
4933407N01Rik	1.021737127
Tram1	1.021446976
Vim	1.021286526
Hs6st1	1.021224289
Ccnd2	1.020920382
Zfhx1a	1.020602168
Rnase4	1.019294908
Ly6e	1.018960192
Arhgap24	1.018820182
Akt1s1	1.018110154
St5	1.016615268
Mfap5	1.016370643
Pcf11	1.015891373
Tor3a	1.015578142
Plagl1	1.015019517
Ptges	1.014950341
Rbpms	1.013524446
4931406C07Rik	1.013135402
Lingo2	1.012444766
Acvr1	1.012319357
Mtap1b	1.01210262
B930062P21Rik	1.012098143
Wbscr24	1.010499316
Tmem34	1.010108453
Hand2	1.009803175
U2af1-rs2	1.009593548
Wnt4	1.009135142
Lrig1	1.008661971
Scotin	1.007691503
Ifitm2	1.005019652
Nid2	1.004758757
AI451557	1.002985917
Clmp	1
Rtp4	1
Lyz	-7.25026225
C1qb	-6.089765961
Lyzs	-5.904591227
Laptm5	-5.617687889
Slc38a5	-5.606399084
4732456N10Rik	-5.329773953
Mrc1	-5.282338788
Ms4a6d	-5.117883555
Krt1-14	-5.070021903
C1qg	-5.068361647
Cldn11	-5.018397731

Pop5	1.114845426
Nlk	1.114370715
Ppa1	1.112769846
Ppp1r9a	1.112058507
Ncdn	1.111884878
Kif22	1.109328411
Tmem46	1.105353
Ifitm6	1.105313544
5730466H23Rik	1.103827363
E130309D02Rik	1.102928755
LOC654467	1.102279684
0610009F02Rik	1.102008512
Krt42	1.101467639
Samd10	1.099665465
Zfp367	1.099535674
Mif	1.099147316
Tek	1.09838474
3230401D17Rik	1.098368745
Ndufa4	1.096648248
Hist2h2ab	1.096533795
Psip1	1.095450703
Gart	1.093996899
Ddx27	1.093652019
Slc12a3	1.093286542
Eras	1.092179533
D11Ertd497e	1.092097545
Mns1	1.091716169
Sfxn1	1.090462165
Adrb2	1.089267338
Ly6f	1.088494886
Vrk1	1.086518429
Kif2c	1.086406051
Tdg	1.084764173
2410015N17Rik	1.084352327
LOC434858	1.082599177
Cdyl	1.07717269
Tgm3	1.074305559
Cd3g	1.072808436
Gmfg	1.072366977
Exosc7	1.070081093
Bex2	1.068171503
Mras	1.067925907
D15Ertd621e	1.065765353
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Slc5a9	1.06534649
Farsb	1.064055394
Smn1	1.063145294
4933432P15Rik	1.061519574
Chaf1b	1.061015775
Kif15	1.057963981
Ris2	1.056603353
Zfand6	1.056586713
Aldoa	1.054529678
2610510J17Rik	1.054072437
D830014E11Rik	1.051505438
Mcm4	1.051488735
Umps	1.050645932
Nlgn3	1.049753035
Dner	1.049048181
Poldip2	1.048096005
Klk7	1.045837536
Sfrs2	1.044547007
Dusp16	1.044238531
Prmt5	1.042228235
Kif23	1.041115854
Abi3	1.039855989
Msh2	1.038238804
Fkbp4	1.037156414
Matr3	1.036835055
Hnrpa1	1.035474802
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Lmtk2	1.034363903
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Deadc1	1.033601814
Hsd3b7	1.03355038
6530405K19	1.033444983
Ard1	1.032472211
Phgdhl1	1.031037794
Pnpo	1.030513308
Mrps18b	1.03018214
Mcph1	1.026609469
Mg29	1.025635927
Ppfibp2	1.02498872
Elmo3	1.024846729
Rps24	1.022615683
BC038156	1.022532213
Sec15l1	1.022186763
Pigq	1.021904693
Dars	1.020479866
Pvrl3	1.019506012
Clspn	1.019300556
Ywhaz	1.017908441
Luc7l	1.017381062
Psmc5	1.016939862
Rps6ka5	1.015305629
Rad51	1.015092525
Erh	1.015036453
Serbp1	1.014936129
Coro1c	1.014751125
Ubap2	1.013487141
Bat1a	1.012833865
Fubp1	1.012128192
Cdc25c	1.01110381
Kctd20	1.010507658
2410001E19Rik	1.010124217
Fancd2	1.00810505
Chaf1a	1.007806143
Rpl29	1.007324771
5832424M12	1.005915209
Mgarp	1.005570258
Acot8	1.0050829
1200006F02Rik	1.004558282
Gbas	1.00433459
2610024G14Rik	1.004230367
Cops4	1.003959912
Rpo1-3	1.00386371
Rps6ka2	1.002608066
B230208J24Rik	1.00080575
Parl	1.000667698
Atp6v1c2	1
Thy1	-5.218218942
Dlk1	-4.987309175
Reg1	-4.498197744
Ptn	-4.463659075
Mmp3	-4.206353219
Lpl	-4.082227952
Lum	-3.830350057
Serpina3g	-3.803560274
Aebp1	-3.7208714
Igfbp7	-3.710233871
Dcn	-3.703901844
Cxcl12	-3.700538098
Adamts2	-3.671241702
Mfap4	-3.628044483
Pdgfra	-3.581795222
Col5a1	-3.574118113
Cyp2f2	-3.553736707
Dpt	-3.528223333
Spp1	-3.522620223
Twist2	-3.485713579
Fbln1	-3.46067425
Avpr1a	-3.42607155
Ptx3	-3.42367546
Itga11	-3.367229493
Loxl1	-3.364483037
Bicc1	-3.319363501
Serpinf1	-3.302646548
Cd248	-3.245235128
Plac8	-3.24252614
Col16a1	-3.198360204
Lox	-3.167208097
Col12a1	-3.159188887
Dkk3	-3.129825282
Lsp1	-3.127797104
Col6a2	-3.117108303
Cpxm1	-3.112591826
Nrp	-3.065895962
Col1a1	-3.055229905
Il1rl1	-3.037389186
Copz2	-3.034184926
Ednra	-3.03030577
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Ifit3	-2.992236447
Gdf10	-2.990635466
Ch25h	-2.989629736
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C1qtnf2	-2.962143312
Tnc	-2.944056395
Mfap2	-2.930713898
Fgf7	-2.897962078
Crabp1	-2.887884597
Polydom	-2.87544678
Smarca1	-2.872429471
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Agpt2	-2.869186933
Cyp1b1	-2.861331913
Rbms3	-2.836844296

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EG243881	0.678071905
Llglh2	0.677413076
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Sfrs2	0.67557994
2310061G07Rik	0.675455957
Ska3	0.674692661
Elmo3	0.674586809
Rhebl1	0.673771768
AB041544	0.673236437
Arhgap4	0.67247403
Ppif	0.671013714
Nr6a1	0.670405437
Card4	0.669566309
Fntb	0.668858727
B3gnt7	0.66871385
Ly6g6e	0.668185978
Hcfc1	0.666780029
Casp2	0.666148319
Slc39a8	0.664815808
Top2a	0.664642623
BC027088	0.664065047
Phox2a	0.663548341
Fzr1	0.663036174
BC037006	0.660109277
Trh	0.659593561
ZBTB45	0.656999681
Wdr5	0.656623486
BC011248	0.656026143
Sall1	0.655665492
Clspn	0.65550398
Akap12	0.654656377
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Gbp1	0.654040883
Cpsf5	0.653163614
Adam19	0.652208902
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4931431L11Rik	0.649571582
Aox3	0.649262817
1600023A02Rik	0.648986646
DXImx50e	0.648964664
Alox15b	0.648649357
Gdf3	0.648569155
AA408296	0.648527629
Ube2c	0.648324562
Jtv1	0.646452529
Gemin4	0.645345835
Cotl1	0.64455806
Zfp322a	0.643261141
Dnmt1	0.643046521
Pnma2	0.642788928
Cenph	0.641912242
Clcn3	0.640815735
Txnip	0.640766405
Rad51	0.640354501
Helz	0.639720308
Dyrk3	0.639533256
Lmnb2	0.6395216
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Tcof1	0.638921849
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2700029E10Rik	0.637610857
Nasp	0.637566313
4921537D05Rik	0.636357484
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Slc28a1	0.631965001
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D6Wsu163e	0.631318136
Rfx4	0.630369712
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Ssx2ip	0.626373995
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2610318I01Rik	0.625107589
Kif15	0.624984347
Prok2	0.624835883
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Add3	0.620865048
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4930547N16Rik	0.616895364
St14	0.61667136
Tipin	0.616307636
D030056L22	0.616193825
Gpr85	0.615659298
Galk1	0.615457004
Esam1	0.6142242
BC003277	0.613526161
Sssca1	0.612713556
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Pdhb	0.611060455
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Slc17a6	0.609111779
Mcm5	0.609102921
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Itgb7	0.605688527
Mrps22	0.605541898
Aldh5a1	0.605282485
Cdca5	0.604801987
Gng13	0.60442693
1600016N20Rik	0.604379955
Wbscr27	0.603982408
Hist2h2ac	0.603344659
Mcam	0.603263317
Zfp296	0.603180359
Snrpa1	0.602854271
Rad1	0.601420122
Nos3as	0.601207831
Prc1	0.600328856
Brp17	0.600267162
Eftud2	0.600154755
Lin28	0.599588064
Mad2l1	0.599315782
Usp37	0.599133401
Gstp1	0.598044129
Abcg1	0.597959841
Prl2c3	0.597515551
Smcr7l	0.596710161
Trub2	0.596452674
Mrpl53	0.596089725
Ahsg	0.596046
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Zfp41	0.593059968
Recql4	0.592967387
Agpat4	0.592215456
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2310057J16Rik	0.590863102
Chek2	0.590517745
Tk1	0.589705893
Cugbp1	0.589466055
2310002J15Rik	0.588298213
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Tfam	0.587341224
Tead4	0.587193358
Cdca2	0.586876207
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Nedd1	0.585633522
Solt	0.584962501
Suhw2	0.584320304
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Actn2	0.583851453
Hist1h3d	0.583195033
Atp1b1	0.583041468
Ccdc58	0.58296951
2410015N17Rik	0.582820125
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Vil2	0.581574566
Zfp160	0.579191713
Psme4	0.578964274
Brf2	0.578435235
Rem2	0.578382352
Rabl3	0.577502638
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A030007D23Rik	0.574458064
Ifitm1	0.574356695
Rdbp	0.574215693
Bnip1	0.573541322
1500001L15Rik	0.573398701
Mre11a	0.572838942
2610009I02Rik	0.572729978
Mcm3	0.572357094
4933411K20Rik	0.572285815
Dctd	0.571998168
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Agrn	0.668032859
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Thy1	0.659693376
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Asna1	0.657983096
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Bxdc2	0.631633871
Pycr2	0.631294818
L3mbtl2	0.6308758
Ndp52	0.630634359
Mtf2	0.630534674
Tulp2	0.630377959
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Sh3bgrl3	0.626552843
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Rpl23	0.624077682
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Mlf2	0.585643122
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Mdm1	0.584284064
Lsm5	0.583600331
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Inpp5f	0.580813246
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Nol9	0.579750177
Pkm	0.579557428

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Fcer1g	-4.778519591
Klk6	-4.641195877
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Ngfa	-4.496724774
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Bglap2	-4.434730896
Atp2a3	-4.406103969
Slc6a12	-4.325453782
Cxcl4	-4.325014075
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Emr1	-4.032321287
Ly6g6c	-4.019116057
Msr2	-3.982230912
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Aif1	-3.397734985
Grb7	-3.38256442
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Cd68	-3.315015312
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Fcrl3	-3.264550204
Ltf	-3.213017696
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Krt1-17	-3.192785959
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Alox5ap	-3.173866794
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Bglap-rs1	-3.139358285
Mgarp	-3.06062277
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Slc2a6	-3.031423242
Casp1	-3.007768974
Trem2	-2.988387844
Lmo2	-2.969528591
Ccr5	-2.914883386
Hemp1	-2.914817511
Itgb4	-2.878118857
Ccl12	-2.872872333
Ush1c	-2.870967429
Stab1	-2.837500479
Gmfg	-2.83507568
Fbxo15	-2.829563093
Lgals7	-2.819027506
Fgd2	-2.785250129
Fetub	-2.772460132
Rpl7a	-2.764015278
Pfkp	-2.761247942
Slpi	-2.751769198
Tyrobp	-2.712550556
Reep1	-2.711363571
Luzp2	-2.683684586
L1td1	-2.664904445
Cldn4	-2.634840106
Rassf4	-2.632268215
Ms4a7	-2.632160233
Lbp	-2.621497243
5730453H04Rik	-2.604039738
Fgfbp1	-2.603415264
AW491445	-2.586689245
Msln	-2.58445136
Aqp3	-2.56780778
Krtdap	-2.550245818
1600023A02Rik	-2.536129908
Krt1-19	-2.507882228
Trf	-2.495634737
Ppp1r1b	-2.486047475
Ramp3	-2.484083138
Aldh3a1	-2.47919522
Krt2-8	-2.471272733
Vav1	-2.456752518
Reln	-2.453815827
Tfrc	-2.449022118
Btk	-2.445287436
Pcdh21	-2.444338056
1110061N23Rik	-2.439146555
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4732474A20Rik	-2.433420959
Mapk13	-2.421592345
Cldn3	-2.418225777
Evi2a	-2.414383957
Edn2	-2.401533235
Tacstd2	-2.395474488
Arg1	-2.388900649
Bex4	-2.386829797
Cd14	-2.350178572
Ncf4	-2.349458777
C1qa	-2.325326671
Avpi1	-2.324679198
Cd86	-2.317810028
Sprr2d	-2.31585358
Apoc4	-2.312611766
Pkp1	-2.307613498
Klhl6	-2.283881191
Ly86	-2.282887679
Mcm6	-2.263767296
P2ry5	-2.26359697
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Gna14	-2.248772826
Cdca7	-2.248063179
Clecsf8	-2.240504717
Itpk1	-2.240172965
Pem	-2.235755161
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Tm4sf3	-2.222059428
Myo1f	-2.204211193
Plcg2	-2.200455429
Tuft1	-2.189142917
St6gal1	-2.166225628
Ccl3	-2.151800454
Chchd4	-2.14998066
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Cotl1	-2.141063667
Aatk	-2.133071277
Itga3	-2.126300187
Dgat2	-2.123168042
Otx1	-2.113524661
Elf3	-2.107528464
2700050C12Rik	-2.107189246
Rps6ka1	-2.10364472
BC049354	-2.09836513
2310006J04Rik	-2.086410419
1810010N17Rik	-2.082211671
Ccl9	-2.075822508
Alox12b	-2.056435946
Cd53	-2.050444499
Aim1	-2.05030748
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Nrip3	-2.044888956
Apoc1	-2.035281132
Pmch	-2.035084829
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Atp1b3	-2.02969373
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Ckmt1	-2.013369846
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Catnal1	-1.964662078
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Tlr7	-1.958777337
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Ii	-1.939470385
Myo1g	-1.938307678
Clec4n	-1.930528024
Elavl2	-1.92977082
2310046K01Rik	-1.920172117
Osm	-1.916979413
Klk24	-1.911943823
Hs3st3a1	-1.907633273
Ptpn18	-1.900920226
Arl11	-1.900525086
6330406L22Rik	-1.895517564
Siat10	-1.890985414
Stxbp2	-1.88367283
Ndrl	-1.87363021
Slco2b1	-1.871415794
Phc1	-1.871232197
Prkcz	-1.866144253
Mif	-1.861161264
Lcp1	-1.85451714
Tpd52	-1.852559209
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D930038M13Rik	-2.824088415
Serpina3n	-2.810113799
Wisp2	-2.796208985
Thbs2	-2.786828277
Ctsk	-2.765235722
Plf2	-2.740740168
2310016C16Rik	-2.725217934
Olfml3	-2.724821803
Olfml2b	-2.718443511
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Sfrp2	-2.712015695
Gpc3	-2.686248366
Prl2c3	-2.674436952
Wisp1	-2.673865223
Gpx3	-2.666734871
Cyp7b1	-2.654124525
Fgf10	-2.649584277
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Hic1	-2.626682486
Tgfb1i1	-2.624490865
Flt1	-2.61147363
Cdkn1c	-2.609889265
Timp2	-2.584136419
H19	-2.578729986
C2	-2.578375725
Acta2	-2.577780159
Gpr49	-2.572381573
Gng8	-2.565840347
Eln	-2.562888333
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Nnmt	-2.540589829
Srpx2	-2.528131278
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Rerg	-2.516372515
Igfbp4	-2.514363142
Epb4.1l3	-2.508572809
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Ppap2b	-2.480470364
Sdc3	-2.473828502
Gas6	-2.456252928
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Cdo1	-2.45025844
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Prickle1	-2.444344474
C1qtnf3	-2.439334049
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Slc1a3	-2.421772333
Cav1	-2.419125728
Cxcl1	-2.414981562
Glipr2	-2.413932409
Lrrc15	-2.407124482
Col6a1	-2.402176174
Bgn	-2.399084786
Slit2	-2.397396188
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Myh10	-2.377311544
Cdh3	-2.374658756
Cklfsf3	-2.36858332
Sema3f	-2.366442158
Maged2	-2.36489004
Aldh1l2	-2.356968665
Tgfbr3	-2.353595025
Mylk	-2.345906958
Igfbp3	-2.343394637
Podn	-2.339999668
Aqp1	-2.334047142
Mfap5	-2.326098284
Fbln2	-2.318774116
Gap43	-2.315926099
Bmp1	-2.312545796
Nope	-2.311159549
Ldb2	-2.310527428
Pftk1	-2.289133442
Fst	-2.28800325
Igf2	-2.284795168
6330406I15Rik	-2.28061379
Arhgap20	-2.270089163
Slit3	-2.266626392
Figf	-2.259168928
Vcam1	-2.256633708
Adamts5	-2.231138824
Galntl4	-2.224721979
Reg3g	-2.222392421
Tnxb	-2.222205386
Inhba	-2.203567171
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D230005D02Rik	-2.193151553
Vegfc	-2.179959766
Steap2	-2.179015738
Tbxa2r	-2.178460813
Fhl1	-2.176322773
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Mrvi1	-2.161700234
Mmp23	-2.155900637
Ube1l	-2.141270732
Fmnl3	-2.132152495
Mmp13	-2.127656259
Efemp2	-2.124497768
0610041G09Rik	-2.118562663
1810054O13Rik	-2.116727116
Reck	-2.115727707
Hs3st1	-2.101616274
Mmp14	-2.098649807
Itgbl1	-2.097170128
Mmp2	-2.090653763
Sema5a	-2.086120175
Rgs16	-2.08181505
1810057P16Rik	-2.07604841
Lrig3	-2.07571971
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Il11ra1	-2.061694922
Serpine2	-2.059555324
Ptpns1	-2.054614363
9330196J05Rik	-2.052485261
Tnfaip2	-2.051743575
Casp4	-2.050463222
Ephb2	-2.047010068
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Zcchc5	-2.037409192
Thbs1	-2.035599491
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Sema3a	-2.027580809
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Emilin2	-2.021061616
Igfbp6	-2.017100497
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6330403K07Rik	-1.995775414
Tpm2	-1.991403976
Nfkbiz	-1.98948649
Ifit2	-1.987408423
Sorcs2	-1.986033821
Jundm2	-1.984425595
Timp3	-1.981246931
Fhl2	-1.977608244
Pdlim2	-1.971099502
P2ry6	-1.963474124
Pmp22	-1.962577559
Adam19	-1.957944546
Ecm1	-1.955728859
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Sfrp1	-1.947603989
Cugbp2	-1.938368131
Usp18	-1.936447137
Col18a1	-1.924730318
Thbd	-1.920760079
Osr2	-1.911881789
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Steap	-1.904241017
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Inhbb	-1.898367972
Rcn3	-1.897711169
Kdelr3	-1.888211147
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Gstm2	-1.882947774
Leprel2	-1.882493026
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Gpx7	-1.875501458
Angptl2	-1.874024459
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Col24a1	-1.856449472
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Pvrl2	-1.850187963
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Vldlr	-1.838863526

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Pdxp	0.569241283
Mybl2	0.568755211
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Gtf2h3	0.568579796
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Glrx	0.567231666
Igf2bp2	0.56703819
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2810408M09Rik	0.565018928
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6330503K22Rik	0.563940915
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Iap	0.563746385
Hist1h2an	0.563222047
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Stk6	0.562669239
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Klk10	0.560099524
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Alox3	0.558079207
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Trim59	0.557132101
Sf3b5	0.555624305
9430034D17Rik	0.555614675
Paox	0.555481632
Mutyh	0.555248277
3732413I11Rik	0.555245795
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Hist1h2bg	0.545333125
Lama1	0.544911553
Ehmt1	0.544883094
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BC060631	0.543035975
1810060D16Rik	0.542120075
Rhoc	0.541732449
Fdps	0.541438245
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Lck	0.540961504
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9330161F08Rik	0.540325973
Ttc4	0.539835863
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Usp28	0.53319153
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Adat1	0.529961112
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Gsta4	0.529394746
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Lmnb1	0.527886612
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5730568A12Rik	0.527385225
Atpbd3	0.527335683
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Edg4	0.576951958
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Fkbp4	0.576369445
6330534C20Rik	0.576029376
Gstp2	0.576000673
40424	0.575743971
4930506L13Rik	0.574838283
Aaas	0.574615704
Cdc34	0.573938276
Gng2	0.572971766
2810037C14Rik	0.572062012
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Fubp1	0.569293781
4833424P18Rik	0.567844726
Ccrn4l	0.567323764
Eif4ebp1	0.566493599
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Ruvbl1	0.565092375
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Tmpo	0.562973497
6330415F13Rik	0.562293425
Zfp219	0.561714431
Cpxm1	0.56097786
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D630023F18Rik	0.549927626
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Amph	0.549388788
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Chc1	0.546106565
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St6galnac2	0.544062547
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Smu1	0.534210378
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Cdca3	0.531129636
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Arhgap8	0.529578692
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Triml1	0.527818594
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Bcas1	0.524628731
Pgm2	0.524567903
Nme4	0.524321945
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Aqr	0.523737648
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Trp53bp1	0.523360251
Rps6kl1	0.523195091
Ndufs4	0.522357964
Fcf1	0.522069402
Pwp2	0.521878671
Ndor1	0.521636565
Idh1	0.520759207
Dolpp1	0.520612089
4930538D17Rik	0.52052891
Ilf3	0.520374422
6430595O10Rik	0.519764235
Slc13a4	0.519528055
Src	0.518705657
2310061I09Rik	0.518516761
Psmd12	0.518315834
Nup62	0.517744278
Rgs10	0.517471474
Llglh2	0.517018738
B130017I01Rik	0.516893826
Nup50	0.516668038
0610010K14Rik	0.51607236
Ass1	0.515682986
Suhw2	0.51521537
1700021C14Rik	0.515051441
2610507L03Rik	0.514691422
Ptpns1	0.514079015
Cdv3	0.514074928
Tcf3	0.513838166
1810073P09Rik	0.513527363
Prss19	0.513513017
Mvd	0.513405576
Ttyh1	0.513242205
Catnal1	0.51305206
Hrsp12	0.5129297
Mgarp	0.51290901
Sfrs2	0.51286239
Serpine2	0.512842285
Odc1	0.512534235
Trim33	0.512327527
Hist1h2bn	0.511308184
A930009M04Rik	0.510972435
Uhrf2	0.510809744
Otx1	0.510700963
Lrpprc	0.510474055
AI326906	0.51033632
Plekha5	0.509949146
D130058I21Rik	0.508867054
Nipsnap3b	0.508751934

Rab8b	-1.848639122	Mx2	-1.836385616	Abcf2	0.517674371	Mpdz	0.508464363
Ret	-1.846927848	Pkd2	-1.83509488	Dact2	0.517595524	Nfyb	0.508452621
Angptl4	-1.845131573	6430411K18Rik	-1.832773371	Tcea3	0.517233411	Ccne1	0.508321832
Stard8	-1.844400283	Ccl11	-1.832193228	1700025B16Rik	0.517217894	Ptdsr	0.508253419
9030611O19Rik	-1.842632019	1190007F08Rik	-1.826080911	Mrps12	0.516166176	Ric3	0.507500526
Insm1	-1.84100266	Bcl11b	-1.822528325	Ezh2	0.515699838	Gad1	0.507207343
Edg7	-1.836912429	Gpr23	-1.818992859	LOC667250	0.515663645	Gpr23	0.507189407
Prkch	-1.827009819	Gp38	-1.815822323	Mif4gd	0.515552599	Snapc3	0.506959989
Pak4	-1.824515473	Lbh	-1.813687171	Ncl	0.514746911	Eed	0.505856931
Nipsnap1	-1.823574641	Ghr	-1.810362531	9430015G10Rik	0.514203204	Pelo	0.505613265
Nudt11	-1.821976354	Rgs10	-1.808886446	C330018L13Rik	0.513926563	Tial1	0.505170762
Sort1	-1.821402697	Slc9a3r2	-1.806701528	Mal	0.51369142	Smyd5	0.505062313
Stmn2	-1.821177446	Msx1	-1.798012494	Acp6	0.513357013	Acrbp	0.504979625
Espn	-1.792276148	Ptgis	-1.797302748	D030060M11Rik	0.513129756	Twsg1	0.504566265
Acas2l	-1.78447631	Igf1	-1.793738652	BC016226	0.512648296	Grm6	0.504472583
Gngt2	-1.783276939	Apbb2	-1.790012313	Dlg7	0.512485839	Gls2	0.504453133
9130213B05Rik	-1.778209936	Il6st	-1.787518506	2310004L02Rik	0.511979796	Lyar	0.504003931
Cd83	-1.775784843	Pltp	-1.785747031	AW540478	0.511745163	BC018242	0.504001584
Eppk1	-1.771101934	BC099439	-1.782465623	Arl6ip4	0.511557435	Mat2a	0.503804273
Nt5c3	-1.765026487	Csf1	-1.777915498	Pml	0.51123746	Snrpd1	0.503636418
Hmgb2l1	-1.763431243	Stk17b	-1.776373979	Mipep	0.51107779	Ddx18	0.503474785
Sult4a1	-1.758366229	6530401D17Rik	-1.776047065	Stk4	0.510893139	Thoc1	0.5024632
E130012A19Rik	-1.750704729	Has2	-1.775522591	Hist1h3c	0.510780688	Rab15	0.502445268
H2-Ab1	-1.750507328	Icam1	-1.770712217	BC027061	0.510498467	MGC58818	0.502094234
Coch	-1.748461233	Lphn3	-1.770561563	Wdhd1	0.510054242	Fbxl10	0.501095739
Ctse	-1.747760797	H6pd	-1.768127657	1110061N23Rik	0.509977786	Psat1	0.500448821
Pglyrp1	-1.746966986	Slc39a13	-1.761481874	BC017634	0.509888509	1190005I06Rik	0.500090144
Itga7	-1.744570752	Sertad4	-1.758598699	Ddx18	0.509870143	Chek1	0.499979583
Sytl1	-1.743999186	B130017I01Rik	-1.757541956	Pithd1	0.509544896	Mphosph6	0.499842471
BC040774	-1.743847695	Adamts1	-1.754745007	Eed	0.509524366	Stat4	0.499627671
Car12	-1.742712788	1200009O22Rik	-1.753894109	Ifdr1	0.509070735	Pls3	0.499208863
Osbpl3	-1.738732187	Ltbp3	-1.747758473	Plch2	0.508597675	Trub2	0.499075981
Prom2	-1.732924429	Nfib	-1.742170108	Cope	0.507882456	Shroom3	0.498966393
Slc35d3	-1.721334942	Atf5	-1.740625441	Bms1l	0.507815807	Thsd2	0.498754359
Selenbp1	-1.719892081	Sdpr	-1.735926242	1110025F24Rik	0.507153457	Acy1	0.498432537
Igfals	-1.714924163	Akr1b8	-1.733246937	D11Ertd707e	0.507087129	Btbd14b	0.498272767
Tcfap2c	-1.709188029	Man2a1	-1.728616213	Pak4	0.507022666	Ctdp1	0.498154548
2310042N02Rik	-1.706707773	Mest	-1.727920455	3930402F13Rik	0.506861763	Arfgap1	0.497958459
BC013481	-1.697094235	Rnf144	-1.727459014	Hdac1	0.506658586	2310057D15Rik	0.497941594
Sla	-1.689972719	Tbc1d2b	-1.727389335	3300001G02Rik	0.506345493	Lypla1	0.49727576
Pdxp	-1.689319457	Irgm	-1.709075012	2610019I03Rik	0.506305557	2010003J03Rik	0.497029956
Ctsc	-1.684842863	LOC381480	-1.707549106	2600003E23Rik	0.506219385	Gpsm1	0.496487313
1110021N19Rik	-1.676877127	Anpep	-1.70576705	5930416I19Rik	0.506124408	Rfx2	0.496299474
BC032204	-1.675505592	Fbn1	-1.705050352	Mad2l2	0.50589093	Zfp278	0.496132824
Apcdd1	-1.674955647	Magee1	-1.701122069	Rnf20	0.505707858	Bst2	0.494764692
Cd84	-1.671041703	1700023M03Rik	-1.7002872	Qdpr	0.505333425	Col1a1	0.494764692
AA467197	-1.668738687	Angptl7	-1.699490889	Fbxo42	0.505212507	Gprin1	0.494374869
Mcm5	-1.665211889	D430039N05Rik	-1.697010444	Nudt4	0.5050697	Kpnb1	0.493697443
E2f2	-1.65971429	Tgfbi	-1.695073356	Dph2	0.505067309	Ypel1	0.493588148
A130092J06Rik	-1.658246927	Fkbp9	-1.69009188	Srfbp1	0.504355743	4432409M07Rik	0.493473485
Mmp9	-1.649379229	Trim30	-1.685276117	Plcg2	0.503604662	Dars	0.492847125
Avil	-1.648865553	Antxr1	-1.682900437	Slc38a2	0.503583738	BC006583	0.492598483
Plek	-1.641724151	Chodl	-1.682530897	Pcbp1	0.503517441	BC016423	0.492415441
Ebi2	-1.641269942	Nedd9	-1.679136676	Gstt2	0.503040777	Dscr2	0.492240596
Syt14l	-1.638715459	Cxcl5	-1.678361341	Gpatch2	0.503002409	Dpysl4	0.492131851
Cyp2s1	-1.638362195	Igtp	-1.676168968	Psmb3	0.502875593	Cdca4	0.491734231
Mbp	-1.638130088	Hoxc9	-1.67262091	F730047E07Rik	0.502800184	Hnrpf	0.491189097
Krt1-13	-1.636036685	Serpinh1	-1.672525533	Scrn2	0.502500341	Sfrs1	0.49049827
Drp2	-1.63297675	Aoc3	-1.669851398	Taldo1	0.502472903	Dhx9	0.490399499
Snrpg	-1.628960056	Adam12	-1.665809961	Sh3d18	0.502262605	C77032	0.489678805
Hk3	-1.628717031	B2m	-1.665200712	Cmas	0.502156883	Zfp334	0.488553449
Gpr65	-1.627487117	Rarres2	-1.662690866	Nr5a2	0.502009711	Slc40a1	0.48815812
Rpl24	-1.625385769	Pcdh7	-1.662669069	Khdc3	0.501852375	Cxxc1	0.487488955
AI467606	-1.623126872	Mapre2	-1.661444203	Ubadc1	0.501558704	Cdr2	0.487320939
Kcnab2	-1.618909833	Gsn	-1.660614708	Gpr20	0.501171836	Hectd2	0.487002252
Cenpa	-1.616294702	Nlgn2	-1.659911689	Mrps31	0.501141104	Epha2	0.486785543
Kcnk1	-1.610751182	Col5a2	-1.658266633	Porcn	0.500964287	Flrt3	0.486768869
Ndg2	-1.603435738	Grb14	-1.657738903	Uqcrc1	0.499665442	Usp52	0.486743155
Liph	-1.602474901	Mlkl	-1.644305791	Ppan	0.499420948	Hexa	0.486296182
Clec4a3	-1.596264177	E130203B14Rik	-1.641335432	Oit1	0.498919909	Gpiap1	0.485931232
Garnl4	-1.594737309	Sprr2k	-1.640276934	Toe1	0.498649386	B430119L13Rik	0.485426827
Ctsh	-1.593435773	Enc1	-1.638833256	Fabp5	0.497793338	A930034L06Rik	0.485426827
E030006K04Rik	-1.593411691	H2-T17	-1.638809787	Chaf1a	0.496970315	Zfp423	0.484991033
Als2	-1.588598021	Cbfa2t1h	-1.638024773	Xab1	0.496709764	Slc16a3	0.484603841
Pfdn2	-1.587202531	Hoxc6	-1.636659756	Crsp9	0.496470476	Tardbp	0.484572572
Oact1	-1.584962501	Siat4a	-1.619576256	Bcl7a	0.496190985	Chga	0.484512572
Gng13	-1.57910246	Rab34	-1.619212063	Hrc	0.496186567	BC030867	0.484004752
Cyp27a1	-1.578189272	Fkbp11	-1.61792386	Ap2a1	0.496093752	Has2	0.483836496
Tspan32	-1.5775307	Tmem98	-1.617217718	Mrpl54	0.495935591	Nme7	0.48378775
Krt2-6b	-1.575247346	Tm4sf6	-1.613766529	Hk2	0.495853951	Slc5a5	0.4835391
Was	-1.574259966	1300018P11Rik	-1.60929183	Pias4	0.495805973	2310007F21Rik	0.483442326
Lpxn	-1.573839122	Colec12	-1.608809243	Smtn	0.495584244	Scly	0.483329886
Ehd4	-1.571236969	Pros1	-1.60853402	Trp53rk	0.49546435	Slc9a3r1	0.48322804
Clcn3	-1.571056899	3110050N22Rik	-1.606641923	2700097O09Rik	0.495344189	Eif5	0.482476772
Mapt	-1.569365646	Ifi47	-1.600210495	Brp16	0.494952335	Pdcd7	0.482435115
LOC434858	-1.562202404	A230050P20Rik	-1.595067807	Sp6	0.49490788	Eif4ebp2	0.481307091
AI847670	-1.560704318	Gbp4	-1.588070845	D12Ertd553e	0.494783904	Ints5	0.48096478
Psmd4	-1.557976248	Il31ra	-1.587718366	2310050B20Rik	0.494430911	Sez6	0.480862135
Abi3	-1.55776669	Npr2	-1.585487403	Cdc45l	0.494416347	Rpp30	0.480636368
Brp17	-1.554190152	4930422J18Rik	-1.584346622	Melk	0.492838695	Rarsl	0.479653375
Tspan7	-1.551241883	Lhfpl2	-1.581976172	Aytl2	0.492703993	2700084L22Rik	0.479580031
Cdc20	-1.550008733	Elk3	-1.581032295	Gnpda1	0.49268788	Tuba1b	0.479256707
Arhgap4	-1.547396309	Arhgap24	-1.581031449	Ddef2	0.492481585	Chst8	0.479099207
1810046I24Rik	-1.545687352	Agrn	-1.58015603	LOC211660	0.492313213	Pik3r3	0.478952796
Arrb2	-1.543142325	Saa3	-1.57779598	Ldh1	0.491786582	Cpsf1	0.478626476
B230208J24Rik	-1.539661375	Mfge8	-1.576534214	Crlf3	0.491782774	Psors1c2	0.478047297
BC003277	-1.539601967	LOC217066	-1.573099496	Stk17b	0.491754447	Olfml3	0.477919291
Med18	-1.519227641	Cdkn2b	-1.572558813	2310033P09Rik	0.491617185	Wdr77	0.477869268
Cbr2	-1.516912187	Nfatc4	-1.572125995	Plcb4	0.491450615	Krt42	0.477484806
1700057K13Rik	-1.516056664	Sec24d	-1.570545728	Plagl2	0.491398089	Gca	0.47740936
Ppp1r9a	-1.514850588	Crtap	-1.569674785	Tmprss4	0.491359783	Nudc-ps1	0.476997491
Lgmn	-1.504759251	Chst2	-1.567271353	Lypla1	0.49129053	Gdf3	0.476694091
Cd151	-1.503404861	AI451557	-1.560317299	3300001P08Rik	0.49055883	LOC245128	0.47662093
Zic3	-1.502985199	Cxcl14	-1.559928142	Tyms	0.490056263	Mep1b	0.476605323
Ngfr	-1.50163939	Tmed3	-1.559081038	BC037034	0.489764612	Meox1	0.476534996
P2ry6	-1.501239995	Cxcl10	-1.551928544	Klf5	0.489707824	Zswim4	0.47616743
Acpp	-1.4973225	Apob48r	-1.551191764	Zfp11	0.489607882	Acly	0.475483105
Lyl1	-1.490605376	G1p2	-1.550302959	Vrk1	0.489542936	Sox9	0.475104068
Plek2	-1.487804344	6030410K14Rik	-1.549410258	1810007P19Rik	0.489083851	Tle1	0.473574723
Sesn1	-1.479148381	Fkbp7	-1.549133199	Pigo	0.488979718	Atm	0.473385484
2410001E19Rik	-1.473712345	Gpr124	-1.546323473	Sfrs9	0.488434821	Dlk1	0.473118173
Fah	-1.473356647	Gpr153	-1.543674292	Elovl6	0.488407429	Sfpq	0.472960414
Pi16	-1.4731516	Lgals3bp	-1.542982123	C77668	0.488141605	Mdn1	0.472739309
Cln3	-1.469420801	Rasl11b	-1.542949384	Lrmp	0.487627559	Idnk	0.47270284
3300001G02Rik	-1.461589838	Ptges3l	-1.542730185	Eppk1	0.487354705	1110033J19Rik	0.472702186
Tnfaip8l2	-1.459143339	Sqrdl	-1.540192631	Smarca4	0.487138548	Mmp15	0.472659531
Prx	-1.457798071	Mpp1	-1.538144346	1810019J16Rik	0.487064857	Dnd1	0.472602787
Rangap1	-1.454027649	1110030H18Rik	-1.537611116	Sorl1	0.486999247	Atp1b2	0.472187626
4930504E06Rik	-1.450736873	Adm	-1.534521377	Pet112l	0.48697271	Pfkm	0.472166855
A030007L17Rik	-1.44969074	Plekha2	-1.533992888	Noc4	0.48623642	Adssl1	0.471953539
Kynu	-1.449456438	BC029169	-1.533278345	Znrd1	0.485797321	Hist1h3h	0.471912021
Ripk4	-1.448862377	Sh3bgrl3	-1.530747369	Dolpp1	0.485684589	Eif2s2	0.471829533
Igfbp2	-1.448618789	Sgk	-1.528737155	Cenpl	0.485590779	Ash2l	0.47171531
Aldh3b1	-1.444930736	Col4a5	-1.527247003	Tpmt	0.485426827	Ddah2	0.471463592
Nt5e	-1.44370911	Tcea3	-1.520612089	Mta3	0.485392693	Srp9	0.471024027
Exosc7	-1.439258078	Gns	-1.520290978	2700082D03Rik	0.485146447	Tubb4	0.470765647
Lst1	-1.438618051	Smtn	-1.513155195	Ppp1r1l1	0.484156663	Tmem170	0.470629825
Sepp1	-1.436153356	Adra2a	-1.511284603	1110001A07Rik	0.484072331	Aars	0.470390319
Mcm10	-1.434468951	H2-T23	-1.509139287	Mbp	0.483565735	Gng5	0.470355802
Sfxn1	-1.432853595	Pea15	-1.508556462	Tarbp2	0.483396292	Tdrkh	0.470142099
EG622339	-1.429651262	Lgals1	-1.50744594	2610209N15Rik	0.483255728	4933405K07Rik	0.469698716
Clrn3	-1.42412475	Micall2	-1.506865078	Grhpr	0.482952614	Pftk1	0.469485283
1200006F02Rik	-1.423572498	Hoxd8	-1.500521211	Bcl2l12	0.482424339	Suz12	0.469457081
Gpr20	-1.423156232	Adcy4	-1.497289093	A630042L21Rik	0.482074202	Ankrd6	0.469121472
Cxadr	-1.422260893	Fgl2	-1.496997591	Suv420h2	0.482016199	Esco2	0.468681023
AK129128	-1.417578798	Rhoc	-1.496675968	B230208J24Rik	0.48173972	Nr1h2	0.468591215
Ryr3	-1.415037499	Vdr	-1.496537175	Chchd8	0.481518141	Sp8	0.468418596
Klk11	-1.412798332	Angptl1	-1.49466263	5830468K18Rik	0.481146106	Tmem90a	0.467667142
Cth	-1.411678487	E430002G05Rik	-1.491722234	Ddc	0.480821818	Srm	0.467419407
Slc2a1	-1.406827461	Actn1	-1.488852701	Mrps5	0.480816386	Sc4mol	0.467413644
Syngr1	-1.398236953	Fcgrt	-1.487392501	Trim23	0.480725402	Stxbp2	0.466925179
Neu1	-1.397349703	Zfhx1b	-1.486630943	1110006G06Rik	0.480156419	5730410I19Rik	0.46662712
Fcho1	-1.391082767	Lip1	-1.482967728	Cox15	0.480126521	2410127E18Rik	0.466470384
Unc93b1	-1.388962317	AI481100	-1.481137344	Hist1h2ak	0.480062611	Bcl11a	0.46614184
Arhgap30	-1.388650733	Atp1b1	-1.480997745	Rpl38	0.480014432	BC057552	0.466111684
Dfy	-1.38602296	Gpc4	-1.478844471	1110007L15Rik	0.479559005	Rfc4	0.465223256
Park7	-1.383009003	Plekha4	-1.475951879	5730410I19Rik	0.479526226	Cdc20	0.464675767
Dok2	-1.380644211	Atp8b1	-1.471017768	Dnajc8	0.479190931	Ednra	0.464668267
1200013B08Rik	-1.376894554	Kif26b	-1.463514572	Nipbl	0.479114588	Snx8	0.464616512
Scin	-1.374525951	Col28a1	-1.462195933	Apex1	0.478872475	2410016F19Rik	0.464395351
Acvr2b	-1.374101956	Plau	-1.459767012	Pdss1	0.478099081	Klhl13	0.464264001
Pdk1	-1.373354019	Adamts4	-1.458343695	Slc9a8	0.477832626	Shd	0.463699618
Cdca3	-1.373049818	G431001E03Rik	-1.457483848	Dok2	0.476853507	Hebp2	0.462971976
Pygl	-1.371300708	St5	-1.452338321	Psmd12	0.476795327	E130016E03Rik	0.462533523
Nptx2	-1.369376998	Sdk1	-1.449246925	Qrsl1	0.476684049	Reprimo	0.462395859
Hcls1	-1.363963315	Ccl5	-1.448132583	Mycbp	0.476572137	6332401O19Rik	0.462343214
Arhgap9	-1.361996101	Stat2	-1.436905653	Mrpl28	0.476256241	Gtf3c5	0.462307984
Slc7a8	-1.360790917	S100a4	-1.435093168	9630048M01Rik	0.4758535	Rpa3	0.462215159
Gusb	-1.359199598	Emilin1	-1.43415221	Ccnf	0.475546482	Pdxp	0.462162869
Eif3s7	-1.358815304	Adh1	-1.433970406	Mccc1	0.475255022	Cer1	0.461904104
Ica1	-1.358748368	LOC435565	-1.4325857	2310031L18Rik	0.474939713	Tnfrsf21	0.461766324
Gpd2	-1.358733005	Frmd6	-1.429259143	4833426J09Rik	0.474652356	Prps1	0.461463652
Slc40a1	-1.356971233	Epb4.1l1	-1.428908313	Sphk2	0.474367505	Hist1h4k	0.46106603
Odz4	-1.353829589	BC034054	-1.42469392	Nos3	0.474318437	Stmn1	0.461027394
BC019731	-1.3517421	Gyg1	-1.424613759	1500001M20Rik	0.473824853	1500001M20Rik	0.460922366
1700019D03Rik	-1.349471406	Oasl2	-1.424147853	Pmf1	0.473591405	Dtx4	0.460612703
Rpl38	-1.347584374	Irx3	-1.424041496	Vps29	0.473344437	3000004C01Rik	0.460540673
Nat1	-1.347350692	Tgfb3	-1.423697837	2810428C21Rik	0.473200525	1700083M11Rik	0.460447959
Pacs1	-1.345927414	Sh3md4	-1.423305115	Gfer	0.472767162	A430005L14Rik	0.460303777
2410002F23Rik	-1.341622922	2300002D11Rik	-1.423195118	Wnt8a	0.472752997	Hdc	0.459958246
Cdh1	-1.340376494	Oat	-1.423183824	2610510J17Rik	0.472127755	Id2	0.459598684
Card4	-1.338895778	Ptges	-1.422493304	Rpain	0.471333708	Hist1h2bf	0.45957632
Mboat2	-1.338726346	Ier3	-1.421716152	Zranb3	0.47112921	Cox7a1	0.459251203
EG638695	-1.337253826	Odz3	-1.419706091	Wdr21	0.470953489	Prss8	0.459168761
Acy1	-1.337173257	Pi16	-1.416450106	Cenpa	0.470857342	9430097H08Rik	0.458930306
BC006705	-1.33273738	Lmcd1	-1.415037499	1810008A14Rik	0.47027961	Fkbp5	0.458866188
Qpct	-1.331438911	Tbx3	-1.414765061	1110037N09Rik	0.470275574	Zbtb8	0.458417707
Dok3	-1.330232101	Slc24a3	-1.41387731	Mgat3	0.470104409	Cd59b	0.458290697

Olig1	-1.329740542	4732435N03Rik	-1.413116109	Arpc1a	0.46956964	Ap4s1	0.458025447
Slc12a3	-1.328150275	Zfp36	-1.412203265	Gstm6	0.469485283	2810405J04Rik	0.457981024
Nppb	-1.324583634	Galnt9	-1.412160739	2610524G07Rik	0.469451	Cdc2l2	0.457552294
Rcl1	-1.322631432	Nipa1	-1.412109217	Rbm14	0.469329644	Accn2	0.457137783
Sdcbp2	-1.321928095	Hist1h2bj	-1.40989617	Sdcbp2	0.468938704	Hrb2	0.456998419
Usp1	-1.320499987	Blvrb	-1.404428091	Coq5	0.468781499	Hmgn1	0.456422566
BC037034	-1.318959149	Slitl2	-1.403687324	Gm347	0.468675463	Tpd52	0.456267067
Rgs10	-1.316253318	Ttyh3	-1.402220161	AW060207	0.46865565	Nol10	0.455828815
2810410M20Rik	-1.316218014	9230117N10Rik	-1.397923478	Rbp7	0.468302649	Psme4	0.455516814
Nup93	-1.31509269	Ncam1	-1.393946086	Mcm8	0.468011964	Myst4	0.454895817
Zfp87	-1.31253496	Sgcb	-1.393161153	Rad50	0.467786308	AI894139	0.454565863
Phtf2	-1.301189973	D0H4S114	-1.391721611	Myg1	0.467613644	2900055D14Rik	0.454565863
Nudt5	-1.298621699	Zfp521	-1.389470835	Tmprss13	0.467588021	Psmc3ip	0.454331166
Gldc	-1.297537545	Igfbp5	-1.386109257	AK122525	0.46719609	Solt	0.454258809
Sorl1	-1.293006486	Gstt1	-1.379072002	Cycs	0.46719609	Pltp	0.453950304
Gnpda1	-1.29180402	Capn6	-1.37768828	2900045N06Rik	0.467102632	Serpina3m	0.453447623
Trpc4	-1.290248248	Irf1	-1.375739323	Sae1	0.466829073	Rnut1	0.45309641
Sema4a	-1.289506617	2310067E08Rik	-1.375422402	2610016F04Rik	0.466256223	Rhebl1	0.452236117
Atp5b	-1.288053597	Efs	-1.374737345	Rfc4	0.466066249	Kcnab2	0.451765533
Cysltr1	-1.285402219	Rabl4	-1.374251884	Tm4sf4	0.465988687	Ttn	0.451024123
Lamb3	-1.283921772	A930021H16Rik	-1.373507926	Ctsd	0.465893869	Diras1	0.450797262
Llglh2	-1.283874749	Mmp11	-1.372250331	C130090K23Rik	0.465756038	Cstf3	0.450573056
Msc	-1.282842887	Cxx1c	-1.372190604	Gpr19	0.465468277	Hip2	0.449428157
Eif4a1	-1.282340219	D10Ertd610e	-1.36953199	Mnd1	0.465373185	Rad1	0.449344776
Cte1	-1.279194496	Ceecam1	-1.369511689	B3gnt3	0.465089993	Plcxd1	0.449307401
Pfkl	-1.277129125	Lynx1	-1.367116869	Plf2	0.464918648	2310057G13Rik	0.448999769
Anp32a	-1.274144242	Zfpm1	-1.365181293	3110009E18Rik	0.464868655	Psmc5	0.448794676
Uhrf1	-1.272437422	Hebp1	-1.363436303	2610029K21Rik	0.464853835	A730024F05Rik	0.448696811
Gm484	-1.268624706	Meox1	-1.361049853	9530027K23Rik	0.464542684	Rbm4b	0.448393592
Arhgap12	-1.268488836	40429	-1.360738231	Lyar	0.464517837	Prkra	0.448075078
Dnajc5b	-1.268309348	Ube2l6	-1.359787639	9130210N20Rik	0.464464632	Palld	0.447902133
9130210N20Rik	-1.267802149	Ier5l	-1.352469489	Gpx4	0.464172562	Orc1l	0.44705267
Itgb7	-1.264354951	Prkr	-1.35228041	Cox7a1	0.464152402	Tuba1a	0.447016704
AI256711	-1.262281237	Tnfrsf1a	-1.351985329	Gtf2e2	0.464049116	Pank4	0.446976873
1110032N12Rik	-1.259633686	Nrap	-1.351384942	Myl4	0.464021464	Hat1	0.446935598
1300013B24Rik	-1.258137118	Thsd2	-1.347729588	Irs3	0.4639471	Igtp	0.445759439
BC004853	-1.257849089	Lamb1-1	-1.347532319	A030007L17Rik	0.463656204	2310069P03Rik	0.445147816
Acot8	-1.257365656	Arsa	-1.346871393	Rabggta	0.46333987	H2afx	0.445059745
Glo1	-1.255816607	Atxn1	-1.346533647	Slc38a5	0.463301767	Sae1	0.444590702
Tpi1	-1.252123196	Myl4	-1.343774109	Prg	0.463273685	Tgfbr3	0.444528796
Suz12	-1.250218222	Fzd1	-1.343671866	Casp8	0.462753639	Pbef1	0.444439986
LOC654467	-1.248368687	Plekhf1	-1.342986405	1110001J03Rik	0.462719522	Dhcr7	0.444265293
Elmo1	-1.244668379	Lrfn3	-1.341772906	Hoxa1	0.462259509	Nsbp1	0.443856336
Mgl2	-1.244374951	F2r	-1.333995928	Hdac6	0.461565368	Thyn1	0.443710864
Egr2	-1.242135469	Tspan11	-1.333926941	Cnot3	0.461526023	Fto	0.443101931
St14	-1.237440224	Colm	-1.331163486	E130012A19Rik	0.461090843	Stx6	0.442964407
Nusap1	-1.235747928	Garnl3	-1.328883434	Taf5	0.461090843	Tlr1	0.442860163
Atad3a	-1.235237495	1700024K14Rik	-1.322740652	Igfals	0.461010924	Zbed4	0.442851988
1300017K07Rik	-1.235009858	Gata6	-1.321612717	0610010E21Rik	0.460867647	Mip	0.442844195
Kcnk13	-1.23230789	Lrrn3	-1.318887641	Ptdss2	0.46055643	Fbxo30	0.442575723
Slc4a8	-1.231804449	Ggcx	-1.31525203	Pla2g6	0.460417403	Vrk1	0.442455687
F11r	-1.231460302	Tnn	-1.312882955	Myo1g	0.460178033	Anp32a	0.442268483
Slc19a1	-1.230819781	Cebpb	-1.310346977	Suclg1	0.459629868	Hspcb	0.44105842
Mrpl46	-1.22964216	Ptprd	-1.30848092	Hax1	0.458832617	BC030499	0.440312826
Bcap29	-1.229123837	Ltbp1	-1.307825695	Acsl3	0.458785395	Gnb4	0.44007405
Ttc5	-1.228844372	Rassf5	-1.307244049	Mrps10	0.458723712	Zfp446	0.439944923
Suv420h2	-1.226275856	Myo7a	-1.306953251	4933403G14Rik	0.458576384	Yeats2	0.439641253
Idh3g	-1.225348504	Fxyd5	-1.306593725	Stard7	0.458572164	E130012A19Rik	0.439373484
Mrpl38	-1.22208293	Tpbg	-1.305930825	D030013I16Rik	0.458555044	Gtf2ird1	0.438655892
Lmnb1	-1.22151264	Gm1012	-1.299878965	Eif2s3x	0.458094084	6330579B17Rik	0.438493469
Kif22	-1.221401219	Pparg	-1.299661819	Ddx25	0.457930982	Ythdf1	0.438406472
Plekha6	-1.220424483	Rbms2	-1.299027693	Nme7	0.457462069	Xrcc2	0.4381575
Mfng	-1.219800908	Nagk	-1.295124306	Klk6	0.457206954	Taf9	0.438074714
Hrmt1l2	-1.216717393	8430417G17Rik	-1.291462814	Dpysl5	0.457019949	Fads1	0.437739491
Cdca2	-1.216214561	Angptl4	-1.28748745	BC038822	0.456857675	Camk2b	0.437504839
Fxyd5	-1.215943711	Snai1	-1.286727063	3830422K02Rik	0.456835027	Lhfpl2	0.43673257
Rab27a	-1.214494436	Matn4	-1.286567339	Ndufv2	0.456726827	Sec22b	0.436662095
Hn1	-1.214090353	Hsd11b1	-1.285469111	Exosc2	0.456470218	Polr2h	0.43662135
Rbm13	-1.213398265	Hexa	-1.284329184	Ret	0.456091153	Hyal1	0.436570661
Nras	-1.212789357	Plvap	-1.270598513	Ctc1	0.455691829	Serpinb6c	0.436502008
Ednrb	-1.212282634	Fmo3	-1.269486803	Cklfsf4	0.454976245	D5Ertd689e	0.436424927
Akr7a5	-1.211612428	Ebf3	-1.26894883	Lmo6	0.454792213	Tekt1	0.436398491
Ptpns1	-1.208092036	Unc5c	-1.266121329	Prpf3	0.454559788	Mcm7	0.435684045
Sh3gl2	-1.208014775	Hist1h2bf	-1.26579622	Rfwd3	0.454518828	Sfrp2	0.435309894
Psmc5	-1.207861557	Cobll1	-1.261549388	Hmgb2	0.454205118	1700001A24Rik	0.434838446
Wasf1	-1.207821994	BC011487	-1.260443125	5830426I05Rik	0.454055243	Mrpl18	0.434418433
Paf53	-1.207239559	Emb	-1.25985451	Slc11a1	0.453598381	Slc5a6	0.434277185
Ltc4s	-1.207198748	Zfpm2	-1.259716417	1500003D12Rik	0.453538927	2310057J16Rik	0.434049468
C130076O07Rik	-1.207090039	Eml1	-1.259633391	D10627	0.453418591	Rnf41	0.433896527
Blmh	-1.205800135	Nicn1	-1.257958384	A930010I20Rik	0.453299856	Stim1	0.433628361
Ak4	-1.20554152	Meis1	-1.256835328	Cd59b	0.453256822	Hspa8	0.433619778
BC018222	-1.204632736	Lhfp	-1.256635653	2310079N02Rik	0.452757613	Prmt5	0.433432451
1600016N20Rik	-1.203872333	2410019G02Rik	-1.253909671	Psmd2	0.452512205	Dbr1	0.433396654
Tufm	-1.20344097	Arhgdib	-1.252499378	A930009M04Rik	0.452480659	F2r	0.433293624
Tmem20	-1.203077278	Sepw1	-1.251483858	Rfc5	0.452153841	2410019G02Rik	0.433221739
Bmp3	-1.202868634	Ccdc3	-1.250827404	Prkcz	0.451650401	Steap	0.43317572
Tlr13	-1.202868634	Hp	-1.25007781	Aldoc	0.451320761	Prdx4	0.432935934
Arpc5	-1.201940105	Adam33	-1.247735269	Mapk1ip1	0.451318973	Tjp2	0.43274895
Pop5	-1.201441606	Hoxb2	-1.24655736	Vgll4	0.451225807	BC055324	0.4325857
Aldh1a3	-1.19939612	2610027C15Rik	-1.245346406	4921528G01Rik	0.451221202	Wt1	0.432288542
LOC239102	-1.198404347	Stat1	-1.24487542	Tuba8	0.451008044	Pdk2	0.431832742
Crip2	-1.197439772	Trib2	-1.244871268	Aqp7	0.450934156	Gna-rs1	0.43171624
Sfn	-1.197372646	Zfp36l1	-1.243569338	Dcun1d2	0.450899834	Cpsf6	0.431588676
Bcl2l13	-1.193808755	Cmya4	-1.242737691	2510038A11Rik	0.450820261	Sec23b	0.431456488
Kif2c	-1.193673604	Cygb	-1.240451998	Armc8	0.45076223	Krba1	0.431385493
Pdyn	-1.193296751	Scgf	-1.240162192	1110014D18Rik	0.450714402	Ncl	0.43106145
Heatr1	-1.193079769	Pold4	-1.238398673	1810008A18Rik	0.450561156	Cds1	0.430951989
BC067047	-1.192998636	Hmox1	-1.238221841	G630055P03Rik	0.450390292	BC024814	0.430834291
Tead4	-1.192645078	Hectd2	-1.237126456	Shprh	0.450013638	LOC545013	0.430812311
Prg	-1.191586375	Hist1h2bn	-1.236918224	2310056P07Rik	0.449560552	BC088983	0.430609103
Capn5	-1.189667702	Gadd45b	-1.234725892	Polr3a	0.449535694	Stc2	0.430155975
Il10ra	-1.189149129	Gbp1	-1.234416115	Mreg	0.449499083	Stk4	0.42932469
Chordc1	-1.188661564	Fndc3b	-1.23354356	Rfx2	0.449484597	Ddx21	0.429278811
Ckb	-1.18422466	Adam9	-1.232439908	Cbs	0.449091678	Sf3a3	0.429276538
D7Rp2e	-1.182768257	Rgs4	-1.232173442	Wdr51b	0.448964095	Tsga2	0.428888102
Gstp2	-1.181083386	Kcnab1	-1.23144567	Thumpd3	0.448889715	Mcm4	0.428742675
5730593N15Rik	-1.180915785	Rin2	-1.229782005	Rage	0.448758117	D030056L22	0.428630062
Prkcb	-1.18078872	a	-1.229278807	Krt20	0.448608649	Syt13	0.428517413
Ndrg1	-1.17634545	Map3k12	-1.22874621	Fbxo30	0.448428763	Icam1	0.428372138
D6Ertd365e	-1.175571565	2310046G15Rik	-1.228268988	Spag7	0.448015895	Ovca2	0.42821172
Pbk	-1.17554265	Wbp5	-1.227096697	Pigf	0.447890211	Rpo2tc1	0.427995299
H2afy	-1.175157309	Zfp37	-1.225420114	Ifi30	0.447823593	Kif1a	0.427982666
Fuom	-1.173762163	Gaa	-1.224895323	Zfp87	0.447650176	Hist1h1b	0.427766259
Ard1	-1.170880823	Lamp2	-1.220580559	Cdk2	0.447620394	Mtch2	0.427748551
Aox3	-1.169654657	Alcam	-1.2197477	Atp5a1	0.447446718	Zfp459	0.427748551
Tnfrsf25	-1.168185347	Edg3	-1.21950703	4930503L19Rik	0.447230504	Mrps31	0.427643828
Aldoa	-1.166754939	Gulp1	-1.218444255	AA589584	0.447174197	E130306D19Rik	0.427353263
Farsb	-1.166494907	Prrx1	-1.214266756	Slc39a4	0.44715506	BC035295	0.427290657
Mrpl12	-1.164762558	Apbb1ip	-1.213190429	EG622339	0.44688788	Uchl3	0.426554792
Rnpep	-1.164424204	Nbl1	-1.212484121	Zc3hc1	0.446764372	Lrrc15	0.426397361
Txnip	-1.164386818	Ccl2	-1.209628993	Mrps2	0.446736546	Ssbp3	0.426286794
9330186A19Rik	-1.164056403	Cish	-1.208921376	Eif2b5	0.446688386	Nsdhl	0.426170242
Pnpla2	-1.16216627	2610001E17Rik	-1.203939501	Clpp	0.44652391	Ruvbl2	0.42603335
Bex2	-1.161688851	Lrrc8a	-1.202389397	Ddx19	0.4464749	Fusip1	0.425990333
4632404H22Rik	-1.161463423	Ubtd2	-1.200716908	Hist1h2ao	0.446305243	1200015N20Rik	0.425844254
Nasp	-1.161360678	Tap1	-1.200471803	Dclre1b	0.446225377	Eif2b1	0.425373744
BC031593	-1.161090344	Dbn1	-1.199564492	Blvrb	0.446058357	2310008H04Rik	0.425190216
Pdgfb	-1.16089119	Sepn1	-1.19758036	Iqgap3	0.445390967	Birc5	0.425037872
H2afz	-1.160776173	Ehbp1	-1.197013331	Sfrs1	0.445143533	Gnas	0.425008189
Cacna2d3	-1.160753356	Irf7	-1.196037842	Fancd2	0.44503224	Jtv1	0.424581272
Tmem8	-1.160616224	P4ha3	-1.196033571	Rps2	0.445015927	Samd3	0.424430634
Lsm8	-1.160013425	Car13	-1.195866788	LOC381881	0.444949318	Notch1	0.424375364
3010033P07Rik	-1.15999952	Ass1	-1.192086651	2700083E18Rik	0.444720415	Wbscr22	0.42421936
Psca	-1.159978889	Hist1h2bc	-1.190366464	Mpp6	0.444450227	Spic	0.424171139
Dhx32	-1.159834108	E130307J07Rik	-1.190237712	Psma7	0.444376541	FHOS2	0.424046694
Zfhx2	-1.15782093	MGC41689	-1.189717728	Mrpl17	0.444169764	Amhr2	0.423957878
Atp5o	-1.157786441	Clmp	-1.189477799	BC018601	0.443665639	Hrmt1l2	0.423734058
Pde1b	-1.157404318	Txndc5	-1.188916298	Gmcl1	0.44363041	Nxt1	0.423508111
Selpl	-1.156119202	Podxl2	-1.183934053	2600001J17Rik	0.443214545	4930427A07Rik	0.423400972
Brp16	-1.154679578	Gm1010	-1.183188484	E130115E03Rik	0.443064532	Slc6a8	0.423348662
Eif2b5	-1.153456979	Xpnpep2	-1.182111517	Cldn5	0.442919817	Cyp27a1	0.423211431
Cox7a1	-1.149867349	Asah2	-1.181460605	LOC380705	0.442814542	Gata2	0.422954013
Adssl1	-1.149829785	Mme	-1.180398333	Mrps7	0.442635234	LOC433182	0.422857004
Snrpd3	-1.149667105	Hist1h2bm	-1.179802454	Pdcd2	0.442395973	Cdc37l1	0.42266794
Slc11a1	-1.147237407	Cacna1h	-1.179727576	Prune	0.442257678	Akap1	0.422596714
Ptgds2	-1.147060893	Ugcg	-1.178838209	4933427D14Rik	0.441786593	Tpst1	0.422327535
2610024G14Rik	-1.146258172	Cyba	-1.178725284	B4galt4	0.44164165	Cdh1	0.422092257
Ccnb1	-1.138598165	B230104P22Rik	-1.178254635	Ccnc	0.441522846	Mapre2	0.42185149
Mrpl2	-1.138028745	Galnt10	-1.177538186	Ecd	0.441512063	Snrpb	0.421685875
Tmc6	-1.137931369	Bnc2	-1.177404967	2610304G08Rik	0.441400341	Slc38a2	0.421558464
Snrpn	-1.137417079	Nox4	-1.176376042	Zfp105	0.441023152	E330018D03Rik	0.42154493
Irf6	-1.135283566	Gbp2	-1.173462609	Txnl4	0.44064663	Rfc5	0.421347025
Dbi	-1.131546068	BC011468	-1.172204741	2610318C08Rik	0.440572591	Fbxo21	0.42134229
Eif2b1	-1.131453898	Gnb5	-1.170145479	Mrpl34	0.440511568	D15Bwg0669e	0.421182239
Ecd	-1.131377421	Hist1h2bh	-1.169696683	Thop1	0.440190977	2610028L19Rik	0.420225917
Fh1	-1.129207659	Gpr177	-1.169299743	Zranb2	0.440117422	2310004L02Rik	0.420116139
C78212	-1.128256147	Hist1h4h	-1.168231555	Nxt1	0.439616702	Pdcl	0.419791854
Gtf2f2	-1.127387357	Amotl2	-1.168105532	1810021J13Rik	0.439332161	Fmn2	0.419783211
Rabggta	-1.126508516	Fmod	-1.167686529	Sptlc1	0.438686539	A930040G15Rik	0.419778126
Rpa1	-1.125893721	Lmo4	-1.166142677	Gsh1	0.438039325	U2af2	0.419642339
2310069P03Rik	-1.122956213	1810008K03Rik	-1.164237581	Pars2	0.438016063	Cdk2	0.419552374
D830014E11Rik	-1.12222032	Ggta1	-1.163684898	MGC118250	0.43789017	Minpp1	0.41917723
Pnma2	-1.121990524	Thbs3	-1.161602159	Dnaja3	0.43784465	Cdca8	0.419050562
Fbl	-1.12160718	Pard6g	-1.160672680	A230051G13Rik	0.437762918	Polrmt	0.419027133
Gtf2h3	-1.118639868	Ankrd50	-1.160194429	Odc1	0.437702151	Tgfb1i1	0.419004219
Mapk14	-1.118630995	Fez2	-1.159342276	Sh3glb2	0.437578252	Sparc	0.41845756
Birc5	-1.115541253	Kai1	-1.158385809	Msh2	0.437360653	Pogz	0.418420139
1500016H10Rik	-1.114297274	Serping1	-1.155447413	2310046K01Rik	0.436873301	BC011248	0.417923852
Deadc1	-1.114202072	Igf2r	-1.155135983	Wwc1	0.436649841	D1Bwg1363e	0.417920008
Mrps22	-1.114009821	Fgfrl1	-1.154112206	BC085271	0.436580412	Tbc1d2b	0.417644937
Pscdbp	-1.113838257	Lrp12	-1.153530563	Oact1	0.436286811	1700007J06Rik	0.417017863
Igsf4a	-1.110915901	Ak5	-1.151606694	Mrpl36	0.436039386	Sema4g	0.416985771
Mterf	-1.109666281	Igsf3	-1.150578678	4930538D17Rik	0.436036051	Slc39a10	0.416919685
2810405K02Rik	-1.108505466	Gng10	-1.149120061	Zfp31	0.43572421	2610033C09Rik	0.416733505
Kcnk6	-1.106756901	Calu	-1.148796693	Etv5	0.435590781	Trim59	0.416680745
Slc7a5	-1.106397556	Vkorc1	-1.147773122	Ccar1	0.435072413	Erh	0.41666248
Rangnrf	-1.105756111	Ddit3	-1.147167302	Rgs19	0.434976346	Magoh	0.416292199
Gale	-1.104859891	Ly6e	-1.146333506	Dnajc7	0.434791734	Khsrp	0.41607833

Dctd	-1.103813497	Glrx	-1.145587487	Heatr1	0.434726443	Sfrs14	0.415981857
2310002J15Rik	-1.103518109	Pdlim7	-1.144136877	Zbtb17	0.434568922	Igsf11	0.415767423
Apitd1	-1.102685664	Gfpt2	-1.142318307	Rpel1	0.434495006	Wdr31	0.4155847
Ptpre	-1.102304763	Tmem176a	-1.140943945	Hrb	0.434490561	Zfpm1	0.415229641
Fcna	-1.101014602	Hoxb6	-1.140913915	LOC432879	0.434450203	Slc4a3	0.415037499
Matk	-1.099310937	Irx5	-1.139041168	2810004N23Rik	0.434350974	LOC211660	0.415037499
Zfp96	-1.097321252	Pls3	-1.136798222	Zfp639	0.434091458	Spo11	0.415037499
Rnaset2	-1.096993066	Armcx3	-1.13571801	Thoc4	0.434072823	Hcfc1	0.415001442
Cerk	-1.096168238	Lypla3	-1.135463417	Wdr9	0.433960363	Ltbp4	0.414882828
Serpina1e	-1.095225902	Bfar	-1.134959536	Acbd4	0.433616106	Tmem14c	0.414663889
Agpat4	-1.095111258	2410008J05Rik	-1.13280452	Igf2bp3	0.433224166	Usp28	0.414315249
A430005L14Rik	-1.095068257	Fzd7	-1.132530137	Ltap	0.433001915	Kcnip3	0.414161812
Tcfap2a	-1.093648159	D15Ertd366e	-1.131935416	Cerk	0.433000924	5730555F13Rik	0.414033047
0610039N19Rik	-1.093282573	Gvin1	-1.129142902	Susd2	0.432719777	Mettl9	0.413990822
Ranbp1	-1.092560356	2310061N23Rik	-1.129080983	Cdk8	0.432623311	2810021B07Rik	0.413513027
Arhgdig	-1.092294916	Polk	-1.123772141	Bid	0.432578349	Copz2	0.413327132
Sumo1	-1.091000934	2810417M05Rik	-1.12307523	2810407K09Rik	0.43225924	Lrfn1	0.413314878
Ppm1b	-1.090810126	Tnfaip3	-1.121121608	9130427A09Rik	0.432023611	Wdr18	0.412969966
Psma5	-1.089626039	Ppapdc1	-1.120074331	Rpa2	0.431961957	Ryr1	0.412951172
Shprh	-1.089040287	Slc2a13	-1.119121742	Paip2	0.431895773	Si	0.412708693
4631426J05Rik	-1.088247371	Rgs3	-1.11862109	Hnrph1	0.431853703	Ard1	0.412682476
Chn2	-1.087325291	Zfh4	-1.117384643	Cd68	0.431559955	BC057371	0.412581848
Pnpo	-1.087147326	Sepm	-1.116172827	Rtn1	0.431525622	Gal	0.412547947
Rbm28	-1.085675697	2410005K17Rik	-1.115802105	Nqo3a2	0.431418205	Vangl1	0.412516627
Rpp38	-1.085154237	Dusp23	-1.115639692	Hspcb	0.431352228	2310008M10Rik	0.412490622
Poll	-1.085026816	Hspg2	-1.112670775	2310066N05Rik	0.431237772	Skd3	0.412484508
Nme1	-1.083866085	Rhbdl4	-1.112642086	Set7	0.431138554	Sca10	0.412424259
Eef1e1	-1.083156327	Lcn2	-1.111518193	Acpp	0.430985693	Hist1h4m	0.412305491
Pcdh20	-1.083141235	Tceal1	-1.111146964	1700007J06Rik	0.430979043	Creld2	0.4119777
Tm6sf1	-1.082973042	1200009F10Rik	-1.109972842	Mrps35	0.430911398	LOC434729	0.411747429
Timm50	-1.081342557	Ets1	-1.108998701	2700038L12Rik	0.430873239	Polr2e	0.411690954
Psmb7	-1.081225328	Hes1	-1.108872994	Xpnpep1	0.430757304	Enah	0.411650094
5730410E15Rik	-1.081049205	Tpm1	-1.106724136	5930412E23Rik	0.430641507	Rbms3	0.411505808
2310010M24Rik	-1.080861833	Slc41a3	-1.105103	Ddx47	0.430041924	F830029L24Rik	0.411426246
Pithd1	-1.080595159	Nelf	-1.104040121	Lgtn	0.429899831	Bxdc1	0.411179627
2410005K20Rik	-1.080104998	Slc6a9	-1.103760561	Sf3b3	0.429880836	Mmp11	0.410915511
Rims2	-1.079461991	Slc44a1	-1.103039063	Spint2	0.4296103	Serbp1	0.410635364
BC025872	-1.079170213	Pkia	-1.102415567	Fnbp3	0.429538484	Atic	0.410380873
Paox	-1.079043433	6230427J02Rik	-1.10106456	Xrcc1	0.429268645	Cbr3	0.409485754
Sh3tc1	-1.078150808	Pcdha6	-1.10057172	1700009P17Rik	0.429167828	BC017133	0.409446543
1810046J19Rik	-1.077567435	Hist1h3f	-1.099941438	Hist1h2ab	0.429036203	Lig1	0.409292824
Hgfac	-1.075989683	Tmem150	-1.099438322	LOC381297	0.428815638	Fjx1	0.409274944
Pik3cg	-1.075387122	Kera	-1.098439817	6330579B17Rik	0.428757362	4930424G05Rik	0.408805546
Tst	-1.074962058	Trim3	-1.098195941	2700084L22Rik	0.428226271	0610007P06Rik	0.408376746
2410015N17Rik	-1.074784442	Cask	-1.096475316	Chaf1b	0.428116078	Cask	0.408208636
Plcd3	-1.074523786	Tbx1	-1.095042693	Acly	0.426574191	Crb3	0.407930613
Ap1b1	-1.074403575	4930402H24Rik	-1.094940286	Nola2	0.426521419	1700012G19Rik	0.407690592
Hmgcl	-1.073681366	Slc8a1	-1.093237479	Zfp213	0.42647844	Grwd1	0.407294524
Timm44	-1.073134705	Tspo	-1.093127496	Tex9	0.426463268	Gemin6	0.407090182
Tcfap2b	-1.070926411	Sytl2	-1.090689364	Mtf2	0.426399801	2610528H13Rik	0.406536031
Kcnk5	-1.069811903	9430063L05Rik	-1.088633209	Dgkz	0.426392737	MGC58426	0.40626729
Atp6v1e1	-1.069724484	Col23a1	-1.086804828	Spc24	0.426389474	Tpd52l1	0.406034693
Fes	-1.0691704	Thsd6	-1.084195127	2310005E10Rik	0.426001857	Tars	0.40531507
Nol10	-1.068670811	Fas	-1.08301405	Spire1	0.425727224	Rnf4	0.405270179
Rnpepl1	-1.06671354	Six1	-1.082274003	Nlk	0.425698309	Nle1	0.405240538
Rpl27	-1.065954775	2810410P22Rik	-1.078727211	1700007I06Rik	0.425684743	3230401I01Rik	0.40508372
Lig1	-1.065543186	Gbp6	-1.078687297	2410016F19Rik	0.425536418	Ttc3	0.404990732
Vnn3	-1.06377591	Osmr	-1.078332759	Eif3s4	0.425392499	D930005D10Rik	0.404432944
Dpep2	-1.063062268	Ncald	-1.07788551	Creb3l4	0.425305835	Nfya	0.404042492
Ela1	-1.062644937	Pik3r1	-1.077286001	Mat2a	0.425246645	Plekhb1	0.403593966
1810042K04Rik	-1.06082184	Rgs17	-1.07723143	Jak3	0.425031468	Hemk1	0.403523511
Ly6f	-1.06015681	Pofut2	-1.074829831	9430029K10Rik	0.425007362	Spc18	0.403397739
Abcb6	-1.057045265	1110019L22Rik	-1.074106999	Mpn	0.424793082	Ppid	0.40309999
Lilrb4	-1.05564803	Crim2	-1.0738013	Fpgs	0.424763347	Klhdc2	0.40214321
Ppp2r5e	-1.05401497	Foxg1	-1.072709322	Pkp3	0.424497829	Usp11	0.401362562
Atp6v1c2	-1.053866872	A4galt	-1.072051493	Hdh	0.424384672	Jmjd5	0.401205226
Trap1	-1.053637964	Fkbp14	-1.07180878	3010026O09Rik	0.424344543	Bzrap1	0.401118998
Phf5a	-1.052831981	Zfyve21	-1.071061657	Nol1	0.424092962	Zfp608	0.400763058
Ebi3	-1.052777031	Gpc1	-1.069383615	5730593N15Rik	0.42389196	Galt	0.400679291
Impdh2	-1.052321532	Serpinb6a	-1.068815779	Sfn	0.423677939	Hmgcl	0.400640071
Pus1	-1.052260402	D9Ertd392e	-1.0675459	Cacnb4	0.42365063	Bcat2	0.400561955
Sae1	-1.050150228	Itga5	-1.067396069	Mrpl12	0.423448814	C80913	0.40053793
Sbsn	-1.050079287	Sspn	-1.066590146	Bub1b	0.42343994	BC027344	0.400396669
Tpcn2	-1.049598797	Shox2	-1.066138464	Rngtt	0.423282615	Gart	0.400391409
Rps3	-1.049543608	Kif3c	-1.065691342	Med19	0.423157307	F730047E07Rik	0.400347128
Sh3bgrl2	-1.049318343	Isgf3g	-1.064763489	Eef1e1	0.423140798	Ina	0.399930607
Tubb2b	-1.049280903	Irx1	-1.064273214	Plcd3	0.423023483	Adra2a	0.399872863
Col14a1	-1.04781148	Ebf1	-1.064254542	Ncaph2	0.422968773	Gas8	0.399855796
Iqsec3	-1.046758099	BC025575	-1.061757539	Ocln	0.422756592	Mrpl45	0.399802986
Blvra	-1.046651246	Glis1	-1.061126659	Bbs5	0.422733676	2610528J11Rik	0.399477214
Pmm1	-1.045560203	Tle2	-1.061051463	2310010M24Rik	0.422584308	Olfr828	0.399384235
Ppp1r10	-1.045082253	EG433180	-1.059027576	3632413B07Rik	0.422551553	Sgol1	0.399231175
D5Bwg0834e	-1.044108352	Whrn	-1.058743791	Pald	0.422435774	Usp14	0.39922855
Cox17	-1.04395541	Scara3	-1.058257533	Eif4g1	0.422358186	Eif5a	0.399193877
P2ry13	-1.043068722	Golph4	-1.05621601	4930432K21Rik	0.422350845	Mrpl24	0.39916342
Ptpro	-1.041177407	Lrrk2	-1.05399489	Thap11	0.422312897	Nip7	0.398840885
1700093E07Rik	-1.039861874	Ctsb	-1.053605969	9330177P20Rik	0.422276326	Jarid1b	0.398743692
Nme2	-1.039676252	Hyal1	-1.052514006	2700038C09Rik	0.422069674	Snip1	0.398637237
Usp20	-1.03736378	Glt8d1	-1.049680973	Magoh	0.421844137	Jub	0.398445946
Mipep	-1.036994207	Rnf11	-1.0489096	Ibtk	0.421554644	Rgl2	0.398219881
4930538D17Rik	-1.036121763	Lgals9	-1.047460647	Stoml1	0.421541019	Elovl6	0.397444732
Corin	-1.033912635	Slco2b1	-1.047092708	Muc1	0.421091621	D330028D13Rik	0.397403825
9530090G24Rik	-1.033276155	2310033K02Rik	-1.045176139	Gapd	0.420784317	Tyms	0.397193476
AI316787	-1.032223499	Cyhr1	-1.044942777	Bcat2	0.420774922	Snrpn	0.397054665
4930547N16Rik	-1.032198822	1200015N20Rik	-1.041994089	Papolg	0.420651106	Cox4i2	0.396758766
Col17a1	-1.031319763	Cst3	-1.040749133	Ttf2	0.420620021	Sfrs7	0.396575257
Tssc1	-1.031205298	Dhrs6	-1.040619546	Plekha7	0.420601313	Hmgcs1	0.396397209
Cct6a	-1.030986078	Evl	-1.038628681	Rdh12	0.420575683	Cdh2	0.396334061
Ivns1abp	-1.030753582	Ppbp	-1.03796785	Chordc1	0.420147172	Rad17	0.396318871
Shf	-1.030333733	Zfp537	-1.037536616	1700011I11Rik	0.41975174	2410017P07Rik	0.395963524
Mrpl17	-1.028982086	Edg2	-1.037259619	Cstf1	0.419513289	Tnpo1	0.395928676
Itpr3	-1.028410667	Kcne4	-1.036525876	Usp52	0.419340597	Rnf126	0.39582802
E130309D02Rik	-1.027678452	AW061290	-1.035877036	Sdccag1	0.419225296	Rhpn1	0.395672174
Parp1	-1.025819984	3110045G13Rik	-1.034157011	Sprr2g	0.419225296	Banf1	0.395338775
Dctn3	-1.025358275	Sulf1	-1.033620981	Incenp	0.418881028	Tuba4	0.395162864
Inpp5d	-1.024189466	Tmem53	-1.033457742	Hpcal1	0.418758665	Amd2	0.394951351
Zfp259	-1.024039403	Rab3il1	-1.033026254	LOC216443	0.418695121	Gprc5c	0.394929926
Eno1	-1.023235278	LOC545007	-1.029781146	B3galt4	0.41846189	2610528A15Rik	0.394819755
Tsga2	-1.023046737	Cbr3	-1.028758993	Hprt	0.418086343	Brp17	0.394813995
Rbm21	-1.022811651	Camk2n1	-1.028569152	Slc45a4	0.418050019	4933425I22Rik	0.394733403
Hpgd	-1.020639766	BC051244	-1.028373711	Mrpl14	0.417475956	4930431B11Rik	0.394429715
Bmx	-1.020103887	Gmds	-1.027159618	Rad9	0.417434667	Fads2	0.394403225
Tm4sf12	-1.019392726	Mmp16	-1.026231542	Fkbp4	0.417372418	Lsm2	0.394145548
Atp6v1c1	-1.018453328	Psmb9	-1.025928465	Upf1	0.417183569	Pep4	0.394006587
ORF9	-1.016891779	Hspa1a	-1.025639821	Glrx2	0.416749897	BC057627	0.39399951
Blm	-1.016282445	4931440N07Rik	-1.024305907	1110032N12Rik	0.416532566	8430427H17Rik	0.393712454
Rab11fip5	-1.015952917	Sntb2	-1.024216237	Ethe1	0.416480627	H2-DMa	0.39362653
Keo4	-1.015701315	Mpdz	-1.024056025	Mllt11	0.416270045	Nipsnap1	0.393507954
Prmt3	-1.014116921	Twsg1	-1.022740939	1110033J19Rik	0.415805503	Vgf	0.393172353
Rac2	-1.013939191	C330023F11Rik	-1.021477249	Ovol1	0.415741768	Cct7	0.393116881
Etfa	-1.012551557	Parp3	-1.021061616	2810452K22Rik	0.415171722	Psmd14	0.392850873
Zdhhc12	-1.012021097	H2-DMa	-1.019931902	Nup37	0.415037499	1200009O22Rik	0.392797761
Plk1	-1.010681027	1190002N15Rik	-1.019921541	Ptpru	0.415037499	1700027M21Rik	0.392655806
Mgst3	-1.010523313	Lrp1	-1.019640425	Xrcc2	0.415037499	Mrps18b	0.392614152
Krt20	-1.010492374	Pbxip1	-1.019083546	Zfp143	0.415037499	1500032D16Rik	0.392463275
Pdss1	-1.010393525	Camk1	-1.018963909	Plekhf2	0.415003123	Ifit2	0.392317423
1700034H14Rik	-1.008859188	Prss35	-1.016186843	Mgst2	0.414559073	5830411K18Rik	0.391982263
BC066028	-1.006484034	Dscr1l1	-1.014778055	Dscr2	0.414436251	Ell3	0.391896922
Dpp3	-1.006003082	Nme4	-1.014362439	Cul2	0.414282754	Strn4	0.391694052
Ccdc53	-1.00551935	Fth1	-1.014019507	Csrp2bp	0.41425036	Btg4	0.391647679
Pald	-1.004650974	Rgl1	-1.014015022	Klk13	0.414215685	Tacc1	0.391578526
Supt3h	-1.003506796	Smad6	-1.013205539	1200011O22Rik	0.414086794	Mrpl11	0.39141775
2610009I02Rik	-1.002611213	1110028E10Rik	-1.013185077	Usp39	0.41356821	Limd1	0.391044644
MGC68323	-1.001636637	Mlf1	-1.01270359	Gbl	0.413556749	Aoc3	0.390951881
Iqgap2	-1.001432666	Ctxn	-1.012056018	Nckipsd	0.413521267	Inpp5d	0.390922301
Ttyh2	-1.001325397	Hist1h2bk	-1.012047201	Pof1b	0.413482033	Mrps28	0.3908738
Ogt	-1.000204218	Trib3	-1.011909388	Pmvk	0.413440714	Hspa5bp1	0.390789953
Slc35f2	-1	Rrbp1	-1.008082346	Snx12	0.413388487	Tmem17	0.390789953
9130005N14Rik	0.999713495	Gpr64	-1.008026141	BC040823	0.41284994	Gpsn2	0.390618244
Fgfr1	0.999011514	Ap3m2	-1.007735649	OTTMUSG00000(	0.412738383	Obfc2b	0.390601713
Cxx1a	0.997901534	Waspip	-1.007545387	Magmas	0.41260831	Alox5ap	0.390567641
Kdt1	0.997653009	Irx2	-1.007503532	Hnrpm	0.412319851	LOC278097	0.390489892
Slco2a1	0.99642011	Vip	-1.007432758	Drg1	0.412255232	Ddx27	0.390354693
Daxx	0.996308095	Syt11	-1.006843986	Cabs1	0.412082972	Bhlhb9	0.389534982
Nsdhl	0.99603655	C86987	-1.005876566	Zbtb24	0.412070633	Kras	0.389420291
Tbx3	0.995918823	Wnt4	-1.00390798	Mettl1	0.412037687	Vps33b	0.389411692
Nox4	0.995567754	1110007C02Rik	-1.002214112	Pold2	0.411902704	E430012M05Rik	0.389294488
Pgrmc1	0.995550177	Prkacb	-1.001705746	Scarb2	0.411748263	Raet1b	0.389191322
Evc	0.994482995	Ifi203	-1.001547126	LOC381066	0.411747429	Parp1	0.389109034
Ephb2	0.994308888	Map1lc3a	-1.001352738	AU022870	0.411678487	0610025P10Rik	0.388873919
Rab22a	0.993859675	Col4a2	-1.001138802	Taf6	0.411018848	C430014N20Rik	0.388798942
Aes	0.992090862	Thra	-1.000424759	Spg4	0.410801047	Ifngr2	0.388637951

Appendix 5.
Common and unique gene lists for last two transition steps

Common in Thy1-toSSEA1+ & SSEA1+toDsRed-	Unique in Thy1-toSSEA1+	Unique in SSEA1+toDsRed-
2410116G06Rik	2010001M09Rik	1110025F24Rik
2410146L05Rik	3110043J09Rik	1500031H04Rik
Car4	Abp1	1700012H05Rik
Chst1	Alox12b	1700029P11Rik
Col18a1	Ap1m2	2410004F06Rik
Dnmt3b	BC013481	2610305D13Rik
Dnmt3l	Bcl2l11	2810004A10Rik
Dppa4	Cdc20	2810046M22Rik
Dppa5	Ckmt1	6030411F23Rik
Esrrb	E130306D19Rik	6330403K07Rik
Gbx2	Egln3	6530401D17Rik
Gldc	Elf3	7420416P09Rik
Igfbp2	Espn	A230098A12Rik
Igsf9	Gpx2	Actb
Lefty2	Grb7	Acvr2b
Mdk	Gstp2	Adam19
Nanog	H2-Bl	Arid3b
Olig1	Kif22	Armcx2
Otx2	Klk11	Atp1b1
Rbpms	Klk7	Axin2
Rbpms2	Krt1-17	B3gnt5
Sall4	Krt1-19	B930096L08Rik
Slc2a3	L1td1	BC030476
Zscan10	Ly6g6c	Bex2
	Mapk13	Bex4
	Med18	C130076O07Rik
	Ndrg1	Cadps2
	Phc1	Car14
	Plekha2	Cd40
	Ppl	Celsr3
	Prom2	Chrd
	Prss19	Cldn6
	Rab15	Cmya4
	Rab25	Cntnap2
	Rbm35a	Cotl1
	Rps6ka1	Crabp1
	Spnb3	Cyp7b1
	Sprr2d	D230005D02Rik
	Tacstd2	Ddx25
	Tcfap2c	Defcr-rs2
	Tpd52	Dgkk
	Zfp473	Dnajc6
		Dppa3
		Dpysl5
		E030006K04Rik
		Egfl7
		Emb
		Enc1
		Eomes
		Epb4.1l3
		Evl
		Fabp3
		Fem1b
		Fgf10
		Fgf15
		Fgf17
		Fgf5
		Fgf8
		Fhl1
		Flt1
		Foxa2
		Foxq1
		Fuom
		Fzd2
		Fzd7
		Gap43
		Gata6
		Gfpt2
		Glipr2
		Gm691
		Gpc3
		Gprasp1
		Greb1
		Gsc
		H19
		Igdcc3
		Igf2bp1
		Igfbp5
		Igsf4a
		Irx3
		LOC545007
		LOC620807
		Lefty1
		Lhx1
		Lin28
		Lmyc1
		Lrig3
		Lrp11
		Mapk12
		Mest
		Mfap2
		Mixl1
		Mlp
		Mnd1
		Mogat2
		Myh10
		Ndg2
		Neurl
		Nid2
		Nptx2
		Nr6a1
		Nudt10
		Nudt11
		Phlda2
		Pitx2
		Pknox2
		Pla2g10
		Pla2g1b
		Pnma2
		Pou3f1
		Ppp1r1a
		Prf1
		Prickle1
		Ptgis
		Ptn
		Ramp2
		Robo4
		Rragb
		Sall2
		Sema3f
		Sertad4
		Sgk
		Slc1a3
		Slc27a2
		Slc29a4
		Slc39a4
		Smarca1
		Snn
		Socs2
		Sox17
		Sp5
		Spink3
		Spp1
		Sqle
		St6gal1
		Stard8
		Stx3
		T
		Tcfl5
		Tdgf1
		Tex19
		Tm4sf6
		Tnfrsf19
		Trh
		Tro
		Utf1
		Whrn
		Wnt8a
		Zbtb2
		Zcchc3

Appendix 6.

Genome-wide RNAi screen and analysis

Gene	Thy1+ log10	Thy1minus log10	SSEA1+ log10	DsREDminus log10
Ism1	2.4336	1.2165	0.6482	0.6482
XM_162370	2.2827	0.9147	0.9565	0.8291
XM_139331	2.2764	0.966	0.6482	0.5184
A930024N18Rik	2.2363	0.3077	1.55	0.8291
Vmn1r81	2.2123	0.8565	0.6482	0.8974
2900092D14Rik	2.2073	1.0119	0.5184	1.2876
XM_286356	2.1998	0.7892	0.3323	1.5209
XM_139236	2.1947		0.6482	0.5184
Fbxo4	2.1921	0.612	0.6482	0.6482
XM_284180	2.1895	0.8565		0.748
XM_155454	2.1895	0.612	0.8974	0.8974
XM_157877	2.1763	0.3077	0.6482	0.3323
Tmf1	2.1709	1.0534	0.748	0.748
Gdpd3	2.1655	0.612		0.5184
XM_161991	2.1458		0.3323	0.5184
Cdkn3	2.1458	1.0913	0.6482	1.0548
XM_287970	2.1429	0.3077	0.8291	0.6482
XM_288726	2.14	0.612	0.6482	
XM_142986	2.1371	0.7096	0.9565	0.5184
1700016D06Rik	2.1341	0.612	1.4562	0.3323
XM_147054	2.1282	1.6757	0.3323	0.3323
XM_145060	2.1252		0.3323	1.2328
Pycrl	2.1252	0.7892		0.3323
Fgf23	2.1252	0.7096	0.5184	1.5209
5031425E22Rik	2.1252	0.612	0.748	1.0967
XM_194204	2.116	0.9147	0.8974	1.0084
XM_149548	2.1098	0.3077	0.3323	0.3323
Taf12	2.1098		0.5184	0.748
Dis3l	2.1067	0.7096	1.0967	0.748
XM_112922	2.1004	0.612	0.5184	1.5773
Anapc10	2.1004	0.3077		0.3323
Speer5-ps1	2.0907		0.5184	
AI182371	2.0907		1.1701	
Olfr1271	2.0874	0.3077	0.3323	
XM_233260	2.0841	0.486	1.5056	
XM_136829	2.0841	0.7096	0.6482	0.5184
Spink5	2.0841	0.7892	0.3323	0.3323
Gm5795	2.0841	0.486	0.5184	
XM_286906	2.0808	1.6362	0.6482	0.5184
Rbfox1	2.0808		0.3323	1.4733
Alpk3	2.0808	0.486	0.3323	0.9565
XM_488263	2.0774	0.612		0.6482
XM_112841	2.0774	0.3077	0.3323	0.6482
Ccl21b	2.0774	0.3077		0.6482
XM_285419	2.0741	1.0913	0.3323	
XM_205385	2.0741		0.3323	0.3323
Idh3b	2.0741	0.486	0.3323	0.3323
XM_152998	2.0707	0.7096	0.5184	0.8974
NM_001002783	2.0707	0.486		0.5184
XM_205489	2.0672	0.8565	0.3323	0.8291
XM_154493	2.0672	0.3077	0.5184	0.3323
Paqr8	2.0672	0.3077	0.3323	0.6482
Ezh2	2.0672	0.7892	0.748	0.8974
XM_148108	2.0638	0.612	0.3323	
XM_129179	2.0638	0.486	0.3323	1.7495
Tle3	2.0638	0.8565	1.0084	0.5184
Krt18	2.0638	0.3077	0.8974	1.55
Clec1a	2.0603	0.486	0.3323	0.3323
Pkhd1	2.0568	0.3077		0.3323
Eps8l3	2.0568	0.9147	0.748	0.8291
XM_194903	2.0532		0.3323	1.7998
XM_149022	2.0532	0.612	0.3323	0.5184
XM_147124	2.0532	0.486	0.8291	
Hs6st1	2.0532	0.3077	0.8974	0.748
Bcl2l12	2.0532		1.4197	0.3323
Rpp40	2.0496	1.0119	0.6482	0.9565
Fut2	2.0496	0.612	0.3323	0.5184
XM_359011	2.046	0.7096	0.8974	0.9565
Kdm6b	2.046	0.486	0.5184	0.6482
Tm2d1	2.0424	0.486	0.5184	0.3323
XM_284944	2.0388	0.486		0.3323
XM_286079	2.0313	0.7096	0.6482	1.0084
XM_147865	2.0276		0.748	0.8291
Syncrip	2.0276		0.3323	0.748
C230029F24Rik	2.0276	0.612	0.6482	0.748
A630034I12Rik	2.0276	0.3077		
Rassf10	2.0238	0.3077	1.2611	0.3323
Mgrn1	2.0238	1.0119	0.6482	0.3323
Cnn1	2.0238	0.3077	0.6482	1.0548
Arhgap11a	2.0238	0.7892	0.8291	1.0548
XM_488695	2.02	0.7096	0.748	0.8291
XM_110047	2.02	0.3077	0.3323	0.3323

XM_288635	2.0161	0.3077	0.3323	0.8974
XM_142984	2.0161	0.7892	0.9565	0.748
Vps37a	2.0161	0.486	0.8974	0.8291
Skint9	2.0161	0.3077	0.5184	0.5184
Krt76	2.0161			0.3323
XM_145067	2.0122	0.3077		
Nbeal1	2.0122	0.3077	0.5184	0.5184
Errfi1	2.0122	1.9216	0.3323	
XM_289391	2.0083	0.9147	0.6482	1.0084
XM_156674	2.0083	0.7096	0.6482	
Dennd2a	2.0083			
Adrb3	2.0083	0.3077	0.3323	1.3587
XM_164931	2.0003	0.612	0.8974	0.9565
Gtf2f2	2.0003	0.486		0.6482
Cnot1	2.0003		0.5184	
XM_142466	1.9963	0.3077	0.3323	1.0967
Tsnax	1.9963	0.3077		1.5639
Prop1	1.9963	0.3077	0.3323	0.5184
XM_355782	1.9922	0.3077	0.6482	0.8974
XM_286351	1.9922	0.7096		0.5184
XM_156900	1.9922			0.3323
Rad17	1.9922	1.0119	0.748	1.0548
Gsta4	1.9922	0.3077	0.3323	0.5184
XM_161868	1.9881	0.7096	1.0548	0.8974
XM_144313	1.9881	0.486	0.5184	1.4197
XM_288245	1.9839	0.7096	0.5184	0.748
XM_283090	1.9839	0.9147	0.8291	0.8974
XM_136832	1.9839	0.486	1.0967	0.9565
Fam82a2	1.9839	0.3077	0.5184	
XM_344980	1.9798	0.3077	0.5184	0.3323
XM_154775	1.9798	0.612	0.3323	0.8291
XM_149081	1.9798	0.7096	0.3323	
Srm	1.9798		1.2026	0.748
XM_164946	1.9755	0.8565	0.5184	0.748
XM_158900	1.9755	0.966	0.3323	0.748
4930578N16Rik	1.9755	0.486	0.6482	1.3587
XM_287355	1.9712	0.3077	0.3323	0.9565
Sprr4	1.9712		0.3323	0.6482
Rdh16	1.9712	0.7096		0.8291
Syt4	1.9669		0.748	1.2876
AK009004	1.9669	0.486		0.5184
Adcyap1	1.9669	1.5692	0.3323	0.6482
XM_286689	1.9626	0.3077	0.748	0.5184
XM_285793	1.9626	0.612	1.2611	0.6482
XM_194054	1.9626	0.3077		0.3323
Lix1l	1.9626	0.3077		1.0967
XM_286753	1.9582	0.3077	0.6482	0.6482
XM_144486	1.9582		0.3323	0.5184
1700092E16Rik	1.9582	0.7892	0.6482	0.8291
XM_165202	1.9537	0.8565	0.8974	0.3323
Pcdhb5	1.9537	1.3348	0.5184	0.6482
XM_206944	1.9492	0.3077	0.5184	0.5184
XM_146458	1.9492	0.3077		
Olr1624	1.9492	0.7096	0.748	
Nav1	1.9492	0.486	0.3323	0.3323
Aass	1.9492	0.612	0.748	0.748
XM_111240	1.9447	0.612	0.6482	0.5184
Xab2	1.9447	0.8565	0.9565	0.8291
Olfr1080	1.9447	0.612	0.8291	1.2328
BC002163	1.9447	0.486	0.3323	0.6482
XM_289420	1.9401	0.9147	0.5184	0.3323
XM_289199	1.9401	0.3077	0.748	0.8974
XM_197786	1.9401	0.486	0.6482	1.0548
XM_164466	1.9401		0.3323	0.5184
Fanci	1.9401	0.3077	0.5184	0.5184
Zeb2	1.9354	0.486	0.3323	0.3323
XM_486342	1.9354	1.0534	0.6482	0.5184
XM_357300	1.9354	0.3077	0.748	0.5184
XM_197290	1.9354	0.3077	0.3323	
XM_146592	1.9354	0.7892	0.748	1.0084
Slc50a1	1.9354	0.3077	0.3323	0.3323
NM_175405	1.9354	1.1584	0.5184	0.6482
XM_162087	1.9307	0.3077	0.3323	
XM_139566	1.9307	0.612	0.3323	0.3323
Tra2a	1.9307	0.7096	0.748	0.5184
Rnf144b	1.9307	0.3077	0.5184	0.3323
Psma1	1.9307	0.612	0.3323	0.3323
Igfn1	1.9307	0.3077	0.748	0.8291
Hist1h2br	1.9307	0.3077	0.5184	1.5773
Fam154a	1.9307	0.612	0.748	0.5184
XM_283017	1.926	0.3077	0.3323	0.5184
XM_194737	1.926	0.486	1.0084	0.5184
XM_144737	1.926	0.486	0.3323	0.6482
Pla2g12b	1.926	1.0913		1.3126
Kcnip4	1.926	0.612	0.748	0.748
Grid1	1.926	0.612	1.0084	0.6482
XM_287151	1.9212	0.3077	0.748	0.3323

XM_284140	1.9212	0.486		0.5184
XM_129420	1.9164	0.3077		
Timp2	1.9164	0.7096	0.5184	0.8291
Serf1	1.9164	0.7892		1.4003
Kdm4a	1.9164	0.486		1.38
Aatk	1.9164	0.486	0.748	1.5639
XM_288837	1.9115	1.3136	0.5184	0.6482
XM_288313	1.9115	0.3077	0.5184	0.8291
XM_285261	1.9115	0.7096	0.3323	1.2876
Olr677	1.9115	0.3077	0.3323	0.6482
Cldn13	1.9115			
XM_286726	1.9065	0.612	0.3323	0.5184
XM_285193	1.9065	0.7096	0.6482	1.0084
XM_155739	1.9065	1.0913	0.748	0.8291
XM_111108	1.9065	0.7096	0.5184	1.2611
Tmc2	1.9065	0.486		0.8974
Ptprn	1.9065	0.7096	0.3323	0.9565
Enam	1.9065	0.3077	0.5184	0.3323
Dctn5	1.9065	0.3077	0.3323	0.6482
XM_288400	1.9015	0.7096	1.0967	0.6482
XM_156418	1.9015		0.3323	0.3323
XM_152880	1.9015		0.748	0.5184
Hmgb1	1.9015	0.486	0.6482	1.4383
Cdc27	1.9015	0.486	0.3323	1.4003
XM_358253	1.8964	0.3077	0.748	
XM_139134	1.8964	0.486	0.6482	0.6482
Mrpl32	1.8964	0.7892	0.5184	1.0967
Gm5105	1.8964	0.486	0.8291	0.6482
Dhodh	1.8964	0.486		0.8291
Ang2	1.8964	0.612	0.3323	1.0548
XM_488731	1.8913	0.612	0.5184	0.3323
XM_357332	1.8913	0.486	0.9565	0.6482
XM_164357	1.8913	0.486	0.5184	0.5184
XM_149292	1.8913	0.612	0.3323	
Trmt61a	1.8913	0.612	0.6482	0.8291
Ssu72	1.8913	0.7096	0.6482	0.9565
Klhdc1	1.8913	0.486	0.8291	1.0548
Il1rap	1.8913	0.7892	1.0967	0.8974
XM_287507	1.8861	0.486	1.0548	0.3323
XM_285807	1.8861	0.7892		1.7918
XM_157008	1.8861	0.7892	0.5184	0.6482
XM_151335	1.8861	0.9147	0.8291	0.8974
XM_143018	1.8861	0.612	1.0084	0.3323
XM_136259	1.8861	0.7096	0.6482	0.8974
Mlec	1.8861	0.7096	0.3323	0.3323
Dpp7	1.8861		0.3323	0.5184
4932443I19Rik	1.8861	0.486	0.5184	0.6482
XM_484838	1.8808	0.612	0.3323	1.2611
XM_153864	1.8808	0.612	0.3323	0.6482
XM_147785	1.8808	0.3077	0.6482	1.4197
XM_143703	1.8808	0.612	0.3323	0.6482
XM_143286	1.8808			0.8291
Mef2c	1.8808	0.3077	0.3323	
Fxn	1.8808		1.4897	
Cldn15	1.8808	0.3077	0.3323	0.8291
Abcg1	1.8808	0.8565	0.748	0.8291
1700018A04Rik	1.8808	0.612	0.6482	0.3323
XM_288891	1.8755	0.486	0.8291	1.0967
XM_159798	1.8755	0.3077		1.0967
Opn1sw	1.8755	0.7892	0.3323	0.8291
XM_142053	1.8701	0.612	0.5184	1.0967
Cst12	1.8701		0.5184	1.6926
XM_287816	1.8646	0.486	0.3323	0.748
XM_163820	1.8646	0.612	0.3323	0.9565
Ube2b	1.8646	0.3077		0.6482
Tex28	1.8646		1.0548	0.6482
Il1f6	1.8646	0.486	0.5184	1.5056
AU019823	1.8646	0.3077	0.6482	0.6482
XM_484194	1.8591	0.7096	0.3323	0.5184
XM_289610	1.8591	0.486	0.748	0.3323
Usp40	1.8591	1.0534	0.8291	0.748
Hnf4g	1.8591	0.7892		0.3323
XM_283133	1.8535	0.612	0.3323	0.8974
XM_206629	1.8535	0.3077	0.3323	0.3323
Nbeal2	1.8535			0.748
Mageb3	1.8535	0.7892	0.748	0.8291
Idh1	1.8535	0.7096	0.5184	1.0548
Chrna7	1.8535			0.748
Abi2	1.8535	0.486	0.748	1.2026
Zc3h6	1.8478	0.486	0.9565	0.748
XM_136658	1.8478	1.3929		0.3323
Sv2b	1.8478	0.486	0.3323	1.2026
Gria3	1.8478		0.3323	0.3323
Atp11c	1.8478	0.486	0.5184	0.748
Adamtsl5	1.8478		0.3323	1.6388
6530415H11Rik	1.8478			0.3323
XM_196330	1.8421	0.7892	0.6482	0.8291

XM_152071	1.8421	0.9147	0.748	0.748
XM_144344	1.8421	0.966	0.3323	0.6482
Olfr1120	1.8421	0.3077	0.3323	0.3323
Nxph4	1.8421	0.3077	0.6482	0.3323
Nobox	1.8421		0.5184	
Ctps	1.8421	0.3077	0.3323	0.3323
XM_146586	1.8363		0.3323	
XM_136755	1.8363	0.612	0.3323	1.8077
Vmn1r27	1.8363		0.3323	0.3323
Vmn1r234	1.8363			1.1701
Rex2	1.8363	0.486	0.3323	
Pi4k2a	1.8363	0.7096	0.6482	0.5184
Oprk1	1.8363	0.486	0.8974	0.6482
Mthfsd	1.8363	0.612	0.3323	1.5357
Mmrn2	1.8363	0.486	0.5184	0.748
Meox1	1.8363		0.5184	0.6482
XM_164457	1.8304	0.486	0.3323	1.38
XM_139900	1.8304	0.3077		
Orc1	1.8304	0.7892	0.3323	0.8974
Kdm1a	1.8304		0.5184	0.8291
Il13ra2	1.8304	0.3077		0.5184
Fads2	1.8304	1.0119	0.748	0.748
Cdc14a	1.8304			1.0084
A630001O12Rik	1.8304	0.3077	0.6482	1.0084
XM_287214	1.8244	0.3077	0.5184	0.5184
XM_286160	1.8244			0.6482
XM_285317	1.8244	0.486		
XM_161612	1.8244		1.4197	
XM_136631	1.8244	0.3077	1.38	
Panx1	1.8244	0.3077	0.6482	
XM_143381	1.8183	0.966	0.748	0.8291
Pigr	1.8183	0.3077	0.3323	1.4733
Phf14	1.8183	0.7892	1.1349	0.5184
Ddb1	1.8183		0.5184	0.3323
Acvr1b	1.8183	0.486	0.3323	0.748
XM_164930	1.8122	0.3077	0.9565	0.5184
XM_143322	1.8122	0.3077		1.0548
XM_142248	1.8122	0.7096	0.5184	0.6482
Nit1	1.8122	0.3077		0.3323
Ndufb5	1.8122	0.3077		0.5184
Lman1	1.8122	0.8565	1.1349	
XM_287088	1.8059	0.486	0.3323	0.5184
XM_155687	1.8059	0.3077		1.4003
XM_153572	1.8059	0.612	0.5184	1.6152
XM_146339	1.8059	0.3077		0.3323
XM_142206	1.8059	0.7096	0.5184	0.3323
Slc25a36	1.8059	0.3077		0.6482
Ndufv3	1.8059	0.486	0.6482	0.6482
Lpcat3	1.8059	0.3077	0.3323	0.5184
Cyp8b1	1.8059	0.7892	0.748	0.8291
Arrdc4	1.8059	0.8565		0.5184
Aldh5a1	1.8059	0.7096	0.5184	1.0967
A130014A01Rik	1.8059	0.486	0.5184	0.748
XM_285042	1.7996	0.7096	0.6482	0.748
XM_156369	1.7996	0.486	0.6482	0.3323
XM_142289	1.7996	0.3077	0.3323	0.748
Uqcrb	1.7996		1.0084	
Esco2	1.7996	1.3348		0.748
Cc2d2a	1.7996	0.486	0.6482	0.8291
BC051070	1.7996	0.7096	1.2876	0.6482
1700027J07Rik	1.7996	0.486	0.3323	0.748
Zfp710	1.7932	0.612	0.748	1.4197
XM_488869	1.7932	0.612	0.5184	0.748
XM_485998	1.7932	0.3077		
XM_288350	1.7932	0.7892	0.748	0.748
XM_198099	1.7932			
XM_151108	1.7932	0.3077	1.3126	0.5184
XM_144978	1.7932		0.3323	
Tkt	1.7932	0.7096	0.5184	0.5184
Slc35d2	1.7932	0.3077	1.1701	0.6482
Otud4	1.7932	0.966	0.5184	0.5184
Nudt7	1.7932	0.3077		0.3323
Hmgcs2	1.7932	0.486	0.8291	1.0548
Ghrhr	1.7932	0.7096	0.8291	0.8974
C80913	1.7932	1.0119	0.5184	0.8291
Ankrd37	1.7932	0.3077	1.5056	0.3323
Aadat	1.7932	0.486		0.8974
4921509J17Rik	1.7932	0.7096	0.748	0.6482
2810030E01Rik	1.7932	0.486	0.5184	0.5184
XM_355324	1.7866			0.5184
XM_289644	1.7866	0.7892	1.1349	0.8291
XM_288189	1.7866	1.5313		
XM_284820	1.7866	1.0119	0.6482	0.9565
XM_283667	1.7866	0.486	0.3323	0.5184
XM_144818	1.7866	0.612	0.8291	0.6482
XM_143128	1.7866	0.3077	0.3323	1.0084
Trpc3	1.7866	0.3077	0.5184	0.5184

Trank1	1.7866	0.3077	0.5184	0.8974
Shb	1.7866	0.3077	0.3323	0.6482
Olr1743	1.7866	0.486	0.3323	
Nmral1	1.7866	0.3077		
NM_175119	1.7866	0.486	0.3323	0.6482
XM_498096	1.78			
XM_287935	1.78	0.3077	0.5184	0.6482
XM_286998	1.78	0.7892	0.5184	0.5184
XM_286820	1.78	1.0119	0.8291	0.6482
XM_162262	1.78	0.3077	0.6482	0.6482
XM_159492	1.78	0.8565	0.6482	1.1349
XM_152291	1.78		0.3323	
XM_149823	1.78	0.9147	1.3126	0.5184
Tshr	1.78	0.486	0.5184	0.5184
Slc26a5	1.78	1.0119	0.8291	0.8291
Slamf1	1.78	0.7096	0.3323	0.3323
Pxmp3	1.78	0.7892	0.3323	0.6482
NM_175693	1.78	0.3077	1.1701	0.8291
Gja3	1.78			
Btbd3	1.78	1.0119	0.5184	0.8974
1700054N08Rik	1.78	0.8565	0.5184	
XM_285563	1.7733	0.612	1.1701	0.6482
XM_138790	1.7733	0.3077	0.3323	1.6926
XM_136747	1.7733	0.8565		1.7495
Tmem38b	1.7733	0.486		0.748
Sox5	1.7733	0.7096	0.8974	0.8974
XM_484598	1.7665	0.3077		
XM_283664	1.7665	1.0119	0.9565	0.5184
XM_145300	1.7665		0.748	
Nasp	1.7665	0.486	0.5184	1.0967
XM_289037	1.7595	0.486	0.3323	0.8291
XM_146492	1.7595	0.612	0.5184	
XM_138116	1.7595	0.3077	0.3323	1.1349
XM_136854	1.7595	0.612	1.4562	0.6482
Unkl	1.7595	0.612	0.5184	0.3323
Tfrc	1.7595	0.7892	1.0967	0.5184
Tbc1d5	1.7595	0.7096	0.5184	0.6482
Rnpc3	1.7595	0.7096	0.5184	1.38
Pvrl3	1.7595	0.612	1.0084	1.0548
Ltbp3	1.7595	0.3077	0.6482	0.3323
Fam33a	1.7595	0.7892	0.3323	0.3323
Cdr2l	1.7595	0.7096	0.3323	0.3323
Cd3g	1.7595	0.9147	0.5184	0.5184
Ywhaz	1.7525	0.3077	0.3323	0.9565
XM_346281	1.7525		0.3323	1.0548
XM_286958	1.7525	0.612	0.6482	0.8974
XM_283807	1.7525	0.486	0.6482	0.5184
XM_235708	1.7525		0.3323	
XM_111995	1.7525	0.486		1.1701
XM_110935	1.7525	0.486	0.6482	0.5184
Ssh3	1.7525	0.7096	0.6482	0.5184
Sp110	1.7525	0.7892	0.6482	1.0084
Slc25a21	1.7525	0.3077	0.3323	0.748
Ptbp1	1.7525		0.5184	0.3323
Pdcl3	1.7525			
Nat8l	1.7525		0.3323	0.3323
Igf1r	1.7525	0.3077	0.6482	0.5184
A430028G04Rik	1.7525	0.612		0.8291
9130024F11Rik	1.7525	0.3077	0.3323	0.3323
XM_143444	1.7453	0.612	0.5184	0.6482
Npc1l1	1.7453	0.612		1.2611
Ecel1	1.7453	0.3077	0.3323	0.9565
4931407J08Rik	1.7453	1.0119	0.3323	0.6482
XM_488597	1.738		1.0548	0.748
XM_289940	1.738	0.612	0.5184	0.8974
XM_289673	1.738	0.612		0.8291
XM_205148	1.738	0.486	0.3323	0.6482
XM_158650	1.738	0.486		0.9565
XM_153209	1.738	0.486	0.6482	0.5184
XM_141449	1.738	0.3077	0.6482	0.3323
XM_135609	1.738	0.3077	0.748	1.4197
P2rx6	1.738	0.3077	0.3323	1.0084
Olr1307	1.738	0.3077	1.2026	0.5184
NM_177072	1.738	0.612		
Msh3	1.738	0.3077	0.6482	0.6482
Ms4a13	1.738	0.7892	0.6482	0.8291
Klk1b5	1.738		0.3323	
XM_487652	1.7306	0.486	0.6482	0.6482
XM_288353	1.7306	0.8565	0.5184	0.6482
XM_285288	1.7306	0.7096	0.6482	0.8291
XM_156778	1.7306	0.7096		0.748
XM_153581	1.7306	1.2165		0.6482
Wdr60	1.7306	0.486	0.9565	0.6482
Per2	1.7306	0.7096		0.9565
NM_177851	1.7306			
Gba2	1.7306	0.486	0.5184	0.5184
Dync2li1	1.7306	0.7096	0.8291	1.0967

Dok4	1.7306	0.3077		
Crnkl1	1.7306	0.3077	0.3323	0.748
Ccr5	1.7306	0.486	0.6482	1.2328
Art4	1.7306	0.612	0.748	0.9565
6330563C09Rik	1.7306	0.486	0.5184	1.5639
6230409E13Rik	1.7306	0.486		0.8291
XM_289912	1.7231	0.9147	0.5184	1.2876
XM_285250	1.7231			0.748
XM_283445	1.7231	0.3077		0.8974
XM_197365	1.7231	0.3077	0.5184	0.6482
XM_196678	1.7231	0.612	0.5184	0.5184
XM_152059	1.7231	0.3077		1.2876
XM_147670	1.7231	0.3077	0.3323	
Wrn	1.7231	0.486	0.3323	1.6719
Trps1	1.7231	0.8565	0.3323	0.5184
Tmem140	1.7231			
Sel1l2	1.7231	0.7096	0.6482	0.8291
Sash3	1.7231	0.486	0.3323	0.3323
Ppapdc1a	1.7231	0.612	0.5184	1.4383
Pcdhb2	1.7231	0.7892		0.8291
Palm2	1.7231	0.3077		1.6388
NM_177154	1.7231	0.7096	0.5184	0.6482
Nlrp4g	1.7231	0.7096	0.6482	0.6482
Mlph	1.7231	0.3077	0.3323	0.3323
Ccnt1	1.7231	0.3077	0.6482	0.6482
Casd1	1.7231	0.3077	0.3323	0.6482
AI836003	1.7231	0.7096	0.3323	1.0967
4933425L06Rik	1.7231	0.612	0.8974	0.6482
XM_285954	1.7154	0.3077	0.3323	0.3323
XM_285724	1.7154	0.3077	0.6482	0.5184
XM_285683	1.7154	1.2913	0.3323	0.748
XM_158203	1.7154	0.612	0.3323	0.5184
XM_154017	1.7154	0.612	0.9565	0.8291
XM_146131	1.7154	0.8565	0.5184	0.748
XM_145383	1.7154	0.7892		0.3323
XM_129620	1.7154	0.3077	0.748	
Wdr95	1.7154		0.3323	
Trim67	1.7154	0.7892	0.6482	
Thap11	1.7154	0.3077		0.5184
Gm16010	1.7154	0.486	0.3323	0.3323
Fgd6	1.7154	0.7096	0.3323	0.8291
Evpl	1.7154	1.0534	0.748	0.6482
Bend6	1.7154	0.8565	0.3323	0.8291
AI662270	1.7154	0.3077	1.2611	
2810407C02Rik	1.7154	0.3077	0.8291	0.8974
XM_286436	1.7076	0.3077	0.3323	
XM_205401	1.7076	0.612		0.5184
XM_205333	1.7076	0.3077	0.3323	0.3323
XM_195702	1.7076	0.486	0.3323	0.3323
XM_161992	1.7076		0.3323	0.8291
XM_147020	1.7076	0.3077	0.748	0.748
Vmn2r1	1.7076	0.7096	1.1701	0.8291
Olr1234	1.7076		0.3323	
Olfr672	1.7076	0.612	0.8291	0.6482
NM_001004175	1.7076	0.3077		0.8291
Efna4	1.7076		0.3323	0.748
Ccr2	1.7076	0.3077	0.748	1.6272
Ap2a1	1.7076	0.3077		
XM_285308	1.6996			
XM_284766	1.6996	0.7096	0.5184	0.6482
XM_196992	1.6996	0.8565	1.2026	0.3323
Tbck	1.6996	0.3077	0.8974	0.5184
Polr2a	1.6996		0.3323	0.3323
NM_001002769	1.6996	0.612	1.0548	0.748
Dusp27	1.6996	0.612	0.748	0.3323
Dsel	1.6996	0.7096		0.5184
Cyp46a1	1.6996	0.3077	0.3323	0.6482
XM_285385	1.6915	0.3077	0.3323	1.0967
XM_196691	1.6915		0.748	0.748
XM_195729	1.6915			1.5903
XM_195223	1.6915	0.7892		0.5184
XM_165310	1.6915	1.0119	0.5184	0.748
XM_140500	1.6915	0.3077	0.748	0.5184
XM_138058	1.6915	0.966	0.3323	0.3323
XM_136897	1.6915	0.966	0.5184	0.748
XM_129229	1.6915	0.7096	0.3323	0.6482
Rad51ap1	1.6915	0.3077	0.5184	
Npr1	1.6915	0.3077		0.748
XM_488148	1.6832	0.9147	0.6482	1.0084
XM_289160	1.6832			
Rbm33	1.6832	0.3077	0.3323	
Pigk	1.6832		0.3323	0.3323
NM_177223	1.6832	0.3077	1.2611	0.8291
NM_175365	1.6832	0.3077	0.748	0.9565
NM_001004165	1.6832	0.3077	1.0548	0.5184
Myo5a	1.6832	0.486		1.0548
Bmp3	1.6832	0.486	0.3323	1.0084

BC030500	1.6832	0.7892	0.8291	0.8974
1700001L19Rik	1.6832			0.8974
Zfp526	1.6748	1.1885	0.5184	0.748
XM_355758	1.6748	1.1584	0.6482	0.5184
XM_289256	1.6748	0.9147		0.5184
XM_288628	1.6748	0.7892	0.5184	0.8291
XM_284400	1.6748	0.9147	0.6482	0.8291
XM_284081	1.6748	0.7892	0.8291	1.0967
XM_161123	1.6748	0.9147	0.5184	0.6482
XM_157769	1.6748	0.7096	0.5184	0.8291
Slc10a1	1.6748	0.8565	0.5184	0.6482
Rabggtb	1.6748		0.3323	0.3323
Ppp4c	1.6748	0.8565	1.2328	0.5184
Olfr887	1.6748	0.486	1.4197	0.3323
Gucy1a3	1.6748	0.3077	1.0967	0.8291
Gna11	1.6748	0.612	0.6482	
Fras1	1.6748	0.3077	1.3126	
XM_288931	1.6662	0.7892	0.6482	1.2611
XM_287220	1.6662	0.3077	0.5184	0.6482
XM_163861	1.6662	0.7892		1.0084
XM_160007	1.6662		0.748	0.5184
XM_139069	1.6662	0.7892		0.5184
XM_136398	1.6662	0.7096	0.748	0.5184
Taf7	1.6662	0.7892	0.6482	1.0967
Rbm25	1.6662	0.612	0.3323	0.5184
Plch2	1.6662	0.3077		0.3323
Obp1a	1.6662	0.8565	0.748	0.8291
NM_183108	1.6662			0.748
NM_177264	1.6662	0.612	0.5184	0.5184
Gpr77	1.6662	0.7892	0.8974	0.8974
Exosc9	1.6662	0.3077		0.3323
Eci3	1.6662	0.486	0.3323	
D19Bwg1357e	1.6662		0.748	0.748
Cideb	1.6662	0.7096	0.3323	1.0967
Cdh12	1.6662	0.612	0.3323	
Adora2b	1.6662	0.486	0.748	0.8974
XM_155270	1.6575		1.2026	1.4197
XM_149933	1.6575	0.3077		0.5184
XM_136197	1.6575	0.612	0.748	0.8974
Rft1	1.6575	0.486		0.6482
Pldi	1.6575			0.748
Piga	1.6575	0.7096		0.3323
NM_027720	1.6575	0.3077		
Il23r	1.6575	0.8565		0.5184
Il17rc	1.6575	0.3077	0.5184	0.748
Fam132b	1.6575	0.486	0.5184	1.0967
Clptm1	1.6575	0.3077	0.3323	0.3323
Cdh24	1.6575	0.3077	0.3323	0.3323
5930416I19Rik	1.6575	0.612	0.3323	0.6482
XM_286393	1.6485	1.0913		0.3323
XM_159854	1.6485	0.7096	0.8291	0.6482
XM_157854	1.6485	0.486	0.3323	0.6482
XM_111099	1.6485	0.7096	0.3323	0.3323
Rab5b	1.6485			
Pole2	1.6485	0.3077		0.5184
Plek	1.6485	0.486	1.2328	
Olfr1302	1.6485	0.3077	0.6482	0.5184
Nudt13	1.6485	0.3077		0.5184
Igfbp4	1.6485	0.486	0.3323	1.0084
Hgd	1.6485	0.3077	0.8291	
Dmbx1	1.6485	0.3077	0.5184	
C030013D06Rik	1.6485		0.6482	0.5184
Zfp120	1.6394	0.7892	0.5184	0.3323
XM_342286	1.6394	0.3077		0.3323
XM_283131	1.6394	0.3077	0.3323	
XM_193686	1.6394	0.612	0.5184	0.6482
XM_164432	1.6394	0.3077	0.5184	0.8291
XM_152301	1.6394	0.7096		0.3323
Tpst2	1.6394	0.3077	0.3323	0.3323
Setd6	1.6394	0.7096	0.5184	0.5184
Pla2g10	1.6394	0.612	0.8291	0.9565
Micall2	1.6394		0.3323	0.5184
Glra1	1.6394	0.3077	0.3323	0.5184
Baiap2l1	1.6394	0.486	1.0548	1.0548
9330155M09Rik	1.6394	0.8565	0.3323	0.8291
4930534B04Rik	1.6394	0.7892		0.6482
XM_487912	1.6301	0.966	0.748	0.8291
XM_287939	1.6301	0.7096	0.6482	0.748
XM_285813	1.6301	0.8565	0.8291	1.0084
XM_144874	1.6301	0.3077	0.6482	0.5184
Pvalb	1.6301	0.612		0.6482
Prdm5	1.6301	0.7892	0.6482	0.6482
Olfr262	1.6301	0.3077	1.0084	0.6482
Obox6	1.6301	0.9147	0.8974	0.8291
Mgrn1	1.6301			0.3323
Gpr61	1.6301		0.5184	0.3323
Dusp21	1.6301	1.0913	0.5184	

Ctnnbl1	1.6301	0.8565	0.5184	0.6482
Cer1	1.6301	0.486	0.3323	0.3323
Ccdc134	1.6301	0.3077	0.748	0.8974
XM_357382	1.6206	0.486	0.3323	0.5184
XM_289357	1.6206	0.966	0.5184	0.8974
XM_287044	1.6206	0.3077	0.3323	1.5209
XM_197039	1.6206	0.7892		0.8291
XM_149341	1.6206	0.9147	0.6482	0.6482
XM_146052	1.6206			0.3323
XM_140287	1.6206			1.2328
Tmem35	1.6206	0.486	0.6482	1.5773
Tmem120b	1.6206	0.3077	0.3323	
Tmed1	1.6206	0.486	0.748	
Ssh1	1.6206	0.7892	0.5184	0.6482
Spink6	1.6206	0.612	0.3323	0.8291
Rbm46	1.6206	0.486	0.6482	0.9565
Htr2a	1.6206	0.3077	1.4897	0.3323
Hspa12a	1.6206	0.7892	0.5184	0.5184
Fitm1	1.6206	0.612	0.3323	0.3323
Defb2	1.6206		0.5184	1.2611
Bub1	1.6206	0.3077	0.5184	0.6482
Alkbh3	1.6206	0.612		0.8291
XM_195531	1.6108	0.7096	0.5184	0.748
XM_154436	1.6108	0.3077	0.5184	0.8974
XM_142683	1.6108	0.486	0.5184	0.748
XM_141920	1.6108	0.486	1.4733	0.3323
XM_127893	1.6108	0.3077		0.3323
Troap	1.6108	0.3077	0.5184	0.5184
Sbpl	1.6108			0.748
Ppp1cc	1.6108	0.612	0.3323	0.5184
Olfr799	1.6108	0.3077	0.5184	0.8974
Olfr1230	1.6108	0.7096	0.5184	0.748
Oas1d	1.6108	0.3077		0.5184
Med21	1.6108	0.612	0.9565	0.3323
Ldhal6b	1.6108		0.3323	
Eif4g2	1.6108			
Col28a1	1.6108		0.3323	0.5184
Abcc4	1.6108	0.7096	0.748	0.5184
2810007J24Rik	1.6108	0.486	1.2026	0.3323
Zfp295	1.6009			
XM_195545	1.6009	0.7096	0.5184	0.748
XM_195373	1.6009	0.486		1.5056
XM_161710	1.6009	0.3077	0.6482	0.8974
XM_142299	1.6009		0.748	0.3323
XM_140147	1.6009	0.486	0.748	0.3323
XM_137491	1.6009	0.3077	0.5184	1.0967
Vmn1r201	1.6009	0.612	0.3323	0.5184
Tomm22	1.6009	0.486	0.748	1.4383
Spag5	1.6009	0.3077	0.3323	0.8291
Olfr1256	1.6009	0.612		0.8291
NM_183125	1.6009	0.612	0.3323	
Hoxb8	1.6009	0.3077		0.8974
Hivep2	1.6009	0.7096	0.5184	1.2328
Gsc	1.6009	0.486	0.6482	0.3323
Foxa2	1.6009	0.612		0.748
Cdh20	1.6009	0.612	0.3323	
B830007D08Rik	1.6009	0.8565	0.5184	0.8974
XM_489005	1.5907	0.3077	1.2328	0.8291
XM_289219	1.5907	0.486	0.5184	1.4197
XM_287278	1.5907			
XM_287013	1.5907	0.3077		0.3323
XM_285464	1.5907		0.5184	0.5184
XM_204855	1.5907	0.3077	0.3323	0.3323
XM_164401	1.5907	0.612	0.5184	0.6482
XM_150641	1.5907	0.3077		0.3323
XM_144457	1.5907	0.486	0.5184	0.8291
XM_137254	1.5907	0.3077		
XM_124482	1.5907		0.3323	0.748
Steap2	1.5907	0.3077		0.5184
Slc12a2	1.5907	0.3077	1.3363	0.5184
Ptprq	1.5907	1.5313	0.3323	0.3323
Olfr954	1.5907	0.9147	0.6482	
Olfr1242	1.5907	0.7096	0.6482	0.5184
Olfml2b	1.5907	0.3077		
Mfsd4	1.5907	0.612		0.5184
Irak2	1.5907	0.3077		0.3323
Igfbp3	1.5907	0.486	0.6482	0.748
Adat2	1.5907	0.612	0.8974	0.8291
Adamts12	1.5907	1.0119	0.5184	1.0084
Zbtb10	1.5802		0.748	0.748
XM_489765	1.5802	0.8565	0.3323	0.8291
XM_158881	1.5802	0.7892	0.3323	1.0084
XM_153340	1.5802	0.486	0.3323	1.0084
XM_145657	1.5802	0.3077	0.3323	0.6482
Usp33	1.5802			0.3323
Suox	1.5802			0.3323
Rnf130	1.5802	0.3077	0.5184	

Rab18	1.5802	0.8565	0.748	0.6482
Gprc5b	1.5802	1.4106	0.3323	0.3323
Glt6d1	1.5802	0.486	0.3323	1.0084
Fabp7	1.5802	0.612	0.748	0.5184
Chd6	1.5802	0.3077		
BC053393	1.5802	1.0534	0.6482	0.8291
Adam7	1.5802	0.3077	0.8974	
6030422M02Rik	1.5802			0.3323
Xpnpep2	1.5695	0.7892	1.1701	
XM_355803	1.5695			0.3323
XM_289314	1.5695	0.3077		0.6482
XM_284316	1.5695	0.3077		0.6482
XM_165008	1.5695	0.486	0.6482	0.3323
XM_155110	1.5695	0.8565	0.5184	0.5184
XM_151594	1.5695	0.3077	0.5184	0.3323
XM_150456	1.5695	0.3077	0.3323	1.1349
XM_141278	1.5695	0.7096	0.6482	0.748
Psmd9	1.5695			
Phkb	1.5695	0.3077	0.5184	
Olr30	1.5695	0.486	0.5184	0.6482
Olfr38	1.5695	0.3077	0.3323	
Olfr116	1.5695	0.486	0.5184	0.8974
NM_177121	1.5695	1.1262	0.6482	0.8291
Mrps28	1.5695	0.3077	0.3323	0.748
Hopx	1.5695		0.3323	1.0967
Gm3286	1.5695	0.486	0.6482	0.6482
Frk	1.5695		0.6482	0.3323
Col18a1	1.5695	0.486		1.2876
Ccl27a	1.5695	0.3077		
Calm2	1.5695			1.2611
Armc3	1.5695		0.3323	0.5184
XM_285406	1.5585	0.612	0.3323	0.5184
Tspan9	1.5585	0.7096	0.5184	0.6482
Psmc2	1.5585	0.3077	0.5184	0.6482
Pcp2	1.5585	0.7096	0.5184	0.3323
Olfr1364	1.5585	0.8565	0.6482	0.748
Noc3l	1.5585	0.486	0.5184	0.3323
NM_177641	1.5585	0.486	0.8291	1.2026
Hmgb3	1.5585	0.3077	0.3323	
Cabyr	1.5585	0.3077		0.5184
2010002N04Rik	1.5585	0.7892		0.5184
Zfp493	1.5473	0.7892		0.8974
XR_000249	1.5473	0.612	0.5184	1.4562
XM_487706	1.5473	0.3077		
XM_164674	1.5473	0.8565		0.6482
XM_162478	1.5473			0.8291
XM_160248	1.5473	1.1885	0.3323	0.8291
XM_153404	1.5473	0.3077	0.3323	0.6482
XM_145247	1.5473	1.0119	0.6482	0.748
XM_140111	1.5473	0.3077	0.3323	0.3323
Slx4	1.5473	0.612	0.5184	0.748
Slco6d1	1.5473	0.7096	0.3323	0.6482
Rfc4	1.5473	0.486	0.8974	0.8291
Ptprk	1.5473	0.3077		
Ptch1	1.5473			0.3323
Olfr745	1.5473	0.7892	0.6482	0.8974
Ncoa2	1.5473		0.8291	0.6482
Nans	1.5473	1.0534	0.5184	0.8291
Grxcr2	1.5473	0.612		
Glmn	1.5473	0.7096	0.3323	0.3323
Fbxl7	1.5473	1.0534		0.9565
Ect2	1.5473	0.612	1.0548	0.3323
Dsg1c	1.5473	0.3077		0.3323
D030056L22Rik	1.5473	0.612	0.748	0.5184
Coro2a	1.5473	0.8565		1.1701
Aqp7	1.5473	0.3077	0.6482	0.5184
AI314278	1.5473	0.7096		1.3363
2610305D13Rik	1.5473	0.7096	0.3323	0.748
XM_289586	1.5357	0.612	0.6482	1.3126
XM_286301	1.5357	0.7096	0.8974	0.748
XM_283866	1.5357	0.3077	0.3323	
XM_197869	1.5357	0.486	0.5184	1.3126
XM_145453	1.5357	0.7096	0.3323	0.5184
XM_145191	1.5357	0.486		0.5184
XM_140162	1.5357	0.3077		
XM_112123	1.5357	0.3077	0.3323	
Tomm20l	1.5357	0.612		
Smc2	1.5357	1.0119	0.6482	0.5184
Siglech	1.5357	0.7096	0.748	0.8291
Rpf1	1.5357	0.3077	0.5184	0.5184
Rfwd3	1.5357		0.8291	0.3323
Ptchd1	1.5357		0.3323	0.6482
Poglut1	1.5357		0.5184	0.8974
Olr772	1.5357	0.612	0.8974	0.8291
Il12b	1.5357	1.0119	0.5184	0.6482
Gpx2	1.5357	0.486	0.3323	1.1701
Fhl1	1.5357	0.7096	0.3323	0.8291

Eif5a2	1.5357	0.486	0.8291	0.3323
Dclre1c	1.5357	0.3077	0.5184	
C2cd2	1.5357	0.3077	0.748	1.0548
Asb4	1.5357		1.3587	0.3323
Acacb	1.5357		0.5184	1.5209
A1cf	1.5357	0.8565	0.5184	0.9565
1700008K24Rik	1.5357	0.486	0.3323	0.8291
Zswim3	1.5238		0.3323	0.748
XM_285923	1.5238	0.7892	0.3323	1.4383
XM_284960	1.5238	0.3077	0.748	0.3323
XM_195159	1.5238	0.612		0.5184
XM_165113	1.5238	0.3077	0.5184	0.5184
XM_152906	1.5238	0.3077	0.3323	0.6482
XM_151864	1.5238	0.486	0.6482	0.5184
XM_147684	1.5238	0.7096		1.0084
XM_143290	1.5238	0.8565		0.6482
XM_139201	1.5238	1.0119	0.3323	0.6482
XM_137953	1.5238			0.6482
XM_112832	1.5238	0.612	0.8291	0.6482
Vwc2l	1.5238	0.7096	0.748	1.1701
Scaf4	1.5238	0.486	0.3323	1.0548
Rsrc2	1.5238	0.8565	0.6482	0.5184
NM_176985	1.5238	0.7892	0.3323	1.2328
Klf5	1.5238	0.3077	0.3323	0.6482
Kif15	1.5238	0.612	0.3323	
Golim4	1.5238			
Cno	1.5238		0.3323	0.5184
C030046I01Rik	1.5238	0.486	0.5184	0.5184
6330578E17Rik	1.5238	0.7096	0.6482	0.8291
4930417G10Rik	1.5238	0.486	0.8291	0.6482
1700061A03Rik	1.5238	0.612		0.748
XM_485773	1.5116		0.6482	1.4562
XM_287631	1.5116	0.7096	0.3323	0.8974
XM_285928	1.5116	0.7892	0.748	1.1349
XM_284831	1.5116	0.3077		0.3323
XM_284767	1.5116			0.5184
XM_283146	1.5116	0.3077	1.3363	0.6482
XM_196837	1.5116	0.3077		0.5184
XM_142669	1.5116			0.5184
Spag9	1.5116	1.1262	0.3323	0.6482
Olfr854	1.5116	0.3077	0.3323	0.5184
Nr2e1	1.5116	0.612	0.3323	
NM_001005857	1.5116	0.612		0.748
Mpo	1.5116	0.7096	0.748	0.5184
Gm22	1.5116	0.486	1.0084	1.0548
Gjb3	1.5116		0.748	0.3323
Fam192a	1.5116	0.3077		0.5184
Casp8ap2	1.5116	0.3077		0.5184
Bap1	1.5116	0.3077		0.3323
4922502B01Rik	1.5116	0.9147	0.6482	0.5184
1700007K09Rik	1.5116	0.3077	0.6482	
XM_194658	1.0832	2.6098	0.6482	0.9565
XM_198119	0.4551	2.4348	0.748	0.8974
Cdh18	0.8166	2.4094	1.2328	0.3323
XM_290100	0.9247	2.4094	0.8974	1.0084
Zfp239		2.3898	1.4897	1.1701
XM_286410	0.9247	2.3879	0.8974	0.6482
Apba3	0.2846	2.3749	0.8291	0.5184
NM_175463	0.7505	2.3749	0.5184	0.5184
XM_140720	0.5772	2.3749	0.3323	0.5184
Fbxo10	0.4551	2.3556	0.748	0.3323
Daxx	0.97	2.3415	1.4383	0.3323
Mdm1	0.2846	2.3374	0.3323	
Stat2		2.3374		0.8974
Gria1	0.2846	2.3312	1.0084	0.9565
XM_287554	0.2846	2.3312		0.6482
XM_488727	0.6724	2.3249	0.5184	1.7837
Pi15	1.0111	2.3185	0.748	1.1349
XM_152039	0.8166	2.3032	0.6482	0.748
Klhl10	0.8166	2.2987	0.3323	1.4003
XM_142770	1.0111	2.2987	0.8974	1.0548
Olfr1406	1.0486	2.2942		0.6482
XM_285604		2.2942	0.3323	
NM_177579		2.2873	1.5773	1.0967
XM_143807	0.8166	2.285		0.8291
Rab9	0.874	2.2803	0.9565	1.1701
Itpr2	0.7505	2.278	0.5184	0.5184
Mrpl18	0.4551	2.2756	0.6482	0.5184
Tpcn1	1.0486	2.2756	0.3323	0.748
XM_160493	0.874	2.2708	0.748	0.5184
XM_287443	1.2693	2.2708	0.6482	0.5184
XM_138422	0.874	2.2684	0.8291	1.0084
Ube2o	1.6915	2.266	0.3323	
Nos3		2.2636	0.6482	
XM_287399	0.4551	2.2587	0.5184	0.8291
Appbp2		2.2562		0.3323
Zfp943		2.2562	0.8291	0.748

Il3	0.7505	2.2537	0.8974	0.748
Sval3	0.874	2.2537	0.3323	0.6482
XM_163867	1.145	2.2537	0.8974	0.5184
XM_284980	0.6724	2.2537	0.6482	0.6482
XM_154613	0.8166	2.2512		1.2328
Stfa3	0.97	2.2461	0.3323	1.4562
Wdr13	0.2846	2.2436	0.3323	
XM_151707		2.2436		0.748
Grpel1	0.7505	2.241	0.6482	0.8291
Lrrc37a	0.5772	2.2359	0.3323	1.4003
Tmcc3	0.7505	2.2359	0.8291	0.6482
Vps8	0.5772	2.2333	0.5184	0.3323
Ddx4	0.2846	2.2306	0.3323	0.748
XM_287996	0.8166	2.2306	0.748	0.6482
Zfp14		2.2306	0.3323	1.0967
Vmn1r208	0.2846	2.228	0.3323	0.6482
XM_139826	1.1152	2.228	0.748	0.6482
Uchl5	0.2846	2.2227	0.8291	1.2026
Hif1an	0.7505	2.2173	0.8291	1.0084
Sec61a1	0.4551	2.2118	0.3323	0.6482
Wdr52	0.4551	2.2118	0.5184	0.8974
XM_285447	0.7505	2.2118	0.3323	0.3323
Pfkl	0.6724	2.209	0.3323	0.748
XM_159819	0.5772	2.209	0.8974	0.748
XM_283622	0.7505	2.209	0.3323	0.748
XM_160677	0.6724	2.2063	0.3323	0.8974
XM_488274		2.2035		0.3323
Arg1	0.5772	2.2007	0.3323	1.2611
Ccdc47	0.5772	2.2007	0.3323	0.748
Gm4841	0.4551	2.195		0.8291
XM_136496	0.874	2.195	0.748	1.2876
Mif	0.4551	2.1921	0.3323	0.5184
2700033N17Rik	0.2846	2.1892		0.5184
NM_183095	0.5772	2.1892	0.5184	0.8291
Taar6	0.4551	2.1863	0.3323	0.5184
Lcn4	0.5772	2.1834	1.1701	0.8291
XM_112000	1.3106	2.1834	0.8291	0.748
Zcchc13	0.6724	2.1834	0.5184	0.3323
R3hdm2	0.5772	2.1805	0.3323	1.0967
Abcb1a	0.2846	2.1775		1.3363
Ankrd61	0.9247	2.1775	0.748	0.3323
Timm8a2	0.9247	2.1775	0.748	1.0084
XM_111960	0.4551	2.1775	0.748	1.6824
XM_155317	0.874	2.1745	0.8974	0.748
XM_487442	0.8166	2.1715	0.5184	1.2876
Ncrna00086	0.5772	2.1654	0.748	0.748
XM_154071	0.6724	2.1654	0.3323	1.6611
XM_157117	0.7505	2.1654	0.748	1.0967
Hdx	0.2846	2.1624	1.0548	0.8291
XM_136226	0.4551	2.1593	1.3587	0.6482
Setd5	0.5772	2.1561	0.748	0.3323
XM_142897		2.1561	0.8291	0.8291
XM_144249	0.5772	2.1561	0.9565	0.6482
XM_158324	0.5772	2.1561	0.8291	1.3363
C030046E11Rik	0.2846	2.153	0.3323	1.1349
XM_152067	0.5772	2.153		0.6482
XM_160027	0.8166	2.153	1.0084	0.748
1700071K01Rik	0.2846	2.1499	0.5184	0.6482
Dpp6	0.4551	2.1467	0.6482	0.6482
Ttc12	0.6724	2.1435	0.5184	0.8974
XM_138891	0.4551	2.1435		0.3323
C3orf77	0.2846	2.1402	0.5184	0.3323
Inpp5b		2.1402		0.5184
Mrpl47	0.5772	2.137	0.748	0.748
Tbce	0.8166	2.137	1.0548	
Fam46a	0.5772	2.1337	0.5184	1.5056
XM_157625	1.3106	2.1337	0.6482	
XM_288365	0.97	2.1337	0.748	1.0548
Zfp623	0.2846	2.1337		1.1349
Grin1	0.2846	2.1304		1.5056
Ireb2	0.5772	2.1304	0.3323	1.0084
Med8		2.1304	0.3323	1.4383
XM_138931	1.1152	2.1304	0.6482	0.5184
Brcc3		2.1271	0.5184	0.748
Kcns2	0.4551	2.1271		0.5184
Srbd1		2.1271	0.3323	0.748
Mcoln1	0.874	2.1237	0.748	0.8291
NM_173366	0.8166	2.1237	1.1701	0.5184
Kcnj15	0.4551	2.1203	0.3323	1.4562
C130030J05	0.7505	2.1135	0.5184	0.5184
XM_286709	0.2846	2.11	0.8291	0.9565
XM_487654	0.2846	2.11	0.748	
Fam176a	0.2846	2.1065	0.3323	
Il34	0.2846	2.1065	0.748	1.4733
XM_140136	0.9247	2.1065	0.748	1.3126
Hsd17b3	0.5772	2.103	1.0548	
XM_284519		2.103	0.3323	0.3323

XM_285814	0.7505	2.103		0.8291
XM_489226		2.0995	1.3587	1.2026
Ano3	0.4551	2.0959	0.8291	0.5184
Slc7a6	1.0486	2.0959	0.6482	1.0967
LOC440248	0.2846	2.0923	0.3323	0.3323
Plagl2	0.4551	2.0923		1.3363
Abcc9	1.0111	2.0887	0.5184	0.6482
Cckbr	0.4551	2.0887	1.0967	0.8291
XM_149369	0.4551	2.0887	0.748	0.6482
Dpcr1	0.6724	2.085	0.8291	0.8974
Klhl2	0.5772	2.0813	0.6482	0.8974
XM_155133	0.6724	2.0813	0.6482	1.2026
XM_288566	1.0832	2.0813	0.5184	1.0084
Cog1	0.2846	2.0776	0.3323	0.5184
Tmem59	0.874	2.0776	0.5184	1.2611
XM_139042	0.6724	2.0776	0.5184	0.6482
XM_142201	0.7505	2.0776	0.6482	0.9565
AY358078	0.4551	2.0738	0.748	0.5184
Pin1-ps1	0.6724	2.0738	0.3323	0.8291
XM_197734	0.4551	2.0738	0.3323	0.3323
Itpr1	0.2846	2.07		0.5184
XM_147954	0.4551	2.07	0.3323	0.8291
Nup155		2.0662		
Ocln	0.8166	2.0662		0.748
Stbd1	0.7505	2.0662	0.6482	0.5184
Wdr44	1.1152	2.0662	0.748	1.0967
XM_153222		2.0662		0.5184
XM_161006	0.5772	2.0662	0.5184	0.5184
XM_161926	0.7505	2.0662	0.6482	0.3323
XM_286001	0.874	2.0662	0.6482	0.8291
XM_288357	0.8166	2.0623	0.748	1.1701
XM_288485	0.5772	2.0623	0.6482	
Cst10	0.5772	2.0584	0.6482	0.5184
Dpys	0.5772	2.0584		0.5184
Rlim	0.874	2.0584	0.6482	0.6482
Tgm5	1.145	2.0584	0.3323	1.4562
XM_128922	0.2846	2.0584	0.3323	
XM_143314	0.6724	2.0584	0.6482	1.0548
Cd24a	0.2846	2.0545	0.3323	
Emr4	0.9247	2.0545	0.5184	0.3323
Xdh	0.2846	2.0545		
XM_157396	0.4551	2.0545	0.748	0.748
6030498E09Rik	0.5772	2.0505	0.5184	0.3323
Ccnk	0.7505	2.0505	0.3323	1.0548
Olfr902	0.6724	2.0505	0.3323	0.748
Pdia3	0.2846	2.0505		
Themis	0.6724	2.0505	0.748	0.9565
Vmn1r195	0.97	2.0505	0.748	0.9565
Alox12b	0.5772	2.0465	1.2876	0.8291
NM_175323	1.0486	2.0465	0.5184	0.6482
XM_146428	1.1152	2.0465	0.5184	0.748
B230219D22Rik	0.7505	2.0425	0.6482	0.6482
Med24	0.7505	2.0425	0.3323	1.1349
Mettl22	0.7505	2.0425	0.5184	1.5056
XM_143530	0.5772	2.0425	0.3323	1.38
XM_356870	0.6724	2.0425	0.6482	0.9565
Rgs2	1.5116	2.0384	0.3323	0.5184
XM_284785	0.4551	2.0384	0.5184	0.5184
XM_140005	1.5695	2.0343	0.3323	0.5184
XM_207320		2.0343	0.3323	
XM_289092	0.5772	2.0343	0.5184	0.6482
FLJ38973	0.2846	2.0301	0.5184	
Uck2	0.5772	2.0301	0.3323	0.9565
XM_138727	0.7505	2.0301	0.9565	0.8974
XM_288757	1.0486	2.0301		0.5184
Galnt10	0.4551	2.0259	1.0967	0.748
Tox	0.7505	2.0259	0.6482	1.1349
XM_158701	0.2846	2.0259		0.748
XM_289459	0.6724	2.0259	0.3323	0.6482
XM_489850		2.0259		0.5184
Akr1c20	0.5772	2.0217	0.3323	0.3323
Mtx2	0.7505	2.0217	0.6482	0.3323
Ttll8	0.2846	2.0217	0.9565	1.0967
XM_154529	0.8166	2.0217	0.3323	0.5184
XM_288366		2.0217		0.3323
XM_290165	0.2846	2.0217	1.7754	0.5184
Csnk2b	1.0111	2.0174	1.0548	0.5184
XM_483933	0.874	2.0174	0.3323	0.9565
Abcb10		2.0131	1.0548	1.3587
Impact	0.8166	2.0131	0.8974	0.6482
Nlrp1a	0.8166	2.0131	0.3323	0.748
Vmn1r32	0.9247	2.0131	0.748	0.3323
1700110C19Rik	0.5772	2.0087		0.3323
Akr1b8	0.6724	2.0087	0.6482	0.5184
Lmo7	0.5772	2.0087	0.748	1.1349
Tnpo1	0.874	2.0087	0.8974	1.0967
XM_356816	0.2846	2.0087		1.5639

Zbtb20	0.8166	2.0087	0.3323	1.0084
Irak1bp1		2.0043		
Rbbp6	0.874	2.0043		0.3323
Rcor2	0.6724	2.0043	0.5184	0.8974
Unc13b		2.0043		1.0967
Ctsz		1.9999	0.3323	1.0084
XM_111991	0.7505	1.9999	1.0548	0.8291
XM_149318	0.5772	1.9999	0.5184	1.0084
Ccdc86	0.97	1.9954	0.6482	0.3323
XM_484255	0.7505	1.9954	0.3323	0.5184
0610010F05Rik	1.0111	1.9908	0.6482	1.0548
XM_147461	0.5772	1.9908		0.3323
XM_196055	0.5772	1.9908	0.5184	0.748
Plxdc2	0.5772	1.9862	1.2026	0.8291
Wdr66	0.6724	1.9862	0.748	1.1701
XM_137301	0.4551	1.9862	0.3323	0.8291
XM_164596	0.9247	1.9862	0.5184	1.3126
Olfr1128	0.6724	1.9816	0.3323	0.5184
Wbp11	0.6724	1.9816	0.748	1.1349
XM_143076	1.3106	1.9816	0.3323	0.8291
XM_165074	0.6724	1.9816	0.8291	1.2328
Adam2	0.5772	1.9769	1.0084	0.5184
CXorf15	0.2846	1.9769		0.5184
NM_172949	0.4551	1.9769		
Srpx	0.5772	1.9721	0.3323	0.3323
XM_147077		1.9721		
XM_196466	0.8166	1.9721		
1700061I17Rik	0.2846	1.9673	0.5184	0.5184
Ccdc87	0.6724	1.9673		
Osbpl10	0.7505	1.9673	0.9565	0.8291
Tspan11	0.5772	1.9673	0.5184	1.1349
XM_145639	1.4449	1.9673	0.5184	0.8291
XM_286939	0.5772	1.9673	1.4562	0.5184
Dcun1d4	0.4551	1.9625	0.748	0.748
Gm4910	0.8166	1.9625	0.5184	0.3323
Mast1		1.9625	0.3323	0.5184
Slc9a1	0.4551	1.9625	0.5184	0.5184
Ube2e1	0.2846	1.9625	0.6482	1.5903
XM_153787	0.2846	1.9625		0.5184
XM_157802	0.4551	1.9625	0.6482	0.748
XM_195450	1.2238	1.9625	0.3323	0.3323
XM_205047	0.2846	1.9625		0.8291
XM_287115	0.6724	1.9625	0.5184	0.748
Ddx25	0.6724	1.9576		1.0967
Rsph6a	0.5772	1.9576		0.8291
Tor1aip2	0.6724	1.9576	0.3323	0.6482
XM_287930	0.5772	1.9576	0.748	0.6482
XM_288883	0.2846	1.9576	0.748	0.6482
Krtap13-1		1.9526		1.4897
Olr1734	0.4551	1.9526	0.6482	
XM_138327	0.7505	1.9526	0.3323	0.3323
XM_286315		1.9526		0.6482
Spats2l		1.9476	0.5184	0.5184
Srp72	0.8166	1.9476	0.5184	1.38
Trmt5	0.4551	1.9476	1.2328	0.5184
Wdr59	0.6724	1.9476	0.3323	
XM_153298	0.4551	1.9476	0.3323	0.748
XM_157269	0.5772	1.9476	0.748	1.0967
XM_160052	0.6724	1.9476	0.748	0.8974
XM_198046	0.4551	1.9476	0.5184	0.6482
XM_205424	0.2846	1.9476		
Cnksr2	0.97	1.9425	0.3323	0.3323
Gcfc1	0.2846	1.9425	0.3323	0.3323
Ltb4r2		1.9425	0.3323	1.2611
Tyk2	0.2846	1.9425	0.3323	
XM_197764	0.4551	1.9425	1.2026	1.1701
XM_287357	0.2846	1.9425	0.3323	
BC005764	0.5772	1.9374	0.748	0.3323
Heatr1	0.97	1.9374	0.5184	0.9565
Ncoa3	0.5772	1.9374		0.5184
XM_160842	0.7505	1.9374	0.8291	1.0084
Ankrd22	0.2846	1.9321	0.3323	1.55
Dock2	0.2846	1.9321	0.6482	0.9565
Naa16		1.9321	0.3323	0.3323
Spp1	1.7231	1.9321		0.748
Ak3		1.9269	0.3323	0.5184
Emb	0.4551	1.9269	0.748	1.5357
XM_288765	0.2846	1.9269	0.6482	0.5184
Fam167b	0.4551	1.9216	0.3323	1.5056
Gfra2		1.9216	0.3323	0.5184
XM_138742	0.6724	1.9216	1.2026	0.3323
XM_163306	0.2846	1.9216	0.3323	1.4733
XM_287222	1.6748	1.9216	0.3323	0.8974
Fcgr3	0.4551	1.9162	0.3323	
Gm4861	0.4551	1.9162	0.8291	0.6482
Myl6	0.2846	1.9162	0.3323	0.6482
XM_151226	0.8166	1.9162	0.5184	0.5184

XM_165182	0.8166	1.9162	0.6482	0.8974
XM_181351	0.6724	1.9162		0.5184
XM_288344	0.6724	1.9162	0.5184	0.6482
XM_289024	0.2846	1.9162		
Amdhd1	0.6724	1.9107	0.8974	0.8291
Ccny	0.4551	1.9107	0.5184	0.748
Fkbp11		1.9107		
Klc2	0.4551	1.9107	0.5184	0.3323
Mageb4	0.8166	1.9107	0.5184	1.0548
Olfr690		1.9107		
Phospho2	0.5772	1.9107	0.6482	0.8974
Smpd2	0.97	1.9107	0.3323	0.8291
XM_112088	0.7505	1.9107	0.5184	0.6482
XM_140510	0.874	1.9107	0.748	0.3323
4921524J17Rik	1.0111	1.9052	0.3323	0.5184
XM_127959	0.4551	1.9052	0.5184	0.3323
XM_130033	0.4551	1.9052		0.3323
XM_137067	1.145	1.9052		0.5184
XM_139608	0.6724	1.9052	1.2876	0.8291
XM_153721	0.7505	1.9052	0.3323	1.6719
XM_154525	0.7505	1.9052	0.5184	1.4733
XM_161619	0.5772	1.9052	0.5184	0.748
XM_286728	0.4551	1.9052	0.3323	0.3323
XM_287668	0.6724	1.9052	0.6482	1.4897
XM_288193	0.5772	1.9052	0.5184	0.6482
A230050P20Rik	0.4551	1.8996	0.9565	0.748
Kcnn1	0.2846	1.8996		0.5184
Slc17a6		1.8996	0.8291	0.3323
XM_285570	0.6724	1.8996	0.8291	1.0967
2310002L09Rik	0.5772	1.8939	0.5184	1.0084
App	0.4551	1.8939	0.8291	1.0967
NM_177065		1.8939	0.5184	1.0084
XM_142475	0.2846	1.8939		0.3323
XM_341661	0.2846	1.8939		0.3323
1100001G20Rik	0.4551	1.8881	0.8974	0.3323
Rnf222	0.4551	1.8881	0.3323	1.2611
XM_141259	0.4551	1.8881	0.748	0.6482
XM_155978	0.4551	1.8881	0.3323	0.3323
XM_163100	0.4551	1.8881	0.8291	0.6482
XM_285637	0.7505	1.8881	0.5184	0.3323
5830433M19Rik	0.2846	1.8823	0.5184	0.8291
Cbfa2t2	0.874	1.8823	0.3323	0.3323
Cox7b	0.6724	1.8823	0.3323	0.748
Gm5068	0.4551	1.8823	0.3323	0.6482
Ints5	0.874	1.8823	0.5184	1.1349
Olig1		1.8823		0.3323
Trim65		1.8823		
XM_165072	0.5772	1.8823	0.3323	0.748
XM_286539	1.6206	1.8823		0.8974
XM_289039	0.7505	1.8823	0.9565	1.1701
Ccdc111	0.97	1.8764	0.8291	1.0084
Dnajb8	0.6724	1.8764	0.5184	1.0084
Hint1	0.7505	1.8764		0.3323
Iqcg	0.7505	1.8764		0.5184
XM_135370	0.5772	1.8764	0.5184	1.1349
XM_285045	0.4551	1.8764	0.5184	1.0084
XM_288778	0.4551	1.8764	0.5184	1.1349
XM_288875	0.4551	1.8764	0.748	0.6482
XM_357237	0.2846	1.8764	0.5184	
Klhl30	0.4551	1.8704		0.3323
XM_109346	0.9247	1.8704		0.8291
XM_285254	0.2846	1.8704		0.8291
XM_289066	0.5772	1.8704	0.5184	0.3323
Agtr1b	0.8166	1.8643		1.6272
Apln	0.7505	1.8643	0.748	0.748
BC031353		1.8643	0.3323	0.3323
Clcn6	0.5772	1.8643	0.748	1.6029
Slc25a17		1.8643		0.3323
XM_152089	0.4551	1.8643	0.3323	0.748
XM_234130		1.8643	0.3323	0.8291
Hpse	0.4551	1.8581	1.1701	0.6482
Olfm4	0.6724	1.8581	0.6482	1.5209
XM_161811	0.8166	1.8581		0.8291
Afap1l2	0.5772	1.8519	0.6482	0.6482
Efhc2	0.9247	1.8519	1.0548	0.748
Erp44	0.6724	1.8519	0.5184	0.3323
Glt25d1	0.2846	1.8519		
Pik3cb	0.2846	1.8519	0.5184	1.6611
Samd7	0.8166	1.8519	0.6482	0.8974
XM_161927	0.4551	1.8519	1.2328	0.5184
XM_287229	0.7505	1.8519	0.5184	0.5184
Abcd1	0.7505	1.8455	0.3323	0.8291
Aplf	0.6724	1.8455	0.5184	0.748
Clps	0.5772	1.8455	0.748	0.9565
Cmtm2a	0.8166	1.8455	1.2026	0.8291
Dmbt1		1.8455		0.3323
Olfr1469	0.5772	1.8455	0.6482	0.748

Sox6	0.2846	1.8455	0.5184	0.3323
XM_163871	0.5772	1.8455	0.5184	0.9565
XM_285628	0.5772	1.8455	0.3323	0.5184
XM_286875	0.6724	1.8455		0.5184
Entpd8	0.4551	1.8391	0.3323	0.5184
XM_139314	0.4551	1.8391	1.2876	0.6482
XM_143834	0.5772	1.8391	1.0084	0.5184
XM_157388	0.5772	1.8391	0.5184	0.5184
XM_163843	0.2846	1.8391	0.6482	1.1349
Gja6	0.2846	1.8326	0.5184	
Mcm3	0.6724	1.8326	0.5184	0.8291
Mrps18a	0.6724	1.8326	0.3323	1.2026
Poldip2		1.8326	0.5184	0.5184
Ptprb	0.6724	1.8326		0.3323
Tlcd2	0.8166	1.8326	0.748	0.8291
XM_155314	0.4551	1.8326	0.5184	0.3323
Ankrd13c	0.2846	1.8259	0.748	
Eya4	0.4551	1.8259	0.3323	0.5184
Gpld1	0.4551	1.8259	0.5184	1.38
Olr1242	0.7505	1.8259	0.5184	1.0548
Otud5	0.9247	1.8259	0.6482	1.2611
XM_157669	0.4551	1.8259	0.5184	0.5184
XM_289504	0.4551	1.8259	0.3323	0.3323
XM_357168		1.8259	0.6482	
Bhlhb9	0.8166	1.8192	0.6482	0.748
Olr346	0.6724	1.8192		0.5184
Scamp5	0.4551	1.8192		
Tdpoz5	0.7505	1.8192		0.6482
XM_194911	0.2846	1.8192	1.4003	0.8291
XM_284355	0.6724	1.8192	0.3323	1.5639
XM_288050	0.7505	1.8192	0.3323	0.3323
4921517D21Rik	0.5772	1.8124		
Abcg8	0.4551	1.8124		0.3323
Ccdc83	0.5772	1.8124	0.5184	0.3323
Prkci	0.2846	1.8124	0.5184	0.6482
Rnf5	0.5772	1.8124	0.3323	0.3323
Sacs	0.6724	1.8124	0.3323	1.0548
XM_221212		1.8124	0.5184	
XM_288944	0.6724	1.8124	0.6482	1.0548
1300015D01Rik	0.874	1.8054	0.5184	0.748
6330531I01Rik	0.4551	1.8054	1.0548	0.5184
9530004P13Rik		1.8054	0.6482	0.3323
Atp5g3	0.2846	1.8054		0.3323
Efcab3	0.4551	1.8054	0.8291	0.3323
Gm12108	0.4551	1.8054		1.0967
Grpel2	0.5772	1.8054	0.5184	0.5184
Porcn	0.2846	1.8054		
Tssc8	0.4551	1.8054	0.748	0.748
Vmn1r227	0.2846	1.8054	0.3323	1.1701
XM_288395	0.5772	1.8054		0.748
XM_487438		1.8054		
4930539M17Rik	0.6724	1.7983	0.3323	0.748
Pltp	0.4551	1.7983	0.3323	
Wars	0.4551	1.7983	0.5184	1.8589
XM_196752	0.5772	1.7983	0.6482	0.5184
XM_285085	1.2904	1.7983	0.3323	1.1349
Adam23	0.6724	1.7912	0.8974	0.3323
Cd163l1	0.97	1.7912	0.5184	
Fgfr2		1.7912		
Pcdhb4	0.9247	1.7912	0.3323	0.5184
Psma5	0.874	1.7912	0.5184	0.8291
Wdr55	0.4551	1.7912	0.5184	1.0548
XM_163503	0.2846	1.7912		
XM_285502	0.2846	1.7912	0.3323	0.3323
XM_288801	0.8166	1.7912	0.3323	0.748
XM_292193		1.7912		1.2026
Adap1	0.5772	1.7839	0.6482	
Krtap7-1		1.7839		0.6482
XM_160229	0.4551	1.7839	0.8291	0.6482
XM_206352	0.9247	1.7839		1.4003
5430411K18Rik	0.6724	1.7764	0.6482	0.8291
Ablim1	0.5772	1.7764	0.8974	
Il1f9		1.7764		
Nat3	0.8166	1.7764	0.748	0.748
Oat	0.5772	1.7764	0.3323	0.6482
Olfr820	0.2846	1.7764	0.3323	1.2876
XM_144264	0.4551	1.7764		1.6272
XM_161895	0.5772	1.7764		
XM_285386	0.2846	1.7764	0.3323	1.4733
XM_289986	0.874	1.7764	0.6482	1.3363
2010107G23Rik		1.7689		
Caps2	0.4551	1.7689		0.8291
Fah	0.2846	1.7689	0.3323	0.3323
Gm5640	0.5772	1.7689	0.3323	0.9565
Npat	0.2846	1.7689	0.5184	0.5184
Spry3	0.4551	1.7689		0.3323
Tmem9	0.2846	1.7689	0.6482	

XM_146593	0.2846	1.7689	0.3323	0.6482
XM_164897	0.5772	1.7689		0.3323
XM_286379	0.8166	1.7689		0.3323
Aif1l		1.7612	0.5184	0.8291
Hba-x		1.7612		1.3587
Sertad3	0.7505	1.7612	0.5184	0.6482
XM_137242		1.7612		
XM_143387	0.97	1.7612	0.5184	0.6482
XM_489678	0.2846	1.7612	0.8974	0.5184
Zfp52		1.7612	1.2026	0.8974
Zfp862	1.0111	1.7612	0.5184	1.1701
Bop1	1.6662	1.7534		0.3323
Ccnj	0.4551	1.7534	0.3323	1.1701
Higd1b	1.5473	1.7534		0.748
Mob3b		1.7534		0.6482
Nlrp9a	0.7505	1.7534	0.8974	1.0084
Sox11	0.2846	1.7534	0.3323	
XM_206777	0.4551	1.7534	0.3323	0.5184
XM_287244	0.4551	1.7534	0.748	0.5184
XM_287323	0.5772	1.7534	0.3323	0.5184
Agbl2	0.9247	1.7454		0.5184
Gm4832	0.2846	1.7454	0.5184	0.3323
Olfr1461	0.6724	1.7454	0.3323	1.2328
Ppargc1a		1.7454	0.5184	
Shc2	0.4551	1.7454	0.6482	1.7124
XM_156861	0.4551	1.7454	1.3126	0.5184
XM_196628	0.9247	1.7454	0.748	0.6482
Cenpe	0.5772	1.7373	1.5773	0.5184
Nf2	0.4551	1.7373		
Ptprz1	0.5772	1.7373	0.3323	0.6482
Sbno1	1.0832	1.7373	0.8974	0.8291
Tmem87a		1.7373	0.6482	0.748
Tmprss11c	0.5772	1.7373		
XM_127049	0.2846	1.7373	0.6482	0.5184
XM_162911	0.4551	1.7373		0.748
XM_289148	0.9247	1.7373	0.5184	0.5184
Antxr2	0.5772	1.729	0.5184	1.1349
Dlec1	0.4551	1.729		0.3323
Smyd3	0.2846	1.729	1.0084	1.38
XM_161867		1.729	0.8291	0.6482
XM_288769	1.145	1.729	0.3323	0.3323
XM_288787	0.2846	1.729	0.6482	0.3323
Cyp4a12b	0.4551	1.7205	0.3323	0.5184
Glipr1l2	0.2846	1.7205	0.5184	0.5184
Slc22a4	0.6724	1.7205	0.3323	1.0084
XM_162358	0.2846	1.7205		0.6482
XM_162980		1.7205	0.3323	0.5184
XM_164043	0.874	1.7205	0.3323	1.2611
XM_288317	0.4551	1.7205		1.6926
XM_288702	0.6724	1.7205	0.3323	1.7124
XM_289503	0.7505	1.7205	0.5184	0.8974
a	0.6724	1.7119	0.3323	
Fam169b	0.874	1.7119	1.0084	0.748
Mfi2		1.7119		
NM_177014		1.7119	0.5184	0.6482
Sgol1	0.2846	1.7119	1.3363	0.748
Slc38a9	0.5772	1.7119	0.6482	1.55
XM_143022	0.5772	1.7119	1.3363	0.748
XM_147435	0.874	1.7119	1.0548	0.6482
XM_164973	0.4551	1.7119	0.3323	0.3323
XM_197853	0.5772	1.7119	0.6482	0.748
XM_285028	0.4551	1.7119	0.6482	1.0084
XM_286123	0.5772	1.7119	0.3323	0.5184
2410002I01Rik	0.4551	1.7032		0.5184
Braf	0.5772	1.7032	0.3323	1.4562
Fancf	0.7505	1.7032	0.6482	1.0548
Gm10590		1.7032	0.3323	0.748
Ngrn	0.6724	1.7032		1.5903
Nup50	0.4551	1.7032		1.2876
Qser1	0.4551	1.7032	0.5184	
Sema4g	0.2846	1.7032	0.748	0.5184
Tmed2	0.2846	1.7032	0.5184	0.3323
XM_112038	0.6724	1.7032	0.748	0.6482
XM_157110	0.4551	1.7032	0.3323	1.3587
Zfp426	0.2846	1.7032	0.3323	
Zfp874a	0.5772	1.7032	0.5184	0.3323
4930433I11Rik	0.4551	1.6942	0.3323	1.0084
6430598A04Rik	0.6724	1.6942	0.3323	0.3323
Atp9b		1.6942		0.3323
Cadps2		1.6942		
Cttnbp2	0.6724	1.6942	0.3323	1.8377
Harbi1	0.7505	1.6942	0.6482	0.8291
Hsd17b7	0.2846	1.6942	0.5184	0.3323
Rfxap		1.6942	0.5184	0.8291
Tspan5		1.6942	0.3323	
Usp34	0.6724	1.6942	0.6482	0.6482
XM_127137		1.6942		0.5184

XM_142047	0.6724	1.6942	1.3587	
XM_149716	0.7505	1.6942	0.6482	1.0967
XM_155802	0.2846	1.6942	0.3323	0.6482
XM_159802	0.7505	1.6942	0.6482	0.3323
XM_288581	0.874	1.6942		0.6482
XM_488669	0.8166	1.6942	0.5184	1.1349
Il15ra	0.6724	1.685	0.3323	1.0084
Olfr594	0.5772	1.685	0.5184	0.3323
Trhde	1.2693	1.685	0.3323	0.5184
Xkrx	0.8166	1.685	0.6482	0.8291
XM_130857		1.685	0.3323	1.4197
XM_156276	0.5772	1.685	0.8974	0.748
XM_198259	0.6724	1.685	0.748	
XM_288146	0.2846	1.685	0.3323	0.6482
XM_289360	1.145	1.685		1.1701
4930544O15Rik	0.2846	1.6757	0.748	0.9565
Acbd7	0.7505	1.6757	0.3323	
Arfip1	0.2846	1.6757	0.5184	
Bpifb1		1.6757	0.748	0.5184
Copb1	0.7505	1.6757	0.3323	1.0084
Dhrs7	0.2846	1.6757	0.5184	0.748
Ext1	0.4551	1.6757	0.3323	0.3323
Samd8	0.5772	1.6757	0.3323	1.6501
XM_156074	0.4551	1.6757	0.3323	0.748
XM_197286	0.2846	1.6757		0.5184
XM_207405	0.5772	1.6757	0.6482	0.5184
XM_284510	0.2846	1.6757	1.6029	0.6482
Adamts14	0.5772	1.6662		0.5184
Agk	0.6724	1.6662	0.5184	0.6482
Ccdc38	0.9247	1.6662	0.5184	0.6482
Chchd8	0.2846	1.6662	0.5184	0.5184
Defb15	1.4302	1.6662	0.5184	0.6482
Hoxa2	1.2238	1.6662		0.8291
Nexn	0.5772	1.6662		0.748
XM_112742	0.4551	1.6662		0.3323
XM_162896	0.6724	1.6662		0.6482
XM_285799	0.4551	1.6662		0.5184
1810011O10Rik	0.5772	1.6564	0.748	0.3323
Akt2	0.2846	1.6564	0.3323	0.9565
Cldn11	0.4551	1.6564	0.9565	0.3323
Dmrt2	0.4551	1.6564	0.3323	0.3323
Gm10488		1.6564	0.3323	0.748
XM_206493	1.0486	1.6564	0.5184	0.6482
XM_288209	0.2846	1.6564	0.748	0.6482
4930438A08Rik		1.6464		0.748
C9orf93	0.2846	1.6464	0.3323	
Cnih2	0.874	1.6464	0.6482	0.748
Eapp	0.4551	1.6464	0.3323	0.9565
Kbtbd3	0.7505	1.6464	0.8291	0.5184
Spint2	0.4551	1.6464	0.748	1.38
XM_198184	0.2846	1.6464		0.5184
XM_206831	0.2846	1.6464	0.5184	0.3323
XM_286605	0.874	1.6464	0.5184	0.6482
XM_288290	0.7505	1.6464	0.5184	1.0084
XM_289589	0.4551	1.6464	0.6482	0.748
6430628N08Rik	0.5772	1.6362	0.6482	0.9565
Ankmy1	0.5772	1.6362	0.5184	0.3323
Btaf1	0.7505	1.6362	0.6482	0.8291
Cyp2c68	0.2846	1.6362	0.5184	0.748
Hadha		1.6362	1.38	1.0548
Pla2r1	0.6724	1.6362	0.3323	1.4197
XM_155407	0.97	1.6362	0.6482	0.8291
XM_157542	0.5772	1.6362	0.5184	0.6482
XM_163082	0.6724	1.6362	0.3323	0.9565
XM_289321	0.7505	1.6362	0.748	0.6482
Actn1	0.6724	1.6257		
Eed		1.6257	0.6482	1.6272
Fam57b	0.7505	1.6257	0.748	0.3323
Inpp5a		1.6257	0.3323	0.6482
Rab3b	0.6724	1.6257		0.748
Slc36a4	0.2846	1.6257	0.6482	0.3323
XM_144125	1.0111	1.6257	0.3323	0.748
XM_153005	0.4551	1.6257	0.3323	0.8291
XM_157855	1.5357	1.6257		1.2026
XM_288426	0.2846	1.6257	0.3323	
XM_289138	0.2846	1.6257		0.6482
XM_289445	0.4551	1.6257	0.3323	0.6482
Cd302	0.2846	1.615	0.6482	0.6482
Dhx38	1.0486	1.615	0.6482	0.3323
Fbxo21	0.4551	1.615	0.5184	0.3323
Igfl3	0.5772	1.615	0.5184	0.6482
Klk8		1.615		0.3323
Krt17	0.2846	1.615	0.3323	0.6482
Nanos3		1.615		0.3323
NM_009882	0.5772	1.615	0.3323	0.5184
Prkcc		1.615	0.5184	0.5184
Ubfd1	0.5772	1.615	1.2611	0.3323

Wdr61	0.2846	1.615	0.5184	0.3323
XM_138607	0.4551	1.615	0.3323	0.3323
XM_142658		1.615	0.3323	1.2328
XM_155373	0.4551	1.615	0.3323	0.8291
XM_195270	0.6724	1.615	0.8291	0.5184
XM_288401	0.8166	1.615	0.5184	0.5184
XM_288741	0.7505	1.615		1.6388
Casp14	0.7505	1.604	1.0084	0.748
Efcab4a	0.6724	1.604	1.0548	0.3323
Frmd5	0.2846	1.604	0.3323	0.748
Lyve1	0.4551	1.604	0.5184	0.5184
Nkx6-3		1.604		
Polr2b	0.8166	1.604	0.3323	0.8291
Tmem26	0.2846	1.604	0.3323	0.8291
Uggt1	0.6724	1.604	0.748	0.5184
XM_142452	0.5772	1.604	0.8291	0.5184
XM_143540	0.5772	1.604	0.9565	0.3323
XM_154092	0.2846	1.604	0.5184	
XM_205369		1.604	0.748	0.5184
4930590J08Rik	0.6724	1.5927	0.3323	
Map3k5	0.4551	1.5927		0.8291
Mylk	0.4551	1.5927	0.748	0.748
Ppm1h	0.97	1.5927	0.748	0.8291
Rab34	1.145	1.5927	0.3323	0.748
Slc5a12	0.6724	1.5927	0.5184	1.38
XM_156542	0.2846	1.5927		1.6272
XM_197970	0.874	1.5927	0.3323	0.3323
XM_288303	1.4991	1.5927		1.3126
XM_288419	0.7505	1.5927	0.5184	0.748
XM_488711	0.5772	1.5927	0.3323	0.748
Zfyve9		1.5927		
4930562A09Rik	0.5772	1.5811	0.8291	1.2611
Ajap1	0.2846	1.5811		0.3323
Araf	0.5772	1.5811	0.748	1.2876
Ccne2	0.6724	1.5811	0.748	0.8974
Chl1	0.5772	1.5811		0.8291
Lrp12		1.5811		0.5184
Myo1a	0.2846	1.5811	0.3323	
Slc9a8	0.8166	1.5811	0.9565	0.5184
U90926	0.2846	1.5811		0.6482
XM_147129	0.5772	1.5811		1.5903
XM_147847	0.8166	1.5811		0.3323
XM_148981	0.2846	1.5811		1.5209
XM_156734	0.5772	1.5811		0.6482
XM_213342	0.4551	1.5811		
XM_287549	0.8166	1.5811	0.6482	0.9565
Cask	0.4551	1.5692	0.3323	0.5184
Commd1	0.5772	1.5692	0.6482	0.3323
Fam98b	0.8166	1.5692	0.8291	0.9565
Mcam	0.2846	1.5692	0.6482	1.4197
Nfxl1	0.6724	1.5692	0.748	0.8291
NM_012059	0.2846	1.5692	0.6482	0.5184
NM_029417		1.5692	0.3323	0.3323
Tk2	0.2846	1.5692	0.3323	0.8291
XM_141439		1.5692	0.3323	
XM_144185	0.4551	1.5692	0.748	1.2876
XM_149892	0.2846	1.5692	0.6482	
Apob	0.874	1.5569	0.5184	0.8291
9-Mar	0.874	1.5569	0.3323	1.0967
V1ra1	0.6724	1.5569	0.8291	0.5184
XM_147625	0.4551	1.5569		0.748
XM_195001	0.7505	1.5569	0.5184	0.8291
XM_288979	0.4551	1.5569	0.3323	
XM_488484	0.2846	1.5569	0.3323	0.8974
Yrdc		1.5569		0.3323
Zdhhc12	0.4551	1.5569	0.5184	0.8291
Cd99	0.2846	1.5443	1.4383	
Cdx2	0.9247	1.5443	0.748	0.8974
Igf2bp3	0.5772	1.5443	0.5184	0.3323
Krt222	0.4551	1.5443	1.0548	0.8291
Opn5	0.6724	1.5443	0.748	0.3323
XM_110990	0.2846	1.5443	0.6482	0.5184
XM_111879	0.6724	1.5443	0.8974	0.8291
XM_142033	1.0111	1.5443		1.1701
XM_145020	1.0486	1.5443	0.3323	0.8974
XM_160751	0.2846	1.5443	0.3323	0.5184
XM_160999	0.2846	1.5443	0.3323	0.9565
XM_287053	0.2846	1.5443	0.5184	0.5184
XM_484607	0.874	1.5443	0.6482	0.5184
1110003E01Rik	0.2846	1.5313	0.748	1.2876
1700024P12Rik		1.5313	0.3323	0.3323
1810014F10Rik	0.5772	1.5313	0.3323	0.5184
Camk4		1.5313	0.3323	
Cbl		1.5313	0.3323	0.3323
Dkk3	0.4551	1.5313	0.5184	
Hs2st1	0.4551	1.5313	0.6482	1.2328
Klhl31	0.2846	1.5313		0.6482

Ncaph2	0.874	1.5313	0.3323	1.0548
NM_183292	0.4551	1.5313	0.8974	0.8974
Oip5	0.97	1.5313	0.3323	0.8974
Pir	0.4551	1.5313		0.6482
Tmem22	0.7505	1.5313	0.8291	1.0967
Tsc22d3	0.7505	1.5313	0.748	0.8974
XM_111753	0.8166	1.5313	1.0084	0.748
XM_140592	0.4551	1.5313	0.3323	0.6482
XM_150977	0.5772	1.5313	0.5184	
XM_151045		1.5313		
XM_152211	0.874	1.5313	0.5184	1.2611
XM_204847	0.7505	1.5313		0.748
XM_288888	0.2846	1.5313	0.3323	0.748
XM_289546	0.5772	1.5313	0.5184	0.6482
XM_346316	0.2846	1.5313	0.748	0.8291
4930504O13Rik	0.9247	1.518		0.3323
4931429I11Rik	0.7505	1.518	0.5184	0.8974
Bola3	0.97	1.518	0.748	0.6482
Hexim1	0.5772	1.518	0.3323	1.38
Mat2b	1.1152	1.518	0.3323	1.0084
Palmd	0.4551	1.518		
Polr3c	0.2846	1.518	0.3323	0.5184
Ptger3	1.0832	1.518	0.8291	0.748
XM_130353		1.518		
XM_136846	0.5772	1.518	1.0967	0.8974
XM_137071		1.518		
XM_152176		1.518		1.2026
XM_158745	0.7505	1.518		1.4383
XM_195255	0.2846	1.518	0.5184	0.3323
XM_206400		1.518	1.3126	0.3323
XM_284852	0.8166	1.518	0.748	1.0967
XM_285518	0.5772	1.518	0.6482	0.748
XM_286390	0.7505	1.518		
XM_487037	0.8166	1.518		0.748
1700093K21Rik	0.874	1.5042	0.5184	0.3323
2900040C04Rik	0.2846	1.5042	1.2328	0.6482
Alas2	0.4551	1.5042		1.2328
Gabrg3	0.6724	1.5042	0.5184	1.0967
NM_175288	0.4551	1.5042	0.5184	0.5184
Plekhf2	0.7505	1.5042	0.6482	1.0548
Sprr2f	0.5772	1.5042	1.38	0.5184
Tcp11l1	0.2846	1.5042		
Tnfrsf10b	0.97	1.5042		1.1701
Vmn1r74	0.7505	1.5042	0.5184	0.3323
Vsig1	0.8166	1.5042	1.38	0.3323
XM_142194	0.2846	1.5042	0.3323	
XM_149397	0.2846	1.5042	0.8974	0.748
XM_154121	1.0111	1.5042		1.0084
XM_163217	0.5772	1.5042	1.0548	0.3323
XM_194973	0.5772	1.5042	0.5184	0.5184
XM_283274	0.6724	1.5042	0.8974	0.3323
Zc3h14	0.5772	1.5042	0.8974	0.5184
XM_145646	0.7505	1.2678	2.5545	
XM_289635		1.3551	2.3502	
4933430L12Rik	0.4551	0.9147	2.3343	0.3323
XM_197033	0.4551	0.612	2.3106	1.2611
Galnt6		0.3077	1.9994	0.5184
XM_282962		0.7096	1.9683	1.5357
Foxn2	0.5772	0.9147	1.9109	0.8291
Myo15			1.9109	
Lcn3	0.2846	1.2678	1.8985	0.5184
Olr1006	0.5772	0.486	1.8857	1.1701
Paip2b	0.4551	0.7096	1.8792	0.6482
XM_484077	0.5772	0.486	1.852	0.6482
Copa	0.5772	0.7892	1.8449	0.6482
XM_285204	0.4551	0.486	1.8377	0.748
XM_198107	0.874	0.612	1.8229	0.5184
Kcnn2	0.6724	0.7892	1.8154	0.6482
Zbtb40	0.874	0.486	1.8154	0.9565
Palld	0.4551	0.966	1.8077	
XM_487526	0.9247	0.612	1.8077	0.5184
Gucy2g		0.3077	1.7998	
XM_111898			1.7998	0.5184
XM_356801	1.0111	0.7892	1.7998	0.8291
Catsper3	0.4551	0.7096	1.7918	0.6482
Dusp19	0.874	0.7096	1.7918	0.8974
XM_483950	0.4551	0.612	1.7918	0.5184
Cabin1	0.4551	0.612	1.7754	0.5184
Vkorc1	0.2846	0.3077	1.7669	0.3323
Sis	0.4551		1.7583	
Tcp11	0.6724	0.486	1.7583	1.1349
Flt1	0.5772	0.486	1.7495	
XM_285224	0.8166	1.1262	1.7495	0.8291
Amd1	1.0111	0.7096	1.7314	1.0548
Fn3krp	0.8166		1.7314	0.3323
Il1rl1	0.2846	0.612	1.7314	0.8974
Prrg4		0.612	1.7314	1.6824

XM_284445	0.874	0.612	1.7314	0.5184
Bdp1	0.9247	0.7892	1.722	0.5184
Nedd9	0.5772	0.612	1.722	0.6482
Sc5d	1.0486	0.7892	1.722	0.8974
Kcnq1ot1	0.6724	0.3077	1.7026	0.748
Olfr1124	0.2846	1.1262	1.7026	0.8291
XM_141574		0.7892	1.7026	0.748
Klhl5	0.5772	0.8565	1.6926	1.0548
AI480653	0.5772	0.3077	1.6824	0.5184
Casr	0.5772	0.7096	1.6824	1.0548
Ly96	0.2846	0.486	1.6824	0.6482
Scn1a	0.8166	0.3077	1.6824	0.6482
XM_163026	0.2846	0.3077	1.6824	0.3323
Olr947			1.6719	0.6482
Ppp2r3c	0.8166	0.8565	1.6719	
XM_139794	1.3829		1.6719	0.3323
XM_163178	0.7505	1.0913	1.6719	0.748
XM_135670	0.7505	0.612	1.6611	0.748
XM_135885	0.8166	0.486	1.6611	1.0967
XM_488756	0.5772	1.5313	1.6611	0.5184
5830426C09Rik	0.9247	0.7892	1.6501	0.5184
Alg6	0.6724	0.612	1.6501	0.8291
Cmtm2b	1.0832	0.612	1.6501	1.0967
Iqub	0.2846	0.7892	1.6501	
Liph	0.2846	1.0534	1.6501	0.6482
XM_143175	0.2846	1.4752	1.6501	0.8291
XM_160344	1.1729	0.486	1.6501	0.3323
XM_287595	0.5772	0.612	1.6501	0.6482
2310061C15Rik		0.7096	1.6388	0.6482
Bmp10	0.4551	1.0534	1.6388	0.5184
NM_174994	0.8166	0.7096	1.6388	1.2611
Tapbp	0.2846	0.612	1.6388	1.0084
XM_156591	0.2846	0.612	1.6388	1.0967
XM_287328		0.486	1.6388	0.8291
XM_489168	0.4551	0.612	1.6388	0.748
Ddit4l	1.0486	0.7892	1.6272	0.8974
Gpc4	0.2846	0.966	1.6272	0.5184
XM_147069	0.2846	0.7096	1.6272	0.6482
XM_284285	0.874	0.3077	1.6272	0.3323
XM_284825	0.6724	0.7892	1.6272	0.3323
XM_288858	0.5772	0.8565	1.6272	0.5184
Odf3l2	0.874	0.7096	1.6152	0.6482
Wdr33	0.5772	0.486	1.6152	0.5184
XM_139078	0.2846	0.3077	1.6152	1.7669
XM_142472	0.5772	0.3077	1.6152	1.1701
XM_195160	0.2846	1.2913	1.6152	0.8291
XM_283958	0.2846	0.612	1.6152	0.8974
XM_289019			1.6152	0.5184
Entpd1	0.6724	0.486	1.6029	1.2328
Mrpl15	0.6724	0.7892	1.6029	0.9565
Pak1	0.4551	0.486	1.6029	0.9565
Pgam1	0.6724	0.7096	1.6029	0.8974
Sucla2	0.2846	0.3077	1.6029	0.748
XM_136410		0.3077	1.6029	0.3323
Zfp947	0.6724	0.7096	1.6029	0.3323
Acoxl	1.2238	1.0119	1.5903	0.3323
Ift74	0.6724	0.7096	1.5903	1.2876
Olfr1457	1.1152	0.612	1.5903	0.5184
Slc16a7	0.4551	0.486	1.5903	0.5184
XM_111304		0.3077	1.5903	0.3323
XM_488956	0.4551	0.612	1.5903	1.38
BC089491	0.8166	0.486	1.5773	0.3323
Cxcr1	0.6724	1.0119	1.5773	0.8974
Gcc1	0.5772	0.486	1.5773	1.2328
Mllt10	0.9247	0.486	1.5773	
Naip1	0.7505	0.7096	1.5773	0.6482
Spata7	1.145	0.3077	1.5773	0.3323
Spg20	0.5772	0.612	1.5773	0.6482
XM_129777	0.4551	1.3744	1.5773	0.5184
XM_145305	0.9247	0.9147	1.5773	0.8291
XM_204027	0.7505	0.7096	1.5773	1.2026
XM_487984	0.4551		1.5773	0.3323
2310033E01Rik	0.2846	0.612	1.5639	1.6824
B230369F24Rik	0.4551	0.7096	1.5639	0.6482
Ccdc138	0.8166	0.8565	1.5639	0.5184
Dchs1	0.6724	0.612	1.5639	0.8974
Gng3	0.2846	0.3077	1.5639	
Gorab	0.2846	0.612	1.5639	0.8291
Lrrc3b	0.5772	0.3077	1.5639	1.2026
XM_111268	0.6724	0.7892	1.5639	0.6482
XM_151755	0.2846	0.7892	1.5639	0.748
XM_284872	0.97	1.2165	1.5639	0.5184
XM_289095	0.5772	1.5042	1.5639	0.3323
XM_289381	1.2472	0.486	1.5639	0.6482
XM_289455	0.2846	0.3077	1.5639	0.6482
XM_345014		0.3077	1.5639	0.3323
Atp13a2	0.2846	0.486	1.55	0.748

D17Wsu92e	1.0486	0.3077	1.55	0.3323
Dhrs11	1.2693	0.3077	1.55	0.748
Lrrc66	0.6724	0.9147	1.55	0.8291
Mak16	0.874	0.612	1.55	1.0967
Olfr1018			1.55	0.3323
Scn3a	0.6724	1.0913	1.55	1.0084
Spnb3	0.2846	0.3077	1.55	1.7314
Ttc28	0.4551	1.0913	1.55	0.9565
XM_144858			1.55	
XM_162488	0.7505	0.7096	1.55	0.8291
XM_197089	0.9247		1.55	0.748
XM_286240	0.2846	0.486	1.55	
XM_486200	0.4551	0.7892	1.55	0.5184
2810417H13Rik	0.8166	0.7892	1.5357	0.5184
Acer2		0.3077	1.5357	0.6482
Chchd10	0.2846	0.9147	1.5357	
Efcab2	0.4551	0.7892	1.5357	1.3363
Efr3b	0.6724	0.486	1.5357	0.8974
Egf	0.2846	0.486	1.5357	0.6482
Fam19a2	0.5772	0.7096	1.5357	0.3323
Fkbp1b	0.6724	0.612	1.5357	1.4197
Neil2	1.2693		1.5357	1.2328
Olfr514	0.2846	0.486	1.5357	0.6482
Rab5c	0.6724	0.9147	1.5357	0.5184
Slco5a1	0.9247	0.7096	1.5357	0.6482
XM_110818		0.612	1.5357	
XM_111481	0.7505	0.9147	1.5357	0.8291
XM_138876	1.1152	0.486	1.5357	1.0967
XM_150524	0.4551	0.3077	1.5357	0.3323
XM_165069	0.4551	0.3077	1.5357	0.748
XM_204981	0.5772	0.3077	1.5357	0.748
XM_285811	0.4551		1.5357	1.0084
XM_288912		0.3077	1.5357	0.3323
Atp8a1	0.2846	0.3077	1.5209	0.8291
Atxn7l3b	0.7505	0.612	1.5209	0.8291
F3	0.8166	0.966	1.5209	0.8974
Klra10	0.8166	0.3077	1.5209	0.9565
Mmp25	0.6724	0.612	1.5209	0.8291
Nmd3	0.7505	0.7096	1.5209	0.748
Pmpca	0.6724	0.612	1.5209	
Ptdss1	0.5772	1.5443	1.5209	
Sema4a	0.2846	0.612	1.5209	0.3323
XM_125126		0.3077	1.5209	0.3323
XM_138920	0.9247	0.966	1.5209	0.8974
XM_139924	0.2846	0.612	1.5209	1.6272
XM_147897	0.4551	0.3077	1.5209	
XM_162309	0.4551	0.612	1.5209	1.5209
XM_287363		0.3077	1.5209	0.6482
XM_288111	0.7505	0.3077	1.5209	0.3323
XM_288710	0.7505	0.3077	1.5209	0.6482
XM_485425		0.3077	1.5209	
XM_487230	0.5772	0.7096	1.5209	0.8974
Zfp125	1.0832	0.8565	1.5209	0.8291
Zfp764		1.2913	1.5209	0.8291
2610301B20Rik	0.4551		1.5056	1.3363
BC023959	0.2846		1.5056	
Bicd1	0.8166	0.486	1.5056	0.3323
Clcnka	0.5772	0.486	1.5056	1.1349
Crebl2	0.2846		1.5056	0.748
Cxcl12	0.6724	0.486	1.5056	0.3323
Depdc1a	0.874	0.7892	1.5056	0.9565
Dlgap1	0.874	0.7096	1.5056	0.6482
Dnaic1	0.5772	0.3077	1.5056	0.3323
Esyt3	0.4551	0.612	1.5056	1.0548
Gfod1	1.0486	0.612	1.5056	0.3323
Mchr1	0.4551		1.5056	0.8291
Mtmr3	0.4551	0.7096	1.5056	0.5184
Olfr418-ps1	0.2846	0.612	1.5056	0.5184
Olfr926	1.1729	0.9147	1.5056	0.6482
Prr13	0.6724	0.612	1.5056	0.6482
Rxfp4	0.2846	0.3077	1.5056	0.3323
Vmn2r10	0.5772	0.7096	1.5056	1.0084
XM_145533		0.7096	1.5056	0.3323
XM_160365	0.2846		1.5056	0.8974
XM_164574	1.0832	0.7096	1.5056	0.6482
XM_194774		0.612	1.5056	1.2026
XM_195245	0.5772	0.3077	1.5056	0.6482
XM_196676	0.4551	1.1885	1.5056	0.5184
XM_205191		0.3077	1.5056	
XM_220047	0.8166	1.1262	1.5056	0.748
XM_283039	0.4551	0.486	1.5056	0.3323
XM_285146	0.6724	0.486	1.5056	0.8974
XM_287127	0.4551	0.7096	1.5056	0.5184
XM_289369		0.3077	1.5056	1.4003
Olr1533	0.2846	0.486	0.8291	2.4852
XM_164238	0.5772	1.0119	0.5184	2.4085
D230038C21	0.4551	0.7096	1.3126	2.3886

C6orf111	0.4551			2.3762
Hspa13	0.2846	0.8565	0.3323	2.372
Cd209c	1.0832	0.7892	0.5184	2.325
Plk2	0.6724	0.3077	0.6482	2.275
Khdrbs3	0.2846	0.7892	1.1701	2.2062
Kcnab3	0.6724	0.612	0.748	2.1672
XM_287689	1.0832	0.8565	0.3323	2.1569
Dgki	0.6724	0.612	0.6482	2.1499
Cuta	0.5772	0.486	1.3587	2.1131
XM_289471	0.4551		0.3323	2.1053
Pqlc3	0.4551		0.3323	2.0811
Agpat2	0.7505	0.612		2.0599
Fam81b	0.9247	0.966	0.3323	2.0555
XM_286624	0.5772	0.612	0.5184	2.0511
Amac1		0.612	1.6388	2.0422
Zfp606	0.5772			2.0376
4921517D16Rik	1.4302	0.486		2.033
XM_154982	0.6724	0.7096		2.0284
XM_287541	0.2846	1.0913	0.6482	2.0237
XM_488610	1.1991	0.3077	0.3323	2.0092
XM_162771	1.0486	0.486	0.8291	1.9841
XM_289299	0.4551	0.966	1.0084	1.9789
XM_285057	0.4551		0.3323	1.9736
XM_138788	0.4551	0.612	0.6482	1.9629
XM_288258	1.0111	0.966	0.5184	1.9629
XM_196816	0.7505	0.8565	0.5184	1.9574
Aida	0.5772	0.3077	0.6482	1.9519
Serpinb9	0.7505	0.486	0.8974	1.9519
Uty	0.5772	0.8565	0.6482	1.9462
XM_285213	0.5772	0.3077	0.3323	1.9462
Coq7		0.966	0.748	1.9406
Rheb	0.4551	0.612	1.1701	1.9406
XM_161191	0.7505	0.612	0.6482	1.9406
XM_284859	0.5772	0.612		1.9348
Pxmp2	0.6724	0.486	0.8291	1.923
Gm11837	0.6724	0.612	0.3323	1.917
Olfr1462	0.5772	0.7892	0.748	1.917
XM_287686	0.6724	0.486	0.3323	1.9109
Prg4	0.7505	0.7892	0.5184	1.9048
XM_288935	0.7505	0.9147	0.6482	1.9048
Gm5094	0.9247	0.3077		1.8922
Ssbp3	0.2846		0.748	1.8857
Tfdp1		0.7892	0.3323	1.8792
XM_145092	0.4551	0.7096	1.2876	1.8792
XM_197034	0.9247	0.3077	1.0967	1.8792
XM_285596	0.4551	0.3077	0.3323	1.8792
Bag4	0.4551		0.3323	1.8725
Fbxo43	0.6724	0.3077	0.5184	1.8725
Fyb	0.2846	0.7096	0.3323	1.8725
Tm9sf4	0.5772	0.8565	0.3323	1.8725
XM_198060	0.6724	1.0119	0.3323	1.8725
XM_205299	0.4551	0.3077	0.5184	1.8725
D3Bwg0562e	0.4551	0.612	0.5184	1.8658
Pag1	0.2846	0.612	0.748	1.8658
XM_141978	0.4551	0.612	0.3323	1.8658
XM_287199	0.2846	0.9147		1.8658
Lipc	0.4551	0.7892	0.3323	1.8589
XM_155926	0.9247	0.7096	0.5184	1.8589
Cyp4a10	0.2846	0.3077	1.2026	1.852
Hspa12b	0.6724	0.612	0.3323	1.852
XM_206778	0.5772	0.8565	0.8291	1.852
AA960436	0.4551	0.612		1.8449
NM_183305	0.5772		0.3323	1.8449
Olfr916	0.2846	0.7892	0.8291	1.8449
Prosc		0.3077	1.3363	1.8449
XM_144247	0.5772	1.1262	0.5184	1.8449
XM_153532	0.97	0.7096	0.748	1.8449
XM_158171	0.2846	1.604		1.8449
XM_158434	0.97	1.0119	0.5184	1.8449
XM_287587	0.4551	0.486	1.5209	1.8449
Gabbr2	1.415	0.7892	0.3323	1.8377
Vapa				1.8377
D17Wsu104e	0.6724	0.612	0.6482	1.8304
Ewsr1			0.6482	1.8304
Gm501	0.5772	0.612		1.8304
XM_286360	0.7505	0.3077	0.6482	1.8304
Cst11	0.5772		0.3323	1.8229
Dep1	0.6724	0.8565	0.748	1.8229
Prl7b1	0.7505	0.7892	0.5184	1.8229
Traf5	0.97	1.0913	0.3323	1.8229
XM_110941	0.2846	0.486	0.5184	1.8229
XM_153001	0.4551	0.486	0.5184	1.8229
XM_161053	0.2846	0.7892	0.5184	1.8229
2700069I18Rik	0.6724	0.9147	0.5184	1.8154
9430031J16Rik	0.6724	0.3077	0.6482	1.8154
Ccdc63	0.5772	0.8565	0.6482	1.8154
LOC399947				1.8154

Rasgef1b	0.5772	0.8565	0.3323	1.8154
Txlna	0.9247	0.486	0.6482	1.8154
XM_146493	0.4551	0.3077		1.8154
XM_163115	0.2846			1.8154
4930431N21Rik	0.2846	0.7096	0.6482	1.8077
C87436	0.4551	0.612	0.8291	1.8077
Cldn16	0.2846	0.486		1.8077
Olfr1344	1.0486	0.486	0.5184	1.8077
Sdk1	0.6724	1.0119	0.5184	1.8077
XM_136251		0.612	0.5184	1.8077
XM_150357	0.2846	0.7096	0.8974	1.8077
XM_284827	0.9247	0.7892	0.6482	1.8077
Aldh1l1	0.2846	0.7096	0.5184	1.7998
Bcl9	0.4551	0.7096	0.748	1.7998
Mex3b	0.6724	0.612	0.3323	1.7998
Nfe2	0.2846	0.3077	0.5184	1.7998
NM_175508	0.874	0.3077	0.5184	1.7998
XM_196735	0.2846	0.3077	0.5184	1.7998
XM_286571	0.2846	0.7096	0.6482	1.7998
Bzw1	0.874		0.3323	1.7918
Dbh		0.486	0.5184	1.7918
Gm12169		0.486		1.7918
Nkx6-2		0.612		1.7918
XM_151259	0.97	0.7892	0.3323	1.7918
XM_197469	0.2846	0.486	0.3323	1.7918
XM_205132	0.2846	1.2913	0.6482	1.7918
2310067B10Rik			0.3323	1.7837
Cyp2c44	0.5772	0.7096	0.748	1.7837
Mbtd1	0.7505	0.3077	0.6482	1.7837
Pappa2	0.5772	0.7096	0.5184	1.7837
Pdc				1.7837
Prdx2	0.97	0.3077	0.748	1.7837
Rassf7	0.2846	0.612	0.6482	1.7837
Serpini2	0.4551	0.7096	0.8291	1.7837
XM_138851	0.2846		0.8291	1.7837
XM_155406	0.7505	0.7096	1.0548	1.7837
XM_156672	0.5772	0.8565	0.748	1.7837
XM_285339	0.4551	0.486	0.3323	1.7837
XM_289302	0.7505	0.3077	0.8974	1.7837
Irf2bp2	0.5772	0.486	0.3323	1.7754
Spdyb	0.6724	0.486		1.7754
XM_111012	0.2846	0.3077	0.5184	1.7754
XM_127178	0.8166	0.7096	0.3323	1.7754
XM_284814	1.4591		0.5184	1.7754
XM_286477	0.2846		0.3323	1.7754
XM_287844		0.7096		1.7754
XM_289078	0.2846	0.612	1.3363	1.7754
Ceacam3	0.2846		0.6482	1.7669
Col3a1	0.4551	0.486	1.2876	1.7669
Epb4.1l2	0.6724	0.3077	0.5184	1.7669
Mcm6	0.8166	0.7096	0.3323	1.7669
Nrxn1	0.6724	0.486		1.7669
XM_143688	0.5772	0.7892	1.0084	1.7669
XM_158861	0.8166	0.7096	0.9565	1.7669
XM_486079	0.97	0.8565	0.6482	1.7669
Zfp53	0.7505	0.7892		1.7669
1600002K03Rik	0.97	1.0534	0.5184	1.7583
4930404I05Rik		0.7892	0.6482	1.7583
C330027C09Rik	0.5772	0.3077	0.5184	1.7583
Cd300c	0.4551			1.7583
Exosc7	0.4551	0.486		1.7583
Gtf2i		1.3744	0.6482	1.7583
XM_144274	0.2846		0.5184	1.7583
XM_195744	0.5772			1.7583
XM_206765		0.3077	0.3323	1.7583
XM_288755	0.2846			1.7583
XM_289567	0.5772	0.486		1.7583
XM_487562	0.7505	0.9147	0.8291	1.7583
Cdca2	0.7505	0.7096	0.5184	1.7495
Fetub	0.6724		0.5184	1.7495
Hspa8				1.7495
Ipo11	0.97	1.0913	0.5184	1.7495
Lce1m	1.2472	0.612	0.6482	1.7495
Mgea5	0.5772	0.7892	0.3323	1.7495
NM_025756	0.8166	0.612	0.6482	1.7495
NM_183277	0.6724	0.7892	0.5184	1.7495
Olr454	0.2846	0.3077		1.7495
Ppp1r12b	1.2472	0.3077		1.7495
Thumpd3	0.2846	0.8565	1.3363	1.7495
Trim68	0.6724	0.486	0.5184	1.7495
XM_136872	0.6724	0.7096	1.0084	1.7495
XM_140535		0.3077	1.0548	1.7495
XM_149838	0.6724	0.486	0.5184	1.7495
XM_196796			0.9565	1.7495
XM_285881	0.5772	0.3077	0.6482	1.7495
XM_288101	0.5772	0.8565	0.748	1.7495
XM_289645	0.6724	0.7096		1.7495

XM_343548		0.486	0.6482	1.7495
XM_485647	0.2846	0.3077	0.8291	1.7495
A630033H20Rik	1.0832	0.7096	0.3323	1.7405
BC031781	0.5772	0.486	1.3126	1.7405
Dnajc25	0.6724	0.7892	0.3323	1.7405
Fan1	0.5772	0.7096		1.7405
Fbxl2	0.4551	0.7096	0.8291	1.7405
Sdhaf2	0.6724	0.3077	0.748	1.7405
Stau2	0.4551	0.3077	0.8291	1.7405
XM_145467	0.4551	1.2165	0.8291	1.7405
XM_159419	0.874	0.3077	0.3323	1.7405
XM_195696	0.2846	0.7096	0.3323	1.7405
XM_289464	0.2846	0.7096	0.748	1.7405
XM_289515	0.5772	0.3077	0.3323	1.7405
XM_489155	0.2846	0.486	0.8291	1.7405
1200011I18Rik	0.8166	1.0534	0.5184	1.7314
1700030J22Rik		0.486		1.7314
4931408C20Rik	0.874	0.9147	0.3323	1.7314
A830073O21Rik	0.5772	0.3077		1.7314
Adamts20	1.0832	0.7892	0.3323	1.7314
Arhgap32	0.2846	0.612	1.1349	1.7314
Cdc42bpb	1.0111	0.7096	0.3323	1.7314
Chmp3	0.4551	0.8565	0.3323	1.7314
Enpp5	0.4551	0.3077	1.2611	1.7314
Hira	0.6724	0.612		1.7314
Klf9	0.8166	0.7096	0.3323	1.7314
Lmbrd2	1.5585	0.3077	0.3323	1.7314
Mosc1	0.8166	0.3077		1.7314
Palb2	0.4551	1.1262		1.7314
V1rb5	0.2846	0.486		1.7314
XM_129976	0.8166	1.4899		1.7314
XM_196410	0.8166	0.486		1.7314
XM_198073	0.5772	1.0119	0.6482	1.7314
XM_287252	0.2846	0.612	1.4003	1.7314
XM_287382	0.6724	0.7892	0.5184	1.7314
XM_289627	0.5772	0.7096	0.6482	1.7314
XM_485288	0.7505	1.0534	0.748	1.7314
Btbd9	0.6724		0.6482	1.722
Elfn2	0.5772	0.3077	1.1701	1.722
H2-DMa		0.9147		1.722
Noxa1	0.2846	1.2165	0.3323	1.722
Speer4d		0.3077	0.3323	1.722
Tatdn3	0.2846	0.612	0.3323	1.722
XM_110688	0.9247	0.486	0.5184	1.722
XM_139179		0.8565		1.722
XM_150633	0.5772	1.2678	0.5184	1.722
XM_162954	0.2846	0.486	0.6482	1.722
XM_194678	0.6724	1.0119	0.8291	1.722
XM_286033	0.4551	0.7892	0.3323	1.722
XM_287622	0.4551	0.3077	0.3323	1.722
Zfp318	0.2846	0.486		1.722
1700009N14Rik		0.9147	0.5184	1.7124
Cct4		0.3077	0.5184	1.7124
Ddrgk1	0.2846		0.5184	1.7124
E330034G19Rik		0.3077	0.3323	1.7124
Fam184a	0.4551	0.3077	0.748	1.7124
Frmd3	0.4551		0.3323	1.7124
Gsdmc2		1.1885	0.3323	1.7124
Olfr1055		0.3077	0.8291	1.7124
Tnfaip2	0.5772	0.3077	1.0084	1.7124
Tomm34		0.3077	0.3323	1.7124
Ufd1l	0.2846	0.3077	0.3323	1.7124
Wee1	1.0111	0.486	0.5184	1.7124
XM_131252	1.1729	0.3077	0.748	1.7124
XM_137022	0.874	0.612	0.8291	1.7124
XM_153882	0.6724	0.7096	0.5184	1.7124
XM_196995	0.7505	1.0534	0.3323	1.7124
XM_231462		0.3077	1.0967	1.7124
XM_283173	0.2846	0.3077		1.7124
1110057K04Rik	0.2846	0.3077	0.748	1.7026
Akap17b	0.874	0.7892	0.6482	1.7026
Arid3b		0.3077	0.3323	1.7026
Dnajb5	0.4551	0.7892	0.748	1.7026
Ehd4	0.7505	0.612	0.3323	1.7026
Gap43	0.4551	1.1262	0.5184	1.7026
Gm5733		0.612		1.7026
Gsta1	0.4551	0.3077	0.5184	1.7026
Gtf2e1	0.2846	0.486	0.3323	1.7026
Ighm		0.612		1.7026
Ikbip	0.4551	0.3077	0.5184	1.7026
Mapk13	0.2846		0.6482	1.7026
Mrpl51	0.6724	0.486	0.8291	1.7026
Myl3	0.5772		0.5184	1.7026
NM_177106	0.2846	0.486		1.7026
Rasef	0.2846			1.7026
Trim61	0.8166	1.0119		1.7026
Vmn2r37		0.7096	1.0967	1.7026

XM_137225	0.6724	1.0119	0.5184	1.7026
XM_138574	0.6724	0.612	0.3323	1.7026
XM_196154		1.2429	0.5184	1.7026
XM_284930		0.612	0.3323	1.7026
XM_485788	0.5772	0.7892	0.3323	1.7026
XM_489108	0.8166	0.486	0.3323	1.7026
Zfp846	0.7505	0.3077	0.3323	1.7026
1700011F14Rik		0.9147	1.2328	1.6926
4930526F13Rik	0.2846	0.486		1.6926
C030048B08Rik	0.8166	0.3077	0.3323	1.6926
Cdc7	0.5772	0.486	0.3323	1.6926
Celf1	1.0111	0.7096	0.748	1.6926
Erlec1	0.2846	0.612	1.0084	1.6926
Fsd1l	1.0486	0.9147		1.6926
Gabrb3	1.0486	0.3077	0.3323	1.6926
Hoxd12				1.6926
Krt77	0.2846	0.9147	0.748	1.6926
Lzts1	0.2846	0.612		1.6926
Nfyc	0.8166	0.7096	0.8291	1.6926
Pola1	0.2846	0.7096		1.6926
Ppp4r4	0.874	0.8565	0.748	1.6926
Tspan33	0.2846	0.7096	0.5184	1.6926
Tstd1	0.97	0.3077	0.8974	1.6926
XM_150881	0.4551		0.3323	1.6926
XM_151728	0.6724	0.612	0.3323	1.6926
XM_154677	0.5772	0.7096	0.5184	1.6926
XM_155816	0.4551	1.2913	0.748	1.6926
XM_282985	0.5772	1.0534	0.6482	1.6926
XM_288957	0.4551			1.6926
XM_487778	0.2846		0.5184	1.6926
Zfp830	0.2846	0.3077	0.748	1.6926
Atg7	0.2846	0.486	0.5184	1.6824
B130021B11Rik	0.6724	0.8565	0.3323	1.6824
C130026I21Rik	1.1729	0.3077	0.3323	1.6824
Isca2	0.7505	0.612	0.3323	1.6824
Lasp1	0.2846	0.3077		1.6824
Pi16	0.2846	0.3077		1.6824
Poc5	0.7505	0.3077	0.3323	1.6824
Pus7l	0.5772	0.612	0.748	1.6824
Snai3	0.5772	0.8565	0.6482	1.6824
Thg1l	0.4551	0.612	0.3323	1.6824
Vip	0.6724	0.612	0.748	1.6824
XM_136261	0.8166	0.486	0.5184	1.6824
XM_143700	0.6724	0.612	0.9565	1.6824
XM_146220	0.5772	0.486	0.5184	1.6824
XM_146705	0.4551		0.5184	1.6824
XM_159533	1.1991	0.7096	0.3323	1.6824
XM_161730	0.2846	0.486	0.9565	1.6824
XM_162569	0.8166	0.3077	0.3323	1.6824
XM_205213		0.7096	0.5184	1.6824
XM_206036				1.6824
XM_286933		1.0119	0.5184	1.6824
XM_288446	0.2846		0.3323	1.6824
XM_289295		0.3077	0.3323	1.6824
Zdhhc11	1.4302	0.486	0.3323	1.6824
9130401M01Rik				1.6719
Anxa11	0.4551		0.748	1.6719
Atat1	0.5772	0.7892	0.5184	1.6719
Bche	0.4551	0.8565	0.5184	1.6719
Ctdp1	0.5772	0.3077		1.6719
Defb3		0.3077	0.748	1.6719
Dfna5	0.4551	0.486	0.3323	1.6719
E030003E18Rik				1.6719
Erf		0.612		1.6719
Gnat2	0.2846	0.612		1.6719
Hint3	0.9247	0.612	0.5184	1.6719
Il33	0.5772	1.0913	0.5184	1.6719
Map3k7	0.874	0.9147	0.3323	1.6719
Olr111	0.8166	0.612	0.6482	1.6719
Pcgf2	1.1152	0.612	0.748	1.6719
Pdzd9	0.874	0.3077	0.748	1.6719
Ppp1r9a	0.4551	0.486	0.3323	1.6719
Prl3c1	0.6724	0.486	0.8291	1.6719
Ptgr2	0.6724	0.966	0.3323	1.6719
Secisbp2l	0.4551	0.966	0.3323	1.6719
Slc15a5	0.4551	0.3077	0.8291	1.6719
Slx1b	0.97		0.3323	1.6719
Tm9sf1	0.4551	0.7892	0.3323	1.6719
Usp12	0.4551	0.486	0.748	1.6719
Wdfy2	0.4551		0.5184	1.6719
XM_145347	0.5772	0.3077	0.6482	1.6719
XM_145934		0.486	0.5184	1.6719
XM_157333	0.6724	0.7096	0.3323	1.6719
XM_160400	0.8166	0.3077	0.8974	1.6719
XM_165238	0.6724	0.486	0.8291	1.6719
XM_204532	0.5772	0.7892		1.6719
XM_286680		0.7096	0.3323	1.6719

XM_288998	0.5772	0.3077	0.6482	1.6719
XM_485871	0.4551	0.486	0.3323	1.6719
1810026J23Rik	0.2846	0.3077	0.5184	1.6611
A530065N20	0.8166	0.612		1.6611
Cnr2	0.2846	0.7892	0.3323	1.6611
Ddx20	0.874	0.7096	0.6482	1.6611
Fxyd6	0.4551	0.7892	0.748	1.6611
Glipr1	0.4551	0.486	0.3323	1.6611
Gm815	0.6724	0.486	0.3323	1.6611
Lin52	0.9247	0.612	0.9565	1.6611
11-Mar	0.8166	1.2165	0.3323	1.6611
Mettl6	0.4551		0.9565	1.6611
Nkrf	0.5772	0.612	0.3323	1.6611
NM_001002770	0.4551	0.8565		1.6611
Proca1		0.612	0.5184	1.6611
Ralgps2		0.3077	0.3323	1.6611
Riok3	0.4551	0.7096	0.3323	1.6611
Vmn1r78	0.6724	0.612	0.9565	1.6611
Wwc1	0.4551	0.7096	0.748	1.6611
XM_111754	0.6724	0.3077	0.748	1.6611
XM_112845	0.5772			1.6611
XM_126301	0.2846	0.3077		1.6611
XM_139089	0.4551	0.3077	0.9565	1.6611
XM_139333	0.4551	0.3077	0.3323	1.6611
XM_139717	0.4551	0.612	0.3323	1.6611
XM_139927	0.4551	1.2678	0.6482	1.6611
XM_151696	1.0832	0.7096	0.5184	1.6611
XM_156372	0.5772	0.3077		1.6611
XM_164994	0.2846	0.3077		1.6611
XM_197443	1.0486	0.3077		1.6611
XM_218013	1.2472	0.3077		1.6611
XM_237458		0.3077		1.6611
XM_283968		0.3077	0.3323	1.6611
XM_286476	0.2846		1.0967	1.6611
XM_289368	0.4551	0.612	1.0548	1.6611
Yme1l1		1.0534	0.748	1.6611
Zfp84	0.5772	0.612	0.5184	1.6611
4932412H11Rik	1.0486	1.1262	0.3323	1.6501
AF529169	0.6724	0.3077	0.6482	1.6501
Arx		0.486	0.9565	1.6501
Fdps	0.2846	0.7096	0.3323	1.6501
Fmo2	1.3829	0.612	0.3323	1.6501
Hoxd4		0.8565	0.3323	1.6501
Ift80				1.6501
NM_177148	0.5772		0.3323	1.6501
NM_177467	0.4551	0.3077	0.5184	1.6501
Rad51l1	0.2846	0.3077		1.6501
Rps19bp1	0.7505	0.7892		1.6501
Sprr2j-ps		0.7096		1.6501
Steap4		0.3077		1.6501
Top2b		0.3077		1.6501
Vav1	0.7505	0.3077	0.5184	1.6501
Wdr96	0.7505	0.612	1.1349	1.6501
XM_111876	0.5772	0.3077		1.6501
XM_126817	0.2846	0.612		1.6501
XM_138084	0.2846	0.486	0.5184	1.6501
XM_138750	0.8166	0.486	0.6482	1.6501
XM_140132	0.4551	0.612	0.3323	1.6501
XM_143154			0.8291	1.6501
XM_146374	0.5772	0.612	1.1701	1.6501
XM_160781	0.2846		0.3323	1.6501
XM_218601	0.4551	0.486		1.6501
XM_223540			0.5184	1.6501
XM_289202		1.1262	0.5184	1.6501
Znhit6	0.4551	0.612	0.5184	1.6501
1700010M22Rik	0.5772	0.612		1.6388
A430005L14Rik	1.0486	0.486	0.6482	1.6388
A430107O13Rik	0.2846	0.7096	0.5184	1.6388
Dbx1				1.6388
Dgkg	0.8166	0.486	0.5184	1.6388
Eif3f	0.6724	0.486		1.6388
Mtap7d2		0.3077	1.1349	1.6388
Nefm			0.3323	1.6388
NM_177902	0.2846	0.3077	0.6482	1.6388
Pgpep1	0.9247	0.486	0.5184	1.6388
Sarm1	0.2846	0.3077	0.748	1.6388
Srsf10	0.4551	0.486	0.3323	1.6388
Trappc10	0.2846	0.3077	0.3323	1.6388
Vegfa	0.6724		0.5184	1.6388
XM_130727	0.8166	0.612	0.8974	1.6388
XM_132334		0.612	0.3323	1.6388
XM_138713	0.4551			1.6388
XM_144941	0.4551	0.3077	0.748	1.6388
XM_146485		0.3077	1.4003	1.6388
XM_206234	0.5772	0.7892	0.748	1.6388
XM_285767	0.5772	0.3077	0.8291	1.6388
XM_289521	0.7505	0.3077	0.5184	1.6388

XM_489181	1.1152	0.7892	0.6482	1.6388
Zfp800	1.0832	0.8565	0.5184	1.6388
2900069M18Rik		0.612	0.8974	1.6272
4933414I06Rik	0.6724	0.7892	0.6482	1.6272
Ankrd28			0.3323	1.6272
Arglu1	0.7505	0.7892	0.5184	1.6272
Arl6ip4	1.3106	0.3077		1.6272
Asxl1	0.4551	0.612	0.3323	1.6272
Bat4	0.6724	0.3077	0.3323	1.6272
Ccng1	1.4302	0.3077	0.3323	1.6272
Cd209d	0.7505		1.0084	1.6272
Crbn	0.2846	0.3077	0.3323	1.6272
D630023F18Rik	0.4551	0.612	0.5184	1.6272
Gm5593	0.5772	0.612	0.748	1.6272
Gm9776	0.7505		0.6482	1.6272
Hist1h1t	0.6724	1.1262	0.5184	1.6272
Krtdap	0.4551		0.5184	1.6272
Olr422	1.0486	0.3077		1.6272
Phyhip	0.7505	0.3077	0.3323	1.6272
Plxnb1	0.2846			1.6272
Ppp4r1	0.7505	0.3077	0.748	1.6272
Prkrir	0.4551	1.1885		1.6272
Prl8a1	0.2846	0.486	0.3323	1.6272
Rhot2	0.5772	0.7892	0.5184	1.6272
Rsu1	0.2846	0.3077	0.6482	1.6272
Tfam	0.6724		0.3323	1.6272
Xcl1	1.2472	0.3077	0.8974	1.6272
XM_141964	0.2846	0.612	0.3323	1.6272
XM_142663	0.4551	0.612	1.1701	1.6272
XM_143134	0.9247	0.8565	0.748	1.6272
XM_145457		0.486	0.3323	1.6272
XM_151703	0.4551			1.6272
XM_153602		0.3077	0.3323	1.6272
XM_153808	0.2846	1.2165	0.3323	1.6272
XM_157965	0.6724	0.7096	0.3323	1.6272
XM_160456	0.4551	0.486		1.6272
XM_164796	0.9247	0.3077	0.6482	1.6272
XM_283269				1.6272
XM_285260	0.2846	0.3077		1.6272
XM_285390	0.2846		0.3323	1.6272
XM_286251	0.2846	0.8565		1.6272
XM_286509	0.97	0.7096		1.6272
XM_288203		0.7892	0.748	1.6272
XM_288578	0.7505	0.3077	0.3323	1.6272
XM_289272	0.4551	0.612	0.6482	1.6272
XM_485248				1.6272
Atad2	0.9247	0.3077	0.6482	1.6152
Dnajc1	0.6724	0.612	1.0084	1.6152
Eef1e1		0.3077		1.6152
Erbb4	0.2846	0.486	0.3323	1.6152
Fgf14	1.145		0.6482	1.6152
Foxn3		1.3929		1.6152
Klk5	0.6724	0.7096	0.3323	1.6152
Krtap3-3		0.7096		1.6152
Lpar1	0.4551	0.3077	0.748	1.6152
Lrrc58	0.4551	0.9147	0.5184	1.6152
Neto2	0.874	0.486	0.3323	1.6152
Nup107	0.4551	0.3077		1.6152
Oit1	0.7505	0.612	0.5184	1.6152
Phlda2	0.5772	0.486	0.8291	1.6152
Ptn	0.4551	0.612	0.3323	1.6152
Rnase10	0.7505	0.7892	0.5184	1.6152
Shd	0.2846	1.3929	0.5184	1.6152
Smr3a	0.6724	1.0913		1.6152
Tbc1d2	0.2846	0.486		1.6152
Urgcp	0.6724	0.612	0.8291	1.6152
XM_110803	0.4551	0.486	0.3323	1.6152
XM_142146	0.5772	0.9147	0.3323	1.6152
XM_150452	0.5772	1.0913	0.8291	1.6152
XM_150607	0.4551	0.3077	0.6482	1.6152
XM_282998		0.612	0.748	1.6152
XM_283529	0.5772		0.6482	1.6152
XM_284221		0.486		1.6152
XM_285500	0.2846	0.3077	0.5184	1.6152
XM_286706	0.5772	0.3077		1.6152
XM_287925	0.2846	0.486	0.5184	1.6152
XM_290020	0.2846	0.612	0.5184	1.6152
XM_489147	0.8166	0.486		1.6152
4930524B15Rik	0.5772	0.612	0.3323	1.6029
4933434C23Rik	1.0111	0.486	0.5184	1.6029
Ar	0.2846	0.612		1.6029
Cldn8	0.4551	0.486	1.1349	1.6029
Cops7b	1.2238	0.3077	0.8974	1.6029
Edn3	1.0111	0.7096	0.6482	1.6029
Fam184b	0.8166	0.8565	0.6482	1.6029
Gm14461	0.9247	0.7096	0.3323	1.6029
Gne	0.2846	0.7892	0.6482	1.6029

Gpr84	0.2846	0.486	0.6482	1.6029
Kif9	0.6724	0.612	0.5184	1.6029
Klre1	0.5772	0.3077	0.748	1.6029
Oc90	0.5772	0.3077		1.6029
Olfr1317		0.3077		1.6029
Olfr608	1.1729	1.0913	0.3323	1.6029
Olfr714	1.1152	0.486	0.5184	1.6029
Olr1084				1.6029
Pbk	0.7505	0.9147	0.8291	1.6029
Pira11	0.4551	0.3077	1.2026	1.6029
Plcd4	0.7505	0.8565	0.3323	1.6029
Ppt1	0.5772	0.3077	0.9565	1.6029
Pramel6	0.8166	0.486	0.5184	1.6029
Reln	0.9247	0.612	0.5184	1.6029
Rinl	0.5772	0.486	0.3323	1.6029
Senp5	0.2846	0.3077	0.6482	1.6029
Sobp	0.5772		0.3323	1.6029
XM_150912	0.7505		0.6482	1.6029
XM_163125	0.5772	0.612		1.6029
XM_164712	0.7505	0.7892	0.748	1.6029
XM_195002	0.2846	0.7892	0.5184	1.6029
XM_196719	0.5772	0.486	0.5184	1.6029
XM_206657	0.2846	0.3077	0.5184	1.6029
XM_284649	0.2846	0.486	0.3323	1.6029
XM_288600	0.5772	0.486	0.3323	1.6029
XM_487514	0.2846	0.3077		1.6029
Zfp595	0.4551	0.486	0.8291	1.6029
Zfp954		0.486	0.5184	1.6029
2410001C21Rik	0.874	0.7892		1.5903
2810459M11Rik	0.4551	0.8565	0.3323	1.5903
BC003266	0.6724	0.486	1.2026	1.5903
Ccin	0.8166	0.7096	0.8974	1.5903
Cnst	0.7505	0.612	0.8291	1.5903
Cryz	0.874	0.612	0.748	1.5903
Ddx24	1.1152	0.486	0.748	1.5903
Gm648	0.7505	0.3077	0.6482	1.5903
Hoxc10	0.4551	0.612		1.5903
Msx3		0.612	0.6482	1.5903
Ndufaf1	0.5772	0.8565	0.5184	1.5903
Npnt	0.4551	0.486	0.5184	1.5903
XM_140063	0.5772	0.3077	0.3323	1.5903
XM_150312	0.2846	0.3077		1.5903
XM_154858	1.1152	0.7892	0.5184	1.5903
XM_155066	0.6724	0.612		1.5903
XM_156262	0.5772	0.3077		1.5903
XM_194805	0.7505	1.2429	0.5184	1.5903
XM_197577	0.4551			1.5903
XM_285452	0.4551	0.486		1.5903
XM_285909		0.486		1.5903
XM_286283	1.3992	0.612	0.3323	1.5903
XM_287316	0.7505	0.612	0.9565	1.5903
XM_287835	0.2846	0.612		1.5903
XM_288633	0.8166	0.7096	0.8291	1.5903
XM_289163	0.4551	0.486	0.3323	1.5903
XM_289443		0.612	1.0548	1.5903
XM_486465	0.5772	0.486	0.3323	1.5903
1500002O10Rik	0.9247	1.0119		1.5773
2700097O09Rik	0.4551	0.486		1.5773
4930468A15Rik	0.6724	0.3077	0.748	1.5773
8430410K20Rik	0.5772	0.7892	0.748	1.5773
A530032D15Rik		1.0913	0.6482	1.5773
Afmid	0.4551			1.5773
Aoc2	0.5772	0.8565	0.8291	1.5773
Arrb1	0.5772	0.486		1.5773
Bbs10		0.7096		1.5773
Card6	0.4551	0.612	0.8291	1.5773
Cd300e	0.97	0.612	0.5184	1.5773
Cd79a	0.2846	1.0119		1.5773
Cyp2a12			0.3323	1.5773
Fabp5	0.2846		0.8291	1.5773
Gbx2	0.4551	1.0119	0.3323	1.5773
Hyal4	0.4551	0.486	0.9565	1.5773
Ido2	0.874	1.0534	0.5184	1.5773
Kl		0.486		1.5773
Matr3	1.0832	0.3077	0.3323	1.5773
Pigc	0.2846	0.486		1.5773
Pitpnm3	0.5772	1.0913	0.5184	1.5773
Rac2	0.5772	0.7892	0.3323	1.5773
Ret		0.3077	0.3323	1.5773
Rfc2		0.3077	0.3323	1.5773
Rnf157	0.2846	0.3077	0.3323	1.5773
Sec31a	0.2846	0.9147	0.8974	1.5773
Sh3pxd2a	1.0832	0.612	0.748	1.5773
Upk1b	0.5772	0.7892	0.748	1.5773
XM_127084	0.5772	0.7892	0.5184	1.5773
XM_136246	0.7505	0.3077		1.5773
XM_138629	0.5772	0.7096		1.5773

XM_146453	0.5772	0.486		1.5773
XM_146465	1.3659	0.3077	0.3323	1.5773
XM_155135	0.2846	0.7892	0.6482	1.5773
XM_156842	0.4551	0.486		1.5773
XM_157736		0.8565	0.3323	1.5773
XM_161863	0.7505	0.612	1.0084	1.5773
XM_163735	1.0832	0.486	0.3323	1.5773
XM_194987	0.5772	0.7892	0.3323	1.5773
XM_197241	0.6724	0.3077	0.6482	1.5773
XM_197490	0.9247	0.966		1.5773
XM_487263	1.0486	0.8565	0.5184	1.5773
2810432L12Rik	0.4551		0.3323	1.5639
5830418K08Rik	0.2846	0.3077	0.5184	1.5639
9530026P05Rik	0.8166	0.3077	0.5184	1.5639
Akap1	0.4551	0.9147	0.9565	1.5639
Arvcf	0.4551		0.3323	1.5639
B4galnt2	1.0486	0.7096	0.6482	1.5639
Batf2	0.6724	1.1262	0.5184	1.5639
BC032203	0.6724	0.7892	0.8974	1.5639
Ccl11	0.5772	0.612	0.6482	1.5639
D330041H03Rik	0.874		0.6482	1.5639
Eya3		0.8565	0.3323	1.5639
Frg1	0.7505	0.612	0.8291	1.5639
Gpr119	1.3298	0.7096		1.5639
Gstt2	0.2846	0.7892		1.5639
Klhdc5	0.8166	0.9147	0.3323	1.5639
Mcart1	0.5772	0.7096	0.3323	1.5639
Mrgprb1	0.874	0.3077	1.1701	1.5639
Ms4a5	0.2846	0.486		1.5639
Myh7	0.2846	0.7096	1.0084	1.5639
NM_175479	0.97	0.7096	0.5184	1.5639
Oxgr1	0.6724	0.9147	0.5184	1.5639
Ppig				1.5639
Wisp2	0.8166		0.5184	1.5639
XM_112298	0.8166	0.7892		1.5639
XM_129867	0.4551	0.8565		1.5639
XM_132134	0.7505	0.9147	0.8291	1.5639
XM_132652	0.4551	0.486	1.0084	1.5639
XM_134412	0.2846	0.3077	0.3323	1.5639
XM_136437	0.4551	0.612	0.5184	1.5639
XM_137215	1.2904	0.7892		1.5639
XM_142892	0.4551	1.0913	0.5184	1.5639
XM_143773	0.6724	0.966	0.5184	1.5639
XM_144221	0.5772	0.3077	0.3323	1.5639
XM_144681	0.4551	0.8565	0.6482	1.5639
XM_151129	0.8166		0.5184	1.5639
XM_152041	0.4551		0.748	1.5639
XM_152187	0.2846		0.748	1.5639
XM_153881	0.2846	0.7096	0.748	1.5639
XM_154522	1.3659	0.486	0.6482	1.5639
XM_154889	0.4551	0.3077	0.6482	1.5639
XM_162513	0.7505	0.7096	0.5184	1.5639
XM_196953	0.2846	0.3077	0.6482	1.5639
XM_206756	0.5772	1.0534	0.5184	1.5639
XM_285001	0.5772	0.8565	0.5184	1.5639
XM_285670	0.4551	0.3077	0.3323	1.5639
XM_286370				1.5639
XM_286808	0.5772	1.2429		1.5639
XM_288561	0.5772	0.486	0.5184	1.5639
XM_288676	0.5772	0.3077	0.3323	1.5639
XM_289251	0.2846	0.486	0.5184	1.5639
XM_289330	0.8166	0.3077		1.5639
XM_289414	0.2846	0.7096	1.2026	1.5639
XM_290060	0.8166	0.7096	0.3323	1.5639
XM_356617	0.5772	0.486	0.8974	1.5639
XM_484644	0.7505	0.612		1.5639
1700028J19Rik	0.7505	0.486	0.6482	1.55
2310036O22Rik	0.2846	0.486		1.55
4921511H03Rik	1.2472			1.55
5730433N10Rik	0.874	1.0913	0.3323	1.55
Accn5	0.6724	0.486	0.3323	1.55
Acsl6	0.7505	0.3077		1.55
Alcam	0.6724	1.0119		1.55
Ankrd1	0.6724	0.612		1.55
Azi1	0.2846	0.7096	0.5184	1.55
C030019G06Rik	0.5772	0.612	0.3323	1.55
Cd68	0.6724	0.3077	0.6482	1.55
Crygs	0.4551		0.6482	1.55
Cstb	0.2846	0.3077	0.5184	1.55
Fam65a	0.6724	0.966	0.5184	1.55
Fbxw8	0.874	0.3077	0.6482	1.55
Fpr-rs3	0.4551	0.3077	0.3323	1.55
G6pdx	0.7505	0.3077	0.5184	1.55
Gimap8	0.4551			1.55
Gm5482	0.8166	0.612	0.5184	1.55
Gsto1	0.7505	0.486	0.8974	1.55
Nat6	0.4551	0.7096	0.3323	1.55

Ncapg		0.3077	0.3323	1.55
Ngb	0.4551	0.612	0.3323	1.55
Oprl1	0.9247	0.612	0.9565	1.55
Osbpl8	0.4551	0.486	0.5184	1.55
Plk3	0.4551		0.5184	1.55
Prdm15	0.4551	0.486	0.3323	1.55
Prkce	0.7505	0.486	1.2026	1.55
Rfc3	0.9247	0.3077	1.0967	1.55
Rpl11	0.97	0.966	0.5184	1.55
St3gal4	0.2846		0.5184	1.55
TEX14	0.5772	0.7892	0.748	1.55
Tmem202	0.6724	0.7096		1.55
Triml1	0.6724	0.7096	0.748	1.55
Ttc33		0.612		1.55
Tusc2	0.7505	1.3136		1.55
Ubd	0.8166		0.3323	1.55
Vamp3		0.486	0.3323	1.55
Vmn1r43	1.0111	0.612	0.6482	1.55
Vmn2r19	0.6724	0.7892	0.5184	1.55
XM_137032	0.5772		0.3323	1.55
XM_139511	0.4551	0.3077		1.55
XM_143050	0.5772	0.486	0.5184	1.55
XM_146303	0.4551	0.7096	0.5184	1.55
XM_158512	0.6724	0.612	0.8974	1.55
XM_285826	0.5772	0.7892	0.3323	1.55
XM_286700	1.1152	0.8565	0.3323	1.55
XM_287191	0.5772	0.3077	0.9565	1.55
XM_288318		0.612		1.55
XM_288853			0.3323	1.55
XM_289282	0.874	0.3077	0.3323	1.55
XM_289348	0.5772	0.612	0.5184	1.55
XM_289482	0.2846	0.7096	0.3323	1.55
XM_356680	0.4551	0.3077	0.6482	1.55
XM_484333	0.2846		0.3323	1.55
Zfp30			0.6482	1.55
Znrf1	0.5772	0.612		1.55
1700021K19Rik	0.5772	0.7892	0.3323	1.5357
2810055F11Rik	0.4551	0.486	0.5184	1.5357
Alg11	0.2846			1.5357
Apcs				1.5357
Arfgap1	0.4551	0.3077		1.5357
C230088H06Rik	0.6724	0.486	0.3323	1.5357
C4b	0.4551	1.2165		1.5357
Cfl1	0.6724		0.748	1.5357
Clcn3	0.4551	0.486		1.5357
Cuedc1	0.9247	0.9147	0.6482	1.5357
Dnm1l	0.8166	0.7892		1.5357
Fhod3	0.6724		0.8291	1.5357
Gpatch3	0.4551	0.486		1.5357
Grik2	1.0832	0.486	0.8974	1.5357
Hcn4	0.2846			1.5357
Iqcf4			0.3323	1.5357
Krt23		0.612		1.5357
Mtap4	0.874	0.612	0.3323	1.5357
NM_175108	1.2238	0.612	0.5184	1.5357
Nup37	0.2846		0.5184	1.5357
Pla2g5	0.5772	0.486	1.0548	1.5357
Sik1	0.6724		0.3323	1.5357
Sphk2			0.6482	1.5357
XM_112201	0.9247		0.5184	1.5357
XM_140869	0.874	0.8565	0.6482	1.5357
XM_141710	0.5772	0.8565		1.5357
XM_145862		0.3077	0.5184	1.5357
XM_154330	0.4551		0.3323	1.5357
XM_157591	0.5772	0.7096	0.5184	1.5357
XM_157701	0.2846	1.2165	0.5184	1.5357
XM_160408	0.2846	0.486	0.3323	1.5357
XM_162184	1.0111	0.7892	0.6482	1.5357
XM_197074	0.6724	0.7096	0.3323	1.5357
XM_205294	0.5772	0.486	0.5184	1.5357
XM_284077	0.2846	0.486	0.3323	1.5357
XM_284639	0.4551	0.7892	0.5184	1.5357
XM_286314		0.3077		1.5357
XM_286647	0.4551	1.3348		1.5357
XM_287784	1.1991	0.7096	0.6482	1.5357
XM_287910	0.2846	0.7892	0.5184	1.5357
XM_289133	0.4551	0.3077	0.5184	1.5357
XM_289382	0.4551		0.3323	1.5357
Xpc		0.486	0.9565	1.5357
Zfp944	1.3992	1.1262		1.5357
Zp1	0.5772	1.2165	0.3323	1.5357
1810030N24Rik	0.8166	0.612		1.5209
4930529M08Rik	1.1991	0.7892	0.5184	1.5209
5830405M20Rik	0.5772	0.8565	0.748	1.5209
6330503K22Rik	0.8166	0.7096	0.8291	1.5209
Ahcyl1				1.5209
Angel1	0.4551	0.612	0.5184	1.5209

Arl8a	0.4551	0.7892	0.8974	1.5209
Cacna1h		0.486	0.3323	1.5209
Ccdc85a	0.5772	0.612		1.5209
Cpe	0.2846		1.2611	1.5209
DKFZP564J086	0.2846	0.612	0.3323	1.5209
Emilin1	0.5772	0.486	0.6482	1.5209
Gltp	0.4551	0.7096	0.8974	1.5209
Gm4825	0.5772	0.7096	0.5184	1.5209
Gm5444	0.7505	0.3077	0.3323	1.5209
Htra3	0.7505	0.966	0.748	1.5209
Klhl6	0.6724	0.7096	0.6482	1.5209
Krtap8-2		0.3077		1.5209
Ltb4r1	0.6724	0.486	0.748	1.5209
Mprip	0.2846	0.3077	0.3323	1.5209
Obscn	0.4551	0.486	0.5184	1.5209
Pcsk6	1.0111	0.7096		1.5209
Pdcd1lg2	0.2846	0.7892	0.3323	1.5209
Plac1l	0.4551	1.2165	0.3323	1.5209
Prl8a6	0.6724	0.966	0.5184	1.5209
Smap1	0.6724	0.3077	0.3323	1.5209
Sox2	1.2472	0.3077	0.6482	1.5209
Tgif2lx1	0.7505	0.486		1.5209
Vmn1r52	0.4551	0.612	0.6482	1.5209
XM_110831	0.9247	0.8565	0.3323	1.5209
XM_110985	0.4551		0.3323	1.5209
XM_134237	1.0111	0.7096	0.8291	1.5209
XM_137221	0.6724	0.612	0.3323	1.5209
XM_138139	0.97	0.486		1.5209
XM_138649	0.4551	0.486	0.5184	1.5209
XM_141865	0.7505	0.486	0.748	1.5209
XM_143206	0.8166	0.7096	0.8291	1.5209
XM_144417		0.3077		1.5209
XM_146363		0.486		1.5209
XM_151047	0.2846	0.7096	0.5184	1.5209
XM_156081	0.4551		0.6482	1.5209
XM_158836	0.8166	0.612	0.8291	1.5209
XM_213907	0.2846	0.7096	0.3323	1.5209
XM_220544	0.5772	0.486		1.5209
XM_287521	0.5772	0.7892	1.0084	1.5209
XM_288438	0.4551	0.486	0.5184	1.5209
XM_288468	0.8166	0.612		1.5209
XM_288750	0.5772			1.5209
XM_288845	0.6724	0.7096	0.6482	1.5209
XM_484058	0.874	0.8565	0.748	1.5209
2610027F03Rik	0.6724	0.3077	1.0084	1.5056
4921517L17Rik	0.6724		0.5184	1.5056
Apobec3	1.145	0.486	0.6482	1.5056
Bcl2l14	1.0111	0.486	0.3323	1.5056
Cav2	0.6724	0.7892	0.3323	1.5056
Ccdc25		0.3077		1.5056
Ccdc41	0.97	0.3077	0.6482	1.5056
Cdkn2aip	0.4551		0.6482	1.5056
Chic2	0.6724	0.486	0.6482	1.5056
Chmp1a	0.7505	0.7892	0.6482	1.5056
Clpx	0.4551	0.7096		1.5056
Ctsj		0.3077		1.5056
D430032J08Rik	0.2846	0.486	0.3323	1.5056
Eid3	0.4551		0.5184	1.5056
Fam117b	1.3106	0.3077	0.748	1.5056
Fam35a	0.5772	0.3077	0.5184	1.5056
Fgd2	0.2846	0.7096		1.5056
Gapdhs	0.2846	0.3077	0.5184	1.5056
Gpr182	0.2846	0.7892	1.2328	1.5056
Hmgxb4	0.8166	0.8565	0.8291	1.5056
Hspa14	0.4551	0.3077	0.6482	1.5056
Itga4	0.8166	0.486	0.748	1.5056
Krt9	1.145	0.3077	0.5184	1.5056
Lrrc8a	0.6724	0.7096	0.3323	1.5056
Mest	0.2846	0.3077	0.3323	1.5056
Nid2	0.7505	0.3077		1.5056
NM_176964	0.5772	0.3077	0.5184	1.5056
Obfc2a	0.874	0.486		1.5056
Odf3l1		0.612		1.5056
Ogfod1	0.5772	0.612	0.748	1.5056
Olfr1206	0.2846	1.0534		1.5056
Olr463	0.2846	0.3077	0.3323	1.5056
Pdxp	0.4551	0.486	0.5184	1.5056
Prickle3	0.5772	0.486	1.0548	1.5056
RGD1310270		0.486		1.5056
Rin1	0.5772	0.3077	0.3323	1.5056
Sgk2	0.4551	0.3077	0.5184	1.5056
Sh3gl2	0.8166	0.966	0.748	1.5056
Slc35b1	0.2846	0.3077	0.5184	1.5056
Slc39a13	0.2846	0.7096	0.8974	1.5056
Slc4a7	0.6724	0.3077	0.748	1.5056
Spast		0.486	0.8974	1.5056
Srp9				1.5056

Tex13	0.4551	0.7096	0.5184	1.5056
Uba1	0.2846	0.3077		1.5056
XM_111216	0.4551	0.8565	0.8291	1.5056
XM_155069	0.5772	0.9147	0.6482	1.5056
XM_155778	0.2846	0.612	0.748	1.5056
XM_157290	0.5772	0.7892	0.5184	1.5056
XM_158035	1.2693	0.486	0.6482	1.5056
XM_158993	0.5772	0.612	0.3323	1.5056
XM_160391	0.5772	0.486	0.6482	1.5056
XM_162361	0.8166	0.486	1.2026	1.5056
XM_163582	0.4551	0.966	0.3323	1.5056
XM_164175			0.8291	1.5056
XM_194974	0.7505	0.8565	0.748	1.5056
XM_196709	0.2846	0.7096	0.6482	1.5056
XM_203293	0.2846	0.3077	0.5184	1.5056
XM_227472	0.5772	0.3077	0.748	1.5056
XM_287062	0.6724	0.7096	0.3323	1.5056
XM_288224	1.2472	0.7096		1.5056
XM_342146	0.4551	0.3077		1.5056
XM_484199	0.6724	0.3077		1.5056
XM_489106	0.8166	0.486	0.5184	1.5056
XM_489872	0.7505	0.9147	0.748	1.5056
Zbtb9	0.4551	0.3077	0.8291	1.5056
Zfp787	1.3659	0.612		1.5056
Zfp956		0.3077		1.5056
0610007P08Rik	1.1152	1.2678	0.8974	0.8974
0610010F05Rik	1.4302	1.4599	1.6719	1.38
0610037L13Rik	1.0111	0.8565	1.5056	1.1701
1110005A03Rik	1.6996	1.3929	1.8154	1.2876
1110049F12Rik	1.1729	1.2429	1.2876	1.0548
1110067D22Rik	1.0486	1.0534	1.1349	1.0084
1200016B10Rik	1.0111	1.0534	1.0548	1.9462
1600012F09Rik	1.0832	1.1262	1.3587	1.38
1600029D21Rik	1.2472	0.8565	0.6482	1.1349
1700001C19Rik	1.6485	1.4277	1.6388	1.1701
1700012P22Rik	0.97	1.0913	1.0084	0.9565
1700018H16Rik	1.2238	1.0534	1.4897	1.55
1700029P11Rik	0.97	0.7892	1.0967	1.2328
1810031K17Rik	1.0111	0.9147	1.3126	2.0189
1810074P20Rik	1.2472	1.4752	1.3363	1.55
2200002K05Rik	1.3829	1.1885	1.1349	1.2328
2210418O10Rik	2.0568	1.2678	1.4733	0.9565
2310002L13Rik	0.6724	0.9147	1.0548	1.2026
2310003L06Rik	1.7595	0.612	1.1701	1.3363
2310057J18Rik	1.5585	0.7096	1.2026	0.9565
2410004P03Rik	1.6108	1.4277	1.2026	1.2876
2610008E11Rik	0.2846	2.0887	1.7918	1.5773
2610019F03Rik	1.2472	0.7892	0.9565	1.3126
2700099C18Rik	1.0111	0.9147	0.8291	1.4733
2810011L19Rik	0.97	1.0913	1.6611	1.6824
2810422O20Rik	1.0832	1.1262	1.5903	1.2611
2810442I21Rik	1.4591	1.7764	1.6272	0.5184
2900064A13Rik	1.3482	1.2165	1.6388	1.3587
3110009E18Rik	0.97	1.5927	0.8291	1.2876
3110047P20Rik	1.5238	1.4106	1.5773	1.7124
3110057O12Rik	1.145	1.0119	1.2026	0.9565
3632451O06Rik	0.9247	1.7983	1.6611	1.1701
4632411B12Rik	1.7665	0.612	1.3126	0.9565
4732471D19Rik	0.9247	1.0119	1.0084	1.2328
4831410D14	1.1152	1.0913	1.4003	1.4197
4831440E17Rik	1.5357	1.4899	0.8974	0.8974
4833438C02Rik	1.3659	1.4441	1.6029	1.3126
4921506M07Rik	1.7076	1.0119	1.3363	0.8974
4921523A10Rik	1.4302	1.3551		1.8077
4921530L21Rik	0.874	1.1262	0.748	1.55
4921536K21Rik	1.0486	1.2913	0.748	1.1701
4930402H05Rik	1.5907	1.4599	1.38	1.0967
4930424E08Rik	1.145	0.966	0.8291	1.6611
4930430F08Rik	2.0351	1.9673	2.1968	1.7583
4930435E12Rik	1.3829	1.3136	2.0284	1.8154
4930443G12Rik	1.0111	1.1584	0.8291	1.2328
4930447C04Rik	1.0111	1.6942	1.1349	0.8291
4930472D16Rik	1.3482	1.3744	1.8589	1.3587
4930503E14Rik	1.6108	0.7892	0.748	1.3126
4930506M07Rik	0.6724	1.3551	1.5209	0.9565
4930510E17Rik	1.3482	1.1584	0.748	0.8291
4930519G04Rik	0.6724	2.3496	1.9629	1.5209
4930535F04Rik	0.8166	1.3551	0.748	1.1701
4930544D05Rik	1.0111	1.0119	0.748	0.9565
4930544G11Rik	1.145	1.0913	1.5639	1.8377
4930544I03Rik	1.1729	1.2165	0.748	1.3363
4930555F03Rik	1.4861	1.5927	1.7124	1.2611
4930556M19Rik	0.7505	0.9147	1.0084	1.1349
4930570G19Rik	1.2904	1.4106	1.3587	1.6388
4930595M18Rik	1.8183	0.8565	1.2328	1.3363
4931406H21Rik	1.145	1.2913	1.1701	1.38
4932411N23Rik	0.8166	1.1885	0.8291	1.55

4932415M13Rik	1.4861	1.3136	1.7314	1.0967
4933403F05Rik	1.1991	1.0913	0.8974	1.3126
4933407H18Rik	0.6724	1.5313	1.2026	1.6926
4933415A04Rik	0.874	1.2913	0.6482	1.2026
4933421E11Rik	1.1152	0.8565	1.4003	1.3363
4933425O20Rik	1.738	1.7839	0.6482	1.4733
4933432B09Rik	0.8166	1.1262	1.1349	1.8229
5033404E19Rik	1.2472	1.2678	1.7124	1.2876
5730508B09Rik	0.2846	1.7373	1.5639	1.8449
5930438M14	1.1991	0.9147	0.5184	1.2611
6330407A03Rik	1.2904	1.0119	1.0967	0.8291
6330407J23Rik	0.7505	0.966	1.2328	1.3363
6720482D04	2.5555	2.4381	2.5531	2.0555
6820408C15Rik	1.1729	1.3348	0.6482	1.1349
6820431F20Rik	2.0496	2.0043	1.1349	1.38
8030423J24Rik	2.02	1.7983	1.2328	2.1569
8430427H17Rik	1.3829	0.966	0.6482	1.4003
9030625A04Rik	1.0486	0.7096	1.0967	1.1701
9130002K18Rik	0.7505	0.9147	1.0967	1.38
9130004C02Rik	0.9247	1.5927	1.1349	0.9565
9230110F15Rik	1.1729	2.0384	1.2611	0.8974
9330117O12	1.2693	1.1584	0.748	1.6824
9330159M07Rik	1.78	2.2827	0.8291	0.748
9930104L06Rik	0.97	0.7892	0.8291	1.7495
9930111J21Rik	1.4449	2.0813	1.2328	1.2876
A030003K21Rik	0.97	0.9147	1.1349	1.7026
A130010C12Rik	0.874	1.4277	1.2328	1.2328
A130030D18Rik	0.874	1.0534	0.8291	0.9565
A130034M23Rik	2.1004	2.6722	1.3363	2.8185
A230061C15Rik	1.2904	0.7892	0.6482	1.4003
A230072E10Rik	2.1921	1.9269	1.9841	1.4562
A430110L20Rik	1.4449	1.3348	1.923	1.6501
A630055G03Rik	1.3992	0.612	1.0967	1.1349
Aadac	2.0122	0.9147	0.5184	1.6824
Aak1	0.97	0.966	0.748	1.4897
AB099516	0.6724	1.0913	0.9565	1.1349
Abca6	1.0832	1.1262	1.2328	1.1349
Abcd3	0.97	1.3136	1.4003	1.1701
Abpb	1.3482	0.9147	1.0548	0.9565
Abtb1	1.3298	0.7096	1.0967	0.8291
Accs	1.9626	1.4899	1.4562	1.1349
Aco1	1.7932	1.6464	1.0548	0.748
Acot11	1.0111	0.7892	1.3126	1.5056
Acpl2	2.0083	2.1135	2.6908	2.2532
Actc1	1.2238	0.7096	1.4003	1.0084
Adam17	1.0111	0.7892	1.2611	1.0548
Adam5	1.415	1.0119	0.9565	0.8291
Adamtsl1	1.4991	1.0119	0.8974	1.7124
Adcy5	0.97	1.9162	1.4562	0.748
Add1	2.0388	1.9673	1.8449	2.033
Add3	1.3482	1.9052	0.5184	1.1349
Adh4	0.874	1.0534	1.4003	1.5903
AF067063	1.2904	2.1499	0.3323	2.2304
Afap1	1.5802	0.9147	1.2328	1.2611
Agbl1	1.415	0.9147	0.5184	1.3363
Agmo	0.7505	1.3551	0.748	1.4003
Agpat6	1.7154	1.1885	1.3587	1.4197
Agt	0.8166	0.9147	1.0548	1.0967
Agtrap	1.145	1.0913	1.2026	1.6824
Ahdc1	1.0111	1.1262	0.9565	2.0555
Ahi1	1.0111	1.7373	0.9565	1.2026
Ahsa1	1.1991	1.1262	1.3363	0.9565
AI646023	1.8244	0.7096	0.8974	1.722
AI849053	0.97	0.7892	1.0967	1.6824
AK048490	1.6748	1.3929	0.3323	1.1349
Akap13	1.0832	1.0534	0.8974	1.0548
Akap7	3.0825	3.1496	3.1869	2.7425
Aldh3b1	1.2472	1.1885	1.6029	1.4003
Alg12	0.874	1.0119	1.1349	1.2328
Alpk1	0.7505	2.4006	1.6029	1.917
Als2	1.2693	1.0119	1.6611	1.55
Als2cr11	0.97	1.6464	1.3363	1.2328
Anapc11	1.1991	1.1262	0.6482	1.2026
Ank2	1.5116	1.518	0.8974	1.3363
Ankib1	0.6724	1.4899	1.2876	1.0548
Ankle2	1.7866	1.6257	0.9565	0.3323
Ankmy2	1.2238	1.3348	1.4733	1.0967
Ankrd11	1.9065	1.9162	2.536	2.1053
Ankrd12	1.2904	0.7096	1.4383	1.4003
Ankrd17	0.4551	1.3348	1.4003	1.4383
Ankrd33b	0.6724	0.966	1.0548	1.6152
Ankrd35	0.874	2.301	1.3363	2.5956
Ankrd36	0.97	1.3348	1.38	0.748
Ankzf1	1.0832	1.3929	0.6482	1.8725
Ano4	1.2904	1.2913	1.0084	1.3363
Aoc3	0.7505	1.2165	1.0084	0.8974
Ap4e1	0.9247	0.8565	1.2611	1.0967

Apitd1	2.9096	2.7216	3.1556	2.5641
Arap2	1.7306	1.8823	2.0974	1.8658
Arhgap20	1.4728	0.7096	0.748	1.7669
Arhgap39	1.0832	0.966	0.8291	1.1701
Arhgap4	1.0832	0.7892	0.748	1.2611
Arid5a	1.4302	1.8054	1.5209	2.4085
Armc2	0.97	1.9862	1.2876	1.8077
Armc5	3.5825	3.6018	3.6889	3.4863
Armc7	2.1571	2.0174	2.1839	1.6719
Armcx2	0.874	1.2165	0.748	1.3587
Arntl2	1.0486	0.7096	0.8291	1.1701
Arpp21	1.7733	1.7032	2.275	1.9943
Arsg	1.3992	1.4752	1.2876	1.1349
As3mt	0.874	1.4752	1.3587	1.0548
Asb3	0.874	1.0913	0.748	1.3126
Asph	1.0111	0.7892	1.3363	1.1349
Atad1	1.1152	1.0119	1.5056	0.748
Atf7ip2	0.874	1.2165	1.0084	1.55
Atm	0.9247	1.7983	0.6482	1.6152
Atp6v1g2	1.3482	1.6564	1.4897	[illegible]
Atp8b3	0.97	1.0119	0.8974	0.8291
Atr	1.9755	1.615	2.1569	1.8154
Atxn7l1	0.5772	1.0913	1.2328	1.4003
AU041133	1.1152	1.2165	1.2328	1.1701
Aurka	1.6206	0.7892	1.4733	1.38
Aurkaip1	1.1991	1.4899	1.7405	1.2876
B430319H21Rik	1.0486	1.0119	0.6482	1.0084
B4galnt3	1.7076	1.5443	0.8974	1.6611
B4galt3	1.3659	1.0119	0.3323	1.5056
B930018H19	1.145	0.612	1.0548	1.1701
Baz1b	1.8122	0.7892	1.2026	0.9565
BC017612	0.7505	1.3136	1.0548	1.2611
BC031181	1.4861	1.4277	1.5357	1.3126
BC043934	0.97	0.8565	1.2026	1.5639
BC048502	1.0832	0.9147	0.9565	1.2876
Bcl2l2	0.9247	0.9147	1.4897	1.2876
Bcl7b	1.9963	0.966	0.8974	1.7026
Bdkrb2	0.97	0.7892	0.9565	1.2876
Bmp4	0.6724	0.9147	1.4003	1.2611
Bmx	1.6575	1.6662	1.8377	1.2611
Bod1l	1.0111	1.1885	1.3587	1.3126
Bpifb9b	1.0832	1.4441	1.2611	0.5184
Brca1	1.145	1.2429	0.9565	1.3363
Brd8	1.0486	1.0913	0.5184	1.7669
Btaf1	1.8913	0.8565	1.3363	0.8974
Btrc	1.0832	0.966	1.4197	1.0084
Bub1b	1.6485	1.2913	1.2611	0.8974
Bub3	0.97	1.2429	1.1349	1.3363
C030014L02	1.3106	1.5443	1.4383	1.0967
C030034L19Rik	1.0486	1.2913	0.9565	1.4197
C030037D09Rik	1.2238	1.2165	0.8291	0.6482
C130074G19Rik	1.2693	1.0119	0.8291	0.8291
C1qbp	0.5772	0.7096	1.5773	1.6029
C230053D17Rik	1.7525	0.7892	0.3323	1.7314
C3ar1	1.2238	1.3744	1.0967	1.0548
Cables1	1.1152	0.7096	0.748	1.4197
Cad	0.874	0.9147	1.0967	1.55
Calb1	1.5802	0.7892	0.6482	1.6029
Caln1	1.3298	1.0119	1.0084	1.2026
Camk1d	0.9247	1.2165	1.4197	1.3363
Camk2a	1.2238	0.9147	1.2026	0.9565
Camkk1	1.2238	1.2165	1.4897	0.9565
Caprin1	1.0486	1.0119	1.0548	1.4003
Car9	0.5772	1.9721	1.5056	0.8291
Casp12	1.0486	1.0534	1.1349	0.9565
Cast	1.415	2.3185	1.7405	1.0548
Catsperg1	1.3829	0.8565	1.6029	1.7405
Ccbe1	1.6301	1.2678	1.3363	1.917
Ccdc112	0.7505	1.0119	0.8974	1.5357
Ccdc14	1.145	1.0119	1.4383	1.2026
Ccdc151	1.6996	1.1584	0.9565	1.0084
Ccdc51	1.1152	1.2165	0.8291	0.9565
Ccdc73	1.1729	2.0995	1.3126	1.8304
Ccdc80	1.6108	1.7373	0.9565	1.8589
Ccdc88a	1.1729	1.2165	1.38	0.748
Ccdc93	1.2904	1.2678	1.2876	1.5209
Cct6a	1.1729	0.966	1.8077	1.2026
Cd177	1.2472	1.0119	1.4197	1.0084
Cd38	1.4449	0.612	1.4197	0.9565
Cd47	1.5357	1.1262	1.38	1.3587
Cd55	0.8166	1.0119	0.8291	1.2876
Cd63	0.874	0.9147	0.9565	1.4733
Cd79b	1.0486	0.3077	1.2611	1.7124
Cdc25a	1.2904	1.3136	2.0189	1.4197
Cdc42bpa	1.0486	1.2678	1.2611	1.4003
Cdca8	0.874	1.1262	0.6482	1.38
Cdh2	1.7076	1.7534	1.3363	1.9289

Cdk13	1.1991	0.966	1.0967	1.5903
Cdk16	0.8166	1.0913	0.8291	1.7495
Cdk5	1.0111	1.1885	0.748	1.0967
Cdk6	1.1729	0.8565	1.2611	1.0967
Cdk8	0.9247	1.0534	0.8974	0.9565
Ceacam11	1.1152	1.6942	0.6482	1.1349
Ceacam12	0.6724	0.8565	1.2611	1.2611
Cebpa	1.8244	0.8565	1.0548	0.8974
Cecr2	1.3482	1.0534	1.2026	1.2876
Celsr3	0.874	1.1584	1.0084	1.8154
Cep120	1.1152	1.1584	1.5357	1.2611
Cep170	0.6724	1.2678	1.0967	1.1701
Cep192	0.9247	0.9147	1.7026	1.6824
Cfc1	1.0111	0.9147	1.4197	1.2876
Cfh	0.97	0.966	0.9565	1.0548
Cflar	1.4302	2.0259	0.8974	0.748
Chmp2b	1.1991	1.0534	1.0084	1.9789
Chmp4c	1.1729	1.2165	1.6272	1.6272
Chrdl2	0.7505	0.7096	1.4897	1.5773
Chrna6	1.0832	1.9052	1.2026	2.1356
Chsy3	1.7595	1.9721	0.748	1.1349
Clasp1	0.7505	1.4106	1.4897	1.7669
Clca6	1.6748	0.612	0.6482	1.5903
Clmn	1.1152	1.2678	0.8291	1.2026
Clvs1	1.5116	0.612	1.2611	1.0967
Cml3	0.874	1.0119	0.8291	1.2876
Cndp1	1.0111	1.0119	0.9565	0.8974
Cnot4	1.7154	1.2678	1.55	1.3363
Cnot8	1.3992	0.9147	1.1701	1.0548
Cntnap5b	1.0486	1.0119	0.6482	1.0967
Col10a1	0.8166	0.9147	0.8974	1.5056
Commd2	0.8166	1.3929	0.8974	1.3363
Cpb1	1.0832	1.1584	1.1701	0.8974
Cpeb2	1.145	1.0534	0.748	1.0084
Cplx2	1.1152	1.0119	0.8291	1.8857
Cpne3	1.0486	1.1584	1.4383	1.0084
Creb3l2	1.1152	1.4277	1.6611	1.2026
Creg1	1.7453	1.9908	1.9406	1.7669
Crlf1	1.0111	1.3744	0.9565	1.8449
Csde1	1.2472	1.0119	1.5903	1.2611
Csrnp1	1.4861	1.0119	1.1701	0.8974
Ctbs	1.415	0.7892	0.748	1.7583
Ctdsp1	0.6724	1.3136	0.748	1.4003
Ctla4	1.0832	1.0913	0.9565	1.6029
Ctr9	1.3482	1.0913	1.0084	0.748
Ctso	1.6206	1.2913	1.6029	1.1701
Ctxn1	0.6724	0.7892	1.0967	1.5903
Cul3	2.2363	2.4771	2.3178	2.1053
Cwf19l1	0.874	1.5443	0.8974	1.2876
Cyb5rl	1.3298	1.0119	1.0084	0.748
Cyba	1.3482		1.4562	1.5357
Cyld	1.3106	1.0119	0.748	1.0084
Cyp2ab1	0.97	0.7096	0.9565	1.5639
Cyp2b23	0.8166	1.0534	1.1701	1.3126
Cyp2c29	0.8166	1.5811	1.4562	1.7124
Cyp4v3	1.3106	2.3476	1.3126	1.3363
Cyth4	1.6915	0.486	1.55	0.748
D030040B21Rik	0.9247	1.0913	1.4733	1.8725
D030051J21Rik	1.8478	1.8519	0.748	0.748
D19Ertd386e	0.874	1.5811	1.4733	1.3126
D5Ertd579e	1.0486	1.0534	0.9565	0.8291
D630003M21Rik	1.3298	1.2429	1.1349	1.4197
D730001G18Rik	0.9247	1.0119	1.1701	1.0548
D930001B02	1.7231	1.6362	0.5184	0.6482
D930030K17Rik	1.2693	1.2678	1.3587	1.9048
Dab1	1.738	1.5811	1.5209	1.1349
Dbr1	1.1152	1.2913	0.8974	0.9565
Dbx2	1.3482	2.0343	1.2026	1.4197
Dcaf12l2	2.0238	1.3551	1.7837	1.2328
Dcbld1	1.2693	1.4752	1.3587	1.2876
Dcst1	1.7231	0.8565	0.748	2.4868
Ddx10	1.2472	0.486	0.8291	1.5639
Ddx52	2.1947	2.1402	1.4897	2.9463
Defa3	1.7595	1.9052	2.2723	1.7837
Dennd1b	1.1729	0.9147	0.5184	1.3363
Denr	1.1729	1.1584	1.0548	1.4003
Derl2	1.4728	1.3744	2.0642	1.6719
Dgat2l6	1.4449	1.1885	0.6482	1.4562
Dgkk	0.97	1.1885	1.2328	1.3126
Dhx9	0.2846	1.7983	1.6501	1.0548
Dido1	0.8166	1.1262	1.0548	1.4383
Dixdc1	0.6724	1.1885	1.1349	1.0084
Dlc1	0.8166	0.8565	1.3126	1.2611
Dlx3	1.4449	1.1262	1.0084	1.7837
Dmrta2	1.1152	1.2678	0.8974	1.4003
Dnahc7b	1.2904	1.3136	1.5903	1.2328
Dnajc17	0.874	0.8565	1.2026	1.3587

Dnajc22	1.6009	1.4599	1.6152	1.0548
Dnch2	1.7665	1.3929	0.3323	2.2031
Dpp10	1.8913	0.8565	1.4733	0.5184
Dr1	1.7076	1.4752	2.0467	1.7754
E130008O17Rik	1.5695	2.0384	0.8291	1.1701
E130119H08	1.0111	1.1885	0.5184	1.9683
E130119H09Rik	0.9247	0.8565	1.0548	1.38
E130309F12Rik	0.4551	1.1885	0.9565	1.8077
E230016D10	1.3829	0.7096	1.5773	1.6272
E330009J07Rik	1.415	0.7892	0.8291	1.1701
E330035G20Rik	1.3106	0.966	1.1349	1.0548
Ear4	0.8166	1.0913	0.8291	1.2328
Ebf2	0.8166	0.966	1.1701	1.4733
Eda2r	0.97	1.8455	0.8291	1.5209
Efna1	1.2238	1.518	0.748	1.4733
Egfl7	0.9247	0.966	0.8974	1.2026
Eif1	0.6724	1.518	0.5184	1.7754
Eif2s1	0.6724	1.1584	1.2026	1.1701
Eif4enif1	0.97	0.7096	1.5639	1.1349
Elavl1	1.2693	1.2165	1.5357	1.7124
Elavl3	0.9247	0.7096	0.9565	1.7026
Ell2	1.1991	1.0913	1.6926	1.5056
Elmo1	1.6206	2.07	1.7669	2.4819
Eml3	0.9247	1.3348	0.8291	1.0967
Eml5	1.0111	1.5811	1.2026	1.0967
Emp2	1.6996	1.7764	2.1806	1.5639
Enpp3	1.2904	1.3348	1.4003	1.1701
Epha8	2.0874	1.8823	1.3126	1.4383
Epsti1	1.9626	1.3348	0.6482	1.4197
Ept1	0.874	1.2429	0.8291	1.3587
Erbb3	1.0111	1.0534	0.9565	1.4003
Ercc5	1.7733	1.6662	0.6482	1.7669
Ermap	0.9247	1.2678	1.0967	0.9565
Esyt2	1.6206	1.1262	1.1701	0.748
Etfa	1.78	1.8192	1.9462	1.8304
Exph5	1.1152	1.6257	0.8291	1.1349
Ext2	0.8166	2.1304	1.0967	1.9109
F2rl2	0.6724	1.7534	1.4733	1.4562
F8	1.2472	0.8565	1.3126	1.0084
F830016B08Rik	0.8166	0.8565	1.0084	1.2026
Fabp1	1.145	1.1584	1.2611	1.0967
Faim3	1.2904	2.1654	1.0967	1.1349
Fam117a	1.0486	1.0534	0.9565	0.8291
Fam120a	1.4991	0.8565	1.1701	1.2328
Fam120c	1.0111	0.966	1.0967	1.4562
Fam122a	1.6915	1.0119	0.8974	0.8974
Fam126b	1.4728	0.9147	0.748	1.2876
Fam154b	1.2238	1.3348	1.4897	1.5056
Fam159b	0.6724	1.2429	0.748	1.4383
Fam26e	1.0486	1.1584	0.8974	1.2611
Fam53b	1.1152	0.9147	1.0548	1.0548
Fam53c	1.1991	1.4441	1.1701	1.5357
Fam71b	2.465	2.2512	3.0142	2.3435
Fancd2	1.2693	1.3348	1.1701	1.0084
Farp2	1.4591	1.5811	1.3126	1.4733
Fat3	1.7932	1.1584	1.4562	1.0084
Fbln5	1.0111	1.7454	1.5357	0.3323
Fbxl17	1.5116	1.0534	1.4197	1.2026
Fbxl21	1.0832	1.2165	0.8974	1.5357
Fbxo34	0.97	1.0534	0.9565	1.0967
Fbxo41	1.0832	1.1262	1.2876	0.6482
Fbxo42	1.1991	1.3551	1.0548	1.3126
Fem1c	1.7932	1.6464	1.5903	1.7754
Fgf15	1.0111	0.9147	0.8974	1.3587
Fgf18	0.874	1.4599	0.748	1.4383
Fgfr1op2	1.1152	0.8565	1.0548	1.3587
Fh1	0.97	1.0913	0.9565	1.7583
Fhod1	0.97	1.0119	0.8291	1.0084
Fignl1	1.1991	1.6257	0.748	0.9565
Flad1	1.8861	1.1885	1.4897	1.4197
Flg	1.2904	2.2461	1.0548	1.6388
Fmnl3	1.0832	1.9999	0.8291	1.9841
Fmo3	0.4551	0.8565	1.55	1.5903
Fndc3a	1.4302	1.615	0.8291	1.0548
Fnip2	1.2238	1.0913	0.5184	1.0967
Folr1	1.3106	1.0119	0.8974	1.6029
Foxc2	1.3829	0.7892	0.748	1.1701
Foxf2	1.5802	2.2919	1.0084	0.5184
Foxl1	1.7154	1.7373	1.2026	2.313
Fpr-rs4	0.7505	1.5443	0.8974	1.2328
Frem1	0.874	1.685	0.8974	1.3126
Fry	1.2238	1.1584	1.4197	1.1349
Fstl5	1.3298	1.2165	0.748	1.38
Fubp3	1.5238	1.4599	1.7026	1.3587
Fus	0.9247	1.1262	1.0548	1.5639
Fut10	1.8059	0.8565	1.3126	0.9565
G3bp1	1.8755	1.0913	1.4733	1.0967

G6pc	0.5772	1.1584	1.0967	1.6272
Gab3	1.9798	0.9147	1.3126	0.8974
Gabra1	1.5907	0.9147	1.5357	0.5184
Gabra4	1.2904	1.0534	1.1349	1.3587
Gas7	1.6485	1.9107	0.8974	0.6482
Gbe1	1.9164	1.2678	1.4562	1.7918
Gda	1.1152	0.7892	0.748	1.0967
Gemin6	0.8166	0.7892	1.1349	1.2328
Ggps1	1.0486	1.2429	0.5184	1.5209
Gins3	0.874	2.0887	1.38	1.2876
Glra2	1.4449	1.3929	1.6719	1.2611
Gm13177	1.6301	1.0534	0.9565	1.7026
Gm14047	1.4861	0.612	0.6482	1.6824
Gm281	1.1152	1.0913	1.2876	1.4197
Gm4423	1.5695	0.7892	0.748	1.5903
Gm4755	1.3659	1.1584	0.5184	1.2611
Gm4758	0.8166	1.3136	1.0548	0.8974
Gm4759	1.0832	0.966	1.2026	1.7754
Gm4890	1.7076	0.612	1.3587	0.8291
Gm4894	0.7505	1.3551	0.5184	1.6719
Gm5084	1.3298	0.8565	0.8974	1.6611
Gm5089	1.5802	1.4277	1.7124	1.4003
Gm5493	1.6575	1.3551	1.3363	1.2328
Gm550	1.9401	1.9769	2.0728	1.722
Gm5615	0.2846	1.5927	1.2328	1.3126
Gm595	0.6724	1.9162	0.748	1.7669
Gm9	1.0486	1.0119	1.0084	1.1349
Gm94	0.2846	0.486	1.7314	2.267
Gm9927	0.97	1.1262	1.3126	1.1701
Gmpr	1.2904	1.1584	1.4003	1.3587
Gna12	0.5772	0.7096	1.38	1.8154
Gnat3	3.1307	3.2437	3.4193	3.2795
Gngt1	0.6724	1.1885	1.7026	1.0967
Gpbp1	1.3659	0.9147	1.2611	1.6501
Gpm6b	1.2472	0.9147	0.8974	0.8291
Gpr126	1.0486	1.0913	1.5639	1.5056
Gpr143	1.2472	0.7096	1.2328	1.6388
Gpr151	1.1991	0.7892	1.5639	1.0084
Gpr31c	1.6009	1.685	1.9462	1.1701
Gpr55	0.8166	0.8565	1.1701	1.3126
Gpr6	0.8166	0.966	1.6272	1.4562
Gpr88	1.0111	0.7892	1.2328	1.2876
Gprasp2	1.5116	1.1584	0.6482	1.3587
Gprc6a	1.1729	0.8565	1.2611	1.5056
Gprin3	1.2472	0.8565	1.3363	1.0967
Grik4	0.874	1.0119	0.8974	1.1701
Grina	1.6009	1.2913	0.8291	1.5639
Grk5	1.5238	1.0119	1.0084	1.55
Grlf1	1.0486	1.2429	1.0967	1.3126
Grm1	1.0111	1.0534	0.748	0.8974
Grrp1	1.1152	0.8565	1.2876	1.6824
Gse1	1.3829	1.5443	1.7669	1.7754
Gtf2h5	0.9247	1.3744	0.9565	1.2611
Gtpbp5	1.8861	1.5569	2.077	1.6272
Gulo	1.145	1.0534	0.748	1.0084
Gzme	1.4591	1.1584	1.38	1.7837
H2afy	1.145	0.966	1.0548	1.38
H2-M2	1.0832	0.8565	1.2026	1.1701
Hao1	1.0486	1.8519	0.9565	1.2026
Haus3	1.3482	0.9147	1.0548	0.8291
Hcn1	0.97	0.966	1.4003	1.38
Heca	0.9247	1.7032	0.8291	1.4562
Hecw2	0.8166	1.0119	0.9565	1.7998
Hilpda	1.6662	1.3929	1.6926	1.4197
Hivep3	1.5802	1.0119	1.0548	1.1701
Hk1	1.3106	0.8565	1.4383	1.7998
Hmga2	1.6915	1.0119	1.2026	1.6388
Hmox2	1.4991	1.4599	0.6482	0.748
Hnrnpa2b1	0.874	0.7892	1.1701	1.3126
Hnrnpab	1.4991	1.4441	1.8154	1.3126
Hnrnpd	1.145	1.1262	1.1701	1.3363
Hormad1	1.1991	1.2165	1.38	1.4197
Hoxb1	1.2472	1.6564	1.4897	1.4897
Hoxc13	1.8122	1.0119	1.0548	0.9565
Hoxc6	0.7505	1.6564	2.8443	0.748
Hps5	0.6724	1.9425	1.0548	1.6272
Hscb	1.1152	1.0534	1.4897	1.0967
Hsd17b12	1.9115	1.5042	1.1349	1.3126
Hsp90aa1	0.7505	1.2165	1.0084	1.4003
Hspa4l	0.9247	0.8565	1.1701	1.6388
Hspb7	1.3659	0.966	1.4003	0.8974
Hydin	1.2472	1.3348	1.0548	1.0967
Iapp	1.4991	1.0534	1.5056	1.0548
Idi2	1.3659	1.1262	1.923	1.2328
Ier3	1.6009	0.612	0.748	1.5357
Ifna11	1.415	0.486	1.0084	1.2328
Igh	1.0486	1.2913	1.3363	1.55

Ikzf5	1.5907	1.2913	1.3587	0.9565
Il18r1	0.874	0.9147	0.8974	1.1349
Il20ra	1.5357	0.486	1.3126	1.4003
Il21r	1.2693	1.2165	1.3363	1.1349
Il6	1.1152	0.8565	0.6482	1.1349
Il6st	1.5238	1.604	1.4197	1.6272
Immp2l	0.9247	0.7892	1.1349	1.0967
Ing1	1.0832	1.0119	0.8974	0.8974
Ing5	0.6724	0.9147	1.3126	1.7124
Inha	1.4591	2.0813	0.3323	1.5209
Insig2	1.0832	1.0534	1.4383	0.8291
Ints6	1.0111	0.8565	0.9565	1.2026
Ipmk	0.7505	1.0534	1.3587	1.0548
Iqcb1	0.7505	0.9147	1.3363	1.4383
Iqch	1.0111	1.0534	1.0967	0.9565
Iqgap3	0.874	1.3929	1.2026	1.0084
Irak4	0.874	1.2165	0.8291	1.5773
Isg20l2	1.7733	1.6757	1.8985	1.6824
Itga2	1.145	1.2429	1.6719	1.5773
Itpkb	0.9247	2.1685	0.8291	1.8304
Itpripl1	0.9247	1.8996	1.4562	1.3126
Jag2	1.1991	1.729	1.0084	0.6482
Jakmip1	1.145	1.2429	1.2328	0.8974
Kcnh3	1.4449	1.4599	1.9574	1.2611
Kcnj16	1.0832	1.7205	0.5184	1.4003
Kcnj6	1.0111	1.0534	0.8974	0.9565
Kcnk5	1.2904	1.2165	1.4197	1.0967
Kcnmb4	1.6748	1.7534	1.4003	1.8377
Kctd15	0.874	0.966	1.0084	0.9565
Kctd4	1.4861	1.3744	1.2328	0.9565
Kdm5c	0.7505	1.0913	0.748	1.6824
Kin	1.3829	1.5569	1.5056	1.0084
Klhdc10	1.145	1.0534	1.3126	1.4897
Klhl25	1.5802	1.0119	0.6482	1.7405
Kng1	0.874	1.0913	1.4003	1.2328
Krba1	1.5585	1.1262	1.2026	1.3363
Krt25	1.9065	1.1262	1.0084	0.8291
Krt35	1.0111	0.8565	1.4383	1.0084
Lair1	1.0486	0.7096	0.9565	1.2328
Larp1	1.3992	1.1584	1.8077	1.4562
Lass5	1.0111	0.966	1.0548	1.2328
Lax1	1.1729	1.3348	1.0967	0.6482
Lce3f	0.874	1.8939	1.2611	1.3587
Lclat1	1.4861	1.9673	0.8974	1.4003
Lcmt2	0.6724	1.0534	1.4197	1.2876
Ldha	1.4591	1.1262	0.8291	1.1349
Lepr	1.3829	0.9147	0.8974	1.0967
Lgals7	1.5695	0.3077	1.1349	2.6646
Lgr6	1.3298	1.2165	1.2328	1.0084
Lhx5	1.2693	2.0995	0.6482	1.2876
Lin9	0.9247	1.2165	0.8291	1.4562
Lingo4	1.0486	0.966	1.4383	1.0084
Lipk	0.6724	1.5569	1.0548	1.0967
Lmnb1	1.0486	0.8565	0.8291	1.5357
Lmod3	1.0832	1.1584	0.5184	1.4897
LOC727924	1.1152	1.6464	0.9565	1.4197
Lpl	1.4991	1.3929	1.4197	1.3587
Lrfn5	1.1729	1.5042	1.5773	1.2611
Lrguk	0.874	0.9147	1.1701	1.0548
Lrrc2	1.3106	0.9147	0.8974	0.9565
Lrrc30	1.0486	0.9147	1.2026	1.2328
Lrrc39	1.0832	0.9147	0.748	1.2328
Lrrc40	1.5238	1.4277	1.722	1.0967
Lrrc52	1.2238	0.486	1.2876	1.3363
Lrrc61	1.1729	1.3929	0.9565	2.1131
Lrrc8d	1.0111	1.0913	0.6482	1.1701
Lrriq3	1.5695	0.966	0.8974	1.0967
Lrrk2	1.6108	1.7032	2.275	1.8922
Lsm11	1.0486	0.7096	1.2026	1.3587
Lsm4	1.7733	0.9147	0.8974	1.2876
Ly6g5b	1.145	1.0534	1.7124	1.2026
Lypd4	0.8166	0.8565	1.2876	1.4897
Lyrm2	1.9626	1.9052	2.0189	1.9048
Lyrm5	0.5772	1.5811	1.5357	0.6482
Lysmd4	1.0111	1.0534	1.3363	1.2026
Macf1	0.97	1.1885	1.5639	1.3126
Mafk	0.874	0.8565	1.4003	1.2876
Maml2	1.5473	1.0119	1.5903	0.748
Man2a1	0.874	1.7119	0.8291	1.852
Map2k3	1.7595	0.9147	1.6824	0.6482
Mapk1ip1l	1.145	1.1885	1.5639	1.0548
Mapk8ip3	1.415	1.4106	1.6719	1.3587
10-Mar	2.14	1.9526	0.6482	2.174
Mark1	1.6832	0.9147	0.748	1.3126
Mau2	0.874	0.7096	1.3587	1.8077
Mc2r	0.4551	2.0623	1.0084	1.9048
Mcpt1	1.2904	1.3744	1.6926	1.4562

Mdga2	1.3659	0.8565	1.2328	1.0084
Mdp1	1.4591	1.1262	0.3323	1.6719
Mecp2	1.2238	1.2678	1.2876	1.2611
Med12l	1.8913	1.3136	1.2328	1.5903
Med18	0.8166	1.2678	0.9565	0.9565
Mei4	0.7505	2.1499	1.55	0.8291
Metap1	0.97	0.966	1.4733	1.0967
Mfsd6	1.1152	1.0534	1.0084	1.4562
Mfsd7b	1.7525	0.7892	1.0084	1.8857
Mgat4a	0.8166	1.0534	0.8291	1.2328
Mipep	1.0832	1.2678	1.1349	1.1701
Mitf	1.3106	1.0913	0.5184	1.3126
Mki67	1.2472	1.2678	0.5184	1.5056
Mll3	1.7866	0.612	0.8291	1.6388
Mlxip	1.4728	1.0913	0.748	1.6029
Mmgt1	0.874	0.7096	1.0548	1.4383
Mmp1a	1.145	1.1262	1.1701	0.9565
Mob2	1.1991	1.0913	1.0084	1.1349
Morn4	0.6724	1.4277	1.3126	1.0967
Mpzl1	1.6108	1.8054	0.5184	1.4003
Mpzl3	1.0832	1.4599	1.3587	1.2026
Mrfap1	1.0486	1.0913	1.5357	1.6824
Mrgpra1	1.7231	1.1584	1.2876	0.3323
Mrpl30	1.2472	1.3348	1.3587	1.3587
Mrps15	1.2238	2.2827	0.748	1.5357
Mrps22	0.9247	1.0913	0.748	1.5056
Mrps33	0.9247	1.0119	0.9565	1.1701
Msrb2	1.3829	1.3348	1.6501	1.0084
Mustn1	0.8166	1.1584	0.6482	1.6029
Mvk	1.0111	0.9147	0.748	1.6611
Mybpc2	1.3992	1.4441	1.1349	1.4197
Mycbp2	0.9247	0.7892	1.1349	1.5903
Myf6	2.2196	1.9052	2.077	1.5357
Myh10	1.2904	1.9216	0.8291	1.0967
Myt1	1.78	1.7612	1.8792	1.7026
Mzt1	0.6724	1.3551	0.8974	1.8922
N4bp1	0.5772	1.1262	1.0084	1.722
Nap1l2	0.874	0.8565	1.2026	1.1701
Nav3	1.2238	1.6257	1.2026	1.3126
Nbea	1.5473	1.0913	1.3363	1.722
Nccrp1	1.9582	1.604	1.38	1.7837
Nckap5	2.1429	1.8192	1.722	1.8589
Ncrna00085	1.9015	0.7892	0.6482	1.7026
Ndufb4	1.8059	0.9147	0.6482	1.3126
Necab1	1.0111	1.1885	0.8974	1.0967
Nek3	1.0111	1.0534	1.38	1.0084
Nemf	1.8122	2.1203	1.2026	0.9565
Neurod1	2.6179	2.2708	2.7654	2.2185
Nfasc	1.2238	1.1584	1.3126	0.9565
Nfe2l1	1.6394	1.5443	1.722	1.6501
Nfia	0.8166	0.8565	0.9565	1.38
Nhedc1	1.3992	0.7096	0.8291	1.3587
Nhp2l1	0.97	0.8565	0.9565	1.1701
Nipbl	1.2238	1.2165	0.9565	1.2328
Nipsnap1	1.5357	1.4441	1.4003	1.5209
Nipsnap3a	1.0832	1.0913	1.2611	0.8974
Nipsnap3a	0.97	0.8565	1.2026	1.0548
Nlrp10	1.1152	1.2165	1.2328	1.2026
NM_001004179	0.2846	1.1885	1.1349	1.4733
NM_008283	1.415	1.3136	1.7583	1.2328
NM_025307	2.046	1.4277	1.0548	1.1701
NM_025726	1.2472	1.0119	1.722	1.3363
NM_025743	1.1991	1.2678	0.6482	1.0548
NM_026226	1.8059	0.7096	0.8974	1.4197
NM_027265	1.145	1.3744	1.3126	0.5184
NM_028564	1.4591	0.486	0.748	1.7124
NM_028588	1.1729	1.2913	1.0084	1.5639
NM_029697	1.1729	1.2165	1.6926	1.4733
NM_030007	1.0486	0.8565	1.7124	0.9565
NM_138946	1.145	0.9147	0.748	1.0084
NM_175354	0.7505	1.0913	1.6029	1.1701
NM_175390	1.3482	1.2913	1.7405	1.5209
NM_176934	1.5116	0.9147	0.8974	0.8974
NM_176955	1.0486	0.966	1.2876	1.0967
NM_177011	1.4991	0.612	1.4197	1.1349
NM_177020	0.8166	1.0913	0.9565	1.0967
NM_177079	1.3106	0.966	1.6611	1.3587
NM_177179	1.1152	1.2165	1.0967	1.1701
NM_177207	1.2472	1.1584	0.6482	2.3273
NM_177858	2.116	0.966	1.6388	1.0084
NM_177896	0.8166	0.8565	0.9565	1.1349
NM_178239	1.9537	1.9052	2.348	1.9574
NM_183110	1.2693	2.2359	1.2876	1.5209
NM_183223	1.0111	1.0534	0.748	0.8291
NM_198008	0.7505	0.966	1.0967	1.4003
NM_199318	1.2472	1.0534	0.8291	1.0548
Nol3	0.6724	0.7096	1.5056	1.6152

Nom1	1.2904	0.7892	0.9565	0.8974
Nphp3	1.3298	1.0534	1.2328	1.1701
Nr0b2	0.874	0.3077	1.4733	2.3435
Nr1i3	1.0832	1.0119	1.55	1.7754
Nr2c1	1.0111	1.1584	1.1349	0.6482
Nr2f1	0.6724	1.3744	1.1349	0.9565
Nr2f2	1.1729	2.0174	1.0084	1.4197
Nrcam	1.4449	1.3348	1.38	1.9289
Nrk	1.2472	0.8565	0.9565	0.8974
Nrsn1	0.97	0.8565	1.0967	1.3587
Nsa2	1.1152	1.0534	0.8291	1.38
Ntf5	1.415	0.7096	0.8974	1.8229
Ntn4	0.4551	1.7689	1.6388	1.2876
Nudt11	0.7505	1.1262	0.748	1.5773
Nudt4	1.0111	0.612	1.1349	1.2328
Nxt1	1.2904	1.4106		1.5639
Obfc1	0.9247	0.7892	0.8974	1.1701
Oit3	0.7505	0.8565	1.3363	1.2026
Olfm3	1.5357	1.7689	2.4582	1.9574
Olfml2a	1.2472	1.1584	1.0084	1.1349
Olfr108	0.874	1.0534	1.0967	0.8974
Olfr1085	0.9247	0.8565	1.4003	1.0548
Olfr1099	0.7505	1.3136	1.3363	1.1349
Olfr1102	1.3829	1.2913	1.1701	0.8974
Olfr1111	1.145	0.9147	1.3126	1.0548
Olfr1112	0.874	1.3744	1.3363	0.8291
Olfr1135	1.5116	1.0119	0.9565	1.6388
Olfr1138	0.6724	1.5313	1.3126	0.8291
Olfr1161	1.6832	0.7096	0.3323	1.7405
Olfr1277	1.5802	1.3744	1.4733	1.1701
Olfr1320		0.9147	1.9406	1.9736
Olfr1325	1.4591	2.2145	1.1349	1.7837
Olfr135	0.97	0.9147	1.8449	1.0084
Olfr1367	1.1991	0.7892	1.0084	0.8974
Olfr1420	1.5585	2.0813	2.0511	1.7754
Olfr1502	0.5772	0.8565	1.3126	1.3587
Olfr154	0.7505	0.9147	0.8974	1.3587
Olfr165	2.02	1.9526	2.0284	1.7583
Olfr183	0.874	2.2487	0.8974	1.4562
Olfr190	0.8166	1.0913	1.1349	0.9565
Olfr196	1.6662	1.3348	1.6152	1.1701
Olfr3	0.874	1.0913	1.0548	1.4197
Olfr301	1.0111	1.1262	1.3363	1.0967
Olfr350	0.874	1.2165	1.3587	0.9565
Olfr419	0.4551	1.6757	1.4003	1.1701
Olfr513	1.4861	1.1262	1.2328	0.5184
Olfr555	0.9247	1.0119	0.748	1.4003
Olfr577	0.9247	0.8565	0.8291	1.0084
Olfr655	1.3659	1.6257	1.2876	1.0084
Olfr716	1.2472	1.1262	1.2328	0.8974
Olfr724	0.7505	1.5692	0.748	1.4383
Olfr821	1.5116	1.4752	1.4562	1.722
Olfr877	0.8166	1.3551	0.8974	1.0967
Olfr934	1.2693	1.0534	1.2611	1.5639
Olr1156	0.874	1.1262	1.3587	1.6719
Olr142	1.8535	2.278	1.1349	1.6029
Olr145	0.5772	1.0534	1.0084	1.6152
Olr1568	2.8642	2.22	1.9841	1.8658
Olr1730	0.9247	0.9147	1.1701	1.3587
Olr237	0.6724	1.0534	1.38	1.9109
Olr357	1.3829	0.7892	0.748	1.6719
Olr461	1.738	1.0119	0.8974	1.4897
Olr559	1.3298	1.1885	1.0548	0.8974
Olr606	1.1729	2.0776	0.6482	1.3126
Olr799	0.9247	1.1262	1.2876	0.748
Olr87	1.2693	1.0913	0.6482	1.1701
Oog1	1.5238	0.7892	1.4733	1.0084
Oog3	1.6108	1.3551	1.7124	1.2611
Oog4	1.0832	1.2165	0.8291	1.55
Opa3	0.97	0.966	0.8974	1.1349
Opcml	0.874	0.9147	1.2611	1.2876
Osbpl5	0.7505	1.2678	0.8974	1.2328
P2rx3	1.6662	0.7096	1.0548	1.2876
P2rx5	1.145	1.1885	1.2328	1.2611
Pacs1	0.5772	2.0259	1.2026	1.5209
Paip2	2.4409	2.2873	2.7764	2.1806
Pak2	0.7505	1.5313	0.748	1.7124
Pak3	1.0486	1.1584	0.748	1.0548
Palm3	1.1729	1.0534	1.4003	1.3363
Pan2	1.0486	0.966	0.748	0.8974
Pan3	1.2904	0.8565	1.2328	1.0548
Parp11	1.0486	1.1262	1.1349	0.8291
Pbrm1	1.6206	1.0119	0.6482	1.1701
Pcdhb13	0.4551	1.2678	1.4003	1.8304
Pcdhb15	1.2238	1.9216	0.8974	1.2611
Pck1	1.3992	1.0534	0.8291	0.8974
Pcsk2	1.3659	0.7892	0.8291	1.5903

Pde4d	1.5238	1.3929	0.6482	0.8291
Pdss2	0.874	1.8939	1.7026	1.3363
Pdxk	1.3298	1.3744	1.7495	1.5056
Pex1	1.8808	0.7096	1.2026	1.0967
Pfdn4	0.7505	0.7892	1.5903	2.3081
Phb	1.1152	1.0119	1.0967	1.2328
Phc2	1.5116	1.2678	1.3126	1.4733
Phex	0.97	1.8823	0.748	1.5209
Phf11	1.0486	1.0119	1.0084	1.38
Phf17	1.2238	1.1885	0.748	1.2611
Phf6	0.9247	1.1262	1.0548	1.2026
Phgdh	1.2472	1.5569	0.8974	1.4003
Pias3	1.7525	2.0343	0.8291	0.748
Pibf1	0.97	1.1262	0.8291	1.0967
Pigp	1.2904	1.4441	1.8725	1.4383
Pigw	0.874	0.966	0.8974	1.5209
Pik3r1	0.9247	0.8565	1.5209	1.1701
Pik3r6	0.4551	1.2429	1.4383	1.4003
Pilrb1	1.1152	1.1584	1.0084	1.0084
Pin1	1.1729	1.1262	1.3126	1.4383
Pja2	1.7996	1.729	0.8974	1.3126
Pkib	1.8363	2.0465	2.1392	1.6719
Pla2g2d	1.3992	1.1584	0.8291	0.8291
Plaur	1.4302	0.7892	0.8974	1.4562
Plk4	0.6724	1.0534	1.0967	1.4562
Plxna4	0.97	0.9147	0.748	1.6029
Pole	1.3482	1.1885	1.8229	1.5357
Polr2c	0.97	0.7892	1.1349	1.0548
Polr2m	1.0832	1.1584	1.4003	1.1349
Pou4f2	0.6724	1.1584	1.2611	1.3126
Pou6f1	2.7639	2.3711	2.4634	2.0284
Ppcdc	0.874	0.8565	1.0548	1.3363
Ppfia1	1.0111	1.8326	0.5184	1.6926
Ppm1b	0.8166	1.2678	1.2876	1.2876
Ppp1r10	1.5357	1.3551	1.4003	1.0967
Ppp1r13b	1.1729	0.966	0.748	1.0084
Ppp1r14a	1.0486	1.0534	1.2026	1.0084
Ppp1r16b	1.4728	1.5927	1.5639	2.6763
Prf1	1.6996	1.8764	1.3126	1.5639
Prkab2	1.6575	2.2436	0.748	1.4197
Prkacb	1.9354	2.0087	2.6591	2.2031
Prlr	1.1152	1.1584	1.0084	1.0967
Prmt5	2.0003	1.8192	2.0189	1.5056
Prmt6	1.0111	0.8565	0.8291	1.4003
Prmt8	1.0111	1.0119	1.0548	1.0084
Prpf19	0.7505	1.1262	0.8974	1.2876
Prpf38a	0.6724	1.2429	1.2328	1.3363
Prr18	0.874	1.7764	1.0967	1.4562
Prr3	0.874	0.9147	1.0084	1.4733
Prss34	0.7505	0.966	0.8974	1.6501
Prss54	2.1222	1.2165	1.3126	1.0967
Psd3	2.3189	1.1584	1.0084	1.3587
Psg23	0.7505	0.612	1.2611	1.6501
Psme3	0.8166	1.0119	1.0967	1.0084
Pstpip1	0.8166	1.1262	0.8974	0.9565
Ptger2	1.4449	1.4106	1.7124	1.1349
Ptgir	1.145	1.1584	1.5209	0.8974
Ptplb	1.2472	1.0534	1.6719	1.0548
Ptpn1	1.7231	0.7096	0.748	1.722
Ptpn13	1.4302	0.966	0.8974	0.9565
Ptpn14	0.9247	1.0119	0.748	1.3587
Ptprd	1.3298	2.0923	1.2876	1.8377
Ptpre	1.0111	0.7892	0.9565	1.2328
Ptprg	1.8363	0.8565	1.0967	0.9565
Ptprj	1.5238	1.3136	1.1349	0.9565
Ptprn2	1.6206	1.0913	1.5357	1.2876
Pxdn	0.97	0.8565	1.0548	1.4897
Qk	0.9247	0.7892	1.6501	1.1349
Qpctl	1.5585	1.4277	1.7495	1.5639
Rab12	1.8122	0.7892	1.3126	0.8291
Rab2b	0.97	0.9147	1.5903	0.9565
Rab39b	1.9401	1.8455	1.0548	0.8291
Rab3il1	1.2472	1.4106	0.8974	0.6482
Rab9b	1.5802	1.4441	2.3081	1.9683
Rad54l2	1.0111	0.966	1.0084	0.8974
Rage	0.6724	0.8565	1.1349	1.2611
Ranbp1	1.0832	1.8823	1.0084	1.3587
Ranbp6	1.0111	0.966	0.8974	1.0084
Rapgef6	0.9247	0.612	1.4003	1.5056
Rarb	2.1543	1.7454	1.9943	1.9736
Rars2	1.5238	2.2827	0.8974	1.38
Rasgrf1	0.97	1.1584	0.5184	1.4197
Rbm26	2.2123	0.9147	1.3126	1.55
Rbm27	1.0832	1.4106	1.0084	1.2328
Rbm39	1.5802	0.486	0.8291	1.4383
Rbm43	1.0111	0.966	0.748	1.0548
Rbp4	1.6394	2.1169	1.9574	1.923

Rcn1	1.4302	0.8565	1.4003	0.8291
Rcsd1	1.1729	1.9216	0.8974	1.2328
Rfpl4	0.97	0.966	0.8974	1.0967
Rfx7	0.6724	1.9862	1.4383	1.5209
Rgs4	1.6394	1.0913	0.6482	1.3363
Rgs7bp	1.8646	1.615	0.3323	1.4003
Rhbdd1	0.7505	1.5313	0.8291	1.2876
Rhbdd2	0.7505	2.0465	0.6482	2.0853
Rif1	1.415	1.0534	0.8974	1.1349
Rin3	1.0486	1.1262	1.1701	0.9565
Ripk2	1.5116	0.7892	1.2328	1.5773
Rmnd5b	1.4728	0.9147	1.0548	0.8974
Rnase6	1.2693	0.9147	0.9565	0.8974
Rnf111	1.7154	0.7892	1.4897	1.9841
Rnf113a1	0.4551	0.9147	1.2328	1.6272
Rnf182	0.6724	1.6662	1.5357	0.8974
Rnf2	1.6206	1.0119	1.0967	1.3363
Rnf24	1.145	1.0119	1.0084	0.8974
Rnft2	1.9669	1.4277	1.4197	2.1638
Robo2	1.0111	0.7892	0.8291	1.55
Rora	1.4302	1.4106	2.0422	1.6824
Rpgr	0.4551	1.3744	0.9565	1.4897
Rpl15	0.5772	0.612	1.5639	1.6388
Rpl36a	1.0832	1.4599	1.5056	1.38
Rpl3l	1.3106	1.3136	0.5184	1.3587
Rpl9	1.0486	1.3551	1.1701	1.1701
Rprd2	0.97	0.9147	0.8291	1.5903
Rps27	1.3659	1.8054	1.0084	1.6719
Rps6ka5	1.3992	0.612	0.8291	1.4897
Rrp15	0.8166	1.9052	0.8291	1.38
Rsph9	1.8244	0.8565	0.9565	1.8154
Sag	0.97	1.0119	0.6482	1.1349
Sall4	0.9247	0.7892	1.0548	1.7918
Samd9l	1.1152	0.7892	1.3126	1.0548
Sar1b	1.5238	1.5811	0.6482	1.0967
Satl1	1.8964	1.1262	1.0084	1.4897
Scai	1.3298	1.1584	1.3587	1.38
Scg5	1.2693	1.1262	1.4562	1.0548
Scgb1a1	2.317	2.0545	0.9565	1.9629
Schip1	1.0111	1.6257	0.3323	1.7495
Scml4	1.0111	1.0534	1.0967	0.748
Sdf2	1.3482	1.3348	0.9565	1.5773
Sdpr	1.738	1.0534	1.0967	1.2328
Sdr42e1	0.7505	0.7892	1.2876	1.7583
Sec16a	0.874	0.7892	0.8974	1.5773
Sec24d	2.1709	1.8881	2.5828	2.2588
Sec31b	1.6485	1.5811	2.1773	1.722
Secisbp2	1.0486	1.2165	1.5209	1.2876
Sele	0.9247	0.9147	0.748	1.5357
Sell	0.874	1.0119	1.0548	0.8974
Sema4d	1.4302	0.8565	1.1349	1.0548
Serbp1	1.4728	1.1885	1.0084	1.2328
Serinc3	0.874	1.0119	1.2328	1.5209
Serpinb1a	0.9247	0.9147	1.2026	1.3126
Serpinb2	2.1998	1.1262	0.8974	1.2026
Serpinb6a	0.9247	0.7096	1.0084	1.6388
Sestd1	1.1152	1.8124	1.4383	1.2026
Sgcz	1.3298	1.1584	1.5357	1.1701
Sh3pxd2b	2.5218	2.3436	1.9574	2.2185
She	0.9247	0.7096	1.0967	1.3587
Shprh	1.2238	0.8565	2.1092	1.4197
Shroom3	1.1991	1.4441	1.2328	1.5056
Siglece	1.145	1.2429	0.9565	0.8291
Sik3	1.6009	1.2165	1.2328	1.1349
Sipa1l2	1.3659	1.2165	1.8857	1.5056
Skil	1.1729	1.2165	1.4197	1.2026
Slc13a3	1.3659	1.2165	1.4733	1.4003
Slc13a4	1.8183	1.7689	1.722	1.2611
Slc13a5	1.1152	1.1262	0.8974	1.2611
Slc16a10	1.2238	1.1885	1.4383	1.2876
Slc16a13	1.5357	0.9147	0.6482	1.7495
Slc16a6	1.5695	1.3136	1.9289	1.1349
Slc17a2	1.2472	1.3551	1.6719	1.1701
Slc17a8	0.5772	1.0534	1.0084	1.4197
Slc1a5	0.874	0.8565	1.2328	1.1349
Slc24a5	1.5357	1.2678	1.3587	1.5639
Slc25a19	1.1152	0.7096	1.2611	1.6152
Slc25a22	1.2904	1.0534	1.4003	1.3126
Slc25a27	1.4728	1.0534	1.1349	1.2026
Slc30a1	0.8166	0.7892	1.0084	1.7754
Slc30a8	1.0111	1.0913	1.0548	1.0084
Slc35d3	0.874	0.966	1.7754	1.7124
Slc35e3	1.0486	1.6942	0.6482	1.4897
Slc35f5	1.2238	1.1584	1.4383	1.5209
Slc39a3	0.2846	1.7764	1.8154	2.0284
Slc39a8	1.0486	0.8565	1.0548	0.8974
Slc39a9	0.874	1.4899	1.1701	1.3126

Slc44a3	0.5772	1.4106	1.1349	1.4383
Slc4a3	1.0832	1.0119	0.748	1.38
Slc4a4	1.3106	0.8565	1.5903	0.6482
Slc4a7	0.874	1.0119	0.9565	1.4562
Slc6a15	1.5238	1.5811	1.6029	1.6272
Slc7a6os	1.4861	1.4752	1.2876	1.3126
Slc7a7	1.1729	1.0534	1.2611	1.2026
Slitrk5	0.9247	0.612	1.1349	1.4733
Slk	2.1191	1.7912	0.8291	1.4383
Smarcc2	1.0111	0.966	1.0084	1.0967
Smc1b	0.97	1.2678	1.5639	1.0967
Smg6	1.2238	1.2429	1.0967	1.4003
Snrpd2	2.9675	2.8675	3.0587	2.5586
Sntn	0.9247	0.9147	0.9565	1.5357
Snx29	1.5585	0.9147	1.2026	1.2328
Soat1	1.415	1.2913	1.7314	1.2876
Sod1	1.6009	1.604	1.7918	1.1349
Sort1	1.1991	0.8565	0.8974	1.3363
Sowaha	1.2904	1.4106	1.8449	1.2026
Sox6	1.1991	0.7892	0.8974	1.0084
Sp2	2.1921	1.3744	0.748	2.0685
Spata1	1.0111	1.0913	0.5184	1.8449
Spata21	1.8421	1.3929	0.5184	1.6501
Spatc1	1.1729	1.0913	1.5357	1.4383
Spc24	1.1152	1.0913	0.748	1.3363
Speer3	0.7505	1.2678	1.3587	0.9565
Spinkl	1.7525	1.5042	1.3587	1.7754
Spna2	1.3482	0.7892	1.2611	1.0548
Spock1	2.1682	2.266	2.6226	1.9736
Spred3	1.926	1.3929	1.9289	1.8304
Srgap2	0.9247	1.0913	0.8291	1.1701
Srp19	1.7154	1.5313	1.0967	1.9892
Srpk2	0.7505	0.966	1.2876	1.0967
Srsf2	1.2693	1.0119	1.4003	0.8974
Ssr1	1.0486	1.0913	0.748	1.5639
St3gal1	1.0832	1.0119	0.6482	1.7124
St6galnac3	1.5116	1.0119	1.1701	0.8291
St7	1.5907	1.3744	0.6482	0.748
Steap3	0.8166	0.612	1.3126	1.5773
Stim2	0.874	1.1262	1.4383	0.9565
Stoml3	1.0111	1.6362	0.8291	1.2876
Stx17	0.9247	0.612	1.2328	1.2876
Sub1	1.0111	1.5042	1.0548	0.9565
Sun2	1.2472	0.7096	0.6482	1.7669
Sycn	1.145	1.2678	0.6482	1.7405
Syne2	1.0832	0.8565	1.0548	1.2328
Syt12	1.2238	0.966	1.4733	1.1349
Tab2	1.1729	1.1262	1.4197	1.0967
Tada2a	1.7665	1.615	1.8229	1.2611
Taf1b	1.1152	1.2678	1.9348	1.5357
Taf1d	0.9247	1.0119	0.748	0.9565
Taf8	1.2693	1.1262	0.8974	1.1701
Tanc2	1.0832	1.2913	1.4733	1.1349
Tas2r139	1.2693	0.7096	0.6482	1.5773
Tbc1d30	0.9247	0.9147	1.5209	1.0548
Tcea3	1.4302	1.2913	1.6926	1.38
Tceb2	0.6724	1.1584	0.8291	1.38
Tchhl1	0.97	0.966	0.9565	1.4383
Tctex1d2	1.3829	0.8565	0.8974	1.1701
Tead2	1.1991	1.1584	0.8291	1.6611
Tekt4	1.4991	1.5927	1.852	1.38
Tex11	1.3106	1.3744	1.1701	1.5773
Tex21	1.6996	0.8565	1.5056	0.9565
Tex9	1.145	1.2165	0.9565	1.3363
Thada	1.2472	1.1584	1.8304	1.8377
Thnsl2	1.4302	1.4752	1.5056	1.8589
Thsd1	1.0832	0.7892	0.748	1.6029
Tigd2	1.2472	1.0119	1.3363	1.1349
Timd2	0.5772	1.0119	1.1349	1.4003
Tiparp	0.97	1.2429	0.8974	1.2876
Tiprl	0.97	1.0119	0.6482	1.4003
Tjap1	1.1152	1.1885	0.5184	1.1349
Tle1	1.7866	1.5811	2.4386	1.7314
Tlr13	1.3298	1.1262	1.7405	1.4003
Tmc3	0.97	1.0534	1.3363	1.55
Tmc4	0.6724	1.0913	0.8974	1.9629
Tmco5	0.97	0.966	1.2328	1.0548
Tmem11	1.7932	1.0119	1.5209	0.5184
Tmem127	0.874	1.3136	1.3363	1.6824
Tmem129	0.6724	1.1885	0.748	1.2876
Tmem139	0.97	0.9147	1.4562	1.4197
Tmem144	0.9247	1.7764	1.2611	0.8291
Tmem14a	1.3829	1.5811	1.6388	2.435
Tmem150b	1.0111	1.0913	1.4733	1.1701
Tmem150c	1.1152	1.0119	0.9565	0.8974
Tmem167	0.874	0.966	1.0084	1.55
Tmem229a	2.2268	2.0776	2.5301	2.1534

Tmem29	1.0111	1.0119	1.2328	1.2026
Tmem44	0.6724	1.0119	1.1349	1.5209
Tmem55a	1.1729	1.8124	1.8377	1.38
Tmem56	2.1627	2.0301	2.0893	1.5903
Tmem89	1.0486	1.1584	1.1349	1.3587
Tmem93	0.4551	1.7119	1.4383	1.0084
Tmod3	0.8166	1.9162	1.3587	1.5773
Tmprss12	0.9247	1.8192	0.5184	1.6272
Tmtc1	0.97	1.1262	1.3126	1.0084
Tmx2	2.5476	2.517	2.4512	1.9048
Tnfaip8l1	0.874	1.8455	1.3587	1.1701
Tnik	1.0111	0.7096	0.8974	1.3363
Tnni1	1.4728	0.9147	0.8291	1.3126
Tnp2	1.1991	0.7892	0.9565	1.2611
Tns1	0.9247	1.1262	0.8291	1.3363
Tom1l2	1.0832	1.0534	1.0084	1.0084
Top2a	0.97	0.8565	0.9565	1.4197
Topors	1.1729	0.9147	1.4562	1.0967
Tpd52	1.6748	0.8565	1.0084	0.9565
Trhr	1.415	1.4599	1.6719	1.3587
Tril	2.0043	1.6257	1.8154	1.4383
Trim15	1.0832	1.2165	1.2026	1.1349
Trim31	1.0486	1.0119	1.5209	0.748
Trim9	1.8421	0.9147	1.2328	1.38
Trpv6	1.0111	0.8565	0.8291	1.1349
Tsku	1.9307	1.9816	2.1053	1.9109
Tslp	0.874	1.8455	1.1701	0.8974
Tspan32	1.7453	1.0534	0.8974	1.2611
Tssk1	1.5695	0.612	0.6482	1.55
Ttbk2	1.0486	0.7892	0.8291	1.5357
Ttc7b	1.3659	1.1262	1.0084	1.1349
Ttll1	1.0832	1.2429	1.1349	1.0548
Ttll5	1.1729	1.3136	1.4003	1.1349
Ttn	0.874	1.0913	1.4733	1.38
Txndc3	1.0486	1.3348	0.5184	1.8377
Txnl4a	0.7505	1.4441	1.2328	1.1349
Uap1l1	1.415	1.6662	2.3906	1.722
Uba3	1.145	0.966	1.3126	1.6824
Uba5	1.5238	1.2913	1.6926	1.3126
Ube2c	1.0111	0.7892	1.0548	1.5357
Ube2cbp	1.9065	1.615	1.0548	1.4562
Ublcp1	1.5802	1.2678	1.0967	1.4733
Ubr2	2.0568	1.1262	1.2611	1.0548
Uckl1	0.5772	1.1885	1.2611	1.2026
Umodl1	0.97	0.966	1.0084	0.9565
Unc5a	0.874	1.3551	0.5184	1.6152
Uqcrfs1	1.3106	1.2165	1.6152	1.2611
Urb1	1.3482	0.3077	1.2026	1.7026
Uros	1.5357	1.0119	0.8291	1.1349
Usp20	1.1152	1.0534	1.2026	1.0548
Usp47	0.7505	1.1262	0.9565	0.8974
Utp20	1.145	0.966	0.8974	0.748
Utrn	2.6885	2.5264	2.9337	2.3297
V1re3	0.9247	1.6564	1.0548	0.8974
Vamp5	1.4861	0.7892	1.1349	1.0084
Vdr	1.0832	0.9147	0.9565	1.1349
Vmn1r148	1.5802	0.8565	1.1349	1.1701
Vmn1r222	1.2472	0.486	1.3126	1.7669
Vmn1r235	1.3829	0.7096	0.6482	1.3126
Vmn1r58	1.5473	1.4277	1.5056	1.4003
Vmn1r73	0.4551	1.5927	1.2026	1.3587
Vmn2r66	1.415	1.5042	1.6152	1.7918
Vmn2r81	2.1627	0.7892	1.0548	1.0548
Vmn2r89	1.7932	0.9147	0.748	1.4003
Vpreb3	1.1991	1.1885	1.7314	1.2611
Vps13a	1.3659	0.8565	0.9565	1.0084
Vps13b	1.2693	1.518	1.1349	1.1701
Vps29	1.3106	1.2429	1.0967	1.6029
Vps4b	2.5206	2.6731	3.1482	2.4313
Vwa5b2	1.0486	1.1584	1.0967	1.0548
Wbp5	0.8166	1.0119	1.2328	1.0084
Wdr17	1.8421	1.8326	2.3906	1.7918
Wdr67	1.0486	2.2333	1.0084	1.0548
Wdr7	1.2238	1.5569	0.748	1.0084
Wdr75	2.3932	2.312	2.7231	2.1773
Whamm	0.7505	1.0534	0.8291	1.0084
Wnt16	0.97	1.0913	1.4562	1.3587
Wnt3	0.5772	0.486	1.9519	2.0974
Wtap	1.3659	1.6564	1.0548	1.7405
Xbp1	1.2904	1.4752	0.748	1.6501
XM_110945	0.8166	0.9147	1.0548	1.3126
XM_111036	1.3829	1.5443	2.0467	1.7669
XM_111056	1.1152	1.0913	1.1701	0.8291
XM_111144	1.7665	1.2678	1.8449	1.3587
XM_111148	1.3482	0.486	1.1701	1.1701
XM_111149	1.3992	1.2429	1.5903	1.1701
XM_111220	1.6996	1.8326	0.748	1.6501

XM_111296	1.3298	0.7892	0.748	1.1349
XM_111450	1.6301	1.8326	0.8291	1.1349
XM_111466	1.1991	0.7892	1.4562	0.8291
XM_111755	0.4551	2.209	1.4897	1.5357
XM_111840	2.6387	2.3934	1.7998	2.6093
XM_112122	1.5357	1.0534	0.748	1.4383
XM_112187	1.0832	1.1584	1.5639	1.0084
XM_112199	0.9247	0.8565	0.8974	1.6272
XM_112296	1.1991	1.3929	0.5184	1.4897
XM_112334	1.2472	1.0534	0.9565	0.6482
XM_112346	1.6394	1.3136	1.6926	1.4897
XM_112375	0.97	1.2913	1.1349	1.0548
XM_112379	1.3482	1.0913	1.0967	0.5184
XM_112423	0.97	0.7892	0.8291	1.2026
XM_112478	1.145	1.0534	0.6482	1.8792
XM_112628	1.8591	1.0119	1.2328	1.1701
XM_112716	1.145	1.1885	0.6482	1.3587
XM_112792	1.1152	1.1584	1.7583	1.6029
XM_126147	0.4551	0.612	1.5639	1.7837
XM_126924	0.97	1.604	0.8291	1.3126
XM_127451	1.7525	1.6757	2.4752	1.7918
XM_129150	1.1152	0.7892	1.2876	0.9565
XM_129740	0.8166	0.7096	1.3126	1.7124
XM_129957	2.0707	0.9147	1.1349	1.7405
XM_131520	1.2693	0.9147	0.6482	1.4897
XM_132758	1.0111	1.0913	0.748	1.5773
XM_132869	0.5772	1.0534	1.2611	1.2328
XM_133116	1.0486	0.612	0.8974	1.5209
XM_133516	1.1729	1.518	0.8974	1.0548
XM_134273	1.2904	1.2913	1.0548	1.0548
XM_135472	1.2693	1.0913	1.5209	1.0548
XM_136298	1.3659	1.2913	0.9565	1.9736
XM_136367	0.7505	2.1685	1.3363	1.7495
XM_136507	2.1371	1.5313	1.5056	1.3126
XM_136558	1.8421	0.7892	0.8974	1.2026
XM_136599	1.2472	1.9721	1.2876	1.0548
XM_136728	1.9492	1.2165	0.748	2.4105
XM_136797	1.6575	0.9147	1.0548	1.5639
XM_136839	1.5357	1.2913	0.8291	0.9565
XM_136848	0.5772	1.518	1.3587	1.2026
XM_136883	0.7505	0.966	0.9565	1.2876
XM_136884	1.0832	1.1262	0.6482	0.8974
XM_136902	1.2472	1.0119	1.2611	1.0548
XM_136930	1.0111	0.966	1.4733	1.2026
XM_136936	0.8166	1.0913	0.8291	0.9565
XM_136961	1.8059	0.7096	1.3587	1.4383
XM_136962	1.2238	1.0119	1.6029	1.3126
XM_136963	1.0832	1.0534	1.2026	1.1349
XM_137008	1.3106	0.9147	0.6482	1.5639
XM_137089	0.874	1.0119	1.0084	1.6272
XM_137095	0.97	0.8565	1.2611	1.0967
XM_137303	0.874	0.7892	0.9565	1.6611
XM_137336	1.7595	1.3744	1.4897	1.4897
XM_137424	1.5238	2.1561	0.8974	0.8974
XM_137575	1.3992	1.1262	1.1349	1.2328
XM_137576	1.7306	1.3348	1.6152	1.1701
XM_137597	1.2693	0.7892	0.6482	1.2328
XM_137860	2.3396	2.3207	2.2588	1.923
XM_137891	1.1152	1.0119	0.5184	1.0967
XM_138065	0.9247	1.0119	0.9565	1.2026
XM_138094	0.874	1.0534	0.9565	1.0967
XM_138105	1.8646	0.8565	1.38	1.1701
XM_138114	0.97	1.2165	0.8291	1.5209
XM_138163	0.8166	0.8565	1.9683	2.0934
XM_138179	0.97	0.8565	0.9565	1.1701
XM_138187	1.0111	0.8565	1.2876	1.5056
XM_138194	1.8421	1.1584	0.9565	1.2328
XM_138345	0.7505	1.0913	1.2026	1.7405
XM_138441	1.4991	1.0534	0.5184	1.4897
XM_138582	0.97	1.3136	0.5184	1.4733
XM_138614	1.2904	0.8565	1.3363	1.0084
XM_138615	1.3659	1.2429	1.7837	1.3126
XM_138638	1.145	0.8565	1.0084	1.1701
XM_138748	0.97	0.966	1.2328	1.3587
XM_138770	1.4449	1.0119	0.6482	1.5903
XM_138775	1.0111	1.7839	1.6824	1.2876
XM_138785	1.1152	0.7096	1.4197	1.1349
XM_138823	1.3659	0.966	0.5184	1.8792
XM_138885	0.97	0.8565	1.2328	1.5357
XM_138909	1.5238	0.966	0.8974	0.9565
XM_138910	1.145	0.9147	1.0084	0.8291
XM_138915	1.3659	1.0534	0.748	1.1701
XM_138950	1.6662	0.612	1.2026	0.9565
XM_139138	0.8166	0.966	1.1701	1.6611
XM_139235	0.8166	1.0119	0.9565	1.7314
XM_139265	1.2238	1.0119	0.6482	1.0548
XM_139330	0.7505	0.9147	1.0548	1.6501

XM_139357	0.97	0.7892	0.8291	1.2876
XM_139386	0.7505	0.8565	1.2876	1.2026
XM_139390	0.7505	1.0534	1.2026	1.1701
XM_139405	1.6575	1.6257	1.2876	1.7583
XM_139419	0.97	0.8565	1.4383	1.5056
XM_139487	1.0486	1.1262	1.55	1.3587
XM_139635	0.2846	1.6564	1.2328	1.2876
XM_139732	0.7505	1.1584	1.2328	1.0548
XM_139770	1.6301	0.966	0.6482	1.7998
XM_139792	1.0111	0.966	1.3363	1.5357
XM_139825	0.9247	1.3929	1.55	1.1701
XM_139878	0.8166	1.0913	1.0548	0.8974
XM_139952	1.2238	1.2429	0.5184	1.5056
XM_139988	1.8861	0.7096	1.3587	1.0084
XM_140059	1.6485	0.612	0.8291	1.4562
XM_140060	0.9247	1.3551	1.0967	0.8974
XM_140071	1.1152	1.0913	1.4897	1.2611
XM_140079	2.1843	1.8581	2.1839	1.7314
XM_140083	1.0832	0.9147	1.0548	1.38
XM_140137	1.1991	1.1584	0.5184	1.0548
XM_140175	2.0841	1.7983	2.2931	1.6388
XM_140228	1.2904	1.2429	1.5056	1.2328
XM_140315	1.0486	1.5443	1.1349	1.1349
XM_140330	1.4991	0.7096	1.1349	1.8725
XM_140422	0.7505	0.8565	1.1701	1.3126
XM_140523	2.046	1.9374	1.9683	1.4897
XM_140530	1.4728	1.0534	1.3363	0.5184
XM_140531	2.6958	2.602	3.063	2.4852
XM_140606	0.874	1.0119	0.748	1.1349
XM_140687	1.2472	1.6257	1.1701	1.5903
XM_140698	1.1729	1.8054	0.9565	1.4003
XM_140790	1.7231	1.2913	1.7314	1.2328
XM_140826	1.3106	1.5042	0.8291	1.2876
XM_141006	1.7306	1.0119	1.2611	0.5184
XM_141013	1.738	1.3744	1.8304	1.7405
XM_141156	1.5585	1.6464	1.7124	1.4562
XM_141313	1.3298	1.3136	1.2026	1.1349
XM_141706	0.874	0.8565	1.3126	1.2328
XM_141815	1.0832	1.0119	1.2611	0.748
XM_141982	1.0486	0.966	0.748	0.9565
XM_142009	1.2904	1.2165	1.5639	1.3363
XM_142021	1.145	1.1262	1.0084	1.2026
XM_142024	1.5695	1.7032	1.9289	1.55
XM_142071	0.97	1.0534	1.2026	0.8974
XM_142085	2.2196	2.1467	2.4668	2.0642
XM_142086	1.8363	1.9526	1.8922	1.6272
XM_142114	0.9247	0.966	0.748	1.1701
XM_142190	2.0874	1.7205	2.2	1.7026
XM_142235	1.2693	0.612	0.9565	1.1701
XM_142285	1.0111	1.4277	0.8974	1.3587
XM_142304	2.0043	1.8939	0.3323	1.1349
XM_142373	0.7505	1.518	1.5209	1.8922
XM_142403	1.3659	1.3348	1.2026	0.8974
XM_142446	1.1729	1.2165	1.1349	1.0967
XM_142454	1.2904	0.612	0.8291	1.6824
XM_142570	0.6724	0.7892	1.1349	1.8077
XM_142587	0.7505	1.1584	1.6388	0.8974
XM_142846	1.5585	1.3929	1.7669	1.38
XM_142855	1.1729	0.8565	0.6482	1.3587
XM_142931	1.2693	1.1885	1.1701	1.2026
XM_143027	1.0111	1.1885	1.2026	1.0548
XM_143109	1.2472	1.2678	1.2611	1.0084
XM_143117	1.0832	1.1885	1.1349	0.9565
XM_143132	1.4449	1.0534	0.6482	1.4897
XM_143147	0.874	1.1262	0.9565	1.0967
XM_143169	1.1729	0.7892	0.748	1.3363
XM_143273	1.3298	1.7119	1.0548	1.6611
XM_143274	0.8166	1.0119	0.748	1.2876
XM_143335	2.4636	3.0716	1.722	2.313
XM_143353	1.2238	1.0119	1.0548	1.1701
XM_143354	1.1729	1.0913	0.9565	1.1349
XM_143379	1.2238	1.615	0.3323	1.3363
XM_143384	0.97	1.4441	1.0548	1.4197
XM_143485	0.5772	0.9147	1.0967	1.3587
XM_143516	0.9247	0.8565	1.2876	1.0967
XM_143644	0.4551	1.4441	0.8974	1.7124
XM_143708	2.0083	1.9999	2.2642	2.0422
XM_143716	1.5802	0.7096	1.0548	1.4383
XM_143850	1.738	1.1885	1.8077	1.3363
XM_143860	1.3298	1.1885	1.1349	1.0548
XM_143975	0.6724	1.518	1.7754	1.6029
XM_144011	0.97	0.966	1.0548	1.2611
XM_144108	0.874	1.0119	0.748	1.1349
XM_144231	1.1729	1.0119	1.4562	1.0548
XM_144394	1.6009	1.1262	0.748	1.2026
XM_144444	0.97	1.1584	1.1701	1.6272
XM_144470	1.1991	1.2913	1.6272	1.2876

XM_144489	0.9247	0.8565	0.8291	1.1349
XM_144539	1.145	1.2678	1.0967	1.1349
XM_144659	1.0111	0.7096	0.9565	1.4003
XM_144701	0.9247	0.8565	0.8291	1.2026
XM_144774	0.97	0.9147	1.2026	1.1701
XM_145066	0.8166	1.0119	1.5056	1.3587
XM_145184	1.3482	1.3136	1.3126	0.8974
XM_145185	1.0111	1.1584	0.6482	1.5903
XM_145256	1.0486	1.6257	1.2328	0.6482
XM_145282	1.0111	1.1885	0.8291	0.9565
XM_145307	1.2472	1.5443	0.8974	0.8974
XM_145430	1.5585	1.5569	2.0141	1.5209
XM_145553	1.1729	1.2165	1.2026	1.7998
XM_145608	1.4991	1.0913	1.0548	0.6482
XM_145635	0.7505	0.8565	1.0084	1.55
XM_145668	0.9247	0.966	1.2026	1.5773
XM_145676	1.145	1.1885	1.0967	1.2611
XM_145691	1.145	0.9147	0.9565	0.8291
XM_145805	0.7505	1.4599	0.5184	1.5903
XM_145886	0.874	1.9576	1.4383	1.0548
XM_145917	0.874	1.0119	1.0084	0.8974
XM_146114	1.0111	1.0119	1.4003	1.0967
XM_146126	1.1152	1.0119	1.3587	1.3363
XM_146477	1.4728	1.0913	1.2026	1.6388
XM_146491	1.0111	1.9862	1.5056	1.3587
XM_146519	1.4449	0.9147	1.2026	0.8974
XM_146561	1.2472	1.2165	1.5639	1.1701
XM_146640	1.3992	1.3348	1.0548	1.55
XM_146661	1.415	1.0913	1.3587	0.8974
XM_146743	1.738	1.3551	1.5056	0.9565
XM_146765	1.6575	0.486	1.4733	1.4733
XM_146929	1.7306	1.2429	1.38	1.6824
XM_146987	1.6108	1.6942	1.2611	0.748
XM_147082	1.1991	1.1584	1.0967	0.5184
XM_147444	0.97	0.966	1.1701	1.5056
XM_147594	1.8304	1.518	1.8922	1.5773
XM_147866	1.1729	1.1885	1.2328	0.748
XM_147945	1.0111	0.966	1.0084	0.8974
XM_148441	1.0111	1.3929	1.3126	1.7405
XM_148582	0.7505	1.2165	0.748	1.2328
XM_148994	1.1991	1.1584	1.4562	1.6501
XM_149327	1.0111	0.7892	1.1349	1.1349
XM_149413	0.7505	1.0534	1.1349	1.1701
XM_149430	1.2238	1.2913	0.5184	1.0548
XM_149849	1.8964	1.0119	1.0548	1.38
XM_150596	1.2472	1.8259	1.0548	1.2026
XM_150759	1.3482	1.9374	0.6482	0.9565
XM_150908	1.7076	1.1262	0.748	1.1701
XM_151001	1.0832	1.2678	1.4897	0.8291
XM_151013	1.5473	1.2913	2.0092	1.5639
XM_151252	0.8166	1.2165	1.0548	1.2876
XM_151296	0.8166	1.1262	0.8291	1.7669
XM_151379	1.6394	0.8565	1.2611	0.6482
XM_151435	1.9881	0.8565	0.8291	1.2876
XM_151483	1.4991	1.4899	1.2876	1.6152
XM_151529	0.97	0.8565	0.8974	1.3126
XM_151591	0.8166	1.518	1.0548	0.9565
XM_151612	1.1152	1.1885	1.0967	1.3126
XM_151641	0.8166	1.4277	1.3126	1.4383
XM_151718	0.9247	0.7892	0.9565	1.0967
XM_151736	1.2904	1.5443	1.0084	1.8725
XM_151750	1.5357	0.9147	1.1701	0.8291
XM_151813	1.5116	0.9147	0.748	1.2876
XM_151837	1.3106	0.8565	0.9565	1.1701
XM_152066	0.8166	1.5811	1.2328	1.7918
XM_152111	1.7231	2.3164	1.7405	1.8229
XM_152202	1.1152	1.4599	0.748	1.6824
XM_152313	1.2238	1.3929	0.6482	1.8725
XM_152438	1.0111	0.7892	1.3587	1.6029
XM_152483	1.2472	1.0119	1.38	1.5056
XM_152931	1.0486	0.612	1.0967	1.38
XM_152972	0.874	0.966	0.748	1.6388
XM_152979	1.145	1.0119	1.0548	0.8974
XM_153060	0.6724	1.0534	0.8974	1.55
XM_153086	1.8304	1.0119	0.748	1.2328
XM_153261	1.3992	1.3348	1.8857	1.4383
XM_153290	1.2472	1.3136	1.1701	0.8291
XM_153523	1.1729	1.2678	1.2876	1.9519
XM_153553	1.7231	1.1885	1.0548	1.923
XM_153624	0.8166	1.0534	1.1349	1.6152
XM_153706	2.0707	0.8565	0.8291	1.3587
XM_153880	1.4302	1.0119	1.917	1.6501
XM_154031	1.4302	0.7892	1.2026	0.748
XM_154068	1.3992	0.7096	0.8291	1.4383
XM_154198	1.7306	1.1584	1.0084	1.2611
XM_154308	1.7525	1.4441	1.0084	0.748
XM_154346	1.1152	1.0534	1.1701	1.1349

XM_154382	1.3298	0.7892	1.0084	0.9565
XM_154395	1.1729	0.966	1.2026	1.2026
XM_154471	1.3482	1.0119	0.8974	0.8291
XM_154560	1.6748	1.0534	0.6482	1.2328
XM_154612	0.97	1.3929	1.0548	0.8291
XM_154614	1.0486	1.1885	1.5639	1.4562
XM_154625	2.1972	0.8565	1.3126	1.2876
XM_154760	1.0832	0.9147	0.748	1.0548
XM_154791	1.1729	1.1584	1.55	1.0967
XM_154905	1.145	0.966	1.4003	1.6152
XM_154981	2.0638	1.5443	1.1701	1.0084
XM_155091	1.2904	1.6564	0.8291	1.3126
XM_155119	1.5357	1.4277	1.4003	1.0084
XM_155150	1.0111	1.0119	0.748	1.3126
XM_155219	1.6485	1.518	2.1773	1.4897
XM_155365	1.2472	1.9625	1.0967	1.2876
XM_155410	1.1991	0.966	1.2876	1.0084
XM_155415	1.2693	1.3348	1.7026	1.9406
XM_155416	0.9247	1.1885	0.748	1.7837
XM_155473	1.0832	0.9147	0.8974	1.3363
XM_155669	1.6996	1.7983	0.8974	0.6482
XM_155748	1.1152	0.9147	0.9565	1.2328
XM_155800	0.97	0.8565	0.8291	1.5209
XM_155805	0.874	1.0534	0.9565	0.8974
XM_155852	1.3298	1.3929	1.4562	1.852
XM_155874	1.0486	1.0119	1.3363	1.0967
XM_156151	1.1991	1.6662	1.5209	1.5056
XM_156163	1.5695	0.8565	0.9565	1.2876
XM_156207	0.9247	0.7892	0.9565	1.2328
XM_156229	0.9247	0.9147	0.8291	1.2026
XM_156387	1.3482	1.1584	0.8974	1.6388
XM_156407	1.4591	0.7096	1.2611	1.0967
XM_156459	1.7076	1.8519	2.3343	2.0974
XM_156469	1.0832	0.9147	0.8291	1.4003
XM_156499	1.0486	1.2429	1.7583	1.4562
XM_156541	1.0111	0.8565	1.2328	1.0548
XM_156577	1.6009	1.4752	1.7583	1.7405
XM_156588	0.9247	0.9147	0.9565	1.0084
XM_156662	1.1152	1.4106	1.1701	1.2876
XM_156683	0.6724	0.7096	1.2876	1.6152
XM_156755	1.3106	1.3551	1.5639	1.38
XM_156764	1.5473	1.1262	1.0967	0.9565
XM_156863	0.7505	1.2429	1.38	1.0084
XM_157041	1.1152	1.4441	0.8291	1.6501
XM_157245	1.0111	1.2678	1.1349	1.0967
XM_157275	1.8701	0.966	0.8291	1.1349
XM_157299	1.2693	1.0913	1.4733	1.2026
XM_157374	1.1729	1.1262	1.5357	1.5209
XM_157391	1.145	1.2429	0.5184	1.0967
XM_157481	0.874	0.7892	1.3587	1.3126
XM_157619	0.97	1.3744	0.8291	0.9565
XM_157639	1.3298	1.1885	1.0967	1.7583
XM_157813	1.0486	1.2678	1.38	1.0548
XM_158270	1.2238	1.2165	1.2876	1.8922
XM_158274	1.8701	1.6662	2.2829	1.917
XM_158492	0.97	1.1885	1.2026	0.748
XM_158570	1.3659	0.966	0.8974	1.2876
XM_158619	0.97	0.612	1.3363	1.55
XM_158620	1.3829	1.0534	1.0967	1.0548
XM_158738	1.0832	1.0119	0.8291	1.5639
XM_158798	1.3298	1.0913	1.4897	1.2026
XM_158839	1.6832	1.7689	2.033	1.55
XM_158953	0.8166	1.3744	1.2611	1.0084
XM_158958	2.4013	1.7032	2.2062	2.2
XM_158978	0.8166	1.3136	1.4003	0.8291
XM_158981	3.1247	3.0982	3.6981	3.1549
XM_158983	1.3106	1.1885	1.5639	1.2876
XM_159156	1.0486	0.9147	1.2876	1.1701
XM_159183	1.8421	0.7892	1.2876	1.6272
XM_159605	0.9247	1.1584	1.2026	1.0084
XM_159758	0.8166	1.3744	2.3106	0.9565
XM_159792	1.0832	1.2429	1.4897	1.4383
XM_159833	1.8304	1.5927	0.3323	1.0084
XM_159867	1.6108	2.0384	0.748	0.8974
XM_159932	1.6394	0.966	1.6388	1.0967
XM_159952	1.5907	0.486	0.5184	1.7837
XM_159966	1.6108	1.3744	1.2876	0.8291
XM_160042	1.0832	1.0119	1.0967	1.2328
XM_160046	0.8166	0.966	1.2026	1.0548
XM_160200	0.6724	0.8565	1.4003	2.0237
XM_160472	0.97	0.7892	0.8291	1.1701
XM_160475	1.7932	1.9052	2.0376	1.7026
XM_160495	1.5116	1.3551	1.6926	1.2876
XM_160586	2.4732	2.373	2.8055	2.1773
XM_160652	1.0486	0.9147	0.6482	1.2611
XM_160654	1.1991	1.4441	1.0084	1.2876
XM_160679	1.7996	0.7892	0.9565	1.1701

XM_160928	1.145	1.0119	1.0548	0.8974
XM_161086	1.5116	0.8565	1.4897	0.8291
XM_161119	0.97	0.7892	1.6029	1.4733
XM_161242	1.0832	0.966	0.9565	0.8291
XM_161321	0.8166	0.7892	1.2328	1.5209
XM_161495	0.6724	1.0534	1.5357	1.3363
XM_161596	1.145	1.3551	0.5184	1.3363
XM_161613	1.3106	1.4752	0.6482	1.8077
XM_161705	1.0486	1.3348	0.748	1.3126
XM_161711	0.9247	1.2165	0.5184	1.6719
XM_161876	1.3106	1.2165	0.8974	1.4733
XM_161886	0.5772	1.9374	1.38	1.55
XM_161922	0.874	1.2678	1.0967	1.2328
XM_161977	1.0111	0.9147	1.0967	1.1349
XM_161990	1.6485	0.7892	0.8974	1.0967
XM_162021	1.0832	0.966	1.0548	1.1349
XM_162034	1.7665	1.7912	0.5184	1.3363
XM_162120	0.8166	0.8565	1.0548	1.2876
XM_162123	1.2693	1.2165	0.8974	1.0084
XM_162180	0.6724	0.486	1.3587	1.7669
XM_162214	1.0111	1.3744	1.4197	1.7583
XM_162216	0.874	1.0119	0.8974	0.8974
XM_162234	0.7505	1.1584	1.2328	1.4197
XM_162261	1.1991	1.1584	1.5639	1.2611
XM_162339	1.0486	0.966	0.6482	1.4897
XM_162376	1.3298	1.3744	0.6482	0.8974
XM_162490	1.0486	1.1262	0.8974	1.5209
XM_162595	1.5116	1.6662	1.8725	1.6029
XM_162814	0.4551	1.3136	0.8291	1.4383
XM_162859	1.145	1.3551	1.8449	1.722
XM_163113	1.3106	1.0119	0.9565	0.8974
XM_163118	1.0486	1.0119	1.38	1.2026
XM_163245	1.145	1.2429	0.748	0.8974
XM_163250	1.0111	1.0913	0.8974	1.0548
XM_163263	1.0832	0.7096	1.2876	1.0548
XM_163311	1.0832	0.9147	0.8291	0.9565
XM_163331	1.145	1.0913	1.1349	1.2026
XM_163520	1.3992	1.1584	1.8304	1.3363
XM_163566	1.6108	1.4277	1.5357	1.2611
XM_163727	1.3482	1.0913	0.8974	1.1349
XM_163859	1.0486	0.9147	0.8974	1.1349
XM_163970	1.2472	0.8565	1.3363	0.748
XM_164132	1.145	2.1435	1.2876	0.748
XM_164144	1.0111	1.1262	1.2026	1.0084
XM_164306	1.8535	1.3744	1.5903	1.4383
XM_164390	1.6996	1.0119	0.8291	1.2876
XM_164400	0.97	0.966	0.748	1.0548
XM_164545	0.8166	0.9147	1.0084	1.0967
XM_164557	1.1729	1.3348	1.38	0.8974
XM_164723	1.7595	1.1262	1.0548	0.8974
XM_164753	1.7231	1.7205	2.2185	1.8304
XM_164789	1.1729	0.966	0.6482	1.6501
XM_164839	1.3482	1.7534	1.2026	1.0548
XM_164993	0.7505	1.0119	0.8291	1.0967
XM_165019	0.874	0.9147	1.2328	1.0967
XM_165026	0.9247	0.486	1.4197	1.5209
XM_165055	0.8166	1.3551	0.9565	1.3363
XM_165073	0.874	1.3744	0.6482	1.2611
XM_165076	0.6724	0.9147	1.2876	1.6388
XM_165150	1.0486	1.1262	1.1701	0.6482
XM_165157	1.8421	1.8881	1.4897	0.748
XM_165188	1.1152	0.486	1.0084	1.2026
XM_165198	0.97	1.1262	1.4897	1.6719
XM_165282	0.8166	1.1885	1.2876	1.1701
XM_165297	1.1729	1.2429	1.0548	1.2328
XM_165355	0.97	1.1584	1.0084	1.1349
XM_165369	0.5772	0.966	1.0548	1.4897
XM_165384	1.2238	1.4899	1.55	1.3587
XM_193814	0.9247	0.7892	1.3126	1.4383
XM_194673	1.3298	1.2429	1.1701	0.9565
XM_194680	1.0832	1.0534	0.748	1.2026
XM_194777	1.4728	1.5443	1.6824	1.4003
XM_194831	1.1729	0.9147	0.8974	0.9565
XM_194834	1.6485	0.9147	0.8974	1.0548
XM_194879	1.415	1.2429	1.0967	0.9565
XM_194897	1.8059	1.8391	1.3587	2.1053
XM_194912	1.1152	0.7096	0.8974	1.6152
XM_194968	0.7505	0.8565	0.9565	1.852
XM_194996	1.0832	1.3929	1.8304	1.38
XM_195006	0.97	0.7892	1.0084	1.0967
XM_195197	1.2904	0.7892	1.2876	0.8291
XM_195224	0.97	0.966	0.8974	1.6152
XM_195256	0.97	1.2165	0.6482	1.0967
XM_195269	0.874	1.2165	1.2328	1.0967
XM_195390	0.874	1.2165	0.6482	1.55
XM_195437	1.0486	1.1885	1.3126	1.0967
XM_195466	0.8166	0.966	0.8291	1.0548

XM_195544	0.97	1.1262	0.8291	1.7918
XM_195678	1.3829	0.612	1.0548	1.8792
XM_195745	1.1729	1.7612	1.4197	1.6029
XM_195748	1.6009	1.8326	1.923	1.55
XM_195831	1.7665	0.966	1.0084	0.8291
XM_196106	1.1729	0.486	1.5209	1.4003
XM_196136	1.0111	0.8565	0.748	1.2328
XM_196240	0.8166	0.486	1.4003	1.8449
XM_196478	0.9247	0.9147	1.0084	1.8377
XM_196607	1.4728	1.3348	0.8974	1.5209
XM_196722	2.1371	2.228	2.792	2.3569
XM_196755	0.6724	1.3929	0.8291	1.4003
XM_196808	1.0486	0.612	0.8974	1.8857
XM_196824	1.1729	1.6464	1.0084	1.4197
XM_196964	0.9247	0.9147	1.2026	1.0967
XM_196981	0.6724	1.0913	0.9565	1.3587
XM_197031	0.9247	1.0534	0.8291	0.8291
XM_197105	0.874	0.8565	0.9565	1.2611
XM_197137	0.8166	1.1584	1.38	1.3126
XM_197266	1.3829	0.3077	1.1349	1.7495
XM_197344	1.3992	0.7892	1.1701	1.3363
XM_197408	0.9247	0.8565	0.8291	1.1349
XM_197431	1.8421	2.0087	0.6482	0.8974
XM_197447	0.874	1.1885	1.3363	1.1701
XM_197724	0.7505	0.966	1.0548	1.2876
XM_197888	1.2238	1.1262	1.3126	1.7124
XM_197895	1.7453	1.0534	0.8291	1.8377
XM_197991	0.874	1.1262	1.1701	1.0967
XM_198071	1.5695	1.8326	1.6388	1.917
XM_198115	1.5802	1.0534	0.8974	0.8291
XM_198196	1.2693	1.0534	0.6482	0.9565
XM_203991	1.0832	1.0913	1.3587	1.4197
XM_204506	1.3298	1.0534	0.9565	0.9565
XM_204714	1.0111	1.5443	1.0084	1.1349
XM_204889	1.145	0.8565	0.8291	1.7583
XM_205290	1.0486	0.966	1.1701	0.8291
XM_205678	1.145	1.1885	0.3323	1.3126
XM_205682	0.8166	1.4277	1.38	1.4003
XM_206401	1.0486	1.0119	0.9565	1.3363
XM_206463	1.0832	0.612	1.0967	1.1701
XM_206504	1.2693	2.397	1.38	1.8377
XM_206658	0.7505	0.9147	0.9565	1.4897
XM_206785	1.415	1.518	1.3363	1.55
XM_206878	1.145	1.0913	1.4733	1.2328
XM_216180	1.415	1.5692	1.8229	1.5639
XM_216345	2.1486	2.5183	2.6202	2.2957
XM_216716	1.6662	1.4441	1.7495	1.1701
XM_216784	1.0832	1.1885	0.6482	1.4383
XM_219399	1.2238	1.1262	1.0548	1.2026
XM_228611	1.2472	1.4106	1.6272	1.1701
XM_230936	0.9247	1.0913	0.6482	1.9519
XM_231152	1.3106	1.2165	1.5357	1.0967
XM_231361	1.4591	1.8581	1.0084	0.8974
XM_232080	0.97	1.1885	0.9565	1.2328
XM_232287	1.0832	0.8565	1.7669	1.0084
XM_236246	2.3523	2.7448	2.6492	3.1646
XM_236351	1.0111	0.966	0.8974	1.1349
XM_236961	0.8166	1.0534	0.748	1.1701
XM_282925	1.0832	1.2429	1.2876	1.3363
XM_282973	1.4728	1.0534	1.5903	1.8077
XM_283001	1.2238	0.7096	1.6272	1.3363
XM_283014	1.0832	1.4752	0.8291	1.0084
XM_283130	1.0486	1.4277	1.8857	1.2876
XM_283332	1.0486	1.4441	1.2026	0.748
XM_283401	1.6485	1.3744	0.8291	0.6482
XM_283523	1.145	1.2165	0.5184	1.4562
XM_283932	1.8646	0.7096	0.748	1.4383
XM_283989	1.2472	0.9147	1.0548	0.748
XM_284122	1.9537	1.0534	0.8291	1.0084
XM_284222	1.1152	1.0119	1.1349	1.0084
XM_284248	1.6662	1.0534	1.6029	0.6482
XM_284262	0.6724	1.685	1.0548	1.2328
XM_284387	1.2693	1.2913	1.7124	1.2328
XM_284405	1.8421	0.7892	1.4383	0.748
XM_284556	0.97	1.4106	0.748	1.1349
XM_284569	1.2693	0.612	0.8291	1.6824
XM_284590	0.9247	0.7892	1.1349	1.4897
XM_284643	1.8363	1.5692	1.5357	0.9565
XM_284775	0.2846	1.7764	1.4562	1.3126
XM_284796	0.7505	1.3136	0.6482	1.7837
XM_284797	0.7505	1.0119	0.8974	1.1349
XM_284838	0.97	0.966	1.2611	1.6388
XM_284840	1.5802	0.8565	0.9565	1.4562
XM_284870	1.1991	1.7764	1.55	1.4562
XM_284875	0.6724	2.3312	1.1349	1.7837
XM_284888	1.0486	0.7096	1.55	1.0548
XM_284893	1.6394	1.0534	0.748	0.9565

XM_284943	1.1152	0.7892	1.5639	1.0084
XM_285066	2.0532	2.11	2.6469	2.3297
XM_285086	1.7453	1.7032	0.3323	0.8974
XM_285089	1.8755	1.8326	2.0555	1.5639
XM_285114	0.6724	1.3348	1.4733	1.1701
XM_285127	0.5772	0.7096	1.7998	2.1773
XM_285153	0.8166	1.0913	1.0967	1.6272
XM_285195	1.2238	0.612	0.8974	1.4003
XM_285268	1.7453	1.6942	0.6482	0.6482
XM_285272	1.1991	0.966	1.4383	1.4383
XM_285283	2.2048	1.7534	1.8922	1.7495
XM_285318	0.8166	1.0119	1.1349	1.0084
XM_285328	0.8166	1.1584	1.0967	1.0967
XM_285543	1.1991	1.0534	1.2876	1.5639
XM_285560	1.2693	0.612	1.4197	0.9565
XM_285625	0.874	0.966	1.3126	1.0548
XM_285653	1.0111	0.3077	1.3363	1.6272
XM_285739	0.97	0.612	1.5773	1.2328
XM_285747	1.0111	0.612	1.1701	1.5903
XM_285756	1.2472	1.1885	1.4197	1.0548
XM_285789	2.1222	0.9147	1.2328	0.8974
XM_285812	1.3298	0.7096	0.8291	1.4383
XM_285819	1.0832	1.1584	1.6719	0.9565
XM_285849	1.2693	1.2165	0.8291	1.2328
XM_285863	1.5585	2.241	1.7754	1.722
XM_285869	0.9247	1.1885	0.9565	1.3587
XM_285934	0.97	0.612	1.2876	1.38
XM_285994	1.0111	0.7892	1.0084	1.3126
XM_286045	0.8166	1.0534	0.8974	1.4897
XM_286054	1.1991	0.8565	1.0548	1.1701
XM_286063	0.874	2.1304	1.0084	1.7314
XM_286080	1.6009	2.0343	0.5184	0.9565
XM_286119	1.5238	0.8565	1.5773	1.6926
XM_286136	1.145	1.0119	1.2611	1.0084
XM_286150	1.2238	0.966	1.5773	1.0084
XM_286231	1.0832	1.1885	1.2876	1.4197
XM_286237	1.4591	1.0119	1.3363	0.6482
XM_286298	1.4449	1.3744	1.7495	1.2328
XM_286346	1.1152	0.8565	1.4197	1.8589
XM_286380	1.4728	1.9425	0.8974	2.3698
XM_286416	1.3482	1.7839	1.1349	0.8974
XM_286421	1.0486	1.0534	0.748	1.1701
XM_286455	2.0672	1.2165	0.6482	1.1701
XM_286467	1.5695	1.518	1.4383	1.5639
XM_286498	1.2238	1.9576	1.0084	0.748
XM_286524	1.1152	2.0776	1.2328	0.8974
XM_286553	0.7505	1.3744	1.2026	1.0084
XM_286564	1.6485	1.3551	0.5184	1.0548
XM_286576	0.8166	1.4599	0.6482	1.3587
XM_286596	0.9247	1.0913	0.6482	1.5056
XM_286597	1.2472	1.2429	1.1701	1.2026
XM_286602	1.3298	2.0343	1.38	0.8291
XM_286644	1.3106	1.2165	0.8974	1.6029
XM_286648	1.6301	0.7892	1.0967	1.8377
XM_286655	1.2472	1.3551	1.2876	1.7026
XM_286732	1.3482	1.2165	1.4383	1.7314
XM_286736	1.1152	1.0119	1.2328	1.38
XM_286790	1.4591	1.3551	1.7405	1.6388
XM_286819	1.0832	1.1584	0.748	0.9565
XM_286826	1.7665	0.8565	1.6152	0.5184
XM_286832	1.1729	1.2165	1.1349	1.0084
XM_286838	0.5772	0.7096	1.5056	1.6272
XM_286861	0.874	1.2429	1.7026	0.748
XM_286867	1.6996	1.4441	1.4733	1.3126
XM_286876	0.97	1.2165	0.748	1.2026
XM_286878	0.8166	1.0119	0.8974	1.1349
XM_286894	0.8166	1.0534	0.8291	1.0548
XM_286915	1.0486	0.7892	1.0084	1.2026
XM_286938	1.3992	0.7096	0.748	1.917
XM_286959	0.97	1.1584	0.9565	1.7314
XM_286984	0.9247	1.3136	1.1701	0.8974
XM_286992	0.97	1.3929	0.8291	1.0548
XM_286995	2.0532	0.8565	1.5357	1.0967
XM_286996	1.3992	0.7892	0.9565	1.1349
XM_287004	1.8478	0.612	1.3363	0.9565
XM_287015	0.8166	1.1262	0.6482	1.6719
XM_287035	1.2472	0.612	0.8291	1.3126
XM_287063	1.1729	0.612	0.8974	1.8449
XM_287068	1.2904	1.3136	1.4733	1.0548
XM_287120	1.5802	1.6464	1.0967	1.7669
XM_287126	0.97	1.3929	1.5056	1.6152
XM_287133	0.6724	0.7096	1.6388	1.7495
XM_287135	1.4991	1.4106	1.5773	1.38
XM_287164	4.2499	3.9118	3.9874	3.435
XM_287198	1.5357	1.2913	1.9519	1.4562
XM_287224	1.1991	1.9908	1.2611	0.6482
XM_287247	0.6724	1.1262	0.8974	1.38

XM_287258	1.0486	0.8565	1.0548	0.9565
XM_287285	1.2472	1.3136	1.2026	1.0967
XM_287310	1.4861	1.518	1.7495	1.1349
XM_287312	2.2432	0.7892	1.1349	1.3126
XM_287332	1.0832	0.9147	0.8291	1.0084
XM_287349	1.7932	1.0913	1.2026	1.0084
XM_287373	1.4302	0.8565	1.1349	1.2026
XM_287400	2.2478	2.0662	1.6926	2.256
XM_287407	0.97	1.0534	1.38	1.2876
XM_287439	1.1152	1.2165	1.1701	1.2611
XM_287455	0.874	0.966	1.2328	1.0084
XM_287504	0.5772	1.3744	1.4197	0.9565
XM_287530	0.9247	0.966	1.0084	0.9565
XM_287625	0.9247	1.1885	0.8974	0.8974
XM_287650	0.9247	1.2165	0.748	1.722
XM_287716	0.97	1.1584	1.5056	1.4733
XM_287749	1.2693	1.0534	1.2876	1.3126
XM_287761	1.2472	1.1262	0.9565	1.3363
XM_287805	1.6996	1.518	0.6482	0.748
XM_287807	1.0832	1.0913	1.1349	1.1349
XM_287817	1.738	1.6942	1.7754	1.55
XM_287837	1.8122	1.3136	0.8291	1.6029
XM_287838	1.145	1.2678	1.3363	1.6388
XM_287845	1.0486	1.0534	0.9565	2.0853
XM_287946	0.6724	0.612	1.4562	1.6824
XM_288010	0.8166	1.1262	1.3363	1.1349
XM_288159	0.6724	1.1885	1.1701	0.9565
XM_288165	1.7076	0.612	0.5184	1.6719
XM_288181	1.6485	1.5042	1.55	1.2026
XM_288186	2.1843	2.3692	2.6624	2.1604
XM_288187	1.7665	1.8391	2.0092	1.5056
XM_288194	0.874	1.0119	1.4003	1.4733
XM_288196	1.3106	0.9147	1.2328	1.2026
XM_288201	1.3829	0.966	1.1349	0.6482
XM_288202	1.9839	1.0913	1.55	0.8974
XM_288223	1.5585	1.4599	1.9048	1.3126
XM_288242	1.145	1.8054	2.077	1.38
XM_288256	0.9247	0.9147	0.8291	1.4003
XM_288279	1.5357	0.9147	0.5184	1.2876
XM_288284	0.8166	1.0119	1.1701	0.9565
XM_288288	1.0486	1.1885	0.748	1.6719
XM_288295	1.3106	1.4899	1.6152	2.3081
XM_288319	1.1991	1.2429	1.2611	0.8974
XM_288371	1.0111	2.07	0.8974	1.2328
XM_288375	0.6724	1.2429	0.9565	1.2876
XM_288394	1.1152	0.612	0.8974	1.4897
XM_288405	1.8122	1.1262	0.8291	0.8974
XM_288421	0.7505	0.7892	1.1701	1.2611
XM_288475	1.5907	1.0119	0.3323	1.7314
XM_288482	1.926	2.3934	0.9565	1.1349
XM_288483	1.738	1.7612	1.9462	1.6611
XM_288490	1.6301	1.3136	0.748	1.4897
XM_288493	0.6724	1.5927	1.2611	0.8974
XM_288504	1.415	1.8939	0.748	1.1701
XM_288521	0.874	1.0913	1.0548	1.0548
XM_288524	1.0111	0.8565	1.38	1.2876
XM_288528	1.2238	1.3929	1.5056	1.722
XM_288531	0.97	0.966	1.1349	1.0084
XM_288537	2.1429	1.3348	0.748	2.1207
XM_288547	0.8166	0.7096	1.5056	1.5209
XM_288555	0.8166	1.7764	1.0967	1.1701
XM_288560	0.7505	0.7892	1.0548	1.5773
XM_288567	1.0111	0.7892	0.8291	1.4003
XM_288602	1.2238	1.6662	0.8974	0.8291
XM_288618	2.9534	3.3258	2.1872	3.1061
XM_288637	1.5238	1.7032	1.9683	1.2876
XM_288654	1.8964	0.7096	2.077	0.5184
XM_288674	1.6009	1.5927	2.0511	1.6501
XM_288681	1.5116	1.1885	0.5184	1.2611
XM_288682	0.874	1.1262	1.7314	1.1349
XM_288685	0.8166	1.2913	1.7124	0.9565
XM_288693	0.5772	0.9147	1.3363	1.8725
XM_288694	0.874	1.2165	0.748	1.4003
XM_288696	1.0111	0.966	0.8974	1.5639
XM_288742	1.2693	0.966	1.0548	0.748
XM_288751	1.738	1.0119	1.7583	1.2328
XM_288763	1.145	0.612	0.8974	1.5903
XM_288775	1.0832	1.0913	1.722	1.4733
XM_288776	1.2238	1.0913	1.1701	1.1701
XM_288781	1.0111	2.2708	0.8974	1.5903
XM_288790	1.1152	0.612	0.8974	1.2876
XM_288794	0.9247	1.2429	0.9565	1.3363
XM_288807	0.97	2.2173	1.3126	1.9994
XM_288813	1.6748	1.9052	1.3363	1.1349
XM_288817	0.874	1.1262	0.6482	1.3363
XM_288819	2.0532	0.7892	1.3587	1.7918
XM_288859	1.0832	1.1885	0.748	0.8291

XM_288867	1.1729	1.0534	1.2026	1.0084
XM_288873	0.874	1.2913	1.1701	1.2026
XM_288879	2.0808	1.3136	1.3363	1.8229
XM_288890	1.8244	1.6757	2.1569	1.5209
XM_288893	1.2904	1.2165	1.6501	1.0548
XM_288897	1.145	1.1584	0.8291	1.3363
XM_288901	1.3298	1.5692	2.1131	1.8857
XM_288905	1.0486	0.966	1.0084	1.6824
XM_288950	1.7665	1.6257	1.5056	1.6926
XM_288952	2.2612	1.0913	0.748	1.7026
XM_288966	1.0111	1.0913	0.8291	1.1349
XM_288991	1.2238	1.2165	0.8974	1.6926
XM_289030	1.6009	1.1262	1.0084	1.852
XM_289038	1.415	1.3136	1.4003	1.2026
XM_289042	1.0832	1.2913	0.8291	1.3587
XM_289050	1.5238	0.9147	0.9565	1.6152
XM_289079	3.2494	3.1509	3.3554	2.8999
XM_289117	2.0388	0.612	1.4562	1.5056
XM_289134	1.0832	0.9147	0.6482	1.0548
XM_289151	1.1729	2.1304	1.6152	2.1428
XM_289166	1.4302	1.8326	0.6482	0.8291
XM_289171	1.1152	0.966	1.2876	1.1349
XM_289186	1.1729	1.2913	1.3126	1.9574
XM_289215	1.0832	0.8565	0.6482	1.4562
XM_289240	0.6724	1.9425	1.55	0.748
XM_289246	0.97	1.4899	1.1349	0.6482
XM_289264	1.0486	1.1584	0.748	1.4897
XM_289284	1.1152	1.518	1.2026	1.5773
XM_289287	0.97	1.0913	1.0084	1.9109
XM_289320	0.97	1.0119	1.2611	1.3587
XM_289335	1.8755	1.9162	1.9406	2.4143
XM_289342	1.2904	1.4599	1.4003	0.748
XM_289350	1.7076	2.137	1.0084	0.3323
XM_289354	1.2238	1.0534	0.8291	0.8974
XM_289407	0.2846	1.4599	1.2876	1.2611
XM_289424	1.0486	1.3929	1.722	1.7495
XM_289438	1.0111	1.1262	1.2611	0.8291
XM_289474	1.2693	2.2227	1.0967	1.2876
XM_289505	0.9247	1.3551	1.3126	1.0084
XM_289514	0.6724	0.9147	1.2026	1.4383
XM_289517	1.2238	1.4106	0.6482	1.3363
XM_289560	0.874	1.4277	0.6482	1.55
XM_289571	1.3659	1.9162	0.6482	1.0084
XM_289572	1.0832	1.2429	0.6482	1.1349
XM_289592	1.6575	1.2165	0.6482	0.8974
XM_289600	2.2123	2.1435	2.275	1.7026
XM_289602	0.9247	1.2165	0.5184	1.3126
XM_289616	1.4302	0.8565	1.0084	0.8974
XM_289632	0.8166	0.8565	0.8974	1.1349
XM_289643	1.1991	1.0119	0.748	1.1701
XM_289649	1.0111	0.9147	1.6501	0.8974
XM_289735	2.0874	1.7119	1.3587	1.6152
XM_289752	1.2238	1.3744	1.5357	0.9565
XM_290029	0.9247	0.966	0.748	1.6501
XM_290137	1.1991	1.1885	0.9565	1.2026
XM_290164	0.7505	1.2165	0.8291	1.1349
XM_343456	1.5357	1.3744	1.5639	1.1701
XM_345593	2.02	2.22	2.435	1.6824
XM_347206	0.97	1.6564	0.6482	1.3587
XM_355246	1.2904	0.7892	1.0548	0.9565
XM_355265	1.0111	1.1885	1.38	1.6152
XM_355456	1.6575	0.7892	1.2876	0.9565
XM_355655	1.1729	0.7892	1.9048	1.4003
XM_356940	0.8166	0.7892	1.4562	1.2328
XM_357883	1.4302	1.8259	1.0084	1.2876
XM_358915	2.3111	1.9862	2.0811	1.6152
XM_359319	0.8166	1.1885	0.8974	1.1701
XM_359409	1.4449	0.9147	1.5357	1.0084
XM_371313	0.874	1.5313	0.6482	1.3587
XM_4	1.4302	1.3348	1.3363	1.3126
XM_484131	1.0486	1.2429	0.6482	1.38
XM_484193	1.5357	1.2429	0.8291	1.2876
XM_484202	1.145	1.6257	0.8291	1.7124
XM_484214	1.3298	1.3551	1.7124	1.1349
XM_484250	1.5238	0.8565	0.8291	1.6824
XM_484476	1.2238	1.2429	1.7405	1.2026
XM_484818	1.3829	0.486	1.7998	1.2026
XM_484819	0.97	2.2708	1.2026	0.9565
XM_485061	2.4139	2.3842	3.2097	2.5012
XM_485180	0.97	0.3077	1.38	1.6029
XM_485292	1.3659	1.2429	1.2876	1.0084
XM_485420	1.7733	[illegible]	1.3363	1.5209
XM_485950	1.0111	0.612	0.9565	1.7669
XM_486612	1.4591	1.1885	0.6482	1.2026
XM_487126	1.145	1.2165	1.6926	1.5209
XM_487177	0.874	1.0119	0.748	1.1349
XM_487447	1.2472	1.2678	1.4733	1.2328

XM_487610	1.3482	1.1885	1.4562	1.1349
XM_487784	0.9247	1.0913	1.1701	1.6926
XM_487875	0.8166	1.3136	1.0967	1.2026
XM_487878	1.0486	0.9147	0.8974	0.8291
XM_487965	1.0832	1.0119	1.0084	0.9565
XM_488011	1.1991	1.3348	1.1349	2.2124
XM_488044	1.6009	1.3744	1.3126	1.2611
XM_488111	1.2904	1.1262	1.7405	0.5184
XM_488203	0.97	1.0119	1.3363	0.8974
XM_488289	1.5473	0.966	1.2328	1.9683
XM_488310	1.4302	1.2165	1.8658	1.2876
XM_488333	1.0486	0.966	0.8974	1.0548
XM_488359	1.0486	0.612	1.2328	1.7405
XM_488393	0.9247	1.4106	1.55	1.0084
XM_488418	0.97	0.966	1.6388	1.2611
XM_488680	0.8166	0.7892	1.0084	1.4897
XM_488721	0.97	1.0119	1.0548	1.2328
XM_488738	0.9247	0.9147	1.0084	1.55
XM_488836	0.9247	1.3744	0.8291	1.5357
XM_488954	0.9247	1.0913	1.38	1.2026
XM_489037	0.97	0.9147	1.2328	1.0548
XM_489132	0.8166	1.4277	0.9565	1.0084
XM_489253	1.1729	1.0534	0.8974	1.0548
XM_489271	1.7665	1.5443	1.4733	1.1349
XM_489273	1.4728	1.4106	1.8154	1.3587
XM_489304	1.3829	2.0465	1.4562	2.1428
XM_489310	1.5907	1.0119	0.6482	1.0967
XM_489320	1.1152	1.3348	1.3126	1.1349
XM_489322	1.6996	1.2165	0.6482	0.8974
XM_489350	0.874	0.612	1.0967	1.4897
XM_489353	1.3829	1.8519	1.8229	1.4733
XM_489372	1.1991	1.0119	1.1349	1.2328
XM_489702	1.3659	1.0119	0.6482	1.2328
XM_489720	1.2693	1.3929	1.2876	1.2611
Yars2	1.6996	1.8259	1.7837	1.5903
Ylpm1	1.3106	1.1262	1.55	1.2026
Ywhaq	1.6485	0.7892	1.0967	1.1349
Zap70	1.7306	1.9954	0.9565	1.6824
Zbed4	1.7525	1.2165	0.748	1.0084
Zbtb24	1.5907	1.5443	1.2611	1.2328
Zbtb44	1.1991	1.3744	1.7837	1.4897
Zbtb6	1.0832	0.8565	1.4562	1.0084
Zc3h12c	1.4861	1.4277	1.6501	1.55
Zc3h6	1.1152	0.7892	0.8291	1.0084
Zcchc5	1.7525	1.729	0.8974	0.6482
Zcrb1	1.7306	0.9147	0.8974	1.0967
Zdhhc20	1.3106	1.0913	0.5184	1.6029
Zer1	1.6748	0.612	1.2876	0.8974
Zfc3h1	1.0486	0.966	1.38	1.2026
Zfhx3	0.874	1.3136	0.8974	1.4197
Zfp111	0.8166	0.612	1.2328	1.8792
Zfp184	0.5772	1.4277	1.38	1.4003
Zfp27	1.2693	0.612	1.3126	1.6152
Zfp326	0.7505	1.5927	0.5184	1.7998
Zfp365	1.5357	1.4599	1.6926	1.5639
Zfp397	1.3829	0.9147	1.1701	0.9565
Zfp422	1.6996	0.8565	1.1349	1.2328
Zfp451	0.874	0.7892	0.8974	1.3587
Zfp507	1.78	1.7912	0.5184	1.1349
Zfp592	0.874	0.9147	1.0967	1.4897
Zfp599	0.7505	2.3395	1.0548	1.55
Zfp612	0.6724	1.8581	1.3126	1.0967
Zfp647	1.145	1.0534	1.2328	1.0084
Zfp668	1.0832	1.0913	1.4003	1.2611
Zfp704	1.0832	0.7892	0.8291	1.4383
Zfp719	1.0486	0.9147	0.6482	1.0967
Zfp750	1.3106	1.1262	0.6482	1.3587
Zfp763	1.0111	1.1584	0.5184	1.1349
Zfp781	1.2238	1.0913	0.8974	1.0084
Zfp788	0.8166	1.2429	0.6482	1.2611
Zfp810	1.1991	0.612	1.1701	1.6388
Zfp819	0.7505	1.3744	1.5056	1.4562
Zfp820	0.8166	0.7096	1.0967	1.5056
Zfp821	0.9247	0.7892	0.8974	1.2876
Zfp866	1.1729	1.5569	0.8291	1.5056
Zfp874b	2.0874	0.612	1.6029	1.6824
Zfp940	1.7733	1.3348	0.748	0.8291
Zmat1	0.874	0.966	1.0084	1.0967
Zmiz2	0.97	1.1885	0.9565	1.2026
ZNF813	1.3992	0.7892	0.8291	2.0189
Zscan20	1.2238	1.1584	0.748	1.2611
Zw10	0.9247	0.966	1.1349	1.0967
Zxdc	1.1729	1.0534	1.4733	1.3363

Appendix 6

Over-representative Networks in shRNA-identified targets

shRNA Group	Top Diseases and Functions	Score	p-value
A	Gene Expression, DNA Replication, Recombination, and Repair, Cellular Assembly and Organization	46	1E-46
	Embryonic Development, Organismal Development, Developmental Disorder	43	1E-43
	Cancer, Hematological Disease, Immunological Disease	41	1E-41
	Cell Morphology, Cell-To-Cell Signaling and Interaction, Cellular Function and Maintenance	32	1E-32
	Cell Signaling, Nucleic Acid Metabolism, Cancer	30	1E-30
B	Protein Synthesis, Hematological System Development and Function, Cancer	39	1E-39
	Cancer, Cell Death and Survival, Tumor Morphology	39	1E-39
	Amino Acid Metabolism, Small Molecule Biochemistry, Cell-To-Cell Signaling and Interaction	32	1E-32
	Cellular Assembly and Organization, Cellular Function and Maintenance, Cell-To-Cell Signaling and Interaction	30	1E-30
	Cell-To-Cell Signaling and Interaction, Cellular Growth and Proliferation, Hair and Skin Development and Function	26	1E-26
C	Cellular Movement, Cellular Function and Maintenance, Hematological System Development and Function	33	1E-33
	Cell-To-Cell Signaling and Interaction, Cell-mediated Immune Response, Cellular Development	28	1E-28
	Developmental Disorder, Hereditary Disorder, Metabolic Disease	26	1E-26
	Cellular Development, Cellular Growth and Proliferation, Embryonic Development	26	1E-26
	Cellular Assembly and Organization, Cellular Function and Maintenance, Protein Degradation	25	1E-25
D	Cell Cycle, Connective Tissue Development and Function, Drug Metabolism	39	1E-39
	Carbohydrate Metabolism, Small Molecule Biochemistry, Behavior	36	1E-36
	Connective Tissue Development and Function, Embryonic Development, Nervous System Development and Function	35	1E-35
	Cellular Movement, Hematological System Development and Function, Hypersensitivity Response	35	1E-35
	Lipid Metabolism, Small Molecule Biochemistry, Cellular Compromise	33	1E-33

Appendix 7.

Gene number and ratio in each shRNA-enriched group

# of genes	Down	Up	None/Minor	Total
shRNA #A	25	100	261	386
shRNA #B	30	80	262	372
shRNA #C	12	35	54	101
shRNA #D	56	99	276	431
shRNA #E	141	209	571	921

%	Down %	Up %	None/Minor	
shRNA #A	6.4766839	25.906736	67.61658	100
shRNA #B	8.0645161	21.505376	70.430108	100
shRNA #C	11.881188	34.653465	53.465347	100
shRNA #D	12.993039	22.969838	64.037123	100
shRNA #E	15.309446	22.692725	61.997828	100

Gene number and ratio in each differential group in transcriptome analysis

# of genes	shRNA #A	#A&B	shRNA #B	shRNA #C	shRNA #D	shRNA #E	Total
mRNA#1	77	0	99	0	62	238	476
mRNA#2	21	11	19	10	32	43	136
mRNA#3	14	0	19	8	31	41	113
mRNA#4	142	0	100	23	97	204	566
mRNA#5	264	0	219	0	185	697	1365

%	shRNA #A	#A&B	shRNA #B	shRNA #C	shRNA #D	shRNA #E	Total
mRNA#1	16.176471	0	20.798319	0	13.02521	50	100
mRNA#2	15.441176	8.0882353	13.970588	7.3529412	23.529412	31.617647	100
mRNA#3	12.389381	0	16.814159	7.079646	27.433628	36.283186	100
mRNA#4	25.088339	0	17.667845	4.0636042	17.137809	36.042403	100
mRNA#5	19.340659	0	16.043956	0	13.553114	51.062271	100

Appendix 8.
Gene properties identified in shRNA Group A

Log Ratio	Symbol	Entrez Gene Name	Location	Type(s)
-1.996	TSNAX	translin-associated factor X	Nucleus	transporter
-1.967	SYT4	synaptotagmin IV	Cytoplasm	transporter
-1.935	SLC50A1	solute carrier family 50 (sugar transporter), member 1	Plasma Membrane	transporter
-1.881	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	Plasma Membrane	transporter
-1.848	ATP11C	ATPase, class VI, type 11C	Plasma Membrane	transporter
-1.848	SV2B	synaptic vesicle glycoprotein 2B	Plasma Membrane	transporter
-1.824	PANX1	pannexin 1	Plasma Membrane	transporter
-1.818	PIGR	polymeric immunoglobulin receptor	Plasma Membrane	transporter
-1.806	SLC25A36	solute carrier family 25 (pyrimidine nucleotide carrier), member 36	Cytoplasm	transporter
-1.793	SLC35D2	solute carrier family 35, member D2	Cytoplasm	transporter
-1.780	GJA3	gap junction protein, alpha 3, 46kDa	Plasma Membrane	transporter
-1.780	SLC26A5	solute carrier family 26, member 5 (prestin)	Plasma Membrane	transporter
-1.760	TFRC	transferrin receptor (p90, CD71)	Plasma Membrane	transporter
-1.752	SLC25A21	solute carrier family 25 (mitochondrial oxoadipate carrier), member 21	Cytoplasm	transporter
-1.745	NPC1L1	NPC1-like 1	Cytoplasm	transporter
-1.708	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	Cytoplasm	transporter
-1.675	SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Plasma Membrane	transporter
-1.639	SLC39A1	solute carrier family 39 (zinc transporter), member 1	Plasma Membrane	transporter
-1.621	TMED1	transmembrane emp24 protein transport domain containing 1	Extracellular Space	transporter
-1.611	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Plasma Membrane	transporter
-1.601	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	Cytoplasm	transporter
-1.591	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	Plasma Membrane	transporter
-1.591	STEAP2	STEAP family member 2, metalloreductase	Plasma Membrane	transporter
-1.580	FABP7	fatty acid binding protein 7, brain	Cytoplasm	transporter
-1.547	AQP7	aquaporin 7	Plasma Membrane	transporter
-1.536	SMC2	structural maintenance of chromosomes 2	Nucleus	transporter
-1.512	GJB3	gap junction protein, beta 3, 31kDa	Plasma Membrane	transporter
-2.060	CLEC1A	C-type lectin domain family 1, member A	Plasma Membrane	transmembrane receptor
-1.891	IL1RAP	interleukin 1 receptor accessory protein	Plasma Membrane	transmembrane receptor
-1.854	CHRNA7	cholinergic receptor, nicotinic, alpha 7 (neuronal)	Plasma Membrane	transmembrane receptor
-1.830	IL13RA2	interleukin 13 receptor, alpha 2	Plasma Membrane	transmembrane receptor
-1.780	SLAMF1	signaling lymphocytic activation molecule family member 1	Plasma Membrane	transmembrane receptor
-1.760	CD3G	CD3g molecule, gamma (CD3-TCR complex)	Plasma Membrane	transmembrane receptor
-1.752	IGF1R	insulin-like growth factor 1 receptor	Plasma Membrane	transmembrane receptor
-1.658	IL17RC	interleukin 17 receptor C	Plasma Membrane	transmembrane receptor
-1.658	IL23R	interleukin 23 receptor	Plasma Membrane	transmembrane receptor
-1.547	PTCH1	patched 1	Plasma Membrane	transmembrane receptor
-1.896	MRPL32	mitochondrial ribosomal protein L32	Cytoplasm	translation regulator
-1.611	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	Cytoplasm	translation regulator
-1.536	EIF5A2	eukaryotic translation initiation factor 5A2	Cytoplasm	translation regulator
-2.171	TMF1	TATA element modulatory factor 1	Cytoplasm	transcription regulator
-2.110	Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Nucleus	transcription regulator
-2.067	EZH2	enhancer of zeste homolog 2 (Drosophila)	Nucleus	transcription regulator
-2.000	GTF2F2	general transcription factor IIF, polypeptide 2, 30kDa	Nucleus	transcription regulator
-1.996	PROP1	PROP paired-like homeobox 1	Nucleus	transcription regulator
-1.935	ZEB2	zinc finger E-box binding homeobox 2	Nucleus	transcription regulator
-1.916	KDM4A	lysine (K)-specific demethylase 4A	Nucleus	transcription regulator
-1.902	Hmgb1	high mobility group box 1	Nucleus	transcription regulator
-1.881	MEF2C	myocyte enhancer factor 2C	Nucleus	transcription regulator
-1.859	HNF4G	hepatocyte nuclear factor 4, gamma	Nucleus	transcription regulator
-1.842	NOBOX	NOBOX oogenesis homeobox	Nucleus	transcription regulator
-1.836	MEOX1	mesenchyme homeobox 1	Nucleus	transcription regulator
-1.793	URI1	URI1, prefoldin-like chaperone	Nucleus	transcription regulator
-1.787	TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1	Nucleus	transcription regulator
-1.773	SOX5	SRY (sex determining region Y)-box 5	Nucleus	transcription regulator
-1.723	CCNT1	cyclin T1	Nucleus	transcription regulator
-1.723	TRPS1	trichorhinophalangeal syndrome I	Nucleus	transcription regulator
-1.666	TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	Nucleus	transcription regulator
-1.648	DMBX1	diencephalon/mesencephalon homeobox 1	Nucleus	transcription regulator
-1.630	Obox6 (includes others)	oocyte specific homeobox 6	Nucleus	transcription regulator
-1.611	MED21	mediator complex subunit 21	Nucleus	transcription regulator
-1.601	FOXA2	forkhead box A2	Nucleus	transcription regulator
-1.601	GSC	goosecoid homeobox	Nucleus	transcription regulator
-1.601	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	Nucleus	transcription regulator
-1.601	HOXB8	homeobox B8	Nucleus	transcription regulator
-1.570	HOPX	HOP homeobox	Nucleus	transcription regulator
-1.570	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Cytoplasm	transcription regulator
-1.547	NCOA2	nuclear receptor coactivator 2	Nucleus	transcription regulator
-1.536	ASB4	ankyrin repeat and SOCS box containing 4	Nucleus	transcription regulator
-1.524	KLF5	Kruppel-like factor 5 (intestinal)	Nucleus	transcription regulator
-1.512	CASP8AP2	caspase 8 associated protein 2	Nucleus	transcription regulator
-2.146	CDKN3	cyclin-dependent kinase inhibitor 3	Nucleus	phosphatase
-1.906	PTPRN	protein tyrosine phosphatase, receptor type, N	Plasma Membrane	phosphatase
-1.891	SSU72	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	unknown	phosphatase
-1.830	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	Nucleus	phosphatase
-1.752	SSH3	slingshot homolog 3 (Drosophila)	Cytoplasm	phosphatase
-1.723	PPAPDC1A	phosphatidic acid phosphatase type 2 domain containing 1A	unknown	phosphatase
-1.700	DUSP27	dual specificity phosphatase 27 (putative)	unknown	phosphatase
-1.675	PPP4C	protein phosphatase 4, catalytic subunit	Cytoplasm	phosphatase
-1.630	Dusp21	dual specificity phosphatase 21	Cytoplasm	phosphatase
-1.621	SSH1	slingshot homolog 1 (Drosophila)	Cytoplasm	phosphatase
-1.611	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme	Cytoplasm	phosphatase
-1.547	PTPRK	protein tyrosine phosphatase, receptor type, K	Plasma Membrane	phosphatase
-2.084	USP24	ubiquitin specific peptidase 24	unknown	peptidase
-1.931	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	Cytoplasm	peptidase
-1.886	DPP7	dipeptidyl-peptidase 7	Cytoplasm	peptidase
-1.859	USP40	ubiquitin specific peptidase 40	unknown	peptidase
-1.745	ECEL1	endothelin converting enzyme-like 1	Plasma Membrane	peptidase
-1.738	KLK3	kallikrein-related peptidase 3	Extracellular Space	peptidase
-1.683	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	Cytoplasm	peptidase
-1.611	TROAP	trophinin associated protein	Cytoplasm	peptidase
-1.601	SPAG5	sperm associated antigen 5	Nucleus	peptidase
-1.591	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	Extracellular Space	peptidase
-1.580	ADAM7	ADAM metallopeptidase domain 7	Plasma Membrane	peptidase
-1.580	RNF130	ring finger protein 130	Cytoplasm	peptidase
-1.580	USP33	ubiquitin specific peptidase 33	Cytoplasm	peptidase
-1.570	XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	Plasma Membrane	peptidase
-1.558	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	Nucleus	peptidase

-1.512	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	Nucleus	peptidase
-2.434	ISM1	isthmin 1 homolog (zebrafish)	unknown	other
-2.236	A930024N18Rik	RIKEN cDNA A930024N18 gene	unknown	other
-2.207	2900092D14Rik	RIKEN cDNA 2900092D14 gene	unknown	other
-2.134	1700016D06Rik	RIKEN cDNA 1700016D06 gene	unknown	other
-2.125	5031425E22Rik	RIKEN cDNA 5031425E22 gene	unknown	other
-2.091	AI182371	expressed sequence AI182371	unknown	other
-2.091	Speer5-ps1	spermatogenesis associated glutamate (E)-rich protein 5, pseudogene 1	unknown	other
-2.084	Gm16440 (includes others)	predicted gene 16440	unknown	other
-2.084	SPINK5	serine peptidase inhibitor, Kazal type 5	Extracellular Space	other
-2.081	RBFOX1	RNA binding protein, fox-1 homolog (C. elegans) 1	Cytoplasm	other
-2.067	PAQR8	progestin and adipoQ receptor family member VIII	Plasma Membrane	other
-2.064	KRT18	keratin 18	Cytoplasm	other
-2.064	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	Nucleus	other
-2.057	EPS8L3	EPS8-like 3	Extracellular Space	other
-2.057	PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	Plasma Membrane	other
-2.053	BCL2L12	BCL2-like 12 (proline rich)	unknown	other
-2.046	KDM6B	lysine (K)-specific demethylase 6B	Extracellular Space	other
-2.028	A630034I12Rik	RIKEN cDNA A630034I12 gene	unknown	other
-2.028	C230029F24Rik	RIKEN cDNA C230029F24 gene	unknown	other
-2.028	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	Nucleus	other
-2.024	ARHGAP11A	Rho GTPase activating protein 11A	Cytoplasm	other
-2.024	CNN1	calponin 1, basic, smooth muscle	Cytoplasm	other
-2.024	RASSF10	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	unknown	other
-2.016	KRT76	keratin 76	Cytoplasm	other
-2.016	Skint9	selection and upkeep of intraepithelial T cells 9	unknown	other
-2.016	VPS37A	vacuolar protein sorting 37 homolog A (S. cerevisiae)	Cytoplasm	other
-2.012	ERRFI1	ERBB receptor feedback inhibitor 1	Cytoplasm	other
-2.012	NBEAL1	neurobeachin-like 1	unknown	other
-2.008	DENND2A	DENN/MADD domain containing 2A	unknown	other
-2.000	CNOT1	CCR4-NOT transcription complex, subunit 1	Cytoplasm	other
-1.984	FAM82A2	family with sequence similarity 82, member A2	Cytoplasm	other
-1.971	SPRR4	small proline-rich protein 4	Cytoplasm	other
-1.967	ADCYAP1	adenylate cyclase activating polypeptide 1 (pituitary)	Extracellular Space	other
-1.963	Gm5102	predicted gene 5102	unknown	other
-1.963	LIX1L	Lix1 homolog (mouse)-like	unknown	other
-1.954	PCDHB4	protocadherin beta 4	Plasma Membrane	other
-1.945	BC002163	NADH dehydrogenase Fe-S protein 5 pseudogene	unknown	other
-1.945	XAB2	XPA binding protein 2	Nucleus	other
-1.940	FANCI	Fanconi anemia, complementation group I	Nucleus	other
-1.935	A930024E05Rik	RIKEN cDNA A930024E05 gene	unknown	other
-1.931	FAM154A	family with sequence similarity 154, member A	unknown	other
-1.931	HIST1H2BN	histone cluster 1, H2bn	Nucleus	other
-1.931	IGFN1	immunoglobulin-like and fibronectin type III domain containing 1	Nucleus	other
-1.931	TRA2A	transformer 2 alpha homolog (Drosophila)	Nucleus	other
-1.916	SERF1A/SERF1B	small EDRK-rich factor 1A (telomeric)	unknown	other
-1.916	TIMP2	TIMP metallopeptidase inhibitor 2	Extracellular Space	other
-1.912	Cldn13	claudin 13	Plasma Membrane	other
-1.906	DCTN5	dynactin 5 (p25)	Cytoplasm	other
-1.906	ENAM	enamelin	Extracellular Space	other
-1.906	TMC2	transmembrane channel-like 2	Plasma Membrane	other
-1.902	CDC27	cell division cycle 27 homolog (S. cerevisiae)	Nucleus	other
-1.896	Gm5105	predicted gene 5105	unknown	other
-1.891	KLHDC1	kelch domain containing 1	Cytoplasm	other
-1.886	4932443I19Rik	RIKEN cDNA 4932443I19 gene	unknown	other
-1.886	MLEC	malectin	Plasma Membrane	other
-1.881	1700018A04Rik	RIKEN cDNA 1700018A04 gene	unknown	other
-1.881	CLDN15	claudin 15	Plasma Membrane	other
-1.870	Cst12	cystatin 12	Extracellular Space	other
-1.865	C11orf57	chromosome 11 open reading frame 57	unknown	other
-1.865	TEX28	testis expressed 28	unknown	other
-1.854	ABI2	abl-interactor 2	Cytoplasm	other
-1.854	MAGEB3	melanoma antigen family B, 3	unknown	other
-1.854	NBEAL2	neurobeachin-like 2	Cytoplasm	other
-1.848	6530415H11Rik	RIKEN cDNA 6530415H11 gene	unknown	other
-1.848	ADAMTSL5	ADAMTS-like 5	Extracellular Space	other
-1.848	ZC3H6	zinc finger CCCH-type containing 6	unknown	other
-1.842	NXPH4	neurexophilin 4	Extracellular Space	other
-1.836	MMRN2	multimerin 2	Extracellular Space	other
-1.836	MTHFSD	methenyltetrahydrofolate synthetase domain containing	unknown	other
-1.836	ZNF41	zinc finger protein 41	Nucleus	other
-1.830	A630001O12Rik	RIKEN cDNA A630001O12 gene	unknown	other
-1.830	ORC1	origin recognition complex, subunit 1	Nucleus	other
-1.818	DDB1	damage-specific DNA binding protein 1, 127kDa	Nucleus	other
-1.818	PHF14	PHD finger protein 14	unknown	other
-1.812	LMAN1	lectin, mannose-binding, 1	Cytoplasm	other
-1.806	A130014A01Rik	RIKEN cDNA A130014A01 gene	unknown	other
-1.806	ARRDC4	arrestin domain containing 4	unknown	other
-1.806	LPCAT3	lysophosphatidylcholine acyltransferase 3	Plasma Membrane	other
-1.800	1700027J07Rik	RIKEN cDNA 1700027J07 gene	unknown	other
-1.800	BC051070	cDNA sequence BC051070	unknown	other
-1.800	CC2D2A	coiled-coil and C2 domain containing 2A	unknown	other
-1.800	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	Nucleus	other
-1.793	4921509J17Rik	RIKEN cDNA 4921509J17 gene	unknown	other
-1.793	ANKRD37	ankyrin repeat domain 37	unknown	other
-1.793	OTUD4	OTU domain containing 4	unknown	other
-1.793	ZNF710	zinc finger protein 710	Nucleus	other
-1.787	NMRAL1	NmrA-like family domain containing 1	Nucleus	other
-1.787	SHB	Src homology 2 domain containing adaptor protein B	Cytoplasm	other
-1.780	BTBD3	BTB (POZ) domain containing 3	unknown	other
-1.780	PTCHD4	patched domain containing 4	unknown	other
-1.766	NASP	nuclear autoantigenic sperm protein (histone-binding)	Nucleus	other
-1.760	CDR2L	cerebellar degeneration-related protein 2-like	unknown	other
-1.760	LTBP3	latent transforming growth factor beta binding protein 3	Extracellular Space	other
-1.760	PVRL3	poliovirus receptor-related 3	Plasma Membrane	other
-1.760	RNPC3	RNA-binding region (RNP1, RRM) containing 3	Nucleus	other
-1.760	TBC1D5	TBC1 domain family, member 5	Extracellular Space	other
-1.760	UNKL	unkempt homolog (Drosophila)-like	unknown	other
-1.752	9130024F11Rik	RIKEN cDNA 9130024F11 gene	unknown	other
-1.752	A430028G04Rik	RIKEN cDNA A430028G04 gene	unknown	other
-1.752	GTSF1	gametocyte specific factor 1	Cytoplasm	other
-1.752	PDCL3	phosducin-like 3	Cytoplasm	other
-1.752	SP110	SP110 nuclear body protein	Nucleus	other
-1.745	4931407J08Rik	RIKEN cDNA 4931407J08 gene	unknown	other
-1.738	BC106179	cDNA sequence BC106179	unknown	other
-1.738	MS4A13	membrane-spanning 4-domains, subfamily A, member 13	unknown	other
-1.731	A530013C23Rik	RIKEN cDNA A530013C23 gene	unknown	other

-1.731	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	Nucleus	other
-1.731	DOK4	docking protein 4	Plasma Membrane	other
-1.731	DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1	Cytoplasm	other
-1.731	PER2	period circadian clock 2	Nucleus	other
-1.731	WDR60	WD repeat domain 60	Extracellular Space	other
-1.723	C12orf68	chromosome 12 open reading frame 68	Cytoplasm	other
-1.723	MLPH	melanophilin	Cytoplasm	other
-1.723	Nlrp4g	NLR family, pyrin domain containing 4G	unknown	other
-1.723	PALM2	paralemmin 2	Plasma Membrane	other
-1.723	PCDHB2	protocadherin beta 2	Plasma Membrane	other
-1.723	SASH3	SAM and SH3 domain containing 3	Cytoplasm	other
-1.723	SEL1L2	sel-1 suppressor of lin-12-like 2 (C. elegans)	unknown	other
-1.723	TMEM140	transmembrane protein 140	unknown	other
-1.715	AI662270	expressed sequence AI662270	unknown	other
-1.715	BEND6	BEN domain containing 6	unknown	other
-1.715	EVPL	envoplakin	Plasma Membrane	other
-1.715	FGD6	FYVE, RhoGEF and PH domain containing 6	Cytoplasm	other
-1.715	Gm16010	predicted gene 16010	unknown	other
-1.715	SELT	selenoprotein T	Cytoplasm	other
-1.715	THAP11	THAP domain containing 11	Nucleus	other
-1.715	TRIM67	tripartite motif containing 67	Cytoplasm	other
-1.715	Wdr95	WD40 repeat domain 95	unknown	other
-1.708	Vmn2r1	vomeronasal 2, receptor 1	Plasma Membrane	other
-1.700	D430018E03Rik	RIKEN cDNA D430018E03 gene	unknown	other
-1.692	RAD51AP1	RAD51 associated protein 1	Nucleus	other
-1.683	BC030500	cDNA sequence BC030500	unknown	other
-1.683	C5orf49	chromosome 5 open reading frame 49	unknown	other
-1.683	D130079A08Rik	RIKEN cDNA D130079A08 gene	unknown	other
-1.683	Gm9837	predicted gene 9837	unknown	other
-1.683	RBM33	RNA binding motif protein 33	unknown	other
-1.675	FRAS1	Fraser syndrome 1	Extracellular Space	other
-1.675	ZNF526	zinc finger protein 526	unknown	other
-1.666	4930479M11Rik	RIKEN cDNA 4930479M11 gene	unknown	other
-1.666	CDH12	cadherin 12, type 2 (N-cadherin 2)	Plasma Membrane	other
-1.666	CIDEB	cell death-inducing DFFA-like effector b	Cytoplasm	other
-1.666	Gm14743 (includes others)	predicted gene 14743	Extracellular Space	other
-1.666	KIAA0020	KIAA0020	Nucleus	other
-1.666	Rbm25	RNA binding motif protein 25	unknown	other
-1.658	4933434M16Rik	RIKEN cDNA 4933434M16 gene	unknown	other
-1.658	CDH24	cadherin 24, type 2	Plasma Membrane	other
-1.658	CLPTM1	cleft lip and palate associated transmembrane protein 1	Plasma Membrane	other
-1.658	FAM132B	family with sequence similarity 132, member B	Extracellular Space	other
-1.658	Pldi	polymorphic derived intron containing	unknown	other
-1.658	RFT1	RFT1 homolog (S. cerevisiae)	unknown	other
-1.648	IGFBP4	insulin-like growth factor binding protein 4	Extracellular Space	other
-1.648	Nudt13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	unknown	other
-1.648	PLEK	pleckstrin	Cytoplasm	other
-1.639	BAIAP2L1	BAI1-associated protein 2-like 1	Cytoplasm	other
-1.639	MICALL2	MICAL-like 2	Cytoplasm	other
-1.639	Zfp932 (includes others)	zinc finger protein 932	Nucleus	other
-1.630	CCDC134	coiled-coil domain containing 134	unknown	other
-1.630	CTNNBL1	catenin, beta like 1	Nucleus	other
-1.630	PRDM5	PR domain containing 5	Nucleus	other
-1.630	PVALB	parvalbumin	Cytoplasm	other
-1.621	Defb2	defensin beta 2	unknown	other
-1.621	FITM1	fat storage-inducing transmembrane protein 1	Extracellular Space	other
-1.621	HSPA12A	heat shock 70kDa protein 12A	unknown	other
-1.621	RBM46	RNA binding motif protein 46	unknown	other
-1.621	Spink6	serine peptidase inhibitor, Kazal type 6	Extracellular Space	other
-1.621	TMEM120B	transmembrane protein 120B	unknown	other
-1.621	TMEM35	transmembrane protein 35	unknown	other
-1.611	COL28A1	collagen, type XXVIII, alpha 1	Extracellular Space	other
-1.611	Sbp/Sbpl	spermine binding protein	Extracellular Space	other
-1.601	B830007D08Rik	RIKEN cDNA B830007D08 gene	unknown	other
-1.601	CDH20	cadherin 20, type 2	Plasma Membrane	other
-1.601	Zfp295	zinc finger protein 295	unknown	other
-1.591	IGFBP3	insulin-like growth factor binding protein 3	Extracellular Space	other
-1.591	MFSD4	major facilitator superfamily domain containing 4	unknown	other
-1.591	OLFML2B	olfactomedin-like 2B	Extracellular Space	other
-1.591	PTPRQ	protein tyrosine phosphatase, receptor type, Q	unknown	other
-1.580	BC053393	cDNA sequence BC053393	unknown	other
-1.580	GLT6D1	glycosyltransferase 6 domain containing 1	unknown	other
-1.580	ZBTB10	zinc finger and BTB domain containing 10	Nucleus	other
-1.570	ARMC3	armadillo repeat containing 3	unknown	other
-1.570	B930095G15Rik	RIKEN cDNA B930095G15 gene	unknown	other
-1.570	C87414 (includes others)	expressed sequence C87414	unknown	other
-1.570	Calm1 (includes others)	calmodulin 1	Nucleus	other
-1.570	COL18A1	collagen, type XVIII, alpha 1	Extracellular Space	other
-1.570	MRPS28	mitochondrial ribosomal protein S28	Cytoplasm	other
-1.558	Cabyr	calcium binding tyrosine-(Y)-phosphorylation regulated	Nucleus	other
-1.558	HMGB3	high mobility group box 3	Nucleus	other
-1.558	KIAA1432	KIAA1432	unknown	other
-1.558	NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	Nucleus	other
-1.558	PCP2	Purkinje cell protein 2	Cytoplasm	other
-1.558	TSPAN9	tetraspanin 9	Plasma Membrane	other
-1.547	2610305D13Rik (includes others)	RIKEN cDNA 2610305D13 gene	unknown	other
-1.547	AI314278	expressed sequence AI314278	unknown	other
-1.547	C9orf40	chromosome 9 open reading frame 40	unknown	other
-1.547	CORO2A	coronin, actin binding protein, 2A	Cytoplasm	other
-1.547	Dsg1c	desmoglein 1 gamma	Plasma Membrane	other
-1.547	ECT2	epithelial cell transforming sequence 2 oncogene	Nucleus	other
-1.547	GLMN	glomulin, FKBP associated protein	Cytoplasm	other
-1.547	Gm7133 (includes others)	predicted gene 7133	unknown	other
-1.547	GRXCR2	glutaredoxin, cysteine rich 2	unknown	other
-1.547	RFC4	replication factor C (activator 1) 4, 37kDa	Nucleus	other
-1.547	SLX4	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae)	Nucleus	other
-1.547	ZNF16	zinc finger protein 16	Nucleus	other
-1.536	1700008K24Rik	RIKEN cDNA 1700008K24 gene	unknown	other
-1.536	C2CD2	C2 calcium-dependent domain containing 2	Cytoplasm	other
-1.536	FHL1	four and a half LIM domains 1	Cytoplasm	other
-1.536	PTCHD1	patched domain containing 1	Plasma Membrane	other
-1.536	RPF1	ribosome production factor 1 homolog (S. cerevisiae)	Nucleus	other
-1.536	Siglech	sialic acid binding Ig-like lectin H	Plasma Membrane	other
-1.536	TOMM20L	translocase of outer mitochondrial membrane 20 homolog (yeast)-like	unknown	other
-1.524	1700061A03Rik	RIKEN cDNA 1700061A03 gene	unknown	other
-1.524	C230013L11Rik	RIKEN cDNA C230013L11 gene	unknown	other
-1.524	GOLIM4	golgi integral membrane protein 4	Cytoplasm	other

-1.524	KIF15	kinesin family member 15	Nucleus	other
-1.524	RSRC2	arginine/serine-rich coiled-coil 2	unknown	other
-1.524	SCAF4	SR-related CTD-associated factor 4	Nucleus	other
-1.524	VWC2L	von Willebrand factor C domain containing protein 2-like	Extracellular Space	other
-1.524	ZSWIM3	zinc finger, SWIM-type containing 3	unknown	other
-1.512	1700007K09Rik	RIKEN cDNA 1700007K09 gene	unknown	other
-1.512	FAM192A	family with sequence similarity 192, member A	Nucleus	other
-1.512	Nr2e1	nuclear receptor subfamily 2, group E, member 1	unknown	other
-1.512	SPAG9	sperm associated antigen 9	Plasma Membrane	other
-1.512	ZNF469	zinc finger protein 469	Nucleus	other
-2.081	ALPK3	alpha-kinase 3	Nucleus	kinase
-1.916	AATK	apoptosis-associated tyrosine kinase	Cytoplasm	kinase
-1.881	FXN	frataxin	Cytoplasm	kinase
-1.836	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	Cytoplasm	kinase
-1.818	ACVR1B	activin A receptor, type IB	Plasma Membrane	kinase
-1.708	EFNA4	ephrin-A4	Plasma Membrane	kinase
-1.700	TBCK	TBC1 domain containing kinase	unknown	kinase
-1.621	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	Nucleus	kinase
-1.591	IRAK2	interleukin-1 receptor-associated kinase 2	Plasma Membrane	kinase
-1.570	FRK	fyn-related kinase	Nucleus	kinase
-1.570	PHKB	phosphorylase kinase, beta	Cytoplasm	kinase
-1.926	GRID1	glutamate receptor, ionotropic, delta 1	Plasma Membrane	ion channel
-1.926	KCNIP4	Kv channel interacting protein 4	Plasma Membrane	ion channel
-1.848	GRIA3	glutamate receptor, ionotropic, AMPA 3	Plasma Membrane	ion channel
-1.787	TRPC3	transient receptor potential cation channel, subfamily C, member 3	Plasma Membrane	ion channel
-1.773	TMEM38B	transmembrane protein 38B	Nucleus	ion channel
-1.738	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6	Plasma Membrane	ion channel
-1.639	GLRA1	glycine receptor, alpha 1	Plasma Membrane	ion channel
-2.125	FGF23	fibroblast growth factor 23	Extracellular Space	growth factor
-1.683	BMP3	bone morphogenetic protein 3	Extracellular Space	growth factor
-2.212	Vmn1r81	vomeronasal 1 receptor 81	Plasma Membrane	G-protein coupled receptor
-2.087	Olfr1271/Olfr142	olfactory receptor 1271	Plasma Membrane	G-protein coupled receptor
-2.042	TM2D1	TM2 domain containing 1	Plasma Membrane	G-protein coupled receptor
-2.008	ADRB3	adrenoceptor beta 3	Plasma Membrane	G-protein coupled receptor
-1.949	OR4N5	olfactory receptor, family 4, subfamily N, member 5	Plasma Membrane	G-protein coupled receptor
-1.945	Olfr1080 (includes others)	olfactory receptor 1082	Plasma Membrane	G-protein coupled receptor
-1.912	Olfr1220	olfactory receptor 1220	Plasma Membrane	G-protein coupled receptor
-1.876	OPN1SW	opsin 1 (cone pigments), short-wave-sensitive	Plasma Membrane	G-protein coupled receptor
-1.842	Olfr1120	olfactory receptor 1120	Plasma Membrane	G-protein coupled receptor
-1.836	OPRK1	opioid receptor, kappa 1	Plasma Membrane	G-protein coupled receptor
-1.836	Vmn1r20/Vmn1r27	vomeronasal 1 receptor 27	Plasma Membrane	G-protein coupled receptor
-1.836	Vmn1r234	vomeronasal 1 receptor 234	Plasma Membrane	G-protein coupled receptor
-1.793	GHRHR	growth hormone releasing hormone receptor	Plasma Membrane	G-protein coupled receptor
-1.787	OR11A1	olfactory receptor, family 11, subfamily A, member 1	Plasma Membrane	G-protein coupled receptor
-1.780	TSHR	thyroid stimulating hormone receptor	Plasma Membrane	G-protein coupled receptor
-1.738	Olfr959	olfactory receptor 959	Plasma Membrane	G-protein coupled receptor
-1.731	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)	Plasma Membrane	G-protein coupled receptor
-1.708	CCR2	chemokine (C-C motif) receptor 2	Plasma Membrane	G-protein coupled receptor
-1.708	Olfr251/Olfr898	olfactory receptor 898	Plasma Membrane	G-protein coupled receptor
-1.708	Olfr672	olfactory receptor 672	Plasma Membrane	G-protein coupled receptor
-1.675	Olfr887	olfactory receptor 887	Plasma Membrane	G-protein coupled receptor
-1.666	ADORA2B	adenosine A2b receptor	Plasma Membrane	G-protein coupled receptor
-1.666	GPR77	G protein-coupled receptor 77	Plasma Membrane	G-protein coupled receptor
-1.648	Olfr1302	olfactory receptor 1302	Plasma Membrane	G-protein coupled receptor
-1.630	GPR61	G protein-coupled receptor 61	Plasma Membrane	G-protein coupled receptor
-1.630	Olfr262	olfactory receptor 262	Plasma Membrane	G-protein coupled receptor
-1.621	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	Plasma Membrane	G-protein coupled receptor
-1.611	Olfr1230	olfactory receptor 1230	Plasma Membrane	G-protein coupled receptor
-1.611	OR6C68	olfactory receptor, family 6, subfamily C, member 68	Plasma Membrane	G-protein coupled receptor
-1.601	Olfr1256	olfactory receptor 1256	Plasma Membrane	G-protein coupled receptor
-1.601	Vmn1r188 (includes others)	vomeronasal 1 receptor 217	Plasma Membrane	G-protein coupled receptor
-1.591	Olfr1242	olfactory receptor 1242	Plasma Membrane	G-protein coupled receptor
-1.591	Olfr951/Olfr954	olfactory receptor 954	Plasma Membrane	G-protein coupled receptor
-1.580	GPRC5B	G protein-coupled receptor, family C, group 5, member B	Plasma Membrane	G-protein coupled receptor
-1.570	Olfr116	olfactory receptor 116	Plasma Membrane	G-protein coupled receptor
-1.570	Olfr38	olfactory receptor 38	Plasma Membrane	G-protein coupled receptor
-1.570	OR14C36	olfactory receptor, family 14, subfamily C, member 36	Plasma Membrane	G-protein coupled receptor
-1.558	Olfr1364	olfactory receptor 1364	Plasma Membrane	G-protein coupled receptor
-1.547	OR11H6	olfactory receptor, family 11, subfamily H, member 6	Plasma Membrane	G-protein coupled receptor
-1.536	Olfr1301	olfactory receptor 1301	Plasma Membrane	G-protein coupled receptor
-1.512	OR7G2	olfactory receptor, family 7, subfamily G, member 2	Plasma Membrane	G-protein coupled receptor
-2.192	FBXO4	F-box protein 4	Nucleus	enzyme
-2.166	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	unknown	enzyme
-2.125	PYCRL	pyrroline-5-carboxylate reductase-like	unknown	enzyme
-2.107	DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	Cytoplasm	enzyme
-2.100	ANAPC10	anaphase promoting complex subunit 10	Nucleus	enzyme
-2.074	IDH3B	isocitrate dehydrogenase 3 (NAD+) beta	Cytoplasm	enzyme
-2.053	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	Plasma Membrane	enzyme
-2.050	FUT2	fucosyltransferase 2 (secretor status included)	Cytoplasm	enzyme
-2.050	RPP40	ribonuclease P/MRP 40kDa subunit	Nucleus	enzyme
-2.024	MGRN1	mahogunin ring finger 1, E3 ubiquitin protein ligase	Cytoplasm	enzyme
-1.992	Gsta4	glutathione S-transferase, alpha 4	Cytoplasm	enzyme
-1.992	RAD17	RAD17 homolog (S. pombe)	Nucleus	enzyme
-1.980	SRM	spermidine synthase	Cytoplasm	enzyme
-1.971	Rdh1 (includes others)	retinol dehydrogenase 1 (all trans)	Cytoplasm	enzyme
-1.949	AASS	aminoadipate-semialdehyde synthase	Cytoplasm	enzyme
-1.949	NAV1	neuron navigator 1	Cytoplasm	enzyme
-1.931	RNF144B	ring finger protein 144B	unknown	enzyme
-1.926	PLA2G12B	phospholipase A2, group XIIB	Extracellular Space	enzyme
-1.896	Ang2 (includes others)	angiogenin, ribonuclease A family, member 2	Cytoplasm	enzyme
-1.896	DHODH	dihydroorotate dehydrogenase (quinone)	Cytoplasm	enzyme
-1.891	TRMT61A	tRNA methyltransferase 61 homolog A (S. cerevisiae)	unknown	enzyme
-1.865	UBE2B	ubiquitin-conjugating enzyme E2B	Cytoplasm	enzyme
-1.854	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	Cytoplasm	enzyme
-1.842	CTPS1	CTP synthase 1	Nucleus	enzyme
-1.830	FADS2	fatty acid desaturase 2	Plasma Membrane	enzyme
-1.830	KDM1A	lysine (K)-specific demethylase 1A	Nucleus	enzyme
-1.812	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	Cytoplasm	enzyme
-1.812	NIT1	nitrilase 1	Cytoplasm	enzyme
-1.806	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	Cytoplasm	enzyme
-1.806	CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1	Cytoplasm	enzyme
-1.806	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	Cytoplasm	enzyme
-1.800	UQCRB	ubiquinol-cytochrome c reductase binding protein	Cytoplasm	enzyme
-1.793	AADAT	aminoadipate aminotransferase	Cytoplasm	enzyme
-1.793	HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	Cytoplasm	enzyme
-1.793	NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	Cytoplasm	enzyme
-1.793	TKT	transketolase	Cytoplasm	enzyme

-1.752	NAT8L	N-acetyltransferase 8-like (GCN5-related, putative)	Cytoplasm	enzyme
-1.752	PTBP1	polypyrimidine tract binding protein 1	Nucleus	enzyme
-1.752	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Cytoplasm	enzyme
-1.738	MSH3	mutS homolog 3 (E. coli)	Nucleus	enzyme
-1.731	ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	Nucleus	enzyme
-1.731	GBA2	glucosidase, beta (bile acid) 2	Cytoplasm	enzyme
-1.723	4933425L06Rik	RIKEN cDNA 4933425L06 gene	unknown	enzyme
-1.723	CASD1	CAS1 domain containing 1	Cytoplasm	enzyme
-1.723	Wrn	Werner syndrome	Nucleus	enzyme
-1.700	CYP46A1	cytochrome P450, family 46, subfamily A, polypeptide 1	Cytoplasm	enzyme
-1.700	DSEL	dermatan sulfate epimerase-like	Extracellular Space	enzyme
-1.700	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	Nucleus	enzyme
-1.692	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	Plasma Membrane	enzyme
-1.683	MYO5A	myosin VA (heavy chain 12, myoxin)	Cytoplasm	enzyme
-1.675	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	Plasma Membrane	enzyme
-1.675	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	Cytoplasm	enzyme
-1.675	RABGGTB	Rab geranylgeranyltransferase, beta subunit	Cytoplasm	enzyme
-1.666	Eci3	enoyl-Coenzyme A delta isomerase 3	unknown	enzyme
-1.666	EXOSC9	exosome component 9	Nucleus	enzyme
-1.666	PLCH2	phospholipase C, eta 2	Cytoplasm	enzyme
-1.658	PIGA	phosphatidylinositol glycan anchor biosynthesis, class A	Cytoplasm	enzyme
-1.648	HGD	homogentisate 1,2-dioxygenase	Cytoplasm	enzyme
-1.648	POLE2	polymerase (DNA directed), epsilon 2, accessory subunit	Nucleus	enzyme
-1.648	RAB5B	RAB5B, member RAS oncogene family	Cytoplasm	enzyme
-1.639	PLA2G10	phospholipase A2, group X	Cytoplasm	enzyme
-1.639	SETD6	SET domain containing 6	Nucleus	enzyme
-1.639	TPST2	tyrosylprotein sulfotransferase 2	Cytoplasm	enzyme
-1.630	MGRN1	mahogunin ring finger 1, E3 ubiquitin protein ligase	Cytoplasm	enzyme
-1.621	ALKBH3	alkB, alkylation repair homolog 3 (E. coli)	Nucleus	enzyme
-1.611	2810007J24Rik	RIKEN cDNA 2810007J24 gene	unknown	enzyme
-1.611	LDHAL6B	lactate dehydrogenase A-like 6B	Cytoplasm	enzyme
-1.611	Oas1d (includes others)	2'-5' oligoadenylate synthetase 1D	Cytoplasm	enzyme
-1.591	ADAT2	adenosine deaminase, tRNA-specific 2	unknown	enzyme
-1.580	CHD6	chromodomain helicase DNA binding protein 6	Nucleus	enzyme
-1.580	RAB18	RAB18, member RAS oncogene family	Cytoplasm	enzyme
-1.580	SUOX	sulfite oxidase	Cytoplasm	enzyme
-1.547	FBXL7	F-box and leucine-rich repeat protein 7	Cytoplasm	enzyme
-1.547	NANS	N-acetylneuraminic acid synthase	Cytoplasm	enzyme
-1.536	A1CF	APOBEC1 complementation factor	Nucleus	enzyme
-1.536	ACACB	acetyl-CoA carboxylase beta	Cytoplasm	enzyme
-1.536	DCLRE1C	DNA cross-link repair 1C	Nucleus	enzyme
-1.536	GPX2	glutathione peroxidase 2 (gastrointestinal)	Cytoplasm	enzyme
-1.536	POGLUT1	protein O-glucosyltransferase 1	Extracellular Space	enzyme
-1.536	RFWD3	ring finger and WD repeat domain 3	Nucleus	enzyme
-1.512	MPO	myeloperoxidase	Cytoplasm	enzyme
-2.077	CCL21	chemokine (C-C motif) ligand 21	Extracellular Space	cytokine
-1.865	IL36A	interleukin 36, alpha	Extracellular Space	cytokine
-1.630	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)	Extracellular Space	cytokine
-1.570	CCL27	chemokine (C-C motif) ligand 27	Extracellular Space	cytokine
-1.536	IL12B	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	Extracellular Space	cytokine

Appendix 8.
Gene properties identified in shRNA Group B

Log Ratio	Symbol	Entrez Gene Name	Location	Type(s)
-2.375	APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	Cytoplasm	transporter
-2.212	SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	Cytoplasm	transporter
-2.183	Lcn4	lipocalin 4	Extracellular Space	transporter
-2.178	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	Plasma Membrane	transporter
-2.096	SLC7A6	solute carrier family 7 (amino acid transporter light chain, y+L system), member 6	Plasma Membrane	transporter
-2.081	KLHL2	kelch-like 2, Mayven (Drosophila)	Cytoplasm	transporter
-2.078	COG1	component of oligomeric golgi complex 1	Cytoplasm	transporter
-2.066	NUP155	nucleoporin 155kDa	Nucleus	transporter
-2.022	MTX2	metaxin 2	Cytoplasm	transporter
-2.013	ABCB10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	Cytoplasm	transporter
-2.009	TNPO1	transportin 1	Nucleus	transporter
-1.948	WDR59	WD repeat domain 59	unknown	transporter
-1.900	SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	Plasma Membrane	transporter
-1.864	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	Cytoplasm	transporter
-1.846	ABCD1	ATP-binding cassette, sub-family D (ALD), member 1	Plasma Membrane	transporter
-1.833	Gja6	gap junction protein, alpha 6	Plasma Membrane	transporter
-1.812	ABCG8	ATP-binding cassette, sub-family G (WHITE), member 8	Plasma Membrane	transporter
-1.805	ATP5G3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	Cytoplasm	transporter
-1.761	HBZ	hemoglobin, zeta	Cytoplasm	transporter
-1.720	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	Cytoplasm	transporter
-1.703	NUP50	nucleoporin 50kDa	Nucleus	transporter
-1.703	TMED2	transmembrane emp24 domain trafficking protein 2	Cytoplasm	transporter
-1.694	ATP9B	ATPase, class II, type 9B	Cytoplasm	transporter
-1.676	COPB1	coatomer protein complex, subunit beta 1	Cytoplasm	transporter
-1.626	SLC36A4	solute carrier family 36 (proton/amino acid symporter), member 4	unknown	transporter
-1.593	SLC5A12	solute carrier family 5 (sodium/glucose cotransporter), member 12	unknown	transporter
-1.581	SLC9A8	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	Cytoplasm	transporter
-1.569	COMMD1	copper metabolism (Murr1) domain containing 1	Nucleus	transporter
-1.557	APOB	apolipoprotein B (including Ag(x) antigen)	Extracellular Space	transporter
-1.922	GFRA2	GDNF family receptor alpha 2	Plasma Membrane	transmembrane receptor
-1.916	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	Plasma Membrane	transmembrane receptor
-1.846	DMBT1	deleted in malignant brain tumors 1	Plasma Membrane	transmembrane receptor
-1.729	ANTXR2	anthrax toxin receptor 2	Plasma Membrane	transmembrane receptor
-1.685	IL15RA	interleukin 15 receptor, alpha	Plasma Membrane	transmembrane receptor
-1.636	PLA2R1	phospholipase A2 receptor 1, 180kDa	Plasma Membrane	transmembrane receptor
-1.615	CD302	CD302 molecule	Plasma Membrane	transmembrane receptor
-1.604	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	Plasma Membrane	transmembrane receptor
-1.581	LRP12	low density lipoprotein receptor-related protein 12	Plasma Membrane	transmembrane receptor
-1.504	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	Plasma Membrane	transmembrane receptor
-2.276	MRPL18	mitochondrial ribosomal protein L18	Cytoplasm	translation regulator
-2.130	IREB2	iron-responsive element binding protein 2	Cytoplasm	translation regulator
-1.544	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	Cytoplasm	translation regulator
-2.342	DAXX	death-domain associated protein	Nucleus	transcription regulator
-2.337	STAT2	signal transducer and activator of transcription 2, 113kDa	Nucleus	transcription regulator
-2.178	Ankrd61	ankyrin repeat domain 61	Nucleus	transcription regulator
-2.092	PLAGL2	pleiomorphic adenoma gene-like 2	Nucleus	transcription regulator
-2.042	MED24	mediator complex subunit 24	Nucleus	transcription regulator
-2.004	RCOR2	REST corepressor 2	Nucleus	transcription regulator
-1.937	NCOA3	nuclear receptor coactivator 3	Nucleus	transcription regulator
-1.932	ANKRD22	ankyrin repeat domain 22	Nucleus	transcription regulator
-1.882	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	Nucleus	transcription regulator
-1.882	OLIG1	oligodendrocyte transcription factor 1	Nucleus	transcription regulator
-1.846	Cmtm2a	CKLF-like MARVEL transmembrane domain containing 2A	Cytoplasm	transcription regulator
-1.846	SOX6	SRY (sex determining region Y)-box 6	Nucleus	transcription regulator
-1.769	NPAT	nuclear protein, ataxia-telangiectasia locus	Nucleus	transcription regulator
-1.761	SERTAD3	SERTA domain containing 3	Nucleus	transcription regulator
-1.753	SOX11	SRY (sex determining region Y)-box 11	Nucleus	transcription regulator
-1.745	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	Nucleus	transcription regulator
-1.694	RFXAP	regulatory factor X-associated protein	Nucleus	transcription regulator
-1.666	HOXA2	homeobox A2	Nucleus	transcription regulator
-1.656	DMRT2	doublesex and mab-3 related transcription factor 2	Nucleus	transcription regulator
-1.636	BTAF1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)	Nucleus	transcription regulator
-1.626	EED	embryonic ectoderm development	Nucleus	transcription regulator
-1.569	NFXL1	nuclear transcription factor, X-box binding-like 1	Nucleus	transcription regulator
-1.544	CDX2	caudal type homeobox 2	Nucleus	transcription regulator
-1.531	CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase	Nucleus	transcription regulator
-1.531	PIR	pirin (iron-binding nuclear protein)	Nucleus	transcription regulator
-1.518	HEXIM1	hexamethylene bis-acetamide inducible 1	Nucleus	transcription regulator
-2.140	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	Plasma Membrane	phosphatase
-1.982	WBP11	WW domain binding protein 11	Nucleus	phosphatase
-1.937	LPPR3	lipid phosphate phosphatase-related protein type 3	unknown	phosphatase
-1.833	PTPRB	protein tyrosine phosphatase, receptor type, B	Plasma Membrane	phosphatase
-1.826	EYA4	eyes absent homolog 4 (Drosophila)	Cytoplasm	phosphatase
-1.737	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	Plasma Membrane	phosphatase
-1.626	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	Plasma Membrane	phosphatase
-1.593	PPM1H	protein phosphatase, Mg2+/Mn2+ dependent, 1H	unknown	phosphatase
-2.223	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	Cytoplasm	peptidase
-2.147	DPP6	dipeptidyl-peptidase 6	Plasma Membrane	peptidase
-2.078	TMEM59	transmembrane protein 59	Plasma Membrane	peptidase
-2.050	PDIA3	protein disulfide isomerase family A, member 3	Cytoplasm	peptidase
-2.000	Ctsz	cathepsin Z	Cytoplasm	peptidase
-1.977	ADAM2	ADAM metallopeptidase domain 2	Plasma Membrane	peptidase
-1.791	ADAM23	ADAM metallopeptidase domain 23	Plasma Membrane	peptidase
-1.791	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	Cytoplasm	peptidase
-1.737	Tmprss11c	transmembrane protease, serine 11c	Plasma Membrane	peptidase
-1.694	USP34	ubiquitin specific peptidase 34	Extracellular Space	peptidase
-1.685	TRHDE	thyrotropin-releasing hormone degrading enzyme	Plasma Membrane	peptidase
-1.666	ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif, 14	Extracellular Space	peptidase
-1.615	KLK8	kallikrein-related peptidase 8	Extracellular Space	peptidase
-1.604	CASP14	caspase 14, apoptosis-related cysteine peptidase	Cytoplasm	peptidase
-1.593	ZFYVE9	zinc finger, FYVE domain containing 9	Cytoplasm	peptidase
-1.581	MYO1A	myosin IA	Cytoplasm	peptidase
-2.409	CDH18	cadherin 18, type 2	Plasma Membrane	other
-2.390	ZNF239	zinc finger protein 239	Nucleus	other
-2.375	A930012O16Rik	RIKEN cDNA A930012O16 gene	unknown	other
-2.337	MDM1	Mdm1 nuclear protein homolog (mouse)	unknown	other
-2.318	PI15	peptidase inhibitor 15	Extracellular Space	other
-2.299	KLHL10	kelch-like 10 (Drosophila)	Nucleus	other
-2.287	Gm9871	predicted gene 9871	unknown	other
-2.256	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Cytoplasm	other
-2.256	Zfp943	zinc finger prtoein 943	unknown	other
-2.254	Sval3	seminal vesicle antigen-like 3	unknown	other
-2.246	Gm4758	predicted gene 4758	unknown	other
-2.244	WDR13	WD repeat domain 13	Nucleus	other
-2.241	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	Cytoplasm	other
-2.236	LRRC37A3 (includes others)	leucine rich repeat containing 37, member A3	unknown	other
-2.236	TMCC3	transmembrane and coiled-coil domain family 3	unknown	other
-2.233	VPS8	vacuolar protein sorting 8 homolog (S. cerevisiae)	unknown	other
-2.231	ZFP14	ZFP14 zinc finger protein	Nucleus	other

-2.212	WDR52	WD repeat domain 52	Extracellular Space	other
-2.201	CCDC47	coiled-coil domain containing 47	Extracellular Space	other
-2.195	Gm4841	predicted gene 4841	unknown	other
-2.189	2700033N17Rik	RIKEN cDNA 2700033N17 gene	unknown	other
-2.183	Zcchc13	zinc finger, CCHC domain containing 13	unknown	other
-2.180	R3HDM2	R3H domain containing 2	Nucleus	other
-2.178	Timm8a2	translocase of inner mitochondrial membrane 8A2	Cytoplasm	other
-2.165	Ncrna00086	non-protein coding RNA 86	unknown	other
-2.162	HDX	highly divergent homeobox	unknown	other
-2.156	SETD5	SET domain containing 5	unknown	other
-2.153	KIAA1432	KIAA1432	unknown	other
-2.150	1700071K01Rik	RIKEN cDNA 1700071K01 gene	unknown	other
-2.144	TTC12	tetratricopeptide repeat domain 12	unknown	other
-2.140	TOPAZ1	testis and ovary specific PAZ domain containing 1	unknown	other
-2.137	MRPL47	mitochondrial ribosomal protein L47	Cytoplasm	other
-2.137	TBCE	tubulin folding cofactor E	Cytoplasm	other
-2.134	FAM46A	family with sequence similarity 46, member A	unknown	other
-2.134	ZNF623	zinc finger protein 623	Nucleus	other
-2.130	MED8	mediator complex subunit 8	Nucleus	other
-2.127	SRBD1	S1 RNA binding domain 1	unknown	other
-2.114	C130030J05	uncharacterized protein C130030J05	unknown	other
-2.106	IL34	interleukin 34	Extracellular Space	other
-2.096	ANO3	anoctamin 3	unknown	other
-2.085	Dpcr1	diffuse panbronchiolitis critical region 1	unknown	other
-2.074	Gm16440 (includes others)	predicted gene 16440	unknown	other
-2.074	Pin1-ps1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1, pseudogene 1	unknown	other
-2.066	STBD1	starch binding domain 1	Cytoplasm	other
-2.066	WDR44	WD repeat domain 44	Cytoplasm	other
-2.058	CST5	cystatin D	Cytoplasm	other
-2.054	Cd24a	CD24a antigen	Plasma Membrane	other
-2.050	6030498E09Rik	RIKEN cDNA 6030498E09 gene	unknown	other
-2.050	THEMIS	thymocyte selection associated	Cytoplasm	other
-2.042	C5orf24	chromosome 5 open reading frame 24	unknown	other
-2.038	RGS2	regulator of G-protein signaling 2, 24kDa	Nucleus	other
-2.026	TOX	thymocyte selection-associated high mobility group box	Nucleus	other
-2.013	IMPACT	impact RWD domain protein	unknown	other
-2.013	NLRP1	NLR family, pyrin domain containing 1	Cytoplasm	other
-2.009	1700110C19Rik	RIKEN cDNA 1700110C19 gene	unknown	other
-2.009	ZBTB20	zinc finger and BTB domain containing 20	Nucleus	other
-2.004	IRAK1BP1	interleukin-1 receptor-associated kinase 1 binding protein 1	unknown	other
-2.004	UNC13B	unc-13 homolog B (C. elegans)	Cytoplasm	other
-1.995	CCDC86	coiled-coil domain containing 86	Nucleus	other
-1.991	KIAA1841	KIAA1841	unknown	other
-1.986	PLXDC2	plexin domain containing 2	Extracellular Space	other
-1.986	WDR66	WD repeat domain 66	unknown	other
-1.977	TXLNG	taxilin gamma	Nucleus	other
-1.972	SRPX	sushi-repeat containing protein, X-linked	Cytoplasm	other
-1.967	1700061I17Rik	RIKEN cDNA 1700061I17 gene	unknown	other
-1.967	CCDC87	coiled-coil domain containing 87	Extracellular Space	other
-1.967	OSBPL10	oxysterol binding protein-like 10	unknown	other
-1.967	TSPAN11	tetraspanin 11	unknown	other
-1.962	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	Nucleus	other
-1.962	Gm4910	predicted pseudogene 4910	unknown	other
-1.958	RSPH6A	radial spoke head 6 homolog A (Chlamydomonas)	Extracellular Space	other
-1.958	TOR1AIP2	torsin A interacting protein 2	Cytoplasm	other
-1.953	KRTAP13-2	keratin associated protein 13-2	unknown	other
-1.948	SPATS2L	spermatogenesis associated, serine-rich 2-like	unknown	other
-1.948	TRMT5	tRNA methyltransferase 5 homolog (S. cerevisiae)	unknown	other
-1.942	CNKSR2	connector enhancer of kinase suppressor of Ras 2	Plasma Membrane	other
-1.942	GCFC1	GC-rich sequence DNA-binding factor 1	Nucleus	other
-1.937	HEATR1	HEAT repeat containing 1	Nucleus	other
-1.932	DOCK2	dedicator of cytokinesis 2	Cytoplasm	other
-1.927	EMB	embigin	Plasma Membrane	other
-1.922	FAM167B	family with sequence similarity 167, member B	unknown	other
-1.916	Gm4861	predicted gene 4861	unknown	other
-1.916	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	Cytoplasm	other
-1.911	CCNY	cyclin Y	Nucleus	other
-1.911	KLC2	kinesin light chain 2	Cytoplasm	other
-1.911	MAGEB4	melanoma antigen family B, 4	Cytoplasm	other
-1.911	PHOSPHO2	phosphatase, orphan 2	unknown	other
-1.905	C16orf87	chromosome 16 open reading frame 87	unknown	other
-1.900	C19orf66	chromosome 19 open reading frame 66	unknown	other
-1.894	2310002L09Rik	RIKEN cDNA 2310002L09 gene	Cytoplasm	other
-1.894	App	amyloid beta (A4) precursor protein	Plasma Membrane	other
-1.888	1100001G20Rik	RIKEN cDNA 1100001G20 gene	Extracellular Space	other
-1.888	RNF222	ring finger protein 222	unknown	other
-1.882	Gm5068	predicted gene 5068	unknown	other
-1.882	INTS5	integrator complex subunit 5	Nucleus	other
-1.882	TRIM65	tripartite motif containing 65	unknown	other
-1.876	CCDC111	coiled-coil domain containing 111	Extracellular Space	other
-1.876	DNAJB8	DnaJ (Hsp40) homolog, subfamily B, member 8	unknown	other
-1.876	IQCG	IQ motif containing G	unknown	other
-1.870	KLHL30	kelch-like 30 (Drosophila)	unknown	other
-1.864	APLN	apelin	Extracellular Space	other
-1.864	FAM214A	family with sequence similarity 214, member A	unknown	other
-1.858	OLFM4	olfactomedin 4	Extracellular Space	other
-1.852	AFAP1L2	actin filament associated protein 1-like 2	Cytoplasm	other
-1.852	EFHC2	EF-hand domain (C-terminal) containing 2	unknown	other
-1.852	GLT25D1	glycosyltransferase 25 domain containing 1	Cytoplasm	other
-1.852	SAMD7	sterile alpha motif domain containing 7	unknown	other
-1.846	CLPS	colipase, pancreatic	Extracellular Space	other
-1.833	MRPS18A	mitochondrial ribosomal protein S18A	Cytoplasm	other
-1.833	POLDIP2	polymerase (DNA-directed), delta interacting protein 2	Nucleus	other
-1.833	TLCD2	TLC domain containing 2	unknown	other
-1.826	ANKRD13C	ankyrin repeat domain 13C	Cytoplasm	other
-1.819	BHLHB9	basic helix-loop-helix domain containing, class B, 9	unknown	other
-1.819	Gm10696 (includes others)	TD and POZ domain containing 3	unknown	other
-1.819	SCAMP5	secretory carrier membrane protein 5	Cytoplasm	other
-1.812	CCDC83	coiled-coil domain containing 83	unknown	other
-1.812	Foxk2	forkhead box K2	unknown	other
-1.812	SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	Nucleus	other
-1.805	1300015D01Rik	RIKEN cDNA 1300015D01 gene	unknown	other
-1.805	6330531I01Rik	RIKEN cDNA 6330531I01 gene	unknown	other
-1.805	9530004P13Rik	RIKEN cDNA 9530004P13 gene	unknown	other
-1.805	EFCAB3	EF-hand calcium binding domain 3	unknown	other
-1.805	Gm12108	predicted gene 12108	unknown	other
-1.805	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	Cytoplasm	other
-1.805	PORCN	porcupine homolog (Drosophila)	Cytoplasm	other
-1.798	4930539M17Rik	RIKEN cDNA 4930539M17 gene	unknown	other
-1.791	Cd163l1	CD163 molecule-like 1	Plasma Membrane	other
-1.791	FREM2	FRAS1 related extracellular matrix protein 2	Extracellular Space	other
-1.791	Pcdhb4	protocadherin beta 4	Plasma Membrane	other
-1.791	WDR55	WD repeat domain 55	Nucleus	other
-1.784	ADAP1	ArfGAP with dual PH domains 1	Nucleus	other
-1.784	KRTAP7-1	keratin associated protein 7-1 (gene/pseudogene)	unknown	other
-1.776	ABLIM1	actin binding LIM protein 1	Cytoplasm	other
-1.769	C10orf35	chromosome 10 open reading frame 35	unknown	other

-1.769	CAPS2	calcyphosine 2	unknown	other
-1.769	DXBay18 (includes others)	predicted pseudogene 5639	unknown	other
-1.769	SPRY3	sprouty homolog 3 (Drosophila)	Plasma Membrane	other
-1.769	TMEM9	transmembrane protein 9	Cytoplasm	other
-1.761	AIF1L	allograft inflammatory factor 1-like	Plasma Membrane	other
-1.761	Zfp52	zinc finger protein 52	unknown	other
-1.761	ZNF862	zinc finger protein 862	unknown	other
-1.753	BOP1	block of proliferation 1	Nucleus	other
-1.753	CCNJ	cyclin J	Nucleus	other
-1.753	HIGD1B	HIG1 hypoxia inducible domain family, member 1B	unknown	other
-1.753	MOB3B	MOB kinase activator 3B	unknown	other
-1.753	Nlrp9a/Nlrp9c	NLR family, pyrin domain containing 9A	unknown	other
-1.745	Gm4832	predicted gene 4832	unknown	other
-1.745	SHC2	SHC (Src homology 2 domain containing) transforming protein 2	Cytoplasm	other
-1.737	CENPE	centromere protein E, 312kDa	Nucleus	other
-1.737	NF2	neurofibromin 2 (merlin)	Plasma Membrane	other
-1.737	TMEM87A	transmembrane protein 87A	unknown	other
-1.729	Dlec1	deleted in lung and esophageal cancer 1 isoform DLEC1-N1	Cytoplasm	other
-1.720	GLIPR1L2	GLI pathogenesis-related 1 like 2	Extracellular Space	other
-1.712	ASIP	agouti signaling protein	Extracellular Space	other
-1.712	Fam169b	family with sequence similarity 169, member B	unknown	other
-1.712	Mfi2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	unknown	other
-1.712	SGOL1	shugoshin-like 1 (S. pombe)	Nucleus	other
-1.712	SLC38A9	solute carrier family 38, member 9	Extracellular Space	other
-1.703	FANCF	Fanconi anemia, complementation group F	Nucleus	other
-1.703	NGRN	neugrin, neurite outgrowth associated	Nucleus	other
-1.703	QSER1	glutamine and serine rich 1	unknown	other
-1.703	SEMA4G	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	Plasma Membrane	other
-1.703	Zfp874a	zinc finger protein 874a	unknown	other
-1.703	ZNF426	zinc finger protein 426	Nucleus	other
-1.694	4930433I11Rik	RIKEN cDNA 4930433I11 gene	unknown	other
-1.694	CADPS2	Ca++-dependent secretion activator 2	Plasma Membrane	other
-1.694	CTTNBP2	cortactin binding protein 2	Cytoplasm	other
-1.694	HARBI1	harbinger transposase derived 1	Cytoplasm	other
-1.694	TSPAN5	tetraspanin 5	Plasma Membrane	other
-1.685	XKRX	XK, Kell blood group complex subunit-related, X-linked	unknown	other
-1.676	ACBD7	acyl-CoA binding domain containing 7	unknown	other
-1.676	ARFIP1	ADP-ribosylation factor interacting protein 1	Cytoplasm	other
-1.676	BPIFB1	BPI fold containing family B, member 1	Extracellular Space	other
-1.676	Dhrs7/LOC690226	dehydrogenase/reductase (SDR family) member 7	unknown	other
-1.676	SAMD8	sterile alpha motif domain containing 8	Cytoplasm	other
-1.666	CCDC38	coiled-coil domain containing 38	unknown	other
-1.666	COA4	cytochrome c oxidase assembly factor 4 homolog (S. cerevisiae)	unknown	other
-1.666	DEFB106A/DEFB106B	defensin, beta 106A	Extracellular Space	other
-1.666	NEXN	nexilin (F actin binding protein)	Plasma Membrane	other
-1.656	C8orf4	chromosome 8 open reading frame 4	unknown	other
-1.656	CLDN11	claudin 11	Plasma Membrane	other
-1.656	Gm4836 (includes others)	predicted gene 4836	Cytoplasm	other
-1.646	4930438A08Rik	RIKEN cDNA 4930438A08 gene	unknown	other
-1.646	CCDC171	coiled-coil domain containing 171	unknown	other
-1.646	CNIH2	cornichon homolog 2 (Drosophila)	Extracellular Space	other
-1.646	EAPP	E2F-associated phosphoprotein	Cytoplasm	other
-1.646	KBTBD3	kelch repeat and BTB (POZ) domain containing 3	Extracellular Space	other
-1.646	SPINT2	serine peptidase inhibitor, Kunitz type, 2	Extracellular Space	other
-1.636	6430628N08Rik	RIKEN cDNA 6430628N08 gene	unknown	other
-1.636	Ankmy1	ankyrin repeat and MYND domain containing 1	unknown	other
-1.626	ACTN1	actinin, alpha 1	Cytoplasm	other
-1.626	FAM57B	family with sequence similarity 57, member B	Cytoplasm	other
-1.615	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta	Nucleus	other
-1.615	Igfl3	IGF-like family member 3	Extracellular Space	other
-1.615	KRT17	keratin 17	Cytoplasm	other
-1.615	NANOS3	nanos homolog 3 (Drosophila)	unknown	other
-1.615	UBFD1	ubiquitin family domain containing 1	unknown	other
-1.615	WDR61	WD repeat domain 61	unknown	other
-1.604	Efcab4a	EF-hand calcium binding domain 4A	Cytoplasm	other
-1.604	FRMD5	FERM domain containing 5	unknown	other
-1.604	Nkx6-3	NK6 homeobox 3	unknown	other
-1.604	TMEM26	transmembrane protein 26	unknown	other
-1.593	C3orf20	chromosome 3 open reading frame 20	Cytoplasm	other
-1.593	Map3k5	mitogen-activated protein kinase kinase kinase 5	Cytoplasm	other
-1.581	4930562A09Rik	RIKEN cDNA 4930562A09 gene	unknown	other
-1.581	Ajap1	adherens junction associated protein 1	unknown	other
-1.581	CCNE2	cyclin E2	Nucleus	other
-1.581	CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	Plasma Membrane	other
-1.581	TRAPPC1	trafficking protein particle complex 1	Cytoplasm	other
-1.581	U90926	cDNA sequence U90926	unknown	other
-1.569	FAM98B	family with sequence similarity 98, member B	unknown	other
-1.569	MCAM	melanoma cell adhesion molecule	Plasma Membrane	other
-1.569	SH3D19	SH3 domain containing 19	Plasma Membrane	other
-1.557	YRDC	yrdC domain containing (E. coli)	unknown	other
-1.557	ZDHHC12	zinc finger, DHHC-type containing 12	unknown	other
-1.544	Cd99	CD99 antigen	unknown	other
-1.544	KRT222	keratin 222	unknown	other
-1.531	1700024P12Rik	RIKEN cDNA 1700024P12 gene	unknown	other
-1.531	4931440L10Rik	RIKEN cDNA 4931440L10 gene	unknown	other
-1.531	Fam48b1/LOC367830	family with sequence similarity 48, member B1	unknown	other
-1.531	KLHL31	kelch-like 31 (Drosophila)	unknown	other
-1.531	NCAPH2	non-SMC condensin II complex, subunit H2	Nucleus	other
-1.531	OIP5	Opa interacting protein 5	Nucleus	other
-1.531	SLC35G2	solute carrier family 35, member G2	Cytoplasm	other
-1.531	SMIM14	small integral membrane protein 14	unknown	other
-1.531	Tsc22d3	TSC22 domain family, member 3	Nucleus	other
-1.518	4930504O13Rik	RIKEN cDNA 4930504O13 gene	unknown	other
-1.518	BOLA3	bolA homolog 3 (E. coli)	unknown	other
-1.518	C11orf63	chromosome 11 open reading frame 63	unknown	other
-1.518	PALMD	palmdelphin	Cytoplasm	other
-1.504	C2orf74	chromosome 2 open reading frame 74	unknown	other
-1.504	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	Cytoplasm	other
-1.504	Sprr2f	small proline-rich protein 2F	Cytoplasm	other
-1.504	TCP11L1	t-complex 11, testis-specific-like 1	Cytoplasm	other
-1.504	Vsig1	V-set and immunoglobulin domain containing 1	Plasma Membrane	other
-1.504	ZC3H14	zinc finger CCCH-type containing 14	Nucleus	other
-2.209	PFKL	phosphofructokinase, liver	Cytoplasm	kinase
-2.050	CCNK	cyclin K	Nucleus	kinase
-2.030	UCK2	uridine-cytidine kinase 2	Cytoplasm	kinase
-2.017	CSNK2B	casein kinase 2, beta polypeptide	Cytoplasm	kinase
-1.962	MAST1	microtubule associated serine/threonine kinase 1	Cytoplasm	kinase
-1.948	SRP72	signal recognition particle 72kDa	Nucleus	kinase
-1.942	TYK2	tyrosine kinase 2	Plasma Membrane	kinase
-1.927	AK3	adenylate kinase 3	Cytoplasm	kinase
-1.894	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	Cytoplasm	kinase
-1.852	PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta	Cytoplasm	kinase
-1.812	PRKCI	protein kinase C, iota	Cytoplasm	kinase
-1.791	FGFR2	fibroblast growth factor receptor 2	Plasma Membrane	kinase
-1.666	AGK	acylglycerol kinase	Cytoplasm	kinase
-1.656	AKT2	v-akt murine thymoma viral oncogene homolog 2	Cytoplasm	kinase
-1.593	MYLK	myosin light chain kinase	Cytoplasm	kinase

-1.581	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	Cytoplasm	kinase
-1.569	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Plasma Membrane	kinase
-1.569	TK2	thymidine kinase 2, mitochondrial	Cytoplasm	kinase
-1.531	CAMK4	calcium/calmodulin-dependent protein kinase IV	Nucleus	kinase
-2.331	GRIA1	glutamate receptor, ionotropic, AMPA 1	Plasma Membrane	ion channel
-2.278	ITPR2	inositol 1,4,5-trisphosphate receptor, type 2	Cytoplasm	ion channel
-2.276	TPCN1	two pore segment channel 1	Plasma Membrane	ion channel
-2.130	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	Plasma Membrane	ion channel
-2.127	KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2	Plasma Membrane	ion channel
-2.124	MCOLN1	mucolipin 1	Cytoplasm	ion channel
-2.120	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	Plasma Membrane	ion channel
-2.089	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	Plasma Membrane	ion channel
-2.070	ITPR1	inositol 1,4,5-trisphosphate receptor, type 1	Cytoplasm	ion channel
-1.962	SLC9A1	solute carrier family 9, subfamily A (NHE1, cation proton antiporter 1), member 1	Plasma Membrane	ion channel
-1.900	KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	Plasma Membrane	ion channel
-1.864	CLCN6	chloride channel, voltage-sensitive 6	Plasma Membrane	ion channel
-1.504	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3	Plasma Membrane	ion channel
-2.294	OR10J1	olfactory receptor, family 10, subfamily J, member 1	Plasma Membrane	G-protein coupled receptor
-2.228	Vmn1r188 (includes others)	vomeronasal 1 receptor 217	Plasma Membrane	G-protein coupled receptor
-2.186	TAAR6	trace amine associated receptor 6	Plasma Membrane	G-protein coupled receptor
-2.089	CCKBR	cholecystokinin B receptor	Plasma Membrane	G-protein coupled receptor
-2.054	EMR4P	egf-like module containing, mucin-like, hormone receptor-like 4 pseudogene	Plasma Membrane	G-protein coupled receptor
-2.050	Olfr902	olfactory receptor 902	Plasma Membrane	G-protein coupled receptor
-2.050	Vmn1r188 (includes others)	vomeronasal 1 receptor 217	Plasma Membrane	G-protein coupled receptor
-2.013	Vmn1r32	vomeronasal 1 receptor 32	Plasma Membrane	G-protein coupled receptor
-1.982	Olfr1128	olfactory receptor 1128	Plasma Membrane	G-protein coupled receptor
-1.953	Olfr103	olfactory receptor 103	Plasma Membrane	G-protein coupled receptor
-1.942	LTB4R2	leukotriene B4 receptor 2	Plasma Membrane	G-protein coupled receptor
-1.911	Olfr690	olfactory receptor 690	Plasma Membrane	G-protein coupled receptor
-1.864	Agtr1b	angiotensin II receptor, type 1b	Plasma Membrane	G-protein coupled receptor
-1.846	OR5B17	olfactory receptor, family 5, subfamily B, member 17	Plasma Membrane	G-protein coupled receptor
-1.826	Olfr906	olfactory receptor 906	Plasma Membrane	G-protein coupled receptor
-1.819	Olfr1451	olfactory receptor 1451	Plasma Membrane	G-protein coupled receptor
-1.805	Vmn1r227	vomeronasal 1 receptor 227	Plasma Membrane	G-protein coupled receptor
-1.776	Olfr820	olfactory receptor 820	Plasma Membrane	G-protein coupled receptor
-1.745	Olfr1461	olfactory receptor 1461	Plasma Membrane	G-protein coupled receptor
-1.685	OR52E2	olfactory receptor, family 52, subfamily E, member 2	Plasma Membrane	G-protein coupled receptor
-1.544	OPN5	opsin 5	Plasma Membrane	G-protein coupled receptor
-1.518	PTGER3	prostaglandin E receptor 3 (subtype EP3)	Plasma Membrane	G-protein coupled receptor
-1.504	Vmn1r74/Vmn1r76	vomeronasal 1 receptor 76	Plasma Membrane	G-protein coupled receptor
-2.356	FBXO10	F-box protein 10	Cytoplasm	enzyme
-2.280	RAB9A	RAB9A, member RAS oncogene family	Cytoplasm	enzyme
-2.266	UBE2O	ubiquitin-conjugating enzyme E2O	unknown	enzyme
-2.264	NOS3	nitric oxide synthase 3 (endothelial cell)	Cytoplasm	enzyme
-2.231	DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	Nucleus	enzyme
-2.217	HIF1AN	hypoxia inducible factor 1, alpha subunit inhibitor	Nucleus	enzyme
-2.201	ARG1	arginase, liver	Cytoplasm	enzyme
-2.127	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	Nucleus	enzyme
-2.103	HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	Cytoplasm	enzyme
-2.066	OCLN	occludin	Plasma Membrane	enzyme
-2.058	DPYS	dihydropyrimidinase	Cytoplasm	enzyme
-2.058	RLIM	ring finger protein, LIM domain interacting	Nucleus	enzyme
-2.058	TGM5	transglutaminase 5	Cytoplasm	enzyme
-2.054	XDH	xanthine dehydrogenase	Cytoplasm	enzyme
-2.046	ALOX12B	arachidonate 12-lipoxygenase, 12R type	unknown	enzyme
-2.042	METTL22	methyltransferase like 22	unknown	enzyme
-2.026	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	Cytoplasm	enzyme
-2.022	Akr1c20	aldo-keto reductase family 1, member C20	unknown	enzyme
-2.022	TTLL8	tubulin tyrosine ligase-like family, member 8	Extracellular Space	enzyme
-2.009	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	Cytoplasm	enzyme
-2.009	LMO7	LIM domain 7	Cytoplasm	enzyme
-2.004	RBBP6	retinoblastoma binding protein 6	Nucleus	enzyme
-1.962	UBE2E1	ubiquitin-conjugating enzyme E2E 1	Cytoplasm	enzyme
-1.958	DDX25	DEAD (Asp-Glu-Ala-Asp) box helicase 25	Nucleus	enzyme
-1.932	NAA16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	Nucleus	enzyme
-1.911	AMDHD1	amidohydrolase domain containing 1	Cytoplasm	enzyme
-1.911	FKBP11	FK506 binding protein 11, 19 kDa	Cytoplasm	enzyme
-1.911	SMPD2	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	Cytoplasm	enzyme
-1.882	COX7B	cytochrome c oxidase subunit VIIb	Cytoplasm	enzyme
-1.876	HINT1	histidine triad nucleotide binding protein 1	Nucleus	enzyme
-1.858	HPSE	heparanase	Plasma Membrane	enzyme
-1.852	ERP44	endoplasmic reticulum protein 44	Cytoplasm	enzyme
-1.846	APLF	aprataxin and PNKP like factor	Cytoplasm	enzyme
-1.839	ENTPD8	ectonucleoside triphosphate diphosphohydrolase 8	unknown	enzyme
-1.833	MCM3	minichromosome maintenance complex component 3	Nucleus	enzyme
-1.826	GPLD1	glycosylphosphatidylinositol specific phospholipase D1	Cytoplasm	enzyme
-1.826	OTUD5	OTU domain containing 5	Cytoplasm	enzyme
-1.812	RNF5	ring finger protein 5, E3 ubiquitin protein ligase	Cytoplasm	enzyme
-1.798	PLTP	phospholipid transfer protein	Extracellular Space	enzyme
-1.798	WARS	tryptophanyl-tRNA synthetase	Cytoplasm	enzyme
-1.776	Nat3	N-acetyltransferase 3	Cytoplasm	enzyme
-1.776	OAT	ornithine aminotransferase	Cytoplasm	enzyme
-1.769	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	Cytoplasm	enzyme
-1.745	AGBL2	ATP/GTP binding protein-like 2	Cytoplasm	enzyme
-1.737	SBNO1	strawberry notch homolog 1 (Drosophila)	unknown	enzyme
-1.729	SMYD3	SET and MYND domain containing 3	Nucleus	enzyme
-1.720	CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22	Cytoplasm	enzyme
-1.703	BRAF	v-raf murine sarcoma viral oncogene homolog B1	Cytoplasm	enzyme
-1.694	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	Cytoplasm	enzyme
-1.676	EXT1	exostosin 1	Cytoplasm	enzyme
-1.636	Cyp2c40 (includes others)	cytochrome P450, family 2, subfamily c, polypeptide 40	Cytoplasm	enzyme
-1.636	HADHA	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	Cytoplasm	enzyme
-1.626	RAB3B	RAB3B, member RAS oncogene family	Cytoplasm	enzyme
-1.615	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	Nucleus	enzyme
-1.615	FBXO21	F-box protein 21	Extracellular Space	enzyme
-1.604	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	Nucleus	enzyme
-1.604	UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	Cytoplasm	enzyme
-1.593	RAB34	RAB34, member RAS oncogene family	Cytoplasm	enzyme
-1.531	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	Cytoplasm	enzyme
-1.518	MAT2B	methionine adenosyltransferase II, beta	Cytoplasm	enzyme
-1.518	POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	Nucleus	enzyme
-1.504	ALAS2	aminolevulinate, delta-, synthase 2	Cytoplasm	enzyme
-2.254	Il3	interleukin 3	Extracellular Space	cytokine
-2.192	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	Extracellular Space	cytokine
-1.932	SPP1	secreted phosphoprotein 1	Extracellular Space	cytokine
-1.776	IL36G	interleukin 36, gamma	Extracellular Space	cytokine
-1.531	DKK3	dickkopf 3 homolog (Xenopus laevis)	Extracellular Space	cytokine

Appendix 8.
Gene properties identified in shRNA Group C

Log Ratio	Symbol	Entrez Gene Name	Location	Type(s)
-1.898	Lcn3	lipocalin 3	Extracellular Space	transporter
-1.845	COPA	coatomer protein complex, subunit alpha	Cytoplasm	transporter
-1.639	TAPBP	TAP binding protein (tapasin)	Cytoplasm	transporter
-1.590	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	Plasma Membrane	transporter
-1.550	ATP13A2	ATPase type 13A2	Cytoplasm	transporter
-1.536	SLCO5A1	solute carrier organic anion transporter family, member 5A1	unknown	transporter
-1.521	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	Cytoplasm	transporter
-1.731	IL1RL1	interleukin 1 receptor-like 1	Plasma Membrane	transmembrane receptor
-1.682	LY96	lymphocyte antigen 96	Plasma Membrane	transmembrane receptor
-1.627	GPC4	glypican 4	Plasma Membrane	transmembrane receptor
-1.521	F3	coagulation factor III (thromboplastin, tissue factor)	Plasma Membrane	transmembrane receptor
-1.521	Klra4 (includes others)	killer cell lectin-like receptor, subfamily A, member 4	Plasma Membrane	transmembrane receptor
-1.879	PAIP2B	poly(A) binding protein interacting protein 2B	unknown	translation regulator
-1.911	FOXN2	forkhead box N2	Nucleus	transcription regulator
-1.722	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	Nucleus	transcription regulator
-1.577	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	Nucleus	transcription regulator
-1.521	Zfp125	zinc finger protein 125	Nucleus	transcription regulator
-1.506	CREBL2	cAMP responsive element binding protein-like 2	Nucleus	transcription regulator
-1.506	DEPDC1	DEP domain containing 1	Nucleus	transcription regulator
-1.792	DUSP19	dual specificity phosphatase 19	Cytoplasm	phosphatase
-1.603	PGAM1	phosphoglycerate mutase 1 (brain)	Cytoplasm	phosphatase
-1.506	MTMR3	myotubularin related protein 3	Cytoplasm	phosphatase
-1.521	MMP25	matrix metallopeptidase 25	Extracellular Space	peptidase
-1.521	PMPCA	peptidase (mitochondrial processing) alpha	Cytoplasm	peptidase
-2.334	4933430L12Rik	RIKEN cDNA 4933430L12 gene	unknown	other
-1.911	MYO15A	myosin XVA	Cytoplasm	other
-1.815	ZBTB40	zinc finger and BTB domain containing 40	Nucleus	other
-1.808	PALLD	palladin, cytoskeletal associated protein	Cytoplasm	other
-1.775	CABIN1	calcineurin binding protein 1	Nucleus	other
-1.758	TCP11	t-complex 11, testis-specific	unknown	other
-1.731	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	Plasma Membrane	other
-1.722	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	Nucleus	other
-1.703	KCNQ1OT1	KCNQ1 opposite strand/antisense transcript 1 (non-protein coding)	unknown	other
-1.693	KLHL5	kelch-like 5 (Drosophila)	Extracellular Space	other
-1.682	XXYLT1	xyloside xylosyltransferase 1	unknown	other
-1.672	PPP2R3C	protein phosphatase 2, regulatory subunit B'', gamma	Cytoplasm	other
-1.650	5830426C09Rik	RIKEN cDNA 5830426C09 gene	unknown	other
-1.650	IQUB	IQ motif and ubiquitin domain containing	Cytoplasm	other
-1.627	DDIT4L	DNA-damage-inducible transcript 4-like	Cytoplasm	other
-1.615	ODF3L2	outer dense fiber of sperm tails 3-like 2	unknown	other
-1.615	WDR33	WD repeat domain 33	Nucleus	other
-1.603	2210404O09Rik/Zfp947	RIKEN cDNA 2210404O09 gene	unknown	other
-1.603	MRPL15	mitochondrial ribosomal protein L15	Cytoplasm	other
-1.590	IFT74	intraflagellar transport 74 homolog (Chlamydomonas)	Cytoplasm	other
-1.577	GCC1	GRIP and coiled-coil domain containing 1	Cytoplasm	other
-1.577	NAIP	NLR family, apoptosis inhibitory protein	unknown	other
-1.577	SELV	selenoprotein V	unknown	other
-1.577	SPATA7	spermatogenesis associated 7	unknown	other
-1.577	SPG20	spastic paraplegia 20 (Troyer syndrome)	Cytoplasm	other
-1.564	B230369F24Rik	RIKEN cDNA B230369F24 gene	unknown	other
-1.564	CCDC138	coiled-coil domain containing 138	unknown	other
-1.564	DCHS1	dachsous 1 (Drosophila)	Plasma Membrane	other
-1.564	GORAB	golgin, RAB6-interacting	Cytoplasm	other
-1.564	LRRC3B	leucine rich repeat containing 3B	unknown	other
-1.550	C6orf106	chromosome 6 open reading frame 106	unknown	other
-1.550	Dhrs11	dehydrogenase/reductase (SDR family) member 11	unknown	other
-1.550	LRRC66	leucine rich repeat containing 66	unknown	other
-1.550	MAK16	MAK16 homolog (S. cerevisiae)	Nucleus	other
-1.550	SPTBN2	spectrin, beta, non-erythrocytic 2	Cytoplasm	other
-1.550	TTC28	tetratricopeptide repeat domain 28	unknown	other
-1.536	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	Cytoplasm	other
-1.536	EFCAB2	EF-hand calcium binding domain 2	unknown	other
-1.536	EFR3B	EFR3 homolog B (S. cerevisiae)	unknown	other
-1.536	FAM19A2	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	Cytoplasm	other
-1.536	KIAA0101	KIAA0101	Nucleus	other
-1.521	ATXN7L3B	ataxin 7-like 3B	unknown	other
-1.521	NMD3	NMD3 homolog (S. cerevisiae)	Nucleus	other
-1.521	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	Plasma Membrane	other
-1.521	ZNF764	zinc finger protein 764	unknown	other
-1.506	BICD1	bicaudal D homolog 1 (Drosophila)	Cytoplasm	other
-1.506	C8orf37	chromosome 8 open reading frame 37	unknown	other
-1.506	DLGAP1	discs, large (Drosophila) homolog-associated protein 1	Plasma Membrane	other
-1.506	DNAI1	dynein, axonemal, intermediate chain 1	Extracellular Space	other
-1.506	ESYT3	extended synaptotagmin-like protein 3	unknown	other
-1.506	PRR13	proline rich 13	Nucleus	other
-1.506	Vmn2r88 (includes others)	vomeronasal 2, receptor 88	unknown	other
-1.750	FLT1	fms-related tyrosine kinase 1	Plasma Membrane	kinase
-1.731	FN3KRP	fructosamine 3 kinase related protein	unknown	kinase
-1.603	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	Cytoplasm	kinase
-1.815	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	Plasma Membrane	ion channel
-1.792	CATSPER3	cation channel, sperm associated 3	unknown	ion channel
-1.682	SCN1A	sodium channel, voltage-gated, type I, alpha subunit	Plasma Membrane	ion channel
-1.550	SCN3A	sodium channel, voltage-gated, type III, alpha subunit	Plasma Membrane	ion channel
-1.506	CLCNKB	chloride channel, voltage-sensitive Kb	Plasma Membrane	ion channel
-1.639	BMP10	bone morphogenetic protein 10	Extracellular Space	growth factor
-1.536	EGF	epidermal growth factor	Extracellular Space	growth factor
-1.886	OR6C2	olfactory receptor, family 6, subfamily C, member 2	Plasma Membrane	G-protein coupled receptor
-1.703	Olfr1124	olfactory receptor 1124	Plasma Membrane	G-protein coupled receptor
-1.682	CASR	calcium-sensing receptor	Plasma Membrane	G-protein coupled receptor
-1.672	Olfr808	olfactory receptor 808	Plasma Membrane	G-protein coupled receptor
-1.590	OR5B3	olfactory receptor, family 5, subfamily B, member 3	Plasma Membrane	G-protein coupled receptor
-1.577	CXCR1	chemokine (C-X-C motif) receptor 1	Plasma Membrane	G-protein coupled receptor
-1.550	Olfr1018	olfactory receptor 1018	Plasma Membrane	G-protein coupled receptor
-1.536	Olfr514	olfactory receptor 514	Plasma Membrane	G-protein coupled receptor
-1.506	MCHR1	melanin-concentrating hormone receptor 1	Plasma Membrane	G-protein coupled receptor
-1.506	Olfr418-ps1	olfactory receptor 418, pseudogene 1	Plasma Membrane	G-protein coupled receptor
-1.506	OR8D2	olfactory receptor, family 8, subfamily D, member 2	Plasma Membrane	G-protein coupled receptor
-1.506	RXFP4	relaxin/insulin-like family peptide receptor 4	Plasma Membrane	G-protein coupled receptor
-1.999	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	Cytoplasm	enzyme
-1.800	Gucy2g	guanylate cyclase 2g	Cytoplasm	enzyme
-1.767	VKORC1	vitamin K epoxide reductase complex, subunit 1	Cytoplasm	enzyme
-1.758	SI	sucrase-isomaltase (alpha-glucosidase)	Cytoplasm	enzyme
-1.731	AMD1	adenosylmethionine decarboxylase 1	Cytoplasm	enzyme
-1.722	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	Cytoplasm	enzyme
-1.650	ALG6	asparagine-linked glycosylation 6, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	Cytoplasm	enzyme
-1.650	Liph	lipase, member H	unknown	enzyme

-1.603	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	Plasma Membrane	enzyme
-1.603	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	Cytoplasm	enzyme
-1.590	ACOXL	acyl-CoA oxidase-like	unknown	enzyme
-1.564	GNG3	guanine nucleotide binding protein (G protein), gamma 3	Plasma Membrane	enzyme
-1.536	ACER2	alkaline ceramidase 2	Cytoplasm	enzyme
-1.536	FKBP1B	FK506 binding protein 1B, 12.6 kDa	Cytoplasm	enzyme
-1.536	NEIL2	nei endonuclease VIII-like 2 (E. coli)	Nucleus	enzyme
-1.536	RAB5C	RAB5C, member RAS oncogene family	Cytoplasm	enzyme
-1.521	PTDSS1	phosphatidylserine synthase 1	Cytoplasm	enzyme
-1.506	GFOD1	glucose-fructose oxidoreductase domain containing 1	unknown	enzyme
-1.506	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	Nucleus	enzyme
-1.650	CMTM2	CKLF-like MARVEL transmembrane domain containing 2	Extracellular Space	cytokine
-1.506	Cxcl12	chemokine (C-X-C motif) ligand 12	Extracellular Space	cytokine

Appendix 8.
Gene properties identified in shRNA Group D

Log Ratio	Symbol	Entrez Gene Name	Location	Type(s)
-1.872	TM9SF4	transmembrane 9 superfamily protein member 4	Cytoplasm	transporter
-1.823	TRAF5	TNF receptor-associated factor 5	Cytoplasm	transporter
-1.808	CLDN16	claudin 16	Plasma Membrane	transporter
-1.767	NRXN1	neurexin 1	Plasma Membrane	transporter
-1.750	IPO11	importin 11	Nucleus	transporter
-1.731	Slco6c1	solute carrier organic anion transporter family, member 6c1	Plasma Membrane	transporter
-1.712	1700009N14Rik	RIKEN cDNA 1700009N14 gene	unknown	transporter
-1.682	LASP1	LIM and SH3 protein 1	Cytoplasm	transporter
-1.672	TM9SF1	transmembrane 9 superfamily member 1	Plasma Membrane	transporter
-1.639	TRAPPC10	trafficking protein particle complex 10	Cytoplasm	transporter
-1.615	NUP107	nucleoporin 107kDa	Nucleus	transporter
-1.577	FABP5	fatty acid binding protein 5 (psoriasis-associated)	Cytoplasm	transporter
-1.577	PITPNM3	PITPNM family member 3	Cytoplasm	transporter
-1.564	FRG1	FSHD region gene 1	Nucleus	transporter
-1.550	NGB	neuroglobin	Cytoplasm	transporter
-1.536	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	Cytoplasm	transporter
-1.536	NUP37	nucleoporin 37kDa	Nucleus	transporter
-1.521	GLTP	glycolipid transfer protein	Cytoplasm	transporter
-1.506	SLC35B1	solute carrier family 35, member B1	Cytoplasm	transporter
-1.506	SLC39A13	solute carrier family 39 (zinc transporter), member 13	Cytoplasm	transporter
-1.506	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	Plasma Membrane	transporter
-1.758	CD300C	CD300c molecule	Plasma Membrane	transmembrane receptor
-1.722	HLA-DMA	major histocompatibility complex, class II, DM alpha	Plasma Membrane	transmembrane receptor
-1.703	IGHM	immunoglobulin heavy constant mu	Plasma Membrane	transmembrane receptor
-1.639	SARM1	sterile alpha and TIR motif containing 1	Plasma Membrane	transmembrane receptor
-1.603	Klre1	killer cell lectin-like receptor family E member 1	Plasma Membrane	transmembrane receptor
-1.603	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Plasma Membrane	transmembrane receptor
-1.577	CD79A	CD79a molecule, immunoglobulin-associated alpha	Plasma Membrane	transmembrane receptor
-1.506	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	Plasma Membrane	transmembrane receptor
-1.792	BZW1	basic leucine zipper and W2 domains 1	Cytoplasm	translation regulator
-1.693	CELF1	CUGBP, Elav-like family member 1	Nucleus	translation regulator
-1.639	EIF3F	eukaryotic translation initiation factor 3, subunit F	Cytoplasm	translation regulator
-1.615	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	Cytoplasm	translation regulator
-1.886	SSBP3	single stranded DNA binding protein 3	Nucleus	transcription regulator
-1.879	TFDP1	transcription factor Dp-1	Nucleus	transcription regulator
-1.800	NFE2	nuclear factor (erythroid-derived 2), 45kDa	Nucleus	transcription regulator
-1.792	NKX6-2	NK6 homeobox 2	Nucleus	transcription regulator
-1.775	IRF2BP2	interferon regulatory factor 2 binding protein 2	Nucleus	transcription regulator
-1.758	GTF2I	general transcription factor IIi	Nucleus	transcription regulator
-1.731	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	Nucleus	transcription regulator
-1.731	KLF9	Kruppel-like factor 9	Nucleus	transcription regulator
-1.703	GTF2E1	general transcription factor IIE, polypeptide 1, alpha 56kDa	Nucleus	transcription regulator
-1.693	HOXD12	homeobox D12	Nucleus	transcription regulator
-1.693	LZTS1	leucine zipper, putative tumor suppressor 1	Nucleus	transcription regulator
-1.693	NFYC	nuclear transcription factor Y, gamma	Nucleus	transcription regulator
-1.682	SNAI3	snail homolog 3 (Drosophila)	Nucleus	transcription regulator
-1.672	ERF	Ets2 repressor factor	Nucleus	transcription regulator
-1.672	PCGF2	polycomb group ring finger 2	Nucleus	transcription regulator
-1.661	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	Nucleus	transcription regulator
-1.661	NKRF	NFKB repressing factor	Nucleus	transcription regulator
-1.661	WWC1	WW and C2 domain containing 1	Cytoplasm	transcription regulator
-1.650	ARX	aristaless related homeobox	Nucleus	transcription regulator
-1.650	E2F8	E2F transcription factor 8	Nucleus	transcription regulator
-1.650	HOXD4	homeobox D4	Nucleus	transcription regulator
-1.650	VAV1	vav 1 guanine nucleotide exchange factor	Nucleus	transcription regulator
-1.639	DBX1	developing brain homeobox 1	Nucleus	transcription regulator
-1.627	ASXL1	additional sex combs like 1 (Drosophila)	Nucleus	transcription regulator
-1.627	TFAM	transcription factor A, mitochondrial	Cytoplasm	transcription regulator
-1.615	FOXN3	forkhead box N3	Nucleus	transcription regulator
-1.590	Msx3	homeobox, msh-like 3	Nucleus	transcription regulator
-1.577	GBX2	gastrulation brain homeobox 2	Nucleus	transcription regulator
-1.550	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	Cytoplasm	transcription regulator
-1.521	SOX2	SRY (sex determining region Y)-box 2	Nucleus	transcription regulator
-1.521	TGIF2LX	TGFB-induced factor homeobox 2-like, X-linked	Nucleus	transcription regulator
-1.506	CDKN2AIP	CDKN2A interacting protein	Nucleus	transcription regulator
-1.866	LPPR4	lipid phosphate phosphatase-related protein type 4	Plasma Membrane	phosphatase
-1.750	PPP1R12B	protein phosphatase 1, regulatory subunit 12B	Cytoplasm	phosphatase
-1.672	CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	Nucleus	phosphatase
-1.627	PPP4R1	protein phosphatase 4, regulatory subunit 1	unknown	phosphatase
-1.564	EYA3	eyes absent homolog 3 (Drosophila)	Nucleus	phosphatase
-1.506	PDXP	pyridoxal (pyridoxine, vitamin B6) phosphatase	Plasma Membrane	phosphatase
-1.784	Pappa2	pappalysin 2	unknown	peptidase
-1.712	UFD1L	ubiquitin fusion degradation 1 like (yeast)	Cytoplasm	peptidase
-1.672	USP12	ubiquitin specific peptidase 12	Cytoplasm	peptidase
-1.661	YME1L1	YME1-like 1 (S. cerevisiae)	Cytoplasm	peptidase
-1.639	PGPEP1	pyroglutamyl-peptidase I	Cytoplasm	peptidase
-1.615	KLK5	kallikrein-related peptidase 5	Extracellular Space	peptidase
-1.603	LOC690251/Senp5	Sumo1/sentrin/SMT3 specific peptidase 5	unknown	peptidase
-1.603	RELN	reelin	Extracellular Space	peptidase
-1.550	CSTB	cystatin B (stefin B)	Cytoplasm	peptidase
-1.521	CPE	carboxypeptidase E	Plasma Membrane	peptidase
-1.521	HTRA3	HtrA serine peptidase 3	Extracellular Space	peptidase
-1.521	PCSK6	proprotein convertase subtilisin/kexin type 6	Extracellular Space	peptidase
-1.506	CHMP1A	charged multivesicular body protein 1A	Extracellular Space	peptidase
-1.506	HSPA14	heat shock 70kDa protein 14	Cytoplasm	peptidase
-1.506	MEST	mesoderm specific transcript	Extracellular Space	peptidase
-2.389	D230038C21	uncharacterized protein D230038C21	unknown	other
-2.376	PNISR	PNN-interacting serine/arginine-rich protein	Nucleus	other
-2.372	HSPA13	heat shock protein 70kDa family, member 13	Cytoplasm	other
-2.325	Cd209c	CD209c antigen	Plasma Membrane	other
-2.206	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	Nucleus	other
-2.113	CUTA	cutA divalent cation tolerance homolog (E. coli)	unknown	other
-2.081	PQLC3	PQ loop repeat containing 3	unknown	other
-2.056	FAM81B	family with sequence similarity 81, member B	unknown	other
-2.042	SLC35G6	solute carrier family 35, member G6	unknown	other
-2.038	ZNF606	zinc finger protein 606	Nucleus	other
-2.033	4921517D16Rik	RIKEN cDNA 4921517D16 gene	unknown	other
-1.952	AIDA	axin interactor, dorsalization associated	Cytoplasm	other
-1.952	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	Cytoplasm	other
-1.946	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	Nucleus	other
-1.923	PXMP2	peroxisomal membrane protein 2, 22kDa	Cytoplasm	other
-1.917	LOC100127983	uncharacterized LOC100127983	unknown	other

-1.905	Prg4	proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein, camptodactyly,	unknown	other
-1.892	Gm5094	predicted gene 5094	unknown	other
-1.872	BAG4	BCL2-associated athanogene 4	Cytoplasm	other
-1.872	FBXO43	F-box protein 43	Nucleus	other
-1.872	FYB	FYN binding protein	Nucleus	other
-1.866	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	Plasma Membrane	other
-1.852	HSPA12B	heat shock 70kD protein 12B	unknown	other
-1.845	USB1	U6 snRNA biogenesis 1	Nucleus	other
-1.838	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	Plasma Membrane	other
-1.830	EWSR1	Ewing sarcoma breakpoint region 1	Nucleus	other
-1.830	Gm501	predicted gene 501	unknown	other
-1.823	CST11	cystatin 11	Extracellular Space	other
-1.823	Prl7b1	prolactin family 7, subfamily b, member 1	Extracellular Space	other
-1.815	2700069I18Rik	RIKEN cDNA 2700069I18 gene	unknown	other
-1.815	CCDC63	coiled-coil domain containing 63	unknown	other
-1.815	RASGEF1B	RasGEF domain family, member 1B	unknown	other
-1.815	Txlna	taxilin alpha	unknown	other
-1.808	4930431N21Rik	RIKEN cDNA 4930431N21 gene	unknown	other
-1.808	C2orf42	chromosome 2 open reading frame 42	unknown	other
-1.808	SDK1	sidekick cell adhesion molecule 1	Plasma Membrane	other
-1.800	BCL9	B-cell CLL/lymphoma 9	Nucleus	other
-1.792	Gm12169	predicted gene 12169	unknown	other
-1.784	KIAA0195	KIAA0195	Extracellular Space	other
-1.784	MBTD1	mbt domain containing 1	unknown	other
-1.784	PDC	phosducin	Cytoplasm	other
-1.784	RASSF7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	unknown	other
-1.784	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2	Extracellular Space	other
-1.775	SPDYE4	speedy homolog E4 (Xenopus laevis)	unknown	other
-1.767	Ceacam3	carcinoembryonic antigen-related cell adhesion molecule 3	unknown	other
-1.767	COL3A1	collagen, type III, alpha 1	Extracellular Space	other
-1.767	EPB41L2	erythrocyte membrane protein band 4.1-like 2	Plasma Membrane	other
-1.767	ZNF571	zinc finger protein 571	Nucleus	other
-1.758	4930404I05Rik	RIKEN cDNA 4930404I05 gene	unknown	other
-1.758	C19orf24	chromosome 19 open reading frame 24	unknown	other
-1.758	KIAA1524	KIAA1524	Cytoplasm	other
-1.750	1500015L24Rik	RIKEN cDNA 1500015L24 gene	unknown	other
-1.750	4933427E11Rik	RIKEN cDNA 4933427E11 gene	unknown	other
-1.750	CDCA2	cell division cycle associated 2	Nucleus	other
-1.750	FETUB	fetuin B	Extracellular Space	other
-1.750	LCE1D	late cornified envelope 1D	Cytoplasm	other
-1.750	PHF3	PHD finger protein 3	Nucleus	other
-1.750	THUMPD3	THUMP domain containing 3	unknown	other
-1.740	DNAJC25	DnaJ (Hsp40) homolog, subfamily C , member 25	unknown	other
-1.740	SDE2	SDE2 telomere maintenance homolog (S. pombe)	unknown	other
-1.740	SDHAF2	succinate dehydrogenase complex assembly factor 2	Extracellular Space	other
-1.740	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	Cytoplasm	other
-1.731	4931408C20Rik	RIKEN cDNA 4931408C20 gene	unknown	other
-1.731	Adamts20	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 20	unknown	other
-1.731	ARHGAP32	Rho GTPase activating protein 32	Cytoplasm	other
-1.731	C16orf46	chromosome 16 open reading frame 46	unknown	other
-1.731	CHMP3	charged multivesicular body protein 3	Cytoplasm	other
-1.731	Gm5545	predicted gene 5545	unknown	other
-1.731	KIAA1704	KIAA1704	unknown	other
-1.731	LMBRD2	LMBR1 domain containing 2	unknown	other
-1.731	PALB2	partner and localizer of BRCA2	Nucleus	other
-1.722	BTBD9	BTB (POZ) domain containing 9	unknown	other
-1.722	ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	unknown	other
-1.722	NOXA1	NADPH oxidase activator 1	unknown	other
-1.722	Speer4a (includes others)	spermatogenesis associated glutamate (E)-rich protein 4a	Nucleus	other
-1.722	TATDN3	TatD DNase domain containing 3	Cytoplasm	other
-1.722	ZNF318	zinc finger protein 318	Nucleus	other
-1.712	CCT4	chaperonin containing TCP1, subunit 4 (delta)	Cytoplasm	other
-1.712	DDRGK1	DDRGK domain containing 1	Extracellular Space	other
-1.712	E330034G19Rik	RIKEN cDNA E330034G19 gene	unknown	other
-1.712	FAM184A	family with sequence similarity 184, member A	Extracellular Space	other
-1.712	FRMD3	FERM domain containing 3	unknown	other
-1.712	GSDMC	gasdermin C	Cytoplasm	other
-1.712	TNFAIP2	tumor necrosis factor, alpha-induced protein 2	Extracellular Space	other
-1.712	TOMM34	translocase of outer mitochondrial membrane 34	Cytoplasm	other
-1.703	Akap17b	A kinase (PRKA) anchor protein 17B	unknown	other
-1.703	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	unknown	other
-1.703	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	Cytoplasm	other
-1.703	GAP43	growth associated protein 43	Plasma Membrane	other
-1.703	IKBIP	IKBKB interacting protein	Cytoplasm	other
-1.703	MRPL51	mitochondrial ribosomal protein L51	Cytoplasm	other
-1.703	MYL3	myosin, light chain 3, alkali; ventricular, skeletal, slow	Cytoplasm	other
-1.703	RASEF	RAS and EF-hand domain containing	unknown	other
-1.703	TRIM61	tripartite motif containing 61	unknown	other
-1.703	ZNF846	zinc finger protein 846	unknown	other
-1.693	4930526F13Rik	RIKEN cDNA 4930526F13 gene	unknown	other
-1.693	ERLEC1	endoplasmic reticulum lectin 1	Extracellular Space	other
-1.693	FSD1L	fibronectin type III and SPRY domain containing 1-like	unknown	other
-1.693	KRT77	keratin 77	unknown	other
-1.693	PPP4R4	protein phosphatase 4, regulatory subunit 4	Cytoplasm	other
-1.693	TSPAN33	tetraspanin 33	Plasma Membrane	other
-1.693	TSTD1	thiosulfate sulfurtransferase (rhodanese)-like domain containing 1	Cytoplasm	other
-1.693	ZNF830	zinc finger protein 830	Nucleus	other
-1.682	A530032D15Rik (includes others)	RIKEN cDNA C130026I21 gene	unknown	other
-1.682	B130021B11Rik	RIKEN cDNA B130021B11 gene	unknown	other
-1.682	ISCA2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)	Cytoplasm	other
-1.682	PI16	peptidase inhibitor 16	Extracellular Space	other
-1.682	POC5	POC5 centriolar protein homolog (Chlamydomonas)	Cytoplasm	other
-1.682	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	unknown	other
-1.682	VIP	vasoactive intestinal peptide	Extracellular Space	other
-1.682	ZDHHC11B	zinc finger, DHHC-type containing 11B	unknown	other
-1.672	ANXA11	annexin A11	Nucleus	other
-1.672	C8orf76	chromosome 8 open reading frame 76	unknown	other
-1.672	Defb3	beta-defensin 3	unknown	other
-1.672	DFNA5	deafness, autosomal dominant 5	Cytoplasm	other
-1.672	E030003E18Rik	RIKEN cDNA E030003E18 gene	unknown	other
-1.672	HINT3	histidine triad nucleotide binding protein 3	unknown	other
-1.672	PDZD9	PDZ domain containing 9	unknown	other
-1.672	PPP1R9A	protein phosphatase 1, regulatory subunit 9A	Plasma Membrane	other
-1.672	Prl3c1	prolactin family 3, subfamily c, member 1	Extracellular Space	other
-1.672	SECISBP2L	SECIS binding protein 2-like	unknown	other
-1.672	SLC15A5	solute carrier family 15, member 5	unknown	other
-1.672	WDFY2	WD repeat and FYVE domain containing 2	unknown	other
-1.661	C19orf52	chromosome 19 open reading frame 52	unknown	other
-1.661	C330011M18Rik	RIKEN cDNA C330011M18 gene	unknown	other
-1.661	FBXL17	F-box and leucine-rich repeat protein 17	unknown	other

-1.661	GLIPR1	GLI pathogenesis-related 1	Extracellular Space	other
-1.661	Gm815	predicted gene 815	unknown	other
-1.661	LIN52	lin-52 homolog (C. elegans)	Nucleus	other
-1.661	PROCA1	protein interacting with cyclin A1	unknown	other
-1.661	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	unknown	other
-1.661	ZNF565	zinc finger protein 565	Nucleus	other
-1.650	B230317F23Rik	RIKEN cDNA B230317F23 gene	unknown	other
-1.650	IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	unknown	other
-1.650	KIAA1024	KIAA1024	unknown	other
-1.650	RPS19BP1	ribosomal protein S19 binding protein 1	Nucleus	other
-1.650	Sprr2j-ps	small proline-rich protein 2J, pseudogene	Cytoplasm	other
-1.650	STEAP4	STEAP family member 4	Plasma Membrane	other
-1.650	WDR96	WD repeat domain 96	unknown	other
-1.650	ZNHIT6	zinc finger, HIT-type containing 6	unknown	other
-1.639	C1orf174	chromosome 1 open reading frame 174	unknown	other
-1.639	MAP7D2	MAP7 domain containing 2	unknown	other
-1.639	NEFM	neurofilament, medium polypeptide	Cytoplasm	other
-1.639	Srsf10	serine/arginine-rich splicing factor 10	Nucleus	other
-1.639	ZNF800	zinc finger protein 800	unknown	other
-1.627	ANKRD28	ankyrin repeat domain 28	Cytoplasm	other
-1.627	ARGLU1	arginine and glutamate rich 1	unknown	other
-1.627	ARL6IP4	ADP-ribosylation-like factor 6 interacting protein 4	Nucleus	other
-1.627	C2orf80	chromosome 2 open reading frame 80	unknown	other
-1.627	Ccnb1/Gm5593	cyclin B1	Nucleus	other
-1.627	CCNG1	cyclin G1	Nucleus	other
-1.627	CLEC4M	C-type lectin domain family 4, member M	Plasma Membrane	other
-1.627	Gm9776	predicted gene 9776	unknown	other
-1.627	HIST1H1T	histone cluster 1, H1t	Nucleus	other
-1.627	KRTDAP	keratinocyte differentiation-associated protein	Extracellular Space	other
-1.627	PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein	unknown	other
-1.627	Plxnb1	plexin B1	unknown	other
-1.627	PRKRIR	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 rep	Nucleus	other
-1.627	Prl8a1	prolactin family 8, subfamily a, member 1	unknown	other
-1.627	RSU1	Ras suppressor protein 1	Cytoplasm	other
-1.615	ATAD2	ATPase family, AAA domain containing 2	Nucleus	other
-1.615	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	Nucleus	other
-1.615	KRTAP3-2	keratin associated protein 3-2	unknown	other
-1.615	LRRC58	leucine rich repeat containing 58	unknown	other
-1.615	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	unknown	other
-1.615	PHLDA2	pleckstrin homology-like domain, family A, member 2	Cytoplasm	other
-1.615	RNASE10	ribonuclease, RNase A family, 10 (non-active)	Extracellular Space	other
-1.615	SHD	Src homology 2 domain containing transforming protein D	Cytoplasm	other
-1.615	Smr3a	submaxillary gland androgen regulated protein 3A	Extracellular Space	other
-1.615	TBC1D2	TBC1 domain family, member 2	Cytoplasm	other
-1.615	URGCP	upregulator of cell proliferation	Cytoplasm	other
-1.603	4933434C23Rik	RIKEN cDNA 4933434C23 gene	unknown	other
-1.603	C5orf47	chromosome 5 open reading frame 47	unknown	other
-1.603	CLDN8	claudin 8	Plasma Membrane	other
-1.603	COPS7B	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)	Cytoplasm	other
-1.603	EDN3	endothelin 3	Extracellular Space	other
-1.603	FAM184B	family with sequence similarity 184, member B	unknown	other
-1.603	Gm14461	predicted gene 14461	unknown	other
-1.603	Pramel6	preferentially expressed antigen in melanoma like 6	unknown	other
-1.603	RINL	Ras and Rab interactor-like	unknown	other
-1.603	SOBP	sine oculis binding protein homolog (Drosophila)	Nucleus	other
-1.603	Zfp954	zinc finger protein 954	unknown	other
-1.603	ZNF676	zinc finger protein 676	Nucleus	other
-1.590	C2orf72	chromosome 2 open reading frame 72	unknown	other
-1.590	CCIN	calicin	Cytoplasm	other
-1.590	CNST	consortin, connexin sorting protein	Cytoplasm	other
-1.590	Gm648	predicted gene 648	unknown	other
-1.590	HOXC11	homeobox C11	Nucleus	other
-1.590	NDUFAF1	NADH dehydrogenase (ubiquinone) complex I, assembly factor 1	Cytoplasm	other
-1.590	NPNT	nephronectin	Plasma Membrane	other
-1.590	SMIM12	small integral membrane protein 12	unknown	other
-1.577	1500002O10Rik	RIKEN cDNA 1500002O10 gene	unknown	other
-1.577	2700097O09Rik	RIKEN cDNA 2700097O09 gene	Extracellular Space	other
-1.577	4930468A15Rik	RIKEN cDNA 4930468A15 gene	unknown	other
-1.577	A530032D15Rik (includes others)	RIKEN cDNA C130026I21 gene	unknown	other
-1.577	Afmid	arylformamidase	unknown	other
-1.577	ARRB1	arrestin, beta 1	Cytoplasm	other
-1.577	BBS10	Bardet-Biedl syndrome 10	unknown	other
-1.577	CARD6	caspase recruitment domain family, member 6	Cytoplasm	other
-1.577	CD300E	CD300e molecule	unknown	other
-1.577	MATR3	matrin 3	Nucleus	other
-1.577	RFC2	replication factor C (activator 1) 2, 40kDa	Nucleus	other
-1.577	RNF157	ring finger protein 157	unknown	other
-1.577	SEC31A	SEC31 homolog A (S. cerevisiae)	Cytoplasm	other
-1.577	SH3PXD2A	SH3 and PX domains 2A	Cytoplasm	other
-1.577	UPK1B	uroplakin 1B	Plasma Membrane	other
-1.564	9530026P05Rik	RIKEN cDNA 9530026P05 gene	unknown	other
-1.564	A330008L17Rik	RIKEN cDNA A330008L17 gene	unknown	other
-1.564	AKAP1	A kinase (PRKA) anchor protein 1	Cytoplasm	other
-1.564	ARVCF	armadillo repeat gene deleted in velocardiofacial syndrome	Plasma Membrane	other
-1.564	BATF2	basic leucine zipper transcription factor, ATF-like 2	unknown	other
-1.564	D330041H03Rik	RIKEN cDNA D330041H03 gene	unknown	other
-1.564	GLTSCR1L	GLTSCR1-like	unknown	other
-1.564	KIAA1731	KIAA1731	Cytoplasm	other
-1.564	KLHDC5	kelch domain containing 5	Nucleus	other
-1.564	MS4A5	membrane-spanning 4-domains, subfamily A, member 5	unknown	other
-1.564	SLC25A52	solute carrier family 25, member 52	unknown	other
-1.550	1700028J19Rik	RIKEN cDNA 1700028J19 gene	unknown	other
-1.550	5730433N10Rik	RIKEN cDNA 5730433N10 gene	unknown	other
-1.550	ALCAM	activated leukocyte cell adhesion molecule	Plasma Membrane	other
-1.550	AZI1	5-azacytidine induced 1	Cytoplasm	other
-1.550	C030019G06Rik	RIKEN cDNA C030019G06 gene	unknown	other
-1.550	C19orf43	chromosome 19 open reading frame 43	Nucleus	other
-1.550	C7orf62	chromosome 7 open reading frame 62	unknown	other
-1.550	CD68	CD68 molecule	Plasma Membrane	other
-1.550	CRYGS	crystallin, gamma S	unknown	other
-1.550	FAM65A	family with sequence similarity 65, member A	Cytoplasm	other
-1.550	FBXW8	F-box and WD repeat domain containing 8	unknown	other
-1.550	GIMAP8	GTPase, IMAP family member 8	unknown	other
-1.550	Gm5482	predicted gene 5482	unknown	other
-1.550	NAT6	N-acetyltransferase 6 (GCN5-related)	Cytoplasm	other
-1.550	NCAPG	non-SMC condensin I complex, subunit G	Nucleus	other
-1.550	OSBPL8	oxysterol binding protein-like 8	Cytoplasm	other
-1.550	PRDM15	PR domain containing 15	Nucleus	other
-1.550	RPL11	ribosomal protein L11	Cytoplasm	other
-1.550	TMEM202	transmembrane protein 202	unknown	other

-1.550	TRIML1	tripartite motif family-like 1	unknown	other
-1.550	TTC33	tetratricopeptide repeat domain 33	unknown	other
-1.550	TUSC2	tumor suppressor candidate 2	Nucleus	other
-1.550	UBD	ubiquitin D	Nucleus	other
-1.550	VAMP3	vesicle-associated membrane protein 3	Plasma Membrane	other
-1.550	Vmn1r51 (includes others)	vomeronasal 1 receptor 51	Plasma Membrane	other
-1.550	Vmn2r19 (includes others)	vomeronasal 2, receptor 19	unknown	other
-1.550	ZFP30	ZFP30 zinc finger protein	Extracellular Space	other
-1.536	AHNAK	AHNAK nucleoprotein	Nucleus	other
-1.536	ALG11	asparagine-linked glycosylation 11, alpha-1,2-mannosyltransferase homolog (yeast)	unknown	other
-1.536	APCS	amyloid P component, serum	Extracellular Space	other
-1.536	C230088H06Rik	RIKEN cDNA C230088H06 gene	unknown	other
-1.536	C4B (includes others)	complement component 4B (Chido blood group)	Extracellular Space	other
-1.536	CFL1	cofilin 1 (non-muscle)	Nucleus	other
-1.536	CUEDC1	CUE domain containing 1	unknown	other
-1.536	Fhod3	formin homology 2 domain containing 3	Nucleus	other
-1.536	GPATCH3	G patch domain containing 3	unknown	other
-1.536	Iqcf4	IQ motif containing F4	unknown	other
-1.536	KIAA0226	KIAA0226	Cytoplasm	other
-1.536	KRT23	keratin 23 (histone deacetylase inducible)	unknown	other
-1.536	MAP4	microtubule-associated protein 4	Cytoplasm	other
-1.536	XPC	xeroderma pigmentosum, complementation group C	Nucleus	other
-1.536	Zfp942/Zfp944	zinc finger protein 944	unknown	other
-1.536	ZP1	zona pellucida glycoprotein 1 (sperm receptor)	Extracellular Space	other
-1.521	4930529M08Rik	RIKEN cDNA 4930529M08 gene	unknown	other
-1.521	5830405M20Rik	RIKEN cDNA 5830405M20 gene	unknown	other
-1.521	ANGEL1	angel homolog 1 (Drosophila)	Extracellular Space	other
-1.521	BC026585	cDNA sequence BC026585	Cytoplasm	other
-1.521	CCDC85A	coiled-coil domain containing 85A	unknown	other
-1.521	EMILIN1	elastin microfibril interfacer 1	Extracellular Space	other
-1.521	Gm5444	predicted gene 5444	unknown	other
-1.521	KLHL6	kelch-like 6 (Drosophila)	unknown	other
-1.521	MPRIP	myosin phosphatase Rho interacting protein	Cytoplasm	other
-1.521	PLAC1L	placenta-specific 1-like	unknown	other
-1.521	Prl8a6	prolactin family 8, subfamily a, member 6	Extracellular Space	other
-1.521	SMAP1	small ArfGAP 1	Cytoplasm	other
-1.521	SMIM8	small integral membrane protein 8	unknown	other
-1.521	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1	Nucleus	other
-1.521	Vmn1r52	vomeronasal 1 receptor 52	unknown	other
-1.506	BCL2L14	BCL2-like 14 (apoptosis facilitator)	Cytoplasm	other
-1.506	CAV2	caveolin 2	Plasma Membrane	other
-1.506	CCDC25	coiled-coil domain containing 25	unknown	other
-1.506	CCDC41	coiled-coil domain containing 41	Extracellular Space	other
-1.506	CGN	cingulin	Plasma Membrane	other
-1.506	CHIC2	cysteine-rich hydrophobic domain 2	Plasma Membrane	other
-1.506	Ctsj	cathepsin J	Cytoplasm	other
-1.506	D430032J08Rik	RIKEN cDNA D430032J08 gene	unknown	other
-1.506	EID3	EP300 interacting inhibitor of differentiation 3	Cytoplasm	other
-1.506	FAM117B	family with sequence similarity 117, member B	unknown	other
-1.506	FAM35A	family with sequence similarity 35, member A	Extracellular Space	other
-1.506	FGD2	FYVE, RhoGEF and PH domain containing 2	Cytoplasm	other
-1.506	HMGXB4	HMG box domain containing 4	Nucleus	other
-1.506	KRT9	keratin 9	Cytoplasm	other
-1.506	LRRC8A	leucine rich repeat containing 8 family, member A	Extracellular Space	other
-1.506	NID2	nidogen 2 (osteonidogen)	Extracellular Space	other
-1.506	ODF3L1	outer dense fiber of sperm tails 3-like 1	unknown	other
-1.506	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	unknown	other
-1.506	PRICKLE3	prickle homolog 3 (Drosophila)	unknown	other
-1.506	RIN1	Ras and Rab interactor 1	Cytoplasm	other
-1.506	SRP9	signal recognition particle 9kDa	Cytoplasm	other
-1.506	TEX13B	testis expressed 13B	unknown	other
-1.506	ZBTB9	zinc finger and BTB domain containing 9	Nucleus	other
-1.506	Zfp956	zinc finger protein 956	unknown	other
-1.506	ZNF787	zinc finger protein 787	unknown	other
-1.603	AR	androgen receptor	Nucleus	ligand-dependent nuclear receptor
-2.275	PLK2	polo-like kinase 2	Nucleus	kinase
-2.150	DGKI	diacylglycerol kinase, iota	Cytoplasm	kinase
-1.800	MEX3B	mex-3 homolog B (C. elegans)	unknown	kinase
-1.731	CDC42BPB	CDC42 binding protein kinase beta (DMPK-like)	Cytoplasm	kinase
-1.712	WEE1	WEE1 homolog (S. pombe)	Nucleus	kinase
-1.703	MAPK13	mitogen-activated protein kinase 13	Cytoplasm	kinase
-1.693	CDC7	cell division cycle 7 homolog (S. cerevisiae)	Nucleus	kinase
-1.672	MAP3K7	mitogen-activated protein kinase kinase kinase 7	Cytoplasm	kinase
-1.661	RIOK3	RIO kinase 3	unknown	kinase
-1.639	DGKG	diacylglycerol kinase, gamma 90kDa	Cytoplasm	kinase
-1.615	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	Plasma Membrane	kinase
-1.603	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	Cytoplasm	kinase
-1.603	PBK	PDZ binding kinase	Cytoplasm	kinase
-1.577	RET	ret proto-oncogene	Plasma Membrane	kinase
-1.550	PLK3	polo-like kinase 3	Nucleus	kinase
-1.550	PRKCE	protein kinase C, epsilon	Cytoplasm	kinase
-1.550	TEX14	testis expressed 14	Plasma Membrane	kinase
-1.536	SIK1	salt-inducible kinase 1	Cytoplasm	kinase
-1.536	SPHK2	sphingosine kinase 2	Cytoplasm	kinase
-1.521	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	Cytoplasm	kinase
-1.506	SGK2	serum/glucocorticoid regulated kinase 2	Cytoplasm	kinase
-2.167	KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	Plasma Membrane	ion channel
-1.693	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	Plasma Membrane	ion channel
-1.661	FXYD6	FXYD domain containing ion transport regulator 6	Plasma Membrane	ion channel
-1.550	ASIC5	acid-sensing (proton-gated) ion channel family member 5	Plasma Membrane	ion channel
-1.536	CLCN3	chloride channel, voltage-sensitive 3	Plasma Membrane	ion channel
-1.536	GRIK2	glutamate receptor, ionotropic, kainate 2	Plasma Membrane	ion channel
-1.536	HCN4	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	Plasma Membrane	ion channel
-1.521	CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	Plasma Membrane	ion channel
-1.639	VEGFA	vascular endothelial growth factor A	Extracellular Space	growth factor
-1.615	FGF14	fibroblast growth factor 14	Extracellular Space	growth factor
-1.615	PTN	pleiotrophin	Extracellular Space	growth factor
-1.564	WISP2	WNT1 inducible signaling pathway protein 2	Extracellular Space	growth factor
-2.485	Olfr194	olfactory receptor 194	Plasma Membrane	G-protein coupled receptor
-1.917	Olfr1462	olfactory receptor 1462	Plasma Membrane	G-protein coupled receptor
-1.845	Olfr916	olfactory receptor 916	Plasma Membrane	G-protein coupled receptor
-1.838	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	Plasma Membrane	G-protein coupled receptor
-1.808	Olfr1344	olfactory receptor 1344	Plasma Membrane	G-protein coupled receptor
-1.750	Olfr1010	olfactory receptor 1010	Plasma Membrane	G-protein coupled receptor
-1.740	A630033H20Rik	RIKEN cDNA A630033H20 gene	Plasma Membrane	G-protein coupled receptor
-1.712	Gpr165	G protein-coupled receptor 165	Plasma Membrane	G-protein coupled receptor
-1.712	Olfr1055	olfactory receptor 1055	Plasma Membrane	G-protein coupled receptor
-1.703	Vmn2r32 (includes others)	vomeronasal 2, receptor 32	Plasma Membrane	G-protein coupled receptor
-1.672	OR52B6	olfactory receptor, family 52, subfamily B, member 6	Plasma Membrane	G-protein coupled receptor
-1.661	CNR2	cannabinoid receptor 2 (macrophage)	Plasma Membrane	G-protein coupled receptor

-1.661	Vmn1r78	vomeronasal 1 receptor 78	Plasma Membrane	G-protein coupled receptor
-1.627	Olr422	olfactory receptor 422	Plasma Membrane	G-protein coupled receptor
-1.615	LPAR1	lysophosphatidic acid receptor 1	Plasma Membrane	G-protein coupled receptor
-1.603	GPR84	G protein-coupled receptor 84	Plasma Membrane	G-protein coupled receptor
-1.603	Olfr1317/Olfr1318	olfactory receptor 1318	Plasma Membrane	G-protein coupled receptor
-1.603	Olfr608	olfactory receptor 608	Plasma Membrane	G-protein coupled receptor
-1.603	Olr1082 (includes others)	olfactory receptor 1082	Plasma Membrane	G-protein coupled receptor
-1.603	OR10A2	olfactory receptor, family 10, subfamily A, member 2	Plasma Membrane	G-protein coupled receptor
-1.564	GPR119	G protein-coupled receptor 119	Plasma Membrane	G-protein coupled receptor
-1.564	MRGPRX2	MAS-related GPR, member X2	Plasma Membrane	G-protein coupled receptor
-1.564	OXGR1	oxoglutarate (alpha-ketoglutarate) receptor 1	Plasma Membrane	G-protein coupled receptor
-1.550	Fpr-rs3	formyl peptide receptor, related sequence 3	Plasma Membrane	G-protein coupled receptor
-1.550	OPRL1	opiate receptor-like 1	Plasma Membrane	G-protein coupled receptor
-1.521	LTB4R	leukotriene B4 receptor	Plasma Membrane	G-protein coupled receptor
-1.506	GPR182	G protein-coupled receptor 182	Plasma Membrane	G-protein coupled receptor
-1.506	OR4C11	olfactory receptor, family 4, subfamily C, member 11	Plasma Membrane	G-protein coupled receptor
-1.506	OR5AP2	olfactory receptor, family 5, subfamily AP, member 2	Plasma Membrane	G-protein coupled receptor
-2.060	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	Cytoplasm	enzyme
-1.941	COQ7	coenzyme Q7 homolog, ubiquinone (yeast)	Cytoplasm	enzyme
-1.941	Rheb	Ras homolog enriched in brain	Plasma Membrane	enzyme
-1.859	LIPC	lipase, hepatic	Extracellular Space	enzyme
-1.852	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	Cytoplasm	enzyme
-1.845	PROSC	proline synthetase co-transcribed homolog (bacterial)	Cytoplasm	enzyme
-1.800	ALDH1L1	aldehyde dehydrogenase 1 family, member L1	Cytoplasm	enzyme
-1.800	PGAP1	post-GPI attachment to proteins 1	Cytoplasm	enzyme
-1.792	DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	Cytoplasm	enzyme
-1.784	Cyp2c44	cytochrome P450, family 2, subfamily c, polypeptide 44	Cytoplasm	enzyme
-1.784	PRDX2	peroxiredoxin 2	Cytoplasm	enzyme
-1.767	MCM6	minichromosome maintenance complex component 6	Nucleus	enzyme
-1.758	EXOSC7	exosome component 7	Nucleus	enzyme
-1.750	HSPA8	heat shock 70kDa protein 8	Cytoplasm	enzyme
-1.750	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	Cytoplasm	enzyme
-1.750	TRIM68	tripartite motif containing 68	Cytoplasm	enzyme
-1.740	FAN1	FANCD2/FANCI-associated nuclease 1	Nucleus	enzyme
-1.740	FBXL2	F-box and leucine-rich repeat protein 2	Cytoplasm	enzyme
-1.731	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)	Extracellular Space	enzyme
-1.731	MARC1	mitochondrial amidoxime reducing component 1	Cytoplasm	enzyme
-1.703	C2orf43	chromosome 2 open reading frame 43	unknown	enzyme
-1.703	EHD4	EH-domain containing 4	Plasma Membrane	enzyme
-1.703	GSTA5	glutathione S-transferase alpha 5	Cytoplasm	enzyme
-1.693	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	Nucleus	enzyme
-1.682	ATG7	autophagy related 7	Cytoplasm	enzyme
-1.682	THG1L	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	Cytoplasm	enzyme
-1.672	ATAT1	alpha tubulin acetyltransferase 1	unknown	enzyme
-1.672	BCHE	butyrylcholinesterase	Plasma Membrane	enzyme
-1.672	GNAT2	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2	Plasma Membrane	enzyme
-1.672	PTGR2	prostaglandin reductase 2	Cytoplasm	enzyme
-1.672	SLX1A/SLX1B	SLX1 structure-specific endonuclease subunit homolog B (S. cerevisiae)	unknown	enzyme
-1.661	METTL6	methyltransferase like 6	unknown	enzyme
-1.661	SETDB2	SET domain, bifurcated 2	Nucleus	enzyme
-1.650	FDPS	farnesyl diphosphate synthase	Cytoplasm	enzyme
-1.650	FMO2	flavin containing monooxygenase 2 (non-functional)	Cytoplasm	enzyme
-1.650	RAD51B	RAD51 homolog B (S. cerevisiae)	Nucleus	enzyme
-1.650	TOP2B	topoisomerase (DNA) II beta 180kDa	Nucleus	enzyme
-1.627	CRBN	cereblon	Cytoplasm	enzyme
-1.627	RHOT2	ras homolog family member T2	Cytoplasm	enzyme
-1.603	KIF9	kinesin family member 9	Cytoplasm	enzyme
-1.603	OC90	otoconin 90	Extracellular Space	enzyme
-1.603	PLCD4	phospholipase C, delta 4	Cytoplasm	enzyme
-1.603	PPT1	palmitoyl-protein thioesterase 1	Cytoplasm	enzyme
-1.590	CRYZ	crystallin, zeta (quinone reductase)	Cytoplasm	enzyme
-1.590	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Nucleus	enzyme
-1.577	AOC2	amine oxidase, copper containing 2 (retina-specific)	unknown	enzyme
-1.577	Cyp2a12/Cyp2a22	cytochrome P450, family 2, subfamily a, polypeptide 12	Cytoplasm	enzyme
-1.577	HYAL4	hyaluronoglucosaminidase 4	unknown	enzyme
-1.577	IDO2	indoleamine 2,3-dioxygenase 2	Cytoplasm	enzyme
-1.577	KL	klotho	Extracellular Space	enzyme
-1.577	PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	Cytoplasm	enzyme
-1.577	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	Cytoplasm	enzyme
-1.564	B4GALNT2	beta-1,4-N-acetyl-galactosaminyl transferase 2	Cytoplasm	enzyme
-1.564	GSTT2/GSTT2B	glutathione S-transferase theta 2	Cytoplasm	enzyme
-1.564	MYH7	myosin, heavy chain 7, cardiac muscle, beta	Cytoplasm	enzyme
-1.564	PPIG	peptidylprolyl isomerase G (cyclophilin G)	Nucleus	enzyme
-1.550	ACSL6	acyl-CoA synthetase long-chain family member 6	Cytoplasm	enzyme
-1.550	G6PD	glucose-6-phosphate dehydrogenase	Cytoplasm	enzyme
-1.550	GSTO1	glutathione S-transferase omega 1	Cytoplasm	enzyme
-1.550	RFC3	replication factor C (activator 1) 3, 38kDa	Nucleus	enzyme
-1.550	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	Cytoplasm	enzyme
-1.550	ZNRF1	zinc and ring finger 1, E3 ubiquitin protein ligase	Cytoplasm	enzyme
-1.536	DNM1L	dynamin 1-like	Cytoplasm	enzyme
-1.536	PLA2G5	phospholipase A2, group V	Extracellular Space	enzyme
-1.521	AHCYL1	adenosylhomocysteinase-like 1	Cytoplasm	enzyme
-1.521	ARL8A	ADP-ribosylation factor-like 8A	Cytoplasm	enzyme
-1.521	PDCD1LG2	programmed cell death 1 ligand 2	Plasma Membrane	enzyme
-1.506	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	Cytoplasm	enzyme
-1.506	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	Cytoplasm	enzyme
-1.506	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	Cytoplasm	enzyme
-1.506	SH3GL2	SH3-domain GRB2-like 2	Plasma Membrane	enzyme
-1.506	SPAST	spastin	Nucleus	enzyme
-1.506	UBA1	ubiquitin-like modifier activating enzyme 1	Cytoplasm	enzyme
-1.830	C19orf10	chromosome 19 open reading frame 10	Extracellular Space	cytokine
-1.672	IL33	interleukin 33	Extracellular Space	cytokine
-1.627	XCL1	chemokine (C motif) ligand 1	Extracellular Space	cytokine
-1.615	FAM3D	family with sequence similarity 3, member D	Extracellular Space	cytokine
-1.564	CCL11	chemokine (C-C motif) ligand 11	Extracellular Space	cytokine