CRLF2 CYTOKINE RECEPTOR SIGNALING IN ACUTE LEUKEMIA

by

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Abstract

Cytokine Receptor Like Factor 2 (CRLF2) is the receptor of the cytokine Thymic Stromal Lymphopoietin (TSLP). CRLF2 plays a role in lymphocyte development, differentiation and homeostasis. Recently, CRLF2 is implicated in a subset of precursor B cell acute lymphoblastic leukemia (pre-B ALL), which is the most common pediatric malignancy. Long-term survival of this disease is stratified into different risk groups dictating treatment plans for patients. Among pre-B ALL risk groups, a much worse prognosis is observed in patients with the gene rearrangement of *CRLF2* as well as with the fusion gene *BCR-ABL1*. Previous transcriptomic analyses indicated a similar gene expression profile for CRLF2 and BCR/ABL1 signaling in pre-B ALL. While both CRLF2 and BCR/ABL1 have potent effects on cell signaling pathways, their total protein and global phosphorylation profiles might be different. In order to interrogate this hypothesis, we leveraged the Ba/F3 cell culture system to carry out a series of quantitative proteomics analysis to compare BCR/ABL1 and multiple forms of aberrant CRLF2 signaling. Our study identified major differences between CRLF2 and BCR/ABL1 signaling including EIF2/EIF4 signaling related to translation initiation regulation, DNA methylation/transcription repression pathways, IKZF2-INPP5D signaling axis, JAK2-mediated H_3Y_{42} phosphorylation, among others. In addition, we took advantage of a kinase and small molecule inhibitor screen to identify PLK1 as a potential therapeutic target downstream of the leukemic CRLF2 signaling. PLK1 dysregulation resulting from the aberrant CRLF2 JAK2 signaling might provide an opportunity to develop CRLF2-targeted therapy in the future. In conclusion, CRLF2 and BCR/ABL1 signaling differs in many aspects that might affect therapy development for the different types of pre-B ALL.

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Preface

It has been my great pleasure and honor to study human genetics, proteomics and leukemia at Hopkins for these years. To me, learning is always humbling and fun. Many times I was awed by the great complexity of biological systems I was studying, and very often the dynamics between each component of this complexity is still beyond my ken. And yet, I am constantly aspired to know it better. As aspired to be a scholar, this is my view carved out through the training I took these years: information is deluging, knowledge is evolving, and yet wisdom is still far and hard to fetch. Luckily, I got unwavering support from my family, my mentors, my friends and so many others that I may not be aware of, and I want to make my acknowledgement to them here as follows: my wife — Mei-Chen Huang; my daughter — Jing-Fei Huang; my parents — Shih-Kai Huang and Yu-Ing Hsiao; my mentors: Akhilesh Pandey, Curt Civin, Judith Karp, Ivana Gojo, William Matsui, Linzhao Cheng, David Weinstock, David Valle, Wen-Chien Chou; all past and current members of Pandey Lab; my classmates at Johns Hopkins.

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Introduction

Cell signaling is a versatile design mediating intricate biological activities not only in all life forms including eukaryotes, bacteria and archaea but also in virus.(Merrick, 2014; Kennelly, 2003; Li and Hayward, 2013) It employs the modification of biomolecules to alter their physicochemical properties, leading to functional changes for intermolecular interactions. This enables cells to carry out countless bioactivities such as proliferation, death, movement, migration, differentiation, transdifferentiation, intercellular communications, and so on.(Hanahan and Weinberg, 2011; van Buul and Hordijk, 2004; Lamouille et al., 2014) This deep involvement of signaling in all facets of cell physiology is also reflected in all sorts of neoplasm.(Hanahan and Weinberg, 2011) In contrast to the controlled and balanced signaling pathways in normal cells, neoplastic cells are a collection of signaling dysregulation related to genome instability and the microenvironment.

Cytokine signaling serves as a good model to illustrate the mechanism of signaling-mediated cell growth and differentiation. In physiological situation, cytokine binds to its receptor, triggers a cascade of downstream protein phosphorylation to modulate gene expression as well as other cellular process. For example, interleukin 2 binds to the interleukin 2 receptor, constituted by α, β, γ subunits, on the surface of T lymphocytes. This engagement between the ligand and the receptor phosphorylates JAK1/JAK3 which in turn phosphorylates SHC1, LCK and PIK3R, leading to the activation of transcription factors such as STAT3/STAT5 and NFKB1. End results of this interleukin 2 signaling cascade are the upregulated transcription of several pro-proliferation genes such as *MYC, FOS, JUN, BCL2, IL2RA, CCND2*, etc.(Malek, 2008) This model epitomizes the importance of cytokine signaling in normal cells.

In cancer, however, the aberrational cytokine signaling may institute and aggravate the neoplastic development. A plethora of studies have characterized the association between dysregulated cytokine signaling and cancer development. For example, upregulated interleukin 1 can promote tumor growth and has been implicated in various malignancies including breast cancer, colon cancer, pancreatic cancer, lung cancer, cervical cancer, head and neck cancer, etc.(Lewis et al., 2006; Kasza, 2013) Likewise, accumulating evidence implicates a cytokine called thymic stromal lymphopoietin (TSLP) in different types of cancers such as breast cancer, pancreatic cancer and cervical cancer.(Kuan and Ziegler, 2014) TSLP is the ligand of a heterodimeric receptor complex composed by Cytokine Receptor Like Factor 2 (CRLF2) and interleukin 7 (IL-7) receptor α subunit.(Pandey et al., 2000) Interestingly, in recent years, CRLF2 was found to be an oncoprotein and emerged as a negative prognostic factor for precursor B cell acute lymphoblastic leukemia (pre-B ALL). Nevertheless, compared with other cytokines, TSLP-CRLF2 signaling is less characterized and the detail of its downstream pathways is lacking, especially in the context of hematological malignancy. This dissertation is motivated to study more about CRLF2 signaling and its dysregulation in acute leukemia.

The objective of this dissertation is two-fold. The first is to study the dysregulated CRLF2 signaling in the context of pre-B ALL. The second is to employ the understanding about leukemic CRLF2 signaling gleaned in this study to identify potential therapeutic targets for CRLF2-rearranged pre-B ALL. To accomplish these goals, this dissertation consists of three chapters with the outline briefly as follows. Chapter 1 is to introduce CRLF2 and the TSLP-CRLF2 signaling in the non-leukemic and leukemic contexts. Chapter 2 is focused on comparing leukemic signaling induced by CRLF2 vs. BCR/ABL1. Chapter 3 delineates the rationale and evidence for a potential therapeutic targets downstream of leukemic CRLF2 signaling.

Chapter 1

CRLF2 signaling pathways

Discovery of CRLF2

The gene *CRLF2* is located in the pseudoautosomal region 1 of chromosome X and Y. It encodes a 42 kDa cell surface cytokine receptor subunit which heterodimerizes with IL-7 receptor α subunit upon the binding of the ligand, TSLP. TSLP was first identified in the conditioned medium from a mouse thymic stromal cell line, several years before CRLF2 was cloned. Independent of IL-7, TSLP was shown to support the differentiation and growth of B and T cells *in vitro*.(Friend et al., 1994) It was unclear how TSLP exerts its function on lymphocytes until its receptor subunit, CRLF2, was cloned in 2000.(Pandey et al., 2000; Park et al., 2000) Taking advantage of the cytoplasmic domain similarity with erythropoietin receptor, interleukin 9 α chain and common γ chain, Pandey *et al* discovered a new murine cytokine receptor, originally named as TSLPR and later called CRLF2, whose affinity to TSLP was greatly enhanced in the presence of IL-7 receptor α subunit. They also demonstrated that TSLP-CRLF2 signaling transduces through STAT5. Soon after that, the human homolog of CRLF2 was also cloned in 2001.(Quentmeier et al., 2001; Reche et al., 2001)

Functions of CRLF2

CRLF2 plays multiple roles in lymphocyte development. Initial functional studies for TSLP and CRLF2 were carried out in mouse cell lines. For mouse B cell development, Tslp is able to stimulate B cell growth through different maturation stages while Il-7 is only effective in the early stage. In mouse long term bone marrow cultures, the growth promoting effect of Tslp persists throughout B220+ IgM-, B220+ IgM^{low} and B220+ IgM^{high} stages. On the contrary, the stimulating effect of Il-7 is more prominent and limited for at the B220+ IgM- stage. (Levin et al., 1999) For mouse T cells, Crlf2 also plays essential roles. Knockout of Crlf2 in mice is not embryonically lethal and allows the evaluations for Crlf2 functions in T cell development. Compared with wild type mice, $Crlf2^{-/-}$ mice had an impaired recovery of CD4+ single positive T cells after sublethal whole body irradiation. In addition, the thymic T cell cellularity was worse in Crlf2 and common γ chain double knockout mice than in common γ chain knockout mice. The administration of Tslp into the common γ chain knockout mice helped expand both T and B cell populations.(Al-Shami et al., 2004) In essence, CRLF2 and its ligand TSLP are needed for normal lymphocyte development and homeostasis.

CRLF2 signaling induced by TSLP

Because the similarity of cytoplasmic domains are shared among CRLF2, common γ chain and erythropoietin receptor, CRLF2 has been known for signaling through the JAK/STAT pathway when it was cloned, before the first draft of Human Genome Project was completed. Nevertheless, it was not until phosphoproteomics analysis was introduced that a global characterization and the greater detail of CRLF2 signaling upon TSLP stimulation became available. To study the TSLP-stimulated CRLF2 signaling, Zhong *et al.* employed a quantitative proteomics technology called stable isotope labeled amino acids in culture (SILAC) to measure phosphoproteomic alterations caused by TSLP in a mouse progenitor B cell line (Ba/F3) reconstituted with CRLF2.(Zhong et al., 2012) By enriching phosphotyrosine (pY), phosphoserine (pS) and phosphothreonine (pT)-containing peptides followed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis, Zhong *et al.* made three insightful observations about CRLF2 signaling. First, in addition to JAK family kinases, TSLP-CRLF2 signaling also involves TEC (Btk-Y551) and SRC (Lyn-Y397) family kinases. Second, phosphatases Ptpn6 (Y538) and Ptpn11 (Y546) are also downstream of TSLP-CRLF2 signaling. Third, a short stimulation of TSLP (15 min) not only activated Stat3, Stat5a and Stat5b but also other transcription factors/co-activators such as Atf7 (T51, T53) and Crtc2 (Y489, T502). This analysis provides an opportunity to examine CRLF2 signaling at an unprecedented depth and might pave the way to understand the mechanism of TSLP-mediated allergy.(Ying et al., 2005, 2008)

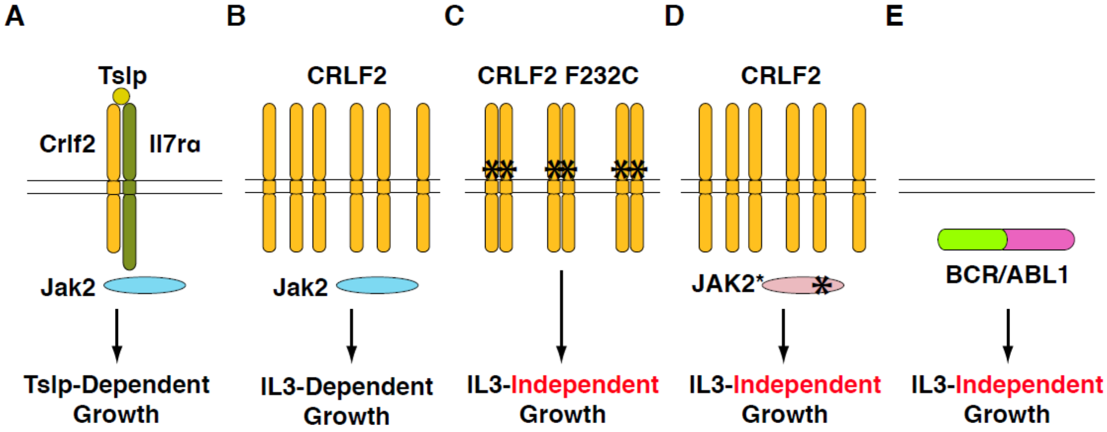
CRLF2 rearrangement in acute lymphoblastic leukemia

Leukemia is hematologic malignancy that results from uncontrolled proliferation of hematopoietic cells. Its molecular mechanism encompasses a wide range of genomic aberrations such as chromosomal translocation, gene deletion, point mutation, gene amplification (i.e. copy number variations), among others. All these genetic events cause dysregulation of gene expression, leading to a series of cell transformation processes that could involve proliferative signaling, evading growth suppressors, resisting cell death, enabling replicative immortality, among other hallmarks of cancer.(Hanahan and Weinberg, 2011) Once lymphoid precursor cells that undertake these transformation processes in an abrupt fashion might develop into acute lymphoblastic leukemia (ALL).

ALL is the most common cancer in children whose genetic heterogeneity is reflected in different clinical outcomes. In recent years, CRLF2 was identified as a negative prognostic factor in ~6% of pediatric and adult patients with precursor B cell ALL (pre-B ALL).(Ensor et al., 2011; Moorman et al., 2012; Harrison, 2013) The Children's Oncology Group reported that high expression of CRLF2 confers an adverse prognosis in high-risk pre-B ALL patients.(Chen et al., 2012) Several independent studies have demonstrated that CRLF2 acts as an oncoprotein. (Mullighan et al., 2009; Russell et al., 2009; Yoda et al., 2010; Chapiro et al., 2010;) In pre-B ALL, both gene duplication or genetic rearrangement involving *CRLF2* locus would result in CRLF2 overexpression. (Roberts et al., 2014) Concerning genetic rearrangement, specifically, chromosomal translocation t(X;14)(p22;q32) or t(Y;14)(p11;q32) juxtapose *CRLF2* to the 3' end of the immunoglobulin heavy chain gene *IGH*; alternatively, an interstitial deletion in the pseudoautosomal region 1 of chromosome X or Y would juxtapose *CRLF2* to the 3' end of the noncoding exon of *P2RY8*. In both scenarios, the expression of *CRLF2* is aberrantly upregulated by the new adjacent promoters.(Russell et al., 2009; Mullighan et al., 2009) Interestingly, about one-half of *CRLF2*-rearranged cases also harbor an activating mutation in exon 16 of *JAK2,* most commonly involving I682 or R683 (Mullighan et al., 2009; Yoda et al., 2010). A rare *CRLF2* gain-of-function mutation

F232C was also observed in pre-B ALL.(Chapiro et al., 2010) In a murine progenitor B cell line, Ba/F3, it has been shown that either CRLF2 F232C or the combination of CRLF2 overexpression and JAK2 R683G mutation would confer IL-3-independent growth, implicating their role in triggering leukemic proliferation (Figure 1).(Chapiro et al., 2010; Yoda et al., 2010)

Figure 1- Progenitor B cell system (Ba/F3 cells) for studying CRLF2 and BCR/ABL1 signaling in leukemia



A, upon the ligand binding, Crlf2 heterodimerizes with Il7α and transduces via Jak2. *B,* wild type CRLF2 is transduced and Ba/F3 cells depend on the growth support from IL-3. *C,* autophosphorylation of CRLF2 F232C confers growth factor independence to transduced Ba/F3 cells. *D,* wild type CRLF2 synergizes with JAK2 mutant (R683G) to confer growth factor independence to transduced Ba/F3 cells. *E,* BCR/ABL1 fusion protein transforms Ba/F3 cells.

Aberrant CRLF2 signaling in acute lymphoblastic leukemia

CRLF2 signaling in pre-B ALL is less studied. Aberrant CRLF2 signaling renders abnormal cell proliferation independent of growth factors in cell culture systems (Figure 1). The altered signaling pathways are even more convoluted in the presence of other genetic abnormalities in pre-B ALL. For example, in around half of CRLF2-rearranged pre-B ALL cases, a gain-of-function mutation of JAK2 exon 16 coexists. This further makes the downstream signaling event distinct from normal CRLF2 signaling.(Bodegom et al., 2012; Huang et al.) To study the additional impact of CRLF2 overexpression on top of JAK2 exon 16 gain-of-function mutation (R683G), Bodegom *et al.* used SILAC to compare Ba/F3 cells with JAK2 R683G alone vs. with JAK2 R683G plus CRLF2. Overall, the addition of CRLF2 to JAK2 R683G alters the phosphotyrosine profiling globally compared with TSLP-stimulated CRLF2 signaling. While TSLP stimulation causes tyrosine hyperphosphorylation of SRC and TEC family kinases, the regulations on these kinases brought by CRLF2 to concurrent JAK2 R683G are in the opposite direction. Having differences stated, CRLF2 JAK2 R683G signaling still activates STAT3, STAT5, MAPK3 and PTPN11, sharing this commonality with TSLP-induced CRLF2 signaling. Another rare *CRLF2* F232C gain-of-function mutation causes autophosphorylation and constitutive activation of CRLF2 signaling, also leading to leukemic growth (Figure 1).(Chapiro et al., 2010) The detail of CRLF2 F232C downstream signaling will be further elucidated in the next chapter.

Chapter 2

Comparison of leukemic signaling induced by CRLF2 and BCR/ABL1

Introduction

Pre-B ALL is the most common pediatric malignancy.(Pui et al., 2012) Prognosis of this disease is stratified into different risk groups, predominantly based on chromosome abnormalities and gene mutation analysis, and treatment plans for patients are made accordingly. One such risk group conferring a markedly negative prognosis is the presence of the BCR-ABL1 fusion gene resulting from Philadelphia chromosome t(9;22) (Ph+).(Schultz et al., 2007; Den Boer et al., 2009) In recent years, the progress in transcriptomic analysis helped identify a new group of pre-B ALL patients who shared similar gene expression profiles as those with BCR-ABL1.(Den Boer et al., 2009; Harvey et al., 2010; Roberts et al., 2014) They are categorized as Philadelphia chromosome-like (Ph-like) pre-B ALL with the prognosis as poor as Ph+ pre-B ALL.(Harvey et al., 2010; Yoda et al., 2010; Izraeli, 2014) One major subset of Ph-like pre-B ALL are the patients with the *CRLF2* rearrangement. Because of their drastic prognoses, for both Ph+ and Ph-like pre-B ALL patients, the current treatment recommendation is still hematopoietic stem cell transplantation at the earliest remission. Given the multitude of adverse effects in transplantation, it is imperative to develop better therapy for these two groups of diseases. At present, a battery of BCR/ABL1-targeted small molecule inhibitors, such as imatinib, dasatinib and ponatinib, are available to be combined with conventional chemotherapy to treat Ph+ pre-B ALL whereas CRLF2-targeted therapy is still out of sight. Even the differences between BCR/ABL1 and CRLF2 signaling pathways have not been sorted out. Therefore, addressing this question may better the understanding of Ph-like pre-B ALL and pave the way for future therapy development.

Rationale of using proteomics analysis

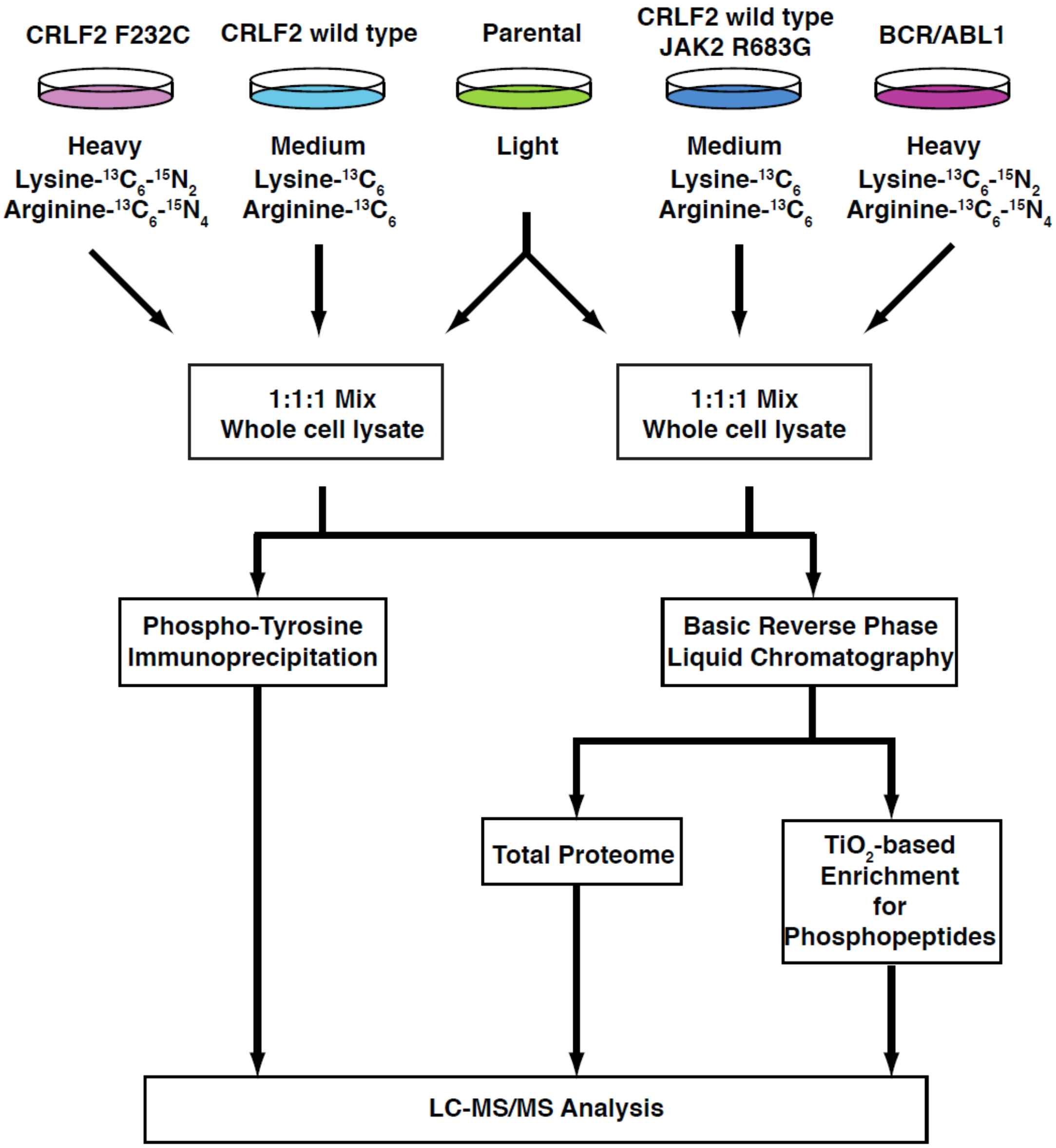
Cell signaling regulation often is not reflected in genomic and transcriptomic profiling. The complexity of posttranscriptional regulation and posttranslational modification confounds these two types of analyses to represent total protein abundance and phosphoproteomic alterations.(Gygi et al., 1999) Current data about the comparison between CRLF2 and BCR/ABL1 signaling pathways only provide transcript level information and how these two pathways differ in protein abundance and phosphorylation regulation is largely unknown. To address this question, we leveraged quantitative proteomics in a mouse progenitor B cell system (Ba/F3 cell line) transduced with BCR-ABL1 or different CRLF2 genotypes for comparison. SILAC was employed for quantifying the differences of total proteome and phosphoproteome in these types of cells. In addition to proteomics analysis, we also used a kinase and small molecule inhibitor screen to query differential pharmacological effects across these cell types as an extraneous perspective for future therapy development.

Experimental procedures

Cell lines and SILAC labeling — Transduction in the Ba/F3 cell line systems was carried out using pMSCV-based vectors and has been previous described.(Bodegom et al., 2012) Ba/F3 parental cells (empty vector control), labeled in the "light" SILAC medium were used as a baseline to link two independent 3-plex SILAC experiments (Figure 2). In the first 3-plex SILAC, Ba/F3 with CRLF2 F232C was labeled with "heavy" isotopes (lysine-$^{13}C_6$,$^{15}N_2$, arginine-$^{13}C_6$,$^{15}N_4$) and Ba/F3 with CRLF2 wild type overexpression was labeled with "medium" isotopes (lysine-$^{13}C_6$, arginine-$^{13}C_6$); in the second 3-plex SILAC, the "heavy" sample (lysine-$^{13}C_6$,$^{15}N_2$, arginine-$^{13}C_6$,$^{15}N_4$) was Ba/F3 with BCR/ABL1 and the "medium" sample (lysine-$^{13}C_6$, arginine-$^{13}C_6$) was Ba/F3 with CRLF2 wild type and JAK2 R683G. Cells were cultured in RPMI-1640 (10% fetal bovine serum, 1% penicillin-streptomycin) supplemented with labeled amino acids (Cambridge Isotope Laboratory) and maintained at 37°C in the CO_2 5% incubator. Ba/F3 parental cells and Ba/F3 cells with CRLF2 wild type alone were maintained with murine IL-3 at 0.5 ng/ml. All groups of cells were washed with phosphate buffered saline for 6 times and subjected to IL-3 deficient media for 6 hr at 37°C prior to protein extraction.

Peptide preparation and phosphopeptide enrichment — Labeled cells were lysed in 9 M urea buffer with protease inhibitors (Halt® Cocktail) (Thermo), sodium pyrophosphate (2.5 mM), sodium orthovanadate (1 mM), sodium fluoride (5 mM), β-glycerophosphate (1 mM) and Equal amounts of protein lysates from each labeling condition were mixed and subjected to trypsin in-solution digestion, followed by lyophilization before downstream fractionation. Forty-five mg of lyophilized tryptic peptides were used for phosphotyrosine enrichment using Cell Signaling Technology PTMScan pY-1000 rabbit monoclonal antibody (#8803). Twelve hundred ug lyophilized tryptic peptides were fractionated into 12 fractions with basic reverse phase liquid chromatography. One tenth of each fraction was used for total proteome analysis whereas the rest of each fraction was subjected to titanium dioxide (TiO2)-based enrichment of phosphopeptides. C18 desalting was performed before LC-MS/MS analysis (Orbitrap-Elite).

Figure 2- SILAC strategy to study proteomic and phosphoproteomic alterations in CRLF2 and BCR/ABL1 signaling networks



Two 3-plex SILAC experiments were intersected with a common cell culture, Ba/F3 parental cells. Extracted proteins were trypsinized and subjected to either anti-phosphotyrosine immunoprecipitation or basic RPLC fractionation, which was followed by TiO2-based enrichment for phosphoserine/threonine peptides.

Phosphopeptide enrichment —The detail of anti-phosphotyrosine immunoprecipitation was described previously.(Kim et al., 2014; Zhong et al., 2012) Briefly, tryptic peptides were lyophilized for 48 hours, followed by binding to PTMScan® Phospho-Tyrosine rabbit monoclonal antibody (P-Tyr-1000) (Cell Signaling Technology, #8803) The method of titanium dioxide (TiO2)-based enrichment of phosphopeptides was described previously.(Zhong et al., 2012) Briefly, tryptic peptides were lyophilized and fractionated with basic reverse phase liquid chromatography.

Liquid chromatography-tandem mass spectrometry—The enriched phosphopeptides were analyzed on an LTQ-Orbitrap Elite mass spectrometer (Thermo Electron, Bremen, Germany) interfaced with Easy-nLC II nanoflow liquid chromatography system (Thermo Scientific, Odense, Denmark). The peptide digests were reconstituted in 0.1% formic acid and loaded onto a trap column (75 µm x 2 cm) packed in-house with Magic C_{18} AQ (Michrom Bioresources, Inc., Auburn, CA, USA). Peptides were resolved on an analytical column (75 µm x 50 cm) at a flow rate of 300 nL/min using a linear gradient of 10-35% solvent B (0.1% formic acid in 95% ACN) over 90 min. The analytical column was heated using column heater at 56°C to reduce the back pressure. The total run time including sample loading and column reconditioning was 120 min. Mass spectrometry data was acquired in a data dependent acquisition mode. The full scans in the range of 350-1700 *m/z* was carried out using an Orbitrap mass analyzer at a mass resolution of 120,000 at 400 *m/z*. Fifteen most intense precursor ions from a survey scan were selected for MS/MS fragmentation using higher energy collisional dissociation (HCD) fragmentation with 32% normalized collision energy and detected and measured using Orbitrap mass analyzer at a mass resolution of 30,000 at 400 *m/z*. AGC target was set to 1×10^6 for MS and 5×10^4 ions for MS/MS with a maximum ion accumulation time of 200 ms. Dynamic exclusion was set for 30 seconds with a 10 ppm mass window. Internal calibration was carried out using lock mass option (m/z 445.1200025) using ambient air.

Database search and other bioinformatics analysis —SILAC LC-MS/MS raw files were analyzed in the MaxQuant 1.5.0.25 software platform including the Andromeda search algorithm. Data analysis parameters are listed below. Fixed modification: carbamidomethylation (cysteine), MS/MS tolerance (FTMS): 20 PPM, top MS/MS peaks per 100 Da (FTMS): 12, MS/MS deisotoping (FTMS): True, PSM FDR: 0.01, Protein FDR: 0.01, Site FDR: 0.01, minimal peptide length: 4, modifications included in protein quantification: acetyl (protein-N-term); deamidation (NQ); oxidation (M), peptides used for protein quantification: unique+razor. Raw files including peak lists are deposited in PRIDE Archive with the dataset identifier PXD001589 (Reviewer account details—Username: reviewer26457@ebi.ac.uk. Password: 4pLeAv9O). Core Analysis settings: reference set: Ingenuity Knowledge Base, direct and indirect relationships, molecules per network: 35, networks per analysis: 25, confidence: only experimentally observed, species: human and mouse with stringent filter.

Kinase and small molecule inhibitor screen — This methodology is described previously. (Tyner et al., 2013; Huang et al.) Briefly, 129 different kinase or small molecule inhibitors were originally stocked in DMSO and diluted with culture media to 50 ul in

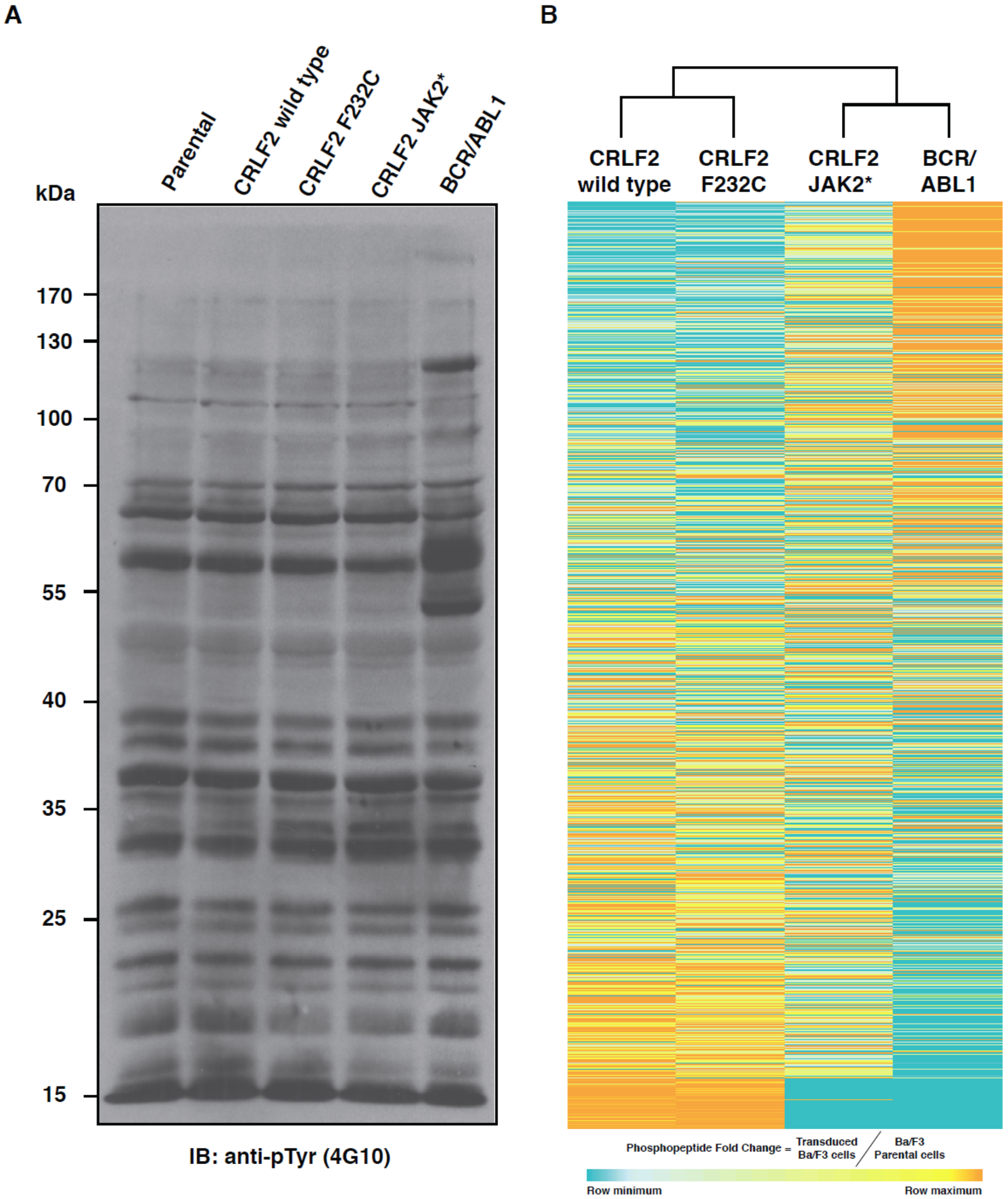
96-well plates kept at -20°C until use. Five types of engineered Ba/F3 cells at the density of 1 million cells per ml of culture media were plated into the inhibitor-laden 96-well plates (50 ul per well). Cells were cultured at 37°C, 5% CO_2 for three days and then coupled to a CellTiter 96 One solution cell proliferation assay (Promega)

Results and discussion

Characterizing tyrosine phosphorylation in CRLF2 and BCR/ABL1 signaling with immunoblotting — Aberration of cell signaling in cancer can be driven by oncogenic mutations and is correlated with neoplastic development.(Hanahan and Weinberg, 2011; Lugo et al., 1990; Skaggs et al., 2006) The mechanistic investigation about how individual genetic lesions lead to signaling alterations in clinical samples, however, is often troubled by the noise from complex genomic changes such as recurrent deletions and rearrangements.(Alexandrov et al., 2013) To study how distinct types of CRLF2 aberrations and the BCR-ABL1 fusion gene affect cell signaling in the context of leukemic growth, we transduced wild type CRLF2 alone, CRLF2 F232C, wild type CRLF2 with JAK2 gain-of-function mutation (R683G) and BCR-ABL1 into a mouse progenitor B cell line (Ba/F3) and used these four cell lines along with Ba/F3 parental cells for subsequent analyses (Figure 1). Among these 5 cell lines, as reported previously, the transduction with CRLF2 F232C, wild type CRLF2 with JAK2 R683G and BCR/ABL1 transformed Ba/F3 cells to be cytokine independent whereas Ba/F3 parental cells and Ba/F3 with wild type CRLF2 alone still require mouse IL-3 to maintain growth in culture.(Yoda et al., 2010)

CRLF2 heterodimerizes with the interleukin 7 receptor α subunit and transduces via non-receptor tyrosine kinase JAK2 in either normal or leukemic context. Wild type ABL1 is a non-receptor tyrosine kinase, and the leukemogenic fusion protein BCR/ABL1 retains the tyrosine phosphorylation activity, causing a wide range of pro-growth signaling activation. To characterize the spectrum of tyrosine phosphorylation events resulting from different CRLF2 aberrations and BCR/ABL1 in immunoblotting, we used an anti-phosphotyrosine antibody (4G-10) to probe phosphotyrosine-containing proteins in cell lysates (Figure 3A). The profiling revealed a distinct banding pattern in BCR/ABL1-transduced cells whereas the disparity between mutant CRLF2 and wild type CRLF2 with/without JAK2 R683G is subtler in band signal intensities.

Figure 3- Phosphoproteome profiling of CRLF2 and BCR/ABL1 signaling in Ba/F3 cells



A, Whole cell lysates of parental and transduced Ba/F3 cells were probed with anti-phosphotyrosine antibody (4G-10) in immunoblotting. *B,* The heat map is showing the phosphorylation signatures of CRLF2 and BCR/ABL1 signaling. The SILAC ratios between transduced vs. parental Ba/F3 cells for all 2,534 phosphosites (pY, pS, pT) commonly identified in all 5 cell lines were plotted.

Different phosphorylation signatures between CRLF2 and BCR/ABL1 signaling revealed through phosphoproteomics analysis — To further quantify these differences in tyrosine phosphorylation as well as other alterations in phosphoproteome (pS and pT) and total proteome, we designed two 3-plex SILAC studies with an overlapping cell line (Ba/F3 parental cells) to compare across 5 cell lines (Figure 2). With the false discovery rate at 1%, in the total proteome analysis, the two 3-plex SILAC experiments generated 293,957 peptide-spectrum matches, corresponding to 50,197 peptides and 5,158 proteins groups including 91 kinases, 74 phosphatases and 298 transcription factors. We used Ba/F3 parental cells as the common denominator for calculating SILAC ratios. Upregulated proteins ≥ 2-fold are listed in Table 1, and all proteins identified commonly in 5 cell lines are in Appendix A. In the phosphoproteome analysis, the two 3-plex SILAC experiments generated 82,119 peptide-spectrum matches, corresponding to 8,488 distinct phosphopeptides belonging to 2,695 protein groups including 91 kinases, 31 phosphatases and 252 transcription factors. Upregulated phosphotyrosine sites ≥ 2-fold are listed in Table 2, and all phosphosites identified commonly in 5 cell lines are in Appendix B. To validate the performance of our SILAC system and proteomics analysis, we referenced several known positive controls for CRLF2 and BCR/ABL1 downstream signaling. In one such sample, both immunoblotting and integrated proteome/phosphoproteome results showed hyperphosphorylation of Stat5a (Y694) downstream of both CRLF2 and BCR/ABL1 (CRLF2 & JAK2 R683G 25.3-fold, BCR/ABL1 10.1-fold) (Figure 4).

Table 1: Proteins that are upregulated ≥ 2-fold in CRLF2 and BCR/ABL1 signaling

CRLF2 wild type		**CRLF2 F232C**		**CRLF2 wild type, JAK2 R683G**		**BCR/ABL1**	
Gene Symbol	**Fold Change***	**Gene Symbol**	**Fold Change***	**Gene Symbol**	**Fold Change***	**Gene Symbol**	**Fold Change***
Hic2	22.02	Dffa	62.07	Anapc1	29.84	S100a8	16.23
S100a9	17.56	Hic2	19.12	Hic2	18.88	Prkar2a	15.84
S100a8	14.05	S100a8	16.69	Scin	11.42	Gm5483	12.49
Lgals3bp	12.68	Lgals3bp	14.34	Ifitm3	9.94	S100a4	10.64
Gfm2	10.47	S100a9	13.89	Lgals3bp	8.50	Anapc1	9.85
Lsp1	8.68	Lsp1	7.67	S100a8	7.91	Mrpl23	9.26
Scin	6.94	Rab38	6.98	Prkar2a	7.47	S100a9	8.21
Dffa	5.44	Scin	6.92	Anxa1	5.17	Trpv2	7.14
Itga4	4.92	Sfxn3	6.90	Gm5483	4.65	Ifitm3	6.30
Fxn	4.83	Ifitm3	6.32	Itga4	4.34	Rasal3	5.15
S100a4	4.56	S100a4	4.97	Gimap8	3.99	Gimap8	5.10
Zc3h14	4.00	Itga4	3.83	S100a9	3.84	Sc4mol	5.06
Cdkn1b	3.98	Tgm2	3.80	Bcl2	3.77	Hmgcs1	4.51
Atg4b	3.55	Atg4b	3.74	Hmgcs1	3.74	Scin	4.08
Anxa1	3.44	Anxa1	3.73	Tmx2	3.62	Mgst2	3.96
Tgm2	3.39	Cdkn1b	3.23	Hsdl1	3.53	Mtap	3.88
Rab38	3.21	Rbmx	2.94	Rab38	3.48	Ldlr	3.87
Ifitm3	3.13	Bcl10	2.76	Tfip11	3.44	Cyp51	3.73
Pgrmc1	3.00	Tmx2	2.76	Golph3	3.27	Osbpl8	3.51
Rbmx	2.99	Tes	2.70	Hmgcl	3.23	Fdps	3.49
Tmx2	2.89	Pdcd4	2.55	Cyp51	3.21	Lcp2	3.37
Acot7	2.79	Rab27b	2.54	Ociad1	3.16	Cotl1	3.04
Rwdd4a	2.75	Cox15	2.49	Acot7	3.02	Ubl7	2.91
Cmc1	2.70	Psmb7	2.43	Rbmx	2.97	Mcl1	2.89
Rassf2	2.69	Acot7	2.34	Zc3h14	2.97	Dok2	2.83
Tes	2.58	Cpne1	2.33	Trpv2	2.91	Nvl	2.76
Akr7a5	2.45	Timm8b	2.30	Eif4g3	2.84	Atxn3	2.75
Hist1h1b	2.44	Rassf2	2.30	Arsb	2.81	Ptcd3	2.73
Eif4g3	2.42	Hnrnph2	2.24	Dak	2.72	Bcl2	2.71
Palm	2.41	Srbd1	2.23	LOC100862446	2.71	Amacr	2.71
Pdcd4	2.39	Dera	2.19	Sqstm1	2.70	Zfp36l2	2.70
Dera	2.30	Dak	2.18	Igfbp4	2.59	Tgs1	2.70
Timm8b	2.28	Atad3a	2.17	Fdps	2.56	Rab27b	2.69
Polr1c	2.26	Akr7a5	2.16	Fut8	2.55	Coro7	2.69
0610011F06Rik	2.22	Bcl2	2.09	Coro7	2.51	Cd63	2.66
Mrps6	2.22	Eif4g3	2.08	Yif1b	2.47	Snap29	2.60
Hist1h1a	2.17	Pet2	2.02	Rassf2	2.43	Efhd1	2.53
Fam76b	2.13	Dffa	62.07	Plac8	2.42	Fhl3	2.51
Rab27b	2.09	Hic2	19.12	Tes	2.41	Emr1	2.49
Cpne1	2.08	S100a8	16.69	Golgb1	2.41	Golt1b	2.41
Hist1h2bk	2.07	Lgals3bp	14.34	Trip12	2.40	Ptgs1	2.41
Coq5	2.07	S100a9	13.89	Clasp2	2.34	Tmx2	2.39
Tbc1d9b	2.07	Lsp1	7.67	Ybx3	2.33	Acat2	2.39
Gbe1	2.07	Rab38	6.98	Ybx3	2.33	Adrm1	2.34
Golga2	2.05	Scin	6.92	Cd63	2.32	1810037I17Rik	2.32
Gimap8	2.05	Sfxn3	6.90	Rasal3	2.31	Igfbp4	2.32
Bphl	2.03	Ifitm3	6.32	Sun2	2.30	Mtch1	2.32
Hist1h1c	2.03	S100a4	4.97	Stub1	2.30	Eif4a2	2.28
Atad3a	2.01	Itga4	3.83	Fam203a	2.29	Uap1l1	2.28
Psmb7	2.00	Tgm2	3.80	Cryzl1	2.27	Lss	2.27
		Atg4b	3.74	Gnl3l	2.26	Fnbp1	2.25
		Anxa1	3.73	Hspa13	2.24	Fads1	2.24
		Cdkn1b	3.23	Lss	2.23	Rab21	2.22
		Rbmx	2.94	Sc4mol	2.21	Ttc1	2.20

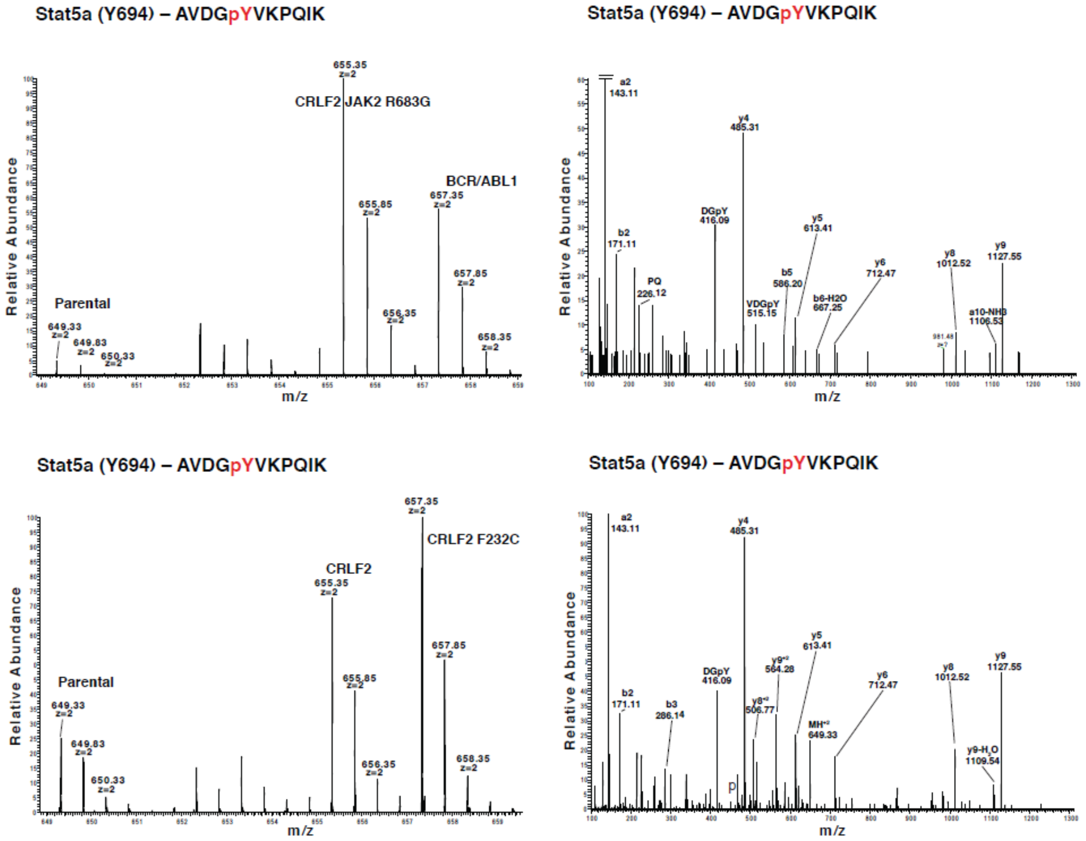
		Bcl10	2.76	Pik3cg	2.18	Armc6	2.19
		Tmx2	2.76	Ppp5c	2.18	Itga2b	2.18
		Tes	2.70	Zfp593	2.18	Acsl4	2.16
		Pdcd4	2.55	Aamp	2.17	Capn2	2.15
		Rab27b	2.54	Cdk6	2.09	Cryzl1	2.12
		Cox15	2.49	Ddx47	2.09	Snx5	2.11
		Psmb7	2.43	Ipo8	2.08	Tuba8	2.10
				Pecam1	2.08	Crlf3	2.09
				Cnot2	2.07	Rcn1	2.09
				Atad2b	2.07	Cd44	2.08
				Fads1	2.06	Zyx	2.08
				Slc18a2	2.06	Dusp3	2.08
				Aarsd1	2.06	Nfatc2	2.07
				Fth1	2.05	Aacs	2.07
				Ddx54	2.03	Slc2a1	2.07
				Dhcr7	2.03	Arrb2	2.06
				Hspbp1	2.02	Dnajb11	2.05
				Cluh	2.00	Commd9	2.05
						Dstyk	2.04
						Casp3	2.04
						Bid	2.03
						Srpr	2.02
						Ndrg3	2.02
						Lpxn	2.00
* The SILAC ratios between engineered Ba/F3 cells vs. parental Ba/F3 cells							

Table 2: Phosphotyrosine sites that are upregulated ≥ 2-fold in CRLF2 and BCR/ABL1 signaling

CRLF2 wild type		**CRLF2 F232C**		**CRLF2 wild type, JAK2 R683G**		**BCR/ABL1**	
Phosphosite	**Fold Change***	**Phosphosite**	**Fold Change***	**Phosphosite**	**Fold Change***	**Phosphosite**	**Fold Change***
Igf2r_Y1396	149.45	Igf2r_Y1396	20.04	Igf2r_Y1396	203.16	Psma2_Y76	60.39
Tgm2_Y369	4.53	Dyrk3_Y368	5.01	Stat5a_Y694	25.27	Exosc6_Y40	38.85
Stat5a_Y694	3.50	Tgm2_Y369	4.78	Stat5b_Y699	22.75	Myh9_Y1805	35.63
Ptpn11_Y542	3.44	Stat5a_Y694	3.93	Lcp1_Y598	6.85	Cct8_Y30	34.29
Acot7_Y164	2.41	Acot7_Y164	3.25	Itsn2_Y554	4.31	Igf2r_Y1396	31.51
Ncl_Y464	2.16	Ptpn11_Y542	2.88	Acot7_Y164	4.18	Ptpn11_Y279	29.76
Stat5b_Y699	2.05			Prpf8_Y2091	3.86	Arhgdib_Y129	27.10
				Snd1_Y109	3.71	Vasp_Y39	18.42
				Pgm2_Y353	3.46	Pik3r1_Y197	16.17
				LOC101056619_Y29	3.26	Vim_Y117	14.28
				LOC100505031_Y156	3.13	Stat5b_Y699	14.11
				Pgam1_Y92	3.07	Hnrnpa3_Y166	13.73
				Ptpn11_Y542	2.93	Vars_Y427	11.79
				G6pdx_Y401	2.82	Itsn2_Y554	10.77
				Ldha_Y239	2.73	Stat5a_Y694	10.14
				Grlf1_Y1105	2.34	Eif4a3_Y202	10.12
				Tln1_Y70	2.26	Ddx17_Y200	9.97
				Vta1_Y280	2.21	Eif4a1_Y197	9.53
				Tuba1b_Y272	2.16	Hnrnpa1_Y167	9.49
				Tars_Y297	2.16	Acot7_Y164	9.22
				Hsp90ab1_Y484	2.01	Wdr18_Y61	9.15
						Ptpn11_Y542	9.06
						Lcp1_Y598	8.88
						Pgam1_Y92	8.64
						Snd1_Y109	8.56
						Tagln2_Y8	8.08
						Calm1_Y100	7.84
						Got2_Y75	7.12
						Psma2_Y57	6.64
						Tuba1b_Y108	6.18
						Pgm2_Y353	6.13
						Prpf8_Y2091	6.12
						Ptbp1_Y126	6.06
						Cap1_Y418	5.81
						Tuba1b_Y272	5.48
						Eif2s1_Y82	5.27
						LOC101056619_Y29	5.19
						Cfl1_Y140	5.14
						Lcp1_Y124	4.91
						Tpi1_Y259	4.91
						Phb_Y107	4.84
						Fasn_Y1057	4.80
						Cd84_Y265	4.72
						Tln1_Y70	4.71
						LOC100505031_Y156	4.56
						G6pdx_Y401	4.49
						Pgk1_Y196	4.40

						Txnrd1_Y131	4.18
						Grlf1_Y1105	4.16
						Hist1h4i_Y52	4.16
						Rdx_Y270	3.97
						Psmb8_Y234	3.95
						Actb_Y198	3.91
						Pacsin2_Y76	3.91
						Tars_Y297	3.68
						Myh9_Y190	3.57
						Actr3_Y16	3.40
						Vta1_Y280	3.32
						Prdx1_Y10	3.26
						Rassf1_Y185	2.90
						Srsf3_Y32	2.86
						Tuba1b_Y399	2.77
						Ldha_Y239	2.49
						Hsp90ab1_Y56	2.38
						Gpx1_Y147	2.34
						Ncl_Y464	2.23
						Eef1d_Y182	2.01
* The SILAC ratios between engineered Ba/F3 cells vs. parental Ba/F3 cells							

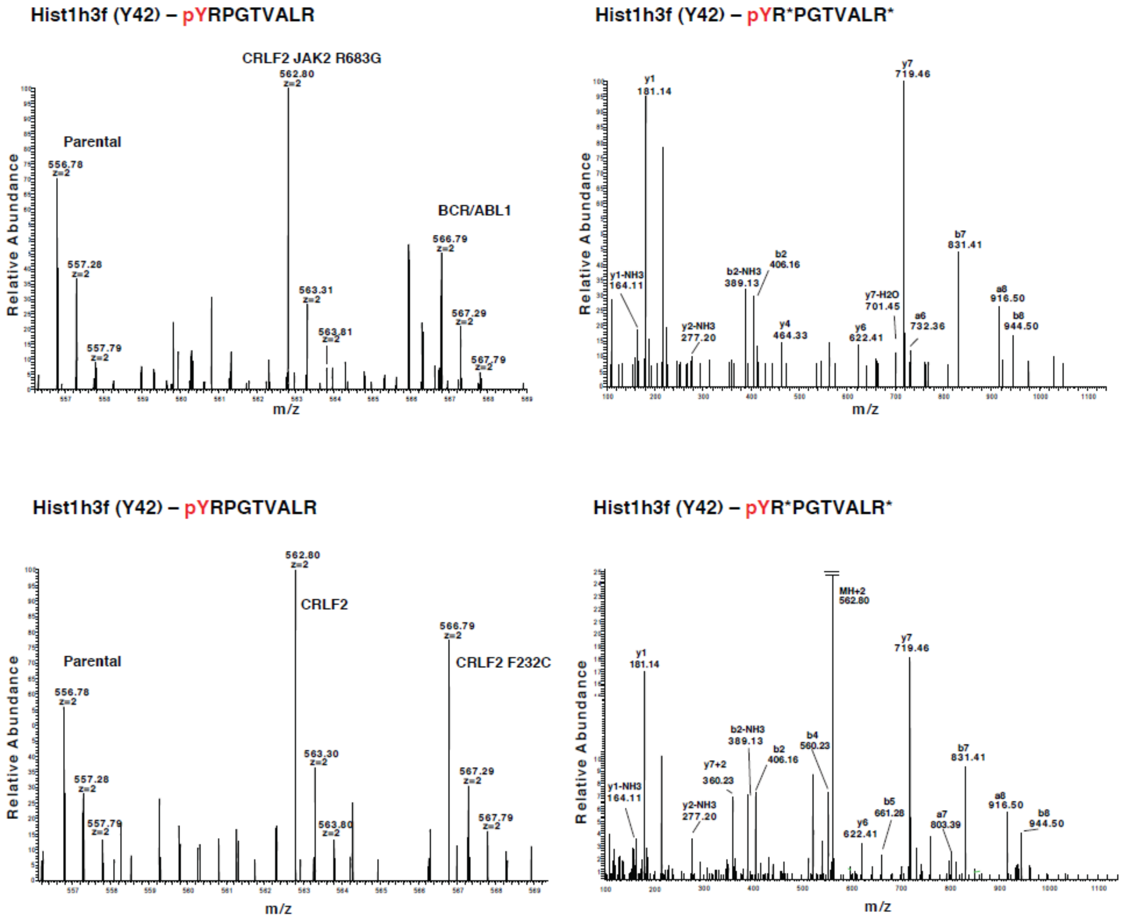
Figure 4- Stat5a (Y694) hyperphosphorylation in Ba/F3 cells with CRLF2 JAK2 R683G



The upper and lower left spectra are from MS1 scans, showing marked upregulation of Stat5a (Y694) in CRLF2 JAK2 mutant Ba/F3 cells. The upper and lower right spectra are from MS2 to confirm the peptide sequence.

Protein phosphorylation of serine, threonine and tyrosine residues in proteins is an instrumental PTM for various biological and pathological processes. The comparison of phosphoproteomic alterations in these engineered Ba/F3 cell lines is designed to help understand how biological processes are differentially regulated between CRLF2 and BCR/ABL1 signaling. All 2,534 non-redundant phosphosites (pY, pS, pT) commonly identified in all 5 cell lines with their SILAC ratios relative to Ba/F3 parental cells were plotted in a heat map in Figure 3B. Interestingly, the unsupervised clustering analysis of phosphosites in the heat map demonstrated that the phosphorylation signature in CRLF2 wild type with JAK2 R683G is distinct from that in BCR/ABL1. Specifically, hyperphosphorylation of Stk10 (T185), Iws1 (S185), Wbp11 (S600), Hirip3 (S152), Dnmt1 (S140) only occurred in CRLF2 JAK2 R683G group whereas Psma2 (Y76,Y57), Hist1h4i (Y52), Vasp (Y39), Srsf3 (Y32) only occurred in BCR/ABL1 group. Most of the hyperphosphorylated tyrosine residues downstream of CRLF2 signaling were more upregulated in BCR/ABL1 group. A noticeable exception existed, however. Histone 3 (Y42) is phosphorylated by nuclear JAK2 and shown related to heterochromatin formation.(Dawson et al., 2009, 2012) In our study, hyperphosphorylation of Hist1h3f (Y42) was common to CRLF2 JAK2 R683G, CRLF2 F232C and CRLF2 wide type alone but not in BCR/ABL1 group (Figure 5). This suggests that CRLF2 signaling might subject Ba/F3 cell growth to different epigenetic regulations, compared with BCR/ABL1 signaling.

Figure 5- H_3Y_{42} hyperphosphorylation in Ba/F3 cells with CRLF2 expression



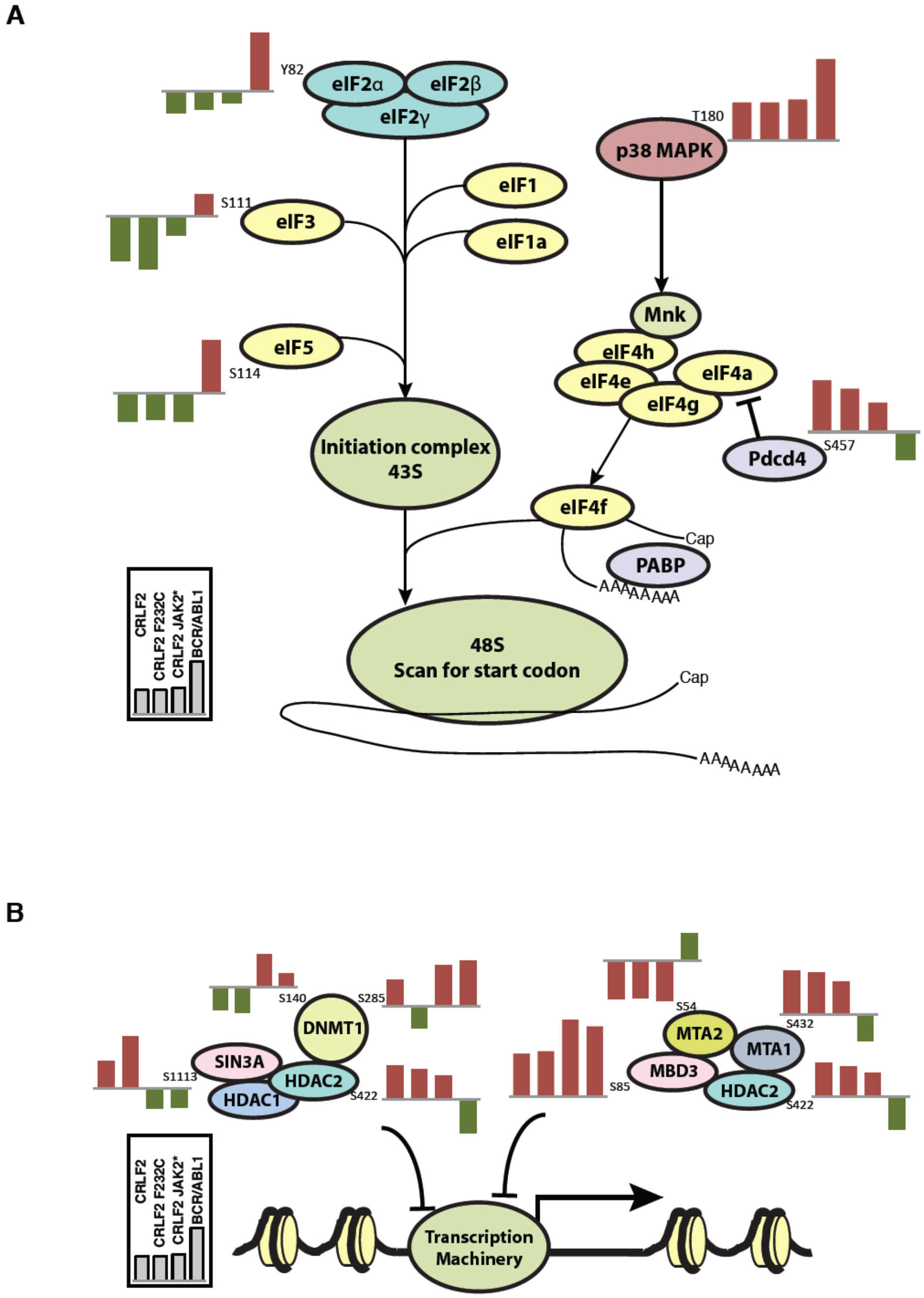
The upper and lower left spectra are from MS1 scans, showing the upregulation of phosphorylation at H_3Y_{42} mediated by JAK2 downstream of CRLF2 signaling but not in BCR/ABL1 signaling. The upper and lower right spectra are from MS2 to confirm the peptide sequence.

Corresponding to phosphoproteomic disparities, a pharmacological approach employed to compare CRLF2 and BCR/ABL1 signaling revealed their dissimilar impacts on cell growth. Ba/F3 parental cell line and 4 engineered cell lines were subjected to a kinase and small inhibitor screen (122 different compounds) which was coupled to a proliferation assay to assess compound potency (Figure 6). As expected, Ba/F3 cells with BCR/ABL1 were sensitive to its targeting compounds with low IC_{50} (nM) including ponatinib (2.2), dasatinib (3.4), nilotinib (23.5), bosutinib (29.8), imatinib (296.1) as well as PD173955 (9.7), an ABL kinase inhibitor. Likewise, Ba/F3 cells with CRLF2 JAK2 R683G were sensitive to JAK inhibitors including tofacitinib (5.3 nM) and ruxolitinib (98.7-437.5 nM) while the IC_{50} of those BCR/ABL1 targeting compounds in CRLF2 cell lines were higher than or equal to 1000 nM. This suggests that current BCR/ABL1-targeted compounds are not effective to curb CRLF2 signaling-mediated leukemic growth.

Figure 6- Kinase and small molecule inhibitor screen for Ba/F3 cell lines

Differential regulation of translation and transcription between CRLF2 and BCR/ABL1 —Molecules and their regulations within a cell can be categorized into various functional modules. In this vein, pathway analysis helps understand and interpret results of global scale experiments. In addition to unsupervised heat map clustering analysis, therefore, we carried out pathway analysis to see what type of biological functions were better represented in our phosphoproteome dataset. Out of >650 pathways annotated in Ingenuity Knowledge Database, two pathways ranked top on the list: EIF2/EIF4 signaling (p= 9.3E-11 – 2.0E-8) and DNA methylation/transcriptional repression signaling (p= 6.6E-9 – 7.8E-9). These two signaling pathways were regulated differently between CRLF2 and BCR/ABL1 signaling networks (Figure 7 A and B). EIF2 and EIF4 signaling is directly related to translational initiation and protein synthesis control. During translation initiation, eIF2 binds to eIF3 and eIF5 to form 43S complex, which subsequently engages eIF4- and PABP-bound mRNA for start codon scanning. Our results of phosphoproteome analysis showed that, compared to CRLF2 signaling, BCR/ABL1 signaling caused opposite regulations of phosphorylation at multiple sites: Eif2s1 (Y82), Eif3b (S111), Eif5b (S114), Eif4a1 (Y197), Eif4a3 (Y202) and PABP (Y297) (Figure 7A). This suggested that BCR/ABL1 signaling upregulates protein synthesis in general while CRLF2-mediated leukemic signaling did not. Another interesting difference lay in the upregulation of DNA synthesis in S phase, during which the activity of Dnmt1 is upregulated to engage Hdac2 repressing transcription. We found CRLF2 JAK2 R683G signaling upregulated the activation phosphosite S140 of Dnmt1 (2.7-fold) whereas this effect in BCR/ABL1 is less prominent (1.1-fold) (Figure 7B).

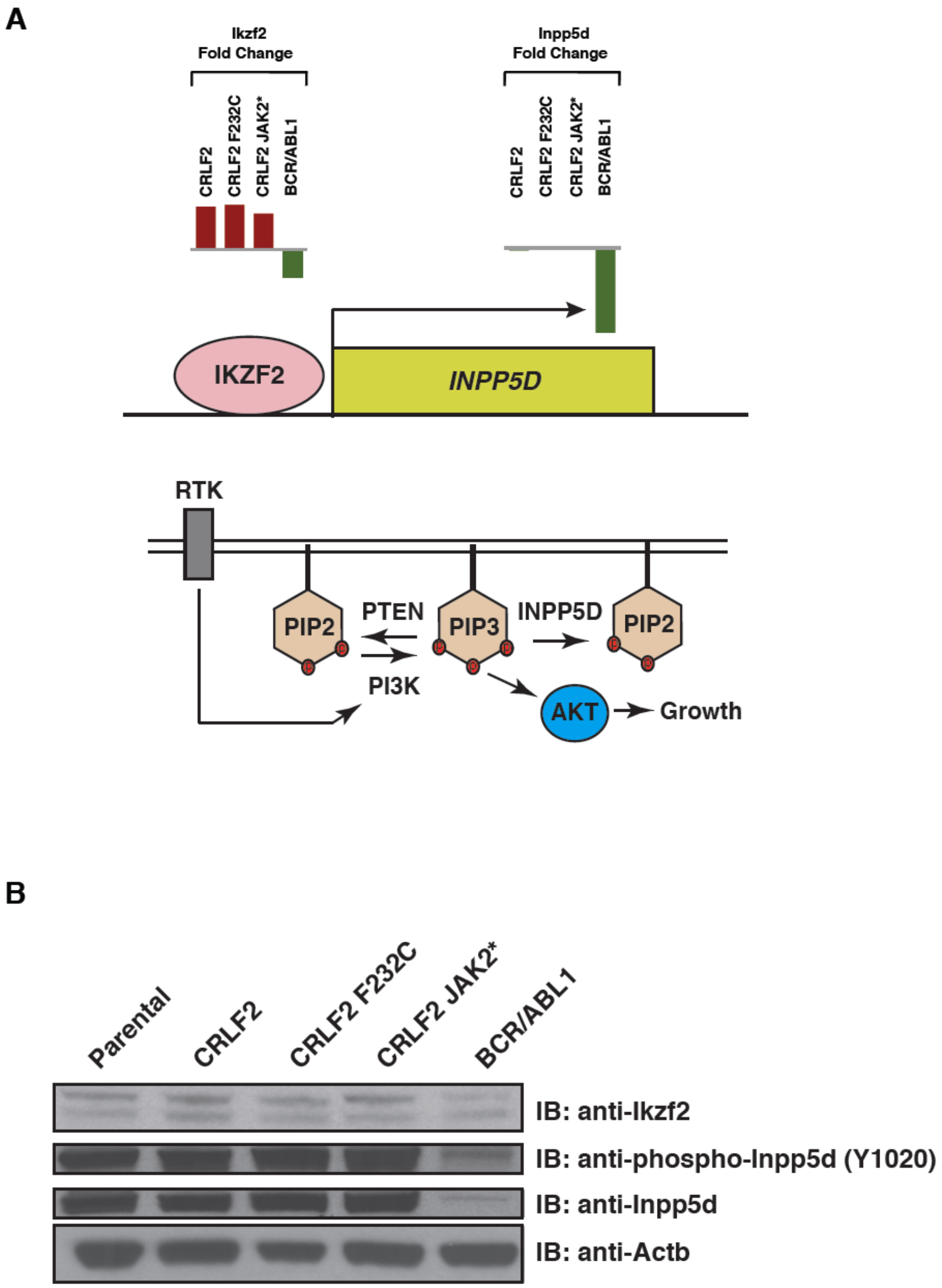
Figure 7- Differential regulation of translation initiation and transcription suppression between CRLF2 and BCR/ABL1 signaling



A, EIF2 and EIF4 signaling were generally upregulated in Ba/F3 cells with BCR/ABL1 signaling while the regulation by CRLF2 signaling was in the opposite direction. Color bars represent the relative values of SILAC ratios between engineered Ba/F3 cell lines vs. parental cells. *B*, Transcription repressors are differentially regulated between CRLF2 and BCR/ABL1 signaling.

The interplay between cell signaling and transcription factors is strongly associated with cancer development, and we would like to examine this type of regulations in BCR/ABL1 and CRLF2 signaling networks, which have been also implicated in Ph+ PRE-B ALL and Ph-like PRE-B ALL, respectively. Recently, evidence for the role of Ikaros family transcription factors in lymphoid differentiation and lymphoid malignancy is accumulating.(Rebollo and Schmitt, 2003; John and Ward, 2011; Asanuma et al., 2013) Ikaros family members may have influenced on their downstream targets including signaling molecules. For example, through knockout mouse experiments, the absence of Ikzf2 (Helios) downregulated protein expression of the phosphoinositol 5 phosphatase, Inpp5d (SHIP1). (Alinikula et al., 2010) This interplay between Ikzf2 and Inpp5d was also uncovered in our system and was regulated differently between CRLF2 and BCR/ABL1 signaling. In our study, total and phospho-Inpp5d and Ikzf2 were commonly identified in all Ba/F3-based cell lines. Phosphorylation of two Ikzf2 activity-related phosphosites (S56 and S78) were upregulated in Ba/F3 cells with CRLF2 wild type alone or with CRLF2 F232C, showed minimal change in CRLF2 JAK2 R683G, and significantly downregulated in Ba/F3 cells with BCR/ABL1 (2-fold). Meanwhile, the difference in Ikzf2 total protein abundance across CRLF2 and BCR/ABL1 signaling was more moderate. Correspondingly, total and phospho-Inpp5d changed in parallel with the trend of Ikzf2. (Figure 8A) Taken together, BCR/ABL1 downregulated the phosphorylation and expression of Ikzf2 and hence Inpp5d while their alterations in CRLF2-mediated signaling is in the opposite direction. Immunoblotting for this regulation was carried out for validation. (Figure 8B)

Figure 8- Differential regulation of Ikzf2-Inpp5d axis between CRLF2 and BCR/ABL1 signaling



A, Ikzf2 promotes transcription of Inpp5d, which dephosphorylates phosphoinositol-(3,4,5)-phosphate to phosphoinositol-(3,4)-phosphate. *B,* the immunoblotting showed that the expression of Ikzf2, Inpp5d and phospho-Inpp5d (Y1020) was downregulated by BCR/ABL1 signaling.

Src signaling and cell cycle entry are similarly regulated between CRLF2 and BCR/ABL1 signaling — The signaling downstream of CRLF2 and BCR/ABL1 still shared some commonalities. For example, Src signaling is downstream both of CRLF2 (Zhong et al., 2012) and BCR/ABL1 (Rubbi et al., 2011) represented by Pgam1 (Y92) (Ferrando et al., 2012), G6pdx (Y401) and Hsp90ab1 (Y484). Markedly, we found that several CDK1- and CDK2-regulated phosphosites were commonly hyperphosphorylated in CRLF2 JAK2 R683G and BCR/ABL1 groups but not in other two groups: Prkar1a (S83), Trp53bp1 (S382), Mta1 (S505), Mcm4 (T19), Mcm2 (S12), Mcm2 (S27), Hmga1 (T53). This finding reflects that CRLF2 JAK2 R683G and BCR/ABL1 tend to activate the entry of cell cycle. Although CRLF2 F232C was able to transform Ba/F3 cells into the growth factor independent state, we noticed that the phosphorylation signature of CRLF2 F232C clustered toward CRLF2 wild type rather than with CRLF2 JAK2 R683G and BCR/ABL1 groups.

Conclusion

CRLF2 gene rearrangement leads to its overexpression and is associated with a pre-B ALL subset with poor prognosis. Based on previous microarray transcriptomic analyses, CRLF2-rearranged pre-B ALL is known as Ph-like pre-B ALL because it harbors a similar gene expression profile as that in Ph+ pre-B ALL. However, taking a quantitative proteomic approach, we characterized proteomic and phosphoproteomic alterations caused by CRLF2 and BCR/ABL1 and found their differences in the regulation of translation initiation, transcription suppression, transcription factor-mediated signaling alterations, the histone mark H_3Y_{42}, among others. Our pharmacological screen showed these two signaling networks conferred disparate sensitivity to a panel of kinase inhibitors. Our results unraveled another layer of comparison between CRLF2 and BCR/ABL1 signaling using phosphoproteomics and suggest further clinical investigations to pave the way toward precision treatment for pre-B ALL.

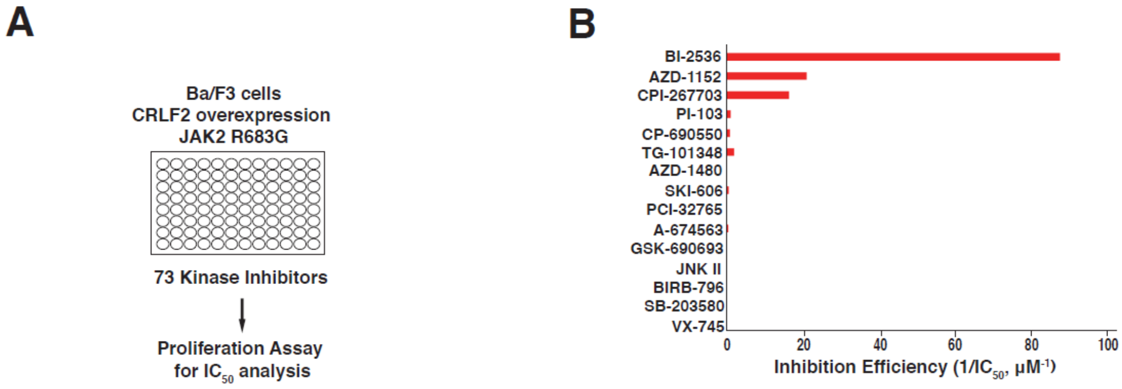
Chapter 3

Identification of a potential therapeutic target for leukemic CRLF2 signaling

Kinase inhibitor screen identifies PLK1 as a therapeutic target

To exploit the differential activation of signaling pathways to identify potential therapeutic targets in *CRLF2*-rearranged pre-B ALL, Ba/F3 cells with CRLF2 overexpression and JAK2 R683G mutation were subjected to a kinase inhibitor screen, which comprised of 73 kinase inhibitors and other small molecules. An *in vitro* cell proliferation assay was used to monitor growth inhibition (Figure 9A) (Tyner et al., 2013). Among all kinase inhibitors, we found that BI 2536, a Polo-like kinase 1 (PLK1) inhibitor, had the lowest IC_{50} (11 nM) while the IC_{50} of p38 mitogen-activated protein kinase inhibitor (VX-745), c-Jun N-terminal kinase inhibitor (JNK II) and pan-Akt kinase inhibitor (GSK-690693) were all 1,000 times higher (Figure 9B).

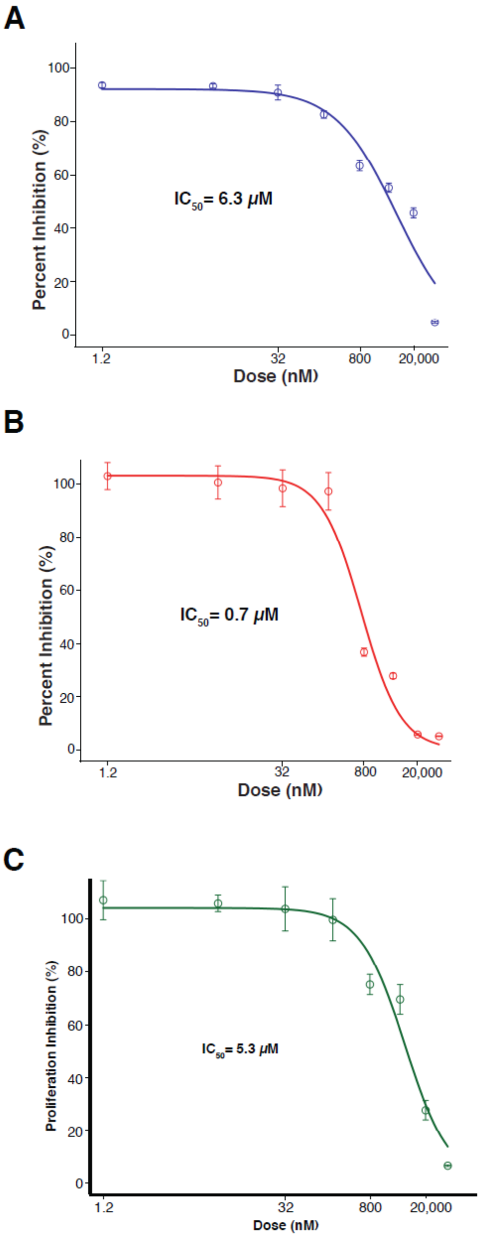
Figure 9- The strategy and result of the kinase and small molecule inhibitor screen for Ba/F3 cells with CRLF2 JAK2 mutation



A, The overall strategy of the high-throughput kinase inhibition screen. *B*, In the kinase inhibition screen, PLK1 inhibitor (BI-2536) has the highest inhibition efficiency, i.e. the lowest IC_{50}, compared to other kinase inhibitors.

Because kinase inhibitors can have off-target effects, we further confirmed the effect of targeting PLK1 by using a different PLK1 inhibitor, volasertib, which has recently been approved by FDA for treating acute myeloid leukemia. In addition, we also tested whether PLK1 inhibition preferentially suppresses the growth of Ba/F3 cells with CRLF2 overexpression and JAK2 R683G over Ba/F3 parental cells or Ba/F3 cells expressing BCR/ABL1. We found that the IC_{50} of volasertib in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G was 9 and 7 times lower than in Ba/F3 parental cells and Ba/F3 cells expressing BCR/ABL, respectively (Figure 10). These findings suggest that the growth of Ba/F3 cells conferred by the combination of CRLF2 overexpression and JAK2 mutation is preferentially inhibited by the PLK1 inhibitor *in vitro*.

Figure 10- Proliferation inhibition of three Ba/F3 cell lines by volasertib

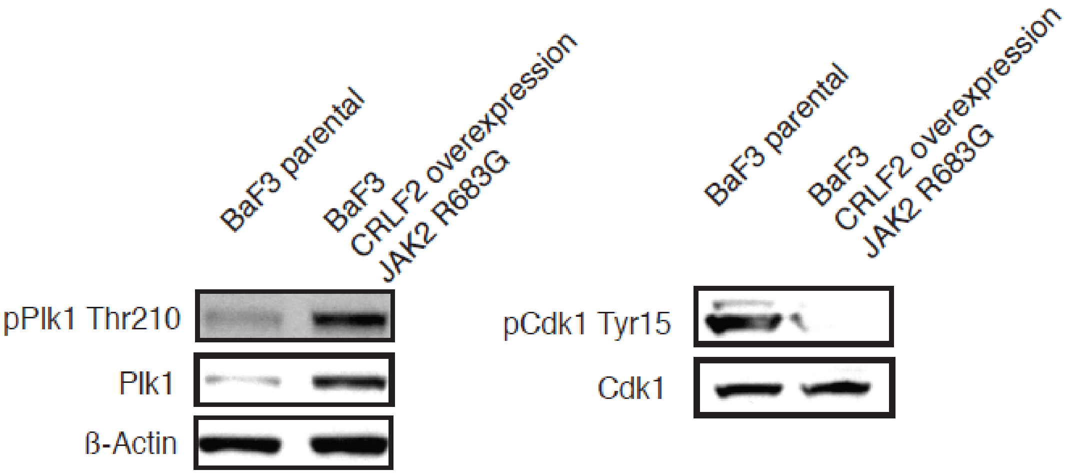


Dose response curve of PLK1 inhibition on Ba/F3 cell lines. Cells were plated in a 96-well plate and treated with volasertib for 48 hr. Fluorescence from 4-hr incubation of AlamarBlue® was measured in 6 replicates of each dose. IC_{50} was derived from the 3-parameter logistic regression modeling in the Package “drc” of R. *A,* Ba/F3 parental cells. *B,* Ba/F3 cells with CRLF2 JAK2 R683G. *C,* Ba/F3 cells with BCR/ABL1.

PLK1 is dysregulated downstream of CRLF2 JAK2 activating mutation

To check if PLK1 is downstream of the aberrant signaling pathway induced by CRLF2 overexpression and JAK2 mutation, we measured the expression of Plk1 protein by immunoblotting. We found that the expression of Plk1 was higher in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G than in parental Ba/F3 cells (Figure 11). Furthermore, the abundance of phospho-Plk1 (Thr210), a major phosphosite in activated Plk1 (Jang et al., 2002), was higher in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G with a concomitant dephosphorylation of Cdk1 as the downstream effect (Figure 11). A synergistic effect between CRLF2 and JAK2 mutation was observed on the upregulation of PLK1 (Figure 12). We immunoprecipitated endogenous Plk1 and carried out a kinase assay, which quantified the amount of ATP converted to ADP as result of Plk1 catalytic activity *in vitro*. As shown in Figure 13, the *in vitro* PLK1 kinase activity from Ba/F3 cells with CRLF2 overexpression and JAK2 R683G is substantially higher than in Ba/F3 parental cells. Taken together, these data indicate that CRLF2 overexpression with concurrent JAK2 activating mutation leads to increased expression and activation of PLK1 kinase.

Figure 11- Upregulation of Plk1 and phospho-Plk1 in Ba/F3 cells with CRLF2 JAK2 R683G is accompanied by downregulation of phosphor-Cdk1



Immunoblotting of Plk1, phospho-Plk1 (Thr210), Cdk1 and phospho-Cdk1 (Tyr15) in Ba/F3 parental cells and Ba/F3 cells with CRLF2 overexpression and JAK2 R683G mutation. β-Actin serves as a loading control.

Figure 12- Immunoblotting of phospho-Plk1 (T210) and Plk1 in different Ba/F3 cell lines revealed the synergism between CRLF2 and JAK2 for the activation of PLK1

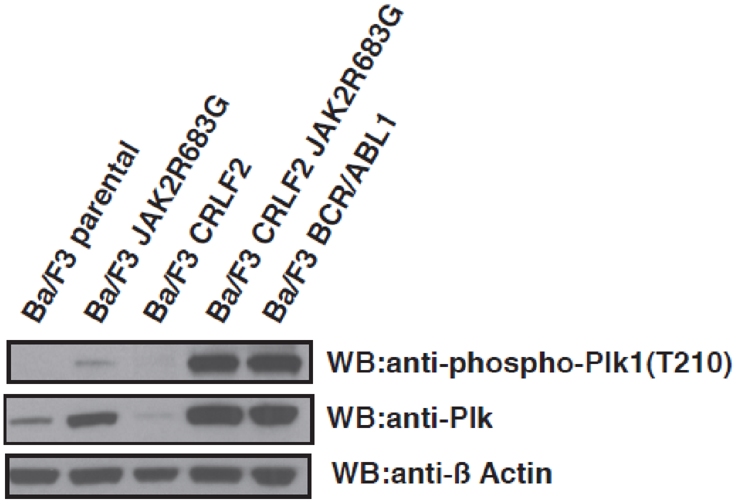
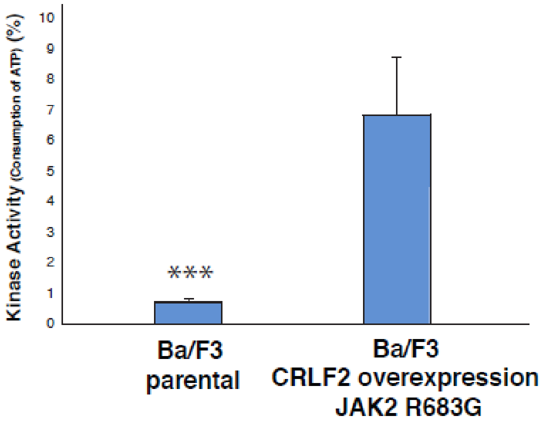


Figure 13- Comparison of kinase activity of Plk1 in Ba/F3 cell lines

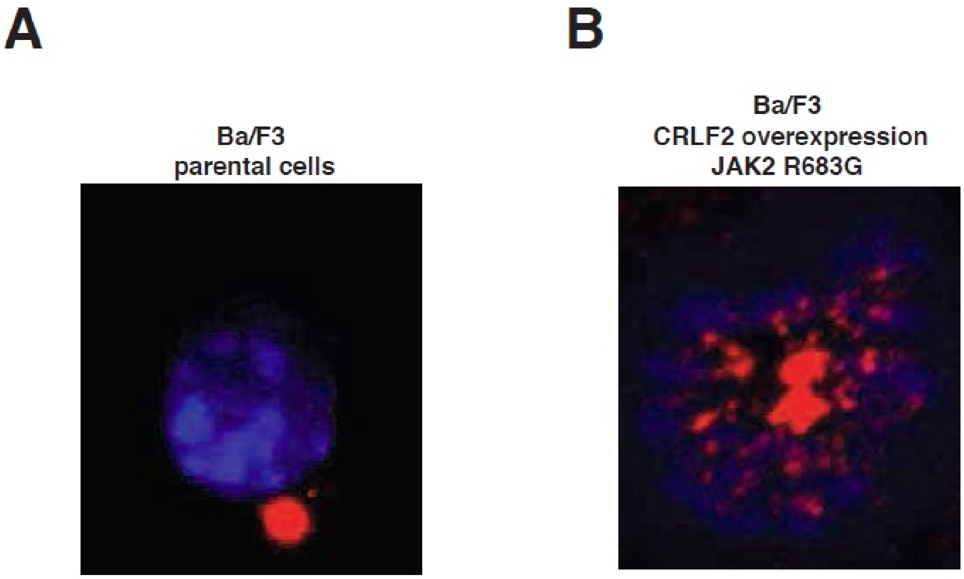


In vitro kinase assay showing that the catalytic activity of immunoprecipitated endogenous Plk1 was higher in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G than in Ba/F3 parental cells (*** p<0.01).

Phenotypes of PLK1 dysregulation downstream of CRLF2 JAK2 activating mutation

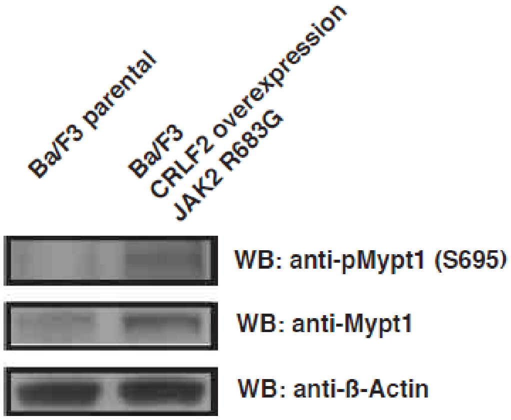
Because PLK1 is a major regulator of centrosomes in mitosis, we further investigated how dysregulation of PLK1 affects cell division. During prophase and metaphase, PLK1 recruits its substrates for centrosomal nucleation of microtubules at their minus ends (Archambault and Glover, 2009). To examine how PLK1 could play a role in mitosis of PRE-B ALL cells, we performed immunofluorescence staining of γ-tubulin, a specific marker for centrosomes in the Ba/F3 system. In normal mitosis, centrioles duplicate and recruit pericentriolar material to form centrosomes that move toward the two poles of the cell as observed in Ba/F3 parental cells (Figure 14A). However, in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G, abnormal separation of centrosomes surrounded by condensed chromosomes was observed (Figure 14B). This abnormal appearance of centrosomes and chromosomes has also been reported when PLK1 function was altered by knockdown in SW962 cells (Yamashiro et al., 2008). When both PLK1 and its negative regulator, myosin phosphatase-targeting subunit 1 (MYPT1), were knocked down, this mitotic abnormality was rescued. This implicates that either overexpression or knockdown of PLK1 causes its imbalanced function and hence abnormal mitosis. Interestingly, we also found that MYPT1 Ser695 was hyperphosphorylated in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G (Figure 15). This would inactivate the function of MYPT1 (Birukova et al., 2004). Taken together, this aberrant pattern of γ-tubulin expression in centrosomes is indicative of PLK1 dysfunction in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G.

Figure 14- Immunofluorescence staining of γ-tubulin in two different Ba/F3 cells



A, In Ba/F3 parental cells, a normal centrosome before duplication and relocation to two poles of the cell. *B,* in Ba/F3 cells with CRLF2 overexpression and JAK2 R683G, failed partition of centrosomes were surrounded by condensed chromosomes.

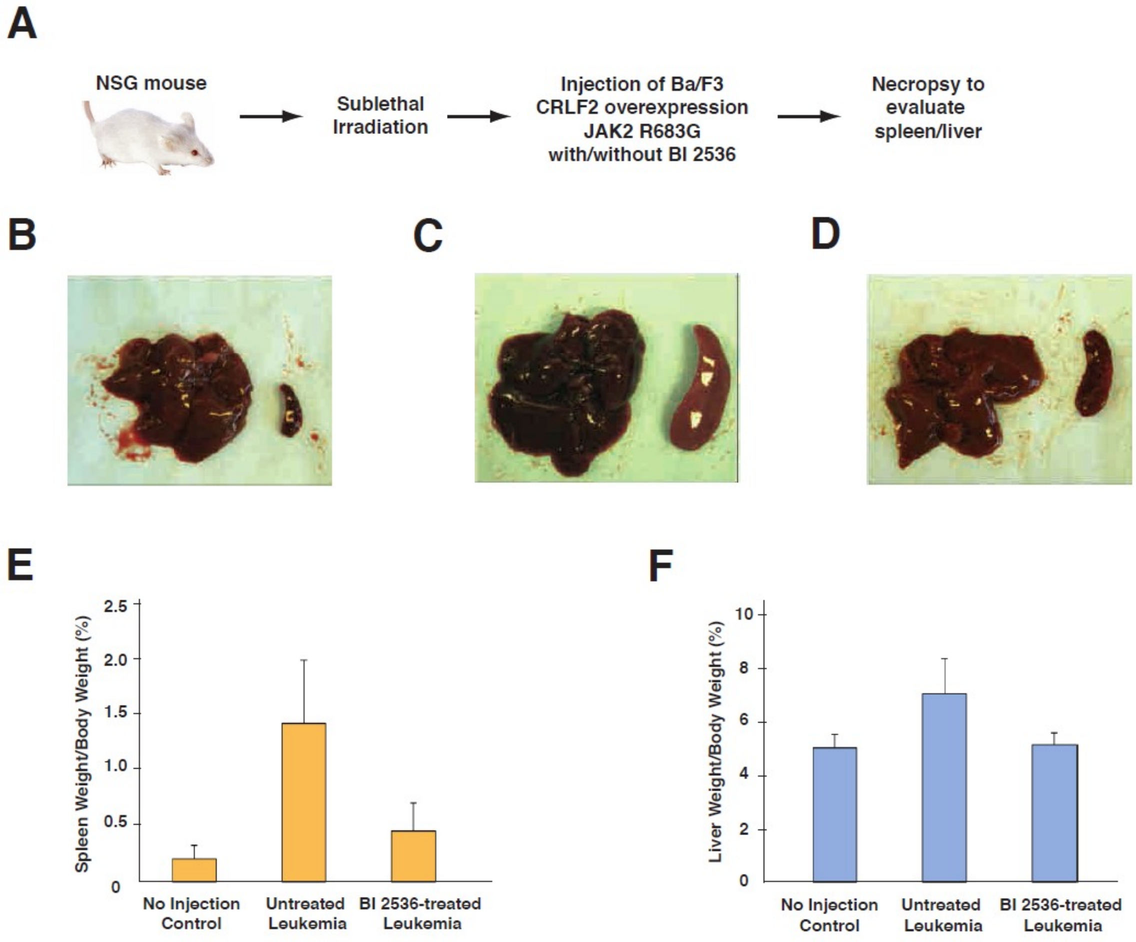
Figure 15- Immunoblotting of phospho-Mypt1 (Ser695) and Mypt1 in Ba/F3 parental cells and Ba/F3 cells with CRLF2 overexpression and JAK2 R683G



In vivo effect of PLK1 inhibition for leukemic CRLF2 JAK2 signaling

We sought to validate the efficacy of PLK1 inhibition *ex vivo*. BI 2536 or vehicle control (DMSO) pre-treated Ba/F3 cells with CRLF2 overexpression and JAK2 R683G were injected into sublethally irradiated NOD-scid IL2Rγ^{null} (NSG) mice that lacked functional T and B lymphocytes and natural killer cells. Fifteen days after cell injection, necropsy was performed to evaluate cell infiltration into spleen and liver (Figure 16A). While the size of spleen and liver from the control mice was consistent with those of regular NSG mice, all mice receiving the injection of Ba/F3 cells with CRLF2 overexpression and JAK2 R683G had hepatosplenomegaly that was reduced upon BI 2536 administration (Figure 16B to 16D). We found Ba/F3 cells with CRLF2 overexpression and JAK2 R683G treated with BI 2536 resulted in significantly smaller spleen (0.5% vs. 1.5% of total body weight, $p<0.01$) and liver size (5.5% vs. 7.6% of total body weight, $p<0.01$) compared to untreated cells (Figure 16E and 16F). These findings suggest that the proliferation of Ba/F3 cells with CRLF2 overexpression and JAK2 R683G in mice was diminished by PLK1 inhibition, consistent with the result of high-throughput kinase inhibitor assay.

Figure 16- *Ex vivo* PLK1 inhibitor therapy involving NOD-scid IL2Rγ^{null} (NSG) mice and the comparison of spleen and liver weights between different treatments

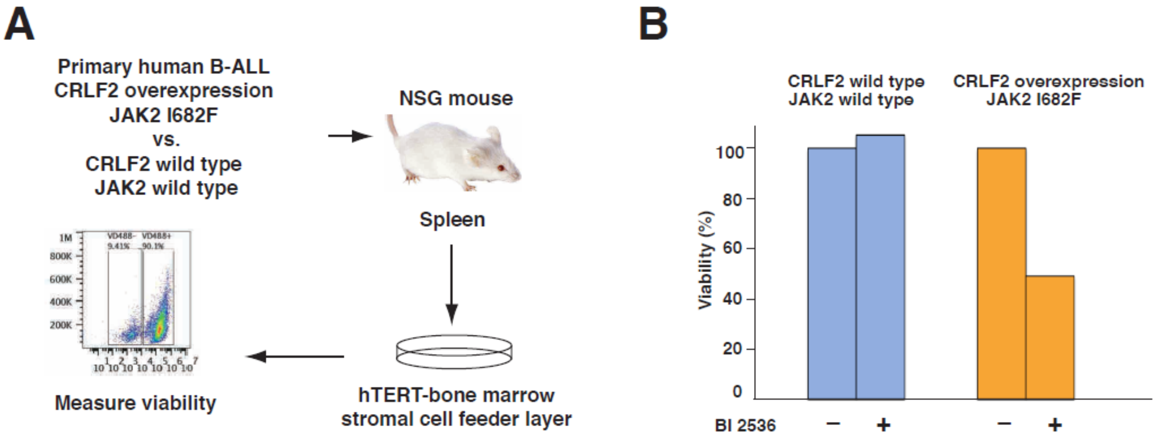


A, The strategy of *ex vivo* treatment using the PLK1 inhibitor and NSG mice. *B,* The sizes of spleen and liver in NSG mice without the injection of Ba/F3 cells with CRLF2 overexpression and JAK2 R683G. *C,* The sizes of spleen and liver in NSG mice receiving injection of Ba/F3 cells with CRLF2 overexpression and JAK2 R683G without BI 2536 pretreatment. *D,* The shrinkage of the spleen and liver in NSG mice receiving injection of Ba/F3 cells with CRLF2 overexpression and JAK2 R683G after BI 2536 pretreatment. *E,* The comparison of spleen weights normalized to body weights from NSG mice with Ba/F3 cells with CRLF2 overexpression and JAK2 R683G. *F,* The comparison of liver weights normalized to body weights from NSG mice with Ba/F3 cells with CRLF2 overexpression and JAK2 R683G. PLK1 inhibition caused smaller spleen and liver sizes.

PLK1 inhibition on CRLF2-rearranged pre-B ALL samples

The efficacy of the PLK1 inhibitor in our Ba/F3 cell system led us to examine the effect of BI 2536 on primary human pre-B ALL samples with CRLF2 overexpression and *JAK2* activating mutation and to compare with those expressing wild-type CRLF2 and *JAK2*. For this, we used two human pre-B ALL xenografts (CRLF2 overexpression/JAK2 I682F vs. CRLF2 normal expression/JAK2 wild type) that had been passaged in NSG mice (Figure 17, 18 and 19). Forty-eight hours prior to culturing the leukemia xenografts, hTERT-transformed human bone marrow stromal cells were seeded as the feeder layer (Campana et al., 1993; Mihara et al., 2003) and leukemia cells were seeded and treated either with BI 2536 or vehicle control (DMSO). Forty-eight hours later, the cells were harvested and assessed for viability. When compared with vehicle control, the viability of *CRLF2*-rearranged pre-B ALL cells treated with BI 2536 was significantly lower (49% of vehicle) than pre-B ALL cells without *CRLF2* rearrangement or *JAK2* mutations (Figure 17). We noticed that the treatment of PLK1 inhibitor caused a differential increase of cleaved poly(ADP-ribose) polymerase in pre-B ALL cells with *CRLF2* rearrangement compared with in those without, implicating the induction of apoptosis (Figure 20). In this particular case of pre-B ALL, *CRLF2* rearrangement was associated with a higher sensitivity to the PLK1 inhibitor.

Figure 17- PLK1 inhibitor treatment for pre-B ALL cells with or without CRLF2 JAK2 mutation



A, The schematic of *in vitro* viability assay for human xenografts. *B,* Human pre-B ALL cells with CRLF2 overexpression and JAK2 I682F was more sensitive to BI 2536 treatment compared to those with wild-type CRLF2 and JAK2.

Figure 18- The detection of pre-B ALL xenografts expressing human CRLF2 in NSG mouse spleens and bone marrow

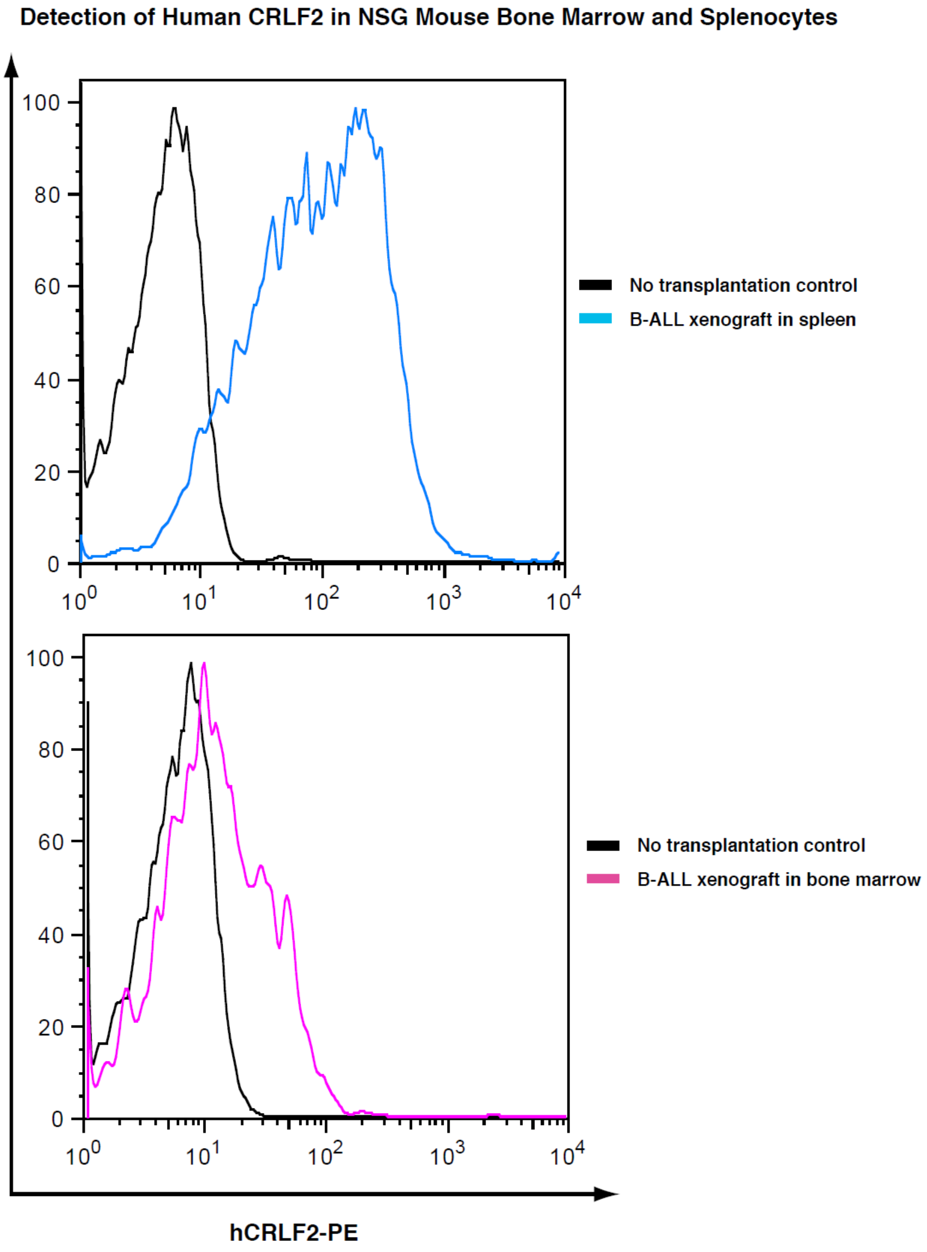


Figure 19- The expression of human CRLF2 on pre-B ALL xenografts in NSG mouse spleens

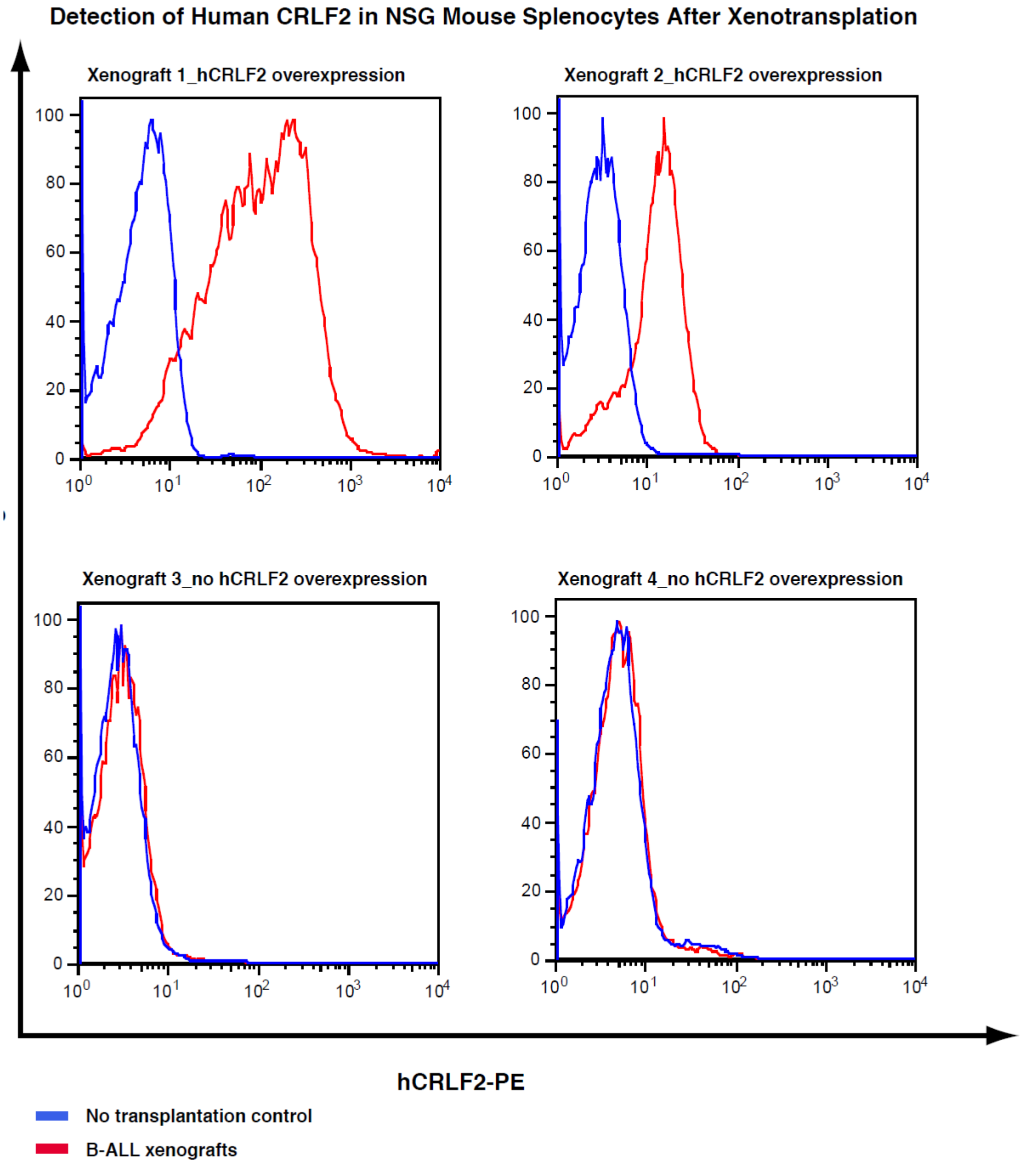
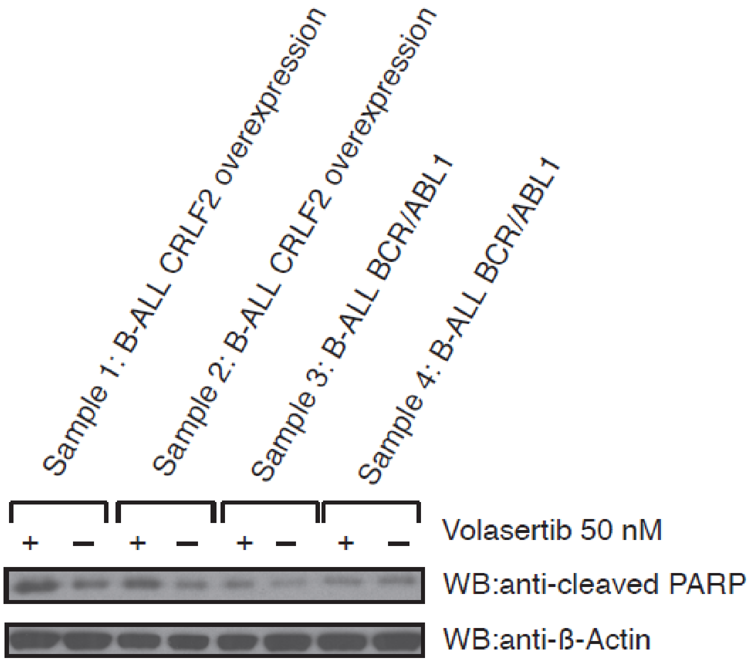


Figure 20- Immunoblotting of cleaved poly(ADP-ribose) polymerase in pre-B ALL xenografts treated with the PLK1 inhibitor



Conclusion

We identified PLK1 as a potential therapeutic target for human *CRLF2*-rearranged pre-B ALL with *JAK2* activating mutations. Based on a high-throughput kinase inhibitor screen, *ex vivo* therapy in mouse transplantation experiments and *in vitro* viability assay for human xenografts, inhibition of PLK1 was shown to have potent activity against Ba/F3 cells with CRLF2 overexpression with JAK2 R683G as well as human pre-B ALL cells with CRLF2 overexpression with JAK2 mutation. In addition, the immunofluorescence imaging implicate that PLK1 is dysregulated downstream of aberrant CRLF2 signaling. More studies are warranted for understanding the particular mechanism behind these observations; however, future therapy for this subset of pre-B ALL could benefit from PLK1 and its associated signaling pathway inhibition.

Appendices

Appendix A: SILAC ratios of all proteins commonly identified in 5 Ba/F3 cell lines

Gene Symbol	CRLF2/ parental	CRLF2 F232C/ parental	CRLF2 JAK2*/ parental	BCR-ABL1/ parental
0610009D07Rik	0.85	0.76	1.00	0.94
0610011F06Rik	2.22	1.91	1.35	0.66
0610037L13Rik	1.57	1.49	1.32	1.20
1110004F10Rik	1.20	1.06	1.53	1.09
1110008F13Rik	0.29	0.30	0.58	0.73
1110057K04Rik	0.96	0.87	0.88	0.58
1110059G10Rik	1.27	1.13	1.00	1.04
1200014J11Rik	0.82	0.95	1.18	1.02
1700074P13Rik	0.03	0.07	0.19	0.04
1810009A15Rik	0.82	0.89	1.01	1.29
1810037I17Rik	0.69	0.64	1.19	2.32
2010107E04Rik	0.93	1.15	0.68	0.90
2310036O22Rik	0.59	0.59	0.73	0.88
2410016O06Rik	1.13	1.00	1.25	1.03
2410127L17Rik	1.08	0.90	1.21	1.10
2610018G03Rik	0.90	0.88	0.92	1.31
2610301G19Rik	1.13	1.03	1.07	0.92
2700029M09Rik	1.01	0.88	0.85	0.89
2700060E02Rik	1.31	1.17	1.13	0.85
3110082I17Rik	1.22	1.03	1.00	0.72
9030617O03Rik	1.00	1.03	0.40	0.55
9030624J02Rik	0.90	0.95	0.82	0.99
Aaas	0.87	0.93	0.89	1.29
Aacs	1.44	1.46	1.89	2.07
Aagab	1.16	1.27	1.24	1.69
Aak1	1.00	0.98	1.06	1.41
Aamp	0.96	1.02	2.17	1.05
Aars	0.76	0.80	0.60	1.38
Aarsd1	1.54	1.68	2.06	1.18
Aatf	1.14	1.09	1.11	1.51
Abcb10	0.93	0.80	0.64	0.75
Abcb7	0.86	0.88	0.75	0.73
Abcc1	1.10	1.04	1.15	1.45
Abcd3	0.76	0.75	0.63	0.71
Abce1	0.85	0.86	0.99	1.15
Abcf1	0.77	0.77	0.99	0.94
Abcf2	0.93	0.92	1.31	1.14
Abhd14b	0.47	0.51	0.34	0.87
Abi1	0.94	1.08	0.89	1.00
Abracl	1.19	1.10	1.26	1.37
Acaa1a	1.48	1.84	1.61	1.13
Acaa2	1.19	1.23	0.99	0.87
Acaca	1.58	1.54	1.65	1.17
Acad8	1.61	1.21	1.02	1.20
Acad9	0.82	0.93	0.75	0.58
Acadl	0.80	0.74	0.58	0.83
Acadm	0.97	1.11	0.76	1.00
Acads	1.08	1.03	0.82	0.79
Acadsb	0.72	0.77	0.57	0.63
Acadvl	1.13	1.18	0.86	0.67
Acap1	1.76	1.37	1.86	1.51
Acat1	1.25	1.31	0.83	0.80
Acat2	1.38	1.64	1.87	2.39
Acbd3	1.02	0.95	0.72	1.01

Acin1	1.05	1.18	1.02	1.04
Acly	0.92	1.03	1.23	1.83
Aco2	1.01	1.04	0.93	0.87
Acot7	2.79	2.34	3.02	1.36
Acot8	1.11	1.24	1.49	1.46
Acot9	0.84	0.73	0.71	0.67
Acox1	1.00	1.19	0.89	0.84
Acsf2	1.95	1.79	1.26	0.79
Acsl1	0.84	0.84	0.73	1.19
Acsl3	1.26	1.41	1.47	1.87
Acsl4	0.95	1.10	1.25	2.16
Acsl5	0.99	1.13	1.03	1.41
Acss2	1.90	1.82	1.67	0.64
Acta1	0.77	0.71	1.47	1.24
Actb	0.64	0.81	1.19	1.23
Actbl2	0.52	0.66	0.98	1.72
Actg1	0.71	0.76	0.89	1.12
Actl6a	1.20	1.26	1.21	1.07
Actn1	1.15	1.15	0.87	1.64
Actn4	0.62	0.65	0.59	1.24
Actr1a	1.29	1.15	1.25	1.41
Actr1b	1.26	1.21	1.03	1.19
Actr2	0.75	0.69	0.75	0.98
Actr3	0.85	0.80	0.69	0.94
Acy1	0.90	0.79	0.66	0.85
Acy3	0.36	0.57	0.43	1.11
Acyp1	1.61	1.57	1.39	1.00
Ada	1.46	1.40	1.13	1.01
Adam10	1.35	1.13	1.64	1.16
Add1	1.05	1.05	0.94	0.76
Add3	0.87	0.91	0.79	0.66
Adh5	1.07	1.16	0.93	1.08
Adi1	0.96	0.77	1.01	0.63
Adk	1.21	1.03	0.82	0.82
Adnp	0.90	0.83	0.56	0.83
Adpgk	1.10	1.06	1.15	1.37
Adprh	1.38	1.06	0.91	0.90
Adrbk1	1.05	1.04	1.07	1.10
Adrm1	0.90	1.01	1.17	2.34
Adsl	1.16	1.04	1.07	1.08
Adss	0.91	0.85	0.95	1.05
Adssl1	1.08	0.83	0.99	1.46
Agfg1	0.82	0.88	0.79	0.82
Agk	0.94	0.85	0.72	0.78
Ago2	0.99	0.96	1.10	1.26
Agps	1.47	1.35	1.38	1.36
Ahctf1	0.58	0.52	0.74	0.76
Ahcy	1.38	1.45	1.08	1.02
Ahcyl2	1.06	1.01	0.91	0.96
Ahsa1	0.99	0.92	1.33	1.23
AI314180	0.75	0.74	0.74	0.80
AI597468	0.74	0.85	1.03	1.15
Aif1	0.26	0.32	0.27	0.44
Aifm1	0.96	0.99	0.81	0.90
Aimp1	0.87	0.88	0.89	0.96
Aimp2	0.99	0.95	0.81	0.90
Aip	1.07	1.18	1.18	1.23
Ak1	0.83	1.00	0.40	0.31
Ak2	0.98	1.07	0.69	0.81
Ak3	1.22	0.94	0.76	0.65
Ak4	1.06	1.18	0.90	0.73
Akap13	0.63	0.61	0.69	0.68
Akap14	0.36	0.29	1.01	1.04

Akap8	0.71	0.76	1.02	1.23
Akr1a1	0.86	0.94	0.76	0.97
Akr1b10	0.65	0.67	0.91	0.99
Akr1b3	0.74	0.75	0.73	0.80
Akr1b7	0.80	0.96	0.57	1.15
Akr1c12	1.72	1.84	1.37	1.05
Akr1c13	1.54	1.57	1.27	1.08
Akr7a5	2.45	2.16	1.88	0.94
Alad	1.07	0.95	0.93	0.59
Alas1	0.59	0.59	0.40	0.89
Aldh16a1	1.97	1.78	1.11	1.23
Aldh18a1	0.86	0.91	0.74	0.99
Aldh2	0.84	0.90	0.77	0.68
Aldh3a2	1.20	1.05	0.84	0.88
Aldh9a1	0.82	0.84	0.73	0.92
Aldoa	1.08	1.00	0.82	0.73
Aldoa	0.70	0.74	0.82	0.73
Alg2	1.17	0.94	0.76	1.02
Alg5	0.68	0.67	0.52	0.72
Alkbh3	1.54	1.38	1.26	1.09
Alkbh5	1.19	0.91	1.09	0.88
Alyref	0.99	0.92	0.92	0.72
Amacr	0.73	0.99	0.73	2.71
Ampd2	0.74	0.70	0.81	1.07
Anapc1	0.94	0.97	29.84	9.85
Anapc4	0.91	0.95	1.12	0.86
Ankfy1	1.58	1.56	1.48	1.35
Ankrd17	1.02	1.02	1.33	1.78
Ankrd28	1.00	1.15	1.26	1.01
Ankrd44	1.07	0.98	0.96	1.28
Ankzf1	1.36	1.28	1.30	1.29
Anln	0.70	0.79	0.45	0.47
Ano6	1.01	0.93	0.58	0.74
Anp32a	0.87	0.91	0.61	0.73
Anp32b	1.36	1.14	0.85	0.88
Anp32e	0.98	1.00	0.74	0.75
Anxa1	3.44	3.73	5.17	0.62
Anxa11	1.07	1.11	1.03	0.85
Anxa2	1.16	1.21	0.82	1.13
Anxa4	1.26	1.11	0.86	0.68
Anxa5	0.67	0.66	0.48	0.67
Anxa6	1.82	1.82	1.23	1.11
Anxa6	1.67	1.52	1.23	1.11
Anxa7	1.30	1.26	1.28	1.22
Ap1b1	1.07	1.02	1.03	1.04
Ap1g1	1.02	0.93	0.74	1.02
Ap1m1	1.09	1.03	1.13	1.02
Ap1s1	1.29	1.07	1.23	1.47
Ap2a1	1.42	1.43	1.28	1.37
Ap2a2	0.98	0.94	0.92	0.70
Ap2b1	0.92	0.99	0.95	0.95
Ap2m1	1.02	1.02	0.99	0.81
Ap3b1	0.88	0.93	1.14	1.13
Ap3d1	0.97	0.89	0.92	1.30
Ap3m1	0.99	1.01	0.63	0.65
Ap3s1	1.01	0.95	1.27	1.12
Apaf1	1.04	0.99	0.84	1.11
Apbb1ip	0.76	0.59	1.00	1.05
Apeh	1.25	1.16	0.99	1.06
Apex1	1.14	1.10	0.89	0.95
Api5	1.10	1.12	1.05	0.92
Apip	1.45	1.29	1.05	0.98
Apoa1bp	1.06	1.10	0.99	0.74

Apoo	1.20	1.18	1.30	1.02
Apool	1.00	0.95	0.89	0.85
Appl1	1.49	1.56	1.39	1.53
Aprt	0.53	0.50	0.53	0.81
Arcn1	0.86	0.82	0.92	1.06
Arf3	1.05	1.06	1.01	1.00
Arf4	0.96	0.93	0.79	0.86
Arf5	0.94	0.87	0.93	1.09
Arf6	0.90	0.94	0.99	1.11
Arfgap1	0.90	0.87	1.21	1.28
Arfgap2	1.23	1.03	1.23	1.41
Arfgap3	1.47	1.47	0.91	0.76
Arfgef1	0.86	0.89	0.82	0.78
Arfip1	1.15	1.04	1.89	1.39
Arfip2	0.97	0.71	0.75	0.81
Arglu1	0.88	0.93	0.80	0.84
Arhgap1	1.04	1.04	0.85	0.85
Arhgap17	0.98	0.97	0.78	0.88
Arhgap6	1.13	0.77	1.38	1.98
Arhgdia	0.84	0.91	0.91	1.01
Arhgdib	1.20	1.25	1.11	1.05
Arhgef1	1.13	1.04	0.95	1.04
Arhgef2	1.03	1.09	1.29	1.67
Arhgef6	1.10	1.16	0.56	0.51
Arhgef7	0.78	0.73	0.95	1.70
Arid1a	1.26	1.23	1.30	1.13
Arid2	1.43	1.61	0.77	0.80
Arih1	1.29	1.05	0.98	1.32
Arih2	0.99	0.97	0.92	1.16
Arl1	1.05	1.08	0.93	0.92
Arl2	1.10	1.01	1.57	1.29
Arl3	1.64	1.43	1.34	0.58
Arl6ip5	1.01	1.00	0.98	1.25
Arl8a	0.78	0.95	1.08	1.53
Arl8b	0.87	0.89	0.77	0.88
Armc1	0.91	0.97	1.01	1.09
Armc10	1.12	1.05	0.90	0.83
Armc6	1.01	0.98	1.54	2.19
Armc8	0.77	0.72	1.02	1.22
Arpc1b	0.78	0.79	1.01	1.08
Arpc2	0.69	0.68	0.75	0.92
Arpc3	0.67	0.67	0.65	0.95
Arpc4	0.68	0.71	0.77	0.86
Arpc5	0.69	0.72	0.74	0.98
Arpc5l	1.40	1.61	1.26	1.65
Arpp19	0.59	0.54	0.88	0.82
Arrb1	1.56	1.62	0.88	0.87
Arrb2	0.59	0.81	0.97	2.06
Arsb	1.78	1.78	2.81	1.13
Asah1	1.16	1.14	1.04	1.57
Ash2l	0.65	0.60	0.53	0.64
Asl	1.43	1.32	1.39	1.29
Asna1	0.79	0.83	0.71	1.27
Asns	0.83	0.73	0.80	1.29
Asph	1.38	1.59	1.45	0.72
Asrgl1	0.86	0.85	0.82	1.03
Asun	1.02	1.13	1.21	1.33
Atad1	0.88	0.96	1.33	1.47
Atad2b	1.12	0.94	2.07	1.19
Atad3a	2.01	2.17	1.81	0.92
Ate1	0.74	0.67	0.41	0.70
Atf1	0.76	0.83	0.83	0.86
Atg3	0.89	0.97	0.97	1.44

Atg4b	3.55	3.74	1.75	1.14
Atic	0.80	0.76	0.80	0.79
Atl2	0.60	0.64	0.67	1.22
Atl3	0.90	0.96	0.81	1.09
Atox1	0.90	0.93	1.06	0.90
Atp11b	1.43	1.33	1.25	1.08
Atp13a1	1.34	1.52	1.72	1.46
Atp1a1	0.71	0.72	0.90	0.94
Atp1b3	0.87	0.88	0.92	0.98
Atp2a2	1.23	1.28	1.48	1.41
Atp2a3	1.37	1.40	1.55	1.62
Atp2b1	0.94	1.03	1.10	1.37
Atp5a1	1.09	1.17	0.92	0.92
Atp5b	1.20	1.28	0.98	0.98
Atp5c1	1.00	1.05	0.97	0.87
Atp5d	0.95	1.07	0.92	0.90
Atp5e	1.30	1.25	1.01	0.90
Atp5f1	1.17	1.18	0.98	0.96
Atp5h	1.11	1.19	0.92	0.89
Atp5j	1.00	1.10	0.85	0.89
Atp5j2	1.07	1.19	0.94	0.95
Atp5k	0.90	0.88	0.84	0.71
Atp5l	1.05	1.11	0.98	0.89
Atp5o	1.23	1.31	0.97	0.82
Atp6v0a1	0.79	0.74	1.07	1.25
Atp6v0d1	0.87	0.99	0.96	1.28
Atp6v1a	0.81	0.84	0.69	1.17
Atp6v1b2	0.76	0.71	0.58	1.01
Atp6v1c1	0.56	0.60	0.69	0.95
Atp6v1d	0.91	1.11	1.15	1.08
Atp6v1e1	0.74	0.77	0.68	1.07
Atp6v1f	0.66	0.70	0.76	0.92
Atp6v1g1	0.00	0.02	0.71	1.11
Atp6v1h	0.80	0.75	0.63	1.26
ATP8	1.17	1.24	0.90	0.94
Atpif1	1.50	1.68	1.02	1.03
Atrx	0.78	0.71	0.68	0.82
Atxn10	1.14	1.06	1.31	1.28
Atxn2l	0.95	0.95	1.16	1.09
Atxn3	1.27	1.24	1.33	2.75
Aup1	0.69	0.71	1.31	1.50
Aurka	0.91	0.83	0.91	0.93
Aurkb	0.66	0.73	0.75	0.64
Babam1	0.89	0.92	1.03	1.05
Bad	0.83	1.06	0.84	1.53
Bag1	0.77	0.75	0.80	0.74
Bag2	0.86	0.70	1.02	0.70
Bag6	1.05	1.05	1.15	1.66
Bak1	0.66	1.08	0.48	0.76
Banf1	1.27	1.03	0.92	0.80
Bax	1.21	1.13	0.87	0.93
Baz1a	1.01	0.93	1.33	1.34
Baz1b	1.16	1.04	1.27	0.90
BC005624	0.93	1.02	1.44	1.31
BC017643	1.20	1.29	1.29	0.94
BC026590	0.92	1.06	1.05	0.88
Bcap29	0.87	0.99	1.12	0.78
Bcap31	0.75	0.91	0.95	1.12
Bcas2	0.79	0.98	0.98	1.03
Bcat2	1.19	1.34	1.04	1.35
Bccip	0.88	0.97	1.17	0.91
Bckdha	1.28	1.04	0.91	0.81
Bckdhb	0.97	0.94	0.98	0.98

Bcl10	1.06	2.76	0.85	1.13
Bcl2	1.88	2.09	3.77	2.71
Bcl2l13	0.80	0.78	0.52	0.62
Bclaf1	0.83	0.93	0.80	0.80
Bclaf1	0.83	0.92	0.80	0.80
Bid	1.48	1.44	1.94	2.03
Bin2	0.74	0.70	1.01	1.26
Birc5	0.77	0.67	0.73	0.66
Birc6	0.80	0.80	0.92	1.17
Blmh	1.13	1.16	0.99	1.11
Blvra	0.97	0.96	1.08	1.04
Blvrb	0.75	1.25	0.71	1.38
Bms1	0.94	0.97	1.45	1.35
Bnip1	1.30	1.41	0.96	1.10
Bnip3	0.84	0.83	1.07	1.11
Bod1l	0.75	0.83	1.07	1.10
Bola1	1.36	1.25	1.27	0.87
Bola2	0.96	0.92	0.95	0.76
Bop1	1.08	1.42	1.04	1.07
Bphl	2.03	1.52	0.80	0.52
Bpnt1	0.63	0.68	0.65	0.75
Brcc3	1.25	1.24	0.90	0.95
Brd2	0.74	0.77	1.00	1.01
Brd4	0.75	0.66	0.74	0.70
Brd7	1.32	1.17	1.06	1.11
Bre	0.98	1.09	1.44	0.88
Bri3bp	1.43	1.46	1.69	1.56
Brix1	0.77	0.79	1.33	0.77
Brk1	1.13	1.12	1.03	1.00
Brox	0.83	1.04	0.61	1.05
Bsg	0.74	0.82	0.93	0.90
Bst2	0.67	0.73	0.70	0.83
Btaf1	1.07	1.02	0.96	1.03
Btf3	1.23	1.14	1.44	1.48
Btf3l4	0.63	0.75	0.88	1.48
Btk	0.65	0.62	0.90	0.98
Bub3	0.96	0.90	1.02	0.85
Bud31	1.23	1.17	1.47	1.12
Bysl	0.88	0.83	1.16	1.38
Bzw1	0.72	0.77	0.64	0.93
Bzw2	0.78	0.88	0.96	0.79
C1qbp	1.51	1.45	1.33	1.31
Cab39	0.70	0.67	0.74	0.80
Cacybp	0.72	0.75	0.85	0.98
Cad	1.30	1.27	1.61	1.18
Calm1	0.91	0.93	0.99	0.99
Calr	0.66	0.67	0.58	0.87
Calu	0.84	0.83	1.17	1.20
Calu	0.89	0.76	1.17	1.20
Camk2g	1.32	1.05	1.24	1.54
Cand1	0.85	0.90	0.80	0.72
Canx	1.38	1.39	1.39	1.38
Cap1	0.97	0.99	1.13	1.89
Capg	0.83	0.97	0.68	1.23
Capn1	0.84	0.92	0.89	1.04
Capn2	0.72	0.73	1.12	2.15
Capns1	0.79	0.84	0.94	1.42
Caprin1	1.11	1.17	1.69	1.34
Capza1	1.04	1.00	1.04	1.06
Capza2	1.44	1.45	1.38	1.25
Capzb	1.15	1.30	1.24	1.19
Carhsp1	0.32	0.36	0.31	0.66
Carkd	1.40	1.41	1.09	1.01

Cars	0.94	1.01	0.97	1.13
Casp1	0.68	0.57	0.40	0.54
Casp2	0.84	0.80	0.79	0.86
Casp3	1.14	0.99	0.79	2.04
Casp7	0.91	0.93	0.97	1.32
Casp8	0.99	0.97	0.71	1.08
Cast	0.77	0.75	0.82	1.00
Cat	0.86	0.99	0.82	0.87
Cbfa2t3	0.73	0.69	1.34	1.09
Cbfb	0.92	0.89	0.98	1.12
Cbl	1.31	1.12	0.70	0.73
Cbll1	1.11	0.94	1.12	1.06
Cbwd1	0.91	0.84	0.88	1.31
Cbx1	1.10	1.05	0.98	0.82
Cbx5	0.78	0.80	0.72	0.69
Cc2d1b	0.90	0.84	0.93	0.96
Ccar1	1.16	1.11	0.80	0.77
Ccbl2	1.16	1.27	1.53	1.07
Ccdc115	1.06	0.91	1.18	1.01
Ccdc12	0.73	0.73	0.96	1.03
Ccdc124	1.06	0.91	1.25	1.48
Ccdc22	1.01	0.95	0.85	1.81
Ccdc43	1.28	1.24	1.08	1.03
Ccdc47	1.10	1.25	1.32	1.58
Ccdc55	1.03	0.94	0.85	0.85
Ccdc58	1.28	1.30	1.22	1.14
Ccdc86	0.61	0.75	1.01	1.06
Ccdc88b	1.47	1.35	1.42	1.54
Ccdc89	0.78	0.79	0.76	0.80
Ccdc93	1.48	0.88	1.44	1.03
Ccna2	0.68	0.56	0.30	0.92
Ccs	1.14	1.17	1.06	1.12
Cct2	1.10	1.17	1.19	1.19
Cct3	1.04	1.11	1.15	1.09
Cct4	1.02	1.14	1.16	1.15
Cct5	1.04	1.07	1.07	1.13
Cct6a	1.12	1.18	1.16	1.18
Cct7	1.01	1.09	1.03	1.05
Cct8	1.02	1.07	1.08	1.12
Cd2ap	0.86	0.79	0.78	1.07
Cd2bp2	0.95	0.75	1.17	1.39
Cd3eap	0.98	0.88	0.98	0.65
Cd44	1.13	0.97	1.44	2.08
Cd47	1.64	1.97	1.89	1.48
Cd63	1.79	1.84	2.32	2.66
Cda	1.44	1.58	0.87	0.84
Cdc16	1.00	1.01	0.88	0.88
Cdc23	0.88	1.00	1.02	0.81
Cdc26	1.13	1.10	0.21	0.37
Cdc37	1.04	0.98	0.78	1.06
Cdc42	1.10	0.94	1.06	0.97
Cdc5l	0.88	0.95	0.92	0.91
Cdc73	0.75	0.72	1.07	1.04
Cdca8	0.68	0.62	0.63	0.47
Cdipt	0.84	0.82	0.87	0.78
Cdk1	0.85	0.99	1.17	0.98
Cdk11b	1.42	1.31	1.34	1.12
Cdk2ap1	0.73	0.89	1.06	1.04
Cdk4	0.92	0.82	1.31	0.91
Cdk5	0.81	0.75	0.88	0.88
Cdk5rap3	1.56	1.51	1.36	1.04
Cdk6	1.61	1.67	2.09	0.80
Cdk9	0.96	1.12	1.07	1.23

Cdkn1b	3.98	3.23	1.88	0.98
Cdkn2aip	0.66	0.68	0.58	0.93
Cdkn2aipnl	1.52	1.55	1.44	0.96
Cds2	1.11	1.15	1.18	1.62
Cdv3	0.74	0.76	0.84	1.12
Cebpe	0.84	0.75	0.77	0.77
Cebpz	0.89	0.93	0.89	0.84
Cecr5	1.97	1.50	1.12	0.85
Celf1	1.13	1.26	1.04	1.28
Celf2	1.38	1.28	1.21	1.22
Cep170	1.02	0.87	0.67	0.79
Cep55	0.67	0.76	0.84	0.98
Cers2	0.82	0.57	1.60	1.70
Ces2g	1.04	1.06	0.75	0.47
Cetn2	1.31	1.19	0.88	0.88
Cfdp1	0.64	0.63	0.52	0.73
Cfl1	0.82	0.89	1.07	1.20
Cggbp1	1.08	0.89	1.10	0.95
Chchd3	0.93	0.92	1.25	0.94
Chchd6	1.62	1.49	0.97	1.05
Chd2	1.57	1.19	0.74	1.05
Chd4	1.01	0.99	0.99	0.92
Cherp	0.78	0.75	0.79	0.91
Chmp1a	0.94	0.88	0.82	0.92
Chmp2a	1.20	1.21	1.08	0.98
Chmp4b	1.13	1.14	0.92	1.31
Chmp5	0.88	0.93	0.84	0.77
Chordc1	0.99	1.01	0.78	1.15
Chp1	0.95	1.07	1.12	0.89
Chtop	1.76	1.40	1.30	0.92
Ciao1	1.25	1.20	1.38	1.45
Ciapin1	1.01	0.88	0.72	0.97
Cirh1a	0.87	0.85	1.14	1.17
Cisd1	1.13	1.26	1.01	0.97
Cisd2	0.81	0.89	0.98	0.98
Ckap5	0.89	0.86	1.02	0.99
Cks2	1.41	1.30	1.03	0.83
Clasp2	1.24	1.30	2.34	0.89
Clic1	0.56	0.58	0.62	1.21
Clic4	0.91	0.92	0.87	0.91
Clint1	0.80	0.85	1.03	1.20
Clip1	0.99	1.15	1.20	0.93
Clns1a	0.67	0.74	0.95	0.75
Clpb	1.09	1.06	1.17	1.02
Clpp	0.98	0.92	0.74	1.25
Clpx	0.81	0.87	1.10	1.04
Clta	1.15	1.12	1.05	0.91
Cltb	1.08	1.00	1.16	0.82
Cltc	1.35	1.33	1.16	0.95
Cluh	1.03	1.27	2.00	1.29
Clybl	1.41	1.36	0.81	0.68
Cmas	1.37	1.50	1.32	0.84
Cmc1	2.70	1.27	0.97	0.91
Cmc2	1.21	1.45	0.83	1.05
Cmpk1	0.88	0.89	0.70	0.74
Cmss1	1.24	1.18	1.14	0.97
Cmtm7	0.88	0.92	1.06	1.21
Cnbp	1.07	1.22	1.52	1.02
Cndp2	0.96	0.96	1.12	1.05
Cnih4	0.93	1.06	0.75	0.97
Cnn2	0.91	0.67	1.10	1.03
Cnot1	1.12	1.16	1.05	1.11
Cnot11	0.81	1.11	0.92	0.91

Cnot2	1.55	1.53	2.07	1.46
Cnot3	1.01	1.25	1.26	1.19
Cnot7	1.33	1.11	1.16	1.25
Cnpy2	1.37	1.33	0.89	1.73
Cnpy3	1.44	1.58	1.34	1.64
Coa3	0.93	0.96	1.39	0.85
Coasy	1.18	1.18	0.92	0.94
Cog4	1.30	1.42	0.94	1.24
Cog7	1.01	0.90	0.83	0.80
Commd3	1.05	1.02	1.16	1.20
Commd5	1.03	1.07	1.36	1.49
Commd6	1.29	1.11	0.96	1.18
Commd9	1.21	1.09	1.50	2.05
Copa	0.95	0.94	1.00	1.00
Copb1	0.89	0.88	0.89	1.07
Copb2	0.98	0.94	0.96	1.04
Cope	1.04	1.04	1.05	1.23
Copg1	0.97	0.90	0.91	0.94
Copg2	1.09	1.21	0.79	1.04
Cops2	1.12	1.06	1.00	0.99
Cops3	1.26	1.18	1.22	1.09
Cops4	1.20	1.14	0.91	0.95
Cops5	0.92	1.05	0.86	0.98
Cops6	1.16	1.37	0.93	0.91
Cops7a	1.54	1.23	1.14	0.92
Cops7b	1.61	1.08	1.08	0.69
Cops8	0.94	1.06	0.96	1.13
Copz1	0.97	0.91	0.98	1.08
Coq5	2.07	1.74	1.15	1.70
Coro1a	0.86	0.91	0.96	1.06
Coro1b	0.93	0.99	1.02	1.13
Coro1c	1.12	1.25	1.45	1.20
Coro7	1.23	1.40	2.51	2.69
Cotl1	0.62	0.54	0.37	3.04
Cox15	1.58	2.49	1.28	0.89
Cox17	0.75	0.75	1.26	1.61
COX2	1.45	1.41	1.07	0.86
Cox4i1	1.26	1.12	1.10	0.97
Cox5a	1.04	1.00	0.95	0.83
Cox6a1	1.19	1.24	0.89	0.95
Cox6b1	0.98	0.99	0.78	0.84
Cox6c	1.20	1.15	0.90	0.79
Cox7a2	1.07	1.14	0.91	0.99
Cox7a2l	1.01	1.05	1.15	1.09
Cox7c	0.94	0.92	1.03	0.79
Cpne1	2.08	2.33	1.09	1.43
Cpne2	1.29	1.17	1.52	1.36
Cpne3	0.94	0.99	0.94	0.64
Cpox	1.31	1.31	1.30	1.20
Cpped1	1.33	1.31	1.59	1.50
Cpsf1	1.14	1.02	1.34	0.99
Cpsf2	1.04	0.94	1.11	0.85
Cpsf3	1.07	1.12	1.11	0.77
Cpsf6	1.21	1.28	0.98	0.91
Cpsf7	1.17	1.11	1.16	1.08
Cpt1a	0.74	0.76	0.74	0.47
Cpt2	1.23	1.04	0.93	0.74
Creg1	0.62	0.54	0.67	0.56
Creld2	1.42	1.17	1.06	1.72
Crkl	1.23	1.15	1.20	1.51
Crlf3	1.26	1.43	1.35	2.09
Crnkl1	1.18	0.99	1.14	0.84
Crocc	1.39	1.18	1.14	1.56

Cryz	0.76	0.77	0.62	0.73
Cryzl1	1.00	0.95	2.27	2.12
Cs	0.84	0.91	0.92	1.02
Csde1	0.91	0.94	1.42	1.44
Cse1l	1.16	1.20	0.99	1.01
Csk	0.92	0.90	0.94	1.26
Csnk1a1	0.95	0.93	1.49	1.14
Csnk2a1	1.57	1.49	1.06	1.26
Csnk2a2	0.47	0.42	0.68	0.97
Csnk2b	0.72	0.77	0.77	1.17
Csrp1	0.64	0.68	0.67	0.86
Cstb	0.41	0.40	0.45	1.07
Cstf1	1.37	1.39	1.19	1.22
Cstf2	1.02	0.87	0.94	1.13
Cstf3	1.14	1.27	1.04	1.13
Ctage5	0.90	1.00	0.99	0.84
Ctbp1	1.45	1.53	1.14	0.97
Ctbp2	0.82	0.95	0.82	0.66
Ctcf	1.31	1.27	0.88	0.81
Ctdp1	0.61	0.91	1.09	0.88
Ctdspl2	1.18	1.41	0.96	0.94
Ctnnbl1	0.98	1.08	1.12	0.94
Ctnnd1	0.10	0.12	0.18	1.10
Ctps	0.79	0.73	0.87	1.08
Ctps2	1.03	1.02	1.14	0.88
Ctr9	0.80	0.84	0.95	1.19
Ctsa	0.86	0.89	0.77	1.09
Ctsb	0.93	1.06	0.78	0.74
Ctsc	1.27	1.31	1.03	0.94
Ctsd	0.80	0.79	0.77	0.99
Ctsz	0.97	1.00	0.74	0.90
Cul1	0.69	0.77	0.78	0.91
Cul2	1.20	1.15	0.97	1.15
Cul3	0.78	0.75	0.71	0.68
Cul4b	1.03	1.08	0.83	1.26
Cux1	1.37	1.21	1.36	1.01
Cwc15	1.06	1.06	1.06	1.02
Cwc22	1.18	0.93	1.04	1.00
Cwc27	1.31	1.20	1.02	0.96
Cwf19l1	0.86	1.23	0.94	1.08
Cyb5	1.07	0.94	1.30	0.73
Cyb5b	0.98	1.10	0.79	1.34
Cyb5r3	0.70	0.72	0.60	0.71
Cyc1	1.07	1.04	0.84	0.80
Cycs	0.85	0.82	0.90	0.88
Cyfip1	1.01	0.99	1.06	1.11
Cyp11a1	0.39	0.44	0.67	1.50
Cyp51	1.74	1.38	3.21	3.73
D10Jhu81e	1.30	1.34	1.16	1.02
D10Wsu52e	1.23	1.30	1.07	0.88
D17Wsu104e	0.96	0.93	1.03	1.45
D19Bwg1357e	0.90	0.79	1.18	0.82
Dad1	1.40	1.25	1.23	1.46
Dak	1.51	2.18	2.72	1.24
Dap	0.95	1.26	0.89	0.85
Dap3	1.12	1.13	0.89	0.87
Dapp1	0.78	0.71	0.86	0.62
Dars	0.91	0.95	0.85	0.79
Dars2	1.20	1.34	0.98	0.71
Dazap1	1.28	1.53	0.87	1.00
Dbi	0.90	0.93	0.97	0.90
Dbnl	1.03	1.15	1.01	1.07
Dbr1	0.59	0.67	0.63	0.88

Dbt	0.88	0.89	0.72	0.85
Dcaf13	0.96	0.97	1.26	0.99
Dcaf7	0.98	0.95	1.10	1.11
Dcaf8	0.70	0.78	0.70	0.93
Dcakd	1.13	1.09	0.93	1.10
Dcp1a	1.33	1.03	0.99	1.04
Dcps	1.40	1.39	0.91	0.95
Dctn1	0.94	0.93	0.99	1.08
Dctn2	0.91	0.89	1.04	1.13
Dctn3	1.15	0.95	1.01	1.00
Dctn4	1.03	0.99	1.03	1.17
Dcun1d1	0.72	0.83	1.01	0.81
Ddb1	0.82	0.81	0.90	1.00
Ddi2	1.19	1.22	1.21	1.23
Ddost	1.07	1.08	1.16	1.11
Ddt	1.14	1.07	1.60	0.96
Ddx1	1.12	1.16	1.11	0.94
Ddx10	0.80	0.80	1.12	1.27
Ddx17	0.78	0.82	0.66	0.84
Ddx18	0.78	0.73	1.00	0.72
Ddx19a	0.85	0.86	0.81	1.08
Ddx20	1.23	1.02	1.09	1.07
Ddx21	1.03	0.91	1.30	0.81
Ddx23	0.76	0.62	0.89	0.88
Ddx24	0.75	0.77	1.19	1.11
Ddx27	0.78	0.84	1.19	1.03
Ddx31	1.69	1.43	1.29	0.99
Ddx39	1.05	1.12	0.94	1.11
Ddx39b	1.09	1.13	1.10	0.84
Ddx3x	0.73	0.79	1.05	1.24
Ddx3y	0.81	0.83	1.46	1.61
Ddx41	0.77	0.81	1.01	0.79
Ddx42	0.95	1.00	0.93	1.02
Ddx46	0.86	0.86	0.88	0.90
Ddx47	1.57	1.62	2.09	0.99
Ddx5	0.95	0.97	1.20	1.14
Ddx51	1.16	1.09	1.38	1.31
Ddx54	1.50	1.18	2.03	1.17
Ddx56	0.99	1.07	1.44	0.91
Ddx6	1.17	1.22	1.13	1.14
Decr1	0.32	0.33	0.32	0.54
Def6	1.59	1.32	1.03	1.12
Degs1	0.73	0.72	1.01	1.62
Dek	0.92	0.86	0.88	0.75
Denr	1.06	1.03	1.06	0.87
Dera	2.30	2.19	1.88	1.31
Dffa	5.44	62.07	1.00	0.68
Dhcr24	0.76	0.87	1.17	1.73
Dhcr7	1.14	1.25	2.03	1.42
Dhfr	1.05	1.13	0.97	0.95
Dhodh	0.70	0.86	0.53	0.60
Dhrs1	0.96	0.89	0.66	0.50
Dhrs4	1.07	1.03	0.81	0.75
Dhx15	1.04	1.06	1.04	1.00
Dhx16	0.91	0.84	0.83	0.71
Dhx29	1.09	1.14	1.41	1.55
Dhx30	1.00	0.86	0.78	0.74
Dhx36	0.78	0.77	0.77	0.75
Dhx38	0.69	0.68	0.50	0.79
Dhx9	0.93	0.97	0.93	0.90
Diap1	0.95	1.08	1.04	1.14
Diap2	1.40	1.30	1.22	0.97
Diap3	0.59	0.61	0.87	0.52

Dimt1	1.01	0.92	1.24	0.83
Dip2b	1.00	1.03	0.99	1.53
Dis3	0.82	0.96	1.32	0.98
Dkc1	0.92	0.93	0.98	0.88
Dlat	0.98	1.07	0.68	0.84
Dld	0.94	0.92	0.95	0.99
Dlst	0.99	1.06	0.93	1.01
Dnaja1	0.61	0.67	0.78	0.78
Dnaja2	0.80	0.75	0.90	1.22
Dnaja3	1.47	1.52	1.18	1.83
Dnajb1	0.74	0.73	0.54	1.03
Dnajb11	1.20	1.27	1.29	2.05
Dnajb6	0.71	0.62	0.91	0.88
Dnajc10	1.30	1.02	0.94	1.07
Dnajc11	0.97	1.08	1.04	1.22
Dnajc13	0.59	0.70	1.03	1.63
Dnajc2	1.16	1.08	1.45	1.14
Dnajc3	1.41	1.39	1.90	1.47
Dnajc5	1.00	1.10	1.11	1.27
Dnajc7	1.12	1.20	1.26	1.34
Dnajc8	1.04	0.90	0.80	0.73
Dnajc9	1.11	1.04	0.75	0.63
Dnm1l	1.19	1.29	1.09	1.06
Dnm2	0.94	0.95	0.80	1.15
Dnm3	1.06	1.15	1.19	1.85
Dnmt1	0.99	0.95	1.12	0.87
Dnmt3a	0.80	0.48	0.74	0.61
Dnpep	0.80	0.73	0.73	0.76
Dnph1	1.03	1.05	0.99	1.16
Dnttip2	0.76	0.81	0.95	0.99
Dock10	1.40	1.35	1.24	1.04
Dock11	1.05	1.00	1.10	1.44
Dock2	1.03	1.02	1.11	1.18
Dock8	1.38	1.34	1.19	1.18
Dohh	1.00	1.01	1.49	1.76
Dok2	0.86	1.37	1.66	2.83
Dpf2	1.45	1.25	1.28	1.05
Dpm1	1.17	1.07	1.29	1.63
Dpp3	0.82	0.90	0.99	1.10
Dpp9	0.73	0.79	0.70	1.22
Dpy30	0.72	0.69	0.82	0.95
Dpysl2	1.67	1.75	1.69	0.76
Dr1	1.48	1.51	1.08	1.24
Drap1	1.01	1.07	1.01	1.10
Drg1	1.19	1.14	1.35	1.24
Drg2	0.97	0.96	0.96	0.90
Dscr3	0.97	0.99	1.02	1.51
Dstn	0.65	0.70	0.70	0.98
Dstyk	0.58	0.70	1.08	2.04
Dtd1	1.76	1.66	1.71	1.72
Dtymk	1.26	1.07	1.26	0.53
Dus3l	1.02	1.03	1.07	1.36
Dusp3	1.29	1.25	1.66	2.08
Dut	1.16	1.06	1.40	1.32
Dync1h1	1.09	1.12	1.15	1.16
Dync1i2	1.26	1.24	1.32	1.14
Dync1li1	0.99	1.00	0.99	1.27
Dynll1	1.24	1.12	1.11	1.11
Dynll2	1.18	1.05	0.84	0.93
Dynlrb1	1.42	1.61	1.58	1.79
Dynlt1f	1.30	1.47	1.43	1.58
Ebna1bp2	0.90	0.83	1.21	1.20
Ebp	0.84	0.75	1.08	1.63

Ech1	0.75	0.88	0.82	0.73
Echs1	1.06	1.09	0.67	0.62
Eci1	1.38	1.32	1.07	0.93
Eci2	0.87	1.10	0.96	0.83
Ecsit	0.87	0.93	0.79	0.82
Edc3	1.31	1.20	0.92	0.98
Edc4	0.74	0.77	0.63	0.83
Edf1	1.29	1.74	1.56	1.23
Eea1	1.60	1.39	1.25	1.64
Eed	0.91	0.92	1.18	0.90
Eef1b2	0.63	0.68	0.89	1.03
Eef1d	0.86	0.90	0.86	1.04
Eef1e1	1.29	1.46	1.03	1.12
Eef1g	0.76	0.80	0.96	1.42
Eef2	0.54	0.59	0.66	1.35
Eefsec	1.36	1.16	1.30	0.96
Efhd1	0.60	0.60	1.37	2.53
Efhd2	0.88	0.94	1.00	0.96
Eftud1	0.79	0.82	0.99	1.89
Eftud2	0.88	0.95	0.96	0.90
Egln1	1.28	1.09	0.77	0.71
Ehd1	0.88	0.83	0.96	1.24
Ehd4	1.20	1.34	1.38	1.34
Ehmt1	0.96	1.23	1.24	1.17
Eif1	0.93	1.00	1.24	1.64
Eif1a	1.22	1.20	1.41	1.67
Eif1ax	0.84	0.83	0.90	1.03
Eif2a	0.88	0.83	1.09	1.04
Eif2ak2	0.81	0.90	0.98	1.32
Eif2b1	1.01	1.04	1.10	1.14
Eif2b2	1.40	1.24	1.36	1.23
Eif2b3	0.97	1.18	1.27	0.81
Eif2b4	1.19	1.15	1.23	1.20
Eif2b5	1.05	1.13	0.83	0.90
Eif2d	0.89	0.92	0.80	0.73
Eif2s1	0.86	0.91	0.95	1.07
Eif2s2	0.88	0.89	0.86	1.04
Eif2s3x	0.91	0.91	0.84	1.13
Eif3a	0.96	1.01	1.26	1.16
Eif3b	1.22	1.10	1.29	1.07
Eif3c	0.93	1.03	1.22	1.14
Eif3d	0.97	1.03	1.14	1.21
Eif3e	0.98	1.03	1.36	1.23
Eif3f	1.02	1.04	1.18	1.24
Eif3g	0.86	0.82	1.19	1.23
Eif3h	1.04	1.11	1.35	1.31
Eif3i	1.11	1.06	1.33	1.23
Eif3j1	0.93	0.99	1.03	1.23
Eif3k	1.02	1.07	1.35	1.28
Eif3l	1.03	1.00	1.28	1.19
Eif3m	1.00	1.06	1.23	1.23
Eif4a1	0.89	0.96	1.29	1.37
Eif4a2	0.92	0.90	0.82	2.28
Eif4a3	1.06	1.06	1.05	1.00
Eif4b	0.83	0.88	1.00	1.15
Eif4e	0.88	0.91	1.45	1.38
Eif4ebp1	1.06	0.95	0.93	1.65
Eif4ebp2	1.36	1.43	1.84	1.45
Eif4g1	0.80	0.78	1.01	1.13
Eif4g2	0.76	0.77	1.07	1.16
Eif4g3	2.42	2.08	2.84	1.81
Eif4h	1.04	1.21	1.40	1.19
Eif5	0.77	0.78	0.99	1.38

Eif5a	1.01	1.03	1.07	1.03
Eif5b	0.83	0.76	0.97	0.97
Eif6	1.50	1.53	1.27	1.34
Elac2	1.11	1.08	0.82	0.72
Elavl1	0.84	0.86	0.87	1.00
Elf1	1.28	1.18	1.24	1.06
Elmo1	1.30	1.25	1.34	1.41
Elmsan1	1.19	1.21	1.42	1.15
Elp2	1.19	1.23	1.22	1.16
Elp3	1.20	1.12	1.01	0.97
Emc1	0.96	0.83	1.16	1.15
Emc2	1.13	0.99	1.17	1.33
Emc3	1.00	1.09	1.47	1.20
Emc7	0.77	0.89	0.85	1.08
Emc8	1.03	1.13	1.09	1.22
Emd	0.88	0.88	1.42	1.20
Emg1	1.26	1.21	1.20	1.06
Emilin1	0.62	0.51	0.99	0.93
Emilin2	0.79	0.75	1.04	1.80
Eml2	1.36	1.32	0.95	1.13
Eml4	1.04	0.84	0.95	1.08
Emr1	0.34	0.32	0.76	2.49
Enah	0.77	0.89	1.30	1.48
Eno3	0.76	0.86	0.93	1.83
Enoph1	1.32	1.40	1.03	1.09
Ensa	0.85	0.95	1.15	1.05
Eny2	0.82	0.96	1.01	0.98
Ep300	0.78	0.81	1.02	1.10
Epb4.1	1.20	1.21	1.09	0.68
Epb4.1l2	1.03	1.01	0.90	0.57
Epdr1	0.90	0.78	0.48	0.97
Epm2aip1	1.03	1.07	1.32	1.77
Eprs	0.89	0.94	0.84	0.88
Eps15	0.78	0.77	0.69	0.67
Eps15l1	1.04	1.13	0.85	1.36
Ept1	1.16	1.20	1.21	1.26
Erap1	1.49	1.28	1.53	1.27
Ercc6l	0.62	0.70	0.81	1.01
Ergic1	0.77	0.84	0.98	0.92
Erh	1.05	1.25	1.05	1.00
Eri1	0.95	0.97	1.20	1.23
Erlin2	1.13	1.28	1.13	1.31
Ermp1	1.16	1.20	1.41	1.02
Ero1l	1.12	0.99	0.41	1.04
Erp29	1.43	1.30	1.40	1.11
Erp44	1.09	1.08	1.10	1.07
Esd	1.29	1.19	1.06	0.83
Esf1	0.95	0.91	1.04	1.77
Esyt1	1.18	1.09	1.53	1.26
Esyt2	1.00	0.97	1.11	1.90
Etf1	0.80	0.77	1.02	1.06
Etfa	1.08	1.16	0.76	0.86
Etfb	1.03	1.02	0.81	0.83
Etfdh	0.94	1.00	0.92	0.93
Ethe1	1.13	1.32	1.22	1.11
Ewsr1	0.98	1.04	0.96	0.97
Exoc1	1.08	1.10	1.49	1.30
Exoc4	1.16	1.04	1.17	1.24
Exosc1	1.20	1.00	0.80	1.00
Exosc10	1.11	1.03	1.10	0.79
Exosc2	1.10	0.97	0.84	0.96
Exosc3	0.98	0.89	0.85	0.88
Exosc5	1.04	1.06	0.73	0.81

Exosc6	1.08	0.93	0.81	0.88
Exosc7	0.92	0.91	0.87	0.84
Exosc8	0.90	0.81	0.75	1.04
Exosc9	1.00	0.92	0.80	0.76
Ezr	0.98	1.00	1.01	1.31
Faah	1.73	1.75	1.35	0.78
Fabp5	1.02	1.12	0.60	0.63
Fads1	1.63	1.46	2.06	2.24
Faf1	0.77	0.73	0.93	1.07
Faf2	1.39	1.15	1.05	1.14
Faim	1.18	0.75	1.08	0.85
Fam107b	0.72	0.69	0.95	0.63
Fam111a	0.60	0.61	0.64	0.58
Fam114a2	1.43	1.44	1.28	1.29
Fam120a	1.10	1.12	1.29	0.85
Fam129b	1.16	1.24	1.91	1.73
Fam136a	1.51	1.46	1.32	1.08
Fam162a	1.04	1.12	0.66	0.96
Fam175b	0.85	0.75	0.98	0.79
Fam192a	0.88	0.92	0.89	1.20
Fam195a	1.03	0.98	1.98	1.34
Fam195b	1.02	1.11	0.87	0.90
Fam203a	1.53	1.71	2.29	1.40
Fam21	0.88	0.92	0.92	1.21
Fam3c	0.98	0.95	0.83	0.58
Fam49b	0.97	1.00	0.85	1.02
Fam50a	0.84	0.81	0.76	1.03
Fam65a	1.34	1.50	0.98	1.01
Fam76b	2.13	1.46	0.96	0.80
Fam96b	1.28	1.24	1.14	1.36
Fam98a	1.15	1.22	1.16	1.41
Fam98b	1.51	1.43	1.27	0.92
Farsa	0.93	0.84	0.89	0.90
Farsb	0.95	0.84	0.86	0.82
Fasn	1.07	1.10	1.44	1.29
Fau	0.82	0.90	1.16	1.00
Fbl	1.09	1.06	0.96	0.93
Fbll1	1.27	1.25	1.13	1.44
Fcer1g	0.17	0.24	0.34	1.53
Fcgr2b	0.38	0.26	0.67	1.07
Fcgr3	0.46	0.45	0.46	1.13
Fdps	1.72	1.71	2.56	3.49
Fdx1	1.30	1.38	0.82	0.85
Fdxr	1.29	1.27	1.19	0.85
Fen1	0.85	0.89	0.87	0.88
Fermt3	0.78	0.73	0.79	1.05
Fes	1.22	0.92	1.48	1.29
Fh1	0.88	0.93	0.80	0.79
Fhl3	0.86	0.79	1.11	2.51
Fip1l1	1.30	1.08	1.25	1.04
Fis1	0.87	0.92	0.84	0.79
Fkbp15	0.86	0.81	0.87	1.20
Fkbp1a	1.36	1.32	1.14	1.41
Fkbp2	1.92	1.73	1.49	1.37
Fkbp3	1.14	1.15	1.12	0.86
Fkbp4	1.14	1.21	1.43	1.13
Fkbp5	0.99	1.12	0.90	0.83
Fkbp8	0.78	0.89	0.92	1.36
Flii	0.98	0.78	0.89	0.97
Flna	0.48	0.51	0.98	1.05
Flnb	1.03	1.04	0.85	0.74
Fmnl1	1.57	1.48	1.63	1.96
Fn3krp	0.88	0.97	0.75	0.63

Fnbp1	1.01	0.94	1.17	2.25
Fnbp4	0.69	0.75	0.67	1.11
Fndc3a	1.51	1.35	1.58	1.42
Fnta	1.09	1.23	1.14	1.15
Frg1	0.98	1.00	0.73	1.01
Fth1	0.65	0.73	2.05	1.05
Ftsj3	0.83	0.84	1.19	1.03
Ftsjd2	0.56	0.51	0.61	0.93
Fubp1	1.14	1.14	1.12	0.71
Fubp3	1.16	1.32	1.15	1.24
Fus	0.87	0.89	0.82	0.78
Fut8	1.48	1.68	2.55	0.88
Fxn	4.83	1.33	0.82	0.91
Fxr1	0.83	0.77	0.88	0.82
Fxr2	1.00	1.09	1.21	1.34
Fyb	0.60	0.63	0.40	0.40
Fyttd1	0.96	1.12	1.57	1.14
G3bp1	0.96	1.00	1.32	1.10
G3bp2	0.86	0.90	1.66	1.25
G6pdx	0.67	0.67	0.75	1.14
Gaa	1.02	0.98	0.97	0.96
Gabpa	0.80	0.96	0.87	0.96
Gadd45gip1	1.03	0.99	1.25	1.01
Galk1	0.99	1.09	0.82	0.88
Galk2	1.05	1.04	1.28	1.74
Ganab	1.20	1.17	1.27	1.37
Gapdh	1.37	1.47	1.07	0.97
Gapvd1	1.07	0.94	1.03	1.47
Gar1	1.20	1.20	1.12	1.09
Gars	0.73	0.73	0.79	1.25
Gart	1.26	1.29	1.55	1.48
Gatad2a	0.83	0.76	1.05	1.24
Gatad2b	1.21	1.18	0.92	1.00
Gba	0.77	0.60	0.52	1.01
Gbas	1.27	1.07	0.86	0.61
Gbe1	2.07	1.76	0.97	1.10
Gbf1	0.85	0.87	0.97	1.11
Gbp7	1.34	1.48	1.34	1.25
Gclm	1.06	1.01	1.24	1.48
Gcn1l1	1.13	1.15	1.12	0.85
Gda	0.50	0.44	0.58	0.38
Gdi1	1.08	1.12	0.96	1.83
Gdi2	1.18	1.25	1.12	1.20
Gemin5	1.27	1.07	1.32	1.16
Gfer	1.68	1.54	1.12	0.75
Gfm1	0.69	0.74	0.77	1.03
Gfm2	0.93	1.07	0.99	1.08
Gfm2	10.47	0.83	0.99	1.08
Gfpt1	0.94	0.76	1.04	1.11
Ggct	0.68	0.68	1.03	1.68
Ggh	0.52	0.43	0.52	0.14
Gigyf2	1.01	0.99	1.05	0.99
Gimap8	2.05	1.84	3.99	5.10
Gins4	1.14	1.07	0.57	0.66
Git2	1.27	1.17	1.14	0.95
Gla	1.17	1.13	0.58	1.34
Glb1	0.84	0.88	0.70	0.82
Glg1	1.00	1.03	0.59	0.67
Glipr2	0.56	0.57	0.64	0.95
Glmn	1.12	1.23	1.21	1.27
Glo1	0.82	0.82	0.78	0.94
Glod4	1.25	1.28	0.96	1.02
Glrx	0.63	0.63	0.46	1.21

Glrx3	0.82	0.84	0.83	0.71
Glrx5	1.09	1.07	0.89	1.13
Gls	0.76	0.84	0.83	0.75
Glt25d1	1.46	1.29	1.47	1.58
Gltp	1.34	1.30	1.10	0.66
Glud1	1.09	1.27	1.00	0.96
Glul	1.18	1.10	0.59	0.64
Glyr1	1.13	1.24	0.85	1.15
Gm10094	0.98	0.93	0.90	0.92
Gm10177	1.35	1.29	1.31	1.88
Gm10349	0.99	1.03	0.81	0.78
Gm12854	0.81	0.84	0.67	0.83
Gm13202	0.90	0.80	0.99	0.67
Gm14680	0.88	0.98	0.90	0.96
Gm15210	0.84	0.87	0.92	1.11
Gm17296	0.75	0.80	1.07	0.77
Gm2001	1.57	1.36	1.83	1.64
Gm20604	1.19	1.18	0.97	1.13
Gm3258	0.83	0.91	0.79	0.81
Gm4832	1.34	1.27	1.59	1.27
Gm5483	1.62	1.75	4.65	12.49
Gm5506	1.32	1.34	1.16	0.99
Gm5621	0.85	0.89	1.34	1.24
Gm8210	0.91	0.80	1.13	0.74
Gm9385	1.04	0.83	1.34	0.50
Gm9386	1.22	1.11	0.78	0.89
Gm9846	0.94	0.97	1.05	1.05
Gmds	1.01	0.89	0.71	1.21
Gmfb	0.91	1.11	0.89	0.95
Gmfg	0.85	1.03	0.61	0.65
Gmip	0.96	1.14	1.31	0.99
Gmppa	0.91	0.75	0.67	0.80
Gmppb	0.47	0.64	0.71	0.93
Gmpr	1.07	1.06	0.99	1.21
Gmpr2	1.21	1.24	1.45	1.89
Gmps	0.93	0.96	0.90	0.95
Gnai2	0.81	0.77	0.79	0.79
Gnai3	0.84	0.85	0.96	0.91
Gnas	1.39	1.23	1.90	1.25
Gnb1	1.20	1.49	0.96	0.69
Gnb2	1.22	1.18	0.79	0.61
Gnb2l1	1.09	1.09	1.13	1.18
Gne	0.88	0.69	1.07	0.91
Gng12	0.67	0.64	0.65	0.61
Gng2	1.67	1.59	1.22	0.54
Gnl1	0.82	0.81	0.74	0.89
Gnl2	1.20	0.98	1.59	1.38
Gnl3	0.92	0.99	1.13	1.14
Gnl3l	1.42	1.49	2.26	1.37
Gnpnat1	1.32	1.03	1.11	1.40
Golga2	2.05	1.93	1.83	1.68
Golgb1	1.11	1.30	2.41	1.61
Golm1	1.25	1.17	1.51	0.96
Golph3	0.79	0.90	3.27	1.01
Golt1b	1.60	1.78	1.42	2.41
Gorasp2	1.15	1.27	1.42	1.58
Got1	1.33	1.21	1.40	1.48
Got2	0.94	0.95	0.73	1.05
Gpatch8	1.38	1.29	1.11	1.17
Gpd1l	0.63	0.70	0.70	0.69
Gpd2	0.94	1.10	1.12	1.32
Gphn	1.53	1.45	1.23	1.28
Gpi1	1.24	1.32	1.12	0.99

Gpkow	0.67	1.02	0.81	1.07
Gpr56	0.86	0.82	0.80	0.78
Gps1	1.45	1.06	1.20	0.99
Gpt2	0.90	1.03	0.71	1.70
Gpx1	0.91	0.85	0.45	0.50
Gpx4	1.11	1.83	0.65	0.96
Grb2	0.89	0.89	0.66	0.79
Grhpr	0.88	0.89	0.64	0.72
Grn	0.82	0.85	1.09	0.95
Grpel1	0.89	0.95	0.78	0.96
Grwd1	1.06	1.10	1.37	1.20
Gsdmd	1.41	1.13	0.85	1.06
Gse1	0.76	0.86	0.89	1.10
Gsk3b	0.96	0.90	1.10	1.43
Gsn	0.82	0.86	0.37	0.58
Gspt1	1.02	1.07	1.13	1.39
Gsr	0.87	0.85	0.64	0.94
Gss	1.78	1.77	1.37	1.75
Gsta4	0.50	0.42	0.49	0.11
Gsto1	0.85	0.87	0.99	0.85
Gstp1	0.87	0.90	0.87	0.86
Gstt3	1.42	1.44	1.02	0.63
Gtf2b	0.77	0.85	0.72	0.89
Gtf2e1	0.99	0.94	0.83	1.21
Gtf2f1	0.65	0.64	1.04	1.13
Gtf2f2	0.88	0.92	0.86	0.87
Gtf2i	1.13	1.07	1.22	1.13
Gtl3	1.29	0.96	0.80	1.05
Gtpbp1	0.82	0.78	0.82	0.95
Gtpbp4	1.02	0.91	1.31	0.91
Guk1	1.09	1.04	0.99	1.08
Gusb	1.48	1.47	1.43	0.86
Gyg	1.12	1.05	0.91	1.23
Gyk	0.79	0.86	0.77	0.78
Gys1	1.41	1.29	0.81	0.91
H13	1.06	1.06	1.06	1.35
H1f0	1.59	0.91	1.09	0.19
H2afy	1.82	1.83	1.38	0.86
H2afz	0.82	0.78	0.73	0.67
H2-K1	0.79	0.80	1.07	1.69
H2-Ke2	0.81	0.82	0.91	1.05
Hadha	1.18	1.22	1.02	0.71
Hadhb	0.99	1.07	0.85	0.68
Hagh	1.13	1.25	0.78	0.99
Hars	0.95	1.05	1.08	0.99
Hat1	1.01	0.93	0.80	0.75
Hbs1l	1.33	1.15	1.25	1.12
Hccs	0.72	0.84	0.94	1.28
Hcfc1	0.73	0.80	0.75	0.83
Hcls1	0.91	0.99	1.17	1.34
Hdac1	1.12	1.06	0.84	0.93
Hdac2	1.18	1.12	1.01	0.78
Hdac6	0.86	0.86	1.17	0.89
Hddc2	1.72	1.53	1.43	1.24
Hdgf	0.93	0.91	0.68	0.76
Hdgfrp2	0.73	0.73	0.71	1.00
Hdhd2	1.24	1.41	1.10	1.13
Hdlbp	0.78	0.76	0.85	0.91
Heatr1	1.15	0.88	0.91	0.95
Heatr1	0.80	0.82	0.91	0.95
Heatr3	1.10	1.17	1.17	1.07
Heatr6	1.10	1.05	1.19	0.81
Helb	1.03	0.96	0.90	0.79

Hells	0.86	0.70	1.56	0.86
Herc4	1.18	1.08	0.98	0.92
Hexa	1.24	1.45	1.42	1.09
Hexb	1.62	1.57	0.98	0.85
Hexim1	0.67	0.72	0.97	1.15
Hgs	1.04	1.13	1.22	1.13
Hibadh	0.90	0.87	0.52	0.73
Hibch	0.87	0.81	0.62	0.45
Hic2	22.02	19.12	18.88	0.81
Hint1	1.28	1.39	1.19	1.05
Hint2	1.14	1.07	0.94	0.72
Hip1r	1.15	1.19	1.23	0.43
Hirip3	0.89	0.79	1.35	0.67
Hist1h1a	2.17	1.20	1.66	0.26
Hist1h1b	2.44	1.38	1.72	0.14
Hist1h1c	2.03	1.19	1.46	0.27
Hist1h1d	1.97	1.13	1.15	0.29
Hist1h1e	1.67	1.00	1.22	0.22
Hist1h2ah	1.81	1.67	1.17	0.89
Hist1h2bk	2.07	1.92	1.03	0.86
Hist1h4i	1.58	1.17	1.16	0.56
Hist2h2ab	1.64	1.42	1.08	1.15
Hist2h2ac	1.04	1.02	0.94	0.85
Hk1	1.65	1.64	1.11	0.84
Hk2	0.54	0.52	0.58	0.91
Hk3	1.87	1.76	1.58	1.59
Hmbs	1.25	1.31	0.83	0.97
Hmg20a	1.36	1.31	0.77	0.85
Hmga1	0.80	0.76	0.65	1.26
Hmga1	0.71	0.74	0.65	1.26
Hmgb2	0.94	0.90	0.82	0.86
Hmgb3	1.04	0.94	0.79	0.69
Hmgcl	1.19	1.25	3.23	0.97
Hmgcs1	1.50	1.50	3.74	4.51
Hmgn1	1.33	1.19	1.05	1.01
Hmgn2	1.23	1.04	0.97	0.75
Hmgn5	0.67	0.66	0.60	0.81
Hmha1	0.91	0.89	1.25	1.96
Hmox1	0.69	0.85	0.35	0.78
Hmox2	0.97	0.99	1.71	1.46
Hn1	0.64	0.66	1.02	0.88
Hn1l	0.74	0.78	0.81	0.73
Hnrnpa0	1.17	1.20	1.09	0.92
Hnrnpa1	1.01	1.03	0.91	0.92
Hnrnpa3	1.70	1.21	0.98	0.99
Hnrnpa3	1.14	1.20	0.98	0.99
Hnrnpab	1.06	1.09	1.09	1.07
Hnrnpf	1.29	1.21	0.99	0.91
Hnrnph1	1.12	1.00	0.84	0.92
Hnrnph2	1.22	2.24	0.90	0.91
Hnrnpk	1.13	1.17	1.04	1.00
Hnrnpl	1.12	1.13	0.95	1.03
Hnrnpm	1.05	0.99	0.89	0.91
Hnrnpr	1.14	1.21	1.09	0.78
Hnrnpu	1.06	1.07	0.98	0.86
Hnrnpul1	1.15	1.08	0.97	1.07
Hnrnpul2	0.99	1.04	0.88	0.97
Hnrpdl	0.94	1.01	1.10	0.97
Hnrpll	0.71	0.84	0.77	0.88
Hook3	1.03	1.14	0.60	0.52
Hp1bp3	1.34	1.19	1.07	0.56
Hprt	0.86	0.89	0.83	0.82
Hrsp12	0.76	0.74	0.51	0.51

Hs1bp3	0.75	0.74	0.73	0.92
Hsbp1	0.78	0.86	0.79	0.89
Hsd17b10	0.94	0.92	1.33	1.27
Hsd17b11	0.71	0.72	0.82	1.26
Hsd17b12	1.15	1.22	1.42	1.94
Hsd17b4	1.37	1.06	0.86	0.72
Hsd17b7	0.73	0.82	1.23	1.45
Hsdl1	1.06	1.21	3.53	1.14
Hsp90aa1	0.91	0.93	1.02	1.14
Hsp90ab1	0.74	0.79	1.03	1.26
Hsp90b1	1.26	1.33	1.08	1.18
Hspa13	1.09	1.53	2.24	1.15
Hspa14	1.27	1.30	1.19	1.11
Hspa2	0.24	0.25	0.25	0.53
Hspa4	1.05	1.14	1.11	1.16
Hspa4l	1.13	1.21	0.97	0.62
Hspa5	1.18	1.22	1.02	1.71
Hspa8	0.87	0.92	1.16	1.27
Hspa9	1.04	1.11	1.03	1.05
Hspbp1	1.40	1.43	2.02	1.08
Hspd1	0.41	0.44	0.37	0.78
Hspe1	0.71	0.76	0.65	0.67
Hsph1	0.90	0.97	0.90	0.92
Htatsf1	0.66	0.64	0.62	0.78
Htra2	0.60	0.57	0.51	0.90
Huwe1	0.99	1.21	0.93	0.90
Huwe1	0.86	0.86	0.93	0.90
Hyou1	0.93	0.96	0.93	1.55
Hypk	0.84	0.84	1.01	1.25
Iah1	1.07	0.86	0.91	0.83
Iars	1.12	1.12	1.09	1.06
Iars2	1.28	1.27	1.05	0.84
Ibtk	0.96	0.82	1.07	0.89
Icam1	0.78	0.79	0.48	0.41
Ide	1.00	1.04	1.09	1.05
Idh1	0.98	0.92	0.85	1.33
Idh2	1.02	1.08	0.70	0.58
Idh3a	0.84	0.92	0.69	0.82
Idh3b	1.10	1.12	0.88	0.96
Idh3g	1.28	1.32	0.84	0.93
Idi1	1.27	1.17	1.54	1.27
Ifi47	1.21	1.47	1.60	1.12
Ifitm3	3.13	6.32	9.94	6.30
Igbp1	0.83	0.97	1.02	1.26
Igf1r	0.76	0.77	0.97	1.07
Igfbp4	0.74	0.61	2.59	2.32
Ik	0.92	0.89	1.02	0.85
Ikbkap	0.85	0.77	0.99	0.93
Ikzf2	1.31	1.33	1.26	0.83
Il16	0.89	0.88	0.74	1.00
Ilf2	0.96	1.04	0.93	1.01
Ilf3	1.10	1.06	0.87	0.97
Ilk	0.80	0.86	0.98	0.94
Ilkap	0.92	0.87	0.97	0.65
Immt	0.97	0.98	0.80	0.89
Imp3	1.15	1.04	1.09	1.08
Imp4	0.82	0.75	1.07	0.99
Impa1	0.87	0.85	0.78	0.87
Impa2	1.42	1.34	1.09	0.98
Impdh1	1.10	1.03	0.99	1.14
Incenp	0.80	0.58	0.59	0.40
Inip	1.07	1.06	1.11	1.07
Inpp5d	0.84	0.88	1.00	0.14

Ints1	0.98	0.99	0.96	1.00
Ints10	1.19	1.13	1.68	1.21
Ints3	1.21	1.20	1.14	0.95
Ints4	0.85	0.83	0.83	1.00
Ints6	0.91	1.22	1.27	1.17
Ints7	0.97	0.80	1.06	1.17
Ipo4	0.94	1.08	1.20	1.26
Ipo5	1.03	1.05	1.10	1.00
Ipo7	0.79	0.87	0.85	0.99
Ipo8	1.00	1.23	2.08	1.32
Ipo9	0.96	0.93	0.92	0.99
Iqgap1	0.72	0.76	0.74	0.53
Iqgap2	1.62	1.77	1.99	1.22
Irak3	0.82	0.78	0.41	0.51
Irf2bp2	0.85	0.91	1.12	1.09
Iscu	1.82	1.50	1.09	1.09
Isoc1	1.04	1.14	0.96	0.57
Ist1	0.71	0.77	0.75	1.16
Isyna1	1.01	1.04	1.01	1.04
Itga2b	1.25	1.39	1.36	2.18
Itga4	4.92	3.83	4.34	0.90
Itga5	0.85	0.79	1.06	1.11
Itgb1	1.33	1.50	1.33	0.97
Itgb2	0.91	0.89	1.64	1.72
Itpa	1.11	1.12	0.98	1.22
Itpr3	1.14	1.39	0.82	1.64
Itsn2	0.89	0.86	0.97	1.77
Iws1	1.03	1.09	1.08	1.01
Jak1	1.41	1.39	1.82	0.91
Jmjd6	0.61	0.68	1.08	0.50
Jund	1.15	0.98	1.13	1.11
Kcmf1	0.96	1.10	1.02	1.40
Kcnab2	0.89	0.88	0.81	0.86
Kdm1a	0.83	0.92	0.88	0.81
Kdm2a	0.93	0.89	0.99	1.03
Kdm3a	0.76	0.76	0.95	0.86
Kdsr	0.77	0.87	0.84	0.50
Khdrbs1	1.01	1.00	0.97	0.94
Khsrp	0.88	0.89	0.91	1.08
Kif11	0.71	0.75	0.97	0.75
Kif15	0.66	0.73	0.92	0.74
Kif22	0.60	0.64	0.88	0.55
Kif23	0.83	0.93	0.81	0.63
Kif23	0.10	0.09	0.81	0.63
Kif2a	1.05	0.97	0.98	1.11
Kif2c	0.58	0.54	0.67	0.71
Kif4	0.59	0.64	0.91	0.92
Kif5b	0.86	0.88	0.93	1.13
Klc1	0.84	0.94	1.03	0.93
Klhdc4	0.58	0.57	0.78	1.05
Kpna1	1.12	1.05	1.06	1.25
Kpna2	0.46	0.46	0.98	0.92
Kpna3	1.03	1.09	1.03	0.88
Kpna4	0.60	0.59	0.59	0.94
Kpnb1	0.99	1.03	0.96	0.92
Krr1	0.90	0.97	0.91	0.76
Kti12	0.74	0.78	1.09	1.29
Ktn1	0.97	0.98	0.92	0.83
l7Rn6	1.08	0.85	1.00	0.63
Lactb2	1.41	1.15	1.23	1.24
Lamp1	0.88	0.95	0.89	1.48
Lamp2	0.60	0.59	0.65	0.92
Lamtor1	1.00	1.11	0.96	0.92

Lamtor2	0.91	1.27	0.87	1.01
Lamtor3	0.81	0.92	0.97	0.97
Lancl1	1.09	1.04	0.69	0.65
Lap3	1.12	1.07	1.12	0.97
Larp1	1.08	1.02	1.54	1.46
Larp4	0.79	0.95	1.87	1.62
Larp4b	1.03	1.15	1.23	0.96
Larp7	0.79	0.73	0.82	0.92
Lars	1.10	1.09	1.12	1.06
Las1l	0.93	1.02	0.99	0.93
Lasp1	1.28	1.30	1.03	1.46
Lbr	0.90	0.90	0.79	0.86
Lcp1	0.69	0.74	0.50	1.17
Lcp2	0.64	0.82	1.03	3.37
Ldha	1.21	1.24	1.10	0.94
Ldlr	0.93	1.12	1.63	3.87
Leo1	0.82	0.72	0.87	1.15
Letm1	1.29	1.29	1.14	0.87
Lgals1	0.81	0.89	0.71	1.75
Lgals3bp	12.68	14.34	8.50	1.10
Lgmn	1.18	0.96	0.98	1.62
Lig1	0.91	0.94	0.98	0.65
Lig3	1.00	0.96	0.95	0.62
Lima1	0.69	0.75	1.20	1.74
Lims1	1.20	1.01	0.98	0.81
Lin7c	1.33	1.28	1.22	0.92
Lman1	1.58	1.85	1.45	1.35
Lman2	1.37	1.46	1.46	0.84
Lmna	0.74	0.84	1.10	1.89
Lmnb1	1.19	1.24	1.01	0.86
Lmnb2	1.35	1.41	1.01	0.94
Lnpep	0.99	1.16	0.87	0.80
LOC100045191	0.94	1.02	0.86	0.90
LOC100045848	0.93	0.98	1.14	0.84
LOC100046079	0.98	1.01	0.89	0.77
LOC100046151	0.98	1.05	0.98	0.97
LOC100505031	1.04	1.09	1.07	1.13
LOC100862446	1.05	0.99	2.71	1.10
LOC100862455	1.00	0.97	1.12	0.98
LOC100862595	1.01	0.92	1.09	0.81
LOC101055761	1.00	0.74	0.98	0.73
LOC101056616	0.74	0.74	0.88	1.00
LOC101056619	0.78	0.82	1.03	1.20
LOC631286	0.71	0.74	0.70	0.68
LOC632329	1.20	1.33	1.52	1.30
LOC635999	0.74	0.72	0.89	0.96
LOC637733	1.29	1.22	1.08	0.72
LOC638399	0.93	1.01	1.16	0.91
LOC674321	1.14	1.06	1.06	1.07
Lonp1	1.14	1.16	0.75	1.09
Lpp	0.61	0.67	0.54	1.80
Lpxn	0.80	0.85	0.53	2.00
Lrba	0.93	0.95	0.86	0.87
Lrch3	1.55	1.22	1.34	1.60
Lrpap1	1.68	1.61	1.51	1.15
Lrpprc	0.86	0.96	1.06	0.94
Lrrc40	0.85	1.08	0.88	0.81
Lrrc47	1.50	1.67	1.46	1.04
Lrrc59	1.10	1.09	1.21	1.15
Lrwd1	1.12	0.97	0.77	0.70
Lsm1	1.05	1.03	0.78	1.18
Lsm12	0.92	0.76	1.57	1.43
Lsm14a	1.42	1.39	1.11	1.13

Lsm14b	0.87	0.84	1.01	0.87
Lsm2	0.89	0.87	0.80	0.85
Lsm3	0.95	0.93	0.90	1.02
Lsm4	0.77	0.77	0.78	0.79
Lsm6	0.82	0.82	0.83	0.84
Lsp1	8.68	7.67	0.56	1.31
Lss	1.83	1.74	2.23	2.27
Lta4h	1.38	1.48	1.37	0.94
Luc7l	0.80	0.77	0.81	0.89
Luc7l2	0.69	0.73	0.75	0.84
Luc7l3	0.93	0.92	1.07	1.07
Lxn	0.83	0.66	0.89	0.80
Ly6e	1.43	1.70	1.72	1.50
Lyar	1.24	1.13	1.33	0.72
Lyn	0.79	0.93	0.87	1.15
Lypla1	0.88	0.91	0.85	0.74
Lypla2	0.94	0.95	0.87	1.06
Lyplal1	1.10	1.04	0.83	0.67
Lzic	1.17	1.11	1.13	1.15
M6pr	0.91	0.89	0.78	0.82
Mad1l1	0.98	0.81	0.92	0.87
Mad2l1	0.65	0.67	0.72	0.65
Maea	0.89	0.82	1.02	0.92
Magoh	0.76	0.67	0.58	0.64
Magt1	1.54	1.43	1.56	1.32
Mak16	0.82	0.78	0.96	1.28
Man1a	1.15	1.17	1.00	0.98
Man2b1	0.53	0.58	0.37	0.34
Man2b2	1.10	1.40	0.79	0.80
Man2c1	1.20	1.10	1.61	1.33
Manba	0.54	0.53	0.60	0.87
Manf	0.86	0.84	0.98	1.17
Map1s	0.77	0.74	0.92	0.98
Map2k1	1.00	0.94	0.89	1.13
Map2k3	1.01	1.17	0.95	1.15
Map2k4	1.18	1.18	1.47	1.10
Map3k19	1.21	1.13	1.41	1.11
Map4	0.96	0.95	0.84	0.61
Map7d1	0.64	0.62	0.96	1.06
Mapk1	1.07	1.05	1.19	1.02
Mapk14	0.70	0.69	0.67	0.91
Mapk15	1.47	1.33	1.56	0.99
Mapk1ip1l	1.09	1.22	1.13	1.23
Mapk3	1.35	1.32	1.07	0.74
Mapkapk2	0.61	0.61	0.63	0.92
Mapre1	1.05	1.08	1.06	1.28
Mapre2	0.73	0.72	0.91	0.93
March2	0.78	0.70	0.62	0.66
Mars	0.98	0.97	0.98	0.98
Mat2a	0.83	0.78	1.35	1.32
Mat2b	0.90	0.98	0.89	1.51
Matr3	1.15	1.09	1.06	1.01
Mavs	0.98	1.11	0.97	1.55
Max	0.65	0.74	1.23	1.32
Mb21d1	0.74	0.75	0.58	0.62
Mbd2	0.73	0.77	0.95	1.03
Mbd3	1.36	1.28	1.21	1.08
Mbnl1	1.05	1.16	0.92	0.89
Mbnl1	1.15	0.82	0.92	0.89
Mcat	1.48	1.30	1.25	1.13
Mccc1	1.20	1.18	0.75	0.61
Mcl1	0.89	1.29	1.91	2.89
Mcm2	0.95	0.92	0.83	0.77

Mcm3	0.82	0.83	0.87	0.81
Mcm4	0.92	0.93	0.91	0.78
Mcm5	0.80	0.79	0.91	0.79
Mcm6	0.81	0.92	0.87	0.80
Mcm7	0.87	0.94	0.89	0.76
Mcmbp	0.67	0.62	1.35	0.97
Mcts1	1.40	1.28	1.00	0.90
Mcu	0.53	0.76	0.57	1.31
Mdc1	0.55	0.56	0.38	0.52
Mdh1	1.42	1.42	1.08	1.21
Mdh2	1.03	1.12	0.87	0.89
Mdn1	0.91	0.91	0.94	0.87
Mdp1	1.20	1.16	1.19	1.19
Me2	1.34	1.40	0.77	0.75
Mecp2	0.67	0.67	0.55	1.27
Mecr	1.19	1.32	0.86	1.01
Med1	1.00	0.93	1.15	0.96
Med8	0.93	1.10	1.04	1.03
Memo1	1.07	0.98	1.03	1.14
Mepce	1.06	1.55	1.02	1.11
Mesdc2	0.92	0.87	1.10	1.06
Metap1	1.06	0.93	0.97	1.20
Metap2	0.94	0.96	1.00	0.96
Mettl13	0.87	0.86	0.87	1.03
Mettl16	1.06	0.75	0.79	0.93
Mfap1a	0.99	1.01	0.96	0.94
Mgea5	0.67	0.69	0.67	1.06
Mgmt	0.70	0.59	0.57	0.89
Mgst2	0.54	0.62	1.11	3.96
Mia3	1.07	0.98	1.12	1.49
Mical1	1.18	1.31	1.45	1.58
Micall2	0.42	0.45	0.56	1.03
Mif	1.59	1.46	1.29	0.98
Mina	0.47	0.45	1.12	0.83
Minpp1	0.92	0.99	1.10	1.06
Mki67	0.99	0.60	0.39	0.24
Mki67ip	0.77	0.77	1.08	0.98
Mlec	1.49	1.39	1.45	1.05
Mlkl	1.01	1.07	0.80	0.96
Mmgt1	0.97	0.94	0.82	0.91
Mms19	1.41	1.35	1.10	1.20
Mnf1	1.51	1.55	1.34	1.59
Mob1b	0.54	0.55	0.77	1.06
Mocs3	0.91	0.94	0.83	0.98
Mogs	1.04	1.04	1.15	1.23
Morc2a	1.25	1.15	1.07	1.33
Mov10	0.95	1.14	1.06	1.20
Mpc2	1.02	1.13	0.76	0.76
Mphosph10	0.80	0.88	0.97	0.93
Mphosph6	1.31	0.94	0.83	0.95
Mpi	1.02	1.09	0.64	0.87
Mpp1	0.98	0.93	0.96	0.75
Mpp6	1.26	1.24	1.03	0.61
Mpst	0.84	0.77	0.77	0.73
Mre11a	1.13	1.15	1.02	0.79
Mri1	0.97	0.93	0.90	0.95
Mrpl1	1.16	1.12	0.75	1.39
Mrpl10	1.09	1.18	0.91	0.79
Mrpl11	0.95	1.01	0.91	0.70
Mrpl12	0.87	1.01	0.95	1.01
Mrpl13	0.97	0.93	0.91	0.73
Mrpl14	1.10	1.01	1.34	0.96
Mrpl15	0.96	0.91	1.07	1.03

Mrpl16	0.84	0.85	1.14	0.69
Mrpl19	0.78	0.89	1.15	1.10
Mrpl2	1.19	1.07	0.97	1.03
Mrpl22	1.31	1.19	1.12	0.92
Mrpl23	1.21	1.23	1.14	9.26
Mrpl24	1.20	1.17	0.99	0.79
Mrpl27	0.81	0.91	0.97	0.58
Mrpl28	0.96	1.17	0.97	0.85
Mrpl3	0.77	0.88	1.23	1.22
Mrpl37	1.18	1.18	1.05	0.88
Mrpl38	0.86	0.94	1.22	1.02
Mrpl39	0.87	0.96	1.22	1.16
Mrpl4	1.44	1.13	1.13	1.11
Mrpl41	0.90	0.80	1.14	0.76
Mrpl45	1.11	1.27	1.16	0.68
Mrpl46	1.06	1.15	1.22	1.02
Mrpl49	1.12	1.17	1.35	1.23
Mrpl53	1.08	1.02	1.39	1.27
Mrpl9	1.20	0.88	1.11	0.94
Mrps15	0.86	0.88	1.08	0.96
Mrps16	1.23	1.16	1.34	1.08
Mrps17	0.93	0.92	1.18	0.73
Mrps2	0.96	1.05	1.01	1.04
Mrps21	1.18	1.16	1.28	0.93
Mrps22	1.41	1.31	0.94	0.94
Mrps23	1.13	1.08	1.28	1.23
Mrps24	0.66	0.72	0.91	1.65
Mrps26	1.16	1.27	1.03	1.50
Mrps27	1.06	1.24	0.94	0.94
Mrps28	1.04	1.08	1.07	0.98
Mrps34	1.27	1.22	1.22	1.01
Mrps35	0.90	0.94	0.95	0.73
Mrps36	1.28	1.35	1.40	0.86
Mrps5	0.86	0.98	1.29	1.23
Mrps6	2.22	1.30	1.07	0.97
Mrps7	1.20	1.00	1.41	1.34
Mrps9	1.00	1.07	1.15	1.16
Mrto4	0.86	0.88	1.17	0.92
Msh2	0.87	0.86	0.82	0.66
Msh6	0.94	1.07	0.73	0.64
Msi2	1.50	1.58	1.31	0.77
Msn	0.70	0.70	0.73	1.26
Msto1	0.95	0.84	0.90	1.24
Mt1	1.75	1.83	1.27	0.92
Mt2	1.29	1.72	1.33	0.87
Mt3	0.59	0.74	0.61	0.43
Mta1	1.01	1.08	1.09	0.78
Mta2	0.78	0.78	0.83	0.76
Mtap	0.47	0.56	0.55	3.88
Mtch1	0.81	0.89	0.54	2.32
Mtch2	1.25	1.36	1.17	1.17
Mtdh	1.00	1.02	1.13	1.49
Mthfd1	1.10	1.11	1.06	1.12
Mthfd1l	1.36	1.39	1.12	1.01
Mthfd2	0.55	0.53	0.49	1.59
Mtpn	0.84	0.84	0.78	1.07
Mtx1	1.01	0.95	0.88	0.87
Mtx2	1.06	1.11	1.10	1.07
Muc13	1.37	1.70	1.19	1.95
Mut	0.65	0.67	0.67	0.84
Mvd	0.80	0.84	0.98	1.83
Mvp	0.51	0.55	0.54	0.60
Mybbp1a	1.01	1.00	1.08	0.93

Mycbp	0.86	0.85	0.85	0.95
Myef2	0.63	0.78	0.71	1.32
Myg1	0.96	0.86	0.86	0.91
Myh14	0.60	0.59	0.83	1.60
Myh9	0.62	0.62	0.89	1.71
Myl1	0.71	0.68	0.96	1.71
Myl12b	0.61	0.63	1.26	1.72
Myl6	0.75	0.73	0.81	1.38
Mylk	0.34	0.36	1.23	1.24
Myo18a	1.17	1.07	1.18	1.35
Myo1c	1.10	1.02	1.18	0.99
Myo1g	1.12	0.99	1.05	1.07
Naa10	0.91	0.96	0.98	1.20
Naa10	0.96	0.93	0.98	1.20
Naa15	0.83	0.85	0.92	1.01
Naa25	1.19	1.05	1.27	1.31
Naa30	1.28	1.21	1.21	1.13
Naa38	1.07	1.05	0.88	0.99
Naa40	1.08	0.93	1.63	1.07
Naa50	0.79	0.80	1.06	1.03
Naca	0.92	0.98	1.22	1.23
Nadk2	1.17	1.13	0.81	0.61
Nae1	1.13	1.11	0.92	0.88
Naglu	1.65	1.30	1.04	1.10
Nampt	0.99	0.90	0.76	0.77
Nans	0.81	0.77	0.72	0.81
Nap1l1	1.11	1.06	1.20	1.13
Nap1l4	1.06	0.91	0.79	0.83
Napa	1.29	1.27	1.62	1.41
Napg	1.01	1.02	1.23	1.20
Nars	0.91	0.90	0.92	1.15
Nasp	0.81	0.85	0.66	0.79
Nat10	1.03	0.99	1.02	1.08
Nbeal2	0.86	0.83	0.96	0.96
Ncapd2	1.19	1.18	1.07	0.92
Ncapd3	1.10	0.91	1.53	1.71
Ncapg	0.97	1.03	1.22	0.93
Ncaph	1.01	1.00	1.27	1.07
Ncbp1	0.87	0.96	0.76	0.69
Ncbp2	0.94	0.89	0.80	0.81
Ncf1	1.70	1.41	1.00	0.89
Ncf2	0.54	0.47	0.61	1.06
Ncf4	0.53	0.45	0.50	0.75
Nck1	0.66	0.54	0.73	1.42
Nckap1l	0.94	1.02	0.86	0.88
Ncl	0.81	0.84	0.83	0.71
Ncln	1.24	1.21	1.36	1.21
Ncoa5	1.02	0.99	1.11	1.56
Ncor1	0.90	0.94	0.88	0.92
Ncstn	0.75	0.87	0.92	0.92
ND4	1.05	1.09	1.20	0.92
Ndc1	0.76	0.74	0.69	0.89
Ndrg1	1.20	1.01	0.76	1.36
Ndrg3	1.23	1.52	1.28	2.02
Ndufa10	0.86	1.00	0.73	0.68
Ndufa12	1.02	0.89	1.05	0.78
Ndufa13	0.95	0.90	1.24	0.90
Ndufa2	1.26	1.16	1.24	0.93
Ndufa4	0.63	0.59	1.51	1.34
Ndufa5	0.89	0.86	0.87	0.73
Ndufa6	0.95	0.89	0.89	0.74
Ndufa7	0.92	0.81	0.89	0.66
Ndufa8	0.84	0.85	0.82	0.68

Ndufa9	0.85	0.89	0.91	0.82
Ndufab1	1.00	1.07	0.85	0.80
Ndufaf7	0.75	0.82	0.70	0.93
Ndufb10	0.85	0.73	1.01	0.76
Ndufb3	0.82	0.73	0.74	0.63
Ndufb4	1.06	1.09	0.78	0.65
Ndufb6	0.89	0.96	0.95	0.90
Ndufb7	0.83	0.77	1.04	0.90
Ndufb9	0.78	0.85	0.79	0.89
Ndufs1	1.17	1.05	1.00	0.96
Ndufs2	0.85	0.79	0.77	0.70
Ndufs3	1.32	1.01	0.99	0.89
Ndufs5	0.91	1.14	0.91	0.70
Ndufs7	1.10	1.13	0.99	0.80
Ndufs8	1.10	1.10	0.94	0.69
Ndufv1	0.89	1.05	1.07	0.83
Ndufv2	1.01	1.18	1.10	1.04
Ndufv3	1.59	1.58	0.69	1.03
Ndufv3	0.54	0.56	0.69	1.03
Necap2	1.08	1.04	0.84	0.99
Nedd4	1.22	1.18	1.02	0.93
Nedd4l	1.67	1.59	1.17	1.02
Nedd8	1.13	1.04	0.95	0.96
Nek9	1.21	1.22	1.37	1.05
Nelfa	1.31	1.29	1.28	0.99
Nelfb	1.44	1.42	1.29	1.13
Nemf	0.92	0.96	0.99	0.95
Nenf	1.24	1.30	1.48	0.79
Nfatc2	0.71	0.77	1.60	2.07
Nfkb1	0.32	0.39	0.29	1.39
Nfkb2	0.78	0.81	0.79	0.88
Nfs1	1.16	1.03	0.97	0.85
Nfu1	0.98	1.26	1.20	0.82
Nfyb	1.11	1.06	1.09	0.98
Ngly1	1.37	0.94	1.11	1.21
Nhp2	1.10	1.15	1.00	1.00
Nhp2l1	0.90	1.11	0.90	0.95
Nif3l1	0.70	0.79	0.62	1.01
Nip7	0.88	1.05	1.03	1.20
Nipbl	0.87	0.87	0.56	0.76
Nipsnap1	1.94	1.67	1.61	0.96
Nisch	1.19	1.08	1.24	1.14
Nit1	0.89	1.00	0.97	0.99
Nit2	1.27	1.24	1.29	1.14
Nkrf	0.99	0.76	1.03	0.86
Nle1	1.04	0.94	1.09	0.54
Nln	0.61	0.68	0.55	0.97
Nme1	1.08	1.13	1.10	0.95
Nme2	1.06	1.00	1.01	1.07
Nmral1	1.51	1.52	1.25	1.79
Nmt1	1.22	1.23	1.19	1.18
Nmt2	1.21	1.06	1.01	1.25
Nnt	1.20	1.23	1.05	0.75
Nob1	1.07	0.90	0.99	1.19
Noc2l	0.94	0.86	1.11	0.79
Noc4l	1.03	1.17	0.80	0.99
Nol10	1.46	1.42	1.49	1.14
Nol11	0.95	1.03	1.18	1.30
Nol6	0.88	0.64	1.02	0.93
Nol7	1.02	1.07	1.12	0.85
Nol8	1.45	1.29	1.40	1.14
Nol9	1.18	1.21	1.39	0.96
Nolc1	0.89	0.88	1.06	1.08

Nomo1	0.92	0.96	1.12	1.06
Nono	0.80	0.81	0.87	0.90
Nop10	1.13	1.07	1.04	1.04
Nop14	1.03	1.00	1.00	0.88
Nop16	0.77	0.85	1.26	1.20
Nop2	0.85	0.90	1.09	0.89
Nop56	1.07	0.99	1.03	0.82
Nop58	0.99	0.99	1.01	0.91
Nop9	0.80	0.75	0.73	0.88
Npc2	0.84	0.94	1.13	1.12
Npepl1	1.36	1.24	1.14	1.17
Npepps	1.12	1.06	0.88	0.87
Nploc4	0.70	0.75	0.75	0.84
Npm1	0.96	1.07	1.02	0.94
Npm3	1.11	1.22	1.40	1.19
Nptn	1.15	1.11	1.29	1.20
Nqo2	0.65	0.74	0.73	1.11
Nrd1	0.86	0.80	0.87	0.90
Nsdhl	0.95	1.03	1.15	1.75
Nsf	0.91	1.08	1.02	1.47
Nsfl1c	1.25	1.32	1.14	1.34
Nsun2	0.96	1.03	0.94	0.88
Nt5c	1.27	1.18	1.08	0.87
Nt5c2	1.20	1.15	1.55	1.39
Nt5c3	0.35	0.38	0.51	0.83
Nt5c3b	1.47	1.28	1.44	1.21
Ntmt1	1.25	1.34	1.39	1.56
Ntpcr	0.97	1.02	0.69	0.60
Nub1	1.87	1.64	1.75	1.48
Nubp1	0.95	0.97	1.06	1.52
Nucb1	1.28	1.22	1.46	1.27
Nucks1	1.34	1.22	1.24	0.78
Nudc	1.03	1.01	1.05	0.99
Nudcd1	1.02	1.02	0.77	0.78
Nudcd2	0.97	1.08	1.02	1.01
Nudcd3	1.03	1.11	1.27	1.39
Nudt16	1.51	1.40	0.99	0.80
Nudt2	0.97	1.11	0.86	0.84
Nudt21	1.05	0.95	0.96	0.86
Nudt3	0.66	0.65	1.12	1.35
Nudt5	1.13	1.12	1.24	1.18
Numa1	0.94	0.93	0.77	0.69
Nup107	0.88	0.88	1.00	1.03
Nup133	0.66	0.78	0.94	0.99
Nup153	1.09	1.51	1.18	1.16
Nup155	0.83	0.92	0.92	0.99
Nup160	0.79	0.71	0.79	0.94
Nup205	0.93	0.97	1.19	1.01
Nup210	1.24	1.24	1.03	0.73
Nup214	1.07	1.04	0.94	0.98
Nup35	0.65	0.59	1.01	1.08
Nup43	0.81	0.85	1.05	0.98
Nup50	0.88	0.89	0.81	1.02
Nup54	1.29	1.10	1.10	0.94
Nup62	1.11	1.31	1.05	1.19
Nup85	0.68	0.88	1.09	0.83
Nup88	1.03	1.03	1.19	1.15
Nup93	0.86	0.89	0.85	1.03
Nup98	0.81	0.83	1.02	1.07
Nupl1	1.25	1.17	1.01	1.18
Nusap1	0.99	0.89	0.79	0.31
Nvl	1.09	0.85	1.12	2.76
Nxf1	0.72	0.81	0.79	0.87

Nxn	1.23	1.10	1.89	1.42
Oat	1.19	1.02	0.70	0.60
Ociad1	1.08	1.16	3.16	1.07
Ogdh	1.36	1.46	1.11	1.00
Ogfr	0.86	0.87	1.32	1.82
Ogt	0.74	0.70	0.73	0.89
Ola1	1.16	1.25	1.17	1.29
Olr1	0.23	0.28	0.56	1.18
Opa1	1.45	1.24	1.18	1.21
Orc1	0.82	0.74	0.96	0.87
Orc3	0.82	0.68	0.73	0.67
Orc5	0.84	0.85	0.62	0.49
Os9	1.16	1.06	1.38	1.28
Osbp	0.94	0.89	0.79	1.32
Osbpl11	1.06	1.04	1.04	1.51
Osbpl3	0.79	0.82	0.93	1.68
Osbpl8	0.80	0.80	0.68	3.51
Osgep	1.30	1.27	0.94	1.09
Ostc	0.96	1.03	0.84	1.07
Ostf1	1.16	1.23	0.86	0.89
Otub1	1.21	0.90	0.97	1.07
Otud4	1.08	1.00	1.05	0.93
Otud6b	0.96	0.81	0.89	0.85
Oxct1	0.96	1.02	0.80	0.84
Oxsr1	1.00	0.94	0.80	1.04
P4ha1	1.07	1.12	1.12	1.29
P4hb	1.06	1.04	0.76	0.94
Pa2g4	1.17	1.21	1.13	1.05
Pabpc1	0.89	0.93	1.18	1.15
Pabpc4	1.11	1.08	1.45	1.24
Pabpn1	1.20	1.15	1.01	0.77
Pacs1	0.72	0.67	0.79	0.78
Pacsin2	0.91	0.91	0.91	1.05
Padi4	0.83	0.83	0.57	0.26
Paf1	0.76	0.84	0.91	0.99
Pafah1b1	1.03	1.08	1.07	1.14
Pafah1b2	1.01	1.20	0.66	0.94
Paics	1.12	1.18	1.17	1.13
Paip1	1.20	1.24	1.27	1.21
Paip1	1.33	1.02	1.27	1.21
Pak1ip1	1.24	1.20	1.67	1.21
Pak2	0.98	1.00	0.99	1.29
Palm	2.41	1.46	1.27	0.82
Pam16	1.32	1.85	1.29	1.54
Paox	1.23	1.29	1.31	0.70
Papola	0.94	0.99	1.05	0.68
Papss1	0.89	0.85	0.80	0.70
Parg	1.16	1.15	1.08	0.89
Park7	1.21	1.28	0.87	1.03
Parn	1.38	1.42	1.21	1.12
Parp1	1.10	0.99	0.88	0.54
Parvg	1.13	1.19	1.19	1.15
Patl1	0.96	0.97	0.85	1.36
Pbdc1	0.78	0.68	0.68	0.87
Pbk	0.88	0.94	1.20	0.77
Pbrm1	1.09	1.11	1.00	1.05
Pcbp1	1.39	1.58	1.50	1.19
Pcbp2	0.81	0.90	0.89	1.05
Pcbp2	0.89	0.84	0.89	1.05
Pcca	1.52	1.31	1.21	0.84
Pccb	1.68	1.87	1.30	0.92
Pcid2	1.18	0.95	1.13	1.43
Pck2	1.46	1.29	1.14	1.58

Pcm1	0.92	0.87	1.18	1.30
Pcmt1	0.95	1.04	0.90	0.94
Pcna	1.08	1.22	1.45	0.98
Pcnp	0.97	0.89	0.90	0.93
Pcx	1.20	1.36	0.84	0.98
Pcyox1	0.67	0.75	0.67	0.74
Pcyox1l	0.95	0.95	0.97	0.83
Pcyt1a	0.84	0.79	0.73	0.97
Pdap1	0.50	0.44	0.54	1.08
Pdcd10	0.93	0.86	0.97	1.21
Pdcd11	0.94	0.91	1.08	0.83
Pdcd4	2.39	2.55	0.80	0.48
Pdcd5	1.21	1.10	1.10	1.09
Pdcd6	1.67	1.44	1.44	1.20
Pdcd6ip	0.94	0.94	0.89	1.08
Pdcl3	0.82	0.86	0.95	1.47
Pde12	1.11	1.10	1.01	1.09
Pdha1	0.85	1.02	0.65	0.82
Pdhb	0.73	0.72	0.64	0.84
Pdhx	1.24	1.34	0.98	1.48
Pdia3	1.15	1.23	1.20	1.53
Pdia4	0.92	0.90	0.84	1.29
Pdia6	1.42	1.34	1.00	1.09
Pdia6	1.06	1.13	1.00	1.09
Pdk3	1.08	1.13	0.58	0.60
Pdlim1	1.31	1.41	1.45	1.36
Pdlim5	0.37	0.44	0.67	0.95
Pds5a	1.01	1.05	1.00	0.76
Pds5b	1.15	1.05	1.00	0.71
Pdxdc1	1.00	1.03	1.10	1.41
Pdxk	1.25	1.23	1.04	1.31
Pdxp	1.39	1.08	0.85	1.05
Pdzd8	1.07	1.06	1.39	1.73
Pebp1	1.45	1.57	1.10	0.97
Pecam1	0.89	0.97	2.08	1.51
Pelo	1.09	1.18	1.04	1.04
Pelp1	0.72	0.80	0.85	0.85
Pepd	1.25	1.32	1.20	1.18
Pes1	1.17	1.04	1.23	0.96
Pet2	1.04	2.02	1.20	1.22
Pex14	1.02	0.96	1.22	1.43
Pex19	0.60	0.60	0.55	1.03
Pfas	1.14	1.12	0.91	0.93
Pfdn1	0.94	0.88	1.01	0.93
Pfdn2	0.80	0.96	0.89	1.07
Pfdn4	1.10	1.07	1.10	1.37
Pfdn5	0.91	0.98	0.92	0.97
Pfkl	1.07	1.11	1.07	1.06
Pfkm	1.17	1.14	0.83	0.71
Pfkp	1.46	1.39	1.28	1.30
Pfn1	0.69	0.72	0.97	1.20
Pgam1	1.25	1.19	1.06	1.20
Pgam5	0.81	0.86	0.83	0.81
Pgd	1.31	1.33	1.19	1.21
Pgk1	1.08	1.12	0.93	1.02
Pgls	1.08	1.01	0.97	1.19
Pgm1	1.17	1.24	1.11	1.25
Pgm2	1.33	1.32	1.04	0.91
Pgm3	1.00	0.97	0.71	1.11
Pgp	1.15	1.20	1.04	0.84
Pgrmc1	3.00	1.03	0.80	0.78
Pgrmc2	0.98	0.91	0.81	0.78
Phax	0.76	0.83	1.26	1.11

Phb	1.17	1.15	1.06	0.91
Phb2	1.05	1.05	0.96	0.79
Phf3	1.51	0.99	1.08	1.02
Phf5a	1.17	1.12	1.08	1.08
Phf6	0.87	0.85	1.00	0.86
Phgdh	0.90	0.92	0.70	0.64
Phip	1.06	1.06	0.87	0.89
Phpt1	1.34	1.23	1.32	1.03
Picalm	0.94	1.19	1.04	0.86
Pigs	1.84	1.77	1.46	1.40
Pih1d1	1.29	1.29	1.65	1.30
Pik3cg	0.91	1.06	2.18	0.95
Pik3r1	1.69	1.83	1.65	1.75
Pin1	0.88	0.91	0.94	0.77
Pip4k2a	1.13	1.14	0.86	1.45
Pitpna	0.81	0.83	0.91	0.97
Pitpnb	0.93	0.96	1.19	1.11
Pitrm1	1.14	1.22	1.04	1.02
Pkm	1.09	1.10	0.85	0.99
Pkm	0.57	0.54	0.85	0.99
Pla2g15	0.91	0.87	1.32	0.75
Pla2g4a	0.69	0.73	0.69	1.50
Plaa	0.63	0.73	0.70	0.87
Plac8	1.31	1.24	2.42	0.43
Plbd2	1.26	1.12	1.08	0.81
Plcb3	1.44	1.21	0.98	1.19
Plcg2	1.08	1.11	0.88	1.02
Plec	0.87	0.92	1.38	1.86
Plek	0.64	0.62	1.05	1.83
Plekha2	0.85	0.96	0.62	0.99
Plin3	0.92	0.95	0.60	1.82
Plk1	0.76	0.55	0.85	0.84
Plod1	1.57	1.30	1.52	1.06
Plod3	0.95	0.92	1.13	1.58
Plrg1	0.95	0.86	0.94	1.02
Plscr1	0.62	0.62	0.63	1.10
Pml	0.92	0.90	0.68	0.92
Pmm2	1.46	1.26	1.35	1.29
Pmpca	1.37	1.59	1.52	1.27
Pmpcb	1.46	1.63	1.26	1.21
Pnkp	1.17	1.18	0.90	1.05
Pnn	0.82	0.89	0.87	0.96
Pno1	0.80	0.73	0.97	0.92
Pnp	0.89	1.03	0.93	0.94
Pnpo	0.93	1.04	0.96	1.15
Pnpt1	1.15	1.23	1.01	1.07
Podxl	0.96	1.26	1.30	0.71
Pogz	0.99	0.97	0.99	0.91
Pola1	0.80	0.89	0.78	0.81
Pola2	0.70	0.64	0.74	0.82
Pold1	1.01	1.14	1.05	0.87
Pold2	1.46	1.30	1.06	0.79
Pold3	0.87	0.88	1.08	0.87
Poldip2	0.93	1.03	1.11	1.01
Poldip3	0.94	0.81	1.17	0.73
Pole3	0.75	0.84	0.81	0.93
Polr1a	0.61	0.62	0.99	0.81
Polr1b	0.69	0.72	1.14	1.05
Polr1c	2.26	0.81	1.01	0.79
Polr1e	1.19	0.91	0.93	0.67
Polr2a	0.87	0.80	0.94	0.94
Polr2b	1.01	0.90	1.06	1.06
Polr2c	1.09	1.31	1.11	1.15

Polr2d	1.20	1.09	1.23	1.06
Polr2e	0.90	0.86	0.79	0.78
Polr2g	0.90	0.99	0.89	0.68
Polr2h	0.88	0.89	0.94	1.03
Polr2i	0.93	1.04	1.07	0.80
Polr2j	0.90	1.03	1.06	1.21
Polr2m	1.58	1.40	1.06	1.33
Pon3	0.83	0.67	0.86	1.07
Pop1	0.96	0.78	0.89	0.96
Por	1.12	1.20	1.35	1.47
Ppa1	0.92	1.03	0.96	0.83
Ppa2	0.79	0.80	0.57	0.70
Ppan	1.18	0.87	1.54	0.82
Ppat	1.26	1.26	1.47	1.20
Ppia	1.24	1.29	1.19	1.18
Ppib	0.94	0.95	1.00	1.08
Ppid	0.71	0.68	0.87	1.38
Ppie	0.95	0.91	1.11	1.06
Ppif	1.78	1.39	1.48	1.24
Ppig	0.94	1.05	0.88	1.10
Ppih	0.67	0.76	0.66	0.83
Ppil1	0.96	0.96	1.04	1.16
Ppil4	0.95	0.96	0.90	1.07
Ppm1a	1.13	1.11	1.07	0.93
Ppm1b	0.80	0.80	0.70	1.07
Ppm1f	1.27	1.22	0.99	1.21
Ppm1g	1.02	1.02	1.16	0.99
Ppme1	0.83	0.74	0.76	0.71
Ppp1ca	1.11	1.08	1.23	1.09
Ppp1cb	1.39	1.35	1.21	1.30
Ppp1cc	1.09	1.06	1.02	1.09
Ppp1r10	1.15	1.04	1.14	1.40
Ppp1r12a	0.73	0.71	1.12	1.74
Ppp1r14b	0.88	0.93	1.08	1.21
Ppp1r18	0.60	1.35	0.55	1.77
Ppp1r2	0.80	0.73	1.00	1.45
Ppp1r7	1.17	1.07	0.99	0.83
Ppp1r8	0.80	0.87	0.77	1.02
Ppp2ca	1.04	1.08	1.56	1.28
Ppp2cb	1.08	1.08	1.18	1.18
Ppp2r1a	0.99	1.03	1.09	1.15
Ppp2r1b	0.68	0.69	0.85	0.82
Ppp2r2a	1.14	1.13	1.22	1.09
Ppp2r4	1.19	1.33	1.12	1.16
Ppp2r5a	0.98	0.70	1.17	0.97
Ppp2r5d	0.84	0.83	0.97	0.87
Ppp2r5e	1.12	1.03	1.19	1.05
Ppp3ca	0.72	0.89	1.70	1.08
Ppp3r1	0.94	0.95	0.88	1.06
Ppp4c	1.07	0.98	1.11	1.07
Ppp4r2	0.94	0.90	1.05	0.98
Ppp5c	1.55	1.52	2.18	1.26
Ppp6c	1.24	1.20	1.11	1.31
Ppp6r3	0.95	0.95	0.95	1.30
Ppt1	1.29	1.18	1.03	1.25
Ppwd1	1.10	0.75	0.97	1.11
Pqbp1	1.04	1.05	1.16	1.01
Prc1	0.95	0.83	0.53	0.45
Prdx1	0.72	0.70	0.62	0.75
Prdx2	0.62	0.63	0.51	1.10
Prdx3	0.80	0.90	0.79	0.95
Prdx4	1.00	0.89	0.78	0.88
Prdx5	0.76	0.66	0.64	0.92

Prdx6	0.49	0.50	0.52	0.68
Preb	1.44	1.31	1.09	1.14
Prep	1.15	1.08	0.94	1.00
Prim1	0.85	0.92	0.93	0.55
Prim2	0.77	0.85	0.68	0.64
Prkaca	0.92	0.95	0.83	1.15
Prkacb	0.89	0.89	0.65	1.13
Prkar1a	1.22	1.23	0.94	0.54
Prkar2a	1.10	1.03	7.47	15.84
Prkar2b	0.75	0.81	0.82	1.95
Prkcd	0.94	0.80	1.10	1.26
Prkcsh	1.05	0.86	1.24	1.47
Prkra	1.20	1.19	0.92	1.19
Prmt1	0.87	0.90	1.16	1.08
Prmt3	1.20	1.24	0.99	1.08
Prmt5	0.93	0.91	0.91	1.07
Prmt7	0.71	0.77	0.72	0.76
Prodh	1.30	1.19	1.17	1.64
Prorsd1	0.91	0.99	1.37	1.42
Prosc	0.73	0.71	1.08	1.17
Prpf19	1.04	1.02	1.04	1.02
Prpf3	0.76	0.85	0.82	0.86
Prpf31	1.27	1.41	1.19	0.98
Prpf38a	0.96	0.95	0.91	1.04
Prpf38b	0.91	0.87	0.81	0.98
Prpf4	0.84	0.93	0.94	0.96
Prpf40a	1.09	1.04	1.02	1.10
Prpf4b	1.09	1.15	0.90	0.90
Prpf6	0.93	1.00	0.74	0.73
Prpf8	0.92	0.90	0.97	0.90
Prps1l1	0.80	0.88	0.86	0.92
Prps1l3	0.80	0.79	0.82	0.87
Prps2	0.77	0.84	0.42	0.59
Prpsap1	0.88	0.95	1.08	1.03
Prrc2a	0.80	0.84	1.11	1.04
Prrc2c	0.90	0.90	1.09	0.99
Prss3	0.02	0.02	0.10	0.03
Prune	0.55	0.50	0.51	1.01
Psap	1.16	1.15	0.75	0.71
Psat1	0.95	0.95	0.85	1.08
Psip1	0.92	0.84	0.85	0.62
Psma1	1.16	1.10	1.03	1.00
Psma2	1.22	1.17	1.09	0.96
Psma3	1.15	1.12	0.99	0.99
Psma4	1.30	1.43	1.01	0.95
Psma5	0.94	1.03	1.00	1.04
Psma6	1.05	1.13	1.05	1.07
Psma7	1.17	1.20	1.06	1.04
Psmb1	1.56	1.42	1.46	1.24
Psmb10	1.20	1.22	0.57	0.64
Psmb3	1.06	1.11	1.04	0.99
Psmb4	1.11	1.32	1.08	1.29
Psmb5	1.15	1.07	1.12	1.16
Psmb6	1.14	1.60	1.25	1.19
Psmb7	2.00	2.43	1.11	1.10
Psmb8	1.35	1.73	1.15	1.10
Psmb9	1.28	1.05	0.97	0.87
Psmc1	0.99	1.00	0.93	1.10
Psmc2	0.85	0.84	0.91	1.09
Psmc3	1.16	1.01	0.91	0.99
Psmc4	0.98	1.02	1.00	1.11
Psmc5	0.89	0.91	0.93	1.01
Psmc6	0.92	0.98	0.95	1.05

Psmd1	0.93	1.03	0.95	1.06
Psmd10	0.71	0.76	0.77	0.85
Psmd11	0.91	0.98	0.99	1.04
Psmd12	0.92	1.03	0.90	1.01
Psmd13	0.85	0.83	0.89	1.01
Psmd14	1.03	1.12	1.07	1.07
Psmd2	0.93	0.90	0.94	1.13
Psmd3	0.98	0.96	0.94	0.91
Psmd4	1.00	0.90	1.05	0.96
Psmd5	1.12	1.06	1.12	1.12
Psmd6	0.84	0.94	0.99	1.10
Psmd7	1.02	0.94	1.06	1.06
Psmd8	1.11	1.13	0.91	1.31
Psmd9	1.14	1.13	1.10	1.14
Psme1	1.00	1.00	0.84	0.83
Psme2	1.05	1.14	0.70	0.82
Psme3	0.90	0.94	1.11	1.05
Psmf1	1.71	1.36	1.12	1.15
Psmg1	1.11	1.18	1.17	1.06
Psmg2	1.45	1.21	1.04	1.17
Psmg3	1.17	1.25	1.40	1.07
Psmg4	1.14	1.17	1.95	1.03
Pspc1	1.17	0.99	0.97	1.16
Ptbp1	1.00	1.01	0.89	0.91
Ptbp3	0.59	0.56	0.62	1.24
Ptbp3	0.58	0.52	0.62	1.24
Ptcd3	0.78	0.87	0.72	2.73
Pter	0.92	1.01	1.09	1.50
Ptges3	1.14	1.33	1.32	1.15
Ptgr1	0.59	0.62	0.53	0.51
Ptgr2	1.18	1.19	1.13	1.05
Ptgs1	0.78	0.84	0.89	2.41
Ptk2b	0.84	0.84	0.84	1.83
Ptma	0.77	0.78	0.72	0.74
Ptp4a2	0.74	0.60	0.96	0.73
Ptplad1	0.79	0.81	0.79	1.31
Ptpn12	0.87	0.90	1.09	1.74
Ptpn18	1.25	1.08	1.52	1.43
Ptpn2	1.77	1.37	1.41	0.82
Ptpn23	0.70	0.68	0.96	1.21
Ptpn6	1.49	1.31	1.00	0.69
Ptpn7	0.93	0.95	0.81	1.28
Ptprc	1.19	1.15	1.17	1.10
Ptrh2	1.48	1.31	0.96	1.13
Puf60	0.93	0.88	0.90	0.96
Pum1	1.06	1.30	1.76	1.58
Pum2	1.31	1.10	1.19	0.88
Pura	1.18	1.15	0.87	0.79
Purb	1.02	1.15	1.08	1.38
Pus10	0.92	0.90	0.73	0.63
Pus7	0.92	1.11	0.80	0.83
Pwp1	1.08	1.10	1.38	0.86
Pwp2	1.06	0.99	1.03	1.03
Pycr2	0.84	0.83	0.71	0.76
Pycrl	0.75	0.68	0.95	1.05
Pygb	1.21	1.17	1.07	1.66
Qars	0.80	0.84	0.92	1.28
Qdpr	1.28	1.25	1.29	0.87
Qk	1.21	1.26	1.08	0.85
Qrich1	1.09	1.10	0.96	0.80
Qtrt1	0.93	0.95	1.44	1.09
Rab1	1.15	1.21	1.08	1.21
Rab10	1.55	1.32	1.00	0.81

Rab11b	0.84	0.86	0.86	1.04
Rab11fip1	0.68	0.60	0.61	1.00
Rab14	1.24	1.22	1.28	1.25
Rab18	1.11	1.00	0.91	0.96
Rab1b	1.03	0.90	0.96	1.26
Rab21	1.38	1.27	1.81	2.22
Rab27b	2.09	2.54	1.72	2.69
Rab2a	0.80	0.91	0.86	0.92
Rab38	3.21	6.98	3.48	0.23
Rab3gap1	0.72	0.76	0.52	0.83
Rab3gap2	0.97	0.93	0.66	0.93
Rab44	0.58	0.63	0.73	0.86
Rab5a	1.32	1.20	0.77	1.20
Rab5c	1.10	1.21	1.11	1.22
Rab6a	0.76	0.81	0.75	1.02
Rab7	1.04	1.03	1.27	1.29
Rab8a	0.97	0.92	1.00	1.24
Rab8b	1.31	1.25	1.03	0.79
Rabep2	1.07	0.94	1.26	1.30
Rabgap1	1.80	1.41	1.38	1.33
Rabggta	1.20	1.19	0.97	1.13
Rabl6	1.18	1.09	0.92	1.02
Rac1	1.04	1.10	1.11	1.02
Rac2	0.77	0.78	0.63	0.78
Racgap1	0.82	0.68	0.63	0.39
Rad21	0.92	0.83	0.76	0.70
Rad23b	0.86	0.79	0.81	0.74
Rad50	1.29	1.21	0.82	0.77
Rae1	1.19	1.27	1.13	1.23
Ralb	0.75	0.81	0.73	0.96
Raly	1.07	1.13	1.09	1.08
Ran	1.17	1.20	1.15	0.94
Ranbp1	1.09	1.19	1.13	1.31
Ranbp10	0.88	0.80	0.66	1.31
Ranbp2	0.94	0.99	0.97	0.87
Ranbp3	0.77	0.79	0.74	1.12
Rangap1	0.81	0.86	1.12	1.02
Rap1a	0.74	0.74	0.71	0.98
Rap1b	0.95	0.89	1.02	1.04
Rap1gds1	1.14	1.09	1.27	1.50
Rap2c	0.94	0.81	0.81	0.91
Rars	0.90	0.93	0.85	1.02
Rasal3	0.62	0.60	2.31	5.15
Rassf2	2.69	2.30	2.43	1.57
Raver1	1.22	1.20	1.01	1.17
Rbbp4	1.49	1.35	1.48	1.22
Rbbp6	1.00	1.04	0.23	0.16
Rbbp7	1.01	0.94	0.82	0.86
Rbm10	1.21	1.10	1.13	1.08
Rbm12	0.89	0.96	0.95	1.09
Rbm14	0.97	1.10	0.91	1.02
Rbm15	1.30	1.25	0.63	0.84
Rbm17	0.82	0.83	0.84	1.00
Rbm22	1.25	1.28	1.42	1.05
Rbm25	1.08	1.01	1.19	0.82
Rbm26	1.15	1.21	0.98	0.92
Rbm28	1.06	0.96	1.02	0.61
Rbm3	1.01	1.10	1.45	1.38
Rbm39	0.91	1.00	0.96	1.11
Rbm4	0.99	1.04	0.96	1.37
Rbm42	1.24	1.14	1.06	0.91
Rbm5	1.06	0.99	0.96	1.28
Rbm6	0.84	0.94	0.80	0.91

Rbm7	1.34	1.17	1.13	1.16
Rbm8a	0.86	0.81	1.07	1.03
Rbmx	2.99	2.94	2.97	0.94
Rbmxl1	0.83	0.85	0.77	0.88
Rbpj	1.21	1.20	1.19	1.35
Rbpms	0.67	0.65	0.55	1.09
Rbx1	0.91	0.81	0.81	0.99
Rcc1	1.10	1.15	0.95	0.92
Rcc2	1.15	1.27	1.23	1.10
Rcl1	0.98	0.76	1.04	0.92
Rcn1	1.64	1.70	1.78	2.09
Rcor1	0.93	0.88	0.82	0.68
Rcsd1	0.82	0.74	0.93	1.20
Rdh11	1.26	1.18	1.50	1.65
Rdx	1.03	1.13	0.84	0.96
Reep5	0.97	1.00	1.11	1.12
Rela	0.67	0.72	0.84	1.08
Renbp	0.72	0.55	1.18	1.38
Reps1	1.68	1.76	1.24	1.85
Rer1	1.80	1.53	1.09	1.66
Rexo2	0.73	0.72	0.66	0.73
Rexo4	0.85	0.82	1.14	0.80
Rfc1	1.51	1.22	1.41	1.35
Rfc2	0.79	0.89	0.98	0.94
Rfc3	1.03	1.14	1.05	0.79
Rfc4	1.00	1.08	0.89	0.77
Rfc5	1.07	1.16	1.19	1.23
Rfk	1.19	0.99	1.36	0.98
Rgs18	0.87	0.77	1.44	0.75
Rheb	1.05	0.87	1.26	1.39
Rhoa	0.93	0.96	0.85	0.97
Rhog	1.16	1.16	1.05	0.84
Rhot1	0.99	0.92	0.95	0.84
Rhox5	0.93	0.89	1.63	1.40
Ric8	0.62	0.58	1.38	1.19
Rif1	1.17	1.05	0.97	1.18
Riok1	1.25	1.13	1.29	1.20
Riok3	1.23	1.09	0.94	0.91
Rnaseh2a	1.42	1.30	1.29	0.81
Rnaseh2b	1.35	1.07	1.28	0.46
Rnaseh2c	1.71	1.62	1.26	0.72
Rnaset2b	0.60	0.50	0.61	0.55
Rnf113a2	1.06	0.99	1.29	1.01
Rnf114	0.92	0.93	0.93	1.54
Rnf2	1.14	0.91	1.02	0.88
Rnf20	0.95	1.05	1.14	1.08
Rnf40	0.98	1.14	0.95	0.91
Rngtt	0.88	0.81	0.89	0.70
Rnh1	1.04	1.04	1.21	1.13
Rnmt	1.10	1.05	0.98	0.90
Rnpep	1.03	1.11	0.95	0.84
Rnps1	0.99	0.99	1.02	1.01
Rock1	1.17	1.05	0.89	0.95
Rock2	0.77	0.81	1.25	0.73
Rpa1	0.91	0.95	0.86	0.83
Rpa2	0.86	1.01	0.76	0.78
Rpa3	0.97	1.01	0.85	0.81
Rpap3	0.92	0.87	0.98	0.98
Rpe	1.10	1.10	0.87	1.04
Rpf2	1.48	1.21	1.75	0.68
Rpia	0.90	0.87	0.84	1.11
Rpl10a	1.07	0.89	1.19	0.80
Rpl11	0.89	0.94	1.11	1.01

Rpl12	0.87	0.84	1.06	1.11
Rpl13	0.95	0.86	1.22	0.88
Rpl13a	0.88	0.89	1.07	0.87
Rpl14	1.20	0.78	1.39	0.46
Rpl15	0.90	0.97	1.11	1.03
Rpl17	1.03	0.90	1.14	0.86
Rpl18	0.96	1.01	1.19	0.50
Rpl18a	0.95	0.85	1.16	0.82
Rpl19	0.95	0.86	1.19	0.73
Rpl22	0.70	0.68	0.76	0.84
Rpl22l1	1.98	1.78	1.94	0.96
Rpl23a	0.97	0.97	1.16	0.99
Rpl26	0.97	0.86	1.19	0.91
Rpl27	1.05	0.93	1.14	0.56
Rpl28	0.98	0.91	1.13	0.75
Rpl3	1.02	1.09	1.09	0.96
Rpl34	1.02	0.78	1.26	0.55
Rpl35	1.35	1.21	1.14	0.68
Rpl36	0.86	0.81	1.10	0.95
Rpl36a	1.00	0.78	1.12	0.77
Rpl37a	0.98	0.96	1.21	1.02
Rpl38	1.04	0.92	1.20	0.61
Rpl39	1.08	1.08	1.28	1.19
Rpl4	0.92	0.96	1.09	0.88
Rpl5	1.03	0.99	1.11	1.11
Rpl6	0.98	0.91	1.17	0.63
Rpl7	1.09	0.98	1.23	0.61
Rpl7a	1.06	0.96	1.21	0.71
Rpl7l1	0.85	0.91	1.17	0.85
Rpl8	1.06	1.08	1.14	0.86
Rplp0	0.94	1.06	1.10	1.15
Rplp1	1.10	1.14	0.94	1.08
Rplp2	1.01	1.05	1.00	1.16
Rpn1	1.40	1.45	1.20	1.27
Rpn2	1.31	1.28	1.23	1.30
Rpp30	1.12	1.11	1.29	1.05
Rprd1b	1.13	1.12	0.92	1.13
Rprd2	0.75	0.96	0.77	0.95
Rps10	0.94	0.88	1.11	0.98
Rps11	0.92	0.78	1.14	0.85
Rps12	1.05	1.15	1.16	1.26
Rps13	0.99	0.88	1.16	0.82
Rps14	0.99	0.85	1.11	0.90
Rps15	0.88	0.89	1.03	1.07
Rps15a	0.96	0.87	1.11	0.95
Rps16	0.98	0.82	1.33	0.54
Rps17	1.04	1.08	1.08	1.07
Rps18	0.90	0.83	1.11	0.92
Rps19	0.89	0.85	1.13	0.92
Rps20	0.90	0.90	1.00	1.02
Rps21	1.22	1.20	1.04	1.15
Rps23	0.98	0.95	1.15	0.82
Rps24	0.96	0.98	1.18	1.06
Rps25	0.93	0.94	1.14	1.04
Rps26	0.87	0.96	1.19	1.12
Rps27a	0.91	0.96	0.94	1.31
Rps27l	1.07	1.03	0.91	0.78
Rps28	1.20	1.16	1.33	1.39
Rps29	0.88	0.86	1.11	0.91
Rps3	0.89	0.85	1.06	1.02
Rps3a1	0.93	0.89	1.08	0.99
Rps4x	0.98	0.94	1.12	0.87
Rps5	1.14	1.16	1.33	1.29

Rps6ka1	1.11	1.08	0.87	0.83
Rps6ka3	1.34	1.13	0.89	0.66
Rps6-ps4	0.96	0.89	1.14	0.93
Rps7	1.00	0.94	1.16	1.02
Rps8	0.97	0.90	1.06	0.95
Rps9	1.00	0.88	1.22	0.96
Rqcd1	1.03	1.06	1.45	1.24
Rras	1.08	1.02	0.90	0.71
Rrbp1	1.03	1.02	1.13	1.53
Rrm2	0.45	0.35	0.50	0.49
Rrp1	0.90	0.82	1.50	1.31
Rrp12	1.02	1.06	1.18	1.07
Rrp15	0.96	0.75	1.04	0.62
Rrp1b	0.88	0.95	0.86	0.71
Rrp7a	0.87	0.99	1.06	0.84
Rrp8	0.64	0.64	1.11	0.95
Rrp9	0.97	0.82	0.63	0.83
Rrs1	1.05	1.03	1.15	1.06
Rsbn1	0.98	0.99	0.80	0.97
Rsf1	0.76	0.81	0.84	0.83
Rsl1d1	1.00	0.89	1.08	0.68
Rsu1	0.82	0.70	0.68	1.22
Rtca	1.02	0.98	1.02	0.99
Rtf1	0.96	0.90	0.85	0.81
Rtfdc1	1.01	1.09	1.43	1.27
Rtn3	1.33	1.23	1.75	1.98
Rtn4	0.70	0.72	1.01	1.82
Rttn	1.44	1.41	1.67	0.72
Runx1	0.91	1.12	0.93	0.87
Ruvbl1	1.13	1.14	1.13	1.05
Ruvbl2	1.17	1.22	1.11	1.13
Rwdd4a	2.75	0.90	0.86	1.61
S100a10	0.91	0.92	0.99	1.29
S100a13	0.64	0.58	0.60	1.22
S100a4	4.56	4.97	0.96	10.64
S100a8	14.05	16.69	7.91	16.23
S100a9	17.56	13.89	3.84	8.21
Saal1	1.55	1.28	1.12	0.99
Sacm1l	0.95	0.89	0.67	1.02
Sae1	1.01	1.09	1.05	0.94
Safb	0.87	0.90	0.70	0.97
Safb2	0.84	0.89	0.89	0.95
Samhd1	0.95	1.15	0.89	1.19
Samm50	0.94	0.98	0.92	0.92
Samsn1	0.88	0.94	0.91	0.99
Sap30	1.24	1.29	0.84	0.74
Sar1a	1.03	0.94	1.06	1.18
Sar1b	0.82	0.82	0.86	1.35
Sarnp	0.98	0.95	0.96	0.98
Sars	0.85	0.80	0.87	1.45
Sart1	0.97	0.95	1.14	1.07
Sart3	1.06	1.12	1.21	1.17
Sash3	1.15	1.10	1.28	1.36
Sbds	1.14	1.14	1.30	1.11
Sbf1	1.08	1.04	1.05	1.57
Sbno1	0.88	0.93	1.03	1.25
Sc4mol	0.97	1.19	2.21	5.06
Scaf11	0.91	0.76	0.69	0.83
Scaf4	0.90	0.88	1.27	1.17
Scaf8	0.72	0.71	0.57	0.53
Sccpdh	1.38	1.17	0.74	0.51
Scfd1	0.99	1.09	0.94	0.87
Scin	6.94	6.92	11.42	4.08

Scly	1.24	1.11	0.87	0.82
Scp2	0.86	0.85	0.60	0.77
Scrib	1.12	1.08	0.87	0.67
Sdad1	1.35	1.00	1.74	1.98
Sdcbp	1.02	1.09	1.18	1.20
Sdf2l1	1.45	1.48	1.23	1.93
Sdha	1.44	1.42	1.13	0.88
Sdhb	1.45	1.47	1.13	1.01
Sdhc	1.79	1.72	1.27	0.92
Sdsl	1.73	1.73	1.71	0.92
Sec11a	0.98	0.98	1.05	1.30
Sec13	0.89	0.75	0.97	1.15
Sec16a	1.57	1.36	1.44	1.45
Sec22b	0.92	0.86	0.68	1.07
Sec23a	0.71	0.74	0.77	0.70
Sec23b	1.21	1.23	1.21	1.40
Sec23ip	0.77	0.70	0.93	0.94
Sec24b	0.87	1.05	0.92	1.01
Sec24c	1.03	1.08	1.13	0.93
Sec24d	1.13	1.05	0.83	1.17
Sec31a	1.06	1.01	1.03	0.95
Sec61a1	0.99	1.00	1.08	1.28
Sec61b	1.29	1.11	1.36	1.61
Sec62	0.80	0.76	0.84	0.84
Sec63	1.18	1.25	1.10	1.33
Seh1l	1.26	1.29	0.83	0.90
Selenbp1	1.39	1.24	0.52	0.35
Senp3	0.93	0.89	0.80	1.08
Sephs1	1.05	1.12	0.93	1.05
Sept1	0.91	0.88	0.91	0.66
Sept11	1.08	1.10	0.95	0.96
Sept15	0.99	0.94	1.01	1.00
Sept2	0.89	1.06	0.93	1.02
Sept6	1.20	1.18	1.15	1.23
Sept7	0.96	0.99	0.86	0.88
Sept9	0.85	0.87	1.28	1.16
Serbp1	0.86	0.84	1.02	1.01
Serpine1	0.30	0.37	0.26	0.27
Set	1.01	0.99	0.83	0.89
Setd1a	0.84	1.17	0.82	0.76
Sf1	0.84	0.87	0.85	1.00
Sf3a1	1.06	1.07	0.86	0.85
Sf3a2	0.85	0.80	0.75	0.77
Sf3a3	0.97	1.00	0.89	0.88
Sf3b1	0.91	0.93	0.87	0.79
Sf3b2	0.95	0.89	0.86	0.92
Sf3b3	0.89	0.91	0.87	0.93
Sf3b4	1.22	1.32	1.01	0.97
Sf3b5	0.81	0.86	0.89	0.89
Sfn	1.01	0.91	0.92	0.94
Sfpq	0.93	1.00	1.21	1.02
Sfr1	0.74	0.77	1.30	1.20
Sfxn1	1.47	1.39	1.28	0.84
Sfxn3	0.89	6.90	0.97	1.00
Sgta	0.91	0.93	1.51	1.74
Sh3bgrl	0.81	0.86	0.80	0.86
Sh3bgrl3	1.27	1.25	1.30	1.67
Sh3bp1	0.67	0.67	0.65	1.25
Sh3gl1	0.89	0.85	0.90	1.56
Sh3kbp1	0.44	0.46	0.51	0.97
Shc1	0.85	0.91	0.90	1.55
Shmt1	0.95	1.06	0.95	1.07
Shmt2	1.32	1.25	1.04	0.96

Shoc2	1.33	1.17	1.84	1.05
Sik3	1.09	1.14	0.89	1.30
Sin3a	1.15	1.16	0.61	0.86
Sipa1l1	0.93	0.96	1.18	0.66
Skap2	0.71	0.69	0.55	0.50
Skiv2l	1.21	0.99	0.83	0.70
Skiv2l2	1.02	1.05	0.96	0.80
Skp1a	0.75	0.76	1.00	1.02
Slc16a1	0.54	0.53	0.87	1.05
Slc18a2	1.18	1.40	2.06	1.38
Slc25a1	1.96	1.81	1.09	1.15
Slc25a10	1.42	1.61	1.29	0.99
Slc25a11	0.92	0.86	0.81	1.12
Slc25a12	1.02	1.10	1.04	1.05
Slc25a13	0.76	0.87	0.82	0.90
Slc25a4	0.80	0.90	0.63	1.13
Slc25a5	0.85	0.89	0.79	0.95
Slc2a1	1.20	1.16	1.25	2.07
Slc2a3	0.58	0.60	0.40	1.11
Slc39a4	0.42	0.35	0.16	0.38
Slc39a7	0.78	0.80	0.80	1.12
Slc3a2	0.61	0.64	0.84	1.14
Slc4a1ap	0.89	0.96	0.93	0.70
Slc7a1	0.66	0.76	1.73	1.70
Slc7a5	0.68	0.69	1.05	1.44
Slc7a6	0.85	0.90	1.07	0.99
Slc9a3r1	1.07	1.19	1.12	0.81
Slirp	1.11	1.14	1.17	1.10
Slk	0.82	0.83	0.88	1.15
Sltm	0.96	0.96	0.98	0.84
Smap1	0.95	0.90	1.41	1.46
Smap2	1.13	1.28	0.77	0.72
Smarca4	1.23	1.27	1.37	1.07
Smarca5	0.81	0.76	1.00	0.83
Smarcb1	1.14	1.23	1.19	0.90
Smarcc1	1.01	1.08	1.21	0.99
Smarcc2	1.03	1.04	0.77	0.79
Smarcd2	1.11	1.21	1.07	1.02
Smarce1	1.16	1.21	1.16	0.99
Smc1a	0.93	0.94	0.93	0.89
Smc2	0.86	0.88	0.88	0.70
Smc3	0.92	0.95	1.01	0.93
Smc4	0.92	0.91	1.09	1.01
Smchd1	0.76	0.77	0.78	0.89
Smek1	1.10	1.01	1.11	0.86
Smn1	0.77	0.77	0.68	0.77
Smndc1	0.98	1.06	1.20	1.22
Smu1	0.83	0.84	0.92	0.94
Smyd5	1.12	1.15	1.49	1.15
Snap23	1.24	1.04	1.09	1.06
Snap29	0.90	1.02	1.41	2.60
Snd1	0.93	0.93	0.89	1.34
Snf8	1.14	1.06	1.17	1.12
Snrnp200	1.03	0.97	1.00	0.90
Snrnp40	0.86	0.91	0.99	0.96
Snrnp70	0.92	0.93	0.81	0.89
Snrpa	0.99	1.06	0.96	0.89
Snrpa1	0.92	0.86	0.86	0.95
Snrpb	1.03	1.01	1.00	0.86
Snrpb2	1.07	1.00	1.00	0.91
Snrpc	1.13	1.09	0.94	1.05
Snrpd1	1.31	1.30	1.23	1.25
Snrpd2	1.34	1.17	1.01	0.91

Snrpd3	1.44	1.41	1.03	0.87
Snrpe	1.91	1.42	1.21	1.28
Snrpf	1.11	1.05	1.04	0.88
Snrpg	1.46	1.43	1.33	1.17
Snw1	1.06	1.02	1.27	1.01
Snx1	0.98	0.97	0.91	1.22
Snx12	0.89	0.85	0.67	0.75
Snx2	1.08	0.99	0.91	1.60
Snx27	1.02	1.03	1.10	1.23
Snx3	0.93	0.92	0.89	0.92
Snx4	0.73	0.88	0.85	1.49
Snx5	1.09	1.06	0.95	2.11
Snx6	0.91	0.99	0.94	1.13
Soat1	1.16	0.97	1.17	1.02
Sod1	1.07	1.22	1.01	1.55
Sod2	0.88	0.85	0.57	0.69
Son	0.92	0.99	0.72	0.95
Sord	1.39	1.16	1.02	1.34
Sp1	0.99	1.05	0.98	0.99
Spag7	1.12	1.02	1.38	1.26
Spats2	0.78	0.66	0.77	0.79
Spcs1	0.94	0.92	0.80	0.97
Spcs2	0.89	0.86	0.88	1.02
Spcs3	0.79	0.85	0.87	0.84
Spin1	0.86	0.74	0.78	0.82
Spn	0.79	0.93	1.12	0.48
Spr	1.07	1.06	0.86	0.72
Sptan1	1.26	1.24	1.05	0.90
Sptbn1	1.38	1.32	0.99	0.91
Sptbn1	1.67	1.15	0.99	0.91
Sptlc1	0.82	0.87	1.45	1.53
Sptlc2	0.89	1.10	1.22	1.18
Sqstm1	1.37	0.88	2.70	1.76
Srbd1	0.72	2.23	0.94	0.73
Srfbp1	0.54	0.55	1.71	1.18
Srgap2	0.83	0.93	0.86	0.93
Sri	1.01	0.94	0.79	0.68
Srm	0.97	1.03	0.97	0.96
Srp14	1.41	1.25	1.18	1.06
Srp19	1.04	1.08	1.23	1.25
Srp54a	1.19	1.05	1.20	1.15
Srp68	0.83	1.03	1.01	1.13
Srp72	0.95	0.98	1.03	1.16
Srp9	0.96	0.87	1.35	1.07
Srpk1	0.76	0.64	0.69	0.87
Srpr	0.92	0.88	1.08	2.02
Srprb	0.85	0.86	1.00	1.34
Srrm1	1.00	1.01	0.90	0.81
Srrm2	0.82	0.82	0.81	0.81
Srrt	1.09	1.11	1.01	0.93
Srsf1	0.90	0.96	1.00	0.99
Srsf10	1.13	1.11	0.98	0.95
Srsf11	0.87	0.83	0.95	1.03
Srsf2	1.04	1.09	1.01	1.04
Srsf3	1.13	1.15	1.03	1.00
Srsf4	1.41	1.23	1.08	1.10
Srsf5	1.08	1.07	1.03	1.05
Srsf6	0.93	0.89	1.03	0.96
Srsf7	1.05	1.03	0.81	0.92
Srsf9	1.24	1.17	0.96	0.77
Ssb	1.19	1.15	1.15	0.98
Ssbp1	1.11	1.10	0.63	0.90
Ssr1	1.00	1.02	1.16	1.06

Ssr3	1.33	1.19	1.33	1.51
Ssr4	1.05	1.07	0.98	1.22
Ssrp1	1.03	1.08	0.99	0.85
Sssca1	0.67	0.67	0.97	1.29
Ssu72	1.10	0.96	1.38	0.89
St13	0.83	0.78	0.75	0.91
Stat1	0.84	0.80	0.87	0.95
Stat3	1.11	1.13	0.99	0.66
Stat5a	1.01	0.99	1.05	0.69
Stim1	0.89	0.89	1.00	1.26
Stim2	0.77	0.67	1.15	0.68
Stip1	0.90	0.95	1.00	1.21
Stk10	1.35	1.04	1.46	1.59
Stk17b	0.54	0.63	0.87	1.26
Stk24	1.14	1.16	0.99	1.10
Stk38	0.71	0.83	0.83	0.72
Stk4	1.11	1.19	1.22	1.11
Stmn1	0.91	0.91	0.92	0.71
Stoml2	1.38	1.23	0.83	0.79
Strap	1.06	1.15	1.36	1.04
Strbp	1.13	1.12	1.10	1.12
Strn	0.74	0.90	0.91	0.91
Stt3a	1.12	1.01	1.06	1.23
Stt3b	1.39	1.30	1.46	1.04
Stub1	1.84	1.61	2.30	1.32
Stx12	1.14	1.22	1.83	1.75
Stx4a	0.90	0.87	1.01	0.81
Stx7	0.71	0.63	0.67	1.29
Stxbp2	0.77	0.68	0.87	1.04
Stxbp3a	1.02	1.07	1.26	1.14
Sub1	0.95	0.98	0.88	1.04
Sucla2	1.07	1.12	0.92	0.75
Suclg1	0.79	1.01	0.78	0.82
Suclg2	0.90	1.05	0.66	0.92
Sugt1	0.92	0.87	1.11	1.18
Sumo1	0.76	0.78	0.75	0.66
Sumo2	0.82	0.83	0.80	0.70
Sumo3	1.13	0.70	1.06	0.71
Sun2	1.08	1.20	2.30	1.19
Supt16	1.02	1.08	0.98	0.85
Supt5	0.84	0.83	1.11	1.11
Supt6	0.83	0.94	1.17	1.17
Surf6	0.98	1.05	0.95	0.90
Suz12	0.89	0.95	1.29	0.67
Swap70	1.01	0.84	0.92	0.94
Syap1	0.78	0.77	0.77	1.02
Syf2	0.92	0.87	1.22	0.94
Syk	1.27	1.26	1.28	1.03
Sympk	1.08	1.12	1.05	0.80
Syncrip	0.91	0.93	0.93	0.95
Synj2bp	1.00	1.03	1.05	1.27
Tab1	0.95	1.28	0.79	0.58
Tacc3	0.60	0.72	0.76	0.71
Taco1	1.27	1.32	1.19	1.11
Taf10	0.97	1.13	0.97	1.40
Taf15	1.14	1.21	0.85	1.37
Taf8	1.05	1.09	1.11	1.13
Tagln2	0.57	0.58	0.71	0.71
Taldo1	0.78	0.79	0.71	0.65
Tamm41	1.15	0.87	0.77	0.56
Taok3	0.91	0.84	1.09	1.26
Tap1	1.22	1.21	1.87	1.47
Tap2	1.44	1.52	1.47	1.94

Tapbp	1.14	1.17	1.06	1.59
Tardbp	1.07	1.11	0.96	0.85
Tars	0.85	0.85	0.88	1.19
Tars2	1.35	0.97	0.70	1.14
Tax1bp1	0.83	0.93	1.28	0.88
Tbc1d1	1.18	1.11	1.01	1.40
Tbc1d15	1.24	1.19	1.09	1.34
Tbc1d5	0.91	0.80	0.95	0.96
Tbc1d5	1.93	0.29	0.95	0.96
Tbc1d9b	2.07	1.89	1.31	1.16
Tbca	1.14	1.11	1.11	1.02
Tbcb	1.99	1.06	1.32	1.67
Tbcc	1.00	1.07	1.07	1.08
Tbcd	1.18	1.40	1.40	1.11
Tbl1x	0.71	0.84	0.69	0.83
Tbl1xr1	0.73	0.72	0.64	0.98
Tbl2	1.29	1.28	1.02	0.66
Tbl3	0.81	0.84	1.05	1.04
Tbrg4	1.00	0.93	1.42	1.18
Tcea1	0.71	0.72	0.75	0.71
Tceb2	0.71	0.72	0.82	0.92
Tceb3	1.07	0.84	0.92	0.73
Tcerg1	0.92	0.95	0.86	0.84
Tcirg1	0.59	0.53	0.70	0.98
Tcof1	0.92	0.80	0.84	0.88
Tcp1	1.30	1.22	1.08	1.09
Tdp1	1.13	1.36	1.04	0.81
Tecr	0.96	0.99	0.97	1.19
Terf2	1.34	0.80	0.66	0.75
Terf2ip	0.80	0.85	0.52	0.63
Tes	2.58	2.70	2.41	1.20
Tex10	0.88	1.10	0.77	0.91
Tfam	1.62	1.53	0.95	0.83
Tfg	1.61	1.05	1.63	1.67
Tfip11	0.86	0.85	3.44	1.20
Tfrc	0.68	0.84	1.42	1.09
Tgfb1	0.77	0.85	1.15	0.72
Tgm2	3.39	3.80	1.73	0.93
Tgs1	0.76	0.72	1.08	2.70
Them6	1.26	1.03	1.29	1.52
Thoc1	1.02	1.12	0.80	0.78
Thoc2	0.95	0.97	1.01	0.87
Thoc3	1.57	1.37	1.18	1.25
Thoc5	1.38	1.19	1.30	0.91
Thoc6	1.37	1.29	1.31	0.95
Thop1	1.10	1.01	0.99	0.87
Thrap3	1.27	1.33	1.14	0.99
Thtpa	1.20	1.14	0.79	1.69
Thumpd1	0.77	0.91	0.82	0.72
Thumpd3	0.85	0.88	0.84	1.06
Thyn1	1.15	1.24	0.90	0.92
Tial1	0.81	1.20	0.94	0.87
Timm10	1.12	1.26	1.41	1.23
Timm13	0.91	1.00	0.92	0.97
Timm17b	1.59	0.95	1.20	1.04
Timm23	1.31	1.17	1.32	1.30
Timm44	0.77	0.80	0.69	0.94
Timm50	1.08	0.99	1.09	1.29
Timm8a1	1.09	1.02	0.71	0.84
Timm8b	2.28	2.30	1.27	1.15
Timm9	1.05	1.16	1.08	1.00
Tjp2	0.77	0.81	1.00	0.90
Tkt	1.35	1.36	1.20	0.97

Tln1	0.54	0.58	0.66	1.21
Tm9sf2	0.95	0.93	1.86	1.02
Tm9sf3	1.12	1.18	1.35	1.17
Tmco1	0.92	0.73	1.30	1.31
Tmed10	1.28	1.21	1.08	0.98
Tmed2	1.10	1.06	1.30	1.23
Tmed5	1.45	1.47	1.09	1.07
Tmed7	1.56	1.48	1.36	0.98
Tmed9	1.14	1.23	1.40	1.23
Tmem11	0.98	0.93	1.09	1.20
Tmem205	1.12	1.32	0.86	1.48
Tmem214	1.33	1.11	1.24	0.89
Tmem30a	0.70	0.82	0.85	1.05
Tmem33	1.33	1.41	1.64	1.40
Tmem43	1.08	1.11	1.33	1.14
Tmem55a	0.62	0.63	0.94	0.87
Tmod3	0.81	0.83	0.81	0.93
Tmpo	1.06	1.20	0.96	0.71
Tmpo	0.98	1.06	0.96	0.71
Tmpo	1.09	1.05	0.96	0.71
Tmsb10	0.50	0.47	0.55	0.63
Tmsb4x	0.34	0.32	0.42	0.78
Tmx1	1.13	1.14	1.03	0.94
Tmx2	2.89	2.76	3.62	2.39
Tmx3	1.30	1.15	1.30	1.11
Tnfaip8	1.06	1.12	1.38	1.53
Tnfrsf10b	0.04	0.04	0.09	0.04
Tnpo1	0.97	0.89	0.83	0.87
Tnpo2	0.79	0.77	0.69	1.29
Tnpo3	0.78	0.78	0.67	0.94
Toe1	0.93	1.07	1.16	1.37
Tollip	1.00	1.02	1.22	1.59
Tomm22	1.06	1.17	1.08	1.26
Tomm34	0.74	0.64	0.77	1.44
Tomm40	1.33	1.27	0.89	1.02
Tomm70a	1.05	1.20	0.90	1.02
Top1	1.16	0.91	1.04	0.92
Top2a	0.51	0.50	0.56	0.59
Top2b	0.99	0.94	0.95	0.93
Tor1aip1	0.89	0.83	0.77	0.75
Tor1aip2	1.22	1.26	1.28	1.21
Tpd52	1.04	0.97	0.88	1.15
Tpd52l2	1.01	1.10	1.40	1.39
Tpi1	1.14	1.20	1.01	0.87
Tpm1	0.80	0.76	0.80	1.36
Tpm3	0.97	1.02	0.99	1.22
Tpm3	0.71	0.78	0.99	1.22
Tpm4	0.26	0.30	0.32	1.22
Tpp2	0.79	0.80	0.92	0.80
Tpr	0.69	0.72	0.71	0.83
Tpt1	0.93	1.01	1.27	1.19
Tpx2	0.97	0.82	0.69	0.61
Tra2a	0.78	0.77	1.00	0.89
Tra2b	1.05	1.02	0.94	1.09
Tradd	0.88	0.81	0.81	1.18
Trap1	1.55	1.50	1.42	1.28
Trappc3	1.30	1.22	1.31	1.14
Trim25	1.46	1.31	1.01	1.15
Trim28	1.13	1.15	1.20	0.93
Trim33	0.95	0.98	0.72	1.07
Trip12	1.65	1.26	2.40	0.82
Trip13	1.30	1.30	1.41	1.78
Trmt1	1.11	1.02	0.96	1.62

Trmt112	1.21	1.09	1.39	1.19
Trmt2a	0.97	0.98	1.16	1.23
Trmt5	1.02	0.86	0.75	1.00
Trmt6	1.36	1.52	1.14	1.12
Trmt61a	1.27	1.24	1.49	1.27
Trnt1	0.84	0.91	0.86	0.97
Trp53bp1	0.98	1.02	1.31	1.64
Trpv2	1.89	1.90	2.91	7.14
Tsc22d1	1.43	1.39	1.75	0.82
Tsfm	1.13	1.12	1.10	1.01
Tsg101	1.16	1.26	1.40	1.48
Tsn	0.94	0.91	0.80	0.93
Tsnax	0.83	0.84	0.71	0.92
Tsr1	1.05	0.93	1.05	1.04
Tsr2	0.79	0.85	0.51	0.55
Tssc1	0.89	0.99	1.37	1.29
Tsta3	1.29	1.34	1.49	1.28
Ttc1	1.08	0.82	1.34	2.20
Ttc33	0.58	0.67	0.58	0.86
Ttc37	1.11	1.39	1.25	1.25
Ttc9c	0.86	0.83	1.04	1.45
Ttll12	0.98	0.93	1.35	1.84
Ttn	0.81	0.68	1.04	0.88
Ttn	0.60	0.61	1.04	0.88
Tuba1b	1.02	0.86	1.03	0.87
Tuba4a	0.66	0.64	1.10	0.90
Tuba8	0.99	1.06	1.82	2.10
Tubb2a	0.96	1.05	0.75	1.01
Tubb4b	1.11	1.13	1.08	0.95
Tubb5	0.76	0.78	0.99	0.87
Tubb6	1.61	1.75	1.31	1.36
Tufm	0.80	0.88	0.75	0.64
Twf1	0.92	0.90	0.99	1.40
Twf2	0.81	0.63	0.73	1.25
Twistnb	0.56	0.66	0.98	0.76
Txlna	0.92	0.93	1.85	1.75
Txn1	0.75	0.79	0.79	0.85
Txn2	0.91	1.14	1.41	1.06
Txndc12	0.90	0.87	1.00	1.08
Txndc17	0.95	0.98	1.10	1.13
Txndc5	1.63	1.66	1.53	1.39
Txnip	1.01	0.89	0.58	0.96
Txnl1	1.16	1.17	0.96	1.01
Txnrd1	0.96	1.00	0.82	0.96
Tyms	0.97	1.03	1.70	1.11
U2af1	1.08	1.16	0.96	0.95
U2af2	1.02	1.03	0.91	0.86
U2surp	0.90	0.85	0.98	0.95
Uap1l1	1.44	1.50	1.25	2.28
Uba1	0.83	0.86	0.76	1.12
Uba2	1.14	1.19	1.09	0.94
Uba3	1.17	1.27	0.85	1.10
Uba5	1.05	0.82	1.18	1.29
Uba6	1.26	1.21	1.03	0.92
Ubap2	0.82	0.90	1.12	0.71
Ubap2l	0.91	0.90	1.02	1.10
Ubap2l	0.85	0.80	1.02	1.10
Ube2c	1.03	0.97	1.96	1.93
Ube2f	0.78	0.62	0.71	0.68
Ube2g1	1.33	1.20	1.66	1.40
Ube2h	1.23	0.98	0.77	0.99
Ube2i	0.99	0.97	0.85	0.81
Ube2k	1.01	0.98	0.96	0.86

Ube2l3	0.89	0.83	0.89	1.14
Ube2m	0.91	0.91	1.04	0.94
Ube2n	0.90	0.90	0.90	0.92
Ube2o	0.94	0.95	0.84	0.84
Ube2v1	1.43	1.38	1.32	1.35
Ube2v2	0.93	0.86	1.18	1.48
Ube2z	1.15	1.35	1.33	1.64
Ube3a	1.09	1.11	1.43	1.38
Ube3c	1.29	1.22	0.93	0.88
Ube4a	1.00	1.03	0.56	0.82
Ube4b	1.26	1.17	1.11	1.24
Ubfd1	0.77	0.62	0.73	0.78
Ubl4a	0.77	0.77	1.02	1.00
Ubl7	0.80	0.64	1.18	2.91
Ubqln1	1.12	1.06	1.18	1.13
Ubqln2	0.65	0.67	0.63	0.66
Ubqln4	0.91	0.97	0.91	0.99
Ubr2	0.90	0.85	1.16	1.90
Ubr4	1.02	1.02	1.14	1.32
Ubr5	0.72	0.62	0.84	1.02
Ubr7	0.86	0.85	0.79	0.96
Ubtf	1.13	1.18	1.17	0.77
Ubxn1	0.73	0.73	0.84	1.15
Ubxn4	0.71	0.73	0.97	1.12
Ubxn7	0.95	0.90	0.75	0.86
Uchl3	1.23	1.26	1.12	1.03
Uchl5	0.92	0.96	1.08	0.92
Uck2	1.34	1.43	1.61	1.20
Ufc1	0.98	0.81	1.02	0.70
Ufd1l	0.69	0.78	0.74	0.99
Ufl1	1.09	1.10	1.71	1.27
Ufm1	0.71	0.75	0.96	1.17
Ugdh	1.24	1.06	1.07	0.92
Uggt1	0.99	0.96	0.93	1.07
Ugp2	1.08	0.96	0.75	1.46
Uhrf1	0.42	0.46	1.60	1.34
Umps	1.11	1.08	1.09	1.08
Unc119	1.54	1.40	1.74	1.90
Unc13d	1.33	1.41	1.58	1.02
Unc45a	0.47	0.55	1.03	1.14
Upf1	1.16	1.08	1.36	1.23
Upf3b	1.06	0.94	1.89	0.50
Uqcr10	1.56	1.19	1.15	1.07
Uqcrb	0.94	0.97	0.91	0.91
Uqcrc1	0.94	1.01	1.06	0.96
Uqcrc2	0.87	0.95	0.90	0.91
Uqcrfs1	1.21	1.14	1.03	0.99
Uqcrh	1.37	1.31	0.99	0.95
Uqcrq	1.20	1.13	0.81	0.76
Urb1	1.23	1.43	1.03	1.00
Urod	0.81	0.79	0.76	0.72
Usmg5	1.35	1.12	0.97	0.91
Uso1	1.08	1.07	0.99	1.23
Usp10	0.85	0.91	1.35	1.03
Usp14	1.04	1.09	1.01	1.02
Usp15	1.10	1.08	1.14	1.35
Usp19	0.74	0.63	0.84	1.10
Usp24	0.83	0.81	1.12	1.27
Usp39	0.84	0.87	1.12	0.93
Usp4	1.07	1.02	1.13	1.04
Usp47	0.95	0.90	1.13	0.95
Usp5	1.25	1.24	1.22	1.16
Usp7	1.15	1.04	1.04	1.07

Usp8	1.27	1.22	1.47	1.74
Usp9x	1.03	0.86	0.98	1.35
Utp14a	0.87	0.88	0.92	1.02
Utp15	0.75	0.67	0.90	1.00
Utp18	1.09	1.10	1.16	0.99
Utp20	1.37	1.34	1.23	1.02
Utp3	0.96	0.92	1.10	0.90
Utp6	1.13	1.02	1.16	1.17
Vac14	0.92	0.95	1.08	0.97
Vamp3	1.30	1.31	1.49	1.27
Vamp4	0.84	0.75	0.82	0.76
Vamp7	0.63	0.60	1.07	1.00
Vamp8	0.94	0.99	0.99	0.95
Vapa	0.89	0.87	0.84	1.53
Vapb	1.27	1.23	1.16	1.42
Vars	1.08	1.03	0.71	0.71
Vasp	0.61	0.52	0.64	0.96
Vat1	0.86	0.96	0.94	0.85
Vav1	0.61	0.61	0.77	1.39
Vbp1	0.82	0.89	0.87	1.04
Vcl	0.65	0.72	0.80	1.13
Vcp	0.81	0.82	0.80	0.80
Vcpip1	0.79	0.86	0.79	1.01
Vdac1	1.33	1.40	0.95	0.90
Vdac2	1.03	1.11	0.94	0.88
Vdac3	0.69	0.74	0.56	0.85
Vim	0.70	0.77	0.86	1.40
Vkorc1	1.19	1.23	1.19	0.56
Vma21	0.84	1.06	0.93	1.52
Vprbp	0.88	1.06	1.11	1.19
Vps11	1.01	1.04	1.02	1.31
Vps13a	1.09	1.08	1.01	1.12
Vps13c	1.29	1.33	0.98	1.14
Vps25	1.20	0.95	1.15	1.01
Vps26a	0.79	0.77	0.87	1.17
Vps26b	1.27	1.21	0.99	1.34
Vps28	0.66	0.72	0.93	1.10
Vps29	0.82	0.97	0.86	0.97
Vps35	0.80	0.94	0.73	1.11
Vps36	1.11	1.20	0.99	1.07
Vps4b	0.76	0.76	0.73	0.87
Vps52	1.00	1.03	1.07	1.04
Vrk1	1.34	1.25	1.30	0.67
Vsx2	1.00	0.96	0.82	0.88
Vta1	1.21	1.41	1.07	1.14
Vwa5a	1.15	1.19	1.23	1.23
Vwa9	0.99	1.04	0.91	0.96
Wapal	1.21	1.22	1.22	1.35
Wars	1.00	1.02	1.31	1.27
Was	1.48	1.45	1.00	1.22
Wasf2	1.34	1.20	1.12	0.91
Wbp11	1.15	1.10	1.31	0.86
Wdfy4	1.24	1.01	0.95	1.16
Wdhd1	0.76	0.68	0.92	0.76
Wdr1	1.02	1.10	1.32	1.36
Wdr12	0.83	0.91	0.92	0.84
Wdr18	0.90	0.97	1.01	1.19
Wdr26	1.25	1.20	1.01	1.25
Wdr3	1.10	1.17	1.37	1.30
Wdr33	0.99	0.99	0.93	0.92
Wdr36	0.82	0.79	1.06	0.94
Wdr43	0.73	0.77	1.13	1.04
Wdr46	1.00	0.88	1.07	0.88

Wdr5	1.03	0.96	1.09	0.93
Wdr61	1.10	1.04	0.99	0.95
Wdr74	1.20	1.14	1.98	1.58
Wdr75	0.93	1.00	1.09	0.84
Wdr77	1.14	1.26	1.31	1.87
Wdr82	1.35	1.34	1.37	0.95
Wibg	0.98	0.96	1.17	0.96
Wipf1	1.38	1.07	1.39	1.29
Wipi2	1.07	1.30	1.08	1.49
Wiz	0.87	0.84	0.92	1.07
Wnk1	1.06	1.00	1.14	1.23
Wtap	1.22	1.06	1.21	1.28
Xab2	1.17	1.11	1.22	1.16
Xpnpep1	0.85	0.87	0.80	1.11
Xpo1	0.97	1.01	0.90	0.89
Xpo4	1.22	1.23	1.32	1.16
Xpo5	0.87	0.86	0.95	1.04
Xpo7	1.89	1.44	1.09	0.89
Xpot	1.18	1.17	1.31	1.15
Xrcc1	0.95	0.99	0.76	0.78
Xrcc5	0.97	1.07	0.75	0.46
Xrcc6	0.95	0.89	0.82	0.49
Xrn1	0.84	0.67	1.43	0.84
Xrn2	1.27	1.27	1.06	1.16
Yars	0.99	1.03	0.98	1.55
Ybx1	0.96	0.97	1.42	1.33
Ybx3	1.37	1.12	2.33	1.64
Ybx3	1.17	1.02	2.33	1.64
Yif1b	1.35	1.20	2.47	1.67
Ykt6	1.04	1.05	1.00	1.23
Ylpm1	0.94	0.97	1.21	1.17
Ythdc1	1.02	1.02	0.93	0.99
Ythdf2	1.12	1.02	1.38	1.18
Ythdf3	0.95	0.98	1.06	1.29
Ywhab	1.13	1.14	1.15	1.27
Ywhae	1.15	1.26	1.02	1.09
Ywhag	1.16	1.11	1.05	1.00
Ywhah	1.08	1.05	1.03	0.97
Ywhaq	0.77	0.80	0.78	0.74
Ywhaz	0.98	1.00	0.90	1.23
Zadh2	0.35	0.38	0.39	0.76
Zbtb8os	1.31	1.29	1.28	1.15
Zc3h11a	0.92	0.77	0.74	0.74
Zc3h13	1.21	1.15	1.18	0.97
Zc3h14	4.00	1.85	2.97	1.34
Zc3h15	1.03	0.99	1.32	1.31
Zc3h18	0.69	0.83	0.58	0.72
Zc3h4	1.04	0.95	1.05	0.93
Zc3hav1	0.92	0.95	1.39	1.56
Zc3hc1	0.96	0.87	0.96	1.06
Zcchc8	1.09	1.02	0.86	0.70
Zfml	0.73	0.80	0.86	1.02
Zfp207	0.92	0.91	1.07	1.19
Zfp259	0.80	0.83	0.86	1.12
Zfp280c	1.11	1.08	1.08	0.97
Zfp326	1.01	0.98	0.76	1.02
Zfp330	0.66	0.75	0.81	1.39
Zfp36l2	0.90	0.90	1.64	2.70
Zfp512	1.46	1.15	0.91	0.39
Zfp593	0.94	0.99	2.18	1.60
Zfp622	0.85	0.92	0.99	1.53
Zfp91	1.55	1.04	0.75	0.83
Zfpl1	1.25	1.39	0.84	1.49

Zfpm1	0.86	0.84	1.27	0.99
Zfr	1.07	1.06	0.98	1.02
Zmpste24	0.79	0.80	0.83	1.02
Znrd1	0.64	0.68	0.84	0.87
Zranb2	0.86	0.83	0.69	0.81
Zw10	1.36	1.31	0.96	0.85
Zwint	0.73	0.88	1.08	1.31
Zyx	0.50	0.51	1.01	2.08

Appendix B: SILAC ratios of all phosphosites commonly identified in 5 Ba/F3 cell lines

Gene Symbol	Phosphosites	CRLF2/ parental	CRLF2 F232C/ parental	CRLF2 JAK2*/ parental	BCR-ABL1/ parental
0610010K14Rik	0610010K14Rik_S62	0.70	0.72	0.66	0.53
1110037F02Rik	1110037F02Rik_S138	0.50	0.50	0.37	0.36
1110037F02Rik	1110037F02Rik_S133	0.43	0.48	0.38	0.36
1110037F02Rik	1110037F02Rik_S173	0.87	0.77	0.70	0.53
1110037F02Rik	1110037F02Rik_S1628	0.99	1.02	1.06	0.77
1110059G10Rik	1110059G10Rik_S50	0.98	0.93	0.95	1.02
1200011I18Rik	1200011I18Rik_S104	0.45	0.29	0.84	0.77
1200014J11Rik	1200014J11Rik_S410	0.52	0.50	0.61	0.40
1700025G04Rik	1700025G04Rik_S115	1.21	1.29	1.36	0.75
1810037I17Rik	1810037I17Rik_S19	0.78	0.88	0.80	1.60
2310022A10Rik	2310022A10Rik_S115	0.89	0.87	0.57	0.26
2310022A10Rik	2310022A10Rik_T119	1.21	1.22	0.57	0.26
2410004B18Rik	2410004B18Rik_S156	0.54	0.52	0.54	0.85
2610018G03Rik	2610018G03Rik_S4	0.66	0.66	0.94	2.70
2610301G19Rik	2610301G19Rik_S612	1.19	1.04	1.31	0.47
2610301G19Rik	2610301G19Rik_S610	0.93	0.93	1.11	0.90
2810004N23Rik	2810004N23Rik_S67	0.73	0.79	0.77	0.62
4932438A13Rik	4932438A13Rik_S2755	0.89	0.91	0.95	0.89
8030462N17Rik	8030462N17Rik_S66	1.04	1.09	1.16	1.35
A730008H23Rik	A730008H23Rik_S491	0.89	1.02	0.38	0.19
A830080D01Rik	A830080D01Rik_S78	0.57	0.58	0.36	0.45
A830080D01Rik	A830080D01Rik_S80	0.57	0.58	0.36	0.45
A830080D01Rik	A830080D01Rik_S205	0.78	0.76	0.64	0.72
A830080D01Rik	A830080D01Rik_S592	0.52	0.62	1.05	1.26
Aaas	Aaas_S495	0.61	0.68	0.83	1.08
Aak1	Aak1_T537	0.39	0.34	0.42	0.69
Aak1	Aak1_S554	2.82	2.74	1.04	0.89
Aak1	Aak1_S541	0.75	0.73	0.85	1.00
Aak1	Aak1_S540	0.76	0.73	0.88	1.03
Aak1	Aak1_T523	0.60	0.61	1.24	1.34
Aarsd1	Aarsd1_S88	1.00	1.33	1.99	4.75
AB124611	AB124611_S179	0.41	0.49	0.00	0.00
Abcc1	Abcc1_S290	1.19	1.15	1.27	1.20
Abcc4	Abcc4_T567	1.58	1.56	0.00	0.00
Abcc4	Abcc4_T571	1.54	1.80	1.33	1.23
Abcf1	Abcf1_S225	0.83	0.70	0.78	0.52
Abcf1	Abcf1_S107	0.70	0.90	0.78	0.81
Abcf1	Abcf1_S138	0.91	0.85	0.85	0.93
Abcf1	Abcf1_S90	0.65	0.44	0.93	1.11
Abi1	Abi1_S178	0.60	0.57	0.60	0.71
Abi1	Abi1_S220	1.05	1.16	1.40	1.99
Abl2	Abl2_S632	0.70	0.71	0.98	0.96
Acaca	Acaca_S79	1.16	1.61	1.95	1.30
Acin1	Acin1_S491	1.78	1.60	0.83	0.39
Acin1	Acin1_S729	0.91	1.00	0.89	0.54
Acin1	Acin1_S657	1.23	1.47	1.75	0.78
Acin1	Acin1_S479	1.55	1.34	1.31	0.88
Acin1	Acin1_S655	1.28	1.20	1.49	0.92
Acin1	Acin1_S886	1.05	1.07	1.18	1.02
Acin1	Acin1_S838	1.11	1.08	0.83	1.08
Acin1	Acin1_S710	1.47	1.37	1.37	1.53

Acly	Acly_S481	1.07	1.05	1.04	2.16
Aco2	Aco2_S559	1.18	1.20	1.13	1.23
Acot7	Acot7_Y164	2.41	3.25	4.18	9.22
Acss2	Acss2_S263	1.49	1.49	1.44	0.63
Actb	Actb_Y198	0.77	0.85	1.11	3.91
Actr3	Actr3_Y16	0.65	0.78	1.28	3.40
Adam17	Adam17_S794	0.54	0.55	0.48	0.73
Adat1	Adat1_S191	0.61	0.65	0.45	0.55
Add1	Add1_T610	0.36	0.39	0.00	0.00
Add1	Add1_T610	0.62	0.73	0.00	0.00
Add1	Add1_S12	0.75	0.68	0.82	1.45
Add3	Add3_T12	0.97	0.89	0.00	0.00
Adnp	Adnp_S904	0.74	0.90	0.63	0.49
Adrbk1	Adrbk1_S628	0.93	1.00	1.08	1.46
Adrm1	Adrm1_S211	1.19	1.04	1.06	1.01
Aebp2	Aebp2_S24	1.25	1.11	2.46	0.87
Aebp2	Aebp2_S199	1.39	1.35	2.81	1.30
Aebp2	Aebp2_S21	1.25	1.11	2.53	1.86
Aff1	Aff1_S1098	1.03	0.80	0.54	0.48
Aftph	Aftph_S151	1.59	1.59	1.62	1.63
Agap3	Agap3_T477	1.41	1.32	0.00	0.00
Agfg1	Agfg1_S181	1.94	2.32	0.90	0.66
Ahctf1	Ahctf1_S1381	0.26	0.33	0.54	0.67
Ahctf1	Ahctf1_T1224	0.91	0.83	0.97	0.92
Ahcyl2	Ahcyl2_S109	0.46	0.44	1.42	4.36
AI597479	AI597479_S193	0.59	0.64	1.50	0.93
AI597479	AI597479_S189	0.76	0.73	1.50	0.93
AI846148	AI846148_S313	0.60	0.64	0.55	0.74
Akap1	Akap1_S101	1.67	1.53	0.74	0.52
Akap1	Akap1_S103	1.93	2.06	1.67	2.43
Akap13	Akap13_S2692	0.39	0.36	0.34	0.39
Akap13	Akap13_S1892	0.73	0.71	0.35	0.48
Akap13	Akap13_S1613	0.81	0.84	0.62	0.51
Akap13	Akap13_S1253	0.45	0.45	0.75	1.06
Akap8	Akap8_S336	0.67	0.70	0.64	1.03
Akap8	Akap8_S320	1.19	1.07	1.68	1.31
Akap8	Akap8_S325	1.19	1.07	1.68	1.31
Aldh18a1	Aldh18a1_S427	0.49	0.51	0.33	0.92
Aldoa	Aldoa_S36	1.00	0.84	0.64	0.58
Aldoa	Aldoa_S46	0.67	0.76	0.74	1.14
Aldoa	Aldoa_Y204	0.61	0.66	0.51	1.22
Als2	Als2_S486	0.91	1.31	1.38	1.16
Amacr	Amacr_S323	0.59	0.58	0.67	5.59
Ampd2	Ampd2_S12	0.96	0.98	0.77	1.51
Ampd2	Ampd2_S87	0.55	0.65	0.75	1.59
Anapc1	Anapc1_S901	0.76	0.83	0.00	0.00
Anapc1	Anapc1_T902	0.84	1.02	0.79	0.89
Anapc1	Anapc1_S688	0.78	0.99	0.99	1.36
Anapc4	Anapc4_S777	0.87	0.96	0.92	1.00
Anapc4	Anapc4_S779	0.73	0.77	0.96	1.00
Ankhd1	Ankhd1_S1678	0.53	0.54	0.78	0.65
Ankib1	Ankib1_S738	1.04	1.01	1.06	1.05
Ankrd17	Ankrd17_S1441	0.52	0.46	1.23	0.63
Ankrd17	Ankrd17_S1789	0.75	0.87	1.05	0.76
Ankrd17	Ankrd17_S1790	0.63	0.88	1.05	0.76

Ankrd17	Ankrd17_S1792	0.65	0.87	1.06	0.77
Anln	Anln_S293	0.66	0.62	0.00	0.00
Anln	Anln_S180	0.50	0.46	0.35	0.32
Anxa5	Anxa5_Y92	0.51	0.43	0.26	0.67
Ap3d1	Ap3d1_T758	0.83	0.97	1.01	0.76
Ap3d1	Ap3d1_S760	1.05	0.96	1.02	0.80
Ap3d1	Ap3d1_S784	0.80	0.71	0.82	0.88
Ap3d1	Ap3d1_S755	1.18	1.33	1.16	1.32
Apbb1ip	Apbb1ip_S537	0.97	1.32	1.23	1.65
Apoa1bp	Apoa1bp_S43	1.14	1.09	0.55	0.50
Apoa1bp	Apoa1bp_T45	1.11	1.04	0.60	0.51
Arfgef2	Arfgef2_S227	1.43	1.12	1.09	0.87
Arglu1	Arglu1_S75	0.91	0.88	0.85	0.75
Arglu1	Arglu1_S74	0.81	0.87	0.70	0.78
Arhgap1	Arhgap1_S51	0.44	0.38	0.93	1.70
Arhgap27	Arhgap27_T265	0.99	0.96	1.19	0.81
Arhgap27	Arhgap27_S263	0.99	0.96	1.16	1.01
Arhgap4	Arhgap4_S918	0.99	1.17	1.51	1.31
Arhgap5	Arhgap5_S1219	0.75	0.71	0.77	1.09
Arhgap6	Arhgap6_S530	0.39	1.02	1.10	1.41
Arhgap9	Arhgap9_S197	0.81	0.95	0.62	0.98
Arhgdib	Arhgdib_Y129	0.89	1.08	1.05	27.10
Arhgef1	Arhgef1_T429	3.17	3.11	4.10	4.21
Arhgef2	Arhgef2_S122	1.27	1.76	1.11	1.78
Arhgef2	Arhgef2_S617	0.75	0.86	1.32	2.46
Arhgef2	Arhgef2_S902	0.96	0.90	1.00	2.64
Arhgef2	Arhgef2_S926	0.75	0.76	2.00	2.82
Arhgef40	Arhgef40_S959	1.17	1.30	1.10	0.60
Arhgef6	Arhgef6_S663	1.61	1.87	0.66	0.42
Arhgef6	Arhgef6_S248	0.54	0.57	0.64	0.75
Arhgef7	Arhgef7_S340	0.73	0.75	0.73	1.17
Arhgef7	Arhgef7_S71	0.54	0.67	0.79	2.09
Arhgef7	Arhgef7_S516	1.01	1.06	1.98	5.12
Arid1a	Arid1a_S697	0.97	0.99	1.26	1.24
Arid1a	Arid1a_S773	1.37	1.70	1.37	1.38
Arid3a	Arid3a_S102	1.28	1.42	0.00	0.00
Arid3a	Arid3a_S101	1.34	1.75	0.00	0.00
Arid3a	Arid3a_S78	1.07	1.32	0.75	0.83
Arid3a	Arid3a_S82	1.15	1.29	0.74	0.87
Arid3a	Arid3a_S77	0.71	0.86	0.73	0.87
Arid3a	Arid3a_S89	0.51	0.60	0.48	0.92
Arid4a	Arid4a_S867	0.85	0.78	0.72	0.52
Arid5a	Arid5a_S225	1.12	1.64	1.38	1.11
Arl13b	Arl13b_S328	1.34	1.21	1.10	1.16
Arl13b	Arl13b_S323	1.40	1.19	1.11	1.20
Arl6ip4	Arl6ip4_S140	2.07	1.24	0.83	1.15
Arl6ip6	Arl6ip6_S80	1.25	1.41	2.00	2.00
Armc10	Armc10_S43	1.47	1.36	1.04	0.89
Arpp19	Arpp19_S62	0.52	0.53	0.80	0.85
Asap1	Asap1_S819	0.68	0.64	0.39	0.23
Asap1	Asap1_S823	0.64	0.68	0.56	0.48
Aspscr1	Aspscr1_S202	0.87	0.82	0.00	0.00
Aspscr1	Aspscr1_T201	0.77	0.92	2.60	2.53
Atf2	Atf2_T53	1.57	1.38	0.83	0.60
Atf2	Atf2_T51	1.94	1.98	0.68	1.03

Atf2	Atf2_S94	1.08	1.00	1.03	1.14
Atf7	Atf7_T51	1.63	1.94	0.00	0.00
Atf7	Atf7_T53	1.63	1.94	0.97	1.03
Atf7ip	Atf7ip_S112	1.57	1.45	1.79	1.10
Atg16l2	Atg16l2_S282	1.00	0.97	0.45	0.52
Atm	Atm_S1987	0.43	0.71	0.25	0.37
Atn1	Atn1_S630	0.92	0.97	1.03	0.92
Atp13a1	Atp13a1_S896	0.56	0.69	0.99	0.99
Atp1a1	Atp1a1_Y55	1.13	1.21	1.14	1.63
Atp2a2	Atp2a2_S663	1.35	1.31	0.98	0.82
Atp2a2	Atp2a2_S661	1.50	1.31	1.35	2.17
Atr	Atr_S431	0.67	0.62	0.74	0.61
Atrip	Atrip_S97	0.87	0.91	0.74	0.53
Atrx	Atrx_S1512	0.34	0.36	0.00	0.00
Atrx	Atrx_S590	0.40	0.39	0.55	0.37
Atrx	Atrx_S315	0.40	0.44	0.51	0.50
Atrx	Atrx_S1290	0.60	0.58	0.63	0.57
Atrx	Atrx_S92	0.61	0.63	0.64	0.77
Atrx	Atrx_S719	0.68	0.64	0.78	0.84
Atrx	Atrx_S717	0.68	0.64	0.91	0.87
Atrx	Atrx_S940	1.00	1.00	0.89	0.97
Atxn2	Atxn2_T710	0.85	1.38	0.98	0.93
Atxn2	Atxn2_S741	0.52	0.49	1.84	1.43
Atxn2l	Atxn2l_S407	1.45	1.59	1.17	0.72
Atxn2l	Atxn2l_S333	1.32	1.32	1.27	1.01
Atxn2l	Atxn2l_S337	1.25	1.34	1.35	1.05
Atxn2l	Atxn2l_S304	0.82	1.20	1.21	1.19
Atxn2l	Atxn2l_S597	0.66	0.55	2.86	1.93
Atxn2l	Atxn2l_T505	0.75	0.71	1.61	3.40
Atxn2l	Atxn2l_S109	0.71	0.87	1.97	3.58
Bag6	Bag6_S1121	0.48	0.30	0.83	0.81
Bag6	Bag6_S977	0.77	0.68	0.86	1.06
Banf1	Banf1_T2	1.58	1.26	1.01	0.70
Banf1	Banf1_S4	1.62	1.68	0.85	0.71
Banf1	Banf1_T3	1.62	1.68	0.90	1.47
Baz1b	Baz1b_S1468	1.45	1.06	1.72	0.53
Baz1b	Baz1b_S1464	0.86	0.79	1.25	0.58
Baz1b	Baz1b_S1338	1.41	1.43	1.38	0.67
Baz2a	Baz2a_S1172	1.07	0.81	1.18	0.83
Baz2a	Baz2a_S1040	0.59	0.55	1.61	1.41
Baz2a	Baz2a_T1039	0.59	0.55	1.61	1.41
Bbc3	Bbc3_S10	1.13	1.43	1.32	1.65
Bckdk	Bckdk_T32	0.89	0.96	0.00	0.00
Bckdk	Bckdk_S31	0.82	0.86	0.64	0.61
Bcl7b	Bcl7b_S122	0.28	0.34	0.97	1.04
Bcl9	Bcl9_S686	0.85	0.78	0.76	0.83
Bcl9l	Bcl9l_S21	0.68	0.67	1.19	1.20
Bclaf1	Bclaf1_S183	0.35	0.42	0.29	0.41
Bclaf1	Bclaf1_S284	0.86	0.94	0.58	0.51
Bclaf1	Bclaf1_S289	1.33	1.16	0.58	0.51
Bclaf1	Bclaf1_S516	0.97	1.18	0.53	0.51
Bclaf1	Bclaf1_S510	0.84	0.82	0.65	0.63
Bclaf1	Bclaf1_S299	0.88	0.86	0.71	0.65
Bclaf1	Bclaf1_S529	0.99	1.02	0.88	0.71
Bclaf1	Bclaf1_S688	1.22	1.13	0.93	0.74

Bclaf1	Bclaf1_S656	1.12	1.28	0.87	0.75
Bclaf1	Bclaf1_S177	0.77	0.90	0.84	0.76
Bclaf1	Bclaf1_S395	1.03	0.95	0.96	0.81
Bclaf1	Bclaf1_S494	0.82	0.82	0.83	0.85
Bclaf1	Bclaf1_S267	0.98	0.85	0.84	0.87
Bclaf1	Bclaf1_T305	0.73	1.37	0.81	0.92
Bcr	Bcr_Y178	0.90	0.76	0.00	0.00
Bicd2	Bicd2_S504	0.67	0.57	0.70	0.73
Bicd2	Bicd2_S743	0.72	0.57	0.78	0.77
Bin2	Bin2_S460	0.33	0.33	0.50	1.41
Bin2	Bin2_S409	1.12	0.87	0.96	2.35
Bmp2k	Bmp2k_S908	0.96	0.84	1.17	1.07
Bnip2	Bnip2_S114	1.48	1.55	0.91	0.78
Bnip3	Bnip3_S79	1.05	1.19	0.58	0.87
Bnip3	Bnip3_S85	1.15	1.18	0.96	0.92
Bnip3	Bnip3_S88	1.41	1.70	0.74	1.03
Bnip3	Bnip3_T86	1.52	1.63	0.73	1.15
Bnip3l	Bnip3l_S63	0.91	0.89	0.91	0.95
Bnip3l	Bnip3l_S64	1.23	0.96	0.91	0.95
Bnip3l	Bnip3l_S62	1.24	0.92	0.85	0.96
Bnip3l	Bnip3l_S61	1.56	1.03	0.85	0.96
Bnip3l	Bnip3l_S119	1.18	1.63	0.76	1.01
Bod1l	Bod1l_S2968	0.75	0.75	0.84	0.47
Bod1l	Bod1l_S3000	0.55	0.57	0.57	0.59
Bod1l	Bod1l_S482	0.78	0.71	0.78	0.87
Bod1l	Bod1l_S480	0.90	0.71	0.78	0.87
Bod1l	Bod1l_S3010	0.68	0.68	0.67	0.88
Bola1	Bola1_S81	1.19	1.10	2.15	1.37
Bop1	Bop1_S11	0.88	0.82	1.08	0.79
Bptf	Bptf_S1197	1.42	1.20	1.22	1.14
Bptf	Bptf_S2353	1.94	2.24	1.35	1.15
Bptf	Bptf_S1559	1.44	1.25	1.47	1.27
Braf	Braf_S135	0.55	0.57	0.54	0.88
Braf	Braf_S454	1.52	1.72	0.84	1.02
Braf	Braf_S766	0.85	0.81	0.66	1.03
Brca1	Brca1_S706	0.88	0.92	0.71	0.35
Brd1	Brd1_S128	0.95	1.06	1.20	1.08
Brd1	Brd1_S906	0.30	0.34	0.82	1.44
Brd2	Brd2_S297	0.65	0.78	0.63	0.58
Brd2	Brd2_S300	0.65	0.78	0.68	0.99
Brd3	Brd3_S262	0.71	0.71	0.52	0.57
Brd4	Brd4_S1086	0.58	0.64	0.56	0.64
Brd4	Brd4_S1153	1.08	1.11	0.78	1.00
Brd7	Brd7_S279	1.24	1.05	1.06	1.06
Brf1	Brf1_S552	0.80	0.80	0.90	0.73
Brwd1	Brwd1_S1830	0.74	0.68	2.01	2.24
Btk	Btk_Y134	0.73	0.53	0.91	1.35
Bud13	Bud13_S297	0.81	0.82	0.85	0.71
Bud13	Bud13_T131	1.00	0.99	0.63	0.72
Bud13	Bud13_S187	2.53	2.58	0.63	0.74
Bud13	Bud13_T183	2.53	2.58	0.63	0.74
Bud13	Bud13_S135	1.00	7.06	0.68	0.75
Bud13	Bud13_S148	0.69	0.63	0.65	0.77
Bud13	Bud13_T144	0.96	0.95	0.65	0.77
Bud13	Bud13_S341	0.59	0.65	0.62	0.78

Bud13	Bud13_S344	1.15	0.95	0.62	0.78
Bud13	Bud13_T196	1.28	1.23	0.80	0.85
Bud13	Bud13_S238	1.13	1.03	0.73	0.99
Bud13	Bud13_S200	1.08	0.96	0.87	1.13
C230081A13Rik	C230081A13Rik_S569	0.55	0.72	2.27	2.31
C230081A13Rik	C230081A13Rik_S282	1.05	1.08	0.98	2.66
C2cd5	C2cd5_S305	1.49	1.52	0.00	0.00
Calm1	Calm1_Y100	0.80	0.89	1.26	7.84
Canx	Canx_S582	1.55	1.59	1.53	1.69
Cap1	Cap1_S307	0.33	0.29	1.48	4.50
Cap1	Cap1_Y418	0.62	0.63	1.89	5.81
Capza1	Capza1_S9	0.53	0.57	0.50	1.05
Capza2	Capza2_S9	1.73	0.90	0.69	1.00
Carhsp1	Carhsp1_S33	0.44	0.44	0.32	0.47
Carhsp1	Carhsp1_S31	0.38	0.38	0.21	0.54
Carhsp1	Carhsp1_S42	0.31	0.35	0.31	0.82
Carhsp1	Carhsp1_S53	0.45	0.46	0.56	1.33
Casp7	Casp7_S16	0.53	0.40	0.00	0.00
Casp7	Casp7_S17	0.70	0.60	0.00	0.00
Casp8	Casp8_S188	1.21	1.15	0.53	0.56
Casp8ap2	Casp8ap2_S560	0.45	0.39	0.52	0.27
Casp8ap2	Casp8ap2_S923	0.57	0.55	0.80	0.50
Cast	Cast_T445	0.46	0.42	1.39	1.19
Cbfa2t3	Cbfa2t3_S39	0.73	0.75	1.16	0.90
Cbfb	Cbfb_S134	0.92	0.91	0.92	0.87
Cbl	Cbl_S481	0.80	0.84	0.00	0.00
Cblb	Cblb_S480	0.96	0.92	1.39	0.57
Cbx5	Cbx5_S93	0.82	0.81	0.74	0.67
Cbx8	Cbx8_S284	2.07	1.76	1.48	1.58
Cc2d1b	Cc2d1b_S520	1.18	1.24	1.74	2.32
Ccdc12	Ccdc12_S165	0.83	0.93	1.01	1.02
Ccdc55	Ccdc55_S33	2.15	1.62	0.87	0.41
Ccdc55	Ccdc55_S31	0.87	0.88	1.03	1.01
Ccdc6	Ccdc6_S237	1.08	1.14	1.05	1.29
Ccdc6	Ccdc6_S233	1.08	1.14	1.22	2.12
Ccdc86	Ccdc86_S18	0.62	0.66	1.36	1.27
Ccdc88b	Ccdc88b_S649	1.26	1.15	1.33	1.17
Ccdc88b	Ccdc88b_S1413	3.36	2.51	1.74	1.24
Ccdc88b	Ccdc88b_S656	0.68	0.75	1.05	1.28
Ccdc94	Ccdc94_S211	0.90	0.86	0.68	0.76
Ccdc94	Ccdc94_S213	0.88	0.78	0.91	1.21
Ccnd3	Ccnd3_S264	0.73	0.47	1.26	1.42
Ccnk	Ccnk_S329	0.73	0.74	0.97	0.80
Ccnk	Ccnk_S325	1.08	1.05	0.97	0.80
Ccnk	Ccnk_S341	1.15	1.14	1.20	1.03
Ccnl1	Ccnl1_S347	0.21	0.20	0.00	0.00
Ccnl1	Ccnl1_S341	0.33	0.31	0.61	0.65
Ccnl1	Ccnl1_S358	0.47	0.49	0.52	0.94
Ccnt2	Ccnt2_S477	1.42	1.40	1.05	0.63
Ccny	Ccny_S326	1.32	1.34	1.44	0.98
Ccnyl1	Ccnyl1_S276	1.31	1.37	1.17	0.76
Cct8	Cct8_S537	0.90	0.96	0.51	0.86
Cct8	Cct8_Y30	0.50	0.84	0.77	34.29
Cd2ap	Cd2ap_S458	0.97	0.79	0.47	0.55
Cd2ap	Cd2ap_S514	0.27	0.27	0.66	0.65

Cd2ap	Cd2ap_S404	0.57	0.60	0.78	1.15
Cd2ap	Cd2ap_S510	0.59	0.54	1.69	1.96
Cd3eap	Cd3eap_S170	0.50	0.51	0.00	0.00
Cd69	Cd69_S26	0.26	0.25	1.07	3.01
Cd69	Cd69_S7	0.40	0.35	1.05	4.99
Cd84	Cd84_Y265	0.23	0.19	0.70	4.72
Cdc23	Cdc23_S588	1.56	1.55	0.80	0.91
Cdc26	Cdc26_S42	0.55	0.59	0.92	1.10
Cdca2	Cdca2_S626	0.94	0.71	1.04	0.77
Cdca8	Cdca8_S228	0.46	0.41	0.71	0.66
Cdk1	Cdk1_Y15	0.67	0.76	0.91	0.53
Cdk1	Cdk1_T14	0.75	0.76	0.92	0.57
Cdk11b	Cdk11b_S578	0.83	0.84	0.71	0.58
Cdk11b	Cdk11b_S741	0.99	0.80	0.78	0.80
Cdk11b	Cdk11b_T740	1.20	1.02	0.78	0.80
Cdk11b	Cdk11b_S270	2.49	2.28	1.63	0.88
Cdk12	Cdk12_S681	0.94	0.79	0.81	0.00
Cdk12	Cdk12_S677	0.99	0.93	0.81	0.00
Cdk12	Cdk12_S1079	0.96	1.08	0.62	0.67
Cdk12	Cdk12_T688	0.87	0.71	0.77	0.69
Cdk12	Cdk12_S331	1.10	0.98	1.27	1.12
Cdk12	Cdk12_S333	1.55	1.56	1.27	1.12
Cdk12	Cdk12_S332	1.55	1.56	1.23	1.16
Cdk12	Cdk12_S302	0.95	0.74	1.36	1.26
Cdk12	Cdk12_S300	1.51	1.48	1.36	1.26
Cdk13	Cdk13_T1185	2.41	2.73	2.05	1.18
Cdk13	Cdk13_S438	1.40	1.46	1.45	1.19
Cdk13	Cdk13_S440	1.40	1.46	1.45	1.19
Cdk13	Cdk13_S326	2.27	2.24	1.69	1.33
Cdk13	Cdk13_S316	2.27	2.24	2.59	1.67
Cdk13	Cdk13_S318	2.27	2.24	2.59	1.67
Cdk2	Cdk2_Y19	0.74	0.87	0.25	0.12
Cdk2	Cdk2_T14	0.32	0.26	0.87	0.27
Cdk2	Cdk2_Y15	0.53	0.63	0.71	0.40
Cdk4	Cdk4_S300	1.04	1.23	0.96	0.87
Cdk5rap2	Cdk5rap2_S1816	0.58	0.62	0.00	0.00
Cdk5rap2	Cdk5rap2_S485	0.90	0.79	2.25	0.87
Cdk7	Cdk7_S164	1.51	1.43	1.49	0.94
Cdkn1a	Cdkn1a_S2	0.67	0.86	0.37	1.66
Cdkn1a	Cdkn1a_S78	0.59	0.59	0.27	1.73
Cdkn1b	Cdkn1b_S10	8.68	14.56	2.47	0.91
Cds2	Cds2_S32	0.61	0.57	0.00	0.00
Cds2	Cds2_T30	0.69	0.74	0.00	0.00
Cebpd	Cebpd_S10	0.42	0.36	1.44	2.82
Cenpc1	Cenpc1_S302	0.76	0.75	0.94	0.42
Cenpc1	Cenpc1_S699	1.19	1.18	1.01	0.46
Cenpc1	Cenpc1_S158	1.00	0.95	1.28	0.55
Cenpc1	Cenpc1_S156	1.13	0.84	1.23	0.60
Cep170	Cep170_S1188	0.46	0.54	0.42	0.32
Cep170	Cep170_S443	0.90	1.07	0.63	0.88
Cep55	Cep55_S433	0.44	2.04	0.34	0.58
Cep55	Cep55_S422	0.24	0.40	0.83	3.78
Cep55	Cep55_S425	0.61	0.53	0.83	3.78
Cfdp1	Cfdp1_S203	0.39	0.47	1.27	2.11
Cfl1	Cfl1_S3	2.28	2.70	0.95	0.96

Cfl1	Cfl1_Y140	0.97	0.99	1.00	5.14
Cgref1	Cgref1_T3	0.01	0.00	0.03	0.01
Champ1	Champ1_S425	0.50	0.40	0.76	0.77
Champ1	Champ1_S603	1.92	1.87	1.18	0.90
Champ1	Champ1_S405	0.95	1.05	1.02	0.98
Champ1	Champ1_S448	0.63	0.63	1.30	1.11
Champ1	Champ1_S532	1.33	1.54	1.44	1.40
Champ1	Champ1_S421	0.62	0.66	1.11	2.85
Champ1	Champ1_S416	0.83	0.90	1.11	2.85
Chd1	Chd1_S1678	1.61	1.61	1.52	1.03
Chd1	Chd1_S1674	1.61	1.58	1.53	1.05
Chd1	Chd1_S5	1.21	1.15	2.50	1.34
Chd2	Chd2_S1365	1.07	1.14	0.73	0.62
Chd3	Chd3_S1653	1.61	1.48	1.35	0.89
Chd3	Chd3_S1651	1.62	1.49	1.40	0.93
Chd3	Chd3_S765	1.51	1.34	0.82	1.10
Chd4	Chd4_S1528	0.67	0.62	0.65	0.64
Chmp2b	Chmp2b_S199	0.97	0.92	0.80	1.38
Chrac1	Chrac1_S122	0.85	0.82	0.66	0.72
Chtf18	Chtf18_S91	0.73	1.14	0.54	0.45
Cic	Cic_S902	0.96	0.76	1.19	1.01
Cic	Cic_S1377	0.80	0.87	0.82	1.17
Ciz1	Ciz1_S731	0.53	0.50	0.66	0.70
Clasp1	Clasp1_S600	1.80	1.94	0.64	0.71
Clasp2	Clasp2_S376	6.18	2.32	0.61	0.81
Clcc1	Clcc1_S429	0.86	0.73	0.62	0.90
Clk4	Clk4_S138	0.89	0.75	0.55	0.77
Clns1a	Clns1a_S3	0.61	0.59	0.90	2.42
Cltc	Cltc_T394	1.08	0.95	0.76	0.27
Cmtm7	Cmtm7_S5	1.08	1.07	1.88	4.43
Cnot4	Cnot4_S429	0.98	0.75	0.00	0.00
Coil	Coil_S225	0.68	0.59	0.68	0.79
Comt	Comt_S261	0.68	0.79	0.75	1.51
Copa	Copa_Y579	0.53	0.49	0.60	0.99
Copa	Copa_S173	0.45	0.49	0.61	2.89
Copb2	Copb2_S860	0.32	0.26	0.00	0.00
Copb2	Copb2_S859	0.31	0.27	0.00	0.00
Coro1a	Coro1a_T418	1.30	1.21	1.53	1.32
Cpne3	Cpne3_Y392	0.66	0.68	0.57	1.02
Cry2	Cry2_S557	0.60	0.67	0.68	0.99
Csf2rb	Csf2rb_S790	0.56	0.82	2.51	3.55
Csf2rb	Csf2rb_S789	0.60	0.73	2.19	4.64
Csnk2b	Csnk2b_S209	0.36	0.37	0.92	0.67
Cstf3	Cstf3_S691	0.92	0.78	0.82	0.77
Ctdp1	Ctdp1_S730	1.99	2.18	1.55	1.07
Ctdspl2	Ctdspl2_S165	0.63	1.03	0.00	0.00
Ctr9	Ctr9_T925	0.83	0.77	1.00	0.70
Cul4b	Cul4b_T106	0.40	0.48	0.48	0.61
D10Wsu102e	D10Wsu102e_S177	1.13	1.38	1.17	0.78
D17Wsu92e	D17Wsu92e_S215	2.19	1.27	0.58	0.70
Dap	Dap_S3	1.27	0.94	1.65	5.29
Dbi	Dbi_S2	0.37	0.36	0.02	8.48
Dbr1	Dbr1_S505	0.62	0.50	0.87	1.02
Dcaf10	Dcaf10_S50	0.79	0.68	0.59	1.02
Dck	Dck_S11	1.51	1.32	1.45	0.67

Dcp1a	Dcp1a_S543	0.56	0.56	0.62	0.54
Dcp1a	Dcp1a_S545	0.43	0.44	1.63	1.28
Ddb1	Ddb1_Y193	0.46	0.58	0.67	1.01
Ddx17	Ddx17_Y200	0.50	0.55	0.85	9.97
Ddx20	Ddx20_S472	0.53	0.49	0.39	0.41
Ddx20	Ddx20_S569	0.47	0.55	0.77	1.22
Ddx21	Ddx21_T114	0.72	0.63	0.00	0.00
Ddx21	Ddx21_S245	0.77	0.63	0.95	0.64
Ddx21	Ddx21_S244	0.75	0.73	0.95	0.64
Ddx21	Ddx21_S243	0.99	0.99	0.95	0.64
Ddx21	Ddx21_S118	0.72	0.63	0.93	0.84
Ddx21	Ddx21_S144	1.01	1.02	2.58	1.04
Ddx21	Ddx21_S155	0.62	0.53	1.03	1.06
Ddx21	Ddx21_S192	0.65	0.61	1.05	1.20
Ddx23	Ddx23_S14	0.75	0.64	0.53	0.73
Ddx23	Ddx23_S106	0.77	0.72	0.74	1.03
Ddx23	Ddx23_S108	0.77	0.72	0.74	1.03
Ddx24	Ddx24_S80	0.84	0.74	1.83	1.71
Ddx42	Ddx42_S185	0.82	0.90	0.88	1.13
Ddx51	Ddx51_S77	1.34	1.17	1.51	1.35
Ddx55	Ddx55_S540	1.00	1.07	1.15	0.59
Dennd1a	Dennd1a_S592	1.33	1.36	0.88	0.92
Dennd1c	Dennd1c_S699	0.40	0.41	0.39	1.09
Dffa	Dffa_S314	1.62	1.56	1.25	0.53
Dgcr14	Dgcr14_S295	1.22	1.03	1.31	1.10
Dhx16	Dhx16_S103	0.85	0.84	0.73	0.61
Dido1	Dido1_S1256	0.91	0.90	0.83	0.91
Dis3l2	Dis3l2_S864	1.10	1.08	0.93	0.78
Dis3l2	Dis3l2_S12	2.23	2.42	1.23	0.96
Dkc1	Dkc1_S453	0.84	0.71	0.58	0.46
Dkc1	Dkc1_S455	0.80	0.68	0.84	0.61
Dkc1	Dkc1_S508	0.98	0.99	0.88	0.69
Dkc1	Dkc1_S451	0.84	0.71	1.74	0.69
Dkc1	Dkc1_S481	0.65	0.63	1.08	1.07
Dlgap5	Dlgap5_S70	0.49	0.58	0.71	0.57
Dlgap5	Dlgap5_S328	0.64	0.58	1.15	0.96
Dnajc21	Dnajc21_S283	0.81	0.74	0.94	1.22
Dnajc5	Dnajc5_S10	1.37	1.32	1.27	1.13
Dnajc6	Dnajc6_S557	2.71	2.81	4.54	2.09
Dnmt1	Dnmt1_S958	0.78	0.81	0.87	0.57
Dnmt1	Dnmt1_S140	0.53	0.47	2.67	1.13
Dnmt1	Dnmt1_S140	0.85	0.84	2.67	1.13
Dnmt1	Dnmt1_S285	1.21	0.98	1.87	2.11
Dnmt3a	Dnmt3a_T120	0.79	0.78	0.74	0.45
Dnmt3a	Dnmt3a_S102	0.54	0.56	0.48	0.50
Dock10	Dock10_S877	2.14	1.89	2.74	1.61
Dock11	Dock11_S1237	1.03	0.76	0.00	0.00
Dock2	Dock2_S1729	0.95	0.87	0.43	0.51
Dock2	Dock2_S1704	2.49	2.12	0.77	0.99
Dock2	Dock2_S1683	0.69	0.77	1.02	2.24
Dock5	Dock5_S1765	1.47	1.04	0.69	0.40
Dock5	Dock5_S1788	1.02	0.88	5.35	4.16
Dock8	Dock8_S2097	0.60	0.75	1.34	2.03
Dok3	Dok3_S274	0.59	0.63	0.69	1.23
Dot1l	Dot1l_S1105	0.67	0.66	0.92	1.04

Dot1l	Dot1l_S373	0.89	1.00	1.26	1.28
Dpf2	Dpf2_S142	1.60	1.40	0.43	0.37
Dpysl2	Dpysl2_T509	0.97	2.60	1.16	0.82
Dsn1	Dsn1_S344	1.06	1.03	0.61	0.38
Dstn	Dstn_S3	3.76	4.42	0.74	0.93
Dtd1	Dtd1_S197	1.11	1.05	1.07	1.72
Dtd1	Dtd1_S196	0.84	0.85	0.97	2.74
Dtl	Dtl_T515	0.62	0.52	0.82	0.60
Dtx3l	Dtx3l_S9	1.14	1.05	0.98	1.11
Dync1li1	Dync1li1_T515	1.17	0.80	0.00	0.00
Dync1li1	Dync1li1_S510	0.57	0.52	0.64	0.59
Dync1li1	Dync1li1_S405	1.30	1.90	0.75	0.92
Dync1li1	Dync1li1_S516	0.70	0.83	1.09	1.00
Dync1li1	Dync1li1_S207	0.53	0.55	1.30	2.81
Dync1li1	Dync1li1_T513	0.62	0.67	7.35	2.96
Dyrk1b	Dyrk1b_Y273	1.25	1.23	1.34	1.59
Dyrk3	Dyrk3_Y368	0.72	5.01	0.55	0.48
E2f8	E2f8_S102	0.71	0.65	0.74	0.50
Eaf1	Eaf1_S165	0.78	0.85	0.95	1.85
Ebag9	Ebag9_S36	0.96	1.03	1.05	1.18
Edc4	Edc4_S868	0.79	0.77	0.40	0.65
Eef1d	Eef1d_S133	0.67	0.69	1.31	1.10
Eef1d	Eef1d_S162	0.75	0.67	1.05	1.16
Eef1d	Eef1d_S118	0.70	0.69	0.92	1.43
Eef1d	Eef1d_Y182	0.72	0.55	0.81	2.01
Eef2	Eef2_T57	0.75	0.74	0.48	1.20
Efhd2	Efhd2_S74	1.14	1.29	0.66	0.69
Efr3a	Efr3a_S692	1.63	1.91	1.25	0.99
Egln1	Egln1_S131	0.54	0.41	0.00	0.00
Egln1	Egln1_S129	0.60	0.40	0.38	0.71
Ei24	Ei24_S348	0.40	0.40	0.27	0.33
Ei24	Ei24_S74	1.03	0.96	0.53	0.62
Eif2ak3	Eif2ak3_S711	0.99	1.20	1.08	1.42
Eif2b5	Eif2b5_S540	1.29	1.24	1.19	0.97
Eif2s1	Eif2s1_Y82	0.51	0.61	0.89	5.27
Eif2s2	Eif2s2_S2	0.86	0.86	0.89	1.03
Eif3a	Eif3a_Y72	0.42	0.51	0.62	1.08
Eif3b	Eif3b_S90	0.61	0.45	0.79	0.84
Eif3b	Eif3b_S120	1.60	1.63	1.29	0.85
Eif3b	Eif3b_S68	0.53	0.57	0.83	1.09
Eif3b	Eif3b_T74	1.05	1.01	1.36	1.23
Eif3b	Eif3b_S79	0.88	0.92	1.45	1.28
Eif3b	Eif3b_S75	0.62	0.69	1.49	1.46
Eif3b	Eif3b_S111	0.28	0.24	0.65	1.75
Eif3c	Eif3c_S39	0.89	0.82	1.20	1.08
Eif4a1	Eif4a1_Y197	0.48	0.49	0.74	9.53
Eif4a3	Eif4a3_S12	1.17	1.22	1.35	0.81
Eif4a3	Eif4a3_Y202	0.44	0.51	1.02	10.12
Eif4b	Eif4b_S498	0.27	0.29	0.74	0.85
Eif4b	Eif4b_S497	0.43	0.54	0.92	1.01
Eif4ebp1	Eif4ebp1_T69	0.54	0.43	0.93	0.97
Eif4enif1	Eif4enif1_S925	0.94	0.89	1.17	0.89
Eif4enif1	Eif4enif1_S539	1.17	1.18	1.18	1.06
Eif4g1	Eif4g1_S1180	1.19	1.48	0.91	0.52
Eif4g1	Eif4g1_S1204	1.05	1.05	0.91	0.71

Eif4g1	Eif4g1_S1182	0.85	0.79	0.76	0.86
Eif4g1	Eif4g1_S1224	0.50	0.53	0.98	1.33
Eif4g2	Eif4g2_T469	0.47	0.54	0.63	0.71
Eif4g3	Eif4g3_S274	2.76	2.77	3.16	1.67
Eif5b	Eif5b_S139	0.97	1.53	0.00	0.00
Eif5b	Eif5b_S215	0.73	0.74	0.70	0.82
Eif5b	Eif5b_S137	0.90	0.93	1.02	0.96
Eif5b	Eif5b_S114	0.69	0.74	0.70	2.63
Elac2	Elac2_S797	1.08	0.93	0.81	0.55
Elf1	Elf1_S334	1.06	1.08	0.85	0.71
Elf1	Elf1_S187	1.00	0.98	1.02	0.94
Elf4	Elf4_S187	0.77	0.72	0.95	0.64
Ell	Ell_S300	0.53	0.57	0.00	0.00
Ell	Ell_S299	0.65	0.66	0.00	0.00
Ell	Ell_S310	0.53	0.52	0.79	1.18
Eml4	Eml4_S144	0.60	0.58	1.24	0.55
Eml4	Eml4_S146	1.27	1.12	0.65	0.78
Enah	Enah_T460	1.49	1.60	1.50	1.12
Enkd1	Enkd1_S52	0.83	0.73	0.88	0.43
Ep400	Ep400_S662	1.31	1.12	2.79	1.51
Epb4.1l2	Epb4.1l2_S38	0.60	0.56	0.41	0.76
Eps15l1	Eps15l1_S255	0.72	0.77	1.31	0.97
Erbb2ip	Erbb2ip_S849	0.63	0.60	1.01	0.62
Ercc5	Ercc5_S341	0.77	0.63	0.55	0.39
Ercc5	Ercc5_S384	1.02	0.97	0.56	0.41
Esco2	Esco2_S200	0.77	0.86	0.68	0.23
Esf1	Esf1_S156	0.58	0.64	0.78	0.68
Espl1	Espl1_S1504	0.48	0.46	0.70	0.60
Etv6	Etv6_S215	0.52	0.52	0.59	1.87
Etv6	Etv6_T18	0.44	0.48	0.53	2.09
Etv6	Etv6_S22	0.41	0.37	0.45	2.47
Evi2a-evi2b	Evi2a-evi2b_S295	1.12	1.02	1.17	1.45
Evi2a-evi2b	Evi2a-evi2b_T250	1.19	1.50	3.64	1.59
Exosc5	Exosc5_S23	0.91	0.86	0.89	0.78
Exosc6	Exosc6_Y40	0.31	0.37	0.36	38.85
Ezh2	Ezh2_S358	2.57	2.42	0.00	0.00
Ezh2	Ezh2_T483	0.68	0.71	0.93	0.62
Ezh2	Ezh2_S359	2.71	2.56	0.90	0.72
Ezh2	Ezh2_T363	2.57	2.42	0.90	0.74
Faf1	Faf1_S581	0.95	0.83	0.71	1.13
Fam104a	Fam104a_S62	0.71	0.67	0.83	0.60
Fam111a	Fam111a_S59	0.61	0.58	0.43	0.31
Fam114a2	Fam114a2_S112	1.11	1.09	2.72	4.98
Fam117b	Fam117b_S10	0.54	0.53	0.37	0.39
Fam117b	Fam117b_S190	0.78	0.64	0.29	0.39
Fam122a	Fam122a_S144	0.98	1.28	1.24	0.95
Fam122a	Fam122a_S34	1.12	1.36	1.00	1.28
Fam122a	Fam122a_S73	1.56	1.88	1.23	1.61
Fam122a	Fam122a_S140	1.55	1.90	1.15	1.73
Fam122b	Fam122b_S115	0.70	0.88	0.25	0.39
Fam122b	Fam122b_S119	0.70	0.88	0.25	0.39
Fam129a	Fam129a_S581	2.70	2.71	0.00	0.00
Fam195b	Fam195b_S21	0.56	0.56	1.36	1.98
Fam207a	Fam207a_S38	0.61	0.67	0.90	0.97
Fam21	Fam21_S157	0.98	1.13	0.35	0.59

Fam21	Fam21_S747	0.96	1.00	0.76	1.05
Fam21	Fam21_S159	0.98	1.13	1.04	1.13
Fam21	Fam21_S533	0.67	0.61	0.64	1.91
Fam53c	Fam53c_S122	0.94	1.00	0.89	0.60
Fam53c	Fam53c_S299	0.83	0.89	1.16	1.04
Fam63a	Fam63a_S103	0.32	0.32	1.66	5.37
Fam64a	Fam64a_S128	0.80	0.76	2.30	0.76
Fam64a	Fam64a_S72	1.36	1.12	4.12	1.51
Fam65a	Fam65a_S347	0.64	0.99	0.74	1.13
Fam83h	Fam83h_S948	0.60	0.44	0.81	0.98
Fam83h	Fam83h_S871	0.43	0.42	0.88	0.98
Fam83h	Fam83h_S915	0.41	0.44	0.75	1.14
Fam98c	Fam98c_S129	1.65	1.59	1.85	1.18
Fasn	Fasn_Y1057	0.79	0.75	0.91	4.80
Fbl	Fbl_S130	0.32	0.32	0.84	1.72
Fbxo42	Fbxo42_S365	0.99	0.88	1.24	0.95
Fcho2	Fcho2_S487	0.82	0.83	0.63	0.43
Fgd3	Fgd3_T732	0.74	0.76	1.24	1.24
Fhod1	Fhod1_S514	0.75	0.78	0.43	0.99
Fhod1	Fhod1_S527	0.50	0.47	0.68	1.15
Fip1l1	Fip1l1_S479	1.32	1.24	1.02	0.71
Fip1l1	Fip1l1_S280	1.35	1.78	0.92	0.80
Fip1l1	Fip1l1_S235	0.64	0.67	1.36	0.85
Fip1l1	Fip1l1_S487	0.82	0.84	0.76	0.86
Flna	Flna_S1459	0.57	0.55	1.28	1.29
Flna	Flna_S1084	0.16	0.28	1.38	2.06
Fmnl1	Fmnl1_S1021	1.09	1.29	1.11	1.95
Fnbp4	Fnbp4_S485	0.77	0.71	0.52	0.81
Fnbp4	Fnbp4_S65	0.57	0.61	0.54	0.86
Fnbp4	Fnbp4_S486	0.84	0.78	0.64	1.00
Fndc3a	Fndc3a_S203	0.92	0.88	1.04	0.97
Fosl2	Fosl2_S200	0.92	0.97	1.16	1.56
Foxj3	Foxj3_S223	1.21	1.22	0.97	0.85
Foxk1	Foxk1_S406	1.98	1.16	0.68	0.55
Foxk1	Foxk1_S402	1.63	1.64	0.68	0.55
Foxk1	Foxk1_S431	0.93	1.15	0.79	0.70
Foxk2	Foxk2_S389	0.75	0.76	1.07	1.01
Frmd4a	Frmd4a_S385	1.27	1.27	1.96	2.17
Fryl	Fryl_S1915	1.99	2.28	1.15	0.67
Fryl	Fryl_T1916	1.99	2.28	1.15	0.67
Fryl	Fryl_S2273	1.04	1.10	1.48	2.40
Ftsjd2	Ftsjd2_S30	0.99	0.78	0.00	0.00
Ftsjd2	Ftsjd2_S27	0.93	0.78	1.41	1.04
Ftsjd2	Ftsjd2_T29	0.60	0.70	1.17	1.11
Fv1	Fv1_S244	0.80	0.82	1.26	1.43
Fxr1	Fxr1_S587	0.39	0.39	0.45	0.68
Fxr2	Fxr2_S603	1.06	1.04	0.96	1.04
Fxr2	Fxr2_S605	1.06	1.04	0.96	1.04
Fyb	Fyb_S203	0.24	0.21	0.00	0.00
Fyb	Fyb_S222	0.43	0.54	0.57	0.58
Fyb	Fyb_S28	1.01	1.05	0.64	0.60
G3bp1	G3bp1_Y125	0.39	0.46	0.82	0.78
G3bp1	G3bp1_S231	0.99	1.08	1.51	1.28
G3bp2	G3bp2_S225	0.38	0.60	0.95	0.54
G3bp2	G3bp2_T227	0.78	0.58	1.06	0.98

G6pdx	G6pdx_Y401	0.35	0.35	2.82	4.49
Gapdh	Gapdh_S208	1.04	0.81	0.85	0.72
Gapdh	Gapdh_S149	1.38	1.40	0.92	0.76
Gapdh	Gapdh_T209	1.02	0.89	0.90	0.80
Gapt	Gapt_T39	0.25	0.21	0.24	0.21
Gapvd1	Gapvd1_S740	0.72	0.66	0.00	0.00
Gapvd1	Gapvd1_S737	0.75	0.67	0.67	0.99
Gapvd1	Gapvd1_S882	2.09	3.14	2.17	2.31
Gapvd1	Gapvd1_S881	1.76	2.43	1.65	2.69
Gatad2a	Gatad2a_S110	2.59	1.16	0.96	0.49
Gatad2a	Gatad2a_S96	2.59	1.16	0.54	0.87
Gatad2a	Gatad2a_S103	0.66	0.67	0.52	0.87
Gatad2a	Gatad2a_T185	0.63	0.74	1.23	0.92
Gatad2b	Gatad2b_S130	0.46	0.50	0.75	0.84
Gatad2b	Gatad2b_S487	0.86	0.93	2.00	1.91
Gbf1	Gbf1_S1298	0.88	1.03	0.82	1.27
Gcfc2	Gcfc2_S118	1.28	1.56	0.70	0.89
Gdpd4	Gdpd4_S210	1.52	42.07	0.00	0.00
Gemin4	Gemin4_S84	0.43	0.52	0.67	1.77
Gemin5	Gemin5_S1413	0.83	0.78	0.89	0.63
Gemin5	Gemin5_S48	1.44	1.48	0.98	1.53
Gfpt1	Gfpt1_S243	0.51	0.60	0.65	0.87
Gigyf2	Gigyf2_S26	0.62	0.44	0.83	1.23
Git1	Git1_S370	1.03	1.31	0.71	2.52
Git1	Git1_S371	1.16	1.17	0.88	2.89
Gltscr1	Gltscr1_S1427	1.07	0.88	0.76	0.68
Gltscr2	Gltscr2_S329	0.87	0.99	1.81	1.03
Gm10257	Gm10257_S29	2.63	2.78	2.06	0.55
Gm13202	Gm13202_S45	0.55	0.57	0.70	0.82
Gm15070	Gm15070_T107	0.06	0.03	0.06	0.03
Gm15070	Gm15070_S109	0.13	0.06	0.05	0.04
Gm2382	Gm2382_S8	1.78	1.45	1.13	1.90
Gm5506	Gm5506_Y25	0.57	0.62	0.48	0.88
Gm5506	Gm5506_S419	1.39	1.03	1.00	1.01
Gm5506	Gm5506_Y44	1.35	1.57	0.83	1.05
Gm7429	Gm7429_S10	0.42	0.43	1.24	1.24
Gm8264	Gm8264_S42	1.51	1.31	1.52	1.03
Gm8264	Gm8264_T41	1.56	1.33	1.60	1.08
Gm9846	Gm9846_S11	0.39	0.37	0.96	0.81
Gmip	Gmip_S433	1.39	1.23	1.43	0.91
Gmip	Gmip_S436	0.96	0.87	0.79	1.21
Gmip	Gmip_S440	1.02	1.02	1.11	1.43
Gmps	Gmps_S332	0.75	0.91	0.69	0.61
Gng12	Gng12_S7	0.81	0.69	0.00	0.00
Gng12	Gng12_S26	0.99	0.85	0.69	0.81
Gnl1	Gnl1_T48	0.87	0.88	0.00	0.00
Gnl1	Gnl1_S51	0.89	0.99	0.67	0.84
Gnl1	Gnl1_T50	0.86	0.90	0.55	1.08
Gnl3	Gnl3_S505	0.83	0.77	1.01	1.00
Gnl3	Gnl3_S95	1.08	1.16	1.28	1.13
Gnl3	Gnl3_S493	0.92	0.88	1.64	4.24
Golga4	Golga4_S93	2.60	2.48	1.03	1.91
Got2	Got2_Y75	0.29	0.37	0.56	7.12
Gpatch4	Gpatch4_S258	0.48	0.51	0.91	0.89
Gphn	Gphn_S194	0.75	0.98	1.16	0.88

Gphn	Gphn_S188	1.13	1.37	1.16	0.88
Gpi1	Gpi1_T109	0.66	0.68	0.60	0.49
Gpkow	Gpkow_S6	0.57	0.63	0.59	0.67
Gpn1	Gpn1_S314	1.11	1.05	1.98	2.90
Gpsm3	Gpsm3_S34	0.54	0.44	0.52	0.83
Gpsm3	Gpsm3_T85	0.53	0.42	0.79	1.24
Gpsm3	Gpsm3_S38	0.33	0.32	0.49	1.50
Gpx1	Gpx1_Y147	0.86	0.86	0.42	2.34
Grb7	Grb7_S364	0.68	0.74	1.02	1.74
Grlf1	Grlf1_Y1105	1.51	1.61	2.34	4.16
Gse1	Gse1_S823	0.77	0.67	0.72	0.48
Gse1	Gse1_S825	0.77	0.67	0.72	0.48
Gsk3b	Gsk3b_S215	1.02	0.99	1.17	1.24
Gsk3b	Gsk3b_Y216	1.07	1.04	1.24	1.28
Gsk3b	Gsk3b_S219	1.50	0.94	1.23	1.49
Gtf2f1	Gtf2f1_T331	1.07	1.07	0.82	0.86
Gtf2f1	Gtf2f1_T389	0.80	0.74	0.69	1.04
Gtf2i	Gtf2i_S634	1.09	1.16	0.96	0.74
Gtf3c3	Gtf3c3_Y467	0.68	0.65	1.44	0.86
Gtpbp1	Gtpbp1_S25	0.72	0.68	0.00	0.00
Gtpbp1	Gtpbp1_S6	0.66	0.47	0.27	0.40
Gtpbp1	Gtpbp1_S8	0.51	0.54	0.61	0.63
Gtpbp1	Gtpbp1_S47	0.82	0.61	0.91	0.93
Gtpbp1	Gtpbp1_S44	0.76	0.62	0.91	0.93
Gys1	Gys1_Y44	0.77	0.59	1.89	1.98
H2afy	H2afy_T177	1.32	1.19	0.00	0.00
H2afy	H2afy_T129	1.23	1.12	2.21	0.97
Hars2	Hars2_S66	0.93	0.86	0.64	0.69
Haus6	Haus6_S500	0.52	0.41	2.17	0.82
Haus6	Haus6_S386	0.48	0.57	0.80	1.28
Hdac1	Hdac1_S393	0.63	0.70	0.63	0.73
Hdac2	Hdac2_S422	1.54	1.38	1.07	0.65
Hdac2	Hdac2_S394	0.86	0.89	0.88	0.67
Hdac4	Hdac4_S629	0.85	0.72	0.71	0.54
Hdac7	Hdac7_S156	0.86	0.78	0.36	0.46
Hdgf	Hdgf_S132	0.68	0.71	0.84	0.74
Hdgf	Hdgf_S133	1.13	0.99	0.84	0.74
Hdgf	Hdgf_S202	0.77	0.86	0.64	0.80
Hdgf	Hdgf_S165	0.85	0.93	0.73	0.86
Hdgfrp2	Hdgfrp2_S366	0.72	0.72	0.78	1.04
Hdgfrp2	Hdgfrp2_S367	0.72	0.72	0.78	1.04
Hdgfrp2	Hdgfrp2_S454	1.16	1.08	0.41	1.66
Hdlbp	Hdlbp_S31	0.43	0.45	1.49	1.00
Heatr3	Heatr3_S144	0.77	0.73	0.78	0.96
Heatr6	Heatr6_S23	0.73	0.68	0.93	1.00
Helb	Helb_S1015	0.45	0.42	0.42	0.24
Helb	Helb_S946	0.79	0.70	0.48	0.44
Helb	Helb_S945	0.84	0.88	0.80	0.50
Helz	Helz_S1637	1.17	1.45	1.29	1.74
Hemgn	Hemgn_S213	4.02	4.67	3.19	1.05
Hipk2	Hipk2_Y354	0.83	0.86	0.95	0.98
Hipk3	Hipk3_Y359	1.36	1.29	0.88	1.01
Hirip3	Hirip3_S207	0.87	0.84	0.59	0.43
Hirip3	Hirip3_S208	0.87	0.84	0.59	0.43
Hirip3	Hirip3_S153	1.56	1.55	2.70	0.50

Hirip3	Hirip3_S134	0.60	0.73	0.68	0.57
Hirip3	Hirip3_T135	0.39	0.40	0.71	0.62
Hirip3	Hirip3_S152	0.91	0.84	3.09	0.66
Hirip3	Hirip3_S575	0.68	0.66	1.31	0.88
Hist1h1a	Hist1h1a_S2	4.07	2.37	2.64	0.52
Hist1h1a	Hist1h1a_S12	5.12	2.67	4.41	0.62
Hist1h1b	Hist1h1b_S2	2.93	1.93	2.00	0.43
Hist1h1b	Hist1h1b_S18	1.87	1.21	3.00	1.59
Hist1h1c	Hist1h1c_S2	4.74	2.52	2.20	0.30
Hist1h1d	Hist1h1d_S37	3.71	2.21	0.72	0.15
Hist1h1d	Hist1h1d_T18	3.78	2.75	1.19	0.33
Hist1h1d	Hist1h1d_T4	3.72	1.82	1.66	0.34
Hist1h1d	Hist1h1d_S2	3.27	2.18	1.86	0.48
Hist1h1e	Hist1h1e_T35	2.28	1.37	1.18	0.13
Hist1h1e	Hist1h1e_T18	2.44	1.87	2.46	0.14
Hist1h1e	Hist1h1e_S36	1.95	1.08	0.99	0.14
Hist1h1e	Hist1h1e_S187	1.27	0.76	2.13	0.26
Hist1h1e	Hist1h1e_S2	2.79	1.66	1.72	0.93
Hist1h2bk	Hist1h2bk_Y41	0.71	0.70	0.48	0.36
Hist1h2bk	Hist1h2bk_Y43	0.59	0.63	0.70	1.54
Hist1h3f	Hist1h3f_S58	2.91	2.21	1.97	0.51
Hist1h3f	Hist1h3f_Y42	1.66	1.29	1.78	0.83
Hist1h4i	Hist1h4i_S48	0.91	0.85	1.96	1.27
Hist1h4i	Hist1h4i_Y52	0.51	0.87	0.60	4.16
Hmg20a	Hmg20a_S104	0.76	0.80	0.87	0.93
Hmga1	Hmga1_S8	1.05	0.66	0.00	0.00
Hmga1	Hmga1_S4	2.20	3.12	0.00	0.00
Hmga1	Hmga1_S44	0.71	0.69	0.22	0.51
Hmga1	Hmga1_T53	1.37	1.45	0.68	0.71
Hmga1	Hmga1_S9	0.70	0.78	0.24	0.92
Hmga1	Hmga1_S103	0.87	0.79	1.08	1.36
Hmga1	Hmga1_S102	0.98	0.84	1.08	1.36
Hmga1	Hmga1_S102	2.24	1.81	1.08	1.36
Hmga1	Hmga1_S99	0.58	0.55	1.07	1.48
Hmga1	Hmga1_S101	0.98	0.84	1.03	1.55
Hmga1	Hmga1_S6	1.73	1.90	1.26	1.76
Hmga1	Hmga1_S2	2.14	2.68	1.75	1.98
Hmha1	Hmha1_S577	0.93	0.72	1.26	1.60
Hmha1	Hmha1_S23	1.47	1.95	1.46	1.69
Hn1	Hn1_S87	0.37	0.46	1.04	0.96
Hnrnpa1	Hnrnpa1_S4	0.82	0.86	0.72	0.96
Hnrnpa1	Hnrnpa1_S2	0.86	0.87	0.98	0.97
Hnrnpa1	Hnrnpa1_S6	0.95	1.09	0.79	1.07
Hnrnpa1	Hnrnpa1_Y167	0.79	0.90	1.08	9.49
Hnrnpa3	Hnrnpa3_Y166	1.51	1.04	1.11	13.73
Hnrnpc	Hnrnpc_S228	0.60	0.67	0.67	0.71
Hnrnpc	Hnrnpc_S216	0.65	0.77	1.07	0.87
Hnrnpc	Hnrnpc_S219	0.60	0.70	0.89	1.19
Hnrnpf	Hnrnpf_S104	0.89	1.01	0.83	1.23
Hnrnph2	Hnrnph2_S104	0.68	0.74	0.66	1.47
Hnrnpk	Hnrnpk_S284	1.07	1.11	0.90	0.83
Hnrnpk	Hnrnpk_S216	1.24	1.28	0.84	1.01
Hnrnpu	Hnrnpu_S58	1.75	1.44	0.52	0.49
Hnrnpu	Hnrnpu_S4	0.76	0.82	0.95	0.53
Hnrnpu	Hnrnpu_S3	0.90	0.89	1.01	0.68

Hnrnpul2	Hnrnpul2_S159	0.62	0.71	0.51	0.74
Hnrpll	Hnrpll_S37	0.61	0.57	0.43	0.80
Hps5	Hps5_S629	0.89	1.21	2.51	2.45
Hsd17b4	Hsd17b4_S3	0.97	0.99	0.65	0.54
Hsf1	Hsf1_S303	0.42	0.35	0.59	0.81
Hsf1	Hsf1_S307	0.65	0.66	0.59	0.81
Hsp90aa1	Hsp90aa1_Y493	0.50	0.56	0.56	1.15
Hsp90aa1	Hsp90aa1_S263	0.75	0.69	1.05	1.20
Hsp90ab1	Hsp90ab1_S255	0.55	0.66	1.18	1.42
Hsp90ab1	Hsp90ab1_Y484	0.40	0.42	2.01	1.99
Hsp90ab1	Hsp90ab1_Y56	0.57	0.54	0.87	2.38
Hspbp1	Hspbp1_S349	1.37	1.60	2.42	2.20
Hsph1	Hsph1_S810	0.91	0.91	1.08	0.95
Htatsf1	Htatsf1_S441	0.75	0.80	0.68	0.57
Htatsf1	Htatsf1_S724	0.73	0.82	0.55	0.66
Htatsf1	Htatsf1_S613	0.99	0.87	0.77	0.67
Htatsf1	Htatsf1_S705	0.83	0.83	0.69	0.70
Huwe1	Huwe1_S1395	0.94	0.95	0.75	0.86
Huwe1	Huwe1_S2363	0.76	0.80	2.01	0.93
Huwe1	Huwe1_S1907	1.60	1.86	1.15	1.12
Huwe1	Huwe1_S2366	0.89	0.80	1.44	1.14
Ibtk	Ibtk_S1046	0.94	1.00	1.31	2.75
Igbp1	Igbp1_S4	0.38	0.38	0.83	1.86
Igf2r	Igf2r_Y1396	149.45	20.04	203.16	31.51
Ighmbp2	Ighmbp2_S800	0.53	0.49	0.85	0.88
Ikzf2	Ikzf2_S373	1.12	0.92	0.00	0.00
Ikzf2	Ikzf2_S375	1.12	1.06	0.00	0.00
Ikzf2	Ikzf2_S78	1.53	1.60	0.85	0.40
Ikzf2	Ikzf2_S79	1.30	1.32	1.27	0.41
Ikzf2	Ikzf2_S56	1.44	1.10	1.09	0.57
Ikzf2	Ikzf2_S369	0.98	0.98	1.23	0.87
Il16	Il16_S917	0.45	0.40	0.71	1.04
Il16	Il16_S930	0.73	0.67	0.76	2.23
Incenp	Incenp_S218	0.72	0.54	0.62	0.30
Incenp	Incenp_T215	0.72	0.54	0.62	0.30
Incenp	Incenp_T195	0.57	0.72	0.76	0.33
Incenp	Incenp_S72	1.36	1.56	1.18	0.75
Inpp5d	Inpp5d_T963	0.20	0.16	0.50	0.05
Inpp5d	Inpp5d_S971	0.52	0.61	0.38	0.09
Inpp5d	Inpp5d_Y867	0.60	0.84	0.73	0.34
Ints1	Ints1_S1347	0.64	0.74	0.65	0.66
Ints1	Ints1_S109	1.02	1.11	0.80	0.67
Ints1	Ints1_T110	1.01	1.03	0.91	0.83
Ints12	Ints12_S354	0.72	0.74	0.00	0.00
Ints12	Ints12_S127	0.88	0.81	0.97	0.77
Ints12	Ints12_S126	0.87	0.89	0.97	0.77
Ints3	Ints3_S993	0.82	1.93	1.10	0.84
Ints3	Ints3_S992	0.81	1.48	1.06	0.89
Ints3	Ints3_S500	1.13	1.23	0.96	0.97
Ints6	Ints6_S800	0.48	0.49	0.67	1.31
Iqgap1	Iqgap1_Y1510	0.37	0.37	0.38	0.77
Irf2bp1	Irf2bp1_S453	1.43	1.53	1.42	0.88
Irf2bp2	Irf2bp2_T387	1.01	1.11	0.00	0.00
Irf2bp2	Irf2bp2_S343	0.85	0.81	0.90	0.65
Irf2bp2	Irf2bp2_S169	1.32	1.35	1.12	0.68

Irf2bp2	Irf2bp2_S250	0.86	0.86	0.94	1.01
Irf2bp2	Irf2bp2_S71	0.80	0.77	1.67	1.54
Irf2bpl	Irf2bpl_S638	0.77	0.68	0.50	0.41
Irf2bpl	Irf2bpl_S526	0.78	0.70	1.06	1.00
Irf2bpl	Irf2bpl_S641	0.77	0.68	0.86	1.08
Irf3	Irf3_S123	0.47	0.51	1.74	1.32
Iscu	Iscu_S15	1.06	0.86	0.48	0.43
Iscu	Iscu_S21	1.06	0.86	0.48	0.43
Iscu	Iscu_S30	1.14	0.91	0.68	0.82
Itpr1	Itpr1_S1755	0.56	0.54	0.58	0.86
Itpr1	Itpr1_S1588	1.73	2.47	0.61	1.67
Itsn2	Itsn2_S843	1.43	1.22	1.22	1.05
Itsn2	Itsn2_S838	2.04	1.03	1.18	1.19
Itsn2	Itsn2_Y554	1.53	1.73	4.31	10.77
Iws1	Iws1_S183	1.15	1.12	0.96	0.46
Iws1	Iws1_S343	0.96	0.94	0.89	0.48
Iws1	Iws1_S345	0.96	0.94	0.75	0.49
Iws1	Iws1_S368	0.86	0.77	1.00	0.80
Iws1	Iws1_S185	1.21	1.04	3.95	0.83
Iws1	Iws1_S666	2.02	2.31	0.89	0.85
Iws1	Iws1_S384	1.09	1.35	1.00	0.93
Iws1	Iws1_S386	1.09	1.35	1.00	0.93
Iws1	Iws1_S366	1.46	1.36	1.29	1.13
Iws1	Iws1_S321	0.97	0.76	1.00	1.14
Iws1	Iws1_S667	1.23	1.44	2.59	1.72
Jakmip1	Jakmip1_S382	1.49	1.35	1.00	1.09
Jmjd1c	Jmjd1c_S471	0.81	0.97	1.01	0.89
Junb	Junb_T252	0.86	0.97	1.05	2.04
Junb	Junb_S256	0.91	0.98	0.98	3.31
Kat7	Kat7_T88	0.70	0.94	0.68	0.38
Kat7	Kat7_S56	0.91	0.81	0.87	0.76
Kat7	Kat7_S57	1.34	1.07	0.85	0.79
Kdm2b	Kdm2b_S458	0.75	1.01	1.15	0.70
Kdm3b	Kdm3b_S799	2.84	4.78	1.96	1.41
Kdm4b	Kdm4b_S418	1.31	1.02	0.72	0.94
Kdm4c	Kdm4c_S395	0.48	0.52	0.33	0.52
Kdm4c	Kdm4c_S475	1.25	1.25	0.61	0.69
Khsrp	Khsrp_S182	0.88	0.92	0.55	1.28
Kidins220	Kidins220_S1578	0.64	0.62	0.75	1.50
Kif11	Kif11_T925	0.73	0.79	0.65	0.46
Kif15	Kif15_S568	0.46	0.43	1.29	1.81
Kif18b	Kif18b_S558	0.70	0.80	1.09	0.57
Kif18b	Kif18b_S561	0.81	0.90	1.02	0.60
Kif20b	Kif20b_S950	0.34	0.30	0.90	0.69
Kif21b	Kif21b_S1217	1.48	1.07	1.34	0.81
Kif5b	Kif5b_S933	0.57	0.57	1.66	2.58
Kif7	Kif7_S662	0.57	0.49	0.78	0.90
Klc2	Klc2_S579	1.16	1.42	0.76	1.03
Klc2	Klc2_S607	1.25	2.31	1.68	1.75
Klc3	Klc3_S501	0.25	0.32	0.07	0.49
Klc4	Klc4_S590	1.08	1.47	0.61	1.21
Kmt2b	Kmt2b_T2079	0.83	0.76	1.26	0.89
Kmt2b	Kmt2b_S866	0.89	0.80	1.68	1.06
Knop1	Knop1_S142	0.49	0.51	1.05	0.57
Kpna2	Kpna2_T61	0.34	0.47	1.30	1.48

Kpna2	Kpna2_S62	0.34	0.46	1.14	1.49
Kpna3	Kpna3_S60	0.77	0.66	0.98	0.83
Kri1	Kri1_S142	1.26	1.19	1.24	1.21
Ksr1	Ksr1_S392	2.12	2.24	1.73	1.47
Kti12	Kti12_S157	0.74	0.57	0.93	1.05
Ktn1	Ktn1_T71	0.98	1.12	0.00	0.00
Ktn1	Ktn1_S75	0.83	0.92	1.01	1.03
L3mbtl2	L3mbtl2_S67	1.06	1.10	0.00	0.00
L3mbtl2	L3mbtl2_T66	1.09	1.13	1.34	1.27
L3mbtl3	L3mbtl3_S605	0.79	0.85	0.00	0.00
Lamtor1	Lamtor1_T28	0.41	0.37	0.58	0.73
Larp1	Larp1_T1047	1.10	1.02	0.00	0.00
Larp1	Larp1_T626	0.96	0.82	1.58	0.83
Larp1	Larp1_S604	0.93	0.79	0.90	0.87
Larp1	Larp1_S608	0.93	0.79	0.90	0.87
Larp1	Larp1_S494	1.18	0.95	1.58	1.06
Larp1	Larp1_S498	1.09	0.92	1.61	1.06
Larp1	Larp1_S751	0.93	0.95	1.15	1.07
Larp1	Larp1_S81	0.92	0.88	0.90	1.09
Larp1	Larp1_T503	1.52	1.54	2.10	1.68
Larp1	Larp1_T1048	1.12	1.04	1.33	2.81
Larp1b	Larp1b_S60	0.87	0.84	1.12	1.02
Larp4	Larp4_S716	0.60	0.63	1.87	1.26
Larp7	Larp7_S253	0.73	0.60	1.04	0.82
Larp7	Larp7_S256	0.73	0.60	0.86	0.88
Larp7	Larp7_T251	2.43	1.33	0.85	1.02
Lats1	Lats1_S612	1.21	1.17	2.08	2.09
Lats1	Lats1_T611	1.23	1.28	2.83	2.32
Lbr	Lbr_S101	0.87	0.84	0.58	1.15
Lbr	Lbr_S103	1.22	1.12	1.24	1.18
Lcor	Lcor_S42	0.47	0.46	0.00	0.00
Lcp1	Lcp1_S257	0.43	0.41	0.95	1.45
Lcp1	Lcp1_S7	0.51	0.53	0.51	2.49
Lcp1	Lcp1_S5	0.55	0.53	2.64	4.68
Lcp1	Lcp1_Y124	0.53	0.29	1.15	4.91
Lcp1	Lcp1_Y598	0.53	0.57	6.85	8.88
Ldha	Ldha_T309	1.72	1.48	1.19	1.42
Ldha	Ldha_Y239	1.30	0.68	2.73	2.49
Ldlrap1	Ldlrap1_S198	0.82	0.75	0.72	1.06
Leo1	Leo1_S631	0.55	0.54	0.68	0.69
Leo1	Leo1_S659	0.54	0.63	0.95	0.73
Leprel2	Leprel2_T522	0.59	196.41	0.71	214.31
Lgalsl	Lgalsl_S25	1.82	1.62	2.35	3.65
Lig1	Lig1_S65	0.79	0.92	0.99	0.38
Lig1	Lig1_S67	0.75	0.82	1.34	0.41
Lig1	Lig1_T93	0.88	0.98	0.85	0.46
Lig1	Lig1_S204	0.62	0.75	1.00	0.68
Lig1	Lig1_S81	0.40	0.41	1.05	1.22
Lig3	Lig3_S211	0.64	0.67	0.53	0.41
Lmna	Lmna_S392	0.32	0.46	0.73	1.60
Lmna	Lmna_S390	0.35	0.52	0.93	1.77
Lmna	Lmna_S22	0.40	0.55	1.08	3.56
Lmnb1	Lmnb1_T5	0.70	0.77	0.74	0.45
Lmnb1	Lmnb1_S17	1.12	0.79	0.45	0.54
Lmnb1	Lmnb1_S14	0.88	1.10	0.45	0.54

Lmnb1	Lmnb1_T21	0.39	0.43	1.07	0.66
Lmnb1	Lmnb1_S24	0.65	0.67	1.46	1.27
Lmnb1	Lmnb1_S405	2.06	1.85	2.09	1.66
Lmnb2	Lmnb2_S383	0.73	0.78	0.94	0.69
Lmnb2	Lmnb2_S385	0.40	0.47	0.87	0.76
Lnp	Lnp_S411	0.57	0.68	2.22	2.24
LOC100040974	LOC100040974_S134	0.93	1.01	0.99	1.73
LOC100505031	LOC100505031_Y156	1.27	1.41	3.13	4.56
LOC100862604	LOC100862604_S93	1.08	1.15	0.57	0.32
LOC100862604	LOC100862604_S95	1.36	1.23	0.73	0.76
LOC101056383	LOC101056383_S152	1.36	1.63	0.98	0.58
LOC101056456	LOC101056456_S53	0.55	0.52	0.93	0.58
LOC101056619	LOC101056619_Y141	0.70	0.73	0.73	1.35
LOC101056619	LOC101056619_Y29	0.43	0.48	3.26	5.19
Lpin2	Lpin2_S186	0.59	0.48	0.63	0.51
Lpin2	Lpin2_S187	0.75	0.83	0.63	0.51
Lpxn	Lpxn_S54	0.30	0.32	1.27	2.26
Lrch1	Lrch1_S518	0.99	0.99	0.87	1.09
Lrrc8c	Lrrc8c_S215	1.56	1.98	2.15	1.57
Lrrfip1	Lrrfip1_S547	0.30	0.35	0.47	0.59
Lrrfip1	Lrrfip1_S16	0.63	0.77	0.99	1.55
Lrrfip1	Lrrfip1_S302	0.22	0.19	0.95	3.59
Lrrfip2	Lrrfip2_S92	0.88	0.89	0.00	0.00
Lrrfip2	Lrrfip2_S88	0.90	0.90	0.85	1.15
Lrrfip2	Lrrfip2_S96	0.76	0.70	0.91	1.23
Lsm11	Lsm11_S21	1.03	1.18	1.08	0.91
Lsm14a	Lsm14a_S216	1.10	1.11	0.91	0.81
Lsm14a	Lsm14a_T194	1.32	1.29	0.93	1.03
Luc7l2	Luc7l2_S373	0.97	0.68	0.75	0.76
Luc7l2	Luc7l2_S374	0.79	0.74	0.75	0.76
M6pr	M6pr_S268	0.75	0.76	0.55	0.58
Map1a	Map1a_S1789	0.66	0.57	0.78	1.11
Map1s	Map1s_S462	0.98	1.00	0.00	0.00
Map2k2	Map2k2_T395	0.79	0.75	0.98	1.06
Map2k2	Map2k2_S295	0.89	1.00	1.36	1.46
Map3k1	Map3k1_S915	1.31	1.48	1.49	1.36
Map3k1	Map3k1_S138	1.33	1.33	1.44	1.61
Map3k1	Map3k1_S142	1.40	1.47	1.47	1.70
Map3k2	Map3k2_S331	1.16	1.09	0.78	0.64
Map3k2	Map3k2_S163	1.11	1.01	0.94	1.35
Map3k2	Map3k2_S239	1.34	1.18	1.35	1.37
Map3k4	Map3k4_S454	0.74	0.65	0.57	0.36
Map3k4	Map3k4_S449	0.74	0.65	0.72	0.68
Map3k7	Map3k7_T415	1.83	2.52	0.93	0.41
Map3k7	Map3k7_S439	2.41	2.96	0.98	0.60
Map4	Map4_S506	0.72	0.62	0.00	0.00
Map4	Map4_S1008	0.79	0.86	0.67	0.61
Map4	Map4_T847	0.99	0.87	1.16	0.62
Map4	Map4_S667	0.48	0.58	0.68	0.79
Map4	Map4_S517	0.78	0.82	3.09	1.00
Map4	Map4_S798	0.64	0.78	1.01	1.40
Map4	Map4_S785	1.01	0.96	2.20	1.69
Map7d1	Map7d1_S329	0.93	0.77	0.72	0.86
Mapk11	Mapk11_T180	1.49	1.48	1.24	2.79
Mapk14	Mapk14_S2	0.36	0.39	0.13	0.43

Mapk14	Mapk14_Y182	1.17	1.31	1.08	1.97
Mapk14	Mapk14_T180	1.15	1.15	1.24	2.47
Mapkap1	Mapkap1_S510	1.93	2.00	0.99	1.14
Mark2	Mark2_S453	1.97	2.08	1.46	1.73
Mars	Mars_S827	0.93	1.08	1.03	1.47
Matr3	Matr3_S188	0.85	0.84	1.17	1.34
Max	Max_S2	0.60	0.54	1.11	0.85
Max	Max_S11	0.63	0.61	0.97	0.96
Mbd3	Mbd3_S85	1.24	1.32	2.24	2.05
Mcm2	Mcm2_S26	1.10	1.17	1.01	0.61
Mcm2	Mcm2_S27	1.14	0.98	0.89	0.63
Mcm2	Mcm2_S41	1.00	0.99	0.66	0.65
Mcm2	Mcm2_S40	0.86	0.96	0.69	0.66
Mcm2	Mcm2_Y137	0.66	0.76	0.95	0.68
Mcm2	Mcm2_S12	1.07	1.21	0.82	0.71
Mcm2	Mcm2_S140	1.11	1.16	0.72	0.77
Mcm2	Mcm2_S139	1.02	1.00	1.02	0.77
Mcm2	Mcm2_S11	0.93	0.95	0.82	0.80
Mcm2	Mcm2_S21	0.85	0.79	0.48	0.91
Mcm2	Mcm2_S381	0.75	0.60	0.62	0.98
Mcm3	Mcm3_S668	0.82	0.88	0.64	0.56
Mcm3	Mcm3_S672	0.89	0.90	1.01	0.75
Mcm4	Mcm4_S3	0.77	0.87	0.66	0.47
Mcm4	Mcm4_S2	1.06	1.20	0.67	0.49
Mcm4	Mcm4_T19	1.88	1.88	0.88	0.69
Mcm6	Mcm6_S13	0.31	0.28	0.14	0.20
Mcm6	Mcm6_S704	0.55	0.50	0.25	0.34
Mcm7	Mcm7_S500	0.57	0.47	0.63	0.74
Mcmbp	Mcmbp_S154	0.52	0.51	0.72	0.69
Mdc1	Mdc1_S596	0.56	0.64	0.20	0.40
Mdc1	Mdc1_S592	0.57	0.65	0.19	0.41
Mdc1	Mdc1_S168	0.58	0.54	0.45	0.68
Mdn1	Mdn1_S4822	0.80	0.82	0.89	0.80
Mecom	Mecom_S527	2.18	2.00	1.71	0.04
Med1	Med1_T1036	0.66	0.71	0.71	0.86
Med12	Med12_S636	0.65	0.61	0.86	0.67
Med24	Med24_S871	1.30	1.64	0.99	0.67
Med24	Med24_S860	1.08	0.95	1.24	1.09
Melk	Melk_S521	0.89	0.91	0.51	0.21
Mepce	Mepce_S192	0.83	0.85	0.49	1.09
Mepce	Mepce_T188	0.90	0.85	0.49	1.10
Mepce	Mepce_S191	0.98	0.84	0.50	1.13
Mettl14	Mettl14_S399	0.97	0.98	0.79	0.52
Mfap1a	Mfap1a_S52	0.73	0.67	0.81	0.73
Mfap1a	Mfap1a_S53	0.73	0.67	0.81	0.73
Mical1	Mical1_S704	0.98	0.92	1.37	1.08
Micall1	Micall1_S651	0.58	0.60	0.62	1.04
Micall1	Micall1_S647	0.49	0.72	0.92	1.15
Micall1	Micall1_S496	2.09	2.79	1.13	1.37
Mis18a	Mis18a_S5	0.49	0.45	0.56	0.53
Mki67	Mki67_S2649	1.59	0.69	0.33	0.11
Mki67	Mki67_S517	0.61	0.37	0.29	0.15
Mki67	Mki67_S2392	0.87	0.85	0.36	0.15
Mki67	Mki67_T3021	1.11	0.58	0.79	0.16
Mki67	Mki67_S767	1.49	0.84	0.19	0.18

Mki67	Mki67_S523	0.71	0.31	0.44	0.21
Mki67	Mki67_S2980	0.99	0.38	1.05	0.24
Mki67	Mki67_S2545	96.87	8.12	0.53	0.26
Mkl1	Mkl1_S457	0.90	0.74	1.19	0.33
Mlf1ip	Mlf1ip_S186	0.95	0.76	0.71	0.59
Mllt1	Mllt1_S284	0.96	1.02	0.88	0.41
Mllt1	Mllt1_S261	0.98	0.97	0.87	0.53
Mllt10	Mllt10_S613	1.27	1.40	1.22	1.38
Mlx	Mlx_S45	0.86	0.70	1.02	0.99
Mon1a	Mon1a_S31	0.76	0.98	0.94	1.08
Morc2a	Morc2a_S614	0.51	0.55	0.88	0.83
Morc2a	Morc2a_S775	1.17	1.23	1.47	1.13
Morc2a	Morc2a_S777	1.33	1.07	0.85	1.29
Morc2a	Morc2a_S716	0.72	0.67	1.26	1.78
Morc2a	Morc2a_S714	1.51	1.48	2.18	1.89
Mov10	Mov10_S970	0.58	0.54	0.00	0.00
Mre11a	Mre11a_S2	1.07	0.83	0.96	0.56
Msh6	Msh6_S137	0.74	0.74	0.55	0.33
Msh6	Msh6_S254	0.82	0.83	0.63	0.38
Msh6	Msh6_S261	0.82	0.83	0.85	0.40
Msh6	Msh6_S63	0.61	0.73	0.58	0.58
Msh6	Msh6_S252	0.60	0.59	1.24	0.60
Msn	Msn_S576	0.37	0.29	0.18	0.34
Mta1	Mta1_S559	0.73	0.90	0.89	0.40
Mta1	Mta1_S432	2.01	1.90	1.48	0.81
Mta1	Mta1_S505	0.95	0.94	1.13	0.95
Mta1	Mta1_S369	1.86	1.47	1.66	1.17
Mta2	Mta2_S435	1.12	1.23	1.13	0.99
Mta2	Mta2_S54	0.57	0.58	0.54	1.24
Mta3	Mta3_S517	0.53	0.56	0.65	0.36
Mtdh	Mtdh_S423	1.11	0.82	1.28	1.55
Mtdh	Mtdh_S297	1.07	0.94	1.19	1.92
Mtdh	Mtdh_T96	0.81	1.28	2.17	2.70
Mtfr1l	Mtfr1l_S100	1.74	1.71	1.67	1.38
Mtmr2	Mtmr2_S6	1.79	1.74	2.59	1.26
Mybbp1a	Mybbp1a_T1191	0.82	0.91	0.00	0.00
Mybbp1a	Mybbp1a_S1323	1.16	1.15	1.21	0.66
Mybbp1a	Mybbp1a_S1164	0.73	0.85	1.11	0.92
Mybbp1a	Mybbp1a_S1160	0.53	0.85	0.87	0.92
Mybbp1a	Mybbp1a_S1253	0.51	0.61	1.36	1.16
Mybbp1a	Mybbp1a_S1325	1.24	1.84	0.94	1.27
Mybbp1a	Mybbp1a_S6	0.46	0.39	1.64	1.96
Mybbp1a	Mybbp1a_S1280	0.78	0.79	2.23	1.97
Mybbp1a	Mybbp1a_T8	0.89	0.73	2.26	1.98
Mycbp2	Mycbp2_S2859	0.98	0.73	0.55	0.51
Mycbp2	Mycbp2_S2861	0.96	1.20	0.96	1.09
Myh9	Myh9_S1943	0.62	0.60	1.04	2.35
Myh9	Myh9_Y190	0.35	0.30	1.37	3.57
Myh9	Myh9_Y1805	0.38	0.43	0.42	35.63
Myl12a	Myl12a_T19	0.96	1.29	0.00	0.00
Myl12a	Myl12a_S20	1.15	1.18	1.19	1.05
Mylk	Mylk_S364	0.19	0.29	0.26	0.22
Myo18a	Myo18a_S2022	1.17	1.23	1.30	1.27
Myo18a	Myo18a_S2024	1.17	1.23	1.30	1.27
Myo19	Myo19_S896	0.60	0.61	0.71	0.72

Myo9b	Myo9b_S1113	0.64	0.67	0.65	1.01
Myo9b	Myo9b_S1264	0.79	0.68	0.74	1.21
Myo9b	Myo9b_S1218	0.79	0.84	1.00	1.31
Myo9b	Myo9b_T1317	1.02	0.99	1.26	1.86
Nab1	Nab1_S401	0.65	0.97	0.71	0.94
Naf1	Naf1_S416	0.60	0.63	1.08	1.08
Nans	Nans_S275	0.69	0.73	0.55	0.63
Nap1l4	Nap1l4_S7	0.49	0.54	1.33	1.13
Nbas	Nbas_S472	0.47	0.41	0.76	0.84
Nbeal2	Nbeal2_S1304	0.77	0.83	0.00	0.00
Nbeal2	Nbeal2_S1303	0.81	0.78	0.69	1.09
Nbeal2	Nbeal2_S2735	0.73	0.73	0.86	1.24
Nbn	Nbn_S398	0.69	0.64	0.25	0.25
Ncapd2	Ncapd2_S1323	0.53	0.40	0.42	0.50
Ncapd2	Ncapd2_S1320	0.43	0.54	1.61	2.98
Ncaph	Ncaph_S25	1.51	1.62	3.17	1.54
Ncbp1	Ncbp1_S22	0.51	0.55	1.85	2.38
Ncf2	Ncf2_S312	0.15	0.15	0.00	0.00
Ncf2	Ncf2_S332	0.29	0.30	0.34	0.78
Ncf2	Ncf2_S324	0.15	0.21	0.38	0.97
Ncf2	Ncf2_S323	0.16	0.24	0.38	0.97
Ncf4	Ncf4_S161	0.55	0.66	0.99	2.49
Nckap5l	Nckap5l_S489	0.78	0.96	1.27	2.90
Ncl	Ncl_S403	0.57	0.28	0.68	0.65
Ncl	Ncl_Y464	2.16	0.48	0.86	2.23
Ncoa1	Ncoa1_S22	0.74	0.79	0.77	0.43
Ncoa2	Ncoa2_S699	0.87	0.77	0.72	0.50
Ncoa5	Ncoa5_S377	0.98	0.99	1.00	0.72
Ncoa5	Ncoa5_S378	1.10	1.03	1.09	0.90
Ncoa5	Ncoa5_S9	0.83	0.90	0.99	1.11
Ncoa5	Ncoa5_S29	0.86	0.86	1.01	1.14
Ncoa5	Ncoa5_S34	1.24	0.91	1.01	1.14
Ncoa7	Ncoa7_S211	0.47	1.46	0.00	0.00
Ncoa7	Ncoa7_S214	0.47	1.46	1.10	0.57
Ncor1	Ncor1_S1154	0.43	0.50	0.58	0.37
Ncor1	Ncor1_S2068	0.68	0.73	0.57	0.55
Ncor1	Ncor1_S2132	0.89	1.22	0.65	0.78
Ncor1	Ncor1_S225	0.86	0.69	0.60	0.83
Ncor1	Ncor1_S1414	1.55	1.56	1.45	1.16
Ncor2	Ncor2_S2211	1.00	0.97	0.66	0.78
Ncor2	Ncor2_S149	0.66	0.72	0.60	0.83
Ncor2	Ncor2_S152	0.66	0.72	0.60	0.83
Ncor2	Ncor2_T1349	0.76	0.72	0.89	0.99
Ndrg1	Ndrg1_S2	0.65	0.65	0.40	0.75
Ndrg1	Ndrg1_S330	3.08	2.20	0.74	1.93
Nedd4	Nedd4_T287	1.50	1.35	0.99	1.00
Nedd4	Nedd4_S309	0.60	0.52	0.62	1.65
Nedd4l	Nedd4l_S328	1.46	1.52	0.66	0.81
Nelfa	Nelfa_S363	1.28	1.17	1.18	1.04
Nelfe	Nelfe_S115	1.59	1.46	1.26	1.26
Nelfe	Nelfe_S51	1.05	0.95	1.26	1.58
Nfatc2ip	Nfatc2ip_S81	0.41	0.41	0.34	0.32
Nfatc2ip	Nfatc2ip_S83	0.41	0.41	0.34	0.32
Nfatc2ip	Nfatc2ip_S79	0.41	0.42	0.34	0.32
Nfix	Nfix_S265	0.25	0.97	1.02	0.65

Nfkb2	Nfkb2_T425	0.29	0.27	0.41	1.37
Nfrkb	Nfrkb_S1288	0.84	1.11	0.77	0.71
Nipbl	Nipbl_S305	1.04	0.88	0.00	0.00
Nipbl	Nipbl_S2652	0.67	0.74	0.70	0.75
Nipbl	Nipbl_S306	1.04	0.80	0.74	0.78
Nmd3	Nmd3_S468	0.68	0.87	0.89	1.10
Nmd3	Nmd3_T470	1.52	1.61	2.21	1.97
Nmt1	Nmt1_S47	0.84	0.77	0.90	1.12
Nolc1	Nolc1_S644	1.08	1.19	1.43	0.78
Nolc1	Nolc1_T608	0.95	0.82	1.19	1.09
Nolc1	Nolc1_S624	1.17	1.20	1.26	1.10
Nolc1	Nolc1_S561	1.03	1.04	1.26	1.12
Nolc1	Nolc1_S623	1.14	1.17	1.48	1.17
Nolc1	Nolc1_S699	0.77	0.83	1.11	1.18
Nolc1	Nolc1_S552	0.89	0.96	1.37	1.34
Nolc1	Nolc1_T611	0.95	0.82	1.65	1.37
Nop14	Nop14_S96	0.56	0.78	1.09	0.86
Nop56	Nop56_S462	1.26	1.28	0.00	0.00
Nop56	Nop56_S465	1.26	1.28	0.00	0.00
Nop56	Nop56_T545	0.79	0.78	0.67	0.50
Nop56	Nop56_S543	0.97	0.73	0.81	0.51
Nop56	Nop56_S529	1.50	1.14	0.82	0.54
Nop56	Nop56_S513	1.23	0.99	1.05	0.74
Nop56	Nop56_S536	1.04	0.94	0.80	0.80
Nop56	Nop56_S554	0.72	0.64	0.94	1.47
Nop56	Nop56_T546	1.19	0.87	1.07	1.73
Nop58	Nop58_S521	1.94	1.80	0.74	0.26
Nop58	Nop58_S509	1.73	1.21	0.95	1.04
Npm1	Npm1_S258	0.70	0.71	0.71	1.01
Npm1	Npm1_S125	1.17	1.25	1.18	1.11
Npm1	Npm1_T217	2.15	2.92	1.66	1.16
Npm1	Npm1_S241	1.14	1.15	1.04	1.39
Npm1	Npm1_S252	0.83	0.93	2.11	2.16
Npm1	Npm1_S252	0.83	0.93	2.11	2.16
Nr2c2	Nr2c2_S68	1.23	1.35	1.53	2.11
Nrd1	Nrd1_S85	4.90	0.58	0.85	1.11
Nsfl1c	Nsfl1c_S178	1.67	1.63	1.05	0.93
Nsfl1c	Nsfl1c_S116	1.51	1.67	1.12	1.20
Nsfl1c	Nsfl1c_S142	1.17	1.25	1.03	1.81
Nsun2	Nsun2_S23	1.04	1.03	0.69	0.74
Nsun2	Nsun2_S723	1.20	1.05	0.72	0.76
Nucks1	Nucks1_S61	0.71	0.73	0.00	0.00
Nucks1	Nucks1_S58	1.04	1.00	0.00	0.00
Nucks1	Nucks1_S180	0.65	0.74	0.56	0.36
Nucks1	Nucks1_S19	0.92	0.80	0.75	0.56
Nucks1	Nucks1_T178	0.91	1.08	0.90	0.64
Nudt5	Nudt5_S10	0.94	0.95	0.00	0.00
Nufip2	Nufip2_S113	1.08	0.89	2.19	2.60
Numa1	Numa1_S2059	0.67	0.71	0.98	0.41
Numa1	Numa1_S167	0.51	0.68	0.78	0.81
Numa1	Numa1_S1844	0.67	0.51	1.81	1.20
Numa1	Numa1_S1835	2.18	1.17	1.51	1.37
Nup107	Nup107_S87	0.62	0.72	0.60	0.64
Nup153	Nup153_S335	0.53	0.51	0.63	1.04
Nup155	Nup155_S992	0.40	0.57	0.57	0.65

Nup188	Nup188_S1718	0.52	0.60	1.24	1.16
Nup188	Nup188_S1719	0.48	0.55	0.87	1.30
Nup210	Nup210_T1844	1.03	0.90	0.70	0.48
Nup88	Nup88_T526	0.79	0.71	0.56	0.55
Nup88	Nup88_S699	0.70	0.65	0.98	0.97
Nup98	Nup98_S888	0.82	0.83	0.58	0.43
Nup98	Nup98_T670	0.63	0.62	1.15	1.24
Nusap1	Nusap1_S152	0.45	0.42	0.58	0.53
Nvl	Nvl_S190	0.63	0.54	2.49	0.90
Ogfr	Ogfr_S403	1.22	1.14	1.63	7.10
Olfr809	Olfr809_S5	19.03	1.06	17.74	3.68
Osbp	Osbp_S188	0.68	0.65	0.90	1.29
Osbp	Osbp_S191	0.68	0.65	0.90	1.29
Osbpl11	Osbpl11_S192	1.01	1.10	1.31	1.27
Osbpl3	Osbpl3_S272	1.12	0.92	2.41	1.30
Osbpl7	Osbpl7_S222	1.41	1.55	0.83	1.46
Otud4	Otud4_S1016	0.82	0.75	1.03	1.03
Otud4	Otud4_S1015	1.05	1.63	1.03	1.03
Otud5	Otud5_S64	0.51	0.36	1.13	1.93
Oxsr1	Oxsr1_S324	2.69	2.94	1.79	2.56
Oxsr1	Oxsr1_S325	2.59	2.96	1.79	2.56
Pa2g4	Pa2g4_S2	1.13	1.15	1.19	1.09
Pabpc1	Pabpc1_Y297	0.43	0.58	0.65	1.29
Pacs1	Pacs1_S493	0.68	0.61	0.39	0.34
Pacsin2	Pacsin2_Y76	0.81	0.53	0.52	3.91
Pag1	Pag1_S247	1.23	0.87	0.00	0.00
Pak2	Pak2_S141	0.54	0.67	0.93	1.72
Pak2	Pak2_S2	0.91	0.97	0.87	2.24
Palm	Palm_S301	0.97	0.95	0.64	0.54
Pank1	Pank1_S30	0.76	0.66	0.64	1.07
Parn	Parn_S556	1.54	1.66	1.18	1.26
Patl1	Patl1_S179	0.84	0.81	0.79	1.16
Pbrm1	Pbrm1_S14	0.99	1.06	0.00	0.00
Pbrm1	Pbrm1_S10	0.71	0.83	0.67	0.79
Pbrm1	Pbrm1_T9	0.87	0.74	0.67	0.85
Pbrm1	Pbrm1_S39	1.25	1.36	0.92	1.00
Pcbp1	Pcbp1_S173	1.43	1.63	2.23	1.96
Pcbp2	Pcbp2_S185	0.70	0.72	0.90	0.88
Pcbp2	Pcbp2_S184	0.94	0.90	0.99	0.93
Pcf11	Pcf11_S510	0.78	0.83	0.85	0.89
Pcf11	Pcf11_S512	0.78	0.83	0.77	0.89
Pcm1	Pcm1_S68	1.51	1.70	1.22	0.94
Pcm1	Pcm1_S645	0.69	0.78	0.81	1.31
Pcm1	Pcm1_S69	0.76	0.78	0.86	1.39
Pcm1	Pcm1_S1769	0.82	0.76	1.26	1.41
Pcm1	Pcm1_S65	0.71	0.76	1.43	1.43
Pcm1	Pcm1_S644	0.76	0.76	0.75	1.46
Pcyt1a	Pcyt1a_T342	0.46	0.55	0.00	0.00
Pcyt1a	Pcyt1a_S343	0.54	0.58	0.30	0.37
Pcyt1a	Pcyt1a_S347	0.66	0.72	0.32	0.42
Pcyt1a	Pcyt1a_S331	0.86	0.87	0.66	0.60
Pcyt1a	Pcyt1a_S323	0.60	0.59	0.46	0.74
Pcyt1a	Pcyt1a_S315	0.75	0.59	0.46	0.74
Pcyt1a	Pcyt1a_S319	0.75	0.59	0.46	0.74
Pcyt1b	Pcyt1b_S285	0.65	0.56	0.34	0.49

Pdcd11	Pdcd11_S1490	0.56	0.51	0.90	0.71
Pdcd11	Pdcd11_S1468	0.73	0.61	1.89	2.16
Pdcd4	Pdcd4_S94	1.02	1.04	0.48	0.22
Pdcd4	Pdcd4_S457	2.90	2.42	1.64	0.65
Pdcd5	Pdcd5_S119	1.10	1.10	0.87	0.97
Pdha1	Pdha1_S232	5.28	4.26	0.55	0.41
Pdha1	Pdha1_T231	5.33	6.25	0.54	0.42
Pdha1	Pdha1_S293	0.65	0.84	0.54	0.44
Pdha1	Pdha1_S300	4.49	4.15	0.54	0.44
Pdha1	Pdha1_S295	4.38	4.22	0.54	0.44
Pdlim2	Pdlim2_S199	0.58	0.57	0.63	0.90
Pdlim2	Pdlim2_S205	0.49	0.51	0.80	1.79
Pdlim2	Pdlim2_S204	0.60	0.58	0.80	1.79
Pdlim5	Pdlim5_S137	0.32	0.47	0.58	0.86
Pdlim5	Pdlim5_S111	0.51	0.57	0.78	0.97
Pdlim7	Pdlim7_T96	0.39	0.30	1.57	1.74
Pdpk1	Pdpk1_S244	1.32	1.21	1.34	1.15
Pds5a	Pds5a_S1300	0.51	0.49	0.37	0.47
Pds5a	Pds5a_S1174	1.04	0.97	1.17	0.75
Pds5b	Pds5b_T1368	0.82	0.87	0.65	0.27
Pds5b	Pds5b_S1182	0.72	0.83	0.58	0.40
Pds5b	Pds5b_S1381	0.81	0.71	0.55	0.40
Pds5b	Pds5b_S1165	1.45	1.20	1.27	0.59
Pds5b	Pds5b_S1166	1.40	1.27	1.36	0.65
Pds5b	Pds5b_S1356	1.02	1.14	0.83	0.86
Pds5b	Pds5b_S1281	1.12	1.04	1.04	0.88
Pdxdc1	Pdxdc1_T687	1.37	1.71	1.37	1.34
Pelp1	Pelp1_T751	0.62	0.63	0.55	0.59
Pelp1	Pelp1_S10	0.96	1.03	0.75	0.86
Pex1	Pex1_S1172	0.85	1.26	0.82	0.84
Pfkl	Pfkl_S775	0.72	0.85	1.49	1.30
Pgam1	Pgam1_S118	0.33	0.45	3.10	2.69
Pgam1	Pgam1_Y92	0.94	0.83	3.07	8.64
Pgk1	Pgk1_S203	1.00	0.84	0.50	0.73
Pgk1	Pgk1_Y196	0.46	0.52	0.38	4.40
Pgm2	Pgm2_S117	1.72	1.49	1.07	0.96
Pgm2	Pgm2_Y353	0.66	0.65	3.46	6.13
Pgm3	Pgm3_S64	2.02	1.77	1.01	1.04
Pgrmc1	Pgrmc1_S181	0.71	0.59	0.64	0.60
Pgrmc2	Pgrmc2_T205	1.02	0.78	0.89	0.97
Phactr4	Phactr4_S91	1.23	1.24	0.96	0.91
Phb	Phb_Y107	0.62	0.72	0.96	4.84
Phc3	Phc3_T574	0.63	0.61	0.35	0.31
Phc3	Phc3_S581	0.63	0.61	0.59	0.44
Phf17	Phf17_S735	0.47	0.49	0.71	0.38
Phf2	Phf2_S536	1.04	1.08	0.00	0.00
Phf2	Phf2_S893	1.49	0.96	1.31	0.58
Phf3	Phf3_S1112	0.65	0.69	0.72	0.78
Phf3	Phf3_S660	1.73	1.40	1.07	0.99
Phf6	Phf6_S155	0.74	0.79	1.01	0.77
Phf8	Phf8_S719	0.76	0.75	0.83	0.70
Phip	Phip_S1281	0.78	0.70	0.62	0.66
Phip	Phip_S1283	0.78	0.70	0.62	0.66
Phrf1	Phrf1_S1201	0.72	0.69	0.75	0.68
Pi4k2a	Pi4k2a_S44	0.83	0.91	1.62	2.94

Pi4k2a	Pi4k2a_S47	0.91	1.01	1.28	3.27
Pi4k2a	Pi4k2a_S51	0.91	0.98	1.29	3.35
Pi4kb	Pi4kb_S413	0.95	0.97	0.94	0.97
Pias1	Pias1_S503	0.96	1.02	0.99	0.88
Pik3r1	Pik3r1_Y197	0.64	0.65	0.67	16.17
Pip5k1b	Pip5k1b_S405	1.43	1.58	2.08	1.57
Pitpnm1	Pitpnm1_S621	1.06	0.99	1.22	1.60
Pja1	Pja1_T231	0.78	0.71	1.64	1.63
Pla2g4a	Pla2g4a_S435	0.97	0.60	0.62	1.23
Pla2g4a	Pla2g4a_S434	0.74	0.71	0.62	1.23
Pla2g4a	Pla2g4a_S728	0.74	1.05	0.51	1.61
Pla2g4a	Pla2g4a_S437	0.45	0.53	1.42	1.79
Plcl2	Plcl2_T585	0.83	0.75	0.63	0.74
Plec	Plec_S21	0.94	1.46	2.82	4.41
Plekha5	Plekha5_S1243	1.85	2.31	1.13	0.61
Plekhg3	Plekhg3_S76	0.57	0.79	1.10	1.99
Plekhg3	Plekhg3_S1141	0.30	0.26	1.45	2.26
Plekho2	Plekho2_S395	0.65	0.67	0.48	1.81
Pmf1	Pmf1_S19	0.73	0.61	0.63	0.55
Pml	Pml_S17	0.97	0.96	0.48	0.58
Pms2	Pms2_S569	1.18	1.24	1.31	0.67
Pnn	Pnn_S66	0.58	0.79	0.87	1.30
Pola1	Pola1_S215	0.78	0.87	0.73	0.61
Pola2	Pola2_T127	1.12	1.37	0.42	0.26
Pola2	Pola2_S126	0.58	0.64	1.98	1.53
Pold3	Pold3_S305	1.05	1.05	0.98	0.75
Poldip3	Poldip3_S127	0.98	0.85	0.83	0.60
Poll	Poll_S175	1.23	0.98	0.97	1.17
Polm	Polm_S12	0.50	0.75	0.96	0.67
Polr2a	Polr2a_S1798	0.65	0.67	0.53	0.57
Polr2a	Polr2a_S1840	0.65	0.68	0.48	0.62
Polr2a	Polr2a_S1875	0.73	0.65	0.57	0.67
Ppfia1	Ppfia1_S238	0.78	0.73	0.00	0.00
Ppfia1	Ppfia1_S242	0.91	0.85	0.00	0.00
Ppfia1	Ppfia1_S239	1.02	0.90	0.00	0.00
Pphln1	Pphln1_S78	0.75	0.74	1.36	0.96
Ppig	Ppig_S685	0.72	0.75	0.84	0.89
Ppig	Ppig_S413	1.28	0.95	0.93	0.96
Ppig	Ppig_S411	0.98	0.98	0.93	0.96
Ppig	Ppig_S395	0.94	0.93	1.16	1.64
Ppip5k2	Ppip5k2_S38	0.97	0.93	0.60	0.66
Ppme1	Ppme1_S243	0.63	0.66	0.42	1.70
Ppp1r10	Ppp1r10_S313	0.78	0.75	1.14	1.65
Ppp1r12a	Ppp1r12a_S422	0.55	0.66	1.29	3.18
Ppp1r12a	Ppp1r12a_S299	0.56	0.55	1.96	3.52
Ppp1r12c	Ppp1r12c_S403	0.61	0.59	0.87	2.17
Ppp1r18	Ppp1r18_S224	0.36	0.54	1.99	3.38
Ppp1r7	Ppp1r7_S24	0.74	0.81	0.86	0.89
Ppp1r7	Ppp1r7_S27	1.25	1.11	0.86	0.89
Ppp2r5a	Ppp2r5a_S42	0.73	0.76	0.77	1.29
Ppp2r5a	Ppp2r5a_S41	0.93	0.87	0.77	1.29
Ppp2r5d	Ppp2r5d_S81	0.61	0.64	0.48	0.54
Ppp2r5d	Ppp2r5d_S44	0.65	0.61	0.74	0.59
Ppp2r5d	Ppp2r5d_S80	0.49	0.55	0.43	0.60
Ppp2r5d	Ppp2r5d_S565	0.90	0.98	1.24	1.03

Ppp2r5e	Ppp2r5e_T7	1.44	1.59	0.00	0.00
Ppp4r2	Ppp4r2_S159	1.04	1.17	0.84	0.81
Ppp6r1	Ppp6r1_S739	0.88	0.93	0.00	0.00
Ppp6r1	Ppp6r1_S529	0.83	0.75	1.12	1.40
Ppp6r1	Ppp6r1_S530	0.88	0.78	1.12	1.40
Ppp6r1	Ppp6r1_T524	1.07	1.13	1.12	1.40
Ppp6r1	Ppp6r1_S531	1.45	1.29	1.12	1.40
Ppp6r2	Ppp6r2_S670	0.68	0.67	0.87	1.16
Prcc	Prcc_S157	0.90	0.91	0.91	0.95
Prcc	Prcc_S159	0.90	0.91	0.91	0.95
Prdx1	Prdx1_Y10	0.60	0.79	1.76	3.26
Prkar1a	Prkar1a_S83	1.28	1.03	0.71	0.24
Prkar2a	Prkar2a_S97	0.99	0.87	0.71	0.56
Prkar2b	Prkar2b_S112	0.92	0.83	0.92	2.34
Prkca	Prkca_S319	3.09	3.78	5.38	5.23
Prkd2	Prkd2_S197	1.97	2.18	1.48	1.27
Prkra	Prkra_T20	0.54	0.49	0.00	0.00
Prkra	Prkra_S18	0.52	0.54	0.90	1.10
Prpf38a	Prpf38a_S226	0.99	1.01	0.66	0.41
Prpf38b	Prpf38b_S321	1.07	0.92	0.86	1.07
Prpf4b	Prpf4b_S240	1.12	1.12	0.96	0.77
Prpf4b	Prpf4b_S242	1.12	1.12	0.96	0.77
Prpf4b	Prpf4b_S88	0.71	0.87	0.68	0.79
Prpf4b	Prpf4b_S94	1.01	1.09	1.15	0.82
Prpf4b	Prpf4b_S258	1.05	1.08	1.04	0.88
Prpf4b	Prpf4b_S387	1.16	1.20	1.14	0.92
Prpf4b	Prpf4b_S366	1.12	1.16	1.01	0.95
Prpf4b	Prpf4b_S368	1.12	1.16	1.01	0.95
Prpf4b	Prpf4b_Y849	1.34	1.48	1.25	1.00
Prpf8	Prpf8_Y2091	0.46	0.54	3.86	6.12
Prpsap2	Prpsap2_S141	1.29	1.31	1.17	1.33
Prrc2a	Prrc2a_S1217	0.76	0.90	0.81	0.98
Prrc2a	Prrc2a_T377	0.79	0.74	0.61	1.02
Prrc2a	Prrc2a_T609	0.40	0.40	1.51	1.05
Prrc2a	Prrc2a_S378	0.65	0.69	0.79	1.22
Prrc2b	Prrc2b_S621	0.76	0.68	0.00	0.00
Prrc2b	Prrc2b_S387	0.87	0.92	1.70	1.31
Prrc2b	Prrc2b_S555	0.83	0.93	2.48	2.68
Prrc2b	Prrc2b_S226	1.04	0.92	3.22	5.06
Prrc2c	Prrc2c_T2625	0.45	0.80	0.78	1.08
Prrc2c	Prrc2c_S853	0.74	0.74	1.27	1.30
Psd4	Psd4_S435	1.28	1.37	0.00	0.00
Psd4	Psd4_S434	1.18	1.30	1.27	0.85
Psd4	Psd4_S968	1.01	1.02	3.59	1.65
Psen1	Psen1_T370	1.22	1.13	1.26	1.04
Psip1	Psip1_T271	1.01	1.00	0.96	0.55
Psip1	Psip1_S106	0.49	0.48	0.42	0.56
Psip1	Psip1_S176	0.82	0.84	0.89	0.56
Psip1	Psip1_S272	0.48	0.50	0.99	0.61
Psip1	Psip1_S274	1.05	0.94	0.99	0.61
Psma2	Psma2_Y57	0.99	1.14	0.72	6.64
Psma2	Psma2_Y76	1.45	1.81	0.83	60.39
Psma3	Psma3_S250	1.18	1.18	0.00	0.00
Psma5	Psma5_S56	0.13	0.13	0.88	1.52
Psma5	Psma5_S16	0.16	0.18	0.47	3.66

Psmb8	Psmb8_Y234	1.06	1.00	0.80	3.95
Psmd1	Psmd1_S315	1.09	1.16	0.78	0.96
Psmd1	Psmd1_T311	1.09	1.16	0.78	0.96
Psmd11	Psmd11_Y415	0.41	0.46	0.39	1.75
Psmd2	Psmd2_T9	0.56	0.52	0.00	0.00
Psmd2	Psmd2_S361	1.09	0.89	1.19	1.23
Psmf1	Psmf1_S153	1.12	1.15	1.10	1.13
Ptbp1	Ptbp1_Y126	0.53	0.53	0.96	6.06
Ptbp3	Ptbp3_S27	0.37	0.30	0.46	0.64
Ptk2b	Ptk2b_S375	1.01	0.86	0.55	0.90
Ptma	Ptma_S9	1.14	1.00	0.61	0.70
Ptma	Ptma_S2	0.85	0.93	0.74	0.72
Ptpn11	Ptpn11_Y542	3.44	2.88	2.93	9.06
Ptpn11	Ptpn11_Y279	0.86	1.71	1.59	29.76
Ptpn12	Ptpn12_S331	0.59	0.47	0.81	1.40
Ptpn12	Ptpn12_S326	0.47	0.43	0.80	1.54
Ptpn12	Ptpn12_S434	0.60	0.65	0.72	2.04
Ptpn12	Ptpn12_S748	0.72	0.67	1.21	6.30
Ptpn6	Ptpn6_S10	1.05	0.67	0.55	0.49
Ptprc	Ptprc_S801	0.85	0.76	1.49	1.62
Pum2	Pum2_S181	1.85	0.92	0.88	0.83
Purb	Purb_S316	1.35	1.22	1.52	1.37
Pus7	Pus7_S40	0.41	0.38	0.19	0.30
Pwp2	Pwp2_S853	1.15	1.31	1.56	1.12
Pwp2	Pwp2_S856	1.15	1.31	1.56	1.12
Pygo2	Pygo2_T264	0.53	0.44	1.15	1.17
R3hdm1	R3hdm1_S381	1.82	2.02	1.15	2.19
Rab11fip1	Rab11fip1_S346	0.50	0.37	0.33	0.41
Rab11fip1	Rab11fip1_S339	0.72	0.78	0.54	0.59
Rab11fip1	Rab11fip1_S541	0.39	0.39	0.46	0.62
Rab11fip1	Rab11fip1_S358	0.89	0.83	0.41	0.67
Rab12	Rab12_S20	1.62	2.01	0.76	1.23
Rab44	Rab44_S268	0.42	0.49	0.52	0.77
Rab44	Rab44_S272	0.54	0.68	0.70	0.82
Rab44	Rab44_S188	0.28	0.28	0.63	1.01
Rab44	Rab44_S221	0.42	0.36	1.12	1.59
Rab44	Rab44_T282	0.60	0.61	0.84	1.60
Rab44	Rab44_S269	0.62	0.61	0.89	1.86
Rabgef1	Rabgef1_T131	1.30	1.74	0.92	1.36
Rabl6	Rabl6_S502	0.89	0.72	0.60	0.97
Rabl6	Rabl6_S482	1.27	1.32	1.02	1.05
Rabl6	Rabl6_S483	1.27	1.32	1.02	1.05
Rad18	Rad18_S158	1.02	0.78	1.04	0.64
Raf1	Raf1_S259	0.72	0.70	0.92	1.19
Raf1	Raf1_S621	0.93	0.89	1.08	1.45
Ralbp1	Ralbp1_S11	1.31	1.44	1.21	1.73
Ralgapa1	Ralgapa1_S859	1.08	0.62	0.43	0.35
Ralgapa1	Ralgapa1_S860	0.69	0.45	0.65	0.79
Ralgapa1	Ralgapa1_S772	0.95	0.79	0.81	1.05
Ralgapb	Ralgapb_S359	1.77	1.41	0.86	0.68
Raly	Raly_T258	1.55	1.59	0.72	0.59
Raly	Raly_S119	1.47	1.45	1.20	0.96
Raly	Raly_S254	1.26	1.38	1.37	1.33
Raly	Raly_T252	1.24	1.61	1.52	1.37
Ranbp2	Ranbp2_S788	0.54	0.59	0.60	0.46

Ranbp2	Ranbp2_S2113	0.38	0.36	0.98	0.57
Ranbp2	Ranbp2_S21	0.64	0.67	0.92	0.58
Ranbp2	Ranbp2_S781	0.58	0.62	0.81	0.83
Ranbp2	Ranbp2_S2117	0.81	0.58	1.82	1.48
Rasa3	Rasa3_S809	0.35	0.36	1.26	2.27
Rasal3	Rasal3_S256	0.55	0.69	2.45	4.44
Rassf1	Rassf1_Y185	0.73	0.89	1.45	2.90
Raver1	Raver1_T23	1.15	1.01	0.63	0.64
Raver1	Raver1_S14	0.89	0.86	0.61	0.66
Raver1	Raver1_S576	1.08	1.58	1.49	2.54
Rb1	Rb1_T364	0.46	0.40	0.68	0.27
Rb1	Rb1_S788	0.60	0.94	0.46	0.28
Rb1	Rb1_S31	0.27	0.25	0.20	0.34
Rb1	Rb1_T367	0.36	0.30	0.41	0.35
Rb1	Rb1_T814	0.30	0.32	0.28	0.36
Rb1	Rb1_S243	0.56	0.44	0.53	0.64
Rb1cc1	Rb1cc1_T238	0.87	0.82	0.74	0.79
Rb1cc1	Rb1cc1_S237	0.75	1.51	0.74	0.79
Rb1cc1	Rb1cc1_S646	0.61	0.46	0.93	1.47
Rbbp6	Rbbp6_S1278	1.19	1.15	1.05	0.63
Rbbp6	Rbbp6_S1179	0.99	1.04	0.80	0.72
Rbbp6	Rbbp6_S862	1.10	1.04	0.75	0.74
Rbbp8	Rbbp8_S325	0.73	0.64	0.58	0.43
Rbbp8	Rbbp8_S326	0.66	0.65	0.76	0.47
Rbl2	Rbl2_S37	1.77	0.92	0.66	1.48
Rbm12b2	Rbm12b2_S277	0.86	0.83	0.78	0.80
Rbm12b2	Rbm12b2_S279	0.86	0.83	0.78	0.80
Rbm12b2	Rbm12b2_S681	0.83	0.79	0.98	1.00
Rbm14	Rbm14_T206	0.95	0.88	0.90	0.78
Rbm14	Rbm14_S215	1.14	1.06	0.90	0.80
Rbm14	Rbm14_S220	0.98	1.07	0.90	0.80
Rbm14	Rbm14_S225	0.83	1.14	0.85	0.89
Rbm15	Rbm15_S256	1.05	0.98	0.85	0.78
Rbm15	Rbm15_S258	1.05	0.98	0.85	0.78
Rbm15	Rbm15_T668	2.05	1.03	0.99	0.83
Rbm15	Rbm15_S670	2.24	1.07	0.99	0.83
Rbm15	Rbm15_S674	2.45	1.12	0.99	0.83
Rbm15	Rbm15_S293	1.31	1.24	0.92	0.85
Rbm15	Rbm15_T567	1.21	1.18	1.10	0.95
Rbm17	Rbm17_S222	0.58	0.60	0.73	0.67
Rbm17	Rbm17_S155	0.87	0.77	0.67	0.80
Rbm25	Rbm25_S670	1.21	1.52	0.96	0.58
Rbm25	Rbm25_S672	0.93	1.15	0.83	0.61
Rbm25	Rbm25_S698	1.15	1.07	0.69	0.74
Rbm26	Rbm26_S127	1.40	1.34	1.04	0.73
Rbm26	Rbm26_S616	0.94	1.06	1.32	0.96
Rbm33	Rbm33_S243	1.22	1.03	0.88	0.85
Rbm33	Rbm33_S816	1.07	0.83	0.91	0.87
Rbm39	Rbm39_S97	1.08	1.25	0.91	0.88
Rbm39	Rbm39_S136	0.98	0.97	1.05	1.01
Rbm4b	Rbm4b_S86	0.63	0.66	1.75	3.65
Rbm6	Rbm6_S888	0.52	0.26	0.60	0.56
Rbm7	Rbm7_S136	1.02	1.22	1.16	1.52
Rbm8a	Rbm8a_S42	1.61	1.35	1.23	1.09
Rbm8a	Rbm8a_S42	1.49	1.45	1.23	1.09

Rbmxl1	Rbmxl1_S88	0.84	0.69	0.79	0.79
Rbmxl1	Rbmxl1_S205	1.08	1.05	0.96	0.91
Rbmxl1	Rbmxl1_S349	1.10	0.99	1.00	1.14
Rcc1	Rcc1_S11	1.02	0.99	0.65	0.79
Rcsd1	Rcsd1_S120	0.52	0.54	0.39	0.33
Rcsd1	Rcsd1_S116	1.67	2.09	0.47	0.39
Rcsd1	Rcsd1_T256	0.37	0.34	0.64	0.54
Rcsd1	Rcsd1_S127	0.39	0.49	0.72	0.59
Rcsd1	Rcsd1_S126	0.43	0.50	1.05	0.66
Rcsd1	Rcsd1_S108	0.94	1.09	0.95	1.11
Rcsd1	Rcsd1_S105	0.61	0.64	2.30	1.47
Rcsd1	Rcsd1_S83	0.72	0.77	1.50	1.88
Rcsd1	Rcsd1_S333	0.37	0.38	0.65	1.91
Rcsd1	Rcsd1_S82	0.75	0.94	1.26	1.95
Rcsd1	Rcsd1_S68	0.75	0.86	1.50	2.17
Rcsd1	Rcsd1_S246	1.04	0.69	2.17	2.91
Rdx	Rdx_Y270	0.44	0.39	0.37	3.97
Reep4	Reep4_S152	1.92	1.81	1.78	2.45
Reps1	Reps1_S681	1.03	1.00	1.32	2.01
Rere	Rere_S656	1.18	1.17	0.92	0.94
Rexo1	Rexo1_S514	0.86	0.80	0.79	1.04
Rfc1	Rfc1_T109	1.63	0.87	0.00	0.00
Rfc1	Rfc1_S107	2.23	1.63	0.00	0.00
Rfc1	Rfc1_S535	1.34	1.16	0.98	0.31
Rfc1	Rfc1_S266	0.89	0.75	1.12	0.34
Rfc1	Rfc1_S155	0.90	0.68	1.49	0.69
Rfc1	Rfc1_S244	1.37	1.28	2.17	0.80
Rfx5	Rfx5_S184	0.94	1.02	0.54	0.45
Rgs18	Rgs18_S218	1.05	0.89	0.98	0.75
Rgs18	Rgs18_T220	1.00	0.79	1.11	0.76
Rhbdf2	Rhbdf2_S359	0.47	0.44	0.67	0.61
Rhbdf2	Rhbdf2_S295	0.31	0.25	1.60	1.07
Rhbdf2	Rhbdf2_S298	0.30	0.26	1.60	1.07
Rhbdf2	Rhbdf2_S60	0.47	0.65	0.51	1.44
Rhbdf2	Rhbdf2_S357	0.45	0.65	1.24	2.54
Ric8	Ric8_S501	1.07	0.89	0.68	0.59
Rictor	Rictor_S21	1.05	0.77	1.04	1.34
Rif1	Rif1_S1690	1.01	0.84	1.10	0.89
Rif1	Rif1_S394	0.80	0.79	0.72	0.90
Rif1	Rif1_S1464	0.66	0.70	1.22	1.36
Rif1	Rif1_S1547	1.21	1.03	1.47	1.39
Riok3	Riok3_S512	0.94	0.90	0.73	0.63
Ripk1	Ripk1_S313	0.97	0.91	1.27	1.51
Rlim	Rlim_S229	0.94	0.90	0.82	1.05
Rmdn3	Rmdn3_S46	1.22	1.31	0.85	0.93
Rnf113a1	Rnf113a1_S6	0.82	0.87	1.83	1.48
Rnf113a2	Rnf113a2_T330	0.38	0.42	0.37	0.56
Rnf113a2	Rnf113a2_S329	0.38	0.42	0.53	0.96
Rnf219	Rnf219_S210	0.46	0.42	0.71	0.53
Rnmt	Rnmt_T34	0.53	0.62	1.42	0.80
Rnmt	Rnmt_S64	0.86	0.87	0.91	0.83
Rnmt	Rnmt_S11	1.34	1.37	0.82	0.95
Rnmt	Rnmt_S15	1.35	1.46	1.00	1.02
Rnmt	Rnmt_S100	0.93	0.84	0.72	1.23
Rnmtl1	Rnmtl1_S42	0.74	0.84	0.86	0.51

Rnps1	Rnps1_S4	0.99	0.77	0.84	0.87
Rnps1	Rnps1_S134	0.91	0.97	0.90	0.93
Rnps1	Rnps1_S132	0.94	0.98	0.97	0.94
Rpap3	Rpap3_S429	0.96	0.89	0.90	0.79
Rpl10a	Rpl10a_Y11	0.44	0.41	0.55	1.40
Rpl12	Rpl12_S38	0.83	0.80	0.95	0.97
Rpl13	Rpl13_T107	0.89	0.82	0.00	0.00
Rpl13	Rpl13_S106	0.98	0.76	1.40	1.09
Rpl14	Rpl14_S139	1.05	0.68	1.69	0.41
Rpl15	Rpl15_Y59	0.51	0.52	0.60	1.01
Rpl15	Rpl15_S97	1.12	0.83	1.13	1.43
Rpl18	Rpl18_S130	1.09	0.99	0.85	0.57
Rpl4	Rpl4_S295	1.08	1.08	1.17	0.71
Rplp0	Rplp0_Y24	0.56	0.62	1.40	1.45
Rplp1	Rplp1_S104	1.08	0.93	0.41	0.61
Rplp1	Rplp1_S101	1.06	0.93	0.67	0.62
Rplp2	Rplp2_S102	0.65	0.75	0.42	0.42
Rplp2	Rplp2_S105	0.81	0.85	0.47	0.64
Rplp2	Rplp2_S16	1.03	0.84	1.29	0.99
Rprd2	Rprd2_S504	0.75	0.80	0.80	0.99
Rprd2	Rprd2_S392	0.73	0.83	1.44	1.15
Rps10	Rps10_S146	1.07	0.87	1.13	1.35
Rps10	Rps10_Y12	0.53	0.53	0.48	1.92
Rps17	Rps17_S113	0.66	0.61	1.04	1.09
Rps20	Rps20_T9	1.09	1.17	1.87	2.34
Rps3	Rps3_T221	0.65	0.66	0.58	1.53
Rps3	Rps3_Y120	0.66	0.67	0.66	1.58
Rps3a1	Rps3a1_S263	1.03	0.80	1.18	0.94
Rps6ka3	Rps6ka3_S715	0.65	0.50	1.29	1.23
Rps6kc1	Rps6kc1_S280	0.75	0.89	0.00	0.00
Rptor	Rptor_S863	0.98	1.06	1.69	1.52
Rras2	Rras2_S186	0.97	1.21	1.23	0.96
Rrbp1	Rrbp1_S135	0.99	0.99	1.18	1.17
Rreb1	Rreb1_S1179	0.71	0.47	0.62	0.56
Rrm2	Rrm2_S20	0.24	0.30	0.29	0.16
Rrp1	Rrp1_S434	0.78	0.79	2.61	1.53
Rrp12	Rrp12_S1081	1.12	1.02	1.32	0.84
Rrp15	Rrp15_S19	0.38	0.44	1.61	1.71
Rrp1b	Rrp1b_S304	0.58	0.54	0.63	0.72
Rrp1b	Rrp1b_S306	0.55	0.46	0.71	1.24
Rrp1b	Rrp1b_S571	0.82	0.50	1.68	4.19
Rrp9	Rrp9_S470	0.80	0.76	0.87	0.87
Rsf1	Rsf1_S401	0.58	0.74	0.68	0.32
Rsrc2	Rsrc2_S32	1.11	1.10	1.44	0.87
Rsrc2	Rsrc2_S17	1.26	1.06	0.75	0.89
Rsrc2	Rsrc2_T16	0.90	0.79	0.91	1.04
Rtn4	Rtn4_S165	0.53	0.53	0.62	1.49
Rtn4	Rtn4_S167	0.46	0.49	1.04	2.97
Rtn4	Rtn4_S105	0.64	0.64	1.35	3.34
Rtn4	Rtn4_S857	0.97	1.78	0.74	3.87
Rtn4	Rtn4_S489	0.31	0.35	0.81	5.19
Runx1	Runx1_T14	1.09	0.46	0.96	0.50
Runx1	Runx1_S21	0.93	1.09	0.96	0.50
Sae1	Sae1_S189	0.73	0.50	0.73	1.34
Safb	Safb_S626	0.73	0.68	0.44	0.69

Safb	Safb_S623	0.81	0.81	0.86	0.76
Safb2	Safb2_S387	0.74	0.73	0.82	1.13
Samd1	Samd1_S150	0.99	0.96	1.18	0.63
Samsn1	Samsn1_S119	1.21	1.29	0.57	0.39
Samsn1	Samsn1_S90	1.81	3.02	0.88	1.36
Samsn1	Samsn1_S23	2.00	2.59	1.09	1.42
Samsn1	Samsn1_S97	0.49	0.43	0.86	1.66
Sap130	Sap130_S416	1.36	1.21	1.04	1.03
Sash3	Sash3_S27	2.09	2.61	0.88	3.90
Sash3	Sash3_S25	2.67	2.44	0.86	4.16
Sash3	Sash3_S26	2.67	2.44	0.86	4.16
Scaf1	Scaf1_S682	0.43	0.42	0.54	0.56
Scaf1	Scaf1_S676	0.54	0.52	0.56	0.67
Scaf1	Scaf1_S240	0.65	0.71	0.59	0.74
Scaf1	Scaf1_S491	0.78	0.76	0.72	0.78
Scaf1	Scaf1_S493	0.78	0.76	0.72	0.78
Scaf1	Scaf1_S577	0.77	0.76	0.74	0.81
Scaf1	Scaf1_S579	0.77	0.76	0.74	0.81
Scaf11	Scaf11_S502	0.93	0.84	0.63	0.67
Scaf11	Scaf11_S857	0.63	0.65	0.75	0.74
Scaf11	Scaf11_S859	1.13	1.01	0.86	0.79
Scaf11	Scaf11_S498	0.78	0.72	0.81	0.84
Scaf8	Scaf8_S617	0.76	0.85	1.00	1.05
Scamp3	Scamp3_S78	0.69	0.69	0.54	1.66
Scnm1	Scnm1_T184	0.42	0.48	0.63	0.69
Scnm1	Scnm1_S182	0.47	0.44	0.72	0.86
Scrib	Scrib_S1485	0.90	0.94	1.16	1.34
Scrib	Scrib_S821	1.00	0.79	2.09	2.37
Sdad1	Sdad1_S585	1.21	1.20	2.57	0.96
Sde2	Sde2_S269	0.49	0.49	0.89	1.38
Sec16a	Sec16a_S2053	1.08	1.07	0.44	1.34
Sec16a	Sec16a_S2058	1.10	1.19	0.44	1.34
Sec16a	Sec16a_S1028	1.36	1.57	1.14	1.46
Sec22b	Sec22b_S137	0.81	0.59	0.53	2.93
Sec23ip	Sec23ip_S748	0.73	0.83	0.66	0.72
Sec31a	Sec31a_S526	0.90	0.90	0.00	0.00
Sec31a	Sec31a_S531	1.06	1.09	0.00	0.00
Sec61b	Sec61b_S14	0.52	0.55	0.81	1.04
Sec61b	Sec61b_S17	0.67	0.74	0.89	1.05
Sec61b	Sec61b_S13	0.70	0.76	2.20	1.49
Senp3	Senp3_S163	0.87	0.86	0.67	1.05
Sept2	Sept2_S178	1.14	1.03	0.86	0.93
Sept9	Sept9_S78	1.33	1.89	1.20	1.04
Sept9	Sept9_S75	1.22	1.97	1.34	1.06
Set	Set_S30	1.02	0.93	0.62	0.54
Set	Set_S160	2.76	3.08	1.55	0.99
Setd1a	Setd1a_S483	0.76	0.85	0.00	0.00
Setd1a	Setd1a_S1160	0.57	0.42	0.46	0.40
Setd1a	Setd1a_S1159	0.57	0.42	0.45	0.41
Setd1a	Setd1a_S578	0.44	0.53	0.46	0.52
Setd1a	Setd1a_T553	0.44	0.53	0.46	0.52
Setd1a	Setd1a_S481	0.75	0.85	0.76	0.74
Setd2	Setd2_S132	0.67	0.68	1.07	0.69
Setd2	Setd2_S624	0.82	0.80	1.26	0.86
Setd2	Setd2_S2053	0.78	0.83	1.04	0.88

Setd2	Setd2_S2055	0.78	0.83	1.04	0.88
Setd2	Setd2_S614	0.74	0.74	1.22	0.89
Setd2	Setd2_S890	0.87	0.83	1.14	1.11
Sf1	Sf1_S80	0.61	0.58	0.62	0.60
Sf1	Sf1_S82	0.61	0.58	0.62	0.60
Sf3b2	Sf3b2_S290	0.82	1.07	1.24	1.39
Sf3b2	Sf3b2_S292	1.26	1.12	1.24	1.39
Sfrs18	Sfrs18_S211	0.70	0.82	0.64	0.62
Sgta	Sgta_T82	1.23	1.05	0.62	0.66
Sh3bp1	Sh3bp1_S535	0.58	0.59	0.44	1.03
Sh3bp5l	Sh3bp5l_S342	0.77	0.91	0.82	1.21
Sh3bp5l	Sh3bp5l_S377	1.16	1.09	1.43	1.38
Sh3kbp1	Sh3kbp1_S193	0.29	0.35	0.71	0.51
Sh3kbp1	Sh3kbp1_S550	0.50	0.52	0.66	1.53
Sik3	Sik3_S551	1.59	1.89	0.69	0.68
Sin3a	Sin3a_S941	1.10	0.95	0.93	0.78
Sin3a	Sin3a_S1113	1.57	2.96	0.85	0.90
Sin3a	Sin3a_S431	1.43	1.44	1.48	1.40
Sipa1l1	Sipa1l1_S1626	1.85	1.52	1.76	0.47
Sipa1l1	Sipa1l1_S1564	1.13	0.95	1.34	0.53
Sipa1l1	Sipa1l1_S1507	0.50	0.54	0.89	0.57
Sipa1l1	Sipa1l1_S1528	0.53	0.57	1.11	0.63
Sipa1l1	Sipa1l1_S1412	0.31	0.39	0.61	0.65
Sipa1l1	Sipa1l1_S1410	0.36	0.40	0.73	0.72
Sipa1l1	Sipa1l1_S1234	0.31	0.36	0.90	0.84
Sipa1l1	Sipa1l1_S1544	0.48	0.56	1.06	1.01
Sipa1l1	Sipa1l1_S1116	0.88	0.97	0.87	1.05
Ska3	Ska3_S119	0.36	0.45	0.48	0.38
Ska3	Ska3_T120	0.36	0.45	0.48	0.38
Skap2	Skap2_S9	0.45	0.50	0.32	0.46
Skap2	Skap2_Y122	0.64	0.78	0.66	0.84
Skiv2l	Skiv2l_S240	1.12	0.93	0.95	0.64
Skiv2l	Skiv2l_S242	0.72	0.74	1.25	1.46
Slc16a1	Slc16a1_S210	0.49	0.56	0.77	0.61
Slc16a1	Slc16a1_S213	0.98	1.04	1.12	0.95
Slc1a5	Slc1a5_S520	0.75	0.81	1.72	1.67
Slc35c2	Slc35c2_S221	1.49	1.53	1.82	1.60
Slc38a1	Slc38a1_T54	0.70	0.98	1.06	1.79
Slc38a1	Slc38a1_S52	0.65	0.90	1.12	1.81
Slc38a1	Slc38a1_S56	0.94	1.15	2.12	2.34
Slc3a2	Slc3a2_S2	0.43	0.54	0.41	0.58
Slc43a2	Slc43a2_S297	0.75	0.80	1.28	0.97
Slc4a1ap	Slc4a1ap_S258	1.00	0.91	1.16	1.10
Slc4a7	Slc4a7_S238	0.86	0.79	0.93	0.74
Slc4a7	Slc4a7_S263	0.90	0.91	1.03	0.94
Slc4a7	Slc4a7_S247	0.98	0.90	1.20	0.98
Slc52a3	Slc52a3_S266	1.49	1.67	1.03	1.28
Slc9a1	Slc9a1_S697	1.41	1.33	1.25	0.61
Slc9a1	Slc9a1_S707	0.83	0.72	1.50	2.21
Slc9a3r1	Slc9a3r1_S286	0.75	0.92	0.00	0.00
Slc9a3r1	Slc9a3r1_S275	0.85	1.04	1.21	0.54
Slc9a3r1	Slc9a3r1_S2	0.92	1.07	1.15	0.62
Slc9a3r1	Slc9a3r1_S297	1.09	1.09	1.96	0.78
Slc9a3r1	Slc9a3r1_S285	1.83	1.61	1.44	0.81
Slirp	Slirp_S105	0.94	0.83	1.15	1.07

Slirp	Slirp_T104	0.80	0.87	1.17	1.08
Slk	Slk_S666	0.93	0.86	0.94	1.36
Sltm	Sltm_S534	1.00	1.04	0.54	0.66
Sltm	Sltm_S532	1.23	1.22	0.88	0.87
Sltm	Sltm_S271	0.95	0.94	0.82	0.88
Slu7	Slu7_S215	0.75	0.78	0.84	0.78
Smad2	Smad2_T8	1.26	1.22	1.58	0.80
Smarca4	Smarca4_S1419	1.13	0.92	0.95	0.68
Smarca4	Smarca4_S695	0.93	0.74	0.94	0.87
Smarca4	Smarca4_S1349	1.42	1.29	0.69	0.89
Smarca4	Smarca4_S699	1.13	1.07	0.90	0.90
Smarca5	Smarca5_S115	0.43	0.46	0.57	0.46
Smarca5	Smarca5_T112	0.46	0.35	1.63	1.08
Smarcad1	Smarcad1_S124	0.57	0.64	1.02	1.08
Smarcad1	Smarcad1_S127	1.17	1.15	1.02	1.08
Smarcc1	Smarcc1_S327	1.15	1.14	0.84	0.65
Smarcc1	Smarcc1_S329	1.13	1.11	0.79	0.70
Smarcc1	Smarcc1_S309	0.97	1.09	1.12	0.82
Smarcc2	Smarcc2_S304	0.68	0.74	0.54	0.51
Smarcc2	Smarcc2_S302	0.78	0.86	0.54	0.51
Smarcc2	Smarcc2_S347	1.10	0.80	0.49	0.66
Smc1a	Smc1a_S360	0.30	0.25	0.16	0.27
Smc3	Smc3_S1067	0.75	0.59	0.72	0.96
Smcr7l	Smcr7l_S94	0.53	0.59	0.51	0.91
Smcr7l	Smcr7l_S55	0.68	0.72	0.90	1.57
Smcr7l	Smcr7l_S59	0.68	0.72	1.17	1.79
Smg1	Smg1_S3567	1.18	0.80	0.59	0.57
Smg1	Smg1_T3570	0.44	0.50	0.56	0.60
Smn1	Smn1_S10	1.16	1.11	1.30	1.14
Snd1	Snd1_Y109	0.58	0.55	3.71	8.56
Snip1	Snip1_S48	0.92	0.81	1.21	0.87
Snip1	Snip1_S50	0.94	0.85	1.21	0.87
Snip1	Snip1_S33	1.15	1.00	1.35	0.93
Snip1	Snip1_S18	1.42	1.40	1.36	1.07
Snrnp200	Snrnp200_S225	1.06	1.14	1.18	1.04
Snrnp70	Snrnp70_S226	1.02	0.92	0.73	0.65
Snrnp70	Snrnp70_Y126	1.29	1.38	1.21	0.79
Snrnp70	Snrnp70_S408	0.75	0.78	0.60	0.86
Sntb2	Sntb2_S88	0.66	0.63	0.54	0.82
Sntb2	Sntb2_S90	0.65	0.61	0.56	0.82
Sntb2	Sntb2_S75	0.69	0.63	0.46	0.83
Snw1	Snw1_S224	0.70	0.53	0.78	0.72
Snw1	Snw1_S232	0.82	0.75	0.98	0.82
Snx2	Snx2_T104	1.25	1.48	1.14	4.02
Son	Son_S2027	1.11	1.09	0.75	0.72
Son	Son_S2031	0.83	1.03	0.69	0.75
Son	Son_S2029	0.83	1.03	0.53	0.93
Son	Son_S1723	0.95	0.99	1.08	1.34
Sos1	Sos1_S1082	1.08	1.20	0.86	2.12
Sox6	Sox6_S357	1.18	1.15	0.98	0.12
Sp1	Sp1_S2	0.69	0.94	1.09	0.93
Sp100	Sp100_S314	0.81	0.72	0.46	0.68
Sp100	Sp100_T313	0.87	0.71	0.47	0.69
Spag9	Spag9_T74	1.47	1.01	1.13	2.36
Spen	Spen_S1303	0.83	0.93	0.97	0.86

Spen	Spen_S748	0.87	0.89	1.13	0.98
Spen	Spen_S750	0.92	0.96	1.13	0.98
Sptan1	Sptan1_S1029	1.25	1.15	0.73	0.39
Sptan1	Sptan1_S1031	1.23	1.14	0.80	0.43
Sptan1	Sptan1_S1197	1.63	1.98	1.58	1.08
Sptbn1	Sptbn1_S2339	0.75	0.82	1.06	0.36
Sptbn1	Sptbn1_S2340	0.76	0.79	1.30	0.45
Sptbn1	Sptbn1_S2137	1.33	1.56	1.61	1.54
Srcap	Srcap_S2845	0.74	0.62	0.00	0.00
Srcap	Srcap_S579	0.62	0.52	0.53	0.50
Srek1	Srek1_S465	0.83	1.00	0.92	0.71
Srf	Srf_S220	0.45	0.46	0.51	1.03
Srp14	Srp14_S45	1.83	2.03	0.47	0.33
Srp72	Srp72_T624	0.68	0.66	0.00	0.00
Srp72	Srp72_T571	0.45	0.46	0.31	0.41
Srp72	Srp72_S621	1.04	0.79	1.09	0.74
Srp72	Srp72_S625	0.66	0.59	0.88	0.91
Srp72	Srp72_S620	0.65	0.69	0.92	1.01
Srpk1	Srpk1_T448	0.66	0.61	0.00	0.00
Srpk1	Srpk1_S450	3.05	1.04	0.55	0.72
Srpk1	Srpk1_S311	0.61	0.52	0.55	0.88
Srrm1	Srrm1_S788	0.70	0.83	0.00	0.00
Srrm1	Srrm1_S567	0.45	0.34	0.47	0.40
Srrm1	Srrm1_S443	0.93	0.94	0.58	0.43
Srrm1	Srrm1_S767	0.38	0.39	0.43	0.45
Srrm1	Srrm1_S769	0.61	0.53	0.38	0.50
Srrm1	Srrm1_S630	0.69	0.64	0.47	0.51
Srrm1	Srrm1_T628	0.80	0.75	0.71	0.60
Srrm1	Srrm1_S545	0.89	0.94	0.70	0.62
Srrm1	Srrm1_S640	0.87	0.84	0.70	0.64
Srrm1	Srrm1_S642	0.87	0.84	0.70	0.64
Srrm1	Srrm1_S697	0.84	0.77	0.68	0.65
Srrm1	Srrm1_S699	0.98	0.95	0.68	0.65
Srrm1	Srrm1_S445	1.09	1.12	0.84	0.66
Srrm1	Srrm1_T399	0.83	0.79	0.77	0.66
Srrm1	Srrm1_S718	1.04	1.04	0.65	0.66
Srrm1	Srrm1_S720	1.04	1.04	0.65	0.66
Srrm1	Srrm1_S586	0.88	0.99	0.77	0.67
Srrm1	Srrm1_T588	0.88	0.99	0.77	0.67
Srrm1	Srrm1_S597	0.93	0.85	0.76	0.67
Srrm1	Srrm1_T595	0.93	0.85	0.76	0.67
Srrm1	Srrm1_S220	0.93	0.88	0.75	0.67
Srrm1	Srrm1_S396	0.66	0.59	0.68	0.68
Srrm1	Srrm1_S395	0.60	0.52	0.68	0.68
Srrm1	Srrm1_S386	1.17	1.28	0.91	0.69
Srrm1	Srrm1_S384	1.14	1.15	0.85	0.70
Srrm1	Srrm1_S652	0.76	0.73	0.74	0.70
Srrm1	Srrm1_S650	0.84	0.82	0.74	0.70
Srrm1	Srrm1_S621	0.88	0.83	1.33	0.70
Srrm1	Srrm1_S619	1.07	0.96	1.33	0.70
Srrm1	Srrm1_S810	1.04	1.08	1.03	0.71
Srrm1	Srrm1_S726	1.50	1.38	0.73	0.71
Srrm1	Srrm1_S765	1.09	1.11	0.62	0.73
Srrm1	Srrm1_S669	0.93	0.89	0.74	0.74
Srrm1	Srrm1_S667	1.02	1.06	0.74	0.74

Srrm1	Srrm1_S260	0.81	0.74	0.66	0.75
Srrm1	Srrm1_S569	0.67	0.66	0.69	0.75
Srrm1	Srrm1_S382	1.16	1.25	0.92	0.76
Srrm1	Srrm1_T885	0.70	0.70	1.25	0.76
Srrm1	Srrm1_T740	1.02	0.95	0.94	0.76
Srrm1	Srrm1_S738	1.00	0.98	0.94	0.76
Srrm1	Srrm1_S556	0.91	0.93	0.86	0.77
Srrm1	Srrm1_S558	0.91	0.93	0.86	0.77
Srrm1	Srrm1_S604	1.11	1.16	0.85	0.77
Srrm1	Srrm1_S606	1.11	1.16	0.85	0.77
Srrm1	Srrm1_S689	1.01	1.01	0.80	0.77
Srrm1	Srrm1_S611	1.09	1.07	0.80	0.77
Srrm1	Srrm1_S728	1.04	0.89	0.94	0.78
Srrm1	Srrm1_S709	1.41	0.96	0.84	0.78
Srrm1	Srrm1_S751	1.16	1.17	0.82	0.80
Srrm1	Srrm1_S887	1.19	1.09	1.28	0.81
Srrm1	Srrm1_S753	0.95	0.87	0.92	0.83
Srrm1	Srrm1_S708	0.83	0.86	0.88	0.84
Srrm1	Srrm1_S424	1.17	1.18	0.88	0.85
Srrm1	Srrm1_S756	1.15	1.09	0.98	0.86
Srrm1	Srrm1_S422	1.00	0.98	1.05	0.89
Srrm1	Srrm1_S782	0.59	0.71	0.83	0.91
Srrm1	Srrm1_S804	1.03	1.04	1.03	1.02
Srrm1	Srrm1_T806	1.04	1.22	1.03	1.02
Srrm1	Srrm1_S815	1.03	1.04	1.01	1.09
Srrm1	Srrm1_S458	0.76	0.82	1.00	1.12
Srrm1	Srrm1_S456	1.57	1.49	1.00	1.12
Srrm2	Srrm2_T727	0.92	1.01	0.00	0.00
Srrm2	Srrm2_S981	0.73	0.87	0.50	0.52
Srrm2	Srrm2_S1979	0.91	0.93	0.56	0.53
Srrm2	Srrm2_S1923	0.84	0.83	0.59	0.54
Srrm2	Srrm2_S1927	0.84	0.90	0.59	0.54
Srrm2	Srrm2_S1180	1.02	0.52	0.54	0.58
Srrm2	Srrm2_T1478	0.76	0.73	0.54	0.59
Srrm2	Srrm2_S1055	0.72	0.65	0.57	0.61
Srrm2	Srrm2_S2439	0.76	0.69	0.56	0.61
Srrm2	Srrm2_T1925	0.91	0.94	0.61	0.61
Srrm2	Srrm2_S1083	0.63	0.51	0.63	0.62
Srrm2	Srrm2_T1294	1.00	1.00	0.73	0.63
Srrm2	Srrm2_T877	0.66	0.69	0.57	0.63
Srrm2	Srrm2_S1534	0.85	0.87	0.69	0.63
Srrm2	Srrm2_S1532	0.88	0.89	0.69	0.63
Srrm2	Srrm2_S1535	0.85	0.91	0.69	0.63
Srrm2	Srrm2_S1736	1.06	0.98	0.57	0.65
Srrm2	Srrm2_S682	1.22	1.62	0.64	0.66
Srrm2	Srrm2_S1209	0.95	1.05	0.81	0.66
Srrm2	Srrm2_S1001	0.73	0.76	0.65	0.66
Srrm2	Srrm2_T1274	0.77	0.82	0.62	0.66
Srrm2	Srrm2_S337	0.91	0.72	1.42	0.68
Srrm2	Srrm2_S2560	0.97	0.87	0.84	0.68
Srrm2	Srrm2_S358	0.78	0.91	0.72	0.69
Srrm2	Srrm2_S1956	0.96	0.92	0.73	0.70
Srrm2	Srrm2_S338	0.82	0.78	0.35	0.71
Srrm2	Srrm2_S339	0.90	0.77	0.45	0.71
Srrm2	Srrm2_S1888	1.00	0.76	0.64	0.71

Srrm2	Srrm2_T2441	0.74	0.86	0.73	0.71
Srrm2	Srrm2_S1120	0.81	1.00	0.78	0.73
Srrm2	Srrm2_S1738	1.03	0.96	0.71	0.74
Srrm2	Srrm2_S356	0.90	0.79	0.85	0.74
Srrm2	Srrm2_S2595	0.86	0.81	0.78	0.75
Srrm2	Srrm2_T2593	0.86	0.81	0.78	0.75
Srrm2	Srrm2_S1182	0.82	0.87	0.65	0.75
Srrm2	Srrm2_T1352	1.07	1.08	0.80	0.75
Srrm2	Srrm2_S2285	1.02	1.03	0.70	0.75
Srrm2	Srrm2_S2308	0.94	0.91	0.68	0.75
Srrm2	Srrm2_S725	0.76	0.76	0.85	0.78
Srrm2	Srrm2_S255	0.81	0.85	0.84	0.78
Srrm2	Srrm2_S253	0.81	0.95	0.84	0.78
Srrm2	Srrm2_S2564	1.10	1.05	0.98	0.78
Srrm2	Srrm2_T1752	0.82	0.84	0.81	0.79
Srrm2	Srrm2_S1750	1.17	1.19	0.81	0.79
Srrm2	Srrm2_S357	0.59	0.61	0.95	0.80
Srrm2	Srrm2_S476	0.94	0.88	0.84	0.80
Srrm2	Srrm2_T478	0.94	0.88	0.84	0.80
Srrm2	Srrm2_S1958	0.99	1.08	0.77	0.80
Srrm2	Srrm2_S1247	0.93	0.76	0.42	0.80
Srrm2	Srrm2_S1244	0.79	0.85	1.46	0.82
Srrm2	Srrm2_S677	0.83	0.74	0.65	0.83
Srrm2	Srrm2_T1740	1.03	0.96	0.88	0.83
Srrm2	Srrm2_S1782	0.97	0.90	0.88	0.83
Srrm2	Srrm2_T1784	0.97	0.90	0.88	0.83
Srrm2	Srrm2_S1886	0.76	0.74	0.84	0.85
Srrm2	Srrm2_T1269	0.88	1.02	1.11	0.85
Srrm2	Srrm2_S1988	1.32	1.57	0.93	0.85
Srrm2	Srrm2_S2552	1.00	1.16	0.86	0.86
Srrm2	Srrm2_T1890	0.97	0.95	0.86	0.86
Srrm2	Srrm2_T2254	1.20	1.10	1.00	0.86
Srrm2	Srrm2_S1831	1.12	1.40	0.87	0.87
Srrm2	Srrm2_S1243	0.83	0.74	1.24	0.87
Srrm2	Srrm2_T1960	0.97	0.83	0.61	0.87
Srrm2	Srrm2_S888	0.74	0.78	1.08	0.87
Srrm2	Srrm2_S1876	1.04	0.97	0.84	0.88
Srrm2	Srrm2_T1878	1.04	0.97	0.84	0.88
Srrm2	Srrm2_S1826	0.98	0.87	0.89	0.89
Srrm2	Srrm2_S2255	1.13	1.11	1.22	0.90
Srrm2	Srrm2_S1780	1.01	1.00	0.85	0.90
Srrm2	Srrm2_S1974	1.13	1.22	1.06	0.90
Srrm2	Srrm2_S604	0.97	0.98	0.98	0.90
Srrm2	Srrm2_S606	1.09	1.29	0.98	0.90
Srrm2	Srrm2_S608	1.09	1.29	0.98	0.90
Srrm2	Srrm2_S679	0.86	0.88	0.81	0.91
Srrm2	Srrm2_S1481	0.93	0.77	1.02	0.92
Srrm2	Srrm2_S1476	0.93	0.78	1.02	0.92
Srrm2	Srrm2_S1702	1.01	1.02	0.87	0.93
Srrm2	Srrm2_T1704	1.04	1.03	0.87	0.93
Srrm2	Srrm2_S1304	0.89	1.03	0.60	0.93
Srrm2	Srrm2_S1977	0.97	0.95	0.90	0.93
Srrm2	Srrm2_S1242	0.74	0.73	1.14	0.94
Srrm2	Srrm2_S1480	0.84	0.77	0.88	0.95
Srrm2	Srrm2_S1553	0.81	0.73	0.78	1.00

Srrm2	Srrm2_S1554	1.06	0.96	0.78	1.00
Srrm2	Srrm2_S1551	1.01	1.09	0.78	1.00
Srrm2	Srrm2_S1263	1.05	0.81	0.95	1.01
Srrm2	Srrm2_S1264	1.01	0.86	1.12	1.05
Srrm2	Srrm2_T1830	0.96	0.82	0.97	1.05
Srrm2	Srrm2_S1828	0.96	0.90	0.97	1.05
Srrm2	Srrm2_S972	1.11	1.06	0.97	1.05
Srrm2	Srrm2_T2266	0.91	0.88	1.16	1.10
Srrm2	Srrm2_S2264	1.00	0.98	1.16	1.10
Srrm2	Srrm2_S1303	0.88	0.89	1.31	1.10
Srrm2	Srrm2_S2548	0.92	0.95	1.16	1.11
Srrm2	Srrm2_S1276	0.63	0.74	0.97	1.13
Srrm2	Srrm2_S342	0.76	0.77	0.62	1.33
Srrm2	Srrm2_S2128	1.02	1.75	1.50	1.34
Srrm2	Srrm2_S2550	1.05	1.05	0.80	1.42
Srrt	Srrt_S67	1.22	1.19	1.07	0.84
Srrt	Srrt_S4	1.20	1.21	1.26	0.95
Srsf1	Srsf1_S201	0.97	0.80	0.83	0.67
Srsf1	Srsf1_S2	1.07	1.02	0.98	0.86
Srsf1	Srsf1_S199	1.09	1.03	0.71	0.88
Srsf1	Srsf1_S205	1.02	1.08	0.71	7.77
Srsf10	Srsf10_S158	0.76	0.77	0.80	0.73
Srsf10	Srsf10_S160	0.80	0.81	0.80	0.73
Srsf10	Srsf10_S156	0.99	1.01	0.80	0.73
Srsf10	Srsf10_S158	0.99	1.01	0.80	0.73
Srsf10	Srsf10_S160	0.99	1.01	0.80	0.73
Srsf10	Srsf10_S133	1.09	1.07	1.05	0.87
Srsf10	Srsf10_S131	1.10	1.06	1.04	0.90
Srsf11	Srsf11_S449	0.77	0.85	0.88	0.75
Srsf11	Srsf11_S359	0.95	0.94	0.86	0.85
Srsf11	Srsf11_S361	0.95	0.94	0.86	0.85
Srsf11	Srsf11_S363	0.95	0.94	0.86	0.85
Srsf11	Srsf11_S200	0.82	0.99	1.53	1.33
Srsf2	Srsf2_T25	1.32	1.29	0.00	0.00
Srsf2	Srsf2_S26	1.70	1.37	0.00	0.00
Srsf2	Srsf2_S187	0.84	0.84	0.79	0.73
Srsf2	Srsf2_S189	0.88	0.90	0.82	0.74
Srsf2	Srsf2_S191	0.88	0.90	0.82	0.74
Srsf3	Srsf3_S138	1.15	1.12	1.01	0.95
Srsf3	Srsf3_S140	1.15	1.12	1.01	0.95
Srsf3	Srsf3_S108	1.06	1.06	0.81	0.99
Srsf3	Srsf3_Y32	0.73	0.97	1.02	2.86
Srsf6	Srsf6_S316	0.63	0.70	0.69	0.66
Srsf6	Srsf6_S314	0.66	0.71	0.69	0.66
Srsf6	Srsf6_S303	0.63	0.67	0.79	0.76
Srsf6	Srsf6_S297	0.93	0.91	1.01	0.87
Srsf6	Srsf6_S299	0.93	0.91	1.01	0.87
Srsf7	Srsf7_S179	1.05	0.92	0.83	0.46
Srsf7	Srsf7_S181	1.12	0.98	1.05	0.88
Srsf7	Srsf7_S171	1.07	0.96	0.95	0.90
Srsf7	Srsf7_S173	1.07	1.10	0.95	0.90
Srsf7	Srsf7_S175	1.07	1.10	0.95	0.90
Srsf7	Srsf7_S183	1.12	1.04	1.11	0.92
Srsf7	Srsf7_Y33	0.87	0.76	0.97	1.60
Srsf9	Srsf9_S212	1.24	1.03	0.73	0.56

Srsf9	Srsf9_S217	1.08	1.13	0.84	0.66
Ssfa2	Ssfa2_S738	1.09	1.05	0.88	1.47
Ssh2	Ssh2_S1216	1.73	1.59	0.00	0.00
Ssh2	Ssh2_S487	0.99	1.10	0.88	1.02
Ssh3	Ssh3_S9	0.76	0.50	0.84	1.03
Ssrp1	Ssrp1_S444	1.17	1.24	0.90	0.86
Stambpl1	Stambpl1_S242	0.62	0.66	0.71	1.56
Stat5a	Stat5a_S779	1.16	1.10	1.82	1.33
Stat5a	Stat5a_Y694	3.50	3.93	25.27	10.14
Stat5b	Stat5b_S128	1.16	0.75	0.00	0.00
Stat5b	Stat5b_Y699	2.05	1.90	22.75	14.11
Stat6	Stat6_Y641	0.15	0.20	0.89	0.88
Steap3	Steap3_S20	0.31	0.40	0.96	0.56
Steap3	Steap3_S17	0.37	0.43	0.76	0.64
Stim1	Stim1_S519	0.72	0.71	0.00	0.00
Stim1	Stim1_S257	0.38	0.28	0.66	0.91
Stim1	Stim1_S575	0.65	0.74	0.68	1.09
Stim2	Stim2_S28	1.37	1.08	0.78	1.51
Stk10	Stk10_T185	1.68	1.09	4.02	1.01
Stk10	Stk10_T950	1.37	1.24	1.66	1.66
Stk24	Stk24_S4	1.10	0.97	2.43	1.95
Stk3	Stk3_S316	0.67	0.72	0.87	1.03
Stmn1	Stmn1_S16	1.15	0.97	0.82	0.63
Stmn1	Stmn1_S63	1.07	1.41	0.90	0.77
Stmn1	Stmn1_S38	0.87	0.91	1.00	0.97
Stmn1	Stmn1_S25	0.73	0.77	1.38	3.38
Stmn2	Stmn2_S80	0.90	0.81	0.79	1.12
Strip1	Strip1_S335	0.97	0.78	1.16	0.85
Strn	Strn_S245	0.99	0.83	0.58	0.86
Strn3	Strn3_S229	0.77	0.95	1.16	1.64
Stub1	Stub1_S20	1.40	1.44	2.31	1.00
Stx4a	Stx4a_S15	0.96	0.82	1.05	0.86
Stx4a	Stx4a_S117	0.55	0.62	1.29	1.74
Stx7	Stx7_S45	0.70	0.72	0.46	0.54
Stx7	Stx7_T79	0.46	0.37	0.53	1.28
Suds3	Suds3_S234	0.76	0.73	0.74	0.43
Suds3	Suds3_S236	0.76	0.73	0.55	0.58
Suds3	Suds3_S237	0.76	0.73	0.56	0.74
Sumo1	Sumo1_S2	0.77	0.87	0.55	0.79
Sumo3	Sumo3_S2	1.05	1.23	0.35	0.76
Sun2	Sun2_T117	1.28	1.29	2.25	0.99
Sun2	Sun2_S120	1.88	1.65	2.25	0.99
Sun2	Sun2_S249	2.73	2.68	5.47	7.97
Supt5	Supt5_S664	0.92	1.04	0.91	0.80
Supv3l1	Supv3l1_S725	0.44	0.42	0.43	1.13
Suv39h1	Suv39h1_S391	0.37	0.41	0.64	0.48
Suz12	Suz12_S525	1.28	1.21	1.61	0.86
Svil	Svil_S960	0.99	1.01	0.93	1.67
Svil	Svil_S227	0.81	0.86	1.31	1.80
Svil	Svil_S233	0.50	0.72	1.01	2.62
Svil	Svil_S241	0.47	0.66	0.93	2.71
Svil	Svil_S234	0.50	0.70	0.87	2.81
Svil	Svil_S1181	0.78	0.74	6.45	2.97
Syap1	Syap1_T262	0.56	0.65	0.75	1.08
Synj1	Synj1_S1339	0.67	1.03	1.00	0.87

Synj1	Synj1_S1215	1.15	0.96	1.43	1.63
Synrg	Synrg_S911	1.30	1.27	1.49	0.87
Szrd1	Szrd1_S38	0.84	0.76	0.97	0.67
Szrd1	Szrd1_S106	0.59	0.64	0.56	1.14
Tab2	Tab2_S450	1.82	1.65	0.00	0.00
Taf12	Taf12_S51	1.38	1.37	0.97	0.80
Taf1c	Taf1c_S576	0.78	0.80	1.52	0.61
Taf1c	Taf1c_S575	0.81	0.87	1.52	0.61
Taf2	Taf2_S1184	1.08	1.05	1.02	0.81
Taf3	Taf3_S291	1.66	1.65	1.29	1.05
Tagln2	Tagln2_S163	0.55	0.48	0.46	0.82
Tagln2	Tagln2_S7	0.88	0.86	1.03	0.90
Tagln2	Tagln2_Y8	0.95	0.82	1.04	8.08
Taldo1	Taldo1_S4	0.73	0.69	0.74	0.50
Tango6	Tango6_S561	0.59	0.57	0.40	0.54
Taok1	Taok1_S421	1.94	1.69	1.97	1.50
Taok3	Taok3_S324	1.25	1.67	0.88	1.17
Tardbp	Tardbp_S183	0.88	0.75	0.37	0.70
Tardbp	Tardbp_S292	2.03	0.96	1.11	3.19
Tars	Tars_S7	0.31	0.38	0.00	0.00
Tars	Tars_S8	0.33	0.41	0.25	0.51
Tars	Tars_S2	0.22	0.32	0.25	0.54
Tars	Tars_Y297	0.41	0.46	2.16	3.68
Tax1bp1	Tax1bp1_S632	0.58	0.61	1.56	1.21
Tbc1d1	Tbc1d1_S1148	0.83	0.66	0.00	0.00
Tbc1d1	Tbc1d1_T1149	0.86	0.92	0.00	0.00
Tbc1d1	Tbc1d1_S231	1.29	1.09	0.86	1.44
Tbc1d10a	Tbc1d10a_S18	1.06	1.01	0.68	0.68
Tbc1d10b	Tbc1d10b_S664	1.11	1.16	0.48	0.35
Tbc1d15	Tbc1d15_S205	1.20	1.25	0.00	0.00
Tbc1d15	Tbc1d15_S662	1.63	1.68	2.18	5.15
Tbc1d25	Tbc1d25_S541	1.40	1.33	1.65	1.37
Tbc1d2b	Tbc1d2b_S959	0.66	0.62	1.21	1.28
Tbc1d5	Tbc1d5_S578	0.68	0.70	0.59	1.01
Tcea1	Tcea1_S100	0.70	0.69	0.61	0.56
Tcf12	Tcf12_S216	1.95	1.93	1.14	0.92
Tcf12	Tcf12_S167	1.25	1.27	1.63	1.08
Tcf12	Tcf12_S413	1.19	1.38	3.09	1.51
Tcf20	Tcf20_T1699	0.58	0.57	0.61	0.83
Tcf20	Tcf20_S588	0.75	0.72	0.80	1.06
Tcof1	Tcof1_S1303	0.57	0.61	0.65	0.45
Tcof1	Tcof1_S1126	0.55	0.51	0.94	0.46
Tcof1	Tcof1_S794	0.63	0.70	0.86	0.55
Tcof1	Tcof1_S1216	0.78	0.80	0.84	0.67
Tcof1	Tcof1_S593	0.77	0.80	1.03	0.74
Tcof1	Tcof1_T171	0.55	0.43	0.82	0.78
Tcof1	Tcof1_S169	0.62	0.77	0.82	0.78
Tcof1	Tcof1_S853	1.12	1.01	1.11	0.90
Tcof1	Tcof1_T860	0.81	0.79	0.96	0.92
Tcof1	Tcof1_S1191	0.85	0.94	1.03	0.95
Tcof1	Tcof1_S852	1.05	1.00	1.11	0.97
Tcp1	Tcp1_S551	1.33	1.24	1.17	0.98
Tcp1	Tcp1_S544	0.96	1.29	1.28	1.03
Tdp1	Tdp1_S132	0.77	0.78	0.92	0.62
Tdp1	Tdp1_S118	0.84	0.77	0.74	0.66

Tdp1	Tdp1_S119	0.59	0.79	0.75	0.67
Terf2	Terf2_S367	0.86	0.83	0.42	0.48
Terf2	Terf2_S399	1.22	1.22	0.71	0.67
Terf2ip	Terf2ip_S200	0.48	0.59	0.42	0.47
Tex264	Tex264_S302	1.13	1.03	1.32	1.93
Tfap4	Tfap4_S123	1.31	1.41	2.46	0.90
Tfap4	Tfap4_S124	1.19	1.12	2.25	1.08
Tfdp1	Tfdp1_S23	0.62	0.80	0.64	0.66
Tfe3	Tfe3_S413	1.13	1.02	0.83	0.80
Tfe3	Tfe3_S405	0.45	0.45	0.55	1.02
Tfip11	Tfip11_S96	0.61	0.69	0.86	1.27
Tfip11	Tfip11_S99	0.61	0.69	0.86	1.27
Tfpt	Tfpt_S180	1.50	1.65	1.19	0.77
Tgm2	Tgm2_Y369	4.53	4.78	1.01	1.96
Tgs1	Tgs1_S431	0.46	0.53	0.82	1.05
Thrap3	Thrap3_S681	1.60	1.29	0.00	0.00
Thrap3	Thrap3_S248	1.66	1.21	1.11	0.74
Thrap3	Thrap3_S264	1.22	1.17	1.05	0.81
Thrap3	Thrap3_S379	0.74	0.80	0.85	0.93
Thrap3	Thrap3_S679	1.29	1.21	1.22	0.97
Thrap3	Thrap3_S243	1.31	1.33	1.51	1.00
Thrap3	Thrap3_S253	0.95	1.18	1.44	1.02
Thrap3	Thrap3_S695	0.79	0.85	1.39	1.37
Thrap3	Thrap3_S572	0.41	0.42	0.95	1.45
Thrap3	Thrap3_S238	1.46	1.44	2.87	1.81
Thumpd1	Thumpd1_S86	0.71	0.78	0.83	0.53
Thumpd1	Thumpd1_S88	0.85	0.84	0.83	0.53
Thumpd1	Thumpd1_S8	0.79	0.97	0.69	0.53
Thumpd2	Thumpd2_S172	0.63	0.51	0.39	0.71
Tiam1	Tiam1_S231	0.34	0.33	1.78	2.86
Ticrr	Ticrr_S599	0.71	0.59	0.61	0.47
Timeless	Timeless_S1165	1.16	1.04	1.13	0.50
Tjap1	Tjap1_T407	0.43	0.43	1.05	1.93
Tjp2	Tjp2_S968	0.59	0.53	0.82	0.82
Tjp2	Tjp2_S107	0.73	0.70	0.97	0.88
Tjp2	Tjp2_S209	1.12	1.07	0.91	0.97
Tjp2	Tjp2_S1136	0.58	0.59	0.93	1.00
Tjp2	Tjp2_S395	0.97	1.01	1.02	1.11
Tk1	Tk1_S13	0.26	0.27	0.00	0.00
Tle4	Tle4_S292	0.86	1.01	0.81	0.88
Tle4	Tle4_S208	1.64	1.66	1.64	0.96
Tln1	Tln1_S425	0.25	0.28	0.57	1.06
Tln1	Tln1_Y70	0.85	1.31	2.26	4.71
Tmcc1	Tmcc1_S378	0.67	0.75	0.57	1.35
Tmem245	Tmem245_S12	0.34	0.35	0.47	0.85
Tmem245	Tmem245_S327	0.57	0.76	0.78	2.64
Tmem40	Tmem40_S14	0.72	0.65	1.46	0.92
Tmem55a	Tmem55a_T22	0.65	0.67	0.00	0.00
Tmem57	Tmem57_S332	0.81	1.07	2.03	1.35
Tmpo	Tmpo_S176	1.63	1.08	0.00	0.00
Tmpo	Tmpo_S79	1.91	2.08	0.00	0.00
Tmpo	Tmpo_S158	2.22	2.29	0.00	0.00
Tmpo	Tmpo_S157	2.18	3.11	0.00	0.00
Tmpo	Tmpo_T74	1.61	1.45	1.09	0.33
Tmpo	Tmpo_T153	3.33	3.86	0.99	0.52

Tmpo	Tmpo_S422	1.42	1.94	1.16	0.58
Tmpo	Tmpo_S155	2.21	2.13	1.02	0.62
Tmpo	Tmpo_T159	2.59	2.56	0.94	0.66
Tmpo	Tmpo_S308	2.54	2.94	1.48	0.77
Tmpo	Tmpo_S66	0.83	0.70	1.14	1.07
Tmpo	Tmpo_S67	1.32	0.88	2.13	1.69
Tmsb4x	Tmsb4x_S2	0.40	0.38	0.63	1.05
Tmx1	Tmx1_S245	0.96	0.80	0.89	0.68
Tnk2	Tnk2_S757	2.37	2.67	1.78	1.47
Toe1	Toe1_S349	0.59	0.76	1.55	1.39
Tom1	Tom1_S462	0.59	0.42	0.74	3.37
Tomm22	Tomm22_S15	1.54	2.44	1.82	3.45
Tomm34	Tomm34_S186	0.84	0.67	0.97	2.53
Tomm70a	Tomm70a_S94	1.13	1.32	0.79	0.83
Top1	Top1_S10	1.82	1.57	1.31	0.63
Top1	Top1_S113	1.26	0.89	1.33	1.09
Top1	Top1_S114	1.31	1.01	1.62	1.30
Top2a	Top2a_S1211	0.54	0.60	0.45	0.36
Top2a	Top2a_S1521	0.43	0.63	0.48	0.42
Top2a	Top2a_S1388	0.38	0.33	0.47	0.43
Top2a	Top2a_T1245	0.46	0.42	0.44	0.58
Top2b	Top2b_S1511	1.60	1.80	1.00	0.57
Top2b	Top2b_S1400	0.65	0.68	0.88	0.65
Top2b	Top2b_S1568	0.60	0.55	0.67	0.72
Top2b	Top2b_S1509	1.89	0.81	0.91	0.75
Top2b	Top2b_S1387	1.01	0.94	0.95	0.97
Top2b	Top2b_S1513	1.03	0.90	0.99	0.97
Top2b	Top2b_S1539	1.13	1.03	1.42	2.07
Top2b	Top2b_S1537	1.07	1.61	1.42	2.07
Topors	Topors_S99	1.81	0.63	0.95	0.97
Tox4	Tox4_S182	0.98	0.88	1.03	1.22
Tox4	Tox4_T175	0.66	0.61	1.07	1.22
Tox4	Tox4_T176	0.85	0.74	0.99	1.22
Tox4	Tox4_S178	0.67	0.61	1.00	1.22
Tpd52l2	Tpd52l2_S206	1.08	1.06	0.00	0.00
Tpd52l2	Tpd52l2_S180	6.43	12.82	1.90	2.30
Tpi1	Tpi1_S130	0.58	0.63	1.16	1.96
Tpi1	Tpi1_Y259	0.85	0.94	0.37	4.91
Tpr	Tpr_S2141	1.07	1.15	0.65	0.66
Tpr	Tpr_S453	0.67	0.76	0.73	1.08
Tpx2	Tpx2_S737	0.82	0.75	0.54	0.66
Tpx2	Tpx2_S486	0.92	0.84	0.77	0.74
Tra2a	Tra2a_T202	0.61	0.55	0.00	0.00
Tra2a	Tra2a_T200	0.63	0.66	0.00	0.00
Tra2a	Tra2a_S14	0.70	0.65	0.74	0.78
Tra2a	Tra2a_S2	0.70	0.63	0.62	0.85
Tra2a	Tra2a_S260	1.21	1.01	1.02	0.92
Tra2a	Tra2a_S262	1.06	1.04	1.02	0.92
Tra2b	Tra2b_S2	1.16	1.22	1.26	1.39
Traf3ip1	Traf3ip1_S409	1.31	1.33	2.42	1.45
Traf7	Traf7_S60	1.29	1.18	2.19	1.29
Tram1	Tram1_S365	0.61	0.68	0.77	0.97
Trim28	Trim28_S23	1.68	1.26	1.17	0.86
Trim28	Trim28_S473	0.77	0.74	1.82	1.29
Trim56	Trim56_S376	0.67	0.62	0.67	0.87

Trip12	Trip12_S310	1.61	1.54	2.11	0.74
Trip12	Trip12_S312	1.80	1.53	2.18	0.78
Trmt10a	Trmt10a_T23	1.51	1.31	1.04	1.28
Trmt6	Trmt6_S11	0.94	0.94	1.01	1.04
Trp53bp1	Trp53bp1_S267	0.98	0.91	0.00	0.00
Trp53bp1	Trp53bp1_S382	1.61	0.95	0.06	0.07
Trp53bp1	Trp53bp1_S1359	0.85	0.96	0.80	0.96
Trp53bp1	Trp53bp1_S1459	1.11	1.13	0.86	1.03
Trp53bp1	Trp53bp1_S268	1.11	0.96	0.83	1.06
Trp53bp1	Trp53bp1_S533	1.34	1.31	0.94	1.14
Trrap	Trrap_S2031	0.54	0.63	1.07	1.56
Tsc22d4	Tsc22d4_S189	0.49	0.45	0.73	0.52
Tsc22d4	Tsc22d4_S62	0.84	0.80	0.98	1.18
Tsr2	Tsr2_S143	1.47	0.95	1.02	0.89
Tssc4	Tssc4_S316	0.53	0.51	0.34	0.45
Tssc4	Tssc4_T124	0.94	0.99	0.95	0.76
Ttc7	Ttc7_S648	1.05	1.03	0.95	0.55
Ttll12	Ttll12_S11	0.79	0.82	0.88	0.97
Tuba1b	Tuba1b_S48	0.62	0.54	5.15	2.67
Tuba1b	Tuba1b_Y399	0.43	0.35	0.55	2.77
Tuba1b	Tuba1b_Y272	0.58	0.41	2.16	5.48
Tuba1b	Tuba1b_Y108	0.34	0.37	0.34	6.18
Tubb4b	Tubb4b_S172	0.39	0.23	3.21	4.46
Twf2	Twf2_S349	0.39	0.41	0.51	1.45
Txlna	Txlna_S523	0.61	0.63	1.70	3.25
Txlna	Txlna_S522	0.65	0.52	2.10	3.73
Txlna	Txlna_S515	0.63	0.64	2.48	9.36
Txnrd1	Txnrd1_Y131	0.58	0.55	0.59	4.18
U2af2	U2af2_S79	1.17	1.00	0.86	0.78
U2af2	U2af2_S2	1.12	1.15	0.83	0.93
U2surp	U2surp_S67	1.23	1.17	0.29	0.39
U2surp	U2surp_S946	0.69	0.68	0.71	0.62
U2surp	U2surp_S948	0.69	0.68	0.71	0.62
Uba1	Uba1_S4	0.95	0.84	0.59	0.70
Uba1	Uba1_S46	0.99	0.92	1.05	2.16
Ubap2	Ubap2_S634	0.66	0.67	1.00	0.64
Ubap2l	Ubap2l_S609	0.36	0.39	0.89	0.62
Ubap2l	Ubap2l_S608	0.26	0.19	0.82	0.69
Ube2j1	Ube2j1_S266	1.38	1.41	0.00	0.00
Ube2j1	Ube2j1_T267	1.23	1.43	0.00	0.00
Ube2o	Ube2o_T835	0.67	0.59	0.00	0.00
Ube2o	Ube2o_S836	0.59	0.63	0.00	0.00
Ube4b	Ube4b_S238	1.00	0.86	0.00	0.00
Ube4b	Ube4b_T234	1.00	0.91	1.00	1.49
Ubl7	Ubl7_S230	1.05	1.03	1.26	1.29
Ubqln2	Ubqln2_S25	0.25	0.27	0.26	0.73
Ubr4	Ubr4_S2715	1.03	1.03	0.89	1.19
Ubr4	Ubr4_S2716	1.08	1.08	1.11	1.57
Ubr4	Ubr4_S619	0.35	0.29	0.78	1.67
Ubr4	Ubr4_S620	0.35	0.29	0.78	1.67
Ubr5	Ubr5_S1543	0.75	0.73	0.97	1.16
Ubxn1	Ubxn1_S188	0.33	0.31	0.00	0.00
Ubxn1	Ubxn1_S200	0.65	0.68	0.50	1.61
Ubxn7	Ubxn7_S350	1.07	1.01	0.63	0.87
Ugdh	Ugdh_T474	0.94	0.92	1.35	1.10

Uhrf1	Uhrf1_S289	0.73	0.75	3.11	2.37
Uimc1	Uimc1_S379	0.99	1.04	1.02	0.83
Uimc1	Uimc1_S665	1.34	1.26	1.18	0.92
Ulk1	Ulk1_S622	0.67	0.73	0.58	0.84
Unc119	Unc119_S37	0.74	0.83	1.56	2.37
Unc119	Unc119_S39	0.74	0.83	1.56	2.37
Unc13d	Unc13d_S149	1.72	1.71	1.71	0.91
Usp10	Usp10_S360	0.31	0.31	0.54	0.86
Usp15	Usp15_S229	0.76	0.74	1.61	1.69
Usp24	Usp24_S2044	0.56	0.59	0.59	0.71
Usp24	Usp24_S2074	0.49	0.56	0.55	0.79
Usp34	Usp34_T3418	1.03	0.91	0.66	1.27
Usp34	Usp34_S3423	0.77	0.74	0.66	1.28
Usp36	Usp36_S578	0.71	0.84	2.06	0.90
Usp39	Usp39_S81	0.97	0.87	0.77	0.83
Usp47	Usp47_S914	0.76	0.58	0.52	0.75
Utp14b	Utp14b_S578	0.90	0.90	2.11	0.93
Utp15	Utp15_S517	0.72	0.66	0.75	0.91
Utp18	Utp18_S114	1.15	1.39	1.05	1.12
Utp18	Utp18_S115	1.15	1.39	1.05	1.12
Utp18	Utp18_S118	1.07	1.28	1.23	1.12
Vamp3	Vamp3_S2	1.44	1.48	1.54	1.69
Vamp3	Vamp3_S15	1.66	1.75	3.74	7.33
Vamp4	Vamp4_S30	0.90	0.92	0.72	0.75
Vamp5	Vamp5_S41	1.91	2.29	1.31	1.12
Vamp8	Vamp8_S55	0.91	0.90	0.80	1.04
Vars	Vars_Y427	0.67	0.65	0.27	11.79
Vasp	Vasp_Y39	0.49	0.52	1.24	18.42
Vcp	Vcp_S3	0.85	0.71	0.85	1.08
Vcpip1	Vcpip1_S993	0.59	0.33	0.45	0.56
Vcpip1	Vcpip1_S997	0.46	0.57	0.46	0.57
Vcpip1	Vcpip1_S756	0.52	0.66	0.48	0.69
Vcpip1	Vcpip1_S767	0.60	0.49	0.80	0.73
Vcpip1	Vcpip1_S746	0.84	0.95	0.81	1.13
Vdac1	Vdac1_S104	1.51	1.41	1.07	0.90
Vdac2	Vdac2_S116	1.12	1.15	0.57	0.70
Vim	Vim_S55	0.41	0.35	0.00	0.00
Vim	Vim_S419	0.63	0.58	0.00	0.00
Vim	Vim_S73	0.85	1.62	0.40	0.72
Vim	Vim_S72	0.45	0.59	0.93	2.09
Vim	Vim_S56	0.44	0.34	2.03	2.77
Vim	Vim_Y117	0.50	0.47	0.45	14.28
Vps35	Vps35_S7	0.27	0.43	0.56	2.39
Vps4b	Vps4b_S102	0.73	0.69	1.00	0.89
Vrk3	Vrk3_S55	0.81	0.83	0.58	0.51
Vrk3	Vrk3_S59	0.58	0.53	0.62	0.55
Vta1	Vta1_Y280	0.85	0.93	2.21	3.32
Wapal	Wapal_S226	1.42	1.43	0.91	0.86
Wapal	Wapal_S77	1.06	1.20	1.09	1.02
Wbp11	Wbp11_S600	1.02	1.21	3.83	0.88
Wbp11	Wbp11_S237	1.95	1.99	2.12	1.41
Wdfy4	Wdfy4_S2963	0.67	0.38	1.41	2.98
Wdhd1	Wdhd1_S784	0.63	0.76	0.69	0.60
Wdr18	Wdr18_Y61	0.50	0.53	0.54	9.15
Wdr26	Wdr26_S101	0.66	0.70	1.34	2.49

Wdr33	Wdr33_S7	0.78	0.76	1.45	0.99
Wdr4	Wdr4_S440	0.89	0.96	0.71	0.71
Wdr43	Wdr43_S432	0.79	1.02	0.92	1.26
Wdr44	Wdr44_S405	0.70	0.64	0.00	0.00
Wdr44	Wdr44_S50	0.54	0.51	2.09	4.65
Wdr59	Wdr59_S564	0.91	0.57	0.69	1.61
Wdr74	Wdr74_S383	1.01	0.94	1.38	1.10
Wdr77	Wdr77_T5	0.60	0.55	0.91	1.14
Wdtc1	Wdtc1_S511	0.66	0.61	0.72	0.82
Whsc1	Whsc1_T110	0.89	0.78	1.41	0.41
Wipf1	Wipf1_S330	1.34	1.37	1.03	2.72
Wipi2	Wipi2_S394	1.11	1.04	1.28	1.58
Wipi2	Wipi2_S395	1.11	1.11	1.31	1.62
Wiz	Wiz_S317	0.76	0.79	0.00	0.00
Wiz	Wiz_T321	0.47	0.69	0.49	0.58
Wiz	Wiz_S322	0.70	0.58	0.47	0.63
Wnk1	Wnk1_S1775	0.59	0.72	1.58	1.91
Wnk1	Wnk1_S165	1.19	1.29	1.81	2.01
Wnk1	Wnk1_S2118	2.00	2.58	1.99	2.45
Wrnip1	Wrnip1_S153	0.92	0.87	0.90	1.02
Wtap	Wtap_S297	0.60	0.55	0.79	0.67
Wtap	Wtap_T298	1.09	1.08	1.03	0.76
Xpc	Xpc_S93	1.28	1.05	1.17	0.62
Xpo4	Xpo4_S521	0.91	1.15	1.30	1.07
Xrcc1	Xrcc1_T452	0.91	0.85	0.48	0.41
Xrcc1	Xrcc1_S446	0.91	0.91	0.48	0.41
Xrn2	Xrn2_S499	2.52	1.89	1.37	0.78
Xrn2	Xrn2_S501	2.44	2.04	0.96	0.92
Xrn2	Xrn2_S471	1.06	0.99	0.88	1.02
Xrn2	Xrn2_S475	0.87	0.80	1.02	1.18
Yaf2	Yaf2_S6	0.62	0.66	0.94	1.02
Ybx3	Ybx3_S259	1.34	1.31	1.46	0.91
Yeats2	Yeats2_S393	0.51	0.50	0.66	0.55
Yeats2	Yeats2_S411	0.86	1.11	1.18	1.01
Ythdf2	Ythdf2_S39	0.54	0.44	2.12	1.34
Ythdf2	Ythdf2_S2	0.88	1.12	1.93	1.35
Zbtb21	Zbtb21_S463	0.97	0.84	1.15	1.09
Zbtb44	Zbtb44_S161	1.27	1.16	0.67	0.72
Zc3h11a	Zc3h11a_T744	0.85	1.06	0.00	0.00
Zc3h11a	Zc3h11a_S743	0.95	0.73	0.67	0.63
Zc3h11a	Zc3h11a_S740	1.23	1.11	0.49	0.66
Zc3h11a	Zc3h11a_S677	0.64	0.60	0.78	0.68
Zc3h11a	Zc3h11a_S312	0.70	0.64	0.92	0.79
Zc3h11a	Zc3h11a_S132	1.46	1.30	1.31	1.06
Zc3h13	Zc3h13_S209	0.95	0.99	0.80	0.58
Zc3h13	Zc3h13_S207	0.95	0.99	0.80	0.58
Zc3h13	Zc3h13_S109	0.95	0.83	0.78	0.61
Zc3h13	Zc3h13_S110	0.95	0.86	0.78	0.61
Zc3h13	Zc3h13_S1069	0.72	0.72	0.79	0.64
Zc3h13	Zc3h13_S242	1.25	1.11	1.10	0.65
Zc3h13	Zc3h13_S379	1.19	1.19	1.00	0.70
Zc3h13	Zc3h13_S369	1.17	1.22	1.00	0.70
Zc3h13	Zc3h13_S371	1.17	1.22	1.00	0.70
Zc3h13	Zc3h13_S198	1.04	1.00	0.94	0.71
Zc3h13	Zc3h13_S953	1.10	1.09	0.96	0.74

Zc3h13	Zc3h13_S77	1.05	1.03	0.92	0.75
Zc3h13	Zc3h13_S951	1.26	1.26	1.22	0.78
Zc3h13	Zc3h13_S265	0.87	0.89	0.83	0.79
Zc3h13	Zc3h13_T263	0.87	0.89	0.83	0.79
Zc3h13	Zc3h13_S1344	1.24	1.29	1.17	0.87
Zc3h14	Zc3h14_S515	1.09	1.05	1.06	0.98
Zc3h14	Zc3h14_S409	1.48	1.45	0.89	1.19
Zc3h18	Zc3h18_S888	0.58	0.56	0.57	0.60
Zc3h18	Zc3h18_S92	0.55	0.51	0.42	0.64
Zc3h18	Zc3h18_S528	0.78	0.79	0.66	0.66
Zc3h18	Zc3h18_S847	0.76	0.75	0.53	0.68
Zc3h18	Zc3h18_S483	0.88	0.88	0.63	0.74
Zc3h18	Zc3h18_S532	0.69	0.74	0.69	0.76
Zc3h18	Zc3h18_S45	1.10	1.06	0.82	0.84
Zc3h18	Zc3h18_S530	0.84	0.80	0.94	0.84
Zc3hav1	Zc3hav1_S324	1.00	1.08	1.32	1.49
Zc3hc1	Zc3hc1_S62	0.84	0.93	0.00	0.00
Zc3hc1	Zc3hc1_S394	0.65	0.74	0.82	0.98
Zc3hc1	Zc3hc1_S393	0.68	0.84	0.84	1.00
Zdhhc5	Zdhhc5_S621	1.21	1.52	1.91	3.74
Zfc3h1	Zfc3h1_S952	1.33	1.42	0.85	0.27
Zfml	Zfml_S1400	0.51	0.54	0.31	0.31
Zfml	Zfml_S606	0.54	0.51	0.72	0.62
Zfml	Zfml_S1571	0.93	0.69	0.55	0.68
Zfml	Zfml_S1099	0.42	0.41	0.55	0.70
Zfml	Zfml_S128	0.42	0.41	1.19	0.75
Zfp106	Zfp106_S1040	0.73	0.70	0.73	0.83
Zfp106	Zfp106_S1041	0.73	0.70	0.73	0.83
Zfp131	Zfp131_S231	0.75	1.07	0.88	0.79
Zfp148	Zfp148_S306	0.93	0.94	0.81	0.85
Zfp219	Zfp219_S657	1.07	1.02	0.48	0.48
Zfp318	Zfp318_S205	1.07	1.19	1.21	1.26
Zfp609	Zfp609_S577	0.73	0.78	0.91	0.68
Zfp609	Zfp609_S575	0.68	0.77	0.55	0.76
Zfp609	Zfp609_S358	2.24	1.93	1.52	1.11
Zfp609	Zfp609_S1057	0.78	0.79	0.86	1.35
Zfp652	Zfp652_S203	2.11	2.17	1.90	0.55
Zfp655	Zfp655_S12	0.89	0.89	0.84	0.92
Zfp655	Zfp655_S28	0.74	0.76	0.86	1.21
Zfp687	Zfp687_S104	0.54	0.99	0.00	0.00
Zfp687	Zfp687_T432	0.70	0.74	0.60	0.84
Zfp692	Zfp692_S3	1.48	1.68	1.77	1.03
Zfp719	Zfp719_S148	1.37	1.66	1.85	2.52
Zfp768	Zfp768_S86	0.90	0.87	0.93	0.58
Zfp800	Zfp800_S337	0.35	0.42	0.71	0.61
Zfp830	Zfp830_S187	1.18	1.26	1.49	1.91
Zfpm1	Zfpm1_S651	0.71	0.74	0.00	0.00
Zfpm1	Zfpm1_S648	0.65	0.76	0.00	0.00
Zfpm1	Zfpm1_S650	0.67	0.77	0.00	0.00
Zfpm1	Zfpm1_S917	0.76	0.70	0.82	0.59
Zfpm1	Zfpm1_S925	0.86	0.87	1.09	0.66
Zfpm1	Zfpm1_S679	1.00	1.00	1.23	0.85
Zfpm1	Zfpm1_S681	1.02	1.11	1.24	0.86
Zfyve19	Zfyve19_S280	0.90	1.06	1.15	1.41
Zhx2	Zhx2_S824	0.85	0.72	0.74	0.63

Zmym4	Zmym4_S121	1.14	1.25	1.09	1.05
Zmynd8	Zmynd8_S754	0.52	0.54	0.46	0.74
Znhit6	Znhit6_S39	1.06	1.07	0.81	0.41
Zranb2	Zranb2_S188	1.13	0.72	0.60	0.71
Zranb2	Zranb2_S120	0.86	0.82	0.72	0.82
Zyx	Zyx_S272	0.43	0.54	2.25	3.25
Zyx	Zyx_S336	0.60	0.42	4.36	4.62
Zzef1	Zzef1_S1538	0.85	0.79	1.02	1.24

Bibliography

Alexandrov, L.B., Nik-Zainal, S., Wedge, D.C., Aparicio, S.A.J.R., Behjati, S., Biankin, A.V., Bignell, G.R., Bolli, N., Borg, A., Børresen-Dale, A.-L., et al. (2013). Signatures of mutational processes in human cancer. Nature *500*, 415–421.

Alinikula, J., Kohonen, P., Nera, K.-P., and Lassila, O. (2010). Concerted action of Helios and Ikaros controls the expression of the inositol 5-phosphatase SHIP. Eur. J. Immunol. *40*, 2599–2607.

Archambault, V., and Glover, D.M. (2009). Polo-like kinases: conservation and divergence in their functions and regulation. Nat. Rev. Mol. Cell Biol. *10*, 265–275.

Asanuma, S., Yamagishi, M., Kawanami, K., Nakano, K., Sato-Otsubo, A., Muto, S., Sanada, M., Yamochi, T., Kobayashi, S., Utsunomiya, A., et al. (2013). Adult T-cell leukemia cells are characterized by abnormalities of Helios expression that promote T cell growth. Cancer Sci. *104*, 1097–1106.

Birukova, A.A., Smurova, K., Birukov, K.G., Usatyuk, P., Liu, F., Kaibuchi, K., Ricks-Cord, A., Natarajan, V., Alieva, I., Garcia, J.G.N., et al. (2004). Microtubule disassembly induces cytoskeletal remodeling and lung vascular barrier dysfunction: Role of Rho-dependent mechanisms. J. Cell. Physiol. *201*, 55–70.

Bodegom, D. van, Zhong, J., Kopp, N., Dutta, C., Kim, M.-S., Bird, L., Weigert, O., Tyner, J., Pandey, A., Yoda, A., et al. (2012). Differences in signaling through the B-cell leukemia oncoprotein CRLF2 in response to TSLP and through mutant JAK2. Blood *120*, 2853–2863.

Den Boer, M.L., van Slegtenhorst, M., De Menezes, R.X., Cheok, M.H., Buijs-Gladdines, J.G., Peters, S.T., Van Zutven, L.J., Beverloo, H.B., Van der Spek, P.J., Escherich, G., et al. (2009). A subtype of childhood acute lymphoblastic leukaemia with poor treatment outcome: a genome-wide classification study. Lancet Oncol. *10*, 125–134.

Van Buul, J.D., and Hordijk, P.L. (2004). Signaling in leukocyte transendothelial migration. Arterioscler. Thromb. Vasc. Biol. *24*, 824–833.

Campana, D., Manabe, A., and Evans, W.E. (1993). Stroma-supported immunocytometric assay (SIA): a novel method for testing the sensitivity of acute lymphoblastic leukemia cells to cytotoxic drugs. Leukemia *7*, 482–488.

Chapiro, E., Russell, L., Lainey, E., Kaltenbach, S., Ragu, C., Della-Valle, V., Hanssens, K., Macintyre, E.A., Radford-Weiss, I., Delabesse, E., et al. (2010). Activating mutation in the TSLPR gene in B-cell precursor lymphoblastic leukemia. Leukemia *24*, 642–645.

Chen, I.-M., Harvey, R.C., Mullighan, C.G., Gastier-Foster, J., Wharton, W., Kang, H., Borowitz, M.J., Camitta, B.M., Carroll, A.J., Devidas, M., et al. (2012). Outcome modeling with CRLF2, IKZF1, JAK, and minimal residual disease in pediatric acute lymphoblastic leukemia: a Children's Oncology Group Study. Blood *119*, 3512–3522.

Dawson, M.A., Bannister, A.J., Göttgens, B., Foster, S.D., Bartke, T., Green, A.R., and Kouzarides, T. (2009). JAK2 phosphorylates histone H3Y41 and excludes HP1α from chromatin. Nature *461*, 819–822.

Dawson, M.A., Foster, S.D., Bannister, A.J., Robson, S.C., Hannah, R., Wang, X., Xhemalce, B., Wood, A.D., Green, A.R., Göttgens, B., et al. (2012). Three Distinct Patterns of Histone H3Y41 Phosphorylation Mark Active Genes. Cell Rep. *2*, 470–477.

Ensor, H.M., Schwab, C., Russell, L.J., Richards, S.M., Morrison, H., Masic, D., Jones, L., Kinsey, S.E., Vora, A.J., Mitchell, C.D., et al. (2011). Demographic, clinical, and outcome features of children with acute lymphoblastic leukemia and CRLF2 deregulation: results from the MRC ALL97 clinical trial. Blood *117*, 2129–2136.

Ferrando, I.M., Chaerkady, R., Zhong, J., Molina, H., Jacob, H.K.C., Herbst-Robinson, K., Dancy, B.M., Katju, V., Bose, R., Zhang, J., et al. (2012). Identification of Targets of c-Src Tyrosine Kinase by Chemical Complementation and Phosphoproteomics. Mol. Cell. Proteomics *11*, 355–369.

Friend, S.L., Hosier, S., Nelson, A., Foxworthe, D., Williams, D.E., and Farr, A. (1994). A thymic stromal cell line supports in vitro development of surface IgM+ B cells and produces a novel growth factor affecting B and T lineage cells. Exp. Hematol. *22*, 321–328.

Gygi, S.P., Rochon, Y., Franza, B.R., and Aebersold, R. (1999). Correlation between Protein and mRNA Abundance in Yeast. Mol. Cell. Biol. *19*, 1720–1730.

Hanahan, D., and Weinberg, R.A. (2011). Hallmarks of Cancer: The Next Generation. Cell *144*, 646–674.

Harrison, C.J. (2013). Targeting signaling pathways in acute lymphoblastic leukemia: new insights. ASH Educ. Program Book *2013*, 118–125.

Harvey, R.C., Mullighan, C.G., Wang, X., Dobbin, K.K., Davidson, G.S., Bedrick, E.J., Chen, I.-M., Atlas, S.R., Kang, H., Ar, K., et al. (2010). Identification of novel cluster groups in pediatric high-risk B-precursor acute lymphoblastic leukemia with gene expression profiling: correlation with genome-wide DNA copy number alterations, clinical characteristics, and outcome. Blood *116*, 4874–4884.

Huang, T.-C., Cutler, J., Bharne, S., Zhong, J., Weinstock, D.M., Tyner, J.W., Gojo, I., Civin, C.I., and Pandey, A. Integrated Analysis of CRLF2 Signaling in Acute Lymphoblastic Leukemia Identifies Polo-Like Kinase 1 as a Potential Therapeutic Target. Leuk. Lymphoma.

Izraeli, S. (2014). Beyond Philadelphia: “Ph-like” B cell precursor acute lymphoblastic leukemias - diagnostic challenges and therapeutic promises. [Miscellaneous Article]. Curr. Opin. Hematol. July 2014 *21*, 289–296.

Jang, Y.-J., Ma, S., Terada, Y., and Erikson, R.L. (2002). Phosphorylation of Threonine 210 and the Role of Serine 137 in the Regulation of Mammalian Polo-like Kinase. J. Biol. Chem. *277*, 44115–44120.

John, L.B., and Ward, A.C. (2011). The Ikaros gene family: Transcriptional regulators of hematopoiesis and immunity. Mol. Immunol. *48*, 1272–1278.

Kasza, A. (2013). IL-1 and EGF regulate expression of genes important in inflammation and cancer. Cytokine *62*, 22–33.

Kennelly, P.J. (2003). Archaeal protein kinases and protein phosphatases: insights from genomics and biochemistry. Biochem. J. *370*, 373–389.

Kim, M.-S., Zhong, Y., Yachida, S., Rajeshkumar, N.V., Abel, M.L., Marimuthu, A., Mudgal, K., Hruban, R.H., Poling, J.S., Tyner, J.W., et al. (2014). Heterogeneity of pancreatic cancer metastases in a single patient revealed by quantitative proteomics. Mol. Cell. Proteomics mcp.M114.038547.

Kuan, E.L., and Ziegler, S.F. (2014). Thymic Stromal Lymphopoietin and Cancer. J. Immunol. *193*, 4283–4288.

Lamouille, S., Xu, J., and Derynck, R. (2014). Molecular mechanisms of epithelial-mesenchymal transition. Nat. Rev. Mol. Cell Biol. *15*, 178–196.

Levin, S.D., Koelling, R.M., Friend, S.L., Isaksen, D.E., Ziegler, S.F., Perlmutter, R.M., and Farr, A.G. (1999). Thymic Stromal Lymphopoietin: A Cytokine That Promotes the Development of IgM+ B Cells In Vitro and Signals Via a Novel Mechanism. J. Immunol. *162*, 677–683.

Lewis, A.M., Varghese, S., Xu, H., and Alexander, H.R. (2006). Interleukin-1 and cancer progression: the emerging role of interleukin-1 receptor antagonist as a novel therapeutic agent in cancer treatment. J. Transl. Med. *4*, 48.

Li, R., and Hayward, S.D. (2013). Potential of protein kinase inhibitors for treating herpesvirus-associated disease. Trends Microbiol. *21*, 286–295.

Lugo, T.G., Pendergast, A.-M., Muller, A.J., and Witte, O.N. (1990). Tyrosine Kinase Activity and Transformation Potency of bcr-abl Oncogene Products. Science *247*, 1079–1082.

Malek, T.R. (2008). The biology of interleukin-2. Annu. Rev. Immunol. *26*, 453–479.

Merrick, M. (2014). Post-translational modification of P II signal transduction proteins. Front. Microbiol. *5*, 763.

Mihara, K., Imai, C., Coustan-Smith, E., Dome, J.S., Dominici, M., Vanin, E., and Campana, D. (2003). Development and functional characterization of human bone marrow mesenchymal cells immortalized by enforced expression of telomerase. Br. J. Haematol. *120*, 846–849.

Moorman, A.V., Schwab, C., Ensor, H.M., Russell, L.J., Morrison, H., Jones, L., Masic, D., Patel, B., Rowe, J.M., Tallman, M., et al. (2012). IGH@ Translocations, CRLF2 Deregulation, and Microdeletions in Adolescents and Adults With Acute Lymphoblastic Leukemia. J. Clin. Oncol. *30*, 3100–3108.

Mullighan, C.G., Collins-Underwood, J.R., Phillips, L.A.A., Loudin, M.G., Liu, W., Zhang, J., Ma, J., Coustan-Smith, E., Harvey, R.C., Willman, C.L., et al. (2009). Rearrangement of CRLF2 in B-progenitor- and Down syndrome-associated acute lymphoblastic leukemia. Nat. Genet. *41*, 1243–1246.

Pandey, A., Ozaki, K., Baumann, H., Levin, S.D., Puel, A., Farr, A.G., Ziegler, S.F., Leonard, W.J., and Lodish, H.F. (2000). Cloning of a receptor subunit required for signaling by thymic stromal lymphopoietin. Nat. Immunol. *1*, 59–64.

Park, L.S., Martin, U., Garka, K., Gliniak, B., Di Santo, J.P., Muller, W., Largaespada, D.A., Copeland, N.G., Jenkins, N.A., Farr, A.G., et al. (2000). Cloning of the murine thymic stromal lymphopoietin (TSLP) receptor: Formation of a functional heteromeric complex requires interleukin 7 receptor. J. Exp. Med. *192*, 659–670.

Pui, C.-H., Mullighan, C.G., Evans, W.E., and Relling, M.V. (2012). Pediatric acute lymphoblastic leukemia: where are we going and how do we get there? Blood *120*, 1165–1174.

Quentmeier, H., Drexler, H.G., Fleckenstein, D., Zaborski, M., Armstrong, A., Sims, J.E., and Lyman, S.D. (2001). Cloning of human thymic stromal lymphopoietin (TSLP) and signaling mechanisms leading to proliferation. Leukemia *15*, 1286–1292.

Rebollo, A., and Schmitt, C. (2003). Ikaros, Aiolos and Helios: Transcription regulators and lymphoid malignancies. Immunol. Cell Biol. *81*, 171–175.

Reche, P.A., Soumelis, V., Gorman, D.M., Clifford, T., Liu Mr, null, Travis, M., Zurawski, S.M., Johnston, J., Liu, Y.J., Spits, H., et al. (2001). Human thymic stromal lymphopoietin preferentially stimulates myeloid cells. J. Immunol. Baltim. Md 1950 *167*, 336–343.

Roberts, K.G., Li, Y., Payne-Turner, D., Harvey, R.C., Yang, Y.-L., Pei, D., McCastlain, K., Ding, L., Lu, C., Song, G., et al. (2014). Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. N. Engl. J. Med. *371*, 1005–1015.

Rubbi, L., Titz, B., Brown, L., Galvan, E., Komisopoulou, E., Chen, S.S., Low, T., Tahmasian, M., Skaggs, B., Muschen, M., et al. (2011). Global Phosphoproteomics Reveals Crosstalk Between Bcr-Abl and Negative Feedback Mechanisms Controlling Src Signaling. Sci. Signal. *4*, ra18.

Russell, L.J., Capasso, M., Vater, I., Akasaka, T., Bernard, O.A., Calasanz, M.J., Chandrasekaran, T., Chapiro, E., Gesk, S., Griffiths, M., et al. (2009). Deregulated expression of cytokine receptor gene, CRLF2, is involved in lymphoid transformation in B-cell precursor acute lymphoblastic leukemia. Blood *114*, 2688–2698.

Schultz, K.R., Pullen, D.J., Sather, H.N., Shuster, J.J., Devidas, M., Borowitz, M.J., Carroll, A.J., Heerema, N.A., Rubnitz, J.E., Loh, M.L., et al. (2007). Risk- and response-based classification of childhood B-precursor acute lymphoblastic leukemia: a combined analysis of prognostic markers from the Pediatric Oncology Group (POG) and Children's Cancer Group (CCG). Blood *109*, 926–935.

Al-Shami, A., Spolski, R., Kelly, J., Fry, T., Schwartzberg, P.L., Pandey, A., Mackall, C.L., and Leonard, W.J. (2004). A role for thymic stromal lymphopoietin in CD4(+) T cell development. J. Exp. Med. *200*, 159–168.

Skaggs, B.J., Gorre, M.E., Ryvkin, A., Burgess, M.R., Xie, Y., Han, Y., Komisopoulou, E., Brown, L.M., Loo, J.A., Landaw, E.M., et al. (2006). Phosphorylation of the ATP-binding loop directs oncogenicity of drug-resistant BCR-ABL mutants. Proc. Natl. Acad. Sci. *103*, 19466–19471.

Tyner, J.W., Yang, W.F., Bankhead, A., Fan, G., Fletcher, L.B., Bryant, J., Glover, J.M., Chang, B.H., Spurgeon, S.E., Fleming, W.H., et al. (2013). Kinase Pathway Dependence in Primary Human Leukemias Determined by Rapid Inhibitor Screening. Cancer Res. *73*, 285–296.

Yamashiro, S., Yamakita, Y., Totsukawa, G., Goto, H., Kaibuchi, K., Ito, M., Hartshorne, D.J., and Matsumura, F. (2008). Myosin Phosphatase-Targeting Subunit 1 Regulates Mitosis by Antagonizing Polo-like Kinase 1. Dev. Cell *14*, 787–797.

Ying, S., O'Connor, B., Ratoff, J., Meng, Q., Mallett, K., Cousins, D., Robinson, D., Zhang, G., Zhao, J., Lee, T.H., et al. (2005). Thymic stromal lymphopoietin expression is increased in asthmatic airways and correlates with expression of Th2-attracting chemokines and disease severity. J. Immunol. Baltim. Md 1950 *174*, 8183–8190.

Ying, S., O'Connor, B., Ratoff, J., Meng, Q., Fang, C., Cousins, D., Zhang, G., Gu, S., Gao, Z., Shamji, B., et al. (2008). Expression and cellular provenance of thymic stromal lymphopoietin and chemokines in patients with severe asthma and chronic obstructive pulmonary disease. J. Immunol. Baltim. Md 1950 *181*, 2790–2798.

Yoda, A., Yoda, Y., Chiaretti, S., Bar-Natan, M., Mani, K., Rodig, S.J., West, N., Xiao, Y., Brown, J.R., Mitsiades, C., et al. (2010). Functional screening identifies CRLF2 in precursor B-cell acute lymphoblastic leukemia. Proc. Natl. Acad. Sci. *107*, 252–257.

Zhong, J., Kim, M.-S., Chaerkady, R., Wu, X., Huang, T.-C., Getnet, D., Mitchell, C.J., Palapetta, S.M., Sharma, J., O'Meally, R.N., et al. (2012). TSLP Signaling Network Revealed by SILAC-Based Phosphoproteomics. Mol. Cell. Proteomics *11*, M112.017764.

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EDUCATION

JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, Baltimore, MD

Ph.D. Human Genetics & Molecular Biology, 2009–2015

Dissertation: CRLF2 cytokine receptor signaling in acute leukemia

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NATIONAL TAIWAN UNIVERSITY HOSPITAL, Taipei, Taiwan

M.D. Clinical Training, 2002-2007

Residency in Internal Medicine, 2002-2005

Clinical Fellow in Hemato-Oncology, 2005-2007

NATIONAL TAIWAN UNIVERSITY SCHOOL OF MEDICINE, Taipei, Taiwan

M.D. Medicine, 1994–2000

EXPERIENCES

Graduate Student, 2009–2015

Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD

Attending Physician, 2007–2009

Department of Internal Medicine, Kinmen Hospital, Kinmen, Taiwan

Clinical Fellow of Hemato-Oncology, 2005–2007

Department of Internal Medicine, National Taiwan University Hospital, Taipei, Taiwan

Medical Resident of Internal Medicine, 2002–2005

National Taiwan University Hospital, Taipei, Taiwan

Military Service as a 2nd Lieutenant M.D. Medical Officer, 2000–2002

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PUBLICATIONS

1. Huang, T. C., Cutler, J., Bharne, S., Zhong, J., Weinstock, D. M., Tyner, J. W., Gojo, I., Civin, C. I. and Pandey, A. (2015). Integrated analysis of *CRLF2* signaling in acute lymphoblastic leukemia identifies Polo-like kinase 1 as a potential therapeutic target. *Leukemia & Lymphoma.* DOI: 10.3109/10428194.2014.963076. In press.
2. Huang, T. C., Renuse, S., Pinto, S., Kumar, P., Yang, Y., Chaerkady, R., Godsey, B., Mendell, J. T., Halushka, M. K., Civin, C. I., Marchionni, L. and Pandey, A. (2015). Identification of miR-145 targets through an integrated omics analysis. *Molecular Biosystems.* 11, 197-207.
3. Kim, M. S., Pinto, S. M., Getnet, D., Nirujogi, R. S., Manda, S. S., Chaerkady, R., Madugundu, A. K., Kelkar, D. S., Isserlin, R., Jain, S., Thomas, J. K., Muthusamy, B., Leal-Rojas, P., Kumar, P., Sahasrabuddhe, N. A., Balakrishnan, L., Advani, J., George, B., Renuse, S., Selvan, L. D. N., Patil, A. H., Nanjappa, V., Radhakrishnan, A., Prasad, S., Subbannayya, T., Raju, R., Kumar, M., Sreenivasamurthy, S. K., Marimuthu, A., Sathe, G. J., Chavan, S., Datta, K. K., Subbannayya, Y., Sahu, A., Yelamanchi, S. D., Jayaram, S., Rajagopalan, P., Sharma, J., Murthy, K. R., Syed, N., Goel, R., Khan, A. A., Ahmad, S., Dey, G., Mudgal, K., Chatterjee, A., Huang, T. C., Zhong, J., Wu, X., Shaw, P. G., Freed, D., Zahari, M. S., Mukherjee, K. K., Shankar, S., Mahadevan, A., Lam, H., Mitchell, C. J., Shankar, S. K., Satishchandra, P., Schroeder, J. T., Sirdeshmukh, R., Maitra, A., Leach, S. D., Drake, C. G., Halushka, M. K., Prasad, T. S. K., Hruban, R. H., Kerr, C. L., Bader, G. D., Iacobuzio-Donahue, C. A., Gowda, H. and Pandey, A. (2014). A draft map of the human proteome. *Nature.* 509, 575-581.

4. Kelkar, D. S., Provost. E., Chaerkady, R., Muthusamy, B., Manda, S. S., Subbannayya, T., Selvan, L. D. N., Wang, C. H., Datta, K. K., Woo, S., Dwivedi, S. B., Renuse, S., Getnet, D., Huang, T. C., Kim, M. S., Pinto, S. M., Mitchell, C. J., Madugundu, A. K., Kumar, P., Sharma, J. Advani, J., Dey, G., Balakrishnan, L., Syed, N., Nanjappa, V., Subbannayya, Y., Goel, R., Prasad, T. S. K., Bafna, V., Sirdeshmukh, R., Gowda, H., Wang, C., Leach, S. D. and Pandey, A. (2014). Annotation of the zebrafish genome through an integrated transcriptomic and proteomic analysis. *Molecular and Cellular Proteomics.* 13, 3184-3198.

5. Sahasrabuddhe, N. A.,* Huang, T. C.,* Ahmad, S., Kim, M. S., Yang, Y., Ghosh, B., Leach, S. D., Gowda, H., Somani, B. L., Chaerkady, R. and Pandey, A. (2014). Regulation of PPAR-alpha pathway by Dicer revealed through proteomic analysis. *Journal of Proteomics.* 108, 306-315.

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6. Marimuthu, A., Huang, T. C., Selvan, L. D. N., Renuse, S., Nirujogi, R. S., Kumar, P., Rajagopalan, S., Pandey, A., Harsha, H. C. and Chatterjee, A. (2014). Identification of targets of miR-200b by a SILAC-based quantitative proteomic approach. *EuPA Open Proteomics.* 4, 10-17.

7. Zhong, J., Sharma, J., Raju, R., Palapetta, S. M., Prasad, T. S. K., Huang, T. C., Yoda, A., Tyner, J. W., van Bodegom, D., Weinstock, D. M., Ziegler, S. F. and Pandey, A. (2014). TSLP signaling pathway map: A platform for analysis of TSLP mediated signaling. *Database*. DOI: 10.1093/database/bau007.

8. Huang, T. C., Pinto, S. M. and Pandey, A. (2013). Proteomics for understanding microRNA biology. *Proteomics*. 13, 558-567.

9. Huang, T. C., Sahasrabuddhe, N. A., Kim, M. S., Getnet, D., Yang, Y., Peterson, J. M., Ghosh, B., Chaerkady, R., Leach, S. D., Marchionni, L., Wong, G. W. and Pandey A. (2012). Regulation of lipid metabolism by Dicer revealed through SILAC Mice. *Journal of Proteome Research*. 11, 2193-2205.

10. Zhong, J., Kim, M. S., Chaerkady, R., Wu, X., Huang, T. C., Getnet, D., Mitchell, C. J., Palapetta, S. M., Sharma, J., O'Meally, R. N., Cole, R. N., Yoda, A., Moritz, A., Loriaux, M. M., Rush, J., Weinstock, D. M., Tyner, J. W. and Pandey, A. (2012). TSLP signaling network revealed by SILAC-based phosphoproteomics. *Molecular and Cellular Proteomics*. 11, M112.017764.

11. Yang, Y., Chaerkady, R., Kandasamy, K., Huang, T. C., Selvan, L. D. N., Dwivedi, S. B., Kent, O. A., Mendell, J. T. and Pandey, A. (2010). Identifying targets of miR-143 using a SILAC-based proteomic approach. *Molecular Biosystems*. 6, 1873-1882.

12. Hou, H.A.,* Huang, T.C.,* Lin, L.I., Liu, C.Y., Chen, C.Y., Chou, W.C., Tang, J.L., Tseng, M.H., Huang, C.F., Chiang, Y.C., Lee, F.Y., Liu, M.C., Yao, M., Huang, S.Y., Ko, B.S., Hsu, S.C., Wu, S.J., Tsay, W., Chen, Y.C., Tien, H.F. (2010). WT1 Mutation in 470 Adult Patients with Acute Myeloid Leukemia: Stability during Disease Evolution and Implication of Its Incorporation into a Survival Scoring System. *Blood* 115: 5222–5231.

*First authors.

13. Huang, T.C., Ko, B.S., Tang, J.L., Hsu, C., Chen, C.Y., Tsay, W., Huang, S.Y., Yao, M., Chen, Y.C., Shen, M.C., Wang, C.H., Tien, H.F. (2007). Comparison of Hypoplastic Myelodysplastic Syndrome (MDS) with Normo-/hypercellular MDS by

International Prognostic Scoring System, Cytogenetic and Genetic Studies. *Leukemia* 22: 544–550.

14. Huang, T.C., Hwang, J.J., Yip, P.K., and Liu, H.M. (2005). Hypotensive Spinal Cord Infarction Associated with Vertebral Body Infarction after Treatment with Short-Acting Antihypertensive Agent. *Journal of the Formosan Medical Association* 104: 607–610.