Title: IRF5 mediates adaptive immunity via altered glutamine metabolism, mTORC1 signaling and post-transcriptional regulation following T cell receptor activation

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ABSTRACT:

Although dynamic alterations in transcriptional, translational, and metabolic programs have been described in T cells, the factors and pathways guiding these molecular shifts are poorly understood, with recent studies revealing a disassociation between transcriptional responses and protein expression following T cell receptor (TCR) stimulation. Previous studies identified interferon regulatory factor 5 (IRF5) in the transcriptional regulation of cytokines, chemotactic molecules and T effector transcription factors following TCR signaling. In this study, we identified T cell intrinsic IRF5 regulation of mTORC1 activity as a key modulator of CD40L protein expression. We further demonstrated a global shift in T cell metabolism, with alterations in glutamine metabolism accompanied by shifts in T cell populations at the single cell level due to loss of *Irf5*. T cell conditional *Irf5* knockout mice in a murine model of experimental autoimmune encephalomyelitis (EAE) demonstrated protection from clinical disease with conserved defects in mTORC1 activity and glutamine regulation. Together, these findings expand our mechanistic understanding of IRF5 as an intrinsic regulator of T effector function(s) and support the therapeutic targeting of IRF5 in multiple sclerosis.

Sentence Summary: Findings provide new insight into the mechanisms by which T cell intrinsic IRF5 regulates the adaptive immune response via modulation of mTORC1 signaling, glutamine metabolism, and protein translation.

Main Text:

INTRODUCTION

The transcription factor interferon (IFN) regulatory factor 5 (IRF5) has been characterized as a regulator of type I IFNs and a key mediator of proinflammatory cytokine expression in response to Toll-like receptor (TLR) signaling. Dysregulation of IRF5 has been linked to infection, autoimmune disease, cancer, metabolic diseases, and neuropathic pain (*1*-*3*). Initial mechanistic studies on IRF5 were performed in myeloid and B cells; however, more recent studies support a role for IRF5 in CD4 T cells (*3*, *4*). Loss of IRF5 expression in CD4 T cells drives Th2 skewing in the context of Th1 and Th17 polarizing conditions, alters inflammatory cytokine production, regulates apoptosis, and inhibits T cell proliferation and chemotaxis (*4*). Many of these IRF5-mediated functions have been reported downstream of IRF5 transcriptional regulation, yet the role of IRF5 in T cell metabolism and translational reprogramming, global shifts of which are required to assume effector function(s), has yet to be examined. Indeed, a lack of correlation between transcriptional responses and protein expression following T cell activation has been documented, with regulation of the T cell proteome occurring far more rapidly than can be explained by *de novo* transcription (*5*). Conversely, rapid metabolic changes in response to T cell stimulation correlate with the kinetics of T activation. One of the key mediators of both normal and pathologic metabolic and translational responses is the mammalian target of rapamycin (mTOR) signaling complex (*6*).

Signaling from mTOR kinase complexes, mTORC1 and mTORC2, regulates T cell effector programs, migration, proliferation, and survival. Similar to previous observations in *Irf5*$^{-/-}$ mice showing skewing towards IL4 secreting Th2 cells, reductions in Th1 and Th17 cells, and increased Treg generation (*4*), reduced mTORC1 signaling is correlated with increased regulatory T cells (Tregs) and a reduction in Th1 and Th17 generation (*7*). In addition, mTORC1 is a key post-transcriptional and translational regulator. Prior studies revealed that naïve CD4 T cells have reserves of ribosomal machinery which, upon TCR stimulation, are activated by mTORC1 to support increased protein synthesis (*8*, *9*). Not only has repression of protein synthesis and mTORC1 signaling been linked to T cell quiescence, but effector immune signaling pathways are also regulated by these translational molecules (*10*, *11*). Further studies elucidating how manipulation of ribosomal machinery regulates T cell function remain to be completed.

The emerging importance of metabolic pathways, mTOR signaling and translational regulation in T cells has inspired a new generation of drug development and target discovery. *In vitro* studies using 2-deoxyglucose and metformin to reprogram reactive T cells from patients with systemic lupus erythematosus (SLE) were met with success (*12*). In the murine model of multiple sclerosis (MS), experimental autoimmune encephalomyelitis (EAE), mTORC1 inhibition with rapamycin protected mice from classical disease development and reversed symptom onset (*7*, *13*, *14*). In addition, manipulation of the Th17-Treg axis through alterations in glutamine metabolism is protective in EAE (*15*). Through a combination of targeted inhibition studies, scRNAseq, flow cytometry, and unbiased metabolomics, we identify IRF5 in the regulation of CD4 T cell metabolism, mTOR signaling and protein translation, and demonstrate a disease modifying role for T cell intrinsic IRF5 in EAE.

RESULTS

IRF5 regulates T cell support of B cell adaptive responses

Previous studies by our lab and others revealed defects in plasmablast (PB) generation and IgG2a/c production in mouse and human *Irf5*-deficient B cells by *in vitro* culture and *in vivo* immunization (*16*, *17*). Although these defects were attributed to B cell intrinsic IRF5 function, more recent studies suggest a role for T cell intrinsic IRF5 in the regulation of B cell adaptive immune responses (*4*) We thus utilized the T cell-dependent antigen NP-conjugated chicken gamma globulin (CGG) emulsified in Complete Freund's Adjuvant (CFA) to assess PB differentiation in 8-10 weeks-old *Irf5*$^{+/+}$ (WT) and *Irf5*$^{-/-}$ (KO) littermate mice. 7 days following immunization, WT and KO spleens were harvested for immunohistochemistry (IHC) and flow cytometric analysis. We detected a significant reduction in B220^{+} staining in KO spleens with no difference in spleen size (**Fig. 1A, B, Supp. 1A, B**). Flow cytometric analysis of KO splenocytes showed reductions in T follicular helper (Tfh) cells (BCL6^{+}CXCR5^{+}) and significantly increased regulatory T cells (Tregs) (CD25^{+}FoxP3^{+}) (**Fig. 1C-E**). Further examination in non-immunized mice revealed significant reductions in splenic Tfh cells in KO compared to WT mice (**Supp. 1C**). Prior studies showed KO T cells to have decreased activation and proliferation following anti-CD3/CD28 stimulation. We confirmed these findings in purified CD4 T cells (**Supp. 1D-G**). Additionally, although KO mice had no significant reductions in NP-specific PBs (CD19^{+}IgD^{low}CD138^{+}), there were significant reductions in IgG2a production (**Fig. 1F-H**). Next, we examined by *in vitro* co-culture assay if KO CD4 T cells were sufficient to replicate the observed B cell defects in the NP-CGG CFA immunization model. B cells (CD45^{+}B220^{+}) and CD4 T cells (CD45^{+}CD4^{+}) were sorted from WT and KO splenocytes and co-cultured for 4 days in the presence of anti-IgM, CpG-B and anti-CD3/CD28 Dynabeads. Of interest, significant reductions in CD19^{+}IgD^{low}CD138^{+} PB generation were observed in KO B cell:KO T cell, WT B cell:KO T cell and KO B cell:WT T cell cocultures as compared to WT B cell:WT T cell cultures with only slight differences in IgG2a production (**Fig. 1I, J, Supp. 1H, I**). Together, these data support a role for CD4 T cell intrinsic *Irf5* in B cell adaptive immunity.

scRNAseq reveals alterations in metabolism, ribosome biogenesis and identifies novel IRF5 transcriptional targets

Current dogma in the field suggests that loss of *Irf5* inhibits Th1 and Th17 effector subsets, enhances Treg differentiation and Th2 responses, and alters Tfh function through transcriptional regulation (*3, 4, 18, 19*). To gain further insight into the cellular pathways by which IRF5 regulates T cell differentiation/function, we performed scRNAseq on 5,000-7,000 TCR-stimulated WT and KO CD4 T cells. Using Seurat, we identified seven distinct T cell clusters (**Fig. 2A**). The subsets were classified as follows: activated naïve (*Nr4a1, Nfkbid, Cd69, Egr3*), naïve (*Sell, Lef1, Klf2, Ifit3*), memory-like (T_{MEM}) (*Spry1, Fabp5, Ccr7*) (*20, 21*), IFN Enriched (*Gbp2, Gbp5, Trat1, Nme1, Nme2)* (*22-25*), Tfh (*Tigit, Il21, Cxcr5, Pdcd1*), Th Complex (*Rora, Ccr5, Ccr2, Serpin6b6)* (*26*), and Treg (*FoxP3, Ikzf2, Il2ra, Il2rb*) (**Fig. 2A, B**). Further subclustering revealed two distinct populations comprising both Treg (termed Treg 0 and Treg 1) and Tfh clusters (identified as Tfh 0 and Tfh 1) (**Supp. Table 1**).

Pseudotime trajectory analysis was performed using Slingshot (*27*) to examine the relationships between each subset. Four trajectory lineages were identified in WT and KO CD4 T cells (**Supp. 2A**). The Tfh and Treg, Th complex subset and IFN enriched, T_{MEM} and activated naïve T cell clusters were predicted to exist within independent lineages. Paired with cluster enrichment analysis (**Fig. 2C**), the pseudotime trajectory findings support that loss of *Irf5* skews T cells toward the specific Tfh/Treg lineage and away from activated naïve and T_{MEM} trajectories. Indeed, further examination of subset enrichment in KO compared to WT CD4 T cells showed KO mice to have reduced activated naïve cells, enrichment in both Treg 0 and Treg 1 and a decrease in T_{MEM} populations, supporting previously described flow cytometric CD4 T cell subset profiling by our lab and others (*4*). There was also a distinct increase in the Tfh 0 and a slight decrease in

Tfh 1 KO T cell populations. The Th complex subset, named thus due to increased expression of genes encoding migratory receptors, inflammatory cytokines, inhibitory molecules, and transcription factors, was also highly enriched in KO CD4 T cells (**Fig. 2C, Supp. 2B**). Of interest, a significant proportion of genes dysregulated in the KO Th complex subset comprised of ribosomal transcripts and alternative splicing machinery**.** In addition, KO Th complex cells had downregulation of proinflammatory and metabolic genes, including *Il18r1*, *Tomm5*, *Nkg7*, *Mif*, *Klrk1* and *Irf8* (**Supp. 2B**) (*28*-*32*). Unlike the Th complex subset, despite the clear shifts in the Tfh and Treg subcluster distribution, few transcripts within each of these clusters demonstrated significant differences with loss of *Irf5* (**Fig. 2C, Supp. 2C, D**). DEG analysis identified only three genes with clear dysregulation across all KO T cell clusters: *Uba52*, *Speckled protein (Sp) 110* (*Sp110*) and *Speckled protein 140* (*Sp140*) (**Fig. 2D-F**). Analysis of the third SP family member, *Sp100*, revealed no change in expression (**Fig. 2G**) (*33*). The specific and dramatic reductions in *Sp110* and *Sp140,* but not *Sp100*, were independently confirmed by *qPCR* in purified WT and KO CD4 T cells (**Fig. 2H-J)**. Of note, previous studies in myeloid cells demonstrated that IRF4 can bind to and regulate similar target genes as IRF5 (*34*). To assess specificity of IRF5 in *Sp* regulation, we examined *Sp100*, *Sp110* and *Sp140* expression in *Irf4*$^{-/-}$ T cells. No significant differences in either *Sp100*, *Sp110* or *Sp140* transcript expression were detected (**Supp. 2E-G**).

SP110 and *SP140* are genes of interest in both inflammatory and autoimmune diseases. Mutations in these factors are associated with Crohn's disease, chronic lymphocytic leukemia, and MS, while hyperactivation of SP110 and SP140 is associated with SLE and MS (*33*). Given the striking reduction in *Sp110* and S*p140* expression in *Irf5*$^{-/-}$ T cells and the implications of elevated IRF5 expression and hyperactivation as a driver of SLE (*35, 36*), we examined *Sp110* and *Sp140* expression in a published RNAseq dataset (GSE149050) from healthy donors and SLE patients with differing IFN levels (*37*). Interestingly, we found increased *SP110* expression in PBMCs from IFN high expressing SLE patients compared to both IFN low SLE patients and healthy controls (HC). Similar trends were observed for *SP140* (**Supp. 2H, I)**. Previous studies from our lab and others demonstrated that SLE is mediated in part by the aberrant production of autoantibodies regulated by B cell intrinsic IRF5 (*16*, *38*). Notably, one of the pathologies associated with speckled protein inactivating mutations is inhibition of B cell antibody production (*39*). Analysis of *Sp110* expression in KO B cells revealed a similar reduction in transcript expression as KO T cells (**Supp. 2J**).

To further assess functional differences between WT and KO T cells, we performed Gene Set Enrichment Analysis (GSEA) using the C5 Gene Ontology (GO) sub-collection. We found significant downregulation in gene sets for Cytoplasmic Translation, Ribosomal Synthesis, Ribosome Metabolism, Ribosome Assembly and Function, RNA Processing, Mitochondrial Depolarization and Mitochondrial structure in KO CD4 T cells (**Fig. 2K**). GSEA using C2 KEGG also revealed significant downregulation of Ribosomes, Oxidative Phosphorylation and Systemic Lupus Erythematosus, supporting conserved regulatory roles for IRF5 in oxidative phosphorylation, mitochondrial function, and ribosome regulation (**Supp. 2K, Supp. Table 2)**. Given these striking reductions in cytoplasmic translation and ribosomal synthesis, we re-examined a previously unpublished study from our lab identifying IRF5-protein interactions in Ramos B cells by immunoprecipitation (anti-IgG control or anti-IRF5 antibodies) and mass spectrometry analysis (**Supp. Table 3**). Among the most significantly enriched for IRF5 interacting partners, as compared to Ig control, were the 60S and 40S ribosomal proteins (RPLs), and translation initiating factors EIF4A2 and EIF6. Despite these studies being performed in B cells, IRF5 interaction with proteins involved in ribosomal assembly and biogenesis (RPLs, EIF6) and translation (EIF4A2) imply a conserved role for cytoplasmic IRF5 in the regulation of the translational apparatus, findings supported by prior independent studies (*40*).

***Irf5*$^{-/-}$ mice are protected from Experimental Autoimmune Encephalomyelitis**

Although inhibition or loss of IRF5 is protective in autoimmune and inflammatory diseases (*4, 35, 41-43*), apart from *Leishmania donovani* and inflammatory bowel disease (IBD) models, the contribution(s) of IRF5 to T cell-mediated disease pathogenesis has remained largely unexplored. Using scRNAseq, we found downregulation of proinflammatory factors previously implicated in EAE disease pathogenesis including *Il18r1*, *Irf8*, and *Mif*, and increased expression of *Rora* in the KO Th complex subset (*28, 32, 44, 45*). In addition, we detected a significant reduction in *Sp110* and *Sp140* expression, gene loci associated with risk of MS (*33*). Thus, we next expanded our studies to examine if loss of *Irf5* impacts the clinical progression of experimental autoimmune encephalomyelitis (EAE) using MOG_{35-55}/PTX injections (*46*). Using a common clinical rating scale (*46*), we found that KO mice had both decreased and delayed incidence and onset of disease as well as significantly attenuated disease progression compared to WT littermate mice, indicating a protective role for loss of *Irf5* in T cell-mediated EAE (**Fig. 3A, B**).

One of the T cell-mediated adaptive immune signaling pathways dysregulated in MS involves the expression and binding of T cell CD40L to its receptor, CD40, on B cells (*47, 48*). Given the observed reductions in PB generation by coculture of WT B cells with KO T cells and the stark protection of *Irf5* KO mice from T cell-mediated EAE disease onset and progression, we next examined if loss of *Irf5* dysregulated the CD40L/CD40 pathway. Following stimulation of WT and KO total splenocytes with either anti-CD3/CD28 Dynabeads or anti-IgM (B cell receptor stimulation), CD40L and CD40 expression was quantified on Live $CD3^{+}CD4^{+}$ T cells and Live

$CD45^+CD19^+B220^+$ B cells, respectively. Anti-CD3/CD28-stimulated KO T cells demonstrated a significant decrease in both CD40L surface expression, as quantified by mean fluorescence intensity (MFI), and CD40L expressing $CD3^+CD4^+$ T cell populations 24 hours following stimulation (**Fig. 3C-E**). There were slight, albeit significant reductions in the percentage of $CD40^+$ B cells and CD40 MFI on unstimulated and anti-IgM stimulated KO B cells (**Supp. 3A, B)**. Examination of basal CD40L expression revealed a slight but significant increase in the percentage of CD40L expressing KO T cells, but no significant difference in MFI (**Supp. 3C, D**). *Cd40l* transcript expression was not significantly detected via scRNAseq, thus we evaluated *Cd40l* transcript expression from sorted $CD3^+CD4^+$ T cells (purity > 95%) from WT and KO mice following 6-hour *in vitro* TCR stimulation. There was no significant difference in expression between genotypes (**Fig. 3F**). This was unsurprising as previous studies have indicated that *Cd40l* expression is extensively regulated post-transcriptionally (*49*, *50*). Notably, flow cytometric examination revealed, like that seen in NP-CGG CFA immunized KO mice, a significant decrease in Tfh cells in KO spleens following EAE induction (**Supp. 3E, F**). Together, aberrant CD40L protein expression on KO CD4 T cells and reductions in Tfh cells supports a role for IRF5 in T cell support of the adaptive immune response and in post-transcriptional or translational regulation of CD40L following TCR signaling.

IRF5 regulates protein translation in T cells via mTORC1

Given our findings, we next sought to examine the function of one of the most highly conserved mediators of translation, metabolism, and post-transcriptional regulation, whose aberrant function also has been implicated in EAE pathogenesis, the mammalian target of rapamycin 1 (mTORC1) signaling complex. mTORC1 is a key regulator of T cell proliferation, differentiation, and effector function (*51-53*). Despite current and prior studies demonstrating KO T cell defects in activation and proliferation, the regulatory mechanisms underlying these dysfunctions have yet to be fully elucidated (*4, 17, 42, 43*). Considering our findings that suggest a role for IRF5 in translational regulation, we next determined if mTORC1 activity was altered in KO T cells by examining total ribosomal S6 protein (RPS6) and phosphorylated RPS6 (phosphoRPS6) levels, both of which are canonical downstream effectors of mTORC1 signaling. Flow cytometric analysis revealed a significant defect in the phosphorylation of RPS6 in TCR stimulated KO T cells, indicating decreased mTORC1 activity (**Figs. 4A, B**). No significant difference in total RPS6 expression was detected (**Supp. 4A**). Examination of phospho(Thr389)-p70 S6 kinase (P70S6K), the kinase responsible for RPS6 phosphorylation, showed decreased phosphorylation, albeit insignificant (**Supp. 4B**). Additional studies revealed similar total mTOR protein expression in KO and WT CD4 T cells basally and following TCR stimulation, further supporting that IRF5 regulates mTORC1 activity rather than mTOR expression (**Supp. 4C**).

One of the main regulators of mTORC1 is the serine/threonine protein kinase, Akt (*54*). Akt activation promotes many of the pathways regulated by mTOR, including proliferation, survival, and metabolism (*55*). Analysis of Akt activity in KO CD4 T cells following 24-hour TCR stimulation revealed a significant reduction in Akt (Ser473) phosphorylation (**Fig. 4C**). This supports previous findings of Akt dysregulation in *Irf5*-deficient myeloid cells (*56*). Akt in T cells can be activated via signaling from IL2 (*57*). Following TCR stimulation, KO CD4 T cells had decreased expression of both IL2 and the IL2 receptor, CD25 (**Fig. 4D, E**). Prior studies have shown that, unlike in humans, IL2 does not regulate murine CD40L expression (*58*). Nonetheless, to confirm that alterations in IL2 expression and signaling through the IL2R were not responsible for reduced CD40L expression in KO CD4 T cells, total splenocytes were harvested and stimulated with anti-CD3/anti-CD28 in the presence or absence of recombinant IL2. Results showed no significant difference in CD40L expression (**Supp. 4D**). Of interest, treatment with the Akt inhibitor, MK2206, inhibited CD40L expression, indicating that Akt activity is required for CD40L expression (**Supp. 4E**). These results provide initial evidence that IRF5 regulates translation through mTORC1 signaling, whose activity is inhibited by reduced Akt activity.

Rapamycin is a small molecule inhibitor of mTORC1 that binds to cytosolic FKBP12 and inhibits mTOR S2448 phosphorylation and subsequent activation (*59*). Given the reduction in phosphoRPS6 in KO CD4 T cells, we next investigated if mTORC1 regulates the expression of CD40L. We stimulated WT CD4 T cells in the presence or absence of rapamycin for 24 hours, then analyzed T cell activation (CD4$^+$CD69$^+$) and CD40L expression. Although there was no change in the activation of CD4 T cells with rapamycin treatment (**Fig. 4F**), there was a significant decrease in CD40L expression that replicated levels seen in KO T cells (**Fig. 4G-I, Fig. 3C-E**). There was no difference in viability following rapamycin treatment (**Supp. 4F**). Next, to examine if T cell intrinsic mTORC1 inhibition was sufficient to inhibit the B cell adaptive response, we sorted and pretreated WT CD4 T cells with rapamycin (+Rap) or PBS (-Rap) then cocultured T cells with B cells as previously described. Quite strikingly, we observed a significant decrease in CD45$^+$CD19$^+$CD138$^+$IgD^{low} PB generation and IgG2a production despite the relative increase in CD45$^+$CD19$^+$ B cells when B cells were cocultured with rapamycin-treated CD4 T cells. Taken together, these findings further support that mTORC1 signaling in CD4 T cells is required for T cell support of B cell adaptive immune responses **(Fig. 4J-M, Supp 4G)**.

Notably, the mTORC1 signaling axis is a key regulator of protein synthesis. With the previous findings demonstrating defects in T cell activation, proliferation, and CD40L expression in the context of mTORC1 dysfunction, we next examined rates of protein translation in unstimulated and TCR stimulated KO T cells by measuring incorporation of an alkyne analog using chemoselective fluorochrome ligation with the OPP assay. We found a significant decrease in the rate of protein translation in TCR stimulated KO T cells, indicating a role for IRF5 in the positive regulation of protein synthesis (**Fig. 4N, O**). Recent studies exploring mechanisms by which mTORC1 regulates translation have revealed ATF4 as a metabolic effector of mTORC1. When expressed, ATF4 promotes protein synthesis and stimulates the uptake of various amino acids. Immunoblot analysis of ATF4 expression in KO T cells following TCR stimulation revealed significantly reduced expression in KO T cells (**Fig. 4P, Q**). We also examined the expression of eukaryotic elongation factor 2 (eEF2), a global mediator of protein translation. Prior studies have demonstrated that NF-kB activating stimuli can activate eEF2 by repressing transcription of the inhibitory calcium/calmodulin dependent eEF2 kinase (eEF2K) (*60*). Other studies have shown that eEF2K inhibitory phosphorylation of eEF2 is regulated through the rapamycin-sensitive mTOR pathway, shown here to be dysregulated in KO T cells (*61*, *62*). We thus examined eEF2 levels following TCR stimulation of purified CD4 T cells and detected a significant reduction in expression within KO T cells (**Fig. 4R, S**). Altogether, these findings support a role for IRF5 in the regulation of protein translation at the transcriptional and post-transcriptional level.

Untargeted metabolomics reveals global metabolic shifts in *Irf5*$^{-/-}$ CD4 T cells

mTORC1 activity is extensively regulated by and responsive to changes in cellular energy levels and metabolites, changes that are mediated in part through ATF4 signaling (*63*). In T cells, metabolites modulate survival, proliferation, and effector fate decision and function (*64*). Results from scRNAseq analysis of KO T cells revealed a significant reduction in the enrichment of genes involved in oxidative phosphorylation (**Supp. 2K**). Prior studies in *Irf5*$^{-/-}$ macrophages have also reported reduced oxidative phosphorylation capacity (*56*, *65*, *66*). Although a role for IRF5 in T cell metabolic regulation has yet to be investigated, the observed alterations in KO T cell function and mTOR signaling provided compelling initial evidence to support this. As such, we performed unbiased LC-MS metabolomics analysis on unstimulated and TCR stimulated WT and KO purified naïve CD4 T cells (**Supp. Table 4**). T cell purity and activation was confirmed by flow cytometric analysis (**Supp. 5A)**. Basally and following TCR stimulation, the metabolic landscapes of WT and KO T cells had dramatic differences (**Supp 5B**). KO T cells significantly downregulating 21 metabolites relative to WT T cells ($p < 0.05$, FC > 1.5) (**Fig. 5A, B**). Following 24 hours of anti-CD3/CD28 stimulation, WT and KO T cells continued to demonstrate distinct metabolic profiles (**Fig. 5A-D**). Anti-CD3/CD28 stimulated KO T cells had 20 significantly upregulated and 4 significantly downregulated metabolites compared to unstimulated KO T cells (**Fig. 5C**), while anti-CD3/CD28 stimulated WT T cells had 28 significantly upregulated and 14 significantly downregulated metabolites compared to unstimulated WT T cells (**Fig. 5D**). Of those metabolites, TCR stimulated WT T cells revealed 10 unique ones that were upregulated while KO T cells had only 2 uniquely upregulated. Conversely, WT T cells showed no uniquely downregulated metabolites while KO T cells had 23 downregulated ($p < 0.05$, FC > 2.0) (**Fig. 5E, F, Supp. Table 5**). Subsequent metabolite enrichment pathway analysis demonstrated regulatory perturbations in some of the most highly enriched metabolite sets following TCR stimulation (**Supp. 5C**). Of particular interest was the significant enrichment in Malate-Aspartate Shuttle (MAS) metabolites: malate, aspartate, glutamate, and α-ketoglutaramate (α-KGM) in KO T cells (**Supp. 5C, Fig. 5G-K)**. We next quantified transcript levels of the cytoplasmic Glutamic-oxaloacetic transaminase 1 (*Got1*) and mitochondrial Glutamic-oxaloacetic transaminase 2 (*Got2*) MAS transaminases. Following anti-CD3/CD28 stimulation, both *Got1* and *Got2* transcript levels were increased in KO compared to WT T cells (**Supp. 5D, E**). Finally, to confirm that the increased levels of MAS metabolites and transaminases were reflective of increased utilization of the MAS in KO T cells, we treated WT and KO T cells with the MAS inhibitor aminooxyacetate acid (AOAA). Following 24 hours of AOAA treatment, anti-CD3/CD28 stimulated KO T cells had significantly increased rates of apoptosis compared to WT T cells (**Supp. 5F**). Together, these findings indicate global shifts in T cell metabolism with loss of *Irf5*, and increased reliance of KO T cells on the malate-aspartate shuttle following T cell receptor stimulation.

IRF5 and glutamine metabolites regulate glutamine transporter protein expression

As previously described, the *in vitro* metabolomics analysis revealed increased levels of glutamate in KO T cells (**Fig. 5J**). However, previous studies demonstrated that inhibition rather than enrichment in glutamine metabolism is a molecular mechanism to inhibit Th1 and Th17 effector functions, drive Treg generation, and inhibit T cell activation and proliferation, phenotypes that have been described by us and others in KO T cells (**Supp. 1**) (*67-70*). Thus, given the results of our *in vitro* metabolic studies that demonstrated increased glutamine metabolites in KO T cells (**Fig. 5**), we next interrogated other factors involved in glutamine transport metabolism in CD4 T cells. Two key murine glutamine transporters expressed in CD4 T cells are ASCT2 and SNAT2. Following TCR stimulation, ASCT2 and SNAT2 expression were downregulated in KO T cells (**Fig. 6A-C**). However, there was no significant difference in *Slc1a5* (ASCT2) or *Slc38a2* (SNAT2) transcript expression (**Fig. 6D, E**). Further evaluation of key glutamine metabolic enzymes, Glutamate dehydrogenase 1 (*Glud1*) and Glutaminase 2 (*Gls2*) revealed no significant differences in transcript expression (**Supp. 6A, B**). Interestingly, although there was no change in GLUD1 expression (**Supp. 6C, D**), there was a dramatic, albeit insignificant reduction in GLS2 protein expression in KO T cells following anti-CD3/CD28 stimulation (**Supp. 6E, F**). Together, these results indicate that the increased levels of glutamine metabolites in the KO T cells are more likely due to contributions from upregulation of the MAS rather than an upregulation in glutamine metabolism.

Given the observed increase in the intermediary metabolite of α-ketoglutarate (α-KG), α-KGM, in KO T cells (**Fig. 5J**), we next examined if ASCT2 expression was influenced by the upregulation of this epigenetic regulator of immune responses (*68, 71-74*). Following treatment of WT CD4 T cells with the cell permeable α-KG analog, dimethyl-ketoglutarate (DMK), we observed a significant reduction in ASCT2 expression (**Fig. 6F**). As previously discussed, glutamine metabolism regulates T helper cell function. Thus, we examined if alterations in metabolites contribute to CD40L dysregulation observed in KO T cells. Following WT T cell DMK treatment, we found a significant downregulation of CD40L expression (**Fig. 6G**). As previously reported, treatment with DMK did not inhibit S6 phosphorylation, indicating that DMK modulation of CD40L expression signals through an mTORC1-independent pathway (**Supp. 6G**) (*75-77*). In support of the previously established regulatory role of α-KG in demethylation via the ten-eleven translocation (Tet) α-KG dependent dioxygenases, increasing levels of DMK resulted in a significant increase in transcript expression for both *Cd40l* and *Slc1a5* despite the significant reductions in CD40L and ASCT2 protein expression (**Fig. 6H, I**) (*77*). These findings indicate a more complex role for α-KG regulation at a post-epigenetic level.

To further elucidate how the reductions in ASCT2 expression mechanistically contribute to defects in KO CD4 T cell function, we sought to mimic the reduction in ASCT2 expression by using the small molecule ASCT2 inhibitor, V-9302. Treatment of WT CD4 T cells with V-9302 dramatically inhibited CD40L expression (**Fig. 6J, K**). Further, inhibition of glutaminase, the enzyme responsible for converting glutamine into glutamate, with CB-839 (Telaglenastat) also inhibited CD40L expression in WT CD4 T cells (**Fig. 6J, L**). Together, our findings indicate that increased intracellular glutamine metabolites act as negative regulators of glutamine transporter and enzyme expression, which in turn are required for the positive regulation of CD40L.

T cell conditional *Irf5*$^{-/-}$ mice are protected from EAE

mTORC1 signaling, ASCT2 expression, and Speckled proteins have been linked as either risk factors for or protective against multiple sclerosis (*7*, *13*, *70*). Thus, to determine the specificity of our findings, we generated *Irf5*$^{fl/fl}$-*Lck-Cre*$^{+}$ T cell-specific KO mice (cKO) and examined if loss of *Irf5* in T cells was sufficient to confer protection from EAE as previously observed in our whole-body KO studies (**Fig. 3**).

cKO mice had significantly attenuated disease progression with a marked improvement in disease scores compared to the *Irf5*$^{fl/fl}$-*Cre*$^{-}$ littermate controls (**Fig. 7A**). Histologic analysis of spinal cord sections from cKO mice showed an intact myelin sheath and reduced inflammatory foci (**Supp. 7A.**), whereas typical demyelination and inflammation were observed in *Irf5*$^{fl/fl}$-*Cre*$^{-}$ littermate mice. To examine the role of IRF5 in disease onset as well as disease progression, we harvested spleens at symptom onset (D13) and peak symptoms (D20). cKO spleen sizes showed trends towards increased size compared to *Irf5*$^{fl/fl}$-*Cre*$^{-}$ mice at D20 (**Fig. 7B, Supp. 7B**). Despite this, flow cytometric analysis of total splenocytes revealed a significant decrease in the overall percentage of CD4 T cells in the spleens of cKO mice at both timepoints (**Fig. 7C**).

We next investigated if effector T cells were impacted by loss of *Irf5*. We observed a significant reduction in splenic IFNγ production by CD4 cKO T cells (**Fig. 7D, E**). There were no differences in IL17 or IL4 expression in cKO CD4 T cells (**Supp. 7C-F**). Despite the protective phenotype in cKO mice, there was no significant alteration in Tfh ($CD4^{+}BCL6^{+}CXCR5^{+}$), Treg ($CD4^{+}FoxP3^{+}$) or CD40L expression (**Supp. 7G-J**). As previously discussed, ASCT2 expression and mTORC1 activity have been implicated in EAE. Examination of the expression and activation of these molecules, respectively, showed significant reductions in ASCT2 expression (**Fig. 7F, G**) and RPS6 phosphorylation (**Fig. 7H, I**) in cKO CD4 T cells following EAE induction, supporting a vital role for the expression of these molecules in EAE disease pathogenesis, as well as their regulation by T cell intrinsic IRF5.

Our previous studies in NP-CGG CFA immunized mice revealed defects in KO splenic follicles (**Fig. 1A**). Thus, we next examined the spleen at both D13 and D20 in cKO and *Irf5*$^{fl/fl}$-*Cre*$^{-}$ mice by IHC. D13 IHC analyses revealed decreased CD4 and B220 cells in cKO spleens, while D20 IHC analyses revealed no significant differences in CD4, but a dramatic increase in B220 coverage (**Figs. 7J, K, Supp. 7K, L**). To better elucidate how these early histologic findings correlated with disease progression, spleens from *Irf5*$^{fl/fl}$-*Cre*$^{-}$ and cKO mice were stratified by disease score (advanced score > 10, moderate score 6 to 8, minimal score 1 - 2) and correlations performed between B or T cell coverage and disease score. Our findings revealed that increasing EAE disease scores inversely correlated with B220 coverage (**Fig. 7L**) and positively correlated with CD4 coverage (**Fig. 7M**), with the coverage of CD4 thus inversely correlated with that of B220 ($R^2 = 0.78$, p-val< 0.005) (**Fig. 7N**).

Notably, Sp110 and Sp140 dysregulation has been implicated in the pathogenesis of MS (*33*). Thus, to further assess the link between loss of *Irf5* expression and *Sp* expression and validate our scRNAseq findings, we performed qPCR on sorted CD4 T cells and B cells from cKO mice following anti-CD3/CD28 stimulation, as previously described. Our findings revealed a select decrease in *Sp110* and *Sp140* in cKO CD4 T cells (**Supp. 7M-O, Fig. 2**). Taken together, these data demonstrate a clear relationship between the presence and function of CD4 T cells and B cells in modulating EAE disease pathogenesis, identifies regulatory pathways by which inhibition of T cell intrinsic IRF5 may offer protection from EAE disease onset and severity, and reveals novel IRF5 translational and transcriptional targets (**Fig. 7O**).

DISCUSSION

Recent studies have demonstrated the vital importance of metabolic and translational regulatory pathways in T cell function (*78-81*). IRF5 was previously implicated as a mediator of T helper cell-intrinsic cytokine/chemokine expression and migration. However, prior to this study, a thorough functional examination of T cell intrinsic IRF5 beyond its canonical role as a transcriptional regulator of proinflammatory cytokines had yet to be conducted (*4, 43, 82*).

Our mechanistic studies using immunophenotyping, targeted inhibitor assays, metabolomics, co-immunoprecipitation and scRNAseq analyses revealed dysregulation of ribosomes, protein translation and metabolism in *Irf5*$^{-/-}$ T cells. Specifically, we found an overall reduction in *Irf5*$^{-/-}$ T cell translational capacity and mTORC1 activity. *Uba52*, ATF4, and eEF2 were identified as candidate regulatory targets of IRF5 that may contribute to the observed reduction in protein translation. UBA52, a ubiquitin-ribosomal fusion protein, is an understudied master regulator of translation that functions through roles in both the assembly of the ribosome translational complex and as a major supplier of ubiquitin. Inhibition of global protein synthesis and decreased proliferation in KO T cells with decreased *Uba52* expression closely replicates findings from prior studies, indicating a likely role for IRF5-dependent UBA52 expression in the regulation of CD4 T cells (*83*). Analysis of IRF5 interacting partners in Ramos B cells revealed significant enrichment for EIF6 and EIF4A2. Both of these factors are of particular interest as EIF6 plays a key role in ribosome biogenesis (*84*) while EIF4A2 is a RNA helicase involved in translational repression via the miRNA degradation pathway (*85, 86*). Thus, it stands to reason that loss of *Irf5* may alter the function and/or expression of EIF6 and EIF4A2 and hence reduce protein translation. Lastly, as previously discussed, ATF4 is a key regulator of protein translation and metabolism, whose expression we reveal as dysregulated with loss of *Irf5*. Further validation of these candidate regulatory targets and their impacts on T cell function will be a focus of future study.

Beyond this, rapamycin inhibition assays provided evidence that mTORC1 signaling is crucial for CD4 T cell support of B cell adaptive immunity through regulation of CD40L expression. Prior studies demonstrated correlations between reduced CD40L expression on T cells and impaired Th1 polarization, recapitulating our findings in KO CD4 T cells (*87, 88*). However, the T cell intrinsic regulatory mechanisms governing CD40L expression have yet to be fully elucidated. Here, we provide compelling evidence that mTORC1 activity and glutamine metabolism are molecular regulators of CD40L expression. We further demonstrate that elevated levels of the metabolite α-KG were sufficient to reduce both glutamine transporter expression and CD40L through post-transcriptional mechanisms, thereby curtailing the adaptive immune response. Interestingly, prior studies showed increased α-KG levels produced from glutamine metabolism drives M2-like macrophage polarization, while other studies have demonstrated the promotion of alternative (M2-like) anti-inflammatory macrophages from M1 occurs with loss of *Irf5* (*89-91*). Our data suggest that IRF5-mediated alterations in α-KG may contribute to its role in macrophage polarization. Beyond glutamine metabolism, another metabolite of interest that was uniquely downregulated in KO but not WT T cells following stimulation was glycerolphosphorylethanolamine (GPE), levels of which directly correlate with phosphatidyl ethanolamine (PE) (**Supp. Table 4, 5)** (*92*). Recent studies have identified PE as a key metabolite in Tfh differentiation and support of humoral immunity. It is tempting to speculate that dysregulation of these metabolic pathways in KO mice may contribute to our findings of reduced Tfh cells (*93*). Lastly, our findings demonstrate increased reliance of KO CD4 T cells on the malate aspartate shuttle. The MAS is an alternative method by which cells can generate NADH and provide electrons to the electron transport chain. Our current findings, along with prior work demonstrating defects in oxidative phosphorylation with loss of *Irf5* (*56*, *65*), suggest that mechanisms exist by which KO T cells compensate for decreased oxidative phosphorylation. Taken together, we propose that loss of *Irf5* in CD4 T cells drives aberrant effector function through a combination of transcriptional, translational, and metabolic reprograming (**Fig. 7O**).

Metabolic intervention to combat disease has been met with success in both preclinical and clinical studies. Increasing our understanding of how immune cells respond to metabolic dysregulation is crucial for continued advancement. Through unbiased metabolomics analysis, we reveal global alterations in T cell metabolism with loss of *Irf5*. Prior studies have shown that reducing glutamine in media drives Tregs while inhibition of glutamate conversion to α-KG with the MAS inhibitor, AOAA, drives Th17 inflammatory cells through 2-hydroxyglutarate dependent methylation of the *FoxP3* promoter. Here, our studies reveal a shift towards a Treg phenotype with loss of *Irf5* and an increase in intracellular α-KG and glutamate, supporting a role for IRF5 in the metabolic regulatory axis governing Th17 and Treg fate decision. Of further interest, α-KGM is an intermediary molecule in the conversion of glutamate to α-KG through the understudied glutaminase II pathway (*94*). Unlike the conversion of glutamate to α-KG by glutamate dehydrogenase, conversion of α-KGM to α-KG results in the production of NH_4^+. High ammonia levels inhibit T cell activation, proliferation and contribute to T cell exhaustion (*95*). Further studies elucidating the role of T cell intrinsic ammonia production in T effector functions, and by extension how increasing levels of α-KGM might contribute to the dysregulation of *Irf5*$^{-/-}$ T cells, remains to be performed.

IRF5 has canonically been described as a transcription factor. Our scRNAseq analyses highlighted the differentiating potential and transcriptional regulation of T cell subsets, particularly the Th complex, by IRF5. DEG analysis in WT CD4 T cells revealed Th complex cells to express chemokines and chemokine receptors in addition to proinflammatory and inhibitory cytokines, transcription factors and proteins. These factors describe a migratory CD4 T cell population poised to rapidly respond to stimuli with the potential to gain proinflammatory or inhibitory effector functions. Notably, we found the Th complex subset to be significantly enriched in *Irf5*$^{-/-}$ mice. Interestingly, analysis of the transcriptional profiles of *Irf5*$^{-/-}$ Th complex subset showed them poised for an anti-inflammatory response with reduced translational capacity compared to their WT counterparts. It is tempting to speculate that these transcriptional differences contribute to the protection observed in EAE cKO mice. Of note, a recent paper revealed that CXCR4-dependent MOG autoreactive T cell migration into the bone marrow was required for CCL5-dependent aberrant inflammatory myelopoiesis that escalates the CNS demyelination characteristic of EAE (*96*). These same pathways were downregulated in *Irf5*$^{-/-}$ Th complex cells.

Our scRNAseq analysis additionally revealed two autoimmune risk genes under IRF5 transcriptional regulation: *Sp110* and *Sp140*. SP110 and SP140 are nuclear body proteins hypothesized to regulate gene transcription, ribosome biogenesis and apoptosis (*97*, *98*). Of interest, *SP110* missense mutations and deletions are associated with Hepatic Venoocclusive Disease with Immunodeficiency (VODI), which clinically presents with severe hypogammaglobulinemia, a T-cell immunodeficiency, absent lymph node germinal centers (GCs) and absent tissue plasma cells; findings remarkably similar to those reported in *Irf5*$^{-/-}$ mice (*99*).

SP140 has been identified as a modulator of chromatin accessibility in macrophages (*100*). Previous ATAC-seq studies performed in *Irf5*$^{-/-}$ T cells revealed significant alterations in chromatin accessibility. This finding was not attributed to IRF5's role as a transcription factor (*4*). Furthermore, analysis of the *SP110* and *SP140* promoter region with Genome.UCSC revealed predicted binding sites for IRF5. We propose that *Sp110* and *Sp140* are IRF5-specific regulatory targets. Examination of this novel IRF5 regulatory axis in other immune cells will be the focus of future studies.

Prior work described alterations in SP110 expression, glutamine transporter expression and aberrant mTORC1 activity as significant risk factors for MS. Here, we show each of these risk factors to be regulated by IRF5 (*101, 102*). cKO protection from EAE further demonstrated the preclinical relevance of IRF5 expression in CD4 T cells. The alterations in secondary lymphoid architecture and reduced B cell egress from the spleens provide additional compelling evidence that the expression of IRF5 in CD4 T cells is crucial for the B cell adaptive response. In the context of MS, mounting evidence demonstrates the crucial role for pathogenic B cell maturation and antibody secretion in driving demyelination (*103*). Treatment with rituximab to deplete B cells is gaining traction as an effective therapy for treatment resistant disease (*104, 105*). However, this fails to counter existing plasma cells which lack CD20 expression (*106*). Thus, inhibiting the generation of pathogenic autoantibody secreting B cells has remained a challenge due to a lack of understanding of modulators of disease pathogenesis (*106-109*). Based on the results of our studies, we propose that inhibiting B cell maturation and autoantibody production by targeting IRF5 activity in CD4 T cells through recently developed IRF5 specific inhibitors is a potential therapeutic strategy for the treatment of MS (*35, 41*).

In summary, our findings highlight novel regulatory roles for IRF5 in mTORC signaling, as well as in the metabolic, transcriptional, and translational regulation of CD4 T cells. We elucidate how subtle shifts in metabolism have a profound impact on the adaptive immune response with clinical implications. Altogether, these data significantly increase our knowledge of IRF5 regulatory pathways in CD4 T cells at a transcriptional, translational and metabolic level, expands our understanding of metabolic regulation of signaling pathway molecules, broadens our knowledge of the KO CD4 single cell landscape, and highlights IRF5 expression in CD4 T cells as a potential therapeutic target in the treatment of multiple sclerosis.

In the context of metabolic dysregulation, previous studies established that disruption of metabolites drives transcriptional alterations and epigenetic remodeling, which in turn reprograms immune cells. Thus, a limitation of this study is an inability to definitively determine the primary perturbation driving dysregulation in these highly interlinked transcription-translation-metabolic feedback loops. We attempted to address this using small molecule inhibitors in unperturbed WT systems. However, our findings only provide partial insight into the complex interplay between metabolism and T cell function. In addition, in the cKO EAE model, we did not observe reductions in CD40L. Review of literature shows that CD40L has historically been difficult to study directly due to the highly transient and early expression of this signaling molecule. Further studies investigating the kinetics of CD40L expression in EAE models are of interest.

MATERIALS AND METHODS

Study design

This study was designed to understand the molecular mechanisms by which IRF5 modulates T cell effector function in response to TCR activation *in vitro* and in the *in vivo* EAE disease model.

Endpoint analyses for *in vitro* and *in vivo* studies included flow cytometry, quantitative polymerase chain reaction (qPCR), scRNAseq, and unbiased metabolomics. All *in vitro* studies used randomly assigned mice without investigator blinding. We compared the clinical response to EAE induction following $MOG_{35\text{-}55}$/PTX injections of 8-12 weeks-old C57BL/6 *Irf5*$^{+/+}$ (WT) and *Irf5*$^{-/-}$ (KO) littermate mice, and *Irf5*$^{fl/fl}$*-Lck-Cre*$^{-}$ and *Irf5*$^{fl/fl}$*-Lck-Cre*$^{+}$ littermate mice. Mechanisms of immunopathology were investigated during early onset and peak disease as determined by a common clinical scoring method. Clinical scoring was performed with investigator blinding. All data points and *n* values reflect biological replicates. The specific numbers and genotypes of the mice and the statistics performed are included in the figure legends such as the two-way unpaired *t* test, 1-way analysis of variance (ANOVA) with Tukey's post-hoc test for multiple comparisons, and 2-way ANOVA with Holm-Sidak correction for multiple comparisons as indicated. Experiments were repeated in multiple settings using complementary methods of molecular interrogation and laboratory techniques to validate findings. All data points from the studies were included unless methodologic errors occurred resulting in decreased cell viability, poor activation, sample contamination or low cell numbers.

Mice

C57BL/6J *Irf5*$^{-/-}$ mice were originally obtained from Taniguchi via the Rifkin Lab and backcrossed 11 generations (*110*). C57BL/6J *Irf5*$^{+/+}$WT littermate mice were used as controls. *Irf5*$^{fl/fl}$*-Lck-Cre*$^{+}$ mice were a kind gift from Simona Stager's lab (1INRS-Institut Armand-Frappier). C57BL/6J *Irf4*$^{-/-}$ mice were a kind gift from Dr. Alessandra Pernis (Hospital for Special Surgery). Genotype was confirmed using PCR. Mice used in experiments were between 6 weeks to 4 months of age and of both genders. Experiments were performed in agreement with our Institutional Care and Use Committee and according to National Institutes of Health guidelines. All mice were bred in house at the Feinstein Institutes for Medical Research. *Irf5*$^{\mathrm{fl/fl}}$ cage-matched littermates (*Irf5*$^{fl/fl}$*-Lck-Cre*$^{-}$) were used as wild-type controls in experiments utilizing *Irf5*$^{fl/fl}$*-Lck-Cre*$^{+}$ (cKO) mice. For all experiments, mice were age- and sex-matched.

Naïve CD4 T cell isolation

Freshly isolated splenocytes from WT and KO mice were homogenized in 4 mL PBS. Red blood cell (RBC) lysis was performed in 8 mL of RBC lysis buffer (Biolegend) for 5 minutes on ice and quenched with excess PBS + 2% FBS (vol/vol). Naïve CD4 T cells were isolated using Miltenyi T cell Isolation Kit following manufacturer’s protocol (Cat#: 130-104-453). Magnetic separation was performed to achieve a >95% enriched population of naïve CD4 T cells. For T cell activation, cells were cultured in RPMI 1640 supplemented with 10% FBS and 1X Pen/Strep in the presence of either 1 ng/mL Recombinant murine IL-7 (PeproTech, Cat#217-17) or stimulated with anti-CD3/CD28 Dynabeads at a 4:1 bead:cell ratio (Fisher Scientific, cat#: 11-452-D).

Total B cell and CD4 T cell isolation

Total splenocytes were isolated from mice and RBCs lysed as previously described. Cells were stained with B220R PerCP and CD4 BV510 in FACS buffer for 30 minutes at room temperature, briefly washed in FACS buffer, and sorted using BDFacsAria.

In vitro CD4 T cell proliferation

CD4 T cells were sorted then stained with CellTrace™ Violet Proliferation Dye as per manufacturer protocols (Invitrogen™ Cat#:C34557). Labeled CD4 T cells were activated with anti-CD3/CD28 Dynabeads and cultured for four days before being analyzed by flow cytometry.

Immunizations

Intraperitoneal injections were performed using 200 µl/mouse. Sterile PBS solution was used to reconstitute 4-Hydroxy-3-nitrophenylacetyl hapten conjugated Chicken Gamma Globulin (NP-

CGG, Ratio 29:20) to a final concentration of 2 mg/mL (Biosearch Technologies, Cat#: N-5055C-5). Complete Freund's Adjuvant (CFA) was purchased from Invivogen (Cat#: vac-cfa-60). Intraperitoneal injections of NP-CGG-CFA were conducted using 100 µg/100 µL NP-CGG emulsified in 100 µL CFA.

Flow cytometry

Samples were harvested, washed in PBS + 2% FBS (vol/vol), blocked with anti-CD16/CD32, and stained with a Live/Dead Fixable Dead Cell stain prior to surface and intracellular stains. For a detailed list of antibodies used in staining panels, see Supplemental Methods. Intracellular staining was performed per manufacturer's protocol using Transcription Factor Staining Buffer Set (Cat#: 00-5523-00, eBioscience^{TM}). Phospho-flow cytometry was performed using the two-step fixation/methanol protocol (Protocol C: Two-step Protocol for Fixation/Methanol, ThermoFisher).

In vitro CD4 T cell activation and cocultures

Sorted CD4$^+$ T cells or total splenocytes were cultured in 24-well flat-bottom plates at a density of 2×10^6 cells/500 µL media (Fischer Scientific, cat# 3473). For T cell activation, cells were cultured in RPMI 1640 supplemented with 10% FBS (v/v) and 1X Penn/Strep and stimulated with anti-CD3/CD28 Dynabeads as per manufacturer's protocol (Fisher Scientific, cat#: 11-452-D). For cocultures, 2 x 10^6 sorted CD4$^+$ T cells and 2 x 10^6 sorted B cells were co-cultured for 4 – 5 days in the presence of Dynabeads, 10 ng/mL CpG-B (ODN 2006) (Fischer Scientific, Cat#: HC4039) and 10 µg/mL anti-IgM (Southern Biotech, Cat#: 1021-01). For rapamycin pretreatment, CD4$^+$ T cells were sorted and plated in RPMI 1640 supplemented with 10% FBS and 1X Penn/Strep and then incubated at 37°C with either 100 nM of rapamycin or equal volume of PBS (control) for 2 hours (Selleck Chemicals, Cat#: S1039). Media was removed and cells were washed three times with excess volume of PBS prior to being plated with sorted B cells. Cocultures were stimulated following rapamycin treatment as previously described.

In vitro protein synthesis quantification

OPP staining was performed using Click-iT plus OPP Alexa-555 protein synthesis kit per manufacturer's protocol (ThermoFischer, Cat#: C10456). Briefly, 2 x 10^6 cells were incubated at 25°C for 30 minutes with 1:400 dilution of the Click-iT OPP reagent. Cells were washed three times with PBS and then fixed in PBS with 4% formaldehyde (v/v). Following fixation, cells were permeabilized in PBS supplemented with 2.0% saponin and 3.0 % FBS (v/v) for 15 minutes. For the Click-iT reaction, cells were incubated in the dark at room temperature for 30 minutes in the Click-iT reaction cocktail. Samples were then washed twice with PBS supplemented with 2% FBS and immediately analyzed by flow cytometry.

qPCR

RNA was isolated from sorted CD4$^+$ T cells following specified stimulation and treatments using the Qiagen RNeasy Mini Kit (Cat#: 74106). cDNA synthesis was performed with the GoScript reverse transcription system (Cat #: A5001). qPCR was performed in triplicate for each sample using the PowerUp SYBR green real-time PCR master mix with 5–10 ng input cDNA (cat#: A25776). Threshold values (C_T) were averaged across sample replicates, followed by normalization *via* the $\Delta\Delta C_T$ method to *β-actin*. For primer sets, see **Supp. Table 6**.

Apoptosis analysis

Total splenocytes were cultured for 24 hours as previously described. All stains were performed protected from light. Cells were washed twice with prewarmed FACS buffer and surface stained as previously described. Cells were then washed once with prewarmed FACS buffer and Annexin V binding buffer. Samples were resuspended in 100 µL binding buffer supplemented with 5 µL of

Annexin V-FITC (Cat#: 10040-02, SouthernBiotech) and stained for 20 minutes at room temperature. Cells were washed once with Annexin V binding buffer (Cat#: 10045-01, SouthernBiotech) then resuspended in 200 μL of binding buffer and stained with 5 μL of 7-AAD (Cat#: 420403, Biolegend) for 15 min at room temperature. Samples were placed on ice and analyzed using Fortessa.

Immunoblot analysis

Briefly, whole cell lysates were prepared using NP-40 lysis buffer (50 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1% NP-40 and 5 mM EDTA) (Thermo Scientific, J60766-AP) supplemented with Halt Protease Inhibitor Cocktail (Thermo Scientific, 87786) and PhosStop Phosphatase Inhibitor Cocktail (Roche, 4906845001). Sample protein concentrations were quantified using the DC protein assay (Bio-Rad, 5000112). 20 μg of protein per sample were separated by SDS-PAGE using the Bolt Bis-Tris system (Invitrogen). Proteins were transferred to 0.45 μm nitrocellulose membranes (MDI, SCNX8402XXXX101) using a wet tank transfer system. The membranes were blocked for 1 hour at room temperature with 5% bovine serum albumin (BSA) in TBST and incubated overnight at 4°C with the primary antibody diluted in the blocking buffer. The membranes were washed three times for 5 min each with TBST and incubated with the secondary antibody diluted in the blocking buffer for 1 hour at room temperature. The membranes were washed five times for 5 min each with TBST and incubated with 1 mL of chemiluminescent detection reagent (Cytiva, RPN2232) for 3 min before image acquisition using a ChemiDoc MP Imaging System (Bio-Rad Laboratories). Horseradish peroxidase (HRP)-conjugated antibodies against β-actin (Cell Signaling, 12620, 1:5000) were used as loading controls for protein normalization. Densitometric analysis was performed using the Image Lab software (Bio-Rad Laboratories).

Metabolomics analysis

For each sample, approximately 3 × 10^6 naïve splenic $CD4^+$ T cells were purified and stimulated as previously described. LC-MS/MS analysis was performed by The Metabolomics Innovation Centre (Alberta, Canada). For detailed protocol, see Supplemental Methods.

Metabolomics Pathways Interpretation

Biological interpretation was performed by MetaboAnalyst 5.0 using the metabolite set library *Homo sapiens* based on normal human metabolic pathways from the Kyoto Encyclopedia of Genes and Genomes (KEGG) database and the Human Metabolome Database (HMDB).

scRNA-Seq sample preparation

FACS-sorted WT and KO $CD4^+$ T cells were purified and stimulated as previously described, then directly processed for scRNA-seq with 10X Genomics 3′ kit (10X Genomics, Pleasanton, CA) following the manufacturer's instructions. 10,000 CD4 T cells were used to construct single-cell libraries with the Chromium Single Cell 3′ Reagent Kits (v2 Chemistry) according to manufacturer's instructions. Libraries were sequenced using the Illumina platform.

scRNA-Seq data analysis

scRNA-seq data were aligned to mm10 using CellRanger v.3.1.0 and downstream processing was performed using Seurat v3.1.1 (*111*). Briefly, cells with fewer than 200 features, higher than 1% mitochondrial gene content, or transcripts expressed by fewer than 3 cells were removed prior to log normalization. Principal component analysis (PCA) was performed, and the subsequent Uniform Manifold Approximation and Projection (UMAP) analysis was conducted using the first 30 principal components. Cluster-specific genes were determined using the FindMarkers algorithm in the Seurat suite. Clustering was performed by calculating a shared nearest neighbor graph with a resolution of 0.5. The FindAllMarkers function determined differentially expressed genes (DEG) based on the non-parametric Wilcoxon rank sum test for each subset. Subsetting was performed using previously published markers of T cell subsets. Trajectory analysis was performed using Slingshot (*112*).

Histological analysis

For histological analysis, spleens, right inguinal lymph nodes, and spinal cords were harvested as indicated and fixed in 10% Neutral Buffer Formalin (NBF) overnight before being transferred to 70% EtOH. For spinal cord harvest, mice were CO_2 euthanized, then immediately perfused with 10 mL PBS followed by 10 mL of 10% NBF. All samples were sent to Histowiz for paraffin embedding and histological analysis (Brooklyn, NY). A minimum of three independent samples were sent for each study. Immune cell infiltration and lymphoid architecture were examined using Hematoxylin and Eosin (H&E), anti-CD4 (Cat# ab183685, Abcam) and anti-B220 (Cat#: NB100-77420, Novus Biologicals). Demyelination was analyzed using Luxol Fast Blue. IHC quantification was performed using ImageJ.

EAE immunization

8-12 weeks-old male and female mice, minimum of 3 per gender and genotype, were subcutaneously injected at three sites with 200 µg of MOG peptide 35–55 emulsified in Complete Freund's Adjuvant (CFA) containing 400 µg of Mycobacterium (Cat#: EK-0111, Hooke Laboratories). On day 0 (D0) and 1 day after (D1) immunization, mice were intraperitoneally injected with 200 ng of pertussis toxin (Cat#: 180, List Biological Laboratories). All mice were examined and graded daily for neurological signs in a blinded manner as previously described. For the tail: 0, no disease; 1, half paralyzed; 2, full paralysis. For each hind and forelimb assessed separately: 0, no disease; 1, weak or altered gait; 2, paresis; 3, limb paralysis; and 5, moribund state (*46*). Average clinical scores were calculated daily for each group of mice and plotted.

Immunological studies were performed on the onset (13 days after immunization) or peak (20 days after immunization) of disease. 4 female mice were chosen for each genotype for further molecular analyses according to typical and representative clinical symptoms.

Statistical analysis

GraphPad Prism v.9.2 was used for statistical analysis. Statistical analysis was performed using . *P* value calculated by two-way unpaired *t* tests, one-way ANOVA with Tukey's post-hoc test for multiple comparisons, or 2-way ANOVA with Holm-Sidak correction for multiple comparisons as indicated. Differences were considered statistically significant when $p < 0.05$.

Supplementary Materials and Methods

Detailed metabolomics analysis, immunoprecipitation and LC/MS/MS, flow cytometry and immunoblot analysis.

Supplementary Figures

Supp. F1 – Supp. F7

Supplementary Tables

Supp. Table 1. scRNA-Seq enrichment analysis comparing Treg0/Treg1 and Tfh0/Tfh1 clusters

Supp. Table 2. scRNA-Seq gene set enrichment analysis using KEGG_Hallmark_C5GO

Supp. Table 3. LC/MS/MS analysis of IRF5 interacting partners from immunoprecipitation in Ramos B cells

Supp. Table 4. Tier 1 and Tier 2 metabolites from Mass Spectrometry Analysis

Supp. Table 5. Fold-change of metabolites from TCR stimulated vs. unstimulated WT and KO T cells

Supp. Table 6. Primers for qPCR analysis

Database Files

Data file S1: scRNAseq files will be made publicly available at GSE267271.

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The Lupus Research Alliance (BJ.B)

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Investigation: ZB, AL, AH, LB

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Supervision: BJB

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Writing – review and editing: ZB, BJB

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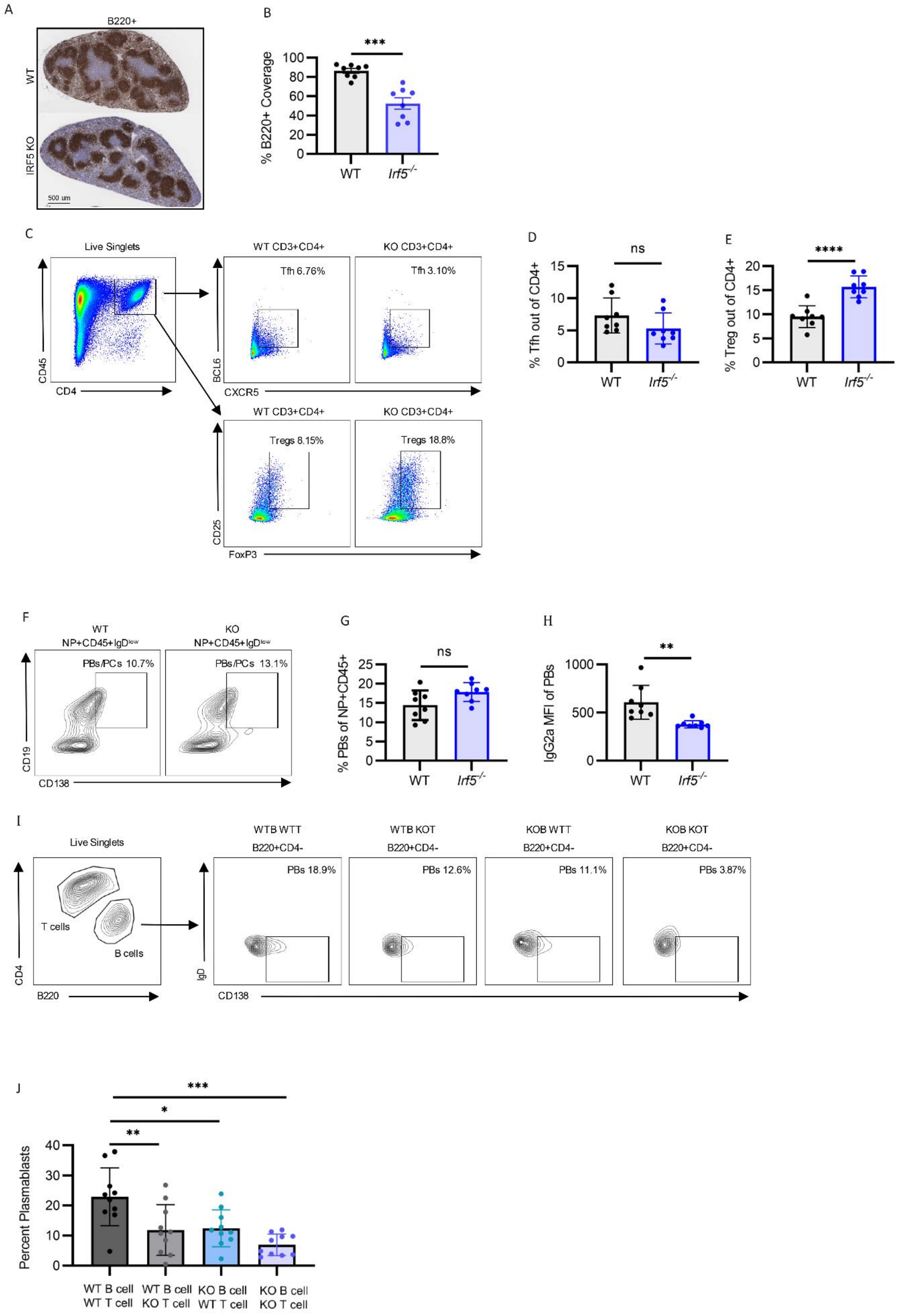
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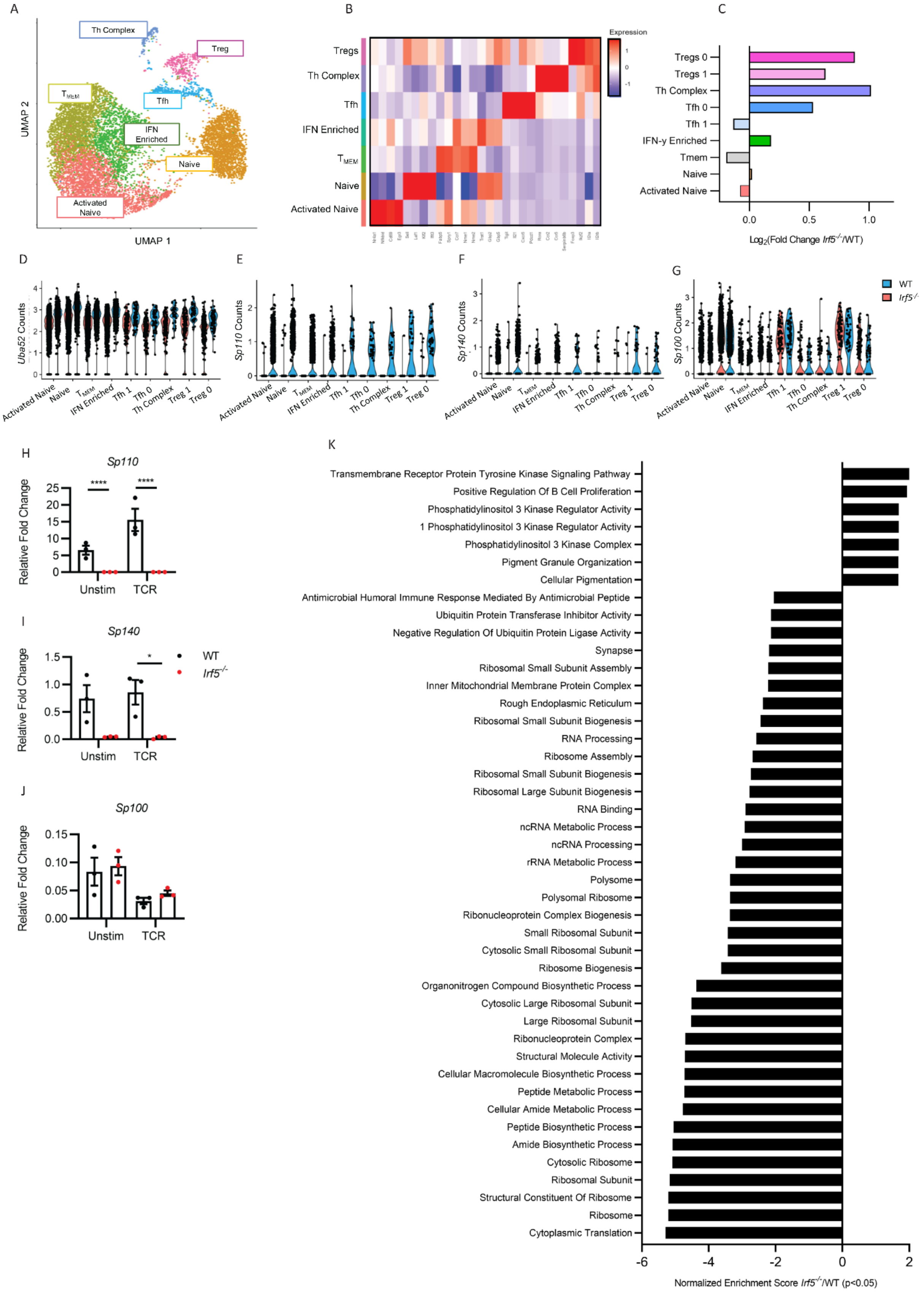
Fig. 1. T cell intrinsic IRF5 regulates T cell dependent B cell maturation

Mice were immunized intraperitoneally with 50 ug NP-CGG/CFA. Spleens harvested 7 days following immunization. (**A**) Representative histology and (**B**) quantification of B220$^+$ staining from WT and *Irf5*$^{-/-}$ spleens; scale bar represents 500µm. (**C**) Representative flow gating strategies for Tfh (CD3$^+$CD4$^+$BCL6$^+$CXCR5$^+$) and Tregs (CD3$^+$CD4$^+$CD25$^+$FoxP3$^+$) and their respective quantification (**D, E**). (**F**) Representative flow cytometric gating strategy for PBs (CD19$^+$IgD^{low}CD138$^+$). (**G**) Quantification of NP specific PBs (NP$^+$CD45$^+$CD19$^+$CD138$^+$IgD^{low}) and (**H**) IgG2a production from (**G**). *P* values calculated by two-way unpaired *t* test. (**I**) Representative flow gating strategy and (**J**) summary graphs of B220$^+$CD138$^+$IgD^{low} plasmablast generation following 4-day *in vitro* coculture. *P* value calculated by one-way analysis of variance (ANOVA) with Tukey's post-hoc test for multiple comparisons. Bar graphs show means +/- SEMs. **p < 0.01, ***p < 0.001, ****p <0.0001, ns = not significant. Data pooled from two to three independent experiments with each point representing an independent biological replicate.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Positive Regulation Of B Cell Proliferation
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1 Phosphatidylinositol 3 Kinase Regulator Activity
Phosphatidylinositol 3 Kinase Complex
Pigment Granule Organization
Cellular Pigmentation
Antimicrobial Humoral Immune Response Mediated By Antimicrobial Peptide
Ubiquitin Protein Transferase Inhibitor Activity
Negative Regulation Of Ubiquitin Protein Ligase Activity
Synapse
Ribosomal Small Subunit Assembly
Inner Mitochondrial Membrane Protein Complex
Rough Endoplasmic Reticulum
Ribosomal Small Subunit Biogenesis
RNA Processing
Ribosome Assembly
Ribosomal Small Subunit Biogenesis
Ribosomal Large Subunit Biogenesis
RNA Binding
ncRNA Metabolic Process
ncRNA Processing
rRNA Metabolic Process
Polysome
Polysomal Ribosome
Ribonucleoprotein Complex Biogenesis
Small Ribosomal Subunit
Cytosolic Small Ribosomal Subunit
Ribosome Biogenesis
Organonitrogen Compound Biosynthetic Process
Cytosolic Large Ribosomal Subunit
Large Ribosomal Subunit
Ribonucleoprotein Complex
Structural Molecule Activity
Cellular Macromolecule Biosynthetic Process
Peptide Metabolic Process
Cellular Amide Metabolic Process
Peptide Biosynthetic Process
Amide Biosynthetic Process
Cytosolic Ribosome
Ribosomal Subunit
Structural Constituent Of Ribosome
Ribosome
Cytoplasmic Translation
-6
-4
-2
0
2
Normalized Enrichment Score Irf5-/-/WT (p<0.05)

Fig. 2. Loss of IRF5 alters CD4 single cell transcriptional landscape

(**A**) Uniform Manifold Approximation and Projection (UMAP) of 5000 - 7000 $CD4^+$ single cells. Each dot corresponds to a single cell, colored according to cell type. Representative graph of two WT and two *Irf5*$^{-/-}$ biological replicates, with one male and one female representing each genotype. (**B**) Heatmap of genes used to identify CD4 T cell clusters. Data are colored according to expression levels. Legend is labeled in log scale. (**C**) Log2 fold change enrichment values of *Irf5*$^{-/-}$ relative to WT T cell clusters. (**D-G**) Violin plots showing the transcript expression of (**D**) *Uba52*, (**E**) *Sp110*, (**F**) *Sp140* and (**G**) *Sp100* in WT and *Irf5*$^{-/-}$ CD4 T cells in indicated T cell cluster. (**H-J**) Sorted $CD3^+CD4^+$ T cells from WT and *Irf5*$^{-/-}$ splenocytes were activated for 6-hours *in vitro* with anti-CD3/CD28 (TCR). (**H**) *Sp110*, (**I**) *Sp140* and (**J**) *Sp100* transcript expression normalized to *β-Actin.* Three biological replicates, representative of two independent experiments. *P* value calculated by two-way unpaired *t* tests. (**K**) Preranked gene set enrichment analyses using C5 gene ontology (GO) gene sets. Top gene ontology (GO) terms sorted by Normalized Enrichment Score (NES). Padj < 0.05. $^*P < 0.05$, $^{****}P < 0.0001$. Each point represents an independent biological replicate.

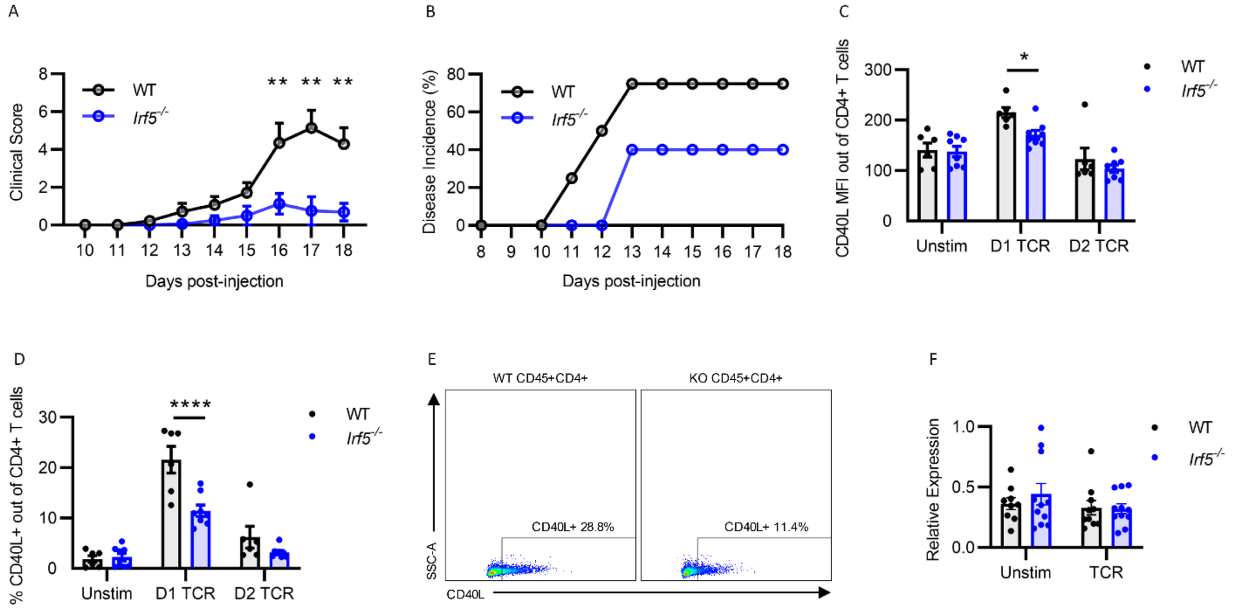
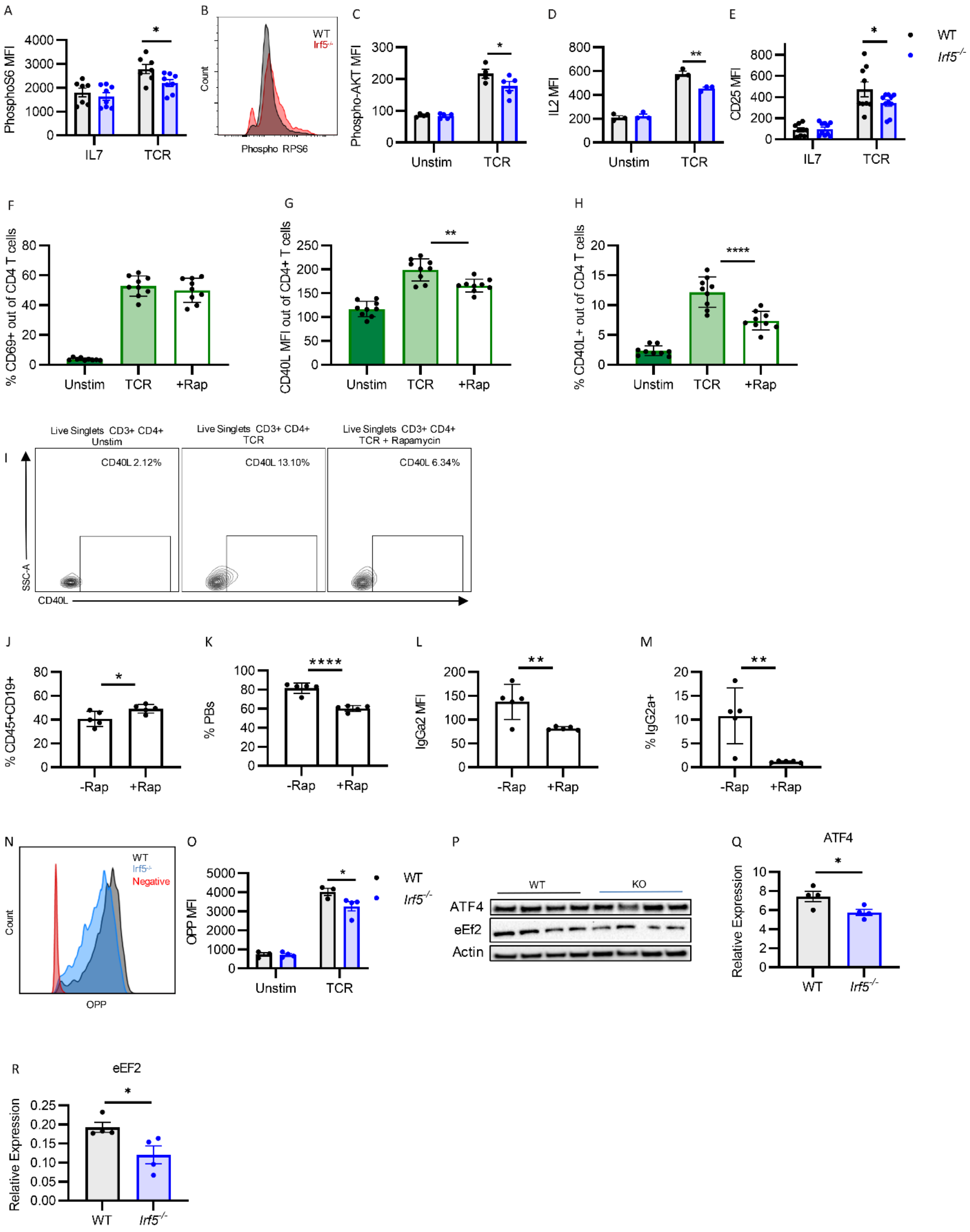


Fig. 3. *Irf5* KO mice are protected from Experimental Autoimmune Encephalomyelitis

(**A**) Composite means +/- SEM of clinical scores. Minimum of 12 biological replicates per experiment. Data pooled from two independent experiments. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**B**) Disease incidence. Minimum of four biological replicates per genotype. (**C, D**) WT and *Irf5*$^{-/-}$ total splenocytes were sorted for CD3$^+$CD4$^+$ T cells, then activated for 24- or 48-hours *in vitro* with anti-CD3/CD28 Dynabeads (TCR). Live CD3$^+$CD4$^+$ T cells were gated for flow cytometric marker analysis. **(E)** Representative CD40L flow cytometry gating in WT and KO CD4 T cells. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**F**) *Cd40l* transcript expression normalized to *β-Actin* following 6-hours *in vitro* anti-CD3/CD28 (TCR) stimulation. Data pooled from two to three independent experiments, with each point representing an independent biological replicate. *P* value calculated by two-way unpaired *t* test. **P* < 0.05, ***P* < 0.01. Bar graphs show means +/- SEMs.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Phospho-AKT MFI
300
200
100
0
*
Unstim
TCR
D
IL2 MFI
800
600
400
200
0
**
Unstim
TCR
E
CD25 MFI
800
600
400
200
0
*
IL7
TCR
● WT
● Irf5-/-
F
% CD69+ out of CD4 T cells
80
60
40
20
0
Unstim
TCR
+Rap
G
CD40L MFI out of CD4+ T cells
250
200
150
100
50
0
**
Unstim
TCR
+Rap
H
% CD40L+ out of CD4 T cells
20
15
10
5
0
****
Unstim
TCR
+Rap
I
Live Singlets CD3+ CD4+ Unstim
Live Singlets CD3+ CD4+ TCR
Live Singlets CD3+ CD4+ TCR + Rapamycin
CD40L 2.12%
CD40L 13.10%
CD40L 6.34%
SSC-A
CD40L
J
% CD45+CD19+
80
60
40
20
0
*
-Rap
+Rap
K
% PBs
100
80
60
40
20
0
****
-Rap
+Rap
L
IgGa2 MFI
200
150
100
50
0
**
-Rap
+Rap
M
% IgG2a+
20
15
10
5
0
**
-Rap
+Rap
N
WT
Irf5-/-
Negative
Count
OPP
O
OPP MFI
5000
4000
3000
2000
1000
0
*
Unstim
TCR
● WT
● Irf5-/-
P
WT
KO
ATF4
eEf2
Actin
Q
ATF4
Relative Expression
10
8
6
4
2
0
*
WT
Irf5-/-
R
eEF2
Relative Expression
0.25
0.20
0.15
0.10
0.05
0.00
*
WT
Irf5-/-

Fig. 4. IRF5 regulates protein translation, mTORC1 and Akt signaling

(**A**) Phosphorylated RPS6 quantification in CD3$^+$CD4$^+$ T cells sorted from WT and *Irf5*$^{-/-}$ splenocytes following 24-hours *in vitro* stimulation with anti-CD3/CD28 (TCR) or without (IL7). Data pooled from three independent experiments. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**B**) Representative histogram of phosphorylated RPS6 quantification from (**A**). (**C-E**) Summary quantification of (**C**) phospho-AKT, (**D**) IL2 and (**E**) CD25 expression in WT and *Irf5*$^{-/-}$ CD3$^+$CD4$^+$ T cells gated from total splenocytes following 24-hours *in vitro* stimulation with anti-CD3/CD28 (TCR) or without (Unstim). Three to five biological replicates, representative of two independent experiments. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**F-H**) Summary quantification of (**F**) CD69, (**G**) CD40L mean fluorescence intensity (MFI) and (**H**) CD40L% expression in Live CD3$^+$CD4$^+$ T cells gated from total splenocytes following 24-hours *in vitro* stimulation in the presence (TCR + Rap) or absence (TCR) of rapamycin. Data pooled from three independent experiments. *P* value calculated by Ordinary 1-way ANOVA with Tukey correction for multiple comparisons. (**I**) Representative gating for CD40L expression in CD3$^+$CD4$^+$ gated on Live Singlets in the absence (TCR) or presence (+Rap) of rapamycin. (**J-M**) Summary quantification of (**J**) CD19$^+$ B cells, (**K**) plasma blasts (PBs) (CD45 $^+$CD19$^+$CD138$^+$IgD^{low}) and (**L, M**) IgG2a production. Five biological replicates. *P* value calculated by two-way unpaired *t* tests. (**N**) CD3$^+$CD4$^+$ T cells gated from total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR) and puromycin incorporation measured via O-propargyl-puromycin assay. Representative histogram of puromycin incorporation is shown. (**O**) Quantification of puromycin incorporation from three to four biological replicates. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**P-R**) Quantification and representative immunoblot of (**P, Q**) ATF4 and (**P, R**) eEF2 in sorted CD4 T cells following anti-CD3/CD28 stimulation. N = 4 biological replicates. *P* value calculated by two-way unpaired t tests. Bar graphs show means +/- SEMs. $^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$. Each point represents an independent biological replicate.

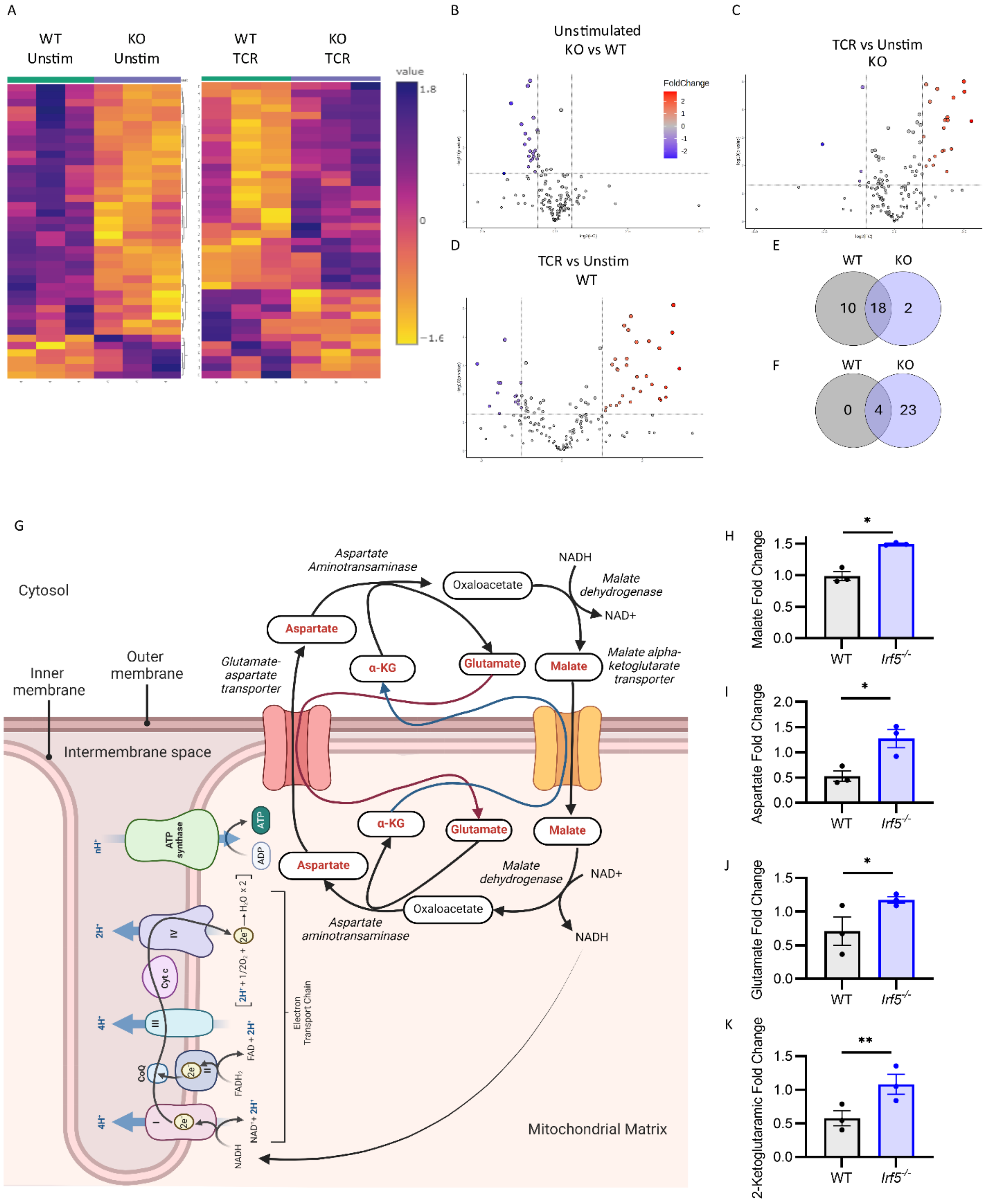

A
WT Unstim
KO Unstim
WT TCR
KO TCR
value
1.8
0
−1.6
B
Unstimulated KO vs WT
FoldChange
2
1
0
-1
-2
C
TCR vs Unstim KO
D
TCR vs Unstim WT
E
WT
KO
10
18
2
F
WT
KO
0
4
23
G
Cytosol
Outer membrane
Inner membrane
Intermembrane space
Aspartate Aminotransaminase
NADH
Oxaloacetate
Malate dehydrogenase
NAD+
Aspartate
α-KG
Glutamate
Malate
Malate alpha-ketoglutarate transporter
Glutamate-aspartate transporter
ATP synthase
ATP
ADP
nH+
2H+
4H+
IV
Cyt c
III
II
I
CoQ
2e
[2H+ + 1/2O2 + 2e → H2O x 2]
FAD + 2H+
FADH2
NAD+ + 2H+
NADH
Electron Transport Chain
α-KG
Glutamate
Malate
Aspartate
Oxaloacetate
Malate dehydrogenase
NAD+
NADH
Aspartate aminotransaminase
Mitochondrial Matrix
H
Malate Fold Change
0.0
0.5
1.0
1.5
*
WT
Irf5-/-
I
Aspartate Fold Change
0.0
0.5
1.0
1.5
2.0
*
WT
Irf5-/-
J
Glutamate Fold Change
0.0
0.5
1.0
1.5
*
WT
Irf5-/-
K
2-Ketoglutaramic Fold Change
0.0
0.5
1.0
1.5
**
WT
Irf5-/-

Fig. 5. IRF5 regulates CD4 T cell metabolism

(**A**) Purified naive CD4 T cells from 3 WT and 3 *Irf5*$^{-/-}$ mouse spleens were analyzed using untargeted LC-MS approach following either 24-hours *in vitro* stimulation with anti-CD3/CD28 (TCR) or IL7 (Unstim). Heatmap of top 40 differentially expressed metabolites in WT and KO CD4 T cells generated using Metaboanalyst 5.0. (**B**-**D**) Volcano plots of significantly altered metabolites in (**B**) IL7 unstimulated (Unstim) KO compared to WT, (**C**) TCR vs Unstim KO, and (**D**) TCR vs Unstim WT. Significance determined by P value < 0.05 and $\log_2$FC >1.5. (**E, F**) Venn diagrams showing shared and unique (**E**) upregulated and (**F**) downregulated metabolites following TCR stimulation in WT and KO T cells. Significance determined by P value < 0.05 and $\log_2$FC >2.0. (**G**) Schematic of the malate-aspartate shuttle. Metabolites significantly enriched in KO T cells are written in red. (**H**-**K**) Summary graphs of the following normalized metabolite levels detected in LC-MS analysis of WT and KO T cells (**H**) malate, (**I**) aspartate, (**J**) glutamate, (**K**) alpha-ketoglutaramate. P value calculated by two-way unpaired T test. *p < 0.05, **p < 0.01.

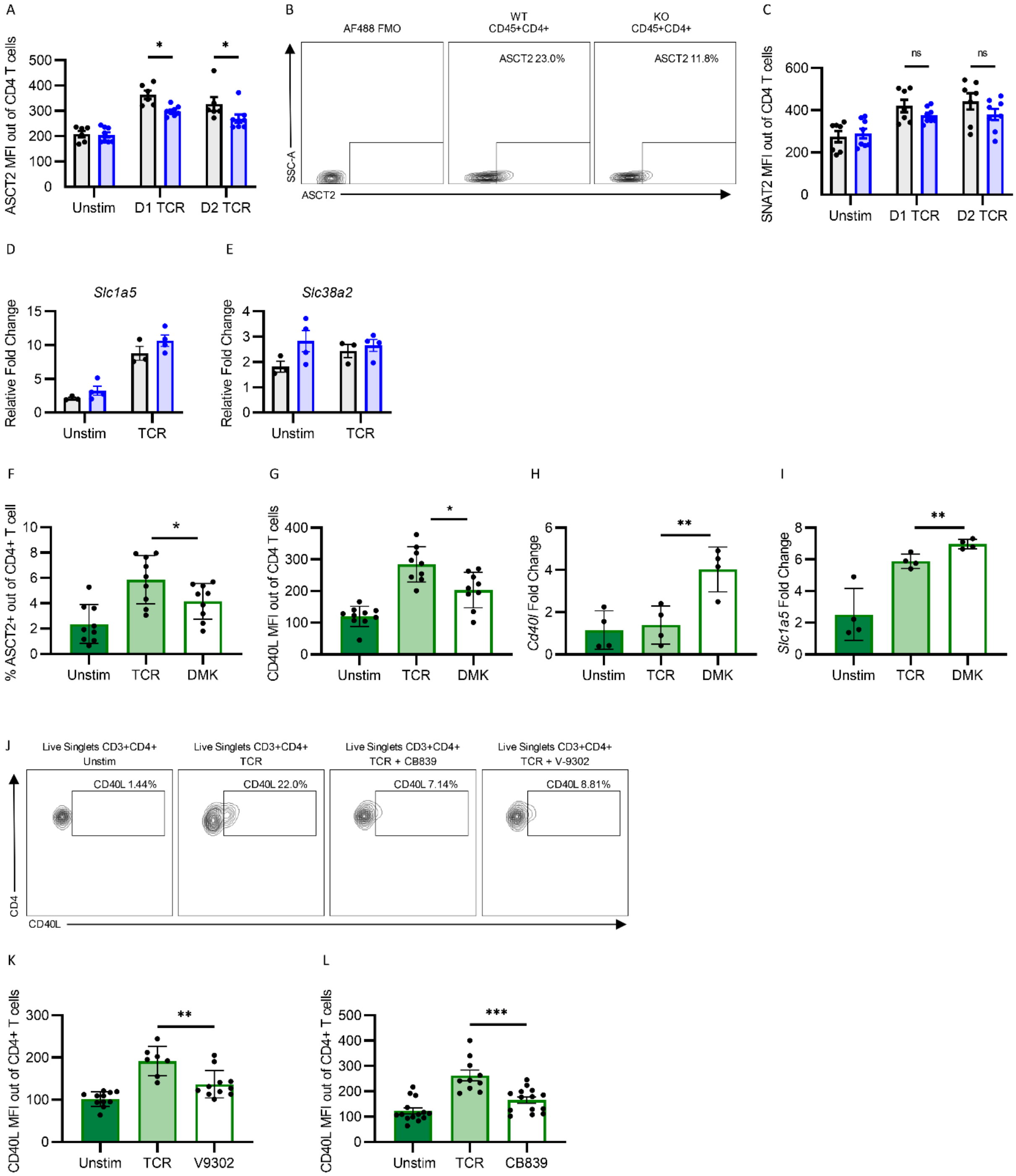


Fig. 6. IRF5 regulation of glutamine metabolism modulates effector protein expression

(**A**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24- (D1) and 48-hours (D2) *in vitro* with anti-CD3/CD28 (TCR). Summary graphs of ASCT2 expression pooled from two independent experiments. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**B**) ASCT2 representative gating strategy in Live CD45$^+$CD4$^+$ T cells gated from WT and *Irf5*$^{-/}$ total splenocytes. (**C**) Summary graph of SNAT2 expression pooled from two independent experiments. Sorted CD3$^+$CD4$^+$ T cells WT and *Irf5*$^{-/-}$ splenocytes were activated for 6 hours *in vitro* with anti-CD3/CD28 (TCR). (**D**) *Slc1a5* and (**E**) *Slc38a2* transcript expression normalized to *β-Actin*. (**F, G**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 in the presence (DMK) or absence (TCR) of dimethyl ketoglutarate (DMK). Summary graphs of (**F**) ASCT2 and (**G**) CD40L expressing CD3$^+$CD4$^+$ T cells pooled from three independent experiments. (**H, I**) WT sorted CD3$^+$CD4$^+$ T cells were activated for 6-hours *in vitro* with anti-CD3/CD28 (TCR) in the presence (DMK) or absence (TCR) of dimethyl-ketoglutarate. Summary graphs of (**H**) *CD40l* expression and (**I**) *Slc1a5* transcript levels normalized to *B-Actin.* Four biological replicates. (**J**) Representative flow gating strategy for CD40L expression in Live CD3$^+$CD4$^+$ T cells under indicated treatment conditions. WT total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR) in the presence of ASCT2 inhibitor (V-9302) or absence (TCR). Summary graph of (**K**) CD40L expression in CD3$^+$CD4$^+$ T cells. Data pooled from three independent experiments. (**L**) WT total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR) in the presence (CB839) or absence (TCR) of CB839. Summary graphs of CD40L expression in activated CD3$^+$CD4$^+$ T cells. Data pooled from three independent experiments. *P* value calculated by one-way analysis of variance (ANOVA) with Tukey's post-hoc test for multiple comparisons unless otherwise noted. Bar graphs show means +/- SEMs. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ns = not significant. Each point represents an independent biological replicate.

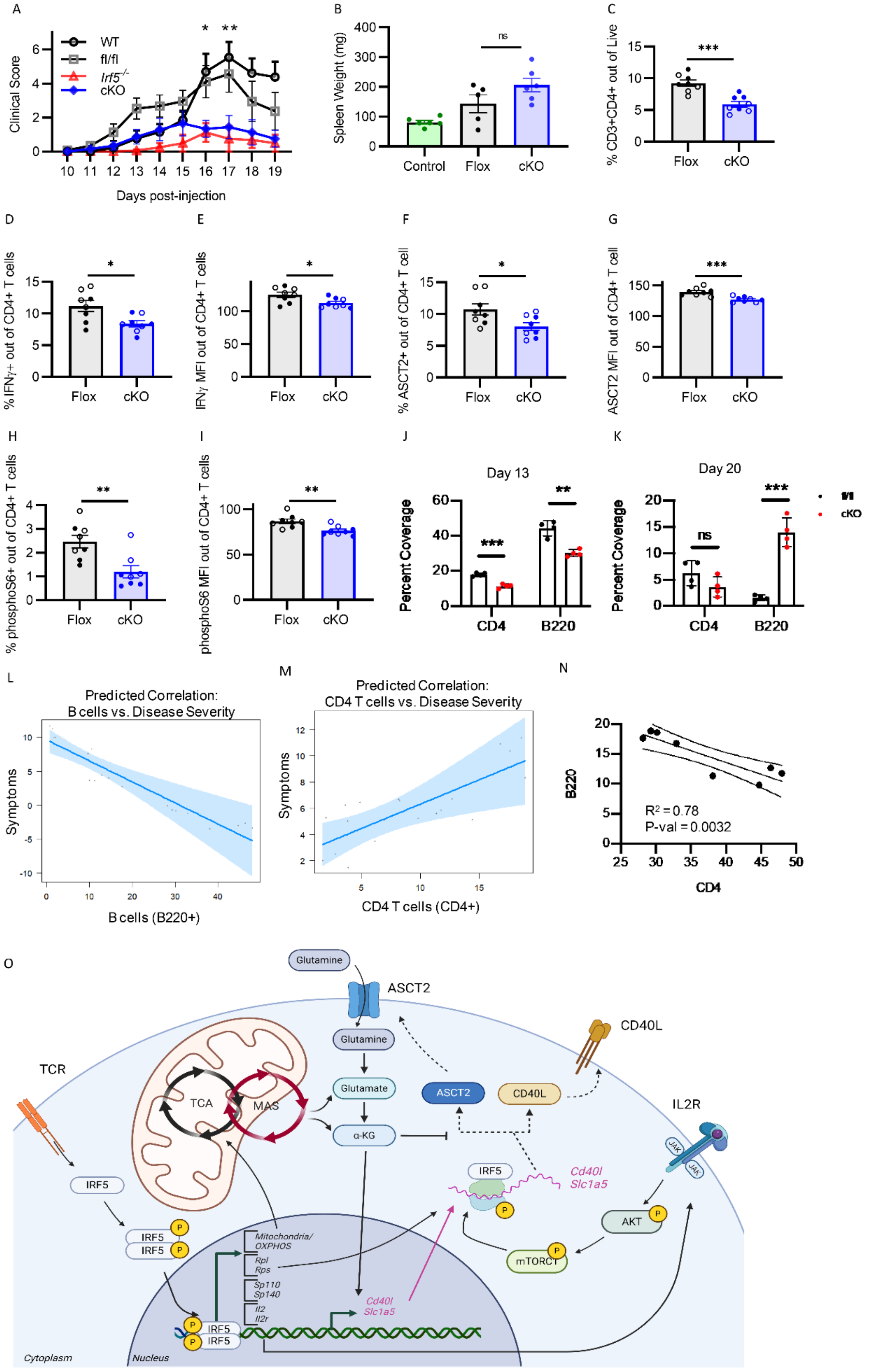

A
Clinical Score
WT
fl/fl
Irf5-/-
cKO
* **
Days post-injection
B
Spleen Weight (mg)
ns
Control
Flox
cKO
C
% CD3+CD4+ out of Live
***
Flox
cKO
D
% IFNγ+ out of CD4+ T cells
*
E
IFNγ MFI out of CD4+ T cells
*
F
% ASCT2+ out of CD4+ T cell
*
G
ASCT2 MFI out of CD4+ T cell
***
H
% phosphoS6+ out of CD4+ T cells
**
I
phosphoS6 MFI out of CD4+ T cells
**
J
Day 13
Percent Coverage
***
**
CD4
B220
K
Day 20
Percent Coverage
ns
***
fl/fl
cKO
CD4
B220
L
Predicted Correlation:
B cells vs. Disease Severity
Symptoms
B cells (B220+)
M
Predicted Correlation:
CD4 T cells vs. Disease Severity
Symptoms
CD4 T cells (CD4+)
N
B220
R² = 0.78
P-val = 0.0032
CD4
O
Glutamine
ASCT2
CD40L
TCR
Glutamine
TCA
MAS
Glutamate
ASCT2
CD40L
IL2R
α-KG
IRF5
IRF5
Cd40l
Slc1a5
JAK
JAK
IRF5
IRF5
P
AKT
Mitochondria/
OXPHOS
Rpl
Rps
mTORC1
Sp110
Sp140
Il2
Il2r
Cd40l
Slc1a5
IRF5
IRF5
Cytoplasm
Nucleus

Fig. 7. T cell conditional *Irf5*$^{-/-}$ mice are protected from EAE

(**A**) Composite means +/- SEM of clinical scores. Minimum of 10 biological replicates per experiment. Pooled data from three independent experiments comparing clinical progression of *Irf5*$^{fl/fl}$*-Lck-Cre*$^{+}$ (cKO), *Irf5*$^{fl/fl}$*-Lck-Cre*$^{-}$ (fl/fl), *Irf5*$^{-/-}$ (KO), and WT mice following EAE induction. (**B**) Spleen weights from WT control, cKO and fl/fl (Flox) mice at peak disease. Five-six biological replicates pooled from two independent experiments. *P* value calculated by one-way analysis of variance (ANOVA) with Tukey's post-hoc test for multiple comparisons. (**C-I**) Summary graphs of flow cytometric analyses from day 13 post immunization (clear circles) and day 20 post immunization (colored circles). (**C**) CD3^{+}CD4^{+} T cells gated from live cells, (**D, E**) IFNγ production from live CD3+CD4+ T cells, (**F, G**) ASCT2 expression, and (**H, I**) S6 phosphorylation (phosphoRPS6). *P* value calculated by multiple T tests with Holm-Sidak correction for multiple comparisons. (**J, K**) Quantification of splenic CD4^{+} and B220^{+} immunohistochemistry staining at (**J**) day 13 post-immunization and (**K**) day 20 post-immunization. Data represents four biological replicates. (**L, M**) Predicted correlation between (**L**) B220 B cells and disease severity and (**M**) CD4 T cells and disease severity. Partial residual plot generated using visreg analysis package (*115*). Shaded area represents 95% confidence interval. (**N**) Linear regression analysis of B220 and CD4 IHC coverage in spleens harvested from mice at Day 13 and Day 20 timepoints post EAE induction. Outer lines represent 95% confidence interval. Bar graphs show means +/- SEMs. *p < 0.05, **p < 0.01, ***p < 0.001, ns = not significant. Each point represents an independent biological replicate. (**O**) Summary schematic of the transcriptional, translational and metabolic regulatory roles for IRF5.

Supplementary Materials and Methods

Detailed Metabolomics Analysis

Chemicals and Reagents

All chemicals and reagents were purchased from Sigma-Aldrich (Markham, ON, Canada), except those specifically stated. LC-MS grade water, acetonitrile, methanol and formic acid were purchased from Canadian Life Sciences (Peterborough, ON, Canada). Metabolome quantification kit for sample normalization and chemical isotope labeling kits for sample labeling were purchased from Nova Medical Testing Inc. (Edmonton, AB, Canada).

Normalization

Samples were randomized before any procedures to eliminate batch variations in sample analysis. Sample normalization was conducted by measuring the total metabolite concentration in each sample usingNova Medical Testing Inc (Product Number: NMT-6001-KT). According to quantification results, different volumes of sample were taken and adjusted to a final concentration of 1.2 mM. The samples were stored in an -80°C freezer and used for the following preparations and analyses.

LC-MS Analysis

Individual samples were labeled with ^{12}C-reagents and a pooled sample, which was generated by mixing an aliquot from each individual sample, was labeled with ^{13}C-reagents. The $^{12}C_2$-labeled individual sample was mixed with $^{13}C_2$-labeled reference sample in equal volumes. The mixture was injected into LC-MS for analysis. Prior to analysis, quality control (QC) samples were prepared by equal volume mix of a ^{12}C-labeled and a ^{13}C-labeled pooled sample. QC samples were run at an interval of one QC injection after 10 sample injections. The peak intensity ratio between ^{12}C-peak and ^{13}C-peak represents the relative quantification result for a specific metabolite in an individual sample. All LC-MS analyses were conducted on an Agilent 1290 LC linked to Bruker Impact II QTOF Mass Spectrometer. The column used was Agilent eclipse plus reversed-phase C18 column (150 × 2.1 mm, 1.8 µm particle size) and the column oven temperature was 40°C. Mobile phase A was 0.1% (v/v) formic acid in water and mobile phase B was 0.1% (v/v) formic acid in acetonitrile. The gradient setting was: t = 0 min, 25% B; t = 10 min, 99% B; t = 15 min, 99% B; t = 15.1 min, 25% B; t = 18 min, 25% B. The flow rate was 400 µL/min. Mass spectral acquisition rate was 1 Hz, with an m/z range from 220 to 1000.

Data Processing and Metabolite Identification

LC-MS data was first converted to .csv files using DataAnalysis 4.4 (Bruker Daltonics). Files were uploaded to IsoMS Pro 1.2.12 (Nova Medical Testing Inc.) for data processing and metabolite identification. Peak pairs that originated from blank samples and those not presented in at least 80.0% of samples in any group were removed. Data was then normalized by Ratio of Total Useful Signal, calculated as sum of all useful ^{12}C-peaks over sum of all useful ^{13}C-peaks. Metabolite identification was carried out using a three-tiered approach against NovaMT Metabolite Databases 2.0 (Nova Medical Testing Inc.) (*113*). In tier 1, peak pairs were searched against a labeled metabolite library (CIL Library) based on accurate mass and retention time. In tier 2, the remaining peak pairs were searched against a linked identity library (LI Library). In tier 3, any remaining peak pairs were searched based on accurate mass match against the MyCompoundID (MCID) library (www.mycompoundid.org) (*114*).

Immunoprecipitation and LC/MS/MS

Briefly, 250µg lysate of unstimulated Ramos B cells was used for immunoprecipitation with either anti-IRF5 or anti-Ig control antibodies (*16*). Samples were processed via 1D gel and in-gel tryptic digestion resulting in peptides fractionated by reversed phase chromatography and analysis by LC/MS/MS on a LTP Orbitrap Velos mass spectrometer at the Center for Advanced

Proteomics Research, New Jersey Medical School Cancer Research Center. Database search was performed using Mascot search engine against SwissPRot human protein database. Listed proteins (**Suppl. Table 3**) had at least 1 unique peptide identified with ≥95% identification probability.

Flow cytometry

The following antibodies were used for surface staining as indicated: AF700-conjugated anti-CD3 (Clone 17A2; Biolegend); BV711-conjugated anti-CD3 (Clone 17A2; Biolegend) BV510-conjugated anti-CD4 (Clone RM4-5; Biolegend); PerCP-conjugated anti-CD45 (Clone 30-F11; Biolegend), PE/CY7-conjugated anti-CD45 (Clone 30-F11; Biolegend), PE/CY7-conjugated anti-CD25 (Clone PC61; Biolegend), PerCP-conjugated anti-CD45R(B220) (Clone RA3-6B2; Biolegend), AF647-conjugated anti-CD38(B220) (Clone 90; Biolegend), BV421-conjugated anti-CD86 (Clone GL-1; Biolegend), FITC-conjugated anti-CD40 (Clone 3/23; Biolegend), Pe-Cy7-conjugated anti-95(Fas) (Cat#: 152617; Biolegend), Pe-Cy5.5-conjugated anti-CXCR4) (Clone#: 2B11; eBioscience), APC/Cy7-conjugated anti-CD69 (Clone#: H1.2F3; Biolegend), BV421-conjugated anti-FoxP3 (Clone#: MF-14; Biolegend), PE-conjugated anti-CD40L(Clone#: 24-31; eBioscience), anti-Asct2 (V501) (Cat#: 5345S; Cell Signaling Technology), and anti-SLC38A2 (Cat#: BS-12125R; Bioss Antibodies).

The following antibodies were used for intracellular staining: PE-conjugated anti-mTOR(7C10) (Cat# 15006S; Cell Signaling Technology), anti-phospho-S6 Ribosomal Protein(Ser235/236) (Cat#: 4857S; Cell Signaling Technology), anti-phospho-Akt(Ser473) (Cat#: 9271T, Cell Signaling Technology), anti-S6 (Cat#2217S; Cell Signaling).

The following secondary antibodies were used: FITC-conjugated anti-Rabbit IgG (Cat#: 65-611-1; Invitrogen), PE-conjugated anti-Rabbit IgG, (Cat#: 12-4739-81, eBioscience).

For dead cell exclusion, either Live/Dead Fixable Yellow Dead Cell Stain (Cat#: 50-112-1528, Thermo Fischer) or Live/Dead Fixable Green Dead Cell Stain (Cat#: L23101, Thermo Fischer)) was used in each experiment.

Immunoblot Analysis

The following antibodies were used as indicated.β-Actin HRP conjugate (Cell Signaling, Cat #: 12620, 1:5000), GLS recombinant antibody (Proteintech, Cat #: 81486-1-RR, 1:1000), GLUD1 monoclonal antibody (Cat #: 67026-1-lg, 1:1000), ATF-4 (Cell Signaling, Cat #: 11815, 1:1000), eEF2 (Cell Signaling, Cat #: 2332, 1:1000).

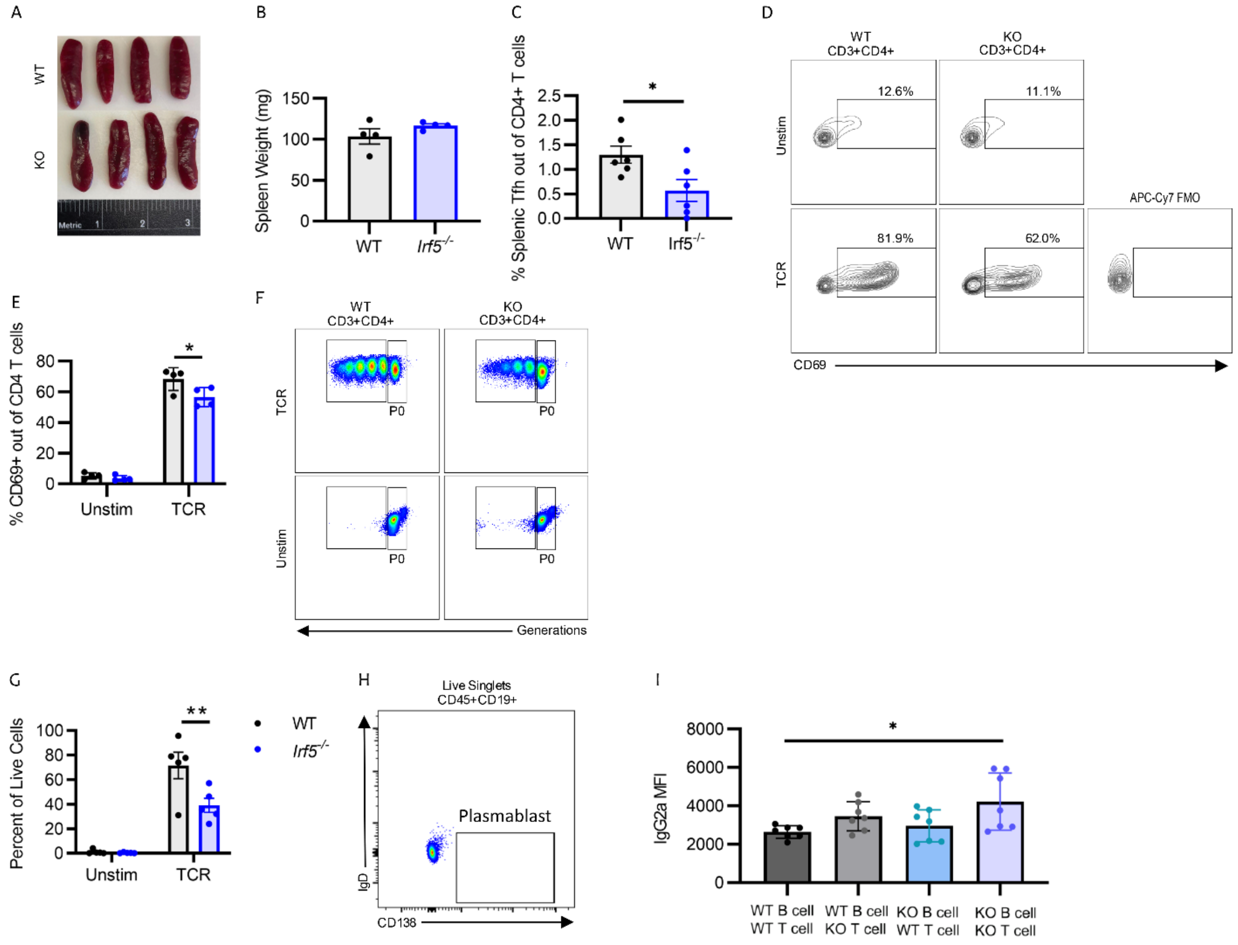
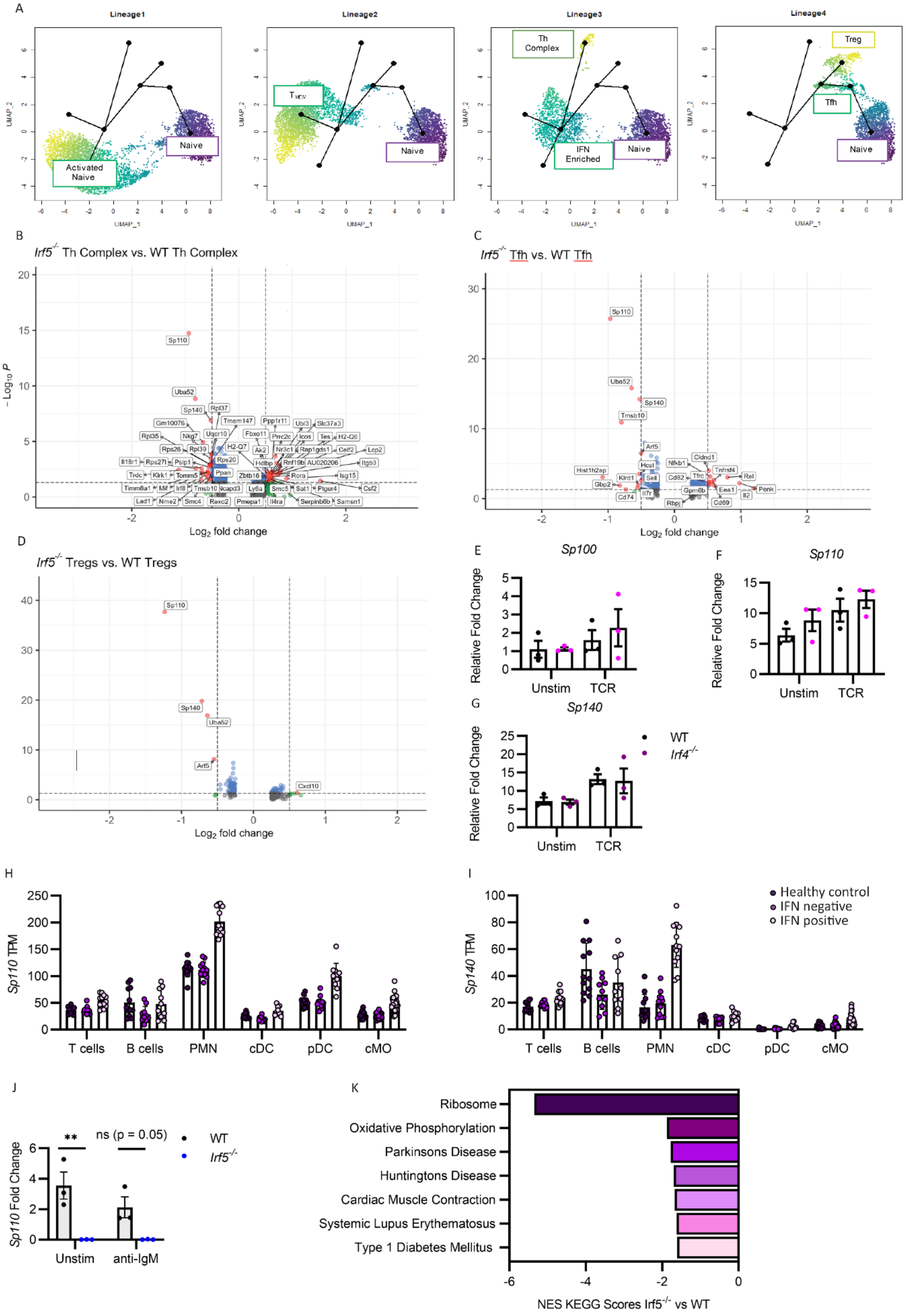


Fig. S1.

(**A**) Spleen images and (**B**) weights from age and gender matched WT and *Irf5*$^{-/-}$ mice. (**C**) Tfh percentages from splenocytes of unimmunized mice as determined by flow cytometry. Six biological replicates. *P* value calculated by two-way unpaired *t* tests. (**D-E**) Sorted CD3^{+}CD4^{+} WT and *Irf5*$^{-/-}$ T cells were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR). (**D**) Representative flow plots and (**E**) summary graphs of frequency of CD69 expression out of live CD3^{+}CD4^{+} T cells. Four biological replicates, representative of three independent experiments. (**F-G**) Sorted CD3^{+}CD4^{+} WT and *Irf5*$^{-/-}$ T cells were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR). (**F**) Representative flow plots and (**G**) summary graphs of T cell proliferation. Five biological replicates. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**H**) Control gating strategy for plasmablasts (CD45$^+$CD19$^+$CD138$^+$IgD^{low}). (**I**) Summary graphs of IgG2a production. *P* value calculated by 1-way ANOVA with Tukey correction for multiple comparisons. *$p < 0.05$, **$p < 0.01$. Each point represents an independent biological replicate. Bar graphs show means +/- SEMs.


A
Lineage1
Lineage2
Lineage3
Lineage4
Activated Naive
Naive
T MEM
Th Complex
IFN Enriched
Treg
Tfh
UMAP_1
UMAP_2
B
Irf5-/- Th Complex vs. WT Th Complex
Sp110
Uba52
Sp140
Rpl37
Tmem147
Ppp1r11
Ubl3
Slc37a3
Gm10076
Fbxo11
Prrc2c
Icos
Tes
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Rpl35
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H2-Q7
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Smc5
Sat1
Ptger4
Csf2
Lad1
Nme2
Smc4
Rexo2
Pmepa1
Il4ra
Serpinb6b
Samsn1
− Log10 P
Log2 fold change
C
Irf5-/- Tfh vs. WT Tfh
Sp110
Uba52
Sp140
Tmsb10
Arl5
Cldnd1
Nfkb1
Tnfrsf4
Hist1h2ap
Hcst
Cd82
Rel
Gbp2
Klrd1
Sell
Tfrc
Gpm6b
Ema1
Penk
Cd74
Il7r
Il2
Rbpj
Cd69
Log2 fold change
D
Irf5-/- Tregs vs. WT Tregs
Sp110
Sp140
Uba52
Arl5
Cxcl10
Log2 fold change
E
Sp100
Relative Fold Change
Unstim
TCR
F
Sp110
Relative Fold Change
Unstim
TCR
G
Sp140
Relative Fold Change
Unstim
TCR
● WT
● Irf4-/-
H
Sp110 TPM
T cells
B cells
PMN
cDC
pDC
cMO
I
Sp140 TPM
● Healthy control
● IFN negative
○ IFN positive
T cells
B cells
PMN
cDC
pDC
cMO
J
Sp110 Fold Change
**
ns (p = 0.05)
● WT
● Irf5-/-
Unstim
anti-IgM
K
Ribosome
Oxidative Phosphorylation
Parkinsons Disease
Huntingtons Disease
Cardiac Muscle Contraction
Systemic Lupus Erythematosus
Type 1 Diabetes Mellitus
NES KEGG Scores Irf5-/- vs WT

Fig. S2.

(**A**) Pseudotime trajectory analysis performed using Slingshot. Depiction of four predicted trajectories. Differential transcript expression in (**B**) *Irf5*$^{-/-}$ vs WT Th Complex cluster (**C**) *Irf5*$^{-/-}$ vs WT Tfh cluster and (**D**) *Irf5*$^{-/-}$ vs WT Treg cluster. (**E-G**) Sorted CD3^{+}CD4^{+} T cells from WT and *Irf4*$^{-/-}$ splenocytes were activated for 6-hours *in vitro* with anti-CD3/CD28 (TCR). (**E**) *Sp100*, (**F**) *Sp110* and (**G**) *Sp140* transcript expression normalized to *β-Actin.* Three biological replicates. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. All comparisons not significant. (**H**) *Sp110* and (**I**) *Sp140* transcripts per million (TPM) in Healthy Control, Interferon (IFN) negative and IFN positive systemic lupus erythematosus (SLE) patient peripheral blood mononuclear cells (PBMCs) analyzed from published scRNAseq dataset (PMC8015858). (**J**) *Sp110* transcript expression normalized to *β-Actin* in sorted CD45^{+}B220^{+} WT and *Irf5*$^{-/-}$ B cells stimulated for 6-hours with anti-IgM. Three biological replicates per genotype. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**K**) Pre-ranked gene set enrichment analyses (GSEA) using Kyoto Encyclopedia of Genes and Genomes (KEGG) C2 gene sets. Top 7 significantly enriched pathways sorted by Normalized Enrichment Score (NES) ($p < 0.05$). Representative graph of two WT and two *Irf5*$^{-/-}$ biological replicates, with one male and one female representing each genotype. Bar graphs show means +/- SEMs. **$p < 0.01$, ns = not significant. Each point represents an independent biological replicate.

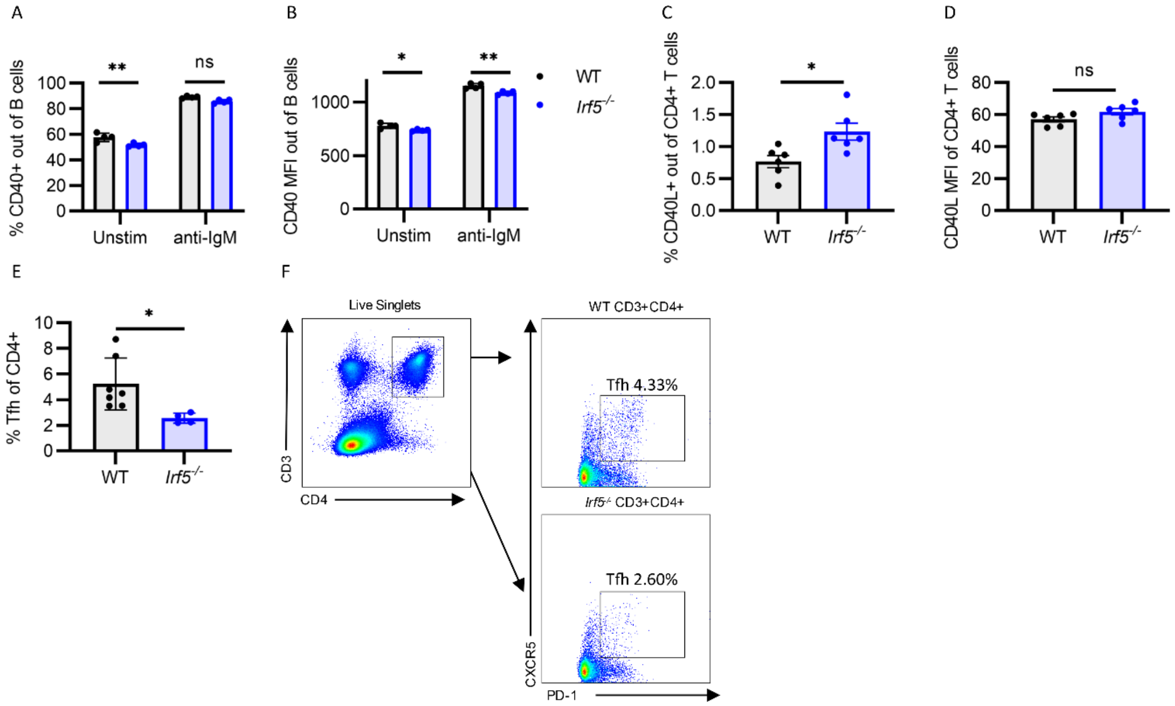

Fig. S3.

(**A,B**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24-hours *in vitro* with anti-IgM. Summary graphs of (**A**) CD40% expression and (**B**) CD40 mean fluorescence intensity (MFI) in CD45^{+}B220^{+} B cells. Four biological replicates, representative of two independent experiments. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. CD40L (**C**) percent expression and (**D**) MFI in CD3^{+}CD4^{+} T cells gated from WT and *Irf5*$^{-/-}$ total splenocytes. Six biological replicates. (**E**) Summary graphs of Tfh (CD3^{+}CD4^{+}PD1^{+}CXCR5^{+}) quantification and (**F**) representative flow cytometric gating. Four to six biological replicates. *P* value calculated by two-way unpaired *t* test.*p < 0.05, **p < 0.01, ns = not significant.

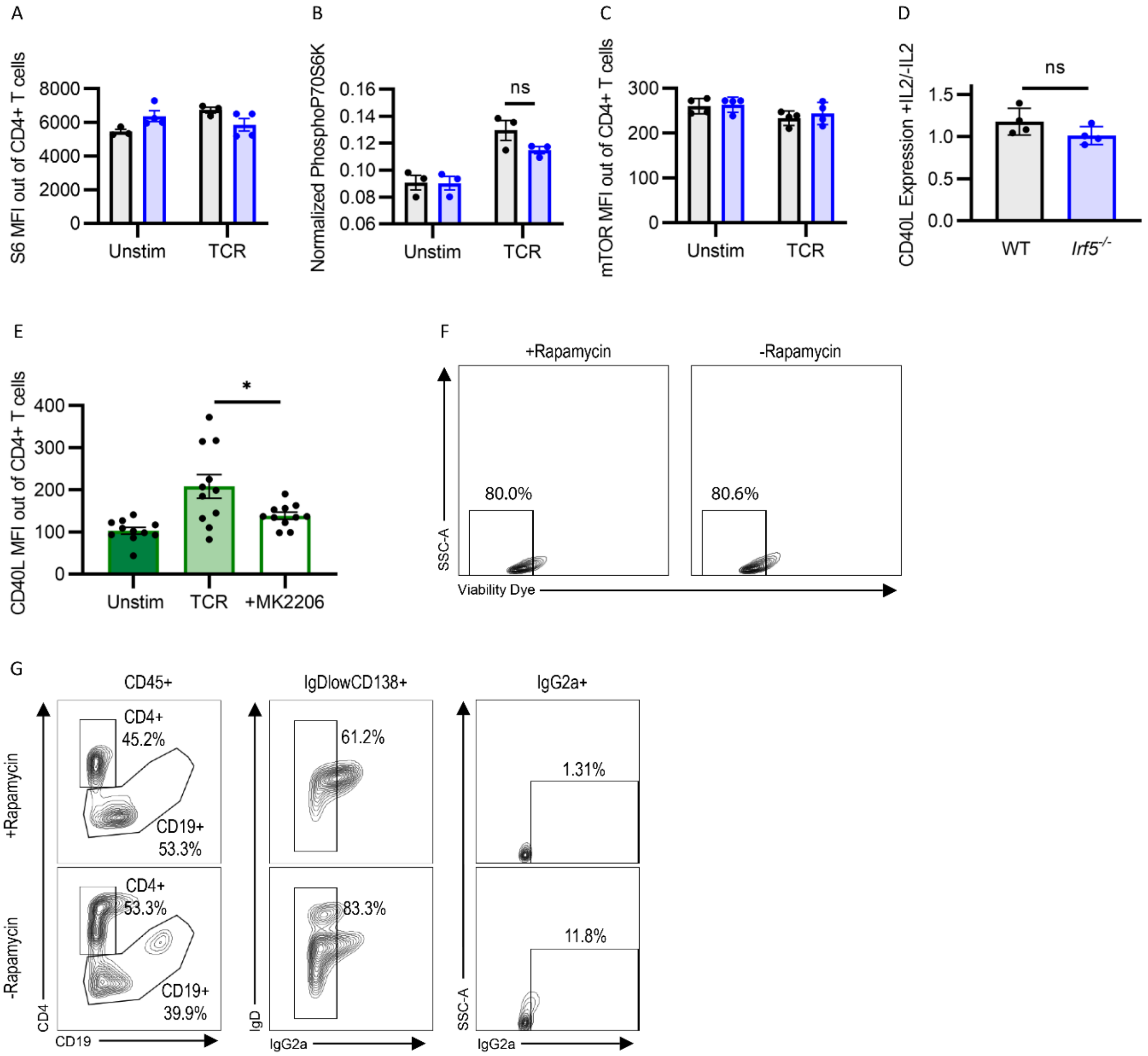

Fig. S4

(**A-C**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR). Summary graphs of indicated intracellular protein expression and/or phosphorylation levels in CD3^{+}CD4^{+} T cells gated from total splenocytes. Three-five biological replicates, representative of a minimum of two independent experiments. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. (**D**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR) in the presence (+IL2) or absence (-IL2) of IL2. Summary graphs of relative CD40L expression comparing

IL2/TCR (+Il2) stimulated vs TCR stimulated (-IL2) CD4$^+$ T cells. *P* value calculated by two-way unpaired *t* test. (**E**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR) in the presence (+MK2206) or absence (TCR) of the ASCT2 inhibitor, MK2206. Summary graphs of CD40L expression on live CD3$^+$CD4$^+$ T cells gated from total splenocytes. Data pooled from three independent experiments. *P* value calculated by 1-way ANOVA with Tukey correction for multiple comparisons. (**F,G**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR) in the presence (+Rapamycin) or absence (-Rapamycin) of Rapamycin. (**F**) Representative flow cytometric gating of CD3$^+$CD4$^+$ T cell viability using cell permeable viability dye. (**G**) Representative gating strategies for CD45$^+$CD19$^+$CD138$^+$IgD^{low} PBs gated from CD4 T cell:B cell cocultures with (+Rapamycin) and without (-Rapamycin) CD4 T cell Rapamycin pretreatment. $^*p < 0.05$, ns = not significant. Each point represents an independent biological replicate. Bar graphs show means +/- SEMs.

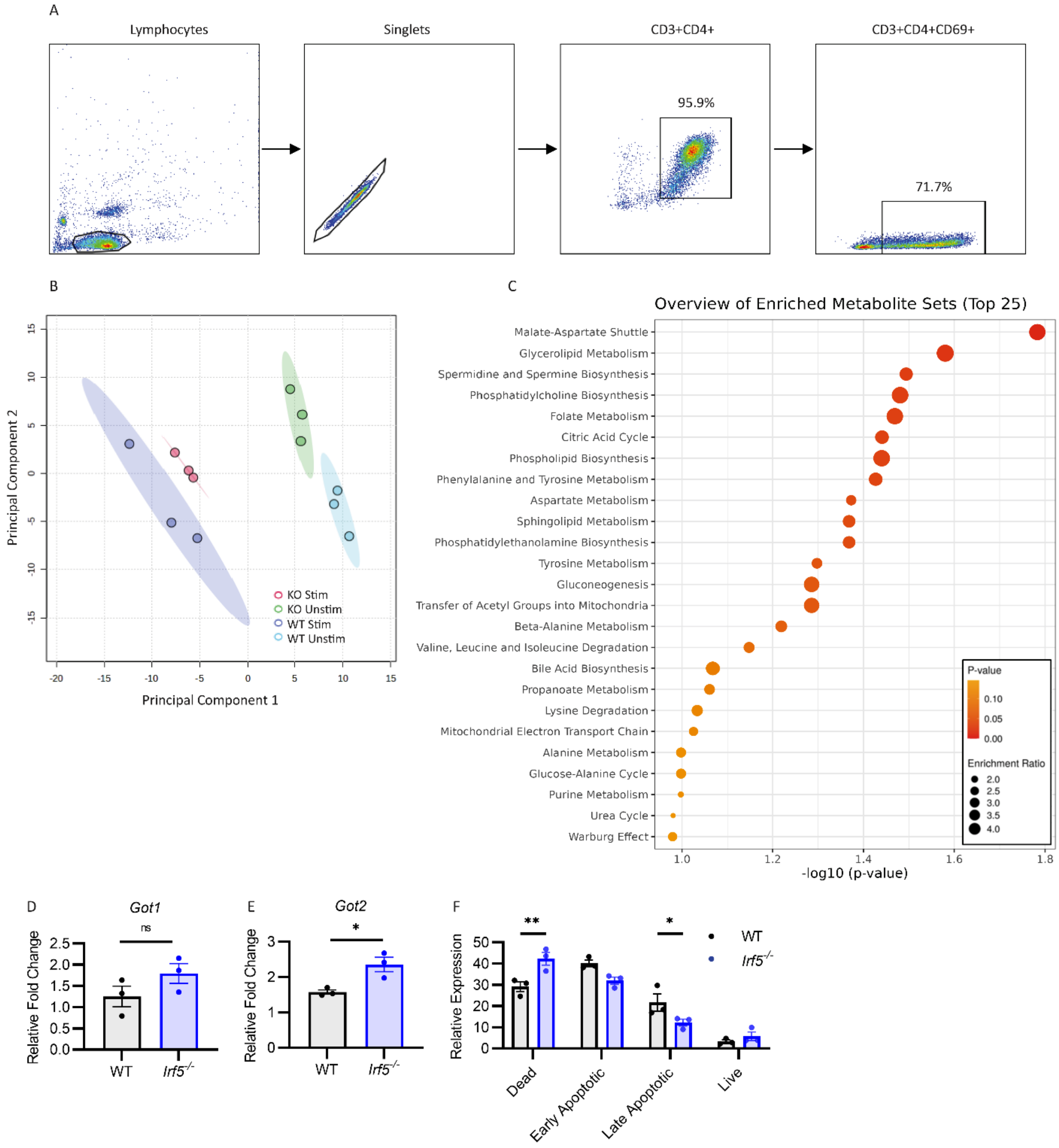

Fig. S5.

(**A**) Representative flow cytometry gating strategy confirming the purity and activation of naïve CD3$^+$CD4$^+$ T cells sorted from total splenocytes. (**B**) Principal component analysis from metabolomics profiling following 24-hours IL7 (Unstim) and anti-CD3/CD28 (Stim) treated CD3$^+$CD4$^+$ T cells sorted from total splenocytes of WT and *Irf5*$^{-/-}$ (KO) mice. Each condition is represented by three independent biological replicates. (**C**) Top 25 significantly enriched metabolite sets. (**D, E**) Sorted $CD3^+CD4^+$ T cells from WT and KO splenocytes were activated for 6-hours *in vitro* with anti-CD3/CD28 (TCR). *Got1* and *Got2* transcript expression normalized to *β-Actin*. *P* value calculated by two-way unpaired *t* test. (**F**) Summary graphs of CD4 T cell apoptosis following AOAA treatment. 3 independent biological replicates. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. Bar graphs show means +/- SEMs. $^*p < 0.05$, $^{**}p < 0.01$, ns = not significant. Each point represents an independent biological replicate.

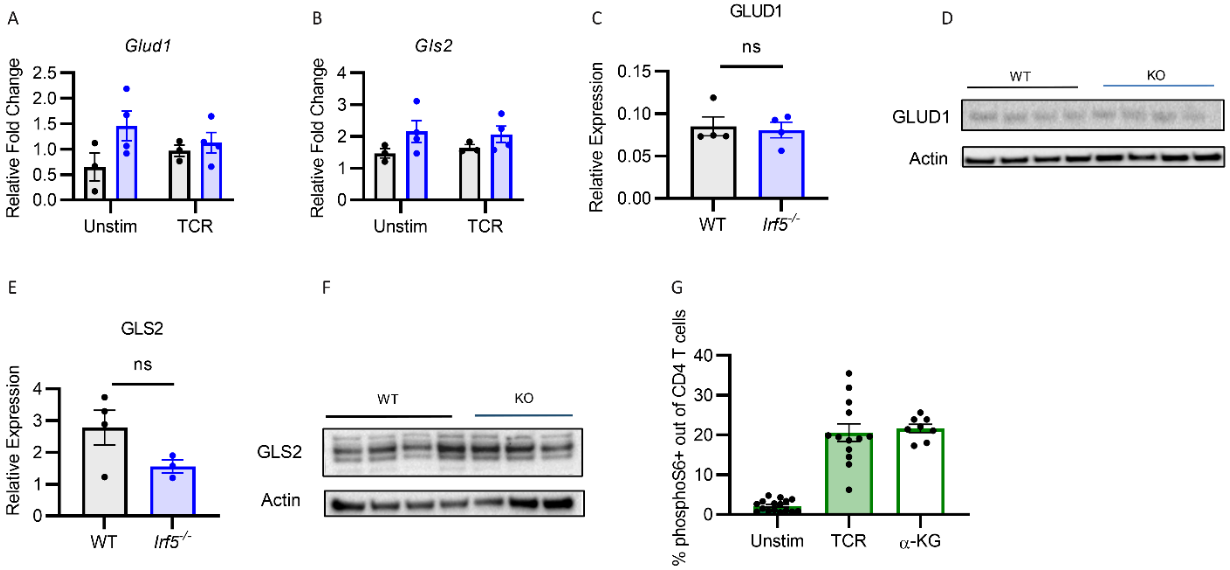

Fig. S6.

(**A,B**) Sorted CD3$^+$CD4$^+$ T cells from WT and *Irf5*$^{-/-}$ splenocytes were activated for 6-hours *in vitro* with anti-CD3/CD28 (TCR). (**A**) *Glud1* and (**B**) *Gls2* transcript expression normalized to *β-Actin.* Four biological replicates. *P* value calculated by 2-way ANOVA with Holm-Sidak correction for multiple comparisons. All comparisons not significant. (**C-F**) Purified CD3$^+$CD4$^+$ T cells were stimulated for 24 hours with anti-CD3/CD28, then analyzed with immunoblot for (**C, D**) GLUD1 (glutamate dehydrogenase) and (**E, F**) GLS (glutaminase). Values representative of 3-4 independent biological replicates normalized to Actin. *P* value calculated by two-way unpaired *t* test. (**G**) WT and *Irf5*$^{-/-}$ total splenocytes were activated for 24-hours *in vitro* with anti-CD3/CD28 (TCR) in the presence (DMK) or absence (TCR) of dimethyl ketoglutarate. Summary graphs of phosphorylated (phospho) S6 expression in CD3$^+$CD4$^+$ T cells. Data pooled from three independent experiments. *P* value calculated by 1-way ANOVA with Tukey correction for multiple comparisons. ns = not significant. Bar graphs show means +/- SEMs. Each point represents an independent biological replicate.

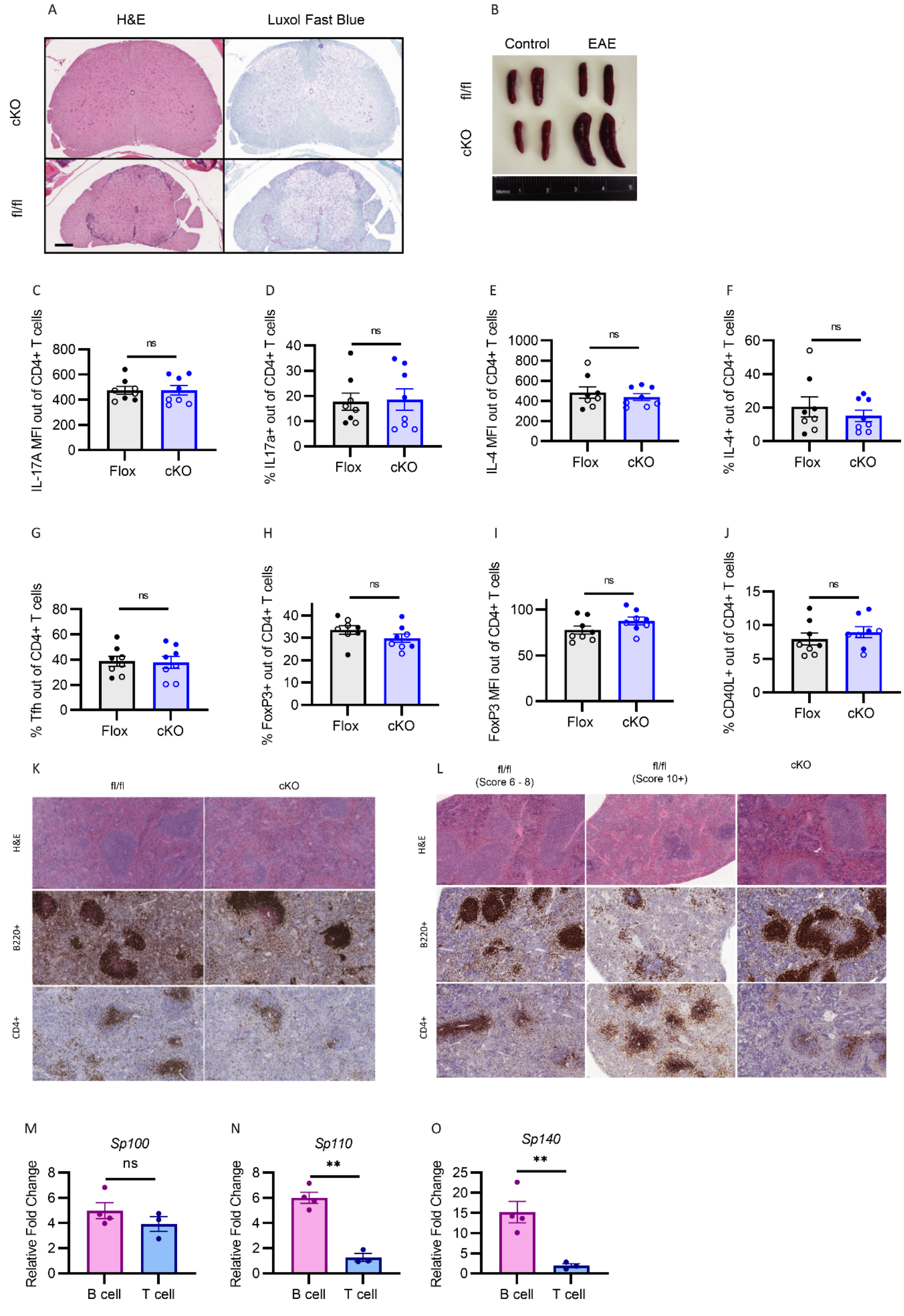
A
H&E
Luxol Fast Blue
cKO
fl/fl
B
Control
EAE
fl/fl
cKO
C
IL-17A MFI out of CD4+ T cells
800
600
400
200
0
ns
Flox
cKO
D
% IL17a+ out of CD4+ T cells
40
30
20
10
0
ns
Flox
cKO
E
IL-4 MFI out of CD4+ T cells
1000
800
600
400
200
0
ns
Flox
cKO
F
% IL-4+ out of CD4+ T cells
60
40
20
0
ns
Flox
cKO
G
% Tfh out of CD4+ T cells
80
60
40
20
0
ns
Flox
cKO
H
% FoxP3+ out of CD4+ T cells
40
30
20
10
0
ns
Flox
cKO
I
FoxP3 MFI out of CD4+ T cells
100
50
0
ns
Flox
cKO
J
% CD40L+ out of CD4+ T cells
15
10
5
0
ns
Flox
cKO
K
fl/fl
cKO
H&E
B220+
CD4+
L
fl/fl
(Score 6 - 8)
fl/fl
(Score 10+)
cKO
H&E
B220+
CD4+
M
Sp100
Relative Fold Change
8
6
4
2
0
ns
B cell
T cell
N
Sp110
Relative Fold Change
8
6
4
2
0
**
B cell
T cell
O
Sp140
Relative Fold Change
25
20
15
10
5
0
**
B cell
T cell

Fig. S7.

(**A**) Spinal cord cross sections stained with H&E and Luxol Fast Blue from cKO and fl/fl mice at peak disease. (**B**) Representative images of spleens from control and experimental cKO and fl/fl mice at clinically determined disease end points. Summary graphs of (**C, D**) IL-17expression, (**E, F**) IL4 expression, (**G**) CD4$^+$CXCR5$^+$BCL6$^+$ Tfh, (**H, I**) CD4$^+$FoxP3$^+$ Tregs, and (**J**) CD40L expression following EAE induction. Clear circles represent day 13 post immunization, filled circles represent day 20 post immunization. (**K,L**) Representative images of spleen sections stained with H&E, anti-B220, and anti-CD4 at (**K**) day 13 and (**L**) day 20 post-immunization. On day 20, spleens were harvested from mice with varying disease severity as indicated by respective scores. (**M-O**) B cells and CD4 T cells were sorted from cKO mice and stimulated for 6 hours with anti-CD3/CD28 Dynabeads. Transcript levels of (**M**) *Sp100*, (**N**) *Sp110* and (**O**) *Sp140* normalized to *β-Actin*. Bar graphs show means +/- SEMs. *P* value calculated by two-way unpaired *t* test. $^{**}p < 0.01$, ns = not significant. Each point represents an independent biological replicate.

Supplemental Table 1

Gene	p_val	avg_log2FC	p_val_adj	Cluster
Tnfrsf4	1.30E-41	1.903773	2.02E-37	Treg0/Treg1
Hspa9	7.52E-35	1.655757	1.16E-30	Treg0/Treg1
Nfkb1	1.12E-34	1.597707	1.74E-30	Treg0/Treg1
Ncl	3.89E-34	1.864491	6.01E-30	Treg0/Treg1
Gadd45b	1.39E-33	2.124907	2.16E-29	Treg0/Treg1
Hsp90ab1	2.53E-32	1.305821	3.91E-28	Treg0/Treg1
Nars	6.92E-31	1.409441	1.07E-26	Treg0/Treg1
Eif3c	1.24E-30	1.394616	1.92E-26	Treg0/Treg1
Srgn	1.60E-30	1.45274	2.48E-26	Treg0/Treg1
Tnfrsf9	4.43E-30	1.954327	6.86E-26	Treg0/Treg1
Odc1	3.42E-29	2.260111	5.30E-25	Treg0/Treg1
Eprs	1.33E-28	1.428333	2.06E-24	Treg0/Treg1
Cd83	1.93E-28	1.739425	2.99E-24	Treg0/Treg1
Bcl2a1b	2.05E-28	1.471618	3.17E-24	Treg0/Treg1
Bcl2l1	2.80E-28	1.440354	4.33E-24	Treg0/Treg1
Junb	5.14E-28	1.506808	7.96E-24	Treg0/Treg1
Mir155hg	9.81E-28	1.794524	1.52E-23	Treg0/Treg1
Hspa5	1.50E-27	1.250327	2.32E-23	Treg0/Treg1
Gnl3	2.87E-27	1.529831	4.45E-23	Treg0/Treg1
Phgdh	4.86E-27	1.466325	7.53E-23	Treg0/Treg1
Lcp1	8.34E-27	1.409625	1.29E-22	Treg0/Treg1
Cd82	6.20E-26	1.333299	9.60E-22	Treg0/Treg1
Nop58	1.63E-25	1.442438	2.52E-21	Treg0/Treg1
Nfkbia	1.64E-25	1.500078	2.54E-21	Treg0/Treg1
Aebp2	2.08E-25	1.201219	3.22E-21	Treg0/Treg1
Anp32b	2.25E-24	1.287919	3.48E-20	Treg0/Treg1
Rel	3.29E-24	1.425403	5.09E-20	Treg0/Treg1
Eif2s2	3.79E-24	1.051991	5.86E-20	Treg0/Treg1
Ppia	6.18E-24	0.743716	9.57E-20	Treg0/Treg1
Ndfip1	7.78E-24	1.108368	1.20E-19	Treg0/Treg1
Nhp2	9.33E-24	1.24194	1.44E-19	Treg0/Treg1
Set	2.82E-23	1.056832	4.36E-19	Treg0/Treg1
Serbp1	2.94E-23	0.969792	4.55E-19	Treg0/Treg1
G3bp1	5.45E-23	1.097696	8.44E-19	Treg0/Treg1
Mthfd2	5.87E-23	1.198097	9.09E-19	Treg0/Treg1
Aldoa	9.08E-23	1.204386	1.40E-18	Treg0/Treg1
Nolc1	3.42E-22	1.314262	5.29E-18	Treg0/Treg1
Slc3a2	4.75E-22	1.213181	7.35E-18	Treg0/Treg1
Ran	1.25E-21	1.005363	1.94E-17	Treg0/Treg1
Nme1	1.42E-21	1.395749	2.21E-17	Treg0/Treg1
Npm1	1.58E-21	1.183829	2.44E-17	Treg0/Treg1

Hsp90aa1	1.77E-21	1.137092	2.74E-17	Treg0/Treg1
Tfrc	1.93E-21	1.295934	2.99E-17	Treg0/Treg1
Slc7a1	3.51E-21	1.183027	5.43E-17	Treg0/Treg1
Orai1	4.54E-21	1.161366	7.02E-17	Treg0/Treg1
Ddx21	5.67E-21	1.274867	8.78E-17	Treg0/Treg1
Wdr43	7.49E-21	1.207209	1.16E-16	Treg0/Treg1
Tnfaip3	7.63E-21	1.219844	1.18E-16	Treg0/Treg1
Ybx1	7.83E-21	0.88417	1.21E-16	Treg0/Treg1
Kdm2b	1.34E-20	1.271768	2.08E-16	Treg0/Treg1
Srsf2	1.59E-20	1.011094	2.46E-16	Treg0/Treg1
Mybbp1a	1.75E-20	1.199887	2.72E-16	Treg0/Treg1
Hopx	2.12E-20	1.572898	3.28E-16	Treg0/Treg1
C1qbp	2.33E-20	1.31199	3.60E-16	Treg0/Treg1
Mat2a	3.12E-20	1.130573	4.84E-16	Treg0/Treg1
Psat1	3.67E-20	1.11184	5.68E-16	Treg0/Treg1
Irf4	4.56E-20	1.55212	7.05E-16	Treg0/Treg1
Gpr183	4.94E-20	1.410184	7.65E-16	Treg0/Treg1
A430093F15Rik	5.98E-20	1.068259	9.25E-16	Treg0/Treg1
Hspd1	5.98E-20	1.388564	9.26E-16	Treg0/Treg1
Pa2g4	1.04E-19	1.166955	1.61E-15	Treg0/Treg1
Etf1	1.32E-19	0.975811	2.05E-15	Treg0/Treg1
Ghitm	3.22E-19	1.025732	4.98E-15	Treg0/Treg1
Fubp1	3.25E-19	0.984224	5.03E-15	Treg0/Treg1
Nop14	3.69E-19	1.034654	5.72E-15	Treg0/Treg1
Mif	3.71E-19	1.472792	5.74E-15	Treg0/Treg1
Eif4a1	4.82E-19	1.023476	7.46E-15	Treg0/Treg1
Srm	6.55E-19	1.167833	1.01E-14	Treg0/Treg1
Bcl2a1d	7.86E-19	1.198991	1.22E-14	Treg0/Treg1
Myo1g	1.17E-18	1.061461	1.82E-14	Treg0/Treg1
Noc2l	1.18E-18	1.040623	1.83E-14	Treg0/Treg1
Mdn1	1.22E-18	1.032258	1.89E-14	Treg0/Treg1
Irf8	1.62E-18	1.805799	2.51E-14	Treg0/Treg1
Itgav	1.81E-18	1.117683	2.80E-14	Treg0/Treg1
Wdr75	3.14E-18	0.973309	4.85E-14	Treg0/Treg1
Snhg15	4.62E-18	1.111293	7.15E-14	Treg0/Treg1
Nop56	7.94E-18	1.094828	1.23E-13	Treg0/Treg1
Tnfrsf18	9.84E-18	0.840409	1.52E-13	Treg0/Treg1
Gtpbp4	1.31E-17	1.029934	2.03E-13	Treg0/Treg1
Eif1a	1.42E-17	1.009072	2.19E-13	Treg0/Treg1
Tomm40	1.71E-17	0.903465	2.65E-13	Treg0/Treg1
Dusp2	1.79E-17	1.400681	2.77E-13	Treg0/Treg1
Ifrd1	1.94E-17	0.985739	3.00E-13	Treg0/Treg1
Nfkb2	2.08E-17	0.962159	3.22E-13	Treg0/Treg1
Timm8a1	2.22E-17	0.953311	3.43E-13	Treg0/Treg1
Eif3a	2.40E-17	0.983529	3.72E-13	Treg0/Treg1

Cct3	2.51E-17	0.966334	3.89E-13	Treg0/Treg1
Iars	3.12E-17	0.845236	4.82E-13	Treg0/Treg1
Ftsj3	3.62E-17	0.95602	5.60E-13	Treg0/Treg1
Mrto4	3.70E-17	1.055935	5.73E-13	Treg0/Treg1
Eif5a	4.79E-17	0.819558	7.41E-13	Treg0/Treg1
Stip1	5.17E-17	0.841316	8.01E-13	Treg0/Treg1
Hnrnpab	5.58E-17	1.011142	8.64E-13	Treg0/Treg1
Timm23	6.45E-17	0.909571	9.99E-13	Treg0/Treg1
Plagl2	7.81E-17	0.95261	1.21E-12	Treg0/Treg1
Rcc2	1.42E-16	0.935192	2.20E-12	Treg0/Treg1
Gar1	1.80E-16	0.979308	2.79E-12	Treg0/Treg1
Lyar	2.08E-16	0.855087	3.22E-12	Treg0/Treg1
Ranbp1	2.24E-16	0.996389	3.47E-12	Treg0/Treg1
Eif4ebp1	2.29E-16	1.118866	3.54E-12	Treg0/Treg1
Cct2	2.97E-16	0.926652	4.60E-12	Treg0/Treg1
Sars	3.41E-16	0.874978	5.28E-12	Treg0/Treg1
Slc7a5	3.44E-16	0.800047	5.33E-12	Treg0/Treg1
Eif4e	3.84E-16	0.829378	5.94E-12	Treg0/Treg1
Tank	4.04E-16	0.897606	6.26E-12	Treg0/Treg1
Tomm20	4.46E-16	0.771639	6.90E-12	Treg0/Treg1
Hif1a	5.01E-16	0.889232	7.76E-12	Treg0/Treg1
Tars	5.36E-16	0.885095	8.29E-12	Treg0/Treg1
Atp5g1	6.11E-16	0.928077	9.46E-12	Treg0/Treg1
Pfn1	6.96E-16	0.700227	1.08E-11	Treg0/Treg1
Cdv3	7.11E-16	1.021175	1.10E-11	Treg0/Treg1
Stap1	7.25E-16	1.319665	1.12E-11	Treg0/Treg1
Tagap	7.52E-16	1.204611	1.16E-11	Treg0/Treg1
Eif1	7.68E-16	0.601016	1.19E-11	Treg0/Treg1
Ddx27	7.83E-16	0.940808	1.21E-11	Treg0/Treg1
Sdf4	8.01E-16	0.989585	1.24E-11	Treg0/Treg1
AI506816	8.20E-16	0.861198	1.27E-11	Treg0/Treg1
Eif3j1	8.83E-16	0.916983	1.37E-11	Treg0/Treg1
Nsun2	9.97E-16	0.85679	1.54E-11	Treg0/Treg1
Icam1	1.01E-15	1.035952	1.57E-11	Treg0/Treg1
Pum3	1.06E-15	0.844983	1.64E-11	Treg0/Treg1
Ppan	1.15E-15	0.812513	1.79E-11	Treg0/Treg1
Mtdh	1.17E-15	0.870659	1.81E-11	Treg0/Treg1
Nr4a1	1.22E-15	1.599514	1.88E-11	Treg0/Treg1
Stat5a	1.25E-15	0.945819	1.93E-11	Treg0/Treg1
Timm10	1.32E-15	0.922593	2.04E-11	Treg0/Treg1
Baz1a	1.62E-15	0.938005	2.51E-11	Treg0/Treg1
Lars	1.98E-15	0.93242	3.07E-11	Treg0/Treg1
Rpf2	1.99E-15	0.782022	3.08E-11	Treg0/Treg1
Cd69	2.01E-15	1.552	3.10E-11	Treg0/Treg1
Ebna1bp2	2.08E-15	0.934349	3.22E-11	Treg0/Treg1

Prpf40a	2.42E-15	0.780143	3.75E-11	Treg0/Treg1
Cd200	2.44E-15	1.073539	3.77E-11	Treg0/Treg1
Plagl1	3.12E-15	1.46938	4.83E-11	Treg0/Treg1
Bhlhe40	3.34E-15	1.192235	5.17E-11	Treg0/Treg1
Tcp1	3.40E-15	0.861025	5.27E-11	Treg0/Treg1
Pdcd11	3.83E-15	0.902111	5.93E-11	Treg0/Treg1
Esf1	4.83E-15	0.875914	7.48E-11	Treg0/Treg1
Prmt1	4.90E-15	0.847052	7.59E-11	Treg0/Treg1
Nr4a3	5.59E-15	1.551603	8.66E-11	Treg0/Treg1
Atf3	6.04E-15	1.628631	9.35E-11	Treg0/Treg1
Cebpz	6.14E-15	0.831289	9.51E-11	Treg0/Treg1
Rrs1	6.57E-15	0.896285	1.02E-10	Treg0/Treg1
Eea1	6.72E-15	1.059113	1.04E-10	Treg0/Treg1
Rrp15	6.77E-15	0.805582	1.05E-10	Treg0/Treg1
Eef1e1	6.77E-15	0.913428	1.05E-10	Treg0/Treg1
Rsl1d1	6.98E-15	0.875364	1.08E-10	Treg0/Treg1
Slc38a1	7.14E-15	0.877766	1.10E-10	Treg0/Treg1
Zfp36l1	9.41E-15	1.083794	1.46E-10	Treg0/Treg1
Ddx18	1.16E-14	0.981934	1.79E-10	Treg0/Treg1
Zfp593	1.17E-14	0.89699	1.81E-10	Treg0/Treg1
Mak16	1.24E-14	0.943894	1.91E-10	Treg0/Treg1
Bzw1	1.63E-14	0.812013	2.52E-10	Treg0/Treg1
Mettl1	1.64E-14	0.939533	2.54E-10	Treg0/Treg1
Traf1	2.61E-14	0.85899	4.04E-10	Treg0/Treg1
Mthfd1l	2.69E-14	0.709425	4.17E-10	Treg0/Treg1
Tgif1	2.84E-14	0.84303	4.39E-10	Treg0/Treg1
Abce1	3.03E-14	0.860526	4.69E-10	Treg0/Treg1
Syncrip	3.27E-14	0.919189	5.07E-10	Treg0/Treg1
Denr	3.36E-14	0.813465	5.20E-10	Treg0/Treg1
Eif3b	3.55E-14	0.812018	5.50E-10	Treg0/Treg1
Cycs	3.61E-14	0.79994	5.59E-10	Treg0/Treg1
Snhg1	3.84E-14	0.828718	5.95E-10	Treg0/Treg1
Eif2s1	4.51E-14	0.806075	6.99E-10	Treg0/Treg1
St13	4.62E-14	0.864324	7.15E-10	Treg0/Treg1
Cct6a	5.08E-14	0.805945	7.86E-10	Treg0/Treg1
Nifk	5.13E-14	0.820002	7.94E-10	Treg0/Treg1
Ier5	5.16E-14	0.920979	7.99E-10	Treg0/Treg1
Apex1	5.29E-14	0.766022	8.19E-10	Treg0/Treg1
Hspe1	5.75E-14	0.934894	8.91E-10	Treg0/Treg1
Cnbp	5.92E-14	0.735874	9.16E-10	Treg0/Treg1
Rrp9	6.17E-14	0.762394	9.54E-10	Treg0/Treg1
Clic4	6.24E-14	0.934422	9.66E-10	Treg0/Treg1
Emc6	6.57E-14	0.764211	1.02E-09	Treg0/Treg1
Rab8b	6.89E-14	0.860968	1.07E-09	Treg0/Treg1
Grwd1	7.10E-14	0.61943	1.10E-09	Treg0/Treg1

Grap	9.50E-14	0.901133	1.47E-09	Treg0/Treg1
Gpatch4	1.04E-13	0.882337	1.61E-09	Treg0/Treg1
Polr3d	1.12E-13	0.759364	1.74E-09	Treg0/Treg1
Shmt2	1.14E-13	0.744727	1.77E-09	Treg0/Treg1
Nop16	1.15E-13	0.789475	1.79E-09	Treg0/Treg1
Jarid2	1.21E-13	1.020995	1.87E-09	Treg0/Treg1
Sms	1.31E-13	0.823166	2.02E-09	Treg0/Treg1
Atad3a	1.64E-13	0.712462	2.54E-09	Treg0/Treg1
Rbm3	1.71E-13	0.616584	2.65E-09	Treg0/Treg1
Cflar	1.92E-13	1.011195	2.97E-09	Treg0/Treg1
Snrpa1	1.97E-13	0.750391	3.05E-09	Treg0/Treg1
Lad1	2.19E-13	1.119193	3.39E-09	Treg0/Treg1
Ssrp1	2.28E-13	0.757752	3.52E-09	Treg0/Treg1
Kdm6b	2.51E-13	1.121731	3.88E-09	Treg0/Treg1
Tcerg1	2.81E-13	0.758115	4.36E-09	Treg0/Treg1
Prmt3	2.87E-13	0.694981	4.45E-09	Treg0/Treg1
Ndufaf4	2.95E-13	0.71866	4.57E-09	Treg0/Treg1
Bmyc	3.29E-13	0.862806	5.09E-09	Treg0/Treg1
Rora	3.52E-13	1.352517	5.46E-09	Treg0/Treg1
Rnf157	3.85E-13	0.8889	5.96E-09	Treg0/Treg1
Rrp1b	3.89E-13	0.762752	6.02E-09	Treg0/Treg1
Nol10	4.69E-13	0.685966	7.26E-09	Treg0/Treg1
Hspa8	5.13E-13	0.77856	7.94E-09	Treg0/Treg1
Tob2	5.75E-13	1.063775	8.90E-09	Treg0/Treg1
Timm9	5.86E-13	0.812739	9.07E-09	Treg0/Treg1
Vsir	5.94E-13	0.830292	9.19E-09	Treg0/Treg1
Calr	6.14E-13	0.769628	9.50E-09	Treg0/Treg1
Imp4	7.44E-13	0.675459	1.15E-08	Treg0/Treg1
Mphosph10	8.44E-13	0.888474	1.31E-08	Treg0/Treg1
Psmd12	8.76E-13	0.752914	1.36E-08	Treg0/Treg1
Nol12	8.80E-13	0.612234	1.36E-08	Treg0/Treg1
Pno1	8.93E-13	0.753295	1.38E-08	Treg0/Treg1
Fbl	9.81E-13	0.901487	1.52E-08	Treg0/Treg1
Gars	1.05E-12	0.797666	1.62E-08	Treg0/Treg1
Hnrnpc	1.07E-12	0.678507	1.65E-08	Treg0/Treg1
Eif6	1.19E-12	0.750965	1.85E-08	Treg0/Treg1
Dnajc21	1.24E-12	0.707753	1.92E-08	Treg0/Treg1
Relb	1.45E-12	0.682357	2.25E-08	Treg0/Treg1
Cyfip1	1.46E-12	1.068703	2.26E-08	Treg0/Treg1
Dkc1	1.59E-12	0.842892	2.46E-08	Treg0/Treg1
Rbpj	1.68E-12	0.925929	2.60E-08	Treg0/Treg1
Nap1l1	1.70E-12	0.811963	2.63E-08	Treg0/Treg1
Cd44	1.88E-12	0.810975	2.91E-08	Treg0/Treg1
Eif3g	2.06E-12	0.735436	3.18E-08	Treg0/Treg1
Eif5b	2.20E-12	0.783732	3.41E-08	Treg0/Treg1

Snrpb	2.21E-12	0.676988	3.42E-08	Treg0/Treg1
Shmt1	2.28E-12	0.580036	3.52E-08	Treg0/Treg1
Nol11	2.42E-12	0.701542	3.74E-08	Treg0/Treg1
Atp5b	2.59E-12	0.589754	4.01E-08	Treg0/Treg1
Hk2	2.75E-12	0.636164	4.26E-08	Treg0/Treg1
Rbm17	2.78E-12	0.762887	4.30E-08	Treg0/Treg1
Ltv1	2.79E-12	0.660151	4.32E-08	Treg0/Treg1
Heatr1	2.88E-12	0.646554	4.46E-08	Treg0/Treg1
Atf4	2.95E-12	0.734191	4.57E-08	Treg0/Treg1
Banf1	3.27E-12	0.748169	5.06E-08	Treg0/Treg1
Srsf7	3.66E-12	0.631769	5.67E-08	Treg0/Treg1
7-Sep	3.75E-12	0.759887	5.81E-08	Treg0/Treg1
Wdr12	4.02E-12	0.730473	6.23E-08	Treg0/Treg1
Nip7	4.27E-12	0.698531	6.61E-08	Treg0/Treg1
Hspa4	4.30E-12	0.761472	6.66E-08	Treg0/Treg1
Ruvbl1	4.53E-12	0.714678	7.00E-08	Treg0/Treg1
Fam162a	4.82E-12	0.840035	7.46E-08	Treg0/Treg1
Mrpl19	4.90E-12	0.708303	7.58E-08	Treg0/Treg1
Nudc	5.36E-12	0.640125	8.30E-08	Treg0/Treg1
Purb	5.51E-12	0.694986	8.52E-08	Treg0/Treg1
Ldha	6.25E-12	0.844625	9.67E-08	Treg0/Treg1
Nol9	6.45E-12	0.61322	9.98E-08	Treg0/Treg1
Btla	6.76E-12	0.780317	1.05E-07	Treg0/Treg1
Syngr2	7.19E-12	0.855496	1.11E-07	Treg0/Treg1
Srsf3	8.35E-12	0.621746	1.29E-07	Treg0/Treg1
Cct5	8.43E-12	0.720355	1.30E-07	Treg0/Treg1
Hnrnpu	8.51E-12	0.602731	1.32E-07	Treg0/Treg1
Slc1a5	8.84E-12	0.72961	1.37E-07	Treg0/Treg1
Ybx3	9.25E-12	0.896094	1.43E-07	Treg0/Treg1
Znhit6	1.05E-11	0.688217	1.62E-07	Treg0/Treg1
Utp20	1.13E-11	0.704806	1.75E-07	Treg0/Treg1
Mrpl12	1.16E-11	0.716102	1.80E-07	Treg0/Treg1
Nme2	1.23E-11	0.943954	1.90E-07	Treg0/Treg1
Hnrnpa1	1.29E-11	0.703603	1.99E-07	Treg0/Treg1
Rps27l	1.30E-11	0.640749	2.02E-07	Treg0/Treg1
Hnrnpa0	1.37E-11	0.631941	2.12E-07	Treg0/Treg1
Serpinb9	1.41E-11	0.794323	2.19E-07	Treg0/Treg1
Mrps6	1.46E-11	0.726599	2.26E-07	Treg0/Treg1
Utp18	1.46E-11	0.760802	2.26E-07	Treg0/Treg1
Srsf10	1.49E-11	0.707127	2.31E-07	Treg0/Treg1
Aars	1.55E-11	0.623321	2.40E-07	Treg0/Treg1
Hivep3	1.60E-11	0.874257	2.48E-07	Treg0/Treg1
Myl12a	1.65E-11	0.75646	2.55E-07	Treg0/Treg1
Ppp4r2	1.67E-11	0.782002	2.59E-07	Treg0/Treg1
Rsl24d1	1.70E-11	0.678095	2.63E-07	Treg0/Treg1

Eif4g1	1.86E-11	0.659469	2.88E-07	Treg0/Treg1
Ddx39	1.96E-11	0.629279	3.03E-07	Treg0/Treg1
Ppp1r14b	1.99E-11	0.768402	3.08E-07	Treg0/Treg1
Wdr18	2.07E-11	0.538591	3.20E-07	Treg0/Treg1
Psma7	2.09E-11	0.631657	3.23E-07	Treg0/Treg1
Zc3h15	2.12E-11	0.737587	3.28E-07	Treg0/Treg1
Mrps18b	2.17E-11	0.568598	3.36E-07	Treg0/Treg1
Txnrd1	2.35E-11	0.749203	3.63E-07	Treg0/Treg1
Rars	2.43E-11	0.675592	3.76E-07	Treg0/Treg1
Usp36	2.59E-11	0.622314	4.01E-07	Treg0/Treg1
Fam107b	2.65E-11	0.759409	4.10E-07	Treg0/Treg1
Nfkbid	2.84E-11	0.955973	4.40E-07	Treg0/Treg1
Rrp12	2.88E-11	0.518009	4.45E-07	Treg0/Treg1
Nol8	3.03E-11	0.83044	4.69E-07	Treg0/Treg1
Tnfrsf1b	3.06E-11	0.754289	4.74E-07	Treg0/Treg1
Dnaja2	3.15E-11	0.676184	4.88E-07	Treg0/Treg1
Llph	3.25E-11	0.65706	5.04E-07	Treg0/Treg1
11-Sep	3.28E-11	0.517923	5.08E-07	Treg0/Treg1
Cish	3.67E-11	0.653589	5.67E-07	Treg0/Treg1
Smyd5	4.24E-11	0.522764	6.57E-07	Treg0/Treg1
Polr2f	4.33E-11	0.674052	6.70E-07	Treg0/Treg1
Tm2d3	4.91E-11	0.57583	7.60E-07	Treg0/Treg1
Hdgf	4.98E-11	0.703456	7.70E-07	Treg0/Treg1
Hsph1	5.20E-11	0.735099	8.05E-07	Treg0/Treg1
Sdad1	5.56E-11	0.70112	8.61E-07	Treg0/Treg1
Cct7	5.62E-11	0.718669	8.70E-07	Treg0/Treg1
Smco4	5.78E-11	0.637097	8.94E-07	Treg0/Treg1
Ppat	6.00E-11	0.6108	9.28E-07	Treg0/Treg1
Wdr74	6.77E-11	0.622988	1.05E-06	Treg0/Treg1
Ppp1r16b	6.92E-11	0.714549	1.07E-06	Treg0/Treg1
Ubl3	7.52E-11	0.838148	1.16E-06	Treg0/Treg1
Dot1l	7.59E-11	0.611676	1.18E-06	Treg0/Treg1
Rheb	7.80E-11	0.713206	1.21E-06	Treg0/Treg1
Hacd3	7.96E-11	0.73078	1.23E-06	Treg0/Treg1
Psme2	8.29E-11	0.668703	1.28E-06	Treg0/Treg1
Hax1	8.34E-11	0.573305	1.29E-06	Treg0/Treg1
Gnl2	8.60E-11	0.660851	1.33E-06	Treg0/Treg1
Lap3	9.02E-11	0.643503	1.40E-06	Treg0/Treg1
Sfxn1	9.02E-11	0.725621	1.40E-06	Treg0/Treg1
Grpel1	9.55E-11	0.535764	1.48E-06	Treg0/Treg1
Cox5a	9.60E-11	0.605862	1.49E-06	Treg0/Treg1
Cebpb	9.67E-11	0.698548	1.50E-06	Treg0/Treg1
Zbtb1	9.70E-11	0.710381	1.50E-06	Treg0/Treg1
Ptma	1.02E-10	0.661642	1.58E-06	Treg0/Treg1
Txnl4a	1.09E-10	0.629175	1.69E-06	Treg0/Treg1

Fabp5	1.10E-10	0.856344	1.70E-06	Treg0/Treg1
Mettl16	1.18E-10	0.523627	1.82E-06	Treg0/Treg1
Batf	1.34E-10	1.128074	2.08E-06	Treg0/Treg1
Ddit3	1.39E-10	0.604748	2.14E-06	Treg0/Treg1
Rps2	1.49E-10	0.514836	2.30E-06	Treg0/Treg1
Myc	1.54E-10	1.025445	2.38E-06	Treg0/Treg1
Wdr46	1.67E-10	0.547116	2.58E-06	Treg0/Treg1
Chchd4	1.68E-10	0.595768	2.60E-06	Treg0/Treg1
Rps19bp1	1.69E-10	0.598233	2.61E-06	Treg0/Treg1
Vars	1.76E-10	0.629566	2.72E-06	Treg0/Treg1
Gspt1	1.77E-10	0.639679	2.74E-06	Treg0/Treg1
Rcl1	1.79E-10	0.570758	2.76E-06	Treg0/Treg1
Smarca5	1.84E-10	0.58953	2.84E-06	Treg0/Treg1
B3gnt2	1.87E-10	0.750308	2.89E-06	Treg0/Treg1
Rangap1	2.44E-10	0.58565	3.77E-06	Treg0/Treg1
Snu13	2.48E-10	0.659599	3.85E-06	Treg0/Treg1
Aatf	2.53E-10	0.654616	3.91E-06	Treg0/Treg1
Ppa1	2.67E-10	0.64485	4.13E-06	Treg0/Treg1
Mea1	2.75E-10	0.60853	4.26E-06	Treg0/Treg1
Pfdn2	2.79E-10	0.601077	4.32E-06	Treg0/Treg1
Cct4	3.00E-10	0.617113	4.65E-06	Treg0/Treg1
Phb2	3.37E-10	0.630329	5.22E-06	Treg0/Treg1
Pdap1	3.38E-10	0.639366	5.23E-06	Treg0/Treg1
Tox	3.38E-10	0.73548	5.23E-06	Treg0/Treg1
Ppp1r15a	3.39E-10	0.569872	5.24E-06	Treg0/Treg1
Hnrnpd	3.54E-10	0.607939	5.48E-06	Treg0/Treg1
Ssb	3.74E-10	0.513467	5.78E-06	Treg0/Treg1
Agpat5	4.02E-10	0.612764	6.22E-06	Treg0/Treg1
Psmb2	4.19E-10	0.523919	6.48E-06	Treg0/Treg1
Aprt	4.34E-10	0.695262	6.72E-06	Treg0/Treg1
Xpot	4.69E-10	0.596869	7.26E-06	Treg0/Treg1
Hirip3	4.90E-10	0.559672	7.58E-06	Treg0/Treg1
Tma16	5.06E-10	0.575292	7.83E-06	Treg0/Treg1
Tuba1b	5.38E-10	0.734447	8.33E-06	Treg0/Treg1
Wnk1	5.46E-10	0.757408	8.45E-06	Treg0/Treg1
Vgll4	6.05E-10	0.786416	9.37E-06	Treg0/Treg1
Areg	6.06E-10	1.490949	9.38E-06	Treg0/Treg1
Aen	6.24E-10	0.587958	9.65E-06	Treg0/Treg1
U2af2	6.40E-10	0.589242	9.91E-06	Treg0/Treg1
Srsf6	6.75E-10	0.641538	1.05E-05	Treg0/Treg1
Pwp1	7.28E-10	0.483275	1.13E-05	Treg0/Treg1
Ifrd2	7.34E-10	0.52318	1.14E-05	Treg0/Treg1
Ramp3	7.39E-10	1.204628	1.14E-05	Treg0/Treg1
Surf2	7.41E-10	0.526102	1.15E-05	Treg0/Treg1
Snrpa	7.88E-10	0.569299	1.22E-05	Treg0/Treg1

Yrdc	9.12E-10	0.544227	1.41E-05	Treg0/Treg1
Tbc1d30	9.23E-10	0.636746	1.43E-05	Treg0/Treg1
Map2k3	9.33E-10	0.759882	1.44E-05	Treg0/Treg1
Canx	9.47E-10	0.560075	1.47E-05	Treg0/Treg1
Rilpl2	9.86E-10	0.67401	1.53E-05	Treg0/Treg1
Ipo4	1.05E-09	0.442796	1.63E-05	Treg0/Treg1
Mrpl15	1.13E-09	0.588504	1.75E-05	Treg0/Treg1
Fdx2	1.27E-09	0.692697	1.96E-05	Treg0/Treg1
Cars	1.28E-09	0.566432	1.97E-05	Treg0/Treg1
Fnbp1	1.28E-09	0.724548	1.98E-05	Treg0/Treg1
Pcbp1	1.29E-09	0.667479	2.00E-05	Treg0/Treg1
Taf15	1.45E-09	0.64767	2.24E-05	Treg0/Treg1
Tm9sf4	1.54E-09	0.530123	2.38E-05	Treg0/Treg1
Nfkbib	1.55E-09	0.586947	2.39E-05	Treg0/Treg1
Egr1	1.57E-09	1.19535	2.42E-05	Treg0/Treg1
Ly75	1.66E-09	0.781311	2.57E-05	Treg0/Treg1
Med11	1.68E-09	0.48442	2.60E-05	Treg0/Treg1
Elp5	1.70E-09	0.528728	2.63E-05	Treg0/Treg1
U2surp	1.72E-09	0.59784	2.66E-05	Treg0/Treg1
Eif1ax	1.91E-09	0.569532	2.96E-05	Treg0/Treg1
Mpp6	2.01E-09	0.619575	3.11E-05	Treg0/Treg1
Cfl1	2.02E-09	0.530545	3.12E-05	Treg0/Treg1
Fam129a	2.19E-09	0.667108	3.40E-05	Treg0/Treg1
Strap	2.23E-09	0.656533	3.45E-05	Treg0/Treg1
Cct8	2.31E-09	0.590671	3.57E-05	Treg0/Treg1
Coq8a	2.38E-09	0.661362	3.68E-05	Treg0/Treg1
Pim3	2.46E-09	0.548175	3.81E-05	Treg0/Treg1
Ap3b1	2.56E-09	0.831274	3.96E-05	Treg0/Treg1
Bcat1	2.80E-09	0.449677	4.34E-05	Treg0/Treg1
Tgfb1	2.84E-09	0.623765	4.40E-05	Treg0/Treg1
Prpf19	2.87E-09	0.545813	4.45E-05	Treg0/Treg1
Timm17a	2.90E-09	0.582286	4.49E-05	Treg0/Treg1
Polr1a	2.93E-09	0.550294	4.54E-05	Treg0/Treg1
Psph	2.98E-09	0.636673	4.61E-05	Treg0/Treg1
Tomm70a	3.02E-09	0.602964	4.68E-05	Treg0/Treg1
Mtap	3.13E-09	0.565577	4.84E-05	Treg0/Treg1
Pgk1	3.16E-09	0.645532	4.90E-05	Treg0/Treg1
Pdcd1lg2	3.33E-09	0.480791	5.16E-05	Treg0/Treg1
Znrd2	3.88E-09	0.514547	6.01E-05	Treg0/Treg1
Nle1	4.15E-09	0.494606	6.42E-05	Treg0/Treg1
Alkbh1	4.16E-09	0.55612	6.44E-05	Treg0/Treg1
Uqcrq	4.45E-09	0.66095	6.89E-05	Treg0/Treg1
Utp14a	4.47E-09	0.551985	6.92E-05	Treg0/Treg1
Scyl2	4.57E-09	0.540405	7.07E-05	Treg0/Treg1
Ddx10	4.71E-09	0.572245	7.29E-05	Treg0/Treg1

Nop2	4.80E-09	0.525456	7.43E-05	Treg0/Treg1
Irf2bp2	4.80E-09	0.662936	7.44E-05	Treg0/Treg1
Pck2	5.15E-09	0.505994	7.96E-05	Treg0/Treg1
Tsr1	5.16E-09	0.397402	7.98E-05	Treg0/Treg1
Rela	5.58E-09	0.493748	8.64E-05	Treg0/Treg1
Serp1	5.65E-09	0.555457	8.75E-05	Treg0/Treg1
Psme3	5.73E-09	0.508174	8.86E-05	Treg0/Treg1
Fosl2	5.80E-09	0.681049	8.97E-05	Treg0/Treg1
Rnps1	5.84E-09	0.561722	9.04E-05	Treg0/Treg1
Utp15	6.05E-09	0.469338	9.36E-05	Treg0/Treg1
Phb	6.05E-09	0.631733	9.37E-05	Treg0/Treg1
Rpl7l1	6.09E-09	0.542701	9.43E-05	Treg0/Treg1
Mrfap1	6.12E-09	0.550038	9.46E-05	Treg0/Treg1
Ipo5	6.26E-09	0.609105	9.68E-05	Treg0/Treg1
Luc7l	6.68E-09	0.519437	0.000103	Treg0/Treg1
Noc3l	6.73E-09	0.544988	0.000104	Treg0/Treg1
Fcf1	6.77E-09	0.405184	0.000105	Treg0/Treg1
Hnrnpf	6.84E-09	0.413867	0.000106	Treg0/Treg1
Cldnd1	6.91E-09	0.811184	0.000107	Treg0/Treg1
Ccdc86	6.94E-09	0.573177	0.000107	Treg0/Treg1
Ndufab1	7.14E-09	0.570803	0.000111	Treg0/Treg1
Ruvbl2	7.44E-09	0.484292	0.000115	Treg0/Treg1
Usp10	7.47E-09	0.465482	0.000116	Treg0/Treg1
Fam136a	7.88E-09	0.545036	0.000122	Treg0/Treg1
Uchl3	7.94E-09	0.495212	0.000123	Treg0/Treg1
Bola2	8.10E-09	0.595687	0.000125	Treg0/Treg1
Ywhag	8.49E-09	0.539505	0.000131	Treg0/Treg1
Gm47283	9.33E-09	0.690825	0.000144	Treg0/Treg1
Herpud1	9.45E-09	0.569591	0.000146	Treg0/Treg1
Dusp5	9.64E-09	0.835305	0.000149	Treg0/Treg1
Prmt7	9.93E-09	0.415446	0.000154	Treg0/Treg1
Ppp1r11	1.03E-08	0.546382	0.00016	Treg0/Treg1
Yars	1.10E-08	0.489009	0.00017	Treg0/Treg1
Morf4l2	1.12E-08	0.496875	0.000173	Treg0/Treg1
Eif2b3	1.22E-08	0.488385	0.000189	Treg0/Treg1
Ccnd2	1.25E-08	0.713128	0.000193	Treg0/Treg1
Slc19a1	1.32E-08	0.410836	0.000204	Treg0/Treg1
Naa15	1.33E-08	0.565113	0.000206	Treg0/Treg1
Snhg6	1.33E-08	0.671347	0.000206	Treg0/Treg1
Colgalt1	1.41E-08	0.459179	0.000218	Treg0/Treg1
Txnl1	1.45E-08	0.445832	0.000224	Treg0/Treg1
Uck2	1.47E-08	0.513777	0.000228	Treg0/Treg1
Ywhae	1.54E-08	0.437145	0.000238	Treg0/Treg1
Bccip	1.65E-08	0.533177	0.000255	Treg0/Treg1
Ctps	1.65E-08	0.47719	0.000255	Treg0/Treg1

Actg1	1.68E-08	0.620908	0.00026	Treg0/Treg1
Itgb1	1.70E-08	0.503305	0.000263	Treg0/Treg1
C9orf72	1.71E-08	0.443632	0.000265	Treg0/Treg1
Rad23b	1.76E-08	0.528695	0.000272	Treg0/Treg1
Sumo2	1.81E-08	0.53106	0.00028	Treg0/Treg1
Btg3	1.96E-08	0.511085	0.000303	Treg0/Treg1
Utp3	1.97E-08	0.499147	0.000306	Treg0/Treg1
Polr2k	2.01E-08	0.517291	0.00031	Treg0/Treg1
Snrpd3	2.11E-08	0.543822	0.000326	Treg0/Treg1
Ptbp1	2.18E-08	0.507122	0.000338	Treg0/Treg1
Dis3	2.27E-08	0.524529	0.000351	Treg0/Treg1
D16Ertd472e	2.38E-08	0.616661	0.000368	Treg0/Treg1
Srrm2	2.38E-08	0.419908	0.000369	Treg0/Treg1
Naa20	2.56E-08	0.509573	0.000396	Treg0/Treg1
Abcf2	2.56E-08	0.502393	0.000396	Treg0/Treg1
Cdk4	2.64E-08	0.506253	0.000409	Treg0/Treg1
Psmc5	2.70E-08	0.495394	0.000418	Treg0/Treg1
Tcof1	2.75E-08	0.574921	0.000425	Treg0/Treg1
Wdr36	2.86E-08	0.498441	0.000443	Treg0/Treg1
Uap1	2.89E-08	0.450718	0.000447	Treg0/Treg1
Cd5	3.03E-08	0.684752	0.000469	Treg0/Treg1
Trmt61a	3.04E-08	0.446638	0.00047	Treg0/Treg1
Pus7	3.15E-08	0.431514	0.000487	Treg0/Treg1
Bysl	3.15E-08	0.401245	0.000488	Treg0/Treg1
Farsa	3.17E-08	0.466153	0.00049	Treg0/Treg1
Thumpd1	3.29E-08	0.511378	0.000509	Treg0/Treg1
Ube2m	3.29E-08	0.460668	0.00051	Treg0/Treg1
Cd3eap	3.31E-08	0.554006	0.000512	Treg0/Treg1
Sla	3.34E-08	0.682058	0.000517	Treg0/Treg1
Txn1	3.35E-08	0.694747	0.000519	Treg0/Treg1
Nfat5	3.53E-08	0.760174	0.000547	Treg0/Treg1
Cluh	3.69E-08	0.396623	0.000571	Treg0/Treg1
St6galnac4	3.86E-08	0.354442	0.000598	Treg0/Treg1
Kti12	3.88E-08	0.377314	0.0006	Treg0/Treg1
Mia2	3.90E-08	0.517473	0.000603	Treg0/Treg1
Pprc1	3.98E-08	0.40067	0.000617	Treg0/Treg1
Isy1	4.00E-08	0.842284	0.000619	Treg0/Treg1
Ube2j2	4.17E-08	0.450154	0.000646	Treg0/Treg1
Naa25	4.20E-08	0.467798	0.000649	Treg0/Treg1
Riox2	4.25E-08	0.530609	0.000658	Treg0/Treg1
Ube2e1	4.34E-08	0.506153	0.000672	Treg0/Treg1
Timm13	4.65E-08	0.500617	0.000719	Treg0/Treg1
Caprin1	4.76E-08	0.579483	0.000736	Treg0/Treg1
Alyref	4.79E-08	0.378898	0.000741	Treg0/Treg1
Sik3	4.93E-08	0.575243	0.000763	Treg0/Treg1

Dcun1d5	4.94E-08	0.47032	0.000764	Treg0/Treg1
Utp11	4.96E-08	0.503926	0.000767	Treg0/Treg1
Bcap29	5.10E-08	0.490028	0.000789	Treg0/Treg1
U2af1	5.34E-08	0.518334	0.000826	Treg0/Treg1
Ptprcap	5.35E-08	0.55477	0.000829	Treg0/Treg1
Ppid	5.37E-08	0.537532	0.000831	Treg0/Treg1
Psmd6	5.68E-08	0.444994	0.000879	Treg0/Treg1
Nom1	5.89E-08	0.486486	0.000912	Treg0/Treg1
2810004N23Rik	6.06E-08	0.532751	0.000938	Treg0/Treg1
Lrig1	6.16E-08	0.536307	0.000953	Treg0/Treg1
Ivns1abp	6.37E-08	0.463438	0.000985	Treg0/Treg1
Gart	6.40E-08	0.522271	0.000991	Treg0/Treg1
Slc26a2	6.95E-08	0.540629	0.001076	Treg0/Treg1
H3f3b	7.06E-08	0.446263	0.001093	Treg0/Treg1
Nudt5	7.07E-08	0.417399	0.001095	Treg0/Treg1
Prelid3b	7.32E-08	0.428716	0.001133	Treg0/Treg1
Pogk	7.36E-08	0.436744	0.001139	Treg0/Treg1
Rasa2	7.84E-08	0.546464	0.001213	Treg0/Treg1
Psma4	7.89E-08	0.508057	0.001221	Treg0/Treg1
2210016F16Rik	7.90E-08	0.51862	0.001223	Treg0/Treg1
M6pr	8.25E-08	0.508611	0.001277	Treg0/Treg1
Ddx3x	8.26E-08	0.50864	0.001278	Treg0/Treg1
Id2	8.28E-08	0.687643	0.001281	Treg0/Treg1
Snhg4	8.86E-08	0.516041	0.001372	Treg0/Treg1
Eif1ad	8.97E-08	0.436165	0.001388	Treg0/Treg1
Trac	9.06E-08	0.669934	0.001403	Treg0/Treg1
Heg1	9.40E-08	0.448606	0.001456	Treg0/Treg1
Zmynd19	9.46E-08	0.382084	0.001465	Treg0/Treg1
Lman2	9.55E-08	0.499935	0.001477	Treg0/Treg1
Ankrd11	9.65E-08	0.564422	0.001493	Treg0/Treg1
Metap2	9.67E-08	0.517875	0.001497	Treg0/Treg1
Ndufa12	9.93E-08	0.483253	0.001537	Treg0/Treg1
Lsm12	1.00E-07	0.472709	0.001552	Treg0/Treg1
Eif4g2	1.01E-07	0.521048	0.001557	Treg0/Treg1
Polr2l	1.05E-07	0.406995	0.001626	Treg0/Treg1
Ppie	1.07E-07	0.390013	0.001656	Treg0/Treg1
Utp6	1.14E-07	0.444327	0.00176	Treg0/Treg1
Tuba1c	1.15E-07	0.466091	0.001773	Treg0/Treg1
Nmd3	1.16E-07	0.530261	0.001793	Treg0/Treg1
Pole4	1.16E-07	0.516409	0.001799	Treg0/Treg1
Mrpl2	1.18E-07	0.401476	0.001823	Treg0/Treg1
Pitrm1	1.20E-07	0.369794	0.001857	Treg0/Treg1
Myo1e	1.21E-07	0.472297	0.001879	Treg0/Treg1
Pgam1	1.24E-07	0.432139	0.001912	Treg0/Treg1
Maf	1.25E-07	1.312816	0.001939	Treg0/Treg1

Cdc37	1.26E-07	0.492336	0.001947	Treg0/Treg1
Pomp	1.27E-07	0.576968	0.001964	Treg0/Treg1
Zfp706	1.28E-07	0.451158	0.001975	Treg0/Treg1
Senp6	1.49E-07	0.463629	0.002312	Treg0/Treg1
Lsg1	1.50E-07	0.43597	0.002317	Treg0/Treg1
Lonp1	1.52E-07	0.498266	0.002355	Treg0/Treg1
Mrps7	1.58E-07	0.456487	0.002444	Treg0/Treg1
Chd4	1.63E-07	0.450334	0.00252	Treg0/Treg1
Polr2h	1.66E-07	0.473797	0.002564	Treg0/Treg1
Rbm15	1.67E-07	0.391934	0.002584	Treg0/Treg1
Ncbp2	1.82E-07	0.397264	0.00282	Treg0/Treg1
Snrpd1	1.83E-07	0.563214	0.002826	Treg0/Treg1
Sfpq	1.86E-07	0.473471	0.002883	Treg0/Treg1
Rpl36al	1.89E-07	0.442536	0.00293	Treg0/Treg1
Dctpp1	1.93E-07	0.415266	0.002982	Treg0/Treg1
Kmt5a	2.04E-07	0.553318	0.003164	Treg0/Treg1
Erh	2.11E-07	0.435255	0.003271	Treg0/Treg1
Zfp507	2.12E-07	0.387907	0.003284	Treg0/Treg1
Dnajc1	2.23E-07	0.524318	0.003446	Treg0/Treg1
Mrpl17	2.32E-07	0.445912	0.00359	Treg0/Treg1
Sec31a	2.41E-07	0.461835	0.003727	Treg0/Treg1
Cyc1	2.47E-07	0.47312	0.003829	Treg0/Treg1
Mrpl54	2.56E-07	0.498365	0.003965	Treg0/Treg1
Psmb5	2.70E-07	0.511407	0.004173	Treg0/Treg1
Ptges3	2.70E-07	0.487152	0.004184	Treg0/Treg1
Glrx5	2.93E-07	0.440096	0.004538	Treg0/Treg1
Ubl4a	2.96E-07	0.403595	0.004586	Treg0/Treg1
Elavl1	3.07E-07	0.451754	0.004754	Treg0/Treg1
Phf10	3.10E-07	0.44187	0.0048	Treg0/Treg1
Psmg2	3.27E-07	0.439614	0.005061	Treg0/Treg1
Abcc1	3.29E-07	0.43947	0.005096	Treg0/Treg1
Psmd11	3.47E-07	0.486469	0.005366	Treg0/Treg1
Mrpl13	3.50E-07	0.399269	0.005419	Treg0/Treg1
Srfbp1	3.60E-07	0.365085	0.005572	Treg0/Treg1
Otud4	3.72E-07	0.376227	0.005764	Treg0/Treg1
Dars	3.78E-07	0.427544	0.005847	Treg0/Treg1
Kdelr2	3.78E-07	0.406718	0.00585	Treg0/Treg1
Dimt1	3.84E-07	0.344085	0.005944	Treg0/Treg1
Larp4	3.97E-07	0.478713	0.006145	Treg0/Treg1
Nucks1	4.19E-07	0.4652	0.006478	Treg0/Treg1
Gadd45gip1	4.22E-07	0.503361	0.006536	Treg0/Treg1
Slco3a1	4.44E-07	0.443939	0.006867	Treg0/Treg1
Sbno1	4.55E-07	0.428508	0.007046	Treg0/Treg1
Impdh2	4.58E-07	0.54247	0.007083	Treg0/Treg1
Psmg1	4.61E-07	0.319612	0.00713	Treg0/Treg1

Lcp2	4.61E-07	0.83797	0.007142	Treg0/Treg1
Rnf220	4.62E-07	0.427279	0.007155	Treg0/Treg1
Got1	4.76E-07	0.698489	0.007369	Treg0/Treg1
Psme1	4.83E-07	0.353407	0.007472	Treg0/Treg1
Ptp4a2	4.91E-07	0.451903	0.007605	Treg0/Treg1
Ube2s	5.04E-07	0.528018	0.007805	Treg0/Treg1
Pes1	5.35E-07	0.399262	0.008273	Treg0/Treg1
Mydgf	5.35E-07	0.450675	0.008276	Treg0/Treg1
Irak1	5.47E-07	0.384603	0.008469	Treg0/Treg1
Pus1	5.55E-07	0.372922	0.00859	Treg0/Treg1
Nab1	5.64E-07	0.406038	0.008733	Treg0/Treg1
Cacybp	5.98E-07	0.612142	0.009251	Treg0/Treg1
Dusp1	6.25E-07	0.57183	0.009669	Treg0/Treg1
Brix1	6.48E-07	0.470516	0.010031	Treg0/Treg1
Ppig	6.63E-07	0.420511	0.010261	Treg0/Treg1
Nfe2l1	6.78E-07	0.459257	0.010488	Treg0/Treg1
Cdk2ap1	6.81E-07	0.326541	0.010538	Treg0/Treg1
Lsm2	6.82E-07	0.474718	0.010551	Treg0/Treg1
Mrpl20	6.85E-07	0.482471	0.010604	Treg0/Treg1
Stx11	7.14E-07	0.57836	0.011046	Treg0/Treg1
Polr1d	7.14E-07	0.521344	0.011048	Treg0/Treg1
Mrps28	7.37E-07	0.41718	0.01141	Treg0/Treg1
Rhog	7.45E-07	0.453386	0.011536	Treg0/Treg1
Impdh1	7.53E-07	0.392641	0.011649	Treg0/Treg1
Umps	7.69E-07	0.390637	0.011903	Treg0/Treg1
Ddx54	7.77E-07	0.370942	0.012026	Treg0/Treg1
Dcaf13	7.99E-07	0.515181	0.012374	Treg0/Treg1
Rbm28	8.14E-07	0.391403	0.012592	Treg0/Treg1
Eif3i	8.30E-07	0.453248	0.012848	Treg0/Treg1
Cinp	8.32E-07	0.321876	0.012877	Treg0/Treg1
Ubfd1	8.37E-07	0.3411	0.012957	Treg0/Treg1
Paics	8.40E-07	0.370582	0.013007	Treg0/Treg1
9130401M01Rik	8.83E-07	0.381216	0.013668	Treg0/Treg1
Mtrex	8.89E-07	0.432659	0.013763	Treg0/Treg1
Nup98	8.95E-07	0.434398	0.013851	Treg0/Treg1
Tnf	9.02E-07	0.536341	0.013963	Treg0/Treg1
Exosc8	9.14E-07	0.407696	0.014152	Treg0/Treg1
Cab39	9.30E-07	0.340279	0.01439	Treg0/Treg1
Uqcc2	9.40E-07	0.385098	0.014556	Treg0/Treg1
Faim	9.58E-07	0.525896	0.014828	Treg0/Treg1
Psma3	9.61E-07	0.351445	0.014871	Treg0/Treg1
Slc41a1	9.66E-07	0.496295	0.014954	Treg0/Treg1
Dph5	9.80E-07	0.428212	0.015175	Treg0/Treg1
Pcgf6	9.91E-07	0.356435	0.015341	Treg0/Treg1
2410002F23Rik	9.93E-07	0.394152	0.015374	Treg0/Treg1

Mrpl33	1.01E-06	0.530661	0.015562	Treg0/Treg1
Dennd4a	1.02E-06	0.574873	0.015757	Treg0/Treg1
Pebp1	1.02E-06	0.516167	0.015838	Treg0/Treg1
Noc4l	1.03E-06	0.358457	0.015865	Treg0/Treg1
Bdp1	1.04E-06	0.48857	0.016119	Treg0/Treg1
Kars	1.04E-06	0.358393	0.016142	Treg0/Treg1
Ubxn2a	1.06E-06	0.395339	0.016443	Treg0/Treg1
Actl6a	1.09E-06	0.399276	0.016884	Treg0/Treg1
Rbmxl1	1.09E-06	0.439366	0.016885	Treg0/Treg1
Pkm	1.09E-06	0.462767	0.016907	Treg0/Treg1
Ubald2	1.10E-06	0.608185	0.016979	Treg0/Treg1
Tmem123	1.11E-06	0.477466	0.017134	Treg0/Treg1
Gid4	1.12E-06	0.306264	0.017339	Treg0/Treg1
Mthfd1	1.13E-06	0.321988	0.017448	Treg0/Treg1
Prdx1	1.15E-06	0.474104	0.017866	Treg0/Treg1
Metap1	1.20E-06	0.380778	0.018621	Treg0/Treg1
Exosc3	1.26E-06	0.445719	0.019431	Treg0/Treg1
D10Wsu102e	1.27E-06	0.501038	0.019686	Treg0/Treg1
Furin	1.28E-06	0.535711	0.01974	Treg0/Treg1
Uhrf1bp1l	1.29E-06	0.369041	0.019894	Treg0/Treg1
Atp2a2	1.29E-06	0.451111	0.019927	Treg0/Treg1
Aasdhppt	1.29E-06	0.389885	0.01996	Treg0/Treg1
Dad1	1.33E-06	0.436854	0.020509	Treg0/Treg1
Mob1b	1.37E-06	0.334038	0.021218	Treg0/Treg1
Slc5a3	1.39E-06	0.479658	0.021443	Treg0/Treg1
Traf4	1.42E-06	0.399982	0.021986	Treg0/Treg1
Ddx1	1.43E-06	0.36465	0.02211	Treg0/Treg1
Mrpl57	1.43E-06	0.483017	0.022152	Treg0/Treg1
Pfkp	1.46E-06	0.450409	0.022641	Treg0/Treg1
Carnmt1	1.55E-06	0.348285	0.023959	Treg0/Treg1
Stt3a	1.55E-06	0.483518	0.023983	Treg0/Treg1
Actr3	1.57E-06	0.461407	0.024342	Treg0/Treg1
Gpr18	1.61E-06	0.566144	0.024854	Treg0/Treg1
Zdhhc21	1.64E-06	0.370909	0.025444	Treg0/Treg1
Nsfl1c	1.66E-06	0.375359	0.025739	Treg0/Treg1
Tdg	1.70E-06	0.318593	0.026238	Treg0/Treg1
Polr1c	1.71E-06	0.368566	0.026477	Treg0/Treg1
Txn2	1.72E-06	0.470713	0.026649	Treg0/Treg1
Cyba	1.79E-06	0.571555	0.027726	Treg0/Treg1
Phf6	1.80E-06	0.386494	0.027794	Treg0/Treg1
Mars	1.88E-06	0.407954	0.029066	Treg0/Treg1
Dnajc2	1.89E-06	0.4305	0.029235	Treg0/Treg1
Rif1	1.90E-06	0.373192	0.029449	Treg0/Treg1
Ubxn4	1.92E-06	0.365733	0.029746	Treg0/Treg1
Hnrnpa3	1.93E-06	0.368021	0.029814	Treg0/Treg1

Vdac2	1.93E-06	0.430219	0.029859	Treg0/Treg1
Malt1	2.01E-06	0.535093	0.031103	Treg0/Treg1
Kpna3	2.01E-06	0.379159	0.031129	Treg0/Treg1
Rnf4	2.02E-06	0.367809	0.03119	Treg0/Treg1
Mbd3	2.10E-06	0.383151	0.032494	Treg0/Treg1
Mrpl35	2.15E-06	0.347774	0.033202	Treg0/Treg1
Exosc1	2.18E-06	0.426922	0.033703	Treg0/Treg1
Dnaja1	2.24E-06	0.47257	0.034626	Treg0/Treg1
Trnt1	2.25E-06	0.584	0.034852	Treg0/Treg1
Cdyl	2.26E-06	0.370797	0.035026	Treg0/Treg1
Ythdf1	2.27E-06	0.319132	0.035072	Treg0/Treg1
Cdk17	2.27E-06	0.412518	0.035177	Treg0/Treg1
Gtf2f1	2.28E-06	0.384428	0.035304	Treg0/Treg1
Npm3	2.40E-06	0.528631	0.037184	Treg0/Treg1
Tfam	2.44E-06	0.376056	0.037706	Treg0/Treg1
Ctsz	2.45E-06	0.41026	0.037983	Treg0/Treg1
Sf1	2.49E-06	0.452994	0.038503	Treg0/Treg1
Ak6	2.62E-06	0.446907	0.04056	Treg0/Treg1
Vapa	2.75E-06	0.398157	0.042551	Treg0/Treg1
Csnk2a1	2.76E-06	0.437736	0.042745	Treg0/Treg1
Lrrc59	2.78E-06	0.31528	0.043044	Treg0/Treg1
Iscu	2.94E-06	0.428799	0.045579	Treg0/Treg1
Aimp2	2.95E-06	0.34093	0.045704	Treg0/Treg1
Psma5	2.96E-06	0.475976	0.045762	Treg0/Treg1
Nfil3	2.96E-06	0.457419	0.045764	Treg0/Treg1
Twistnb	3.12E-06	0.472756	0.048249	Treg0/Treg1
Sec61a1	3.17E-06	0.323851	0.049039	Treg0/Treg1
Trmt1	3.28E-06	0.41544	0.050714	Treg0/Treg1
Adipor2	3.28E-06	0.410641	0.050842	Treg0/Treg1
Leo1	3.33E-06	0.413543	0.051505	Treg0/Treg1
Idh3a	3.56E-06	0.309555	0.055109	Treg0/Treg1
Gorasp2	3.74E-06	0.391589	0.057824	Treg0/Treg1
Sec13	3.80E-06	0.336455	0.058883	Treg0/Treg1
Jagn1	3.81E-06	0.325962	0.058936	Treg0/Treg1
2900097C17Rik	3.84E-06	0.392663	0.059489	Treg0/Treg1
Prkar1a	3.88E-06	0.472021	0.060036	Treg0/Treg1
Map4k1	4.02E-06	0.371984	0.062176	Treg0/Treg1
Clpp	4.15E-06	0.385615	0.064231	Treg0/Treg1
Larp1	4.26E-06	0.483273	0.065938	Treg0/Treg1
Hnrnpk	4.29E-06	0.316492	0.066392	Treg0/Treg1
Mfsd14a	4.40E-06	0.293595	0.068109	Treg0/Treg1
Erg28	4.40E-06	0.361633	0.068109	Treg0/Treg1
Ak2	4.40E-06	0.515904	0.068172	Treg0/Treg1
Ighm	4.46E-06	1.07367	0.069048	Treg0/Treg1
Tm2d1	4.70E-06	0.393787	0.072781	Treg0/Treg1

Spata5	4.78E-06	0.38454	0.074024	Treg0/Treg1
Hsd17b12	4.89E-06	0.347774	0.075687	Treg0/Treg1
Psmb4	4.99E-06	0.39088	0.077248	Treg0/Treg1
Pdcd5	5.00E-06	0.42994	0.07744	Treg0/Treg1
Utp25	5.07E-06	0.282274	0.078464	Treg0/Treg1
Krtcap2	5.10E-06	0.470513	0.078968	Treg0/Treg1
Usp1	5.26E-06	0.415632	0.08145	Treg0/Treg1
Lzic	5.37E-06	0.384928	0.083041	Treg0/Treg1
Pou2f2	5.42E-06	0.510571	0.083893	Treg0/Treg1
Ehd1	5.51E-06	0.39448	0.085317	Treg0/Treg1
Sf3a1	5.56E-06	0.29667	0.086132	Treg0/Treg1
Mrps14	5.63E-06	0.392145	0.087082	Treg0/Treg1
Selenos	5.69E-06	0.424734	0.08803	Treg0/Treg1
Tuba4a	5.75E-06	0.388138	0.08902	Treg0/Treg1
Sinhcaf	5.82E-06	0.366288	0.090111	Treg0/Treg1
Nkapd1	5.92E-06	0.386679	0.091646	Treg0/Treg1
Top1	6.22E-06	0.432314	0.096293	Treg0/Treg1
Mrpl52	6.28E-06	0.461495	0.097167	Treg0/Treg1
Rpia	6.28E-06	0.330445	0.097271	Treg0/Treg1
Adsl	6.88E-06	0.357488	0.106534	Treg0/Treg1
Rps12	6.99E-06	0.272543	0.108122	Treg0/Treg1
Anapc16	7.07E-06	0.333616	0.109364	Treg0/Treg1
Dnajc15	7.11E-06	0.319062	0.110093	Treg0/Treg1
Psmb7	7.17E-06	0.394829	0.110999	Treg0/Treg1
Rap1b	7.80E-06	0.411333	0.120748	Treg0/Treg1
Psma6	8.12E-06	0.335875	0.125738	Treg0/Treg1
Sugt1	8.12E-06	0.393891	0.125748	Treg0/Treg1
Prpf38a	8.14E-06	0.336748	0.125926	Treg0/Treg1
Dusp4	8.35E-06	0.436078	0.129185	Treg0/Treg1
Cops7a	8.36E-06	0.356685	0.129439	Treg0/Treg1
Nob1	8.60E-06	0.361102	0.133145	Treg0/Treg1
Tagln2	8.62E-06	0.422063	0.133384	Treg0/Treg1
Ptpn6	9.05E-06	0.421996	0.140149	Treg0/Treg1
Arhgef3	9.17E-06	0.39875	0.141986	Treg0/Treg1
Il2ra	9.23E-06	0.495375	0.142792	Treg0/Treg1
Ubb	9.26E-06	0.283117	0.143345	Treg0/Treg1
Mrpl51	9.42E-06	0.320452	0.145841	Treg0/Treg1
Szrd1	9.57E-06	0.289911	0.148056	Treg0/Treg1
Seh1l	9.73E-06	0.379756	0.150628	Treg0/Treg1
Snrpd2	9.89E-06	0.40717	0.153039	Treg0/Treg1
Ociad1	9.99E-06	0.348421	0.154596	Treg0/Treg1
Gnl1	1.00E-05	0.349196	0.15511	Treg0/Treg1
Lrrc32	1.01E-05	0.49832	0.155803	Treg0/Treg1
Lman1	1.02E-05	0.346087	0.157293	Treg0/Treg1
Ndufa5	1.02E-05	0.365442	0.158446	Treg0/Treg1

Cdc34	1.04E-05	0.334023	0.160922	Treg0/Treg1
Btf3	1.05E-05	0.339946	0.162031	Treg0/Treg1
Bag5	1.05E-05	0.33155	0.163013	Treg0/Treg1
Pfdn6	1.07E-05	0.401739	0.165151	Treg0/Treg1
Riox1	1.08E-05	0.287678	0.166935	Treg0/Treg1
Clec2d	1.10E-05	0.472189	0.1696	Treg0/Treg1
Trmt6	1.11E-05	0.460296	0.171957	Treg0/Treg1
Mrps23	1.13E-05	0.347716	0.175328	Treg0/Treg1
Dtymk	1.16E-05	0.378733	0.17964	Treg0/Treg1
Mrps18a	1.17E-05	0.363383	0.18098	Treg0/Treg1
Prpf31	1.17E-05	0.406667	0.181025	Treg0/Treg1
Thumpd3	1.18E-05	0.382861	0.182402	Treg0/Treg1
Sf3b4	1.18E-05	0.276862	0.182497	Treg0/Treg1
Hilpda	1.18E-05	0.435211	0.182706	Treg0/Treg1
Mrpl3	1.20E-05	0.29635	0.185287	Treg0/Treg1
Slc25a3	1.21E-05	0.429172	0.186669	Treg0/Treg1
Rpl22l1	1.23E-05	0.361731	0.189729	Treg0/Treg1
Serpinb6b	1.24E-05	0.49539	0.191179	Treg0/Treg1
Taf1d	1.25E-05	0.380613	0.193266	Treg0/Treg1
Cd6	1.25E-05	0.523363	0.19399	Treg0/Treg1
Ppil1	1.27E-05	0.35417	0.196181	Treg0/Treg1
Mif4gd	1.27E-05	0.488452	0.1972	Treg0/Treg1
Foxn2	1.29E-05	0.31086	0.199821	Treg0/Treg1
Lrpprc	1.31E-05	0.365538	0.202839	Treg0/Treg1
Il2rg	1.32E-05	0.437908	0.203966	Treg0/Treg1
Hdgfl3	1.41E-05	0.414045	0.218816	Treg0/Treg1
Sfr1	1.42E-05	0.418907	0.220241	Treg0/Treg1
Smn1	1.46E-05	0.35965	0.226143	Treg0/Treg1
Slc25a5	1.47E-05	0.452685	0.227844	Treg0/Treg1
Supt16	1.54E-05	0.361852	0.238848	Treg0/Treg1
Fasn	1.55E-05	0.315609	0.240214	Treg0/Treg1
Smarcc1	1.57E-05	0.399024	0.242778	Treg0/Treg1
Psmc1	1.59E-05	0.295547	0.246655	Treg0/Treg1
Emc4	1.64E-05	0.301884	0.253093	Treg0/Treg1
Rbis	1.65E-05	0.34262	0.254697	Treg0/Treg1
Rpf1	1.66E-05	0.336875	0.257631	Treg0/Treg1
Swap70	1.67E-05	0.553456	0.259125	Treg0/Treg1
Prpf8	1.73E-05	0.347197	0.267366	Treg0/Treg1
Nfatc1	1.74E-05	0.347814	0.269818	Treg0/Treg1
Fyttd1	1.75E-05	0.28628	0.270568	Treg0/Treg1
Rbm38	1.77E-05	0.25519	0.273807	Treg0/Treg1
Kpnb1	1.77E-05	0.387499	0.274097	Treg0/Treg1
Vcp	1.82E-05	0.354043	0.281647	Treg0/Treg1
Yif1b	1.86E-05	0.322988	0.287156	Treg0/Treg1
Pak1ip1	1.89E-05	0.40665	0.29272	Treg0/Treg1

Snx1	1.91E-05	0.274712	0.294904	Treg0/Treg1
Ahsa1	1.91E-05	0.398476	0.295701	Treg0/Treg1
Selenot	1.92E-05	0.412767	0.297173	Treg0/Treg1
Naa50	1.92E-05	0.329847	0.29772	Treg0/Treg1
Mrpl21	1.93E-05	0.36815	0.298938	Treg0/Treg1
Tmem167	1.95E-05	0.403533	0.301362	Treg0/Treg1
Pim1	2.01E-05	0.438167	0.311494	Treg0/Treg1
Stub1	2.06E-05	0.359033	0.318986	Treg0/Treg1
Abracl	2.07E-05	0.421191	0.320598	Treg0/Treg1
Pmepa1	2.16E-05	0.408902	0.334942	Treg0/Treg1
Srsf9	2.17E-05	0.314882	0.336051	Treg0/Treg1
Gata3	2.22E-05	0.59023	0.343252	Treg0/Treg1
Fkbp4	2.22E-05	0.389598	0.34374	Treg0/Treg1
1110038B12Rik	2.23E-05	0.379729	0.344872	Treg0/Treg1
Adrm1	2.23E-05	0.375035	0.345626	Treg0/Treg1
Arpp19	2.24E-05	0.349686	0.346341	Treg0/Treg1
Arf1	2.24E-05	0.37587	0.347192	Treg0/Treg1
Ubap2	2.28E-05	0.347593	0.352846	Treg0/Treg1
Chchd1	2.28E-05	0.406196	0.353194	Treg0/Treg1
Eftud2	2.31E-05	0.374253	0.357643	Treg0/Treg1
Eny2	2.33E-05	0.392722	0.359966	Treg0/Treg1
Med1	2.35E-05	0.260674	0.363604	Treg0/Treg1
Atad1	2.37E-05	0.36405	0.367212	Treg0/Treg1
Ube2a	2.39E-05	0.306636	0.36986	Treg0/Treg1
Srsf5	2.40E-05	0.327908	0.37091	Treg0/Treg1
Rpp14	2.42E-05	0.322887	0.374925	Treg0/Treg1
Knop1	2.43E-05	0.311297	0.375551	Treg0/Treg1
Farsb	2.52E-05	0.354097	0.390753	Treg0/Treg1
Agfg1	2.54E-05	0.424025	0.392576	Treg0/Treg1
S100a11	2.58E-05	0.669582	0.398665	Treg0/Treg1
Eif5	2.73E-05	0.392316	0.42239	Treg0/Treg1
Trim27	2.75E-05	0.27326	0.425375	Treg0/Treg1
Ilf3	2.80E-05	0.265229	0.432771	Treg0/Treg1
Tardbp	2.80E-05	0.326431	0.433419	Treg0/Treg1
Rrp8	2.90E-05	0.282446	0.44916	Treg0/Treg1
Arf4	2.94E-05	0.345613	0.45492	Treg0/Treg1
Usp14	2.95E-05	0.354268	0.457106	Treg0/Treg1
Parp1	2.96E-05	0.291257	0.458746	Treg0/Treg1
Fam104a	2.98E-05	0.342936	0.461296	Treg0/Treg1
Abcf1	3.02E-05	0.36102	0.468004	Treg0/Treg1
Ccdc50	3.03E-05	0.402976	0.469521	Treg0/Treg1
Tnpo1	3.14E-05	0.336697	0.485302	Treg0/Treg1
Thoc3	3.26E-05	0.329276	0.504786	Treg0/Treg1
Sde2	3.28E-05	0.342189	0.507486	Treg0/Treg1
Chordc1	3.30E-05	0.351684	0.511476	Treg0/Treg1

Snrpf	3.41E-05	0.326305	0.527839	Treg0/Treg1
Pfdn4	3.43E-05	0.311885	0.530787	Treg0/Treg1
Yae1d1	3.53E-05	0.313242	0.54684	Treg0/Treg1
Hdac2	3.56E-05	0.26359	0.55143	Treg0/Treg1
Glrx3	3.62E-05	0.409917	0.55978	Treg0/Treg1
Mphosph8	3.66E-05	0.355137	0.566103	Treg0/Treg1
Stoml2	3.67E-05	0.333293	0.568175	Treg0/Treg1
Chchd2	3.68E-05	0.321257	0.56982	Treg0/Treg1
Ncbp1	3.82E-05	0.310202	0.591976	Treg0/Treg1
Dennd5a	3.91E-05	0.419333	0.605827	Treg0/Treg1
Timm50	4.01E-05	0.326888	0.62054	Treg0/Treg1
Ssr4	4.08E-05	0.388283	0.631504	Treg0/Treg1
Ubqln1	4.20E-05	0.251916	0.650703	Treg0/Treg1
Ndufs8	4.21E-05	0.311839	0.651721	Treg0/Treg1
Zhx2	4.28E-05	0.329896	0.661728	Treg0/Treg1
Ndufb2	4.31E-05	0.306653	0.66636	Treg0/Treg1
Uqcrb	4.33E-05	0.406558	0.669804	Treg0/Treg1
Hdac7	4.38E-05	0.455465	0.678359	Treg0/Treg1
Ccdc124	4.42E-05	0.261089	0.684825	Treg0/Treg1
Clptm1l	4.45E-05	0.339382	0.688208	Treg0/Treg1
Eef1g	4.47E-05	0.353672	0.692611	Treg0/Treg1
Reps1	4.63E-05	0.381243	0.715903	Treg0/Treg1
Bmp2k	4.64E-05	0.402938	0.718918	Treg0/Treg1
Mrpl38	4.81E-05	0.28985	0.74467	Treg0/Treg1
Rab11fip1	4.90E-05	0.476108	0.759157	Treg0/Treg1
Psmc2	4.91E-05	0.326283	0.760025	Treg0/Treg1
Dennd2d	5.02E-05	0.312128	0.776398	Treg0/Treg1
Pdia6	5.14E-05	0.365672	0.795923	Treg0/Treg1
Ssbp1	5.14E-05	0.32738	0.796251	Treg0/Treg1
Timm44	5.26E-05	0.349209	0.813578	Treg0/Treg1
Ywhab	5.26E-05	0.327837	0.81488	Treg0/Treg1
Zfp52	5.31E-05	0.416754	0.822474	Treg0/Treg1
Ube2v2	5.36E-05	0.314867	0.830285	Treg0/Treg1
Ola1	5.50E-05	0.300716	0.851483	Treg0/Treg1
Tpr	5.60E-05	0.329578	0.86684	Treg0/Treg1
Ddx49	5.70E-05	0.280659	0.881949	Treg0/Treg1
Cfdp1	5.77E-05	0.286207	0.893788	Treg0/Treg1
Huwe1	5.79E-05	0.387392	0.896397	Treg0/Treg1
Zmiz2	5.91E-05	0.313373	0.915402	Treg0/Treg1
Ythdf2	5.96E-05	0.327387	0.923244	Treg0/Treg1
Pcna	5.97E-05	0.331171	0.924033	Treg0/Treg1
Nufip1	6.14E-05	0.340844	0.950261	Treg0/Treg1
Gramd1b	6.16E-05	0.361422	0.953776	Treg0/Treg1
Rybp	6.31E-05	0.33337	0.976308	Treg0/Treg1
Mafg	6.60E-05	0.379404	1	Treg0/Treg1

Arfrp1	6.63E-05	0.30657	1	Treg0/Treg1
Csrnp1	6.72E-05	0.317987	1	Treg0/Treg1
AI662270	6.77E-05	0.354603	1	Treg0/Treg1
9530068E07Rik	7.20E-05	0.294117	1	Treg0/Treg1
Snhg12	7.27E-05	0.456561	1	Treg0/Treg1
Nup54	7.37E-05	0.308712	1	Treg0/Treg1
Tkt	7.59E-05	0.378235	1	Treg0/Treg1
Lrrfip1	7.65E-05	0.46028	1	Treg0/Treg1
Wdr83os	7.69E-05	0.32941	1	Treg0/Treg1
Nudt4	7.76E-05	0.402585	1	Treg0/Treg1
Afg3l2	7.82E-05	0.305425	1	Treg0/Treg1
Ero1l	7.85E-05	0.378873	1	Treg0/Treg1
C1qtnf12	7.89E-05	0.425759	1	Treg0/Treg1
Tomm6	8.06E-05	0.374409	1	Treg0/Treg1
Ube2n	8.08E-05	0.303978	1	Treg0/Treg1
Mmadhc	8.51E-05	0.258123	1	Treg0/Treg1
Gps1	8.61E-05	0.283289	1	Treg0/Treg1
Mir17hg	8.62E-05	0.373478	1	Treg0/Treg1
Pgrmc2	8.67E-05	0.298762	1	Treg0/Treg1
Erap1	8.72E-05	0.345957	1	Treg0/Treg1
Smad7	8.74E-05	0.727821	1	Treg0/Treg1
Ube2i	8.87E-05	0.352285	1	Treg0/Treg1
Snx5	8.95E-05	0.326738	1	Treg0/Treg1
Atp5md	9.00E-05	0.36672	1	Treg0/Treg1
Tmem248	9.15E-05	0.286692	1	Treg0/Treg1
Bms1	9.20E-05	0.396625	1	Treg0/Treg1
Acsl4	9.34E-05	0.329465	1	Treg0/Treg1
Stk40	9.49E-05	0.377024	1	Treg0/Treg1
Tmpo	9.55E-05	0.461213	1	Treg0/Treg1
Dnajc8	9.67E-05	0.359851	1	Treg0/Treg1
Tpd52l2	9.71E-05	0.273706	1	Treg0/Treg1
Plcxd2	9.73E-05	0.397244	1	Treg0/Treg1
Stx6	9.78E-05	0.395518	1	Treg0/Treg1
Sh3bgrl	9.96E-05	0.520002	1	Treg0/Treg1
Sf3a2	9.99E-05	0.288191	1	Treg0/Treg1
Pin1	0.0001	0.33612	1	Treg0/Treg1
Arih2	0.000103	0.266223	1	Treg0/Treg1
Ahi1	0.000104	0.333608	1	Treg0/Treg1
Atp6v0b	0.000104	0.339377	1	Treg0/Treg1
Tespa1	0.000104	0.419825	1	Treg0/Treg1
A930024E05Rik	0.000106	0.274328	1	Treg0/Treg1
Ndufb7	0.000106	0.311849	1	Treg0/Treg1
Zdhhc5	0.000106	0.251037	1	Treg0/Treg1
BC005561	0.000107	0.273754	1	Treg0/Treg1
Krr1	0.000108	0.278316	1	Treg0/Treg1

Zranb2	0.000111	0.388957	1	Treg0/Treg1
Cox7a2	0.000111	0.347385	1	Treg0/Treg1
Bag1	0.000112	0.334678	1	Treg0/Treg1
Tiam1	0.000114	0.503038	1	Treg0/Treg1
Snrpb2	0.000116	0.282178	1	Treg0/Treg1
Zmpste24	0.000116	0.314822	1	Treg0/Treg1
Wdr3	0.000118	0.317006	1	Treg0/Treg1
Nol7	0.000118	0.336793	1	Treg0/Treg1
Rbm8a	0.000119	0.328958	1	Treg0/Treg1
Rock2	0.000119	0.284827	1	Treg0/Treg1
Dnttip2	0.000119	0.362944	1	Treg0/Treg1
Rbm34	0.000121	0.350447	1	Treg0/Treg1
Nasp	0.000128	0.298553	1	Treg0/Treg1
Trappc4	0.00013	0.276596	1	Treg0/Treg1
Cmtm7	0.000131	0.384671	1	Treg0/Treg1
Gfer	0.000133	0.262976	1	Treg0/Treg1
Atp5g3	0.000137	0.358309	1	Treg0/Treg1
Zbtb11	0.000139	0.292522	1	Treg0/Treg1
Ndufaf8	0.00014	0.28491	1	Treg0/Treg1
Psmd7	0.000142	0.314071	1	Treg0/Treg1
Cebpg	0.000142	0.250205	1	Treg0/Treg1
Clcn3	0.000143	0.304202	1	Treg0/Treg1
Pitpna	0.000143	0.281913	1	Treg0/Treg1
Cox17	0.000144	0.406959	1	Treg0/Treg1
Uqcrc1	0.000144	0.339833	1	Treg0/Treg1
Bloc1s2	0.000146	0.305934	1	Treg0/Treg1
Trp53	0.000146	0.341609	1	Treg0/Treg1
Mrps10	0.000147	0.302503	1	Treg0/Treg1
Rdx	0.000151	0.280383	1	Treg0/Treg1
Psmd14	0.000153	0.308758	1	Treg0/Treg1
Rpap3	0.000154	0.316958	1	Treg0/Treg1
Klhdc4	0.000161	0.2741	1	Treg0/Treg1
Aqr	0.000161	0.347845	1	Treg0/Treg1
Amd1	0.000165	0.294585	1	Treg0/Treg1
Aldh18a1	0.000168	0.293977	1	Treg0/Treg1
Ap1ar	0.000169	0.266037	1	Treg0/Treg1
Aig1	0.000172	0.28207	1	Treg0/Treg1
2310001H17Rik	0.000174	0.33869	1	Treg0/Treg1
Mgat2	0.000175	0.329334	1	Treg0/Treg1
Sdhaf1	0.000175	0.321997	1	Treg0/Treg1
Wdr1	0.000177	0.374526	1	Treg0/Treg1
Pitpnb	0.000185	0.293362	1	Treg0/Treg1
Hnrnpdl	0.000187	0.277384	1	Treg0/Treg1
Ahcyl1	0.000187	0.295871	1	Treg0/Treg1
Parl	0.000188	0.272385	1	Treg0/Treg1

Ndufb9	0.000192	0.292103	1	Treg0/Treg1
Usp24	0.000193	0.263461	1	Treg0/Treg1
Azin1	0.000195	0.268677	1	Treg0/Treg1
Gabpb1	0.000199	0.424123	1	Treg0/Treg1
Prmt5	0.000203	0.255892	1	Treg0/Treg1
Qdpr	0.000205	0.288848	1	Treg0/Treg1
Slfn2	0.000207	0.537546	1	Treg0/Treg1
Ddb1	0.000209	0.408931	1	Treg0/Treg1
Trim28	0.000221	0.266233	1	Treg0/Treg1
Stat3	0.000223	0.485421	1	Treg0/Treg1
Dock10	0.000226	0.314536	1	Treg0/Treg1
Wdr61	0.000229	0.261747	1	Treg0/Treg1
Atp6v0c	0.00024	0.360747	1	Treg0/Treg1
Eif2s3x	0.000242	0.250957	1	Treg0/Treg1
Polr2b	0.000244	0.352068	1	Treg0/Treg1
Ankib1	0.000245	0.348489	1	Treg0/Treg1
Higd1a	0.000247	0.292839	1	Treg0/Treg1
Trim44	0.000248	0.295013	1	Treg0/Treg1
Ccdc9	0.000248	0.320472	1	Treg0/Treg1
Mesd	0.00025	0.273829	1	Treg0/Treg1
Slc25a1	0.000254	0.363859	1	Treg0/Treg1
Mrps5	0.000256	0.273136	1	Treg0/Treg1
Mta1	0.000275	0.284893	1	Treg0/Treg1
Psmg4	0.000276	0.414358	1	Treg0/Treg1
Hnrnpr	0.000284	0.307157	1	Treg0/Treg1
Tgs1	0.000295	0.289623	1	Treg0/Treg1
Lsm7	0.000297	0.340752	1	Treg0/Treg1
Zcrb1	0.000301	0.262995	1	Treg0/Treg1
Nampt	0.000302	0.374479	1	Treg0/Treg1
Dhx15	0.000313	0.33811	1	Treg0/Treg1
Rwdd1	0.000314	0.322441	1	Treg0/Treg1
Actb	0.000314	0.296386	1	Treg0/Treg1
Dcun1d1	0.000319	0.28772	1	Treg0/Treg1
Clns1a	0.000322	0.257937	1	Treg0/Treg1
Ubc	0.000323	0.348231	1	Treg0/Treg1
Psmd1	0.000333	0.276675	1	Treg0/Treg1
Bax	0.000335	0.390076	1	Treg0/Treg1
Htatsf1	0.000336	0.28965	1	Treg0/Treg1
Creb1	0.00034	0.410762	1	Treg0/Treg1
Tet2	0.00034	0.378559	1	Treg0/Treg1
Mapkapk3	0.000342	0.253805	1	Treg0/Treg1
Rest	0.000344	0.265722	1	Treg0/Treg1
Sar1a	0.00035	0.376214	1	Treg0/Treg1
Tgoln1	0.000351	0.26611	1	Treg0/Treg1
Mdh2	0.000354	0.378972	1	Treg0/Treg1

Tmem243	0.000357	0.35538	1	Treg0/Treg1
Ttc1	0.000359	0.28174	1	Treg0/Treg1
Smap2	0.000368	0.322226	1	Treg0/Treg1
Gm16286	0.000371	0.303456	1	Treg0/Treg1
Ccdc115	0.000374	0.269753	1	Treg0/Treg1
Rrp7a	0.00038	0.259368	1	Treg0/Treg1
Rwdd4a	0.000383	0.264042	1	Treg0/Treg1
Bzw2	0.000386	0.326998	1	Treg0/Treg1
Cltc	0.00039	0.281267	1	Treg0/Treg1
Zap70	0.000394	0.358147	1	Treg0/Treg1
Stk11	0.000397	0.305717	1	Treg0/Treg1
Eif4h	0.000399	0.318276	1	Treg0/Treg1
Sh2d2a	0.000401	0.399198	1	Treg0/Treg1
Zfr	0.000402	0.302148	1	Treg0/Treg1
Wbp4	0.000404	0.328308	1	Treg0/Treg1
Emc7	0.000405	0.292192	1	Treg0/Treg1
Slc38a2	0.000409	0.282551	1	Treg0/Treg1
Gapdh	0.000414	0.372759	1	Treg0/Treg1
Itgb8	0.000417	0.419954	1	Treg0/Treg1
Gtf2f2	0.000422	0.274231	1	Treg0/Treg1
Srsf1	0.00043	0.330076	1	Treg0/Treg1
Edf1	0.000437	0.300441	1	Treg0/Treg1
Tra2b	0.000437	0.305053	1	Treg0/Treg1
Lsm6	0.000444	0.353915	1	Treg0/Treg1
Ubap2l	0.000445	0.329456	1	Treg0/Treg1
Thap2	0.000449	0.389599	1	Treg0/Treg1
Eif3d	0.000455	0.491728	1	Treg0/Treg1
Fyn	0.000467	0.353571	1	Treg0/Treg1
Gpr65	0.000469	0.258458	1	Treg0/Treg1
Dda1	0.000474	0.25088	1	Treg0/Treg1
Ddx24	0.000493	0.290457	1	Treg0/Treg1
Dhx36	0.000496	0.289536	1	Treg0/Treg1
Gng5	0.000537	0.325639	1	Treg0/Treg1
Snrpe	0.000573	0.265844	1	Treg0/Treg1
Psmd8	0.000575	0.27931	1	Treg0/Treg1
Txlna	0.000591	0.250872	1	Treg0/Treg1
Fkbp3	0.000596	0.382097	1	Treg0/Treg1
Prrc2a	0.000603	0.308326	1	Treg0/Treg1
Ddx39b	0.00061	0.315509	1	Treg0/Treg1
Ranbp2	0.000613	0.29503	1	Treg0/Treg1
Ier2	0.000621	0.498638	1	Treg0/Treg1
Ptpn7	0.000627	0.25466	1	Treg0/Treg1
Thy1	0.000642	0.298571	1	Treg0/Treg1
Pla2g12a	0.000656	0.335838	1	Treg0/Treg1
Ogfr	0.000675	0.267488	1	Treg0/Treg1

Morf4l1	0.000692	0.314799	1	Treg0/Treg1
Grb2	0.000696	0.269276	1	Treg0/Treg1
Ncoa7	0.000696	0.832848	1	Treg0/Treg1
Sap18	0.000699	0.306899	1	Treg0/Treg1
Nfkbiz	0.000702	0.270947	1	Treg0/Treg1
Srpr	0.000729	0.292097	1	Treg0/Treg1
Gcn1	0.000746	0.343987	1	Treg0/Treg1
Zfp445	0.000752	0.299703	1	Treg0/Treg1
Arhgap5	0.000758	0.254865	1	Treg0/Treg1
Col4a3bp	0.000762	0.266135	1	Treg0/Treg1
Eml4	0.000769	0.344204	1	Treg0/Treg1
Desi2	0.000786	0.269457	1	Treg0/Treg1
Mrpl42	0.0008	0.295886	1	Treg0/Treg1
Trps1	0.000803	0.274438	1	Treg0/Treg1
Rad23a	0.000806	0.334012	1	Treg0/Treg1
Bsg	0.000845	0.274718	1	Treg0/Treg1
Papola	0.000881	0.283891	1	Treg0/Treg1
Tm9sf2	0.000901	0.279303	1	Treg0/Treg1
Lat	0.000903	0.401913	1	Treg0/Treg1
Bri3	0.000905	0.338771	1	Treg0/Treg1
Zfp131	0.00092	0.263867	1	Treg0/Treg1
Pom121	0.000949	0.25415	1	Treg0/Treg1
Ube2v1	0.000952	0.269082	1	Treg0/Treg1
Bop1	0.001038	0.250305	1	Treg0/Treg1
Ankrd13c	0.001057	0.263459	1	Treg0/Treg1
Nop10	0.0011	0.340793	1	Treg0/Treg1
Rbm26	0.00113	0.271568	1	Treg0/Treg1
Atic	0.001132	0.252268	1	Treg0/Treg1
Sec22b	0.001162	0.272342	1	Treg0/Treg1
Brd2	0.001168	0.298969	1	Treg0/Treg1
Micos10	0.001196	0.27669	1	Treg0/Treg1
Ewsr1	0.001205	0.285672	1	Treg0/Treg1
Psmb3	0.001215	0.267624	1	Treg0/Treg1
Rtcb	0.001234	0.289356	1	Treg0/Treg1
Zwint	0.001277	0.265039	1	Treg0/Treg1
Ets2	0.00131	0.253933	1	Treg0/Treg1
Dpm2	0.001314	0.275382	1	Treg0/Treg1
Erp44	0.001436	0.28452	1	Treg0/Treg1
Arglu1	0.001563	0.252001	1	Treg0/Treg1
Znrd1	0.001598	0.262853	1	Treg0/Treg1
Capzb	0.00161	0.301031	1	Treg0/Treg1
Eif4a3	0.001631	0.255288	1	Treg0/Treg1
Pcgf5	0.001662	0.31153	1	Treg0/Treg1
Psmd4	0.001664	0.259098	1	Treg0/Treg1
Il21r	0.00168	0.283313	1	Treg0/Treg1

Rbm25	0.001695	0.260491	1	Treg0/Treg1
Pbdc1	0.00172	0.281845	1	Treg0/Treg1
Pabpn1	0.001738	0.285233	1	Treg0/Treg1
Larp7	0.001749	0.264372	1	Treg0/Treg1
Tomm5	0.001834	0.399747	1	Treg0/Treg1
Rraga	0.001847	0.250396	1	Treg0/Treg1
Gnb1	0.001885	0.253033	1	Treg0/Treg1
Hprt	0.001945	0.279246	1	Treg0/Treg1
Baz1b	0.00195	0.326827	1	Treg0/Treg1
Vps35	0.002011	0.252353	1	Treg0/Treg1
Cyp51	0.002017	0.326627	1	Treg0/Treg1
Dynll1	0.002019	0.270332	1	Treg0/Treg1
Ifi27	0.002094	0.264373	1	Treg0/Treg1
Slc14a1	0.002146	0.2625	1	Treg0/Treg1
Fam49b	0.002169	0.259284	1	Treg0/Treg1
Vasp	0.002173	0.294518	1	Treg0/Treg1
Fam241a	0.002195	0.254568	1	Treg0/Treg1
Pum1	0.002329	0.284202	1	Treg0/Treg1
Crlf2	0.002344	0.25414	1	Treg0/Treg1
Tmed9	0.00235	0.260645	1	Treg0/Treg1
Gramd3	0.002398	0.311362	1	Treg0/Treg1
Ube2d3	0.002444	0.28969	1	Treg0/Treg1
Ap2b1	0.002542	0.25717	1	Treg0/Treg1
H13	0.002585	0.279921	1	Treg0/Treg1
Fip1l1	0.00263	0.28027	1	Treg0/Treg1
Tasor2	0.002636	0.340891	1	Treg0/Treg1
Rnf19b	0.002704	0.3612	1	Treg0/Treg1
Lmnb1	0.00283	0.259712	1	Treg0/Treg1
Bcl10	0.002945	0.270597	1	Treg0/Treg1
BC003965	0.002964	0.253514	1	Treg0/Treg1
Katna1	0.002985	0.276631	1	Treg0/Treg1
Cd164	0.003153	0.257704	1	Treg0/Treg1
Hcls1	0.003302	0.29355	1	Treg0/Treg1
Tubb4b	0.003317	0.272452	1	Treg0/Treg1
Cd53	0.003415	0.264862	1	Treg0/Treg1
Ube2k	0.003421	0.274889	1	Treg0/Treg1
Samsn1	0.003439	0.281447	1	Treg0/Treg1
Zfc3h1	0.003592	0.260326	1	Treg0/Treg1
Tmem131l	0.003823	0.303195	1	Treg0/Treg1
Atp5j	0.003844	0.252598	1	Treg0/Treg1
Bclaf3	0.003849	0.256572	1	Treg0/Treg1
Gna13	0.003899	0.287248	1	Treg0/Treg1
Emg1	0.004093	0.264126	1	Treg0/Treg1
Prdx2	0.004491	0.267186	1	Treg0/Treg1
Ago2	0.004507	0.371574	1	Treg0/Treg1

Exoc3	0.00517	0.250216	1	Treg0/Treg1
D8Ertd738e	0.005402	0.253979	1	Treg0/Treg1
Rab10	0.005414	0.296293	1	Treg0/Treg1
Epb41	0.005715	0.334956	1	Treg0/Treg1
Tnfsf8	0.008407	0.824363	1	Treg0/Treg1
Prkca	0.008695	0.291037	1	Treg0/Treg1
Atxn2l	0.008707	0.292092	1	Treg0/Treg1
Sell	8.17E-47	2.186305	1.26E-42	Treg0/Treg1
Ms4a4b	4.59E-46	2.33617	7.11E-42	Treg0/Treg1
Samhd1	1.78E-42	1.881488	2.75E-38	Treg0/Treg1
Ms4a6b	8.03E-42	1.944982	1.24E-37	Treg0/Treg1
Itih5	2.26E-36	1.985036	3.49E-32	Treg0/Treg1
Txk	1.70E-35	1.90623	2.63E-31	Treg0/Treg1
Ecm1	2.74E-35	2.115111	4.24E-31	Treg0/Treg1
Klf2	3.93E-34	1.783168	6.09E-30	Treg0/Treg1
Fyb	3.16E-31	1.42384	4.90E-27	Treg0/Treg1
Rabgap1l	5.11E-31	1.725235	7.91E-27	Treg0/Treg1
Lef1	1.63E-29	1.480334	2.53E-25	Treg0/Treg1
Tmem64	4.13E-29	1.399503	6.39E-25	Treg0/Treg1
Gpr83	2.06E-28	1.83853	3.18E-24	Treg0/Treg1
Itm2b	3.78E-26	1.139569	5.85E-22	Treg0/Treg1
Tmsb10	9.63E-26	0.892623	1.49E-21	Treg0/Treg1
Itga6	1.61E-25	1.582217	2.49E-21	Treg0/Treg1
Fau	1.95E-25	0.556563	3.01E-21	Treg0/Treg1
Trpc4ap	1.08E-24	1.356521	1.67E-20	Treg0/Treg1
Ets1	1.10E-23	1.099702	1.70E-19	Treg0/Treg1
Nsd3	3.02E-23	1.0442	4.67E-19	Treg0/Treg1
Ifi27l2a	7.55E-23	1.020841	1.17E-18	Treg0/Treg1
Tmsb4x	9.01E-23	0.846328	1.39E-18	Treg0/Treg1
Cox7a2l	3.15E-22	1.073146	4.87E-18	Treg0/Treg1
Cytip	1.09E-21	1.041729	1.69E-17	Treg0/Treg1
Ftl1	1.41E-21	0.809069	2.19E-17	Treg0/Treg1
Rpl37a	1.26E-20	0.624658	1.94E-16	Treg0/Treg1
Foxn3	1.47E-20	1.2527	2.28E-16	Treg0/Treg1
Rpl39	2.16E-20	0.676574	3.35E-16	Treg0/Treg1
Rps21	1.49E-19	0.563766	2.31E-15	Treg0/Treg1
Cast	3.03E-19	1.138737	4.68E-15	Treg0/Treg1
H2-T23	5.03E-19	1.000521	7.78E-15	Treg0/Treg1
Atp1b1	6.66E-19	1.563777	1.03E-14	Treg0/Treg1
Ube2h	2.44E-18	1.048677	3.78E-14	Treg0/Treg1
S1pr1	3.00E-18	1.200231	4.65E-14	Treg0/Treg1
Rps24	3.62E-18	0.410416	5.61E-14	Treg0/Treg1
Rps11	3.66E-18	0.512282	5.67E-14	Treg0/Treg1
Tpt1	1.12E-17	0.376497	1.73E-13	Treg0/Treg1
Sipa1l1	1.28E-17	1.162526	1.98E-13	Treg0/Treg1

Ifngr1	2.29E-17	0.997615	3.54E-13	Treg0/Treg1
Pitpnc1	2.69E-17	1.090964	4.17E-13	Treg0/Treg1
Gm8369	7.68E-17	1.005148	1.19E-12	Treg0/Treg1
Patj	7.80E-17	1.030563	1.21E-12	Treg0/Treg1
Rpl13a	9.79E-17	0.40875	1.52E-12	Treg0/Treg1
Rpl27a	1.13E-16	0.461055	1.74E-12	Treg0/Treg1
Mcl1	1.13E-16	0.994982	1.75E-12	Treg0/Treg1
Ssh2	3.19E-16	0.91764	4.93E-12	Treg0/Treg1
Tecpr1	4.72E-16	1.112359	7.30E-12	Treg0/Treg1
Jun	8.72E-16	1.479655	1.35E-11	Treg0/Treg1
Tubgcp4	9.01E-16	1.00741	1.39E-11	Treg0/Treg1
Treml2	1.31E-15	0.950689	2.02E-11	Treg0/Treg1
Elovl6	2.16E-15	1.113278	3.34E-11	Treg0/Treg1
Ptpn18	2.16E-15	0.770844	3.34E-11	Treg0/Treg1
Rps16	2.31E-15	0.418027	3.58E-11	Treg0/Treg1
Rpl19	2.56E-15	0.330848	3.97E-11	Treg0/Treg1
Ahcyl2	2.76E-15	1.179139	4.27E-11	Treg0/Treg1
Pdia4	2.82E-15	0.992097	4.37E-11	Treg0/Treg1
Rps10	2.92E-15	0.40978	4.52E-11	Treg0/Treg1
Casp8	5.82E-15	1.043413	9.01E-11	Treg0/Treg1
Rps29	6.44E-15	0.392913	9.96E-11	Treg0/Treg1
Sp100	8.67E-15	1.004214	1.34E-10	Treg0/Treg1
Mllt3	8.69E-15	0.969893	1.35E-10	Treg0/Treg1
Rps15	9.33E-15	0.462655	1.44E-10	Treg0/Treg1
Gm26740	1.14E-14	1.077728	1.76E-10	Treg0/Treg1
Senp7	1.56E-14	0.996897	2.42E-10	Treg0/Treg1
Cnp	2.47E-14	0.787505	3.83E-10	Treg0/Treg1
Gpr146	3.89E-14	0.952276	6.02E-10	Treg0/Treg1
Ppm1l	4.08E-14	1.043811	6.31E-10	Treg0/Treg1
Psmb8	4.23E-14	0.723538	6.55E-10	Treg0/Treg1
Npc2	6.22E-14	0.938638	9.62E-10	Treg0/Treg1
Kat2b	9.50E-14	0.714192	1.47E-09	Treg0/Treg1
Rhoh	9.97E-14	0.828029	1.54E-09	Treg0/Treg1
Gbp2	1.07E-13	1.156262	1.65E-09	Treg0/Treg1
Akap13	1.50E-13	0.621196	2.32E-09	Treg0/Treg1
Ly6c1	1.62E-13	1.457018	2.51E-09	Treg0/Treg1
Rps27	1.77E-13	0.349268	2.74E-09	Treg0/Treg1
Ifi209	1.88E-13	1.09755	2.90E-09	Treg0/Treg1
Sh3bp5	2.12E-13	0.930557	3.29E-09	Treg0/Treg1
Tnrc6b	2.52E-13	0.940617	3.90E-09	Treg0/Treg1
Ssbp2	3.21E-13	1.082429	4.97E-09	Treg0/Treg1
Ift80	4.31E-13	0.820184	6.67E-09	Treg0/Treg1
Rpl18a	5.45E-13	0.38428	8.43E-09	Treg0/Treg1
Resf1	5.53E-13	1.068969	8.55E-09	Treg0/Treg1
Zscan29	6.03E-13	1.088963	9.34E-09	Treg0/Treg1

Bin2	6.14E-13	0.91663	9.50E-09	Treg0/Treg1
Tnks2	7.26E-13	1.021743	1.12E-08	Treg0/Treg1
Gm42418	8.81E-13	0.411736	1.36E-08	Treg0/Treg1
Ablim1	8.83E-13	1.029798	1.37E-08	Treg0/Treg1
Rgs1	8.86E-13	1.041813	1.37E-08	Treg0/Treg1
Rps14	8.92E-13	0.333899	1.38E-08	Treg0/Treg1
Mbd2	9.78E-13	0.810026	1.51E-08	Treg0/Treg1
Rps3	1.21E-12	0.367005	1.88E-08	Treg0/Treg1
Dgka	1.87E-12	0.872052	2.90E-08	Treg0/Treg1
Mtmr3	1.93E-12	0.933003	2.98E-08	Treg0/Treg1
Trib2	2.51E-12	0.904348	3.89E-08	Treg0/Treg1
S100a13	2.61E-12	1.057024	4.04E-08	Treg0/Treg1
Snap23	2.62E-12	1.059577	4.06E-08	Treg0/Treg1
Smchd1	2.79E-12	0.880557	4.32E-08	Treg0/Treg1
Arl6ip1	2.90E-12	0.65047	4.49E-08	Treg0/Treg1
Rps7	3.39E-12	0.385374	5.25E-08	Treg0/Treg1
Rpl9	4.19E-12	0.367757	6.49E-08	Treg0/Treg1
Arid4b	4.98E-12	1.012277	7.70E-08	Treg0/Treg1
Rpl30	8.29E-12	0.375694	1.28E-07	Treg0/Treg1
Tax1bp1	8.46E-12	0.86218	1.31E-07	Treg0/Treg1
Rpl27	9.34E-12	0.347882	1.45E-07	Treg0/Treg1
Pdcd4	9.69E-12	0.812624	1.50E-07	Treg0/Treg1
Rpl11	1.02E-11	0.359655	1.58E-07	Treg0/Treg1
Malat1	1.09E-11	0.384783	1.68E-07	Treg0/Treg1
Prkcq	1.63E-11	0.876043	2.52E-07	Treg0/Treg1
Slc12a6	1.82E-11	0.782181	2.82E-07	Treg0/Treg1
Dnah8	1.90E-11	0.821573	2.94E-07	Treg0/Treg1
Rnasel	1.90E-11	0.814262	2.95E-07	Treg0/Treg1
Wdr82	2.39E-11	0.931002	3.70E-07	Treg0/Treg1
Atp11b	2.55E-11	0.560693	3.95E-07	Treg0/Treg1
Hipk2	3.58E-11	0.921225	5.55E-07	Treg0/Treg1
AI480526	3.67E-11	0.887131	5.67E-07	Treg0/Treg1
Rpl17	4.76E-11	0.371797	7.37E-07	Treg0/Treg1
Arhgdib	5.40E-11	0.728804	8.35E-07	Treg0/Treg1
Nin	5.70E-11	0.904988	8.82E-07	Treg0/Treg1
Vim	6.62E-11	1.032459	1.02E-06	Treg0/Treg1
Zbp1	1.07E-10	0.869159	1.65E-06	Treg0/Treg1
Rps4x	1.22E-10	0.360124	1.88E-06	Treg0/Treg1
Ly6e	1.43E-10	0.566246	2.21E-06	Treg0/Treg1
Twf2	2.12E-10	0.918198	3.29E-06	Treg0/Treg1
Inpp4b	2.15E-10	0.792226	3.33E-06	Treg0/Treg1
Rps23	2.24E-10	0.276676	3.46E-06	Treg0/Treg1
Phc3	4.02E-10	0.907506	6.22E-06	Treg0/Treg1
H2-T22	4.90E-10	0.774157	7.58E-06	Treg0/Treg1
P2ry10	5.72E-10	0.691487	8.85E-06	Treg0/Treg1

Rasa3	5.86E-10	0.748288	9.07E-06	Treg0/Treg1
Arhgef18	6.03E-10	0.625106	9.34E-06	Treg0/Treg1
Cd27	7.49E-10	0.785623	1.16E-05	Treg0/Treg1
Sgpp1	7.50E-10	0.80416	1.16E-05	Treg0/Treg1
Bcl2	7.61E-10	0.666221	1.18E-05	Treg0/Treg1
Rps9	8.00E-10	0.354377	1.24E-05	Treg0/Treg1
Traf3ip3	9.70E-10	0.782653	1.50E-05	Treg0/Treg1
Vps37b	1.08E-09	0.554577	1.68E-05	Treg0/Treg1
Arid4a	1.27E-09	0.784919	1.97E-05	Treg0/Treg1
A930005H10Rik	1.33E-09	0.660904	2.06E-05	Treg0/Treg1
Gbp7	1.52E-09	0.692673	2.35E-05	Treg0/Treg1
Tmem71	1.52E-09	0.607643	2.36E-05	Treg0/Treg1
Ptprc	1.74E-09	0.577098	2.69E-05	Treg0/Treg1
Grap2	1.77E-09	0.597723	2.75E-05	Treg0/Treg1
Rps19	1.81E-09	0.372527	2.80E-05	Treg0/Treg1
Tbc1d4	1.97E-09	0.825802	3.05E-05	Treg0/Treg1
Mbnl1	2.14E-09	0.505736	3.32E-05	Treg0/Treg1
Bnip3l	2.22E-09	0.75384	3.43E-05	Treg0/Treg1
Stk38	3.00E-09	0.767308	4.64E-05	Treg0/Treg1
Rps13	3.07E-09	0.29347	4.75E-05	Treg0/Treg1
Clk1	3.59E-09	0.684222	5.56E-05	Treg0/Treg1
Utrn	3.68E-09	0.951331	5.70E-05	Treg0/Treg1
Cdk19	3.75E-09	0.736876	5.81E-05	Treg0/Treg1
Rpl38	8.12E-09	0.352622	0.000126	Treg0/Treg1
4930523C07Rik	1.03E-08	0.736724	0.000159	Treg0/Treg1
Slfn1	1.07E-08	0.702777	0.000165	Treg0/Treg1
Mov10	1.43E-08	0.64571	0.000221	Treg0/Treg1
Zfp652	1.49E-08	0.742537	0.000231	Treg0/Treg1
2810013P06Rik	1.76E-08	0.54115	0.000272	Treg0/Treg1
Foxp1	1.78E-08	0.715819	0.000276	Treg0/Treg1
Rpl10	1.85E-08	0.388008	0.000286	Treg0/Treg1
Nabp1	2.02E-08	0.567652	0.000312	Treg0/Treg1
Itgb7	2.14E-08	0.702025	0.00033	Treg0/Treg1
Pja1	2.23E-08	0.863916	0.000345	Treg0/Treg1
Mbnl3	2.55E-08	0.809075	0.000395	Treg0/Treg1
Crebrf	2.78E-08	0.709563	0.000431	Treg0/Treg1
Cd47	3.64E-08	0.551759	0.000563	Treg0/Treg1
Gm2682	4.18E-08	0.762009	0.000647	Treg0/Treg1
Ppp3ca	5.24E-08	0.785616	0.000811	Treg0/Treg1
Galnt6	5.84E-08	0.759022	0.000904	Treg0/Treg1
Fam102a	6.58E-08	0.731035	0.001019	Treg0/Treg1
Tmem50a	6.63E-08	0.595558	0.001026	Treg0/Treg1
Uqcrh	6.95E-08	0.553798	0.001075	Treg0/Treg1
Lyst	7.22E-08	0.742923	0.001117	Treg0/Treg1
P4ha1	8.96E-08	0.708142	0.001387	Treg0/Treg1

Samd9l	1.08E-07	0.756073	0.00167	Treg0/Treg1
Atox1	1.16E-07	0.717876	0.001789	Treg0/Treg1
Ltb	1.21E-07	0.433778	0.001872	Treg0/Treg1
Rpl13	1.23E-07	0.301589	0.001898	Treg0/Treg1
Iigp1	1.33E-07	0.655677	0.002053	Treg0/Treg1
Sec24a	1.33E-07	0.742641	0.002065	Treg0/Treg1
Rabac1	1.40E-07	0.594513	0.002168	Treg0/Treg1
Frat2	1.49E-07	0.538587	0.002307	Treg0/Treg1
9930111J21Rik2	1.66E-07	0.63013	0.002565	Treg0/Treg1
Ifi206	1.78E-07	0.598851	0.002751	Treg0/Treg1
Cyb5a	1.95E-07	0.671583	0.003014	Treg0/Treg1
Ifi47	1.98E-07	0.490357	0.003072	Treg0/Treg1
Tle5	2.09E-07	0.669471	0.003233	Treg0/Treg1
Trim12a	2.14E-07	0.57879	0.003311	Treg0/Treg1
Rpl21	2.21E-07	0.288984	0.003418	Treg0/Treg1
Myb	2.22E-07	0.964187	0.003431	Treg0/Treg1
Prrc2c	2.33E-07	0.646882	0.003612	Treg0/Treg1
Hmgb2	2.48E-07	0.731154	0.003845	Treg0/Treg1
Cdkn1b	2.69E-07	0.575401	0.00416	Treg0/Treg1
Supt4a	2.72E-07	0.578667	0.004207	Treg0/Treg1
Il2rb	3.16E-07	0.660897	0.004893	Treg0/Treg1
Neat1	3.20E-07	0.610859	0.004952	Treg0/Treg1
Ifi214	3.60E-07	0.690564	0.005566	Treg0/Treg1
Uba52	3.60E-07	0.403826	0.005572	Treg0/Treg1
Kmt2c	3.70E-07	0.757199	0.005731	Treg0/Treg1
Crybg1	3.84E-07	0.535905	0.00594	Treg0/Treg1
Etnk1	3.85E-07	0.704898	0.005954	Treg0/Treg1
Tspo	3.86E-07	0.580208	0.005971	Treg0/Treg1
Rpl23a	4.26E-07	0.306296	0.0066	Treg0/Treg1
Evl	4.74E-07	0.684854	0.007343	Treg0/Treg1
Rpl26	5.00E-07	0.253381	0.007736	Treg0/Treg1
Add1	5.04E-07	0.6459	0.007804	Treg0/Treg1
Cnot4	5.31E-07	0.719135	0.008213	Treg0/Treg1
Rps28	6.55E-07	0.305131	0.010135	Treg0/Treg1
Phf14	6.81E-07	0.642062	0.010539	Treg0/Treg1
Arnt	7.16E-07	0.664656	0.011075	Treg0/Treg1
Tnfrsf13b	8.64E-07	0.705424	0.013374	Treg0/Treg1
Gimap3	8.97E-07	0.488673	0.01388	Treg0/Treg1
Pfdn5	9.64E-07	0.382271	0.014928	Treg0/Treg1
BE692007	1.10E-06	0.553097	0.016969	Treg0/Treg1
Dcaf17	1.37E-06	0.844448	0.021152	Treg0/Treg1
Ms4a4c	1.37E-06	0.670699	0.021173	Treg0/Treg1
Klf3	1.71E-06	0.671416	0.026514	Treg0/Treg1
Ifi208	2.00E-06	0.626517	0.030915	Treg0/Treg1
Nek7	2.02E-06	0.572619	0.0313	Treg0/Treg1

Ypel3	2.33E-06	0.610059	0.036118	Treg0/Treg1
Crlf3	2.53E-06	0.696482	0.039213	Treg0/Treg1
Ezh2	2.72E-06	0.56885	0.042152	Treg0/Treg1
Usp3	2.86E-06	0.603756	0.04428	Treg0/Treg1
Ifi203	3.19E-06	0.58006	0.04931	Treg0/Treg1
Cwc15	3.20E-06	0.557083	0.049549	Treg0/Treg1
Mxd1	3.24E-06	0.598522	0.050212	Treg0/Treg1
Macf1	3.45E-06	0.632595	0.053468	Treg0/Treg1
Thap3	3.53E-06	0.585914	0.054585	Treg0/Treg1
Ccnd3	3.63E-06	0.636261	0.056202	Treg0/Treg1
Ankrd44	4.14E-06	0.554959	0.064132	Treg0/Treg1
Zfp36l2	4.23E-06	0.690047	0.065421	Treg0/Treg1
Gpsm3	5.12E-06	0.600955	0.079234	Treg0/Treg1
Smc4	5.78E-06	0.455842	0.089439	Treg0/Treg1
Irf7	6.11E-06	0.660124	0.094562	Treg0/Treg1
Ifit1	6.47E-06	0.56918	0.100161	Treg0/Treg1
Dtx3l	7.00E-06	0.625987	0.108394	Treg0/Treg1
Slamf6	7.15E-06	0.528449	0.110623	Treg0/Treg1
Mcub	9.33E-06	0.494127	0.144378	Treg0/Treg1
Irf2	1.03E-05	0.498418	0.159522	Treg0/Treg1
Shisa5	1.20E-05	0.359506	0.185923	Treg0/Treg1
Igtp	1.34E-05	0.485128	0.207679	Treg0/Treg1
Rasa1	1.38E-05	0.729432	0.213225	Treg0/Treg1
Foxp3	1.39E-05	0.422321	0.215238	Treg0/Treg1
Cd3d	1.46E-05	0.395915	0.225844	Treg0/Treg1
Eif3f	1.49E-05	0.489107	0.23085	Treg0/Treg1
Slc44a2	1.56E-05	0.505463	0.241703	Treg0/Treg1
Paip2	1.58E-05	0.557013	0.244504	Treg0/Treg1
Ralbp1	1.69E-05	0.510604	0.261117	Treg0/Treg1
Rnf167	1.69E-05	0.668166	0.261957	Treg0/Treg1
Bcl11b	1.74E-05	0.520101	0.269892	Treg0/Treg1
Hectd1	1.78E-05	0.533853	0.276022	Treg0/Treg1
Tut4	1.86E-05	0.529766	0.287365	Treg0/Treg1
Arl6ip5	1.95E-05	0.599676	0.301717	Treg0/Treg1
4930581F22Rik	2.04E-05	0.657585	0.31523	Treg0/Treg1
Mxd4	2.15E-05	0.54253	0.332725	Treg0/Treg1
Ube2d2a	2.16E-05	0.49056	0.334309	Treg0/Treg1
Rb1cc1	2.23E-05	0.598699	0.345471	Treg0/Treg1
Klhl24	2.35E-05	0.501773	0.363551	Treg0/Treg1
Arl4c	2.45E-05	0.547194	0.379714	Treg0/Treg1
Trbc2	2.46E-05	0.613613	0.380286	Treg0/Treg1
Arhgap15	2.46E-05	0.707811	0.381474	Treg0/Treg1
4932438A13Rik	2.49E-05	0.794071	0.385389	Treg0/Treg1
Chd3	2.63E-05	0.703885	0.406949	Treg0/Treg1
Gnai2	2.65E-05	0.437414	0.410799	Treg0/Treg1

Pum2	2.96E-05	0.556667	0.4587	Treg0/Treg1
Gbp5	3.02E-05	0.443044	0.467928	Treg0/Treg1
C2cd5	3.04E-05	0.483258	0.469969	Treg0/Treg1
Trim12c	3.18E-05	0.574653	0.491633	Treg0/Treg1
H2afv	3.20E-05	0.435041	0.495487	Treg0/Treg1
Cmtm6	3.23E-05	0.564348	0.500119	Treg0/Treg1
H2afy	3.24E-05	0.473223	0.502096	Treg0/Treg1
Ddx5	3.35E-05	0.274608	0.519025	Treg0/Treg1
Rapgef6	3.42E-05	0.506682	0.529716	Treg0/Treg1
Btg1	3.87E-05	0.312863	0.598814	Treg0/Treg1
Izumo1r	4.16E-05	0.63046	0.64435	Treg0/Treg1
Gimap1	4.21E-05	0.498914	0.651165	Treg0/Treg1
Gimap4	4.22E-05	0.311851	0.652981	Treg0/Treg1
Lsp1	4.88E-05	0.447407	0.756065	Treg0/Treg1
Cnst	5.05E-05	0.46033	0.782075	Treg0/Treg1
AY036118	5.33E-05	0.31385	0.825197	Treg0/Treg1
Gm20559	6.12E-05	0.586038	0.947259	Treg0/Treg1
Uqcc3	6.38E-05	0.590272	0.986862	Treg0/Treg1
Il4ra	6.38E-05	0.562391	0.987739	Treg0/Treg1
Elf1	7.11E-05	0.545792	1	Treg0/Treg1
Aven	7.25E-05	0.57815	1	Treg0/Treg1
Trim34a	7.82E-05	0.536188	1	Treg0/Treg1
Ubn1	7.95E-05	0.502551	1	Treg0/Treg1
Pcmtd2	8.68E-05	0.605404	1	Treg0/Treg1
Rsbn1l	9.68E-05	0.443453	1	Treg0/Treg1
Txnip	9.85E-05	0.480501	1	Treg0/Treg1
Tsc22d3	0.000108	0.495707	1	Treg0/Treg1
Ccs	0.00011	0.529928	1	Treg0/Treg1
Rap1gds1	0.000113	0.518649	1	Treg0/Treg1
Bach2	0.000115	0.492443	1	Treg0/Treg1
Ccdc82	0.000128	0.46538	1	Treg0/Treg1
Nt5e	0.000134	0.671266	1	Treg0/Treg1
Bptf	0.000142	0.406602	1	Treg0/Treg1
4833420G17Rik	0.000148	0.367298	1	Treg0/Treg1
Tuba1a	0.000148	0.427389	1	Treg0/Treg1
Arhgap45	0.00015	0.48172	1	Treg0/Treg1
Peli1	0.000156	0.41635	1	Treg0/Treg1
Msn	0.00017	0.361644	1	Treg0/Treg1
Kif21b	0.000176	0.50449	1	Treg0/Treg1
Wls	0.000182	0.595615	1	Treg0/Treg1
Stat2	0.000183	0.464895	1	Treg0/Treg1
Kmt2a	0.000187	0.376067	1	Treg0/Treg1
Gbp4	0.00019	0.322754	1	Treg0/Treg1
Mindy2	0.00019	0.453904	1	Treg0/Treg1
Ntan1	0.000239	0.473774	1	Treg0/Treg1

Rexo2	0.000242	0.481726	1	Treg0/Treg1
Emsy	0.000243	0.487317	1	Treg0/Treg1
Arhgef1	0.000271	0.538094	1	Treg0/Treg1
Rpl36a	0.000278	0.284774	1	Treg0/Treg1
Emp3	0.000281	0.361932	1	Treg0/Treg1
Crip1	0.000286	0.282109	1	Treg0/Treg1
Selplg	0.000323	0.435674	1	Treg0/Treg1
Zdhhc20	0.00033	0.491094	1	Treg0/Treg1
Rbms1	0.000344	0.510608	1	Treg0/Treg1
Rtp4	0.000348	0.417393	1	Treg0/Treg1
Cyth3	0.000351	0.482551	1	Treg0/Treg1
Arid5a	0.000377	0.54026	1	Treg0/Treg1
Setx	0.000384	0.536477	1	Treg0/Treg1
Acaa1a	0.000409	0.371356	1	Treg0/Treg1
Gbp3	0.000429	0.444165	1	Treg0/Treg1
S100a10	0.000455	0.310583	1	Treg0/Treg1
Pkn1	0.000457	0.53467	1	Treg0/Treg1
Phf20l1	0.000504	0.42556	1	Treg0/Treg1
Ndufa6	0.000506	0.417868	1	Treg0/Treg1
Mkln1	0.000536	0.547541	1	Treg0/Treg1
Ripor2	0.000537	0.482809	1	Treg0/Treg1
Osbpl9	0.000538	0.398525	1	Treg0/Treg1
Skap1	0.000549	0.445626	1	Treg0/Treg1
Cd3e	0.00056	0.418491	1	Treg0/Treg1
Helz	0.00063	0.521049	1	Treg0/Treg1
Cbx3	0.00063	0.395826	1	Treg0/Treg1
Sesn3	0.000669	0.620844	1	Treg0/Treg1
Ccm2	0.000701	0.423115	1	Treg0/Treg1
Cux1	0.000717	0.645874	1	Treg0/Treg1
Heca	0.00075	0.434945	1	Treg0/Treg1
Setd1b	0.000761	0.463944	1	Treg0/Treg1
Rsrp1	0.000784	0.610977	1	Treg0/Treg1
Cd3g	0.000794	0.354105	1	Treg0/Treg1
Stat1	0.00082	0.260315	1	Treg0/Treg1
Zfp281	0.000844	0.435919	1	Treg0/Treg1
Hist1h1c	0.000858	0.53181	1	Treg0/Treg1
Ly6a	0.000859	0.330042	1	Treg0/Treg1
Nipbl	0.000883	0.441249	1	Treg0/Treg1
Numa1	0.000885	0.562251	1	Treg0/Treg1
Ndufb10	0.000995	0.410096	1	Treg0/Treg1
Gabarap	0.001126	0.312528	1	Treg0/Treg1
Smim14	0.001136	0.403812	1	Treg0/Treg1
Usp25	0.00116	0.474928	1	Treg0/Treg1
Pcnt	0.001238	0.368703	1	Treg0/Treg1
Mier1	0.001265	0.364716	1	Treg0/Treg1

Tspan32	0.001324	0.435803	1	Treg0/Treg1
Tapbp	0.001343	0.380266	1	Treg0/Treg1
Klhl28	0.001405	0.446732	1	Treg0/Treg1
Ppm1h	0.00159	0.427929	1	Treg0/Treg1
Xaf1	0.001654	0.514166	1	Treg0/Treg1
Pik3r1	0.001655	0.476462	1	Treg0/Treg1
Hp1bp3	0.00171	0.383702	1	Treg0/Treg1
Scp2	0.001785	0.393487	1	Treg0/Treg1
Mapk9	0.001792	0.452121	1	Treg0/Treg1
Socs2	0.001835	0.403743	1	Treg0/Treg1
Tacc1	0.002034	0.380489	1	Treg0/Treg1
Hcst	0.002101	0.428342	1	Treg0/Treg1
Zbtb20	0.002108	0.492337	1	Treg0/Treg1
Zc3hav1	0.002174	0.344897	1	Treg0/Treg1
Coro1a	0.002179	0.333037	1	Treg0/Treg1
Add3	0.002186	0.464365	1	Treg0/Treg1
Hbp1	0.002261	0.388416	1	Treg0/Treg1
Slc9a3r1	0.002297	0.346738	1	Treg0/Treg1
Kbtbd11	0.002369	0.376896	1	Treg0/Treg1
Cog5	0.002407	0.394092	1	Treg0/Treg1
Zfp260	0.002469	0.37527	1	Treg0/Treg1
Cyld	0.002491	0.550308	1	Treg0/Treg1
Frmd6	0.002509	0.552731	1	Treg0/Treg1
Klf13	0.002512	0.518075	1	Treg0/Treg1
Hist1h1e	0.002586	0.427017	1	Treg0/Treg1
Daxx	0.002684	0.324468	1	Treg0/Treg1
Gbp6	0.002756	0.294182	1	Treg0/Treg1
Cd247	0.002787	0.31338	1	Treg0/Treg1
Mndal	0.00316	0.336738	1	Treg0/Treg1
Trbc1	0.003351	0.574262	1	Treg0/Treg1
Atp2b1	0.003379	0.574957	1	Treg0/Treg1
Bbx	0.003619	0.625784	1	Treg0/Treg1
Pink1	0.003786	0.280344	1	Treg0/Treg1
Gltp	0.003939	0.443515	1	Treg0/Treg1
Baz2b	0.004159	0.377071	1	Treg0/Treg1
Fxyd5	0.004307	0.392894	1	Treg0/Treg1
Cndp2	0.004407	0.45076	1	Treg0/Treg1
Atf7ip	0.004437	0.398621	1	Treg0/Treg1
Thoc7	0.004504	0.491696	1	Treg0/Treg1
Saraf	0.004696	0.352309	1	Treg0/Treg1
Tbca	0.004761	0.449429	1	Treg0/Treg1
Dennd1c	0.004781	0.3313	1	Treg0/Treg1
Anapc5	0.004922	0.320055	1	Treg0/Treg1
Dip2b	0.005421	0.401057	1	Treg0/Treg1
Ing4	0.005522	0.340779	1	Treg0/Treg1

Epsti1	0.005573	0.389278	1	Treg0/Treg1
Pecam1	0.005731	0.407801	1	Treg0/Treg1
Parp9	0.006425	0.342163	1	Treg0/Treg1
Bcl2l11	0.006527	0.444925	1	Treg0/Treg1
Prkacb	0.006568	0.439436	1	Treg0/Treg1
Chd2	0.006733	0.37892	1	Treg0/Treg1
Auh	0.006965	0.333943	1	Treg0/Treg1
Psmb9	0.006973	0.301959	1	Treg0/Treg1
Dok2	0.007263	0.491688	1	Treg0/Treg1
Apobec3	0.0073	0.338868	1	Treg0/Treg1
Sun2	0.008357	0.297358	1	Treg0/Treg1
Rbm5	0.008362	0.321318	1	Treg0/Treg1
Lncpint	0.008543	0.320371	1	Treg0/Treg1
Tcf12	0.00858	0.457702	1	Treg0/Treg1
Cir1	0.008608	0.443442	1	Treg0/Treg1
Phf11b	0.008868	0.324659	1	Treg0/Treg1
Fam53b	0.008913	0.532042	1	Treg0/Treg1
Man2b1	0.008973	0.371877	1	Treg0/Treg1
Actr10	0.009256	0.466252	1	Treg0/Treg1
Ttc3	0.009316	0.471926	1	Treg0/Treg1
Itpr2	0.009442	0.550074	1	Treg0/Treg1
Tnrc6c	0.009464	0.442439	1	Treg0/Treg1
Amn1	0.009514	0.497653	1	Treg0/Treg1
Tmem59	0.009823	0.412256	1	Treg0/Treg1
Irf4	2.84E-44	2.502032	4.40E-40	Tfh0/Tfh1
Hsp90ab1	1.17E-42	1.526967	1.82E-38	Tfh0/Tfh1
Mthfd2	7.18E-38	1.788234	1.11E-33	Tfh0/Tfh1
Eif2s2	1.10E-37	1.70553	1.70E-33	Tfh0/Tfh1
Nme1	1.13E-37	1.788023	1.74E-33	Tfh0/Tfh1
Eif3c	2.36E-36	1.629357	3.66E-32	Tfh0/Tfh1
Mir155hg	9.65E-36	1.919681	1.49E-31	Tfh0/Tfh1
Tnfrsf4	1.13E-35	2.33769	1.74E-31	Tfh0/Tfh1
Anp32b	5.06E-35	1.576317	7.84E-31	Tfh0/Tfh1
Serbp1	1.85E-34	1.275598	2.86E-30	Tfh0/Tfh1
Nop58	2.52E-34	1.747317	3.90E-30	Tfh0/Tfh1
Hspa5	2.46E-33	1.519852	3.81E-29	Tfh0/Tfh1
Hsp90aa1	5.19E-33	1.516205	8.04E-29	Tfh0/Tfh1
Hnrnpab	1.27E-32	1.436669	1.96E-28	Tfh0/Tfh1
Eea1	2.08E-32	2.051938	3.22E-28	Tfh0/Tfh1
Mettl1	3.77E-32	1.412138	5.84E-28	Tfh0/Tfh1
Nfkb1	3.99E-32	1.476352	6.18E-28	Tfh0/Tfh1
Nars	7.56E-32	1.454123	1.17E-27	Tfh0/Tfh1
Nop56	7.57E-32	1.757487	1.17E-27	Tfh0/Tfh1
Tfrc	1.78E-31	1.723941	2.75E-27	Tfh0/Tfh1
Phgdh	2.88E-31	1.67156	4.45E-27	Tfh0/Tfh1

Psat1	7.02E-31	1.531919	1.09E-26	Tfh0/Tfh1
Shmt2	9.79E-31	1.397628	1.52E-26	Tfh0/Tfh1
Eif4a1	1.21E-30	1.465561	1.87E-26	Tfh0/Tfh1
Ncl	1.68E-30	1.941302	2.59E-26	Tfh0/Tfh1
Klf2	2.76E-30	-2.16851	4.28E-26	Tfh0/Tfh1
Gnl3	2.87E-30	1.725482	4.45E-26	Tfh0/Tfh1
Npm1	5.03E-30	1.708239	7.79E-26	Tfh0/Tfh1
Hspd1	7.14E-30	1.725589	1.11E-25	Tfh0/Tfh1
Hspa9	1.21E-29	1.585891	1.87E-25	Tfh0/Tfh1
Tnfsf8	1.68E-29	2.349519	2.61E-25	Tfh0/Tfh1
Set	1.94E-29	1.411794	3.00E-25	Tfh0/Tfh1
Eif5a	3.21E-29	1.579107	4.97E-25	Tfh0/Tfh1
Ddx21	3.60E-29	1.470408	5.57E-25	Tfh0/Tfh1
Ets1	3.85E-29	-1.63196	5.96E-25	Tfh0/Tfh1
Gm26740	5.07E-29	-1.70312	7.84E-25	Tfh0/Tfh1
Bcl2a1b	7.27E-29	1.296374	1.13E-24	Tfh0/Tfh1
Mrto4	1.81E-28	1.375118	2.80E-24	Tfh0/Tfh1
Ifngr1	2.20E-28	-2.46724	3.40E-24	Tfh0/Tfh1
Cycs	2.29E-28	1.25102	3.54E-24	Tfh0/Tfh1
Ran	3.09E-28	1.40173	4.78E-24	Tfh0/Tfh1
Il7r	3.93E-28	-2.69677	6.08E-24	Tfh0/Tfh1
Lars	4.31E-28	1.366296	6.68E-24	Tfh0/Tfh1
Gtpbp4	5.53E-28	1.393471	8.56E-24	Tfh0/Tfh1
Srgn	1.09E-27	1.192537	1.69E-23	Tfh0/Tfh1
Btla	1.14E-27	1.379948	1.77E-23	Tfh0/Tfh1
Nme2	2.28E-27	1.399109	3.53E-23	Tfh0/Tfh1
Il2ra	6.86E-27	1.616471	1.06E-22	Tfh0/Tfh1
Emb	2.78E-26	-1.85506	4.30E-22	Tfh0/Tfh1
Gar1	3.38E-26	1.272593	5.23E-22	Tfh0/Tfh1
Ndfip1	4.88E-26	1.192902	7.55E-22	Tfh0/Tfh1
Cd200	7.71E-26	1.926204	1.19E-21	Tfh0/Tfh1
Fyb	9.03E-26	-1.45509	1.40E-21	Tfh0/Tfh1
Nhp2	9.36E-26	1.393227	1.45E-21	Tfh0/Tfh1
Cdkn1b	9.59E-26	-1.41848	1.48E-21	Tfh0/Tfh1
S1pr1	1.15E-25	-1.74966	1.78E-21	Tfh0/Tfh1
C1qbp	1.38E-25	1.444731	2.14E-21	Tfh0/Tfh1
Kdm6b	1.50E-25	1.570387	2.32E-21	Tfh0/Tfh1
Tmsb10	1.93E-25	-1.10806	2.99E-21	Tfh0/Tfh1
Snrpd1	2.72E-25	1.055334	4.21E-21	Tfh0/Tfh1
Ranbp1	2.77E-25	1.355787	4.29E-21	Tfh0/Tfh1
Srm	3.85E-25	1.305314	5.97E-21	Tfh0/Tfh1
Mat2a	4.16E-25	1.347064	6.44E-21	Tfh0/Tfh1
Nolc1	4.36E-25	1.42142	6.74E-21	Tfh0/Tfh1
Rbpj	4.53E-25	1.505252	7.01E-21	Tfh0/Tfh1
Rel	5.68E-25	1.686712	8.79E-21	Tfh0/Tfh1

Malat1	6.31E-25	-0.84634	9.77E-21	Tfh0/Tfh1
Arhgap45	7.54E-25	-1.39279	1.17E-20	Tfh0/Tfh1
Ebna1bp2	1.05E-24	1.307341	1.62E-20	Tfh0/Tfh1
G3bp1	1.07E-24	1.110263	1.66E-20	Tfh0/Tfh1
Pa2g4	1.28E-24	1.279298	1.99E-20	Tfh0/Tfh1
Hivep3	1.33E-24	1.840807	2.05E-20	Tfh0/Tfh1
Cd69	1.45E-24	2.113447	2.25E-20	Tfh0/Tfh1
Rps8	1.88E-24	0.637014	2.90E-20	Tfh0/Tfh1
Laptm5	1.90E-24	-1.29759	2.94E-20	Tfh0/Tfh1
Neurl3	2.19E-24	-1.92557	3.38E-20	Tfh0/Tfh1
Tspo	2.20E-24	-1.43302	3.41E-20	Tfh0/Tfh1
Ybx3	3.25E-24	1.522234	5.03E-20	Tfh0/Tfh1
Timm10	4.95E-24	1.128042	7.66E-20	Tfh0/Tfh1
Plscr1	5.69E-24	1.441484	8.81E-20	Tfh0/Tfh1
Hspe1	5.77E-24	1.314537	8.93E-20	Tfh0/Tfh1
Gpatch4	7.28E-24	1.056464	1.13E-19	Tfh0/Tfh1
Sp100	7.40E-24	-1.35598	1.15E-19	Tfh0/Tfh1
Fam162a	7.78E-24	1.032898	1.20E-19	Tfh0/Tfh1
Atp5g1	1.26E-23	1.10682	1.95E-19	Tfh0/Tfh1
Cct3	1.28E-23	1.097864	1.97E-19	Tfh0/Tfh1
Cct2	1.62E-23	1.070721	2.51E-19	Tfh0/Tfh1
Fbl	1.73E-23	1.210182	2.68E-19	Tfh0/Tfh1
Slc7a1	1.83E-23	1.130901	2.84E-19	Tfh0/Tfh1
Slc1a5	2.56E-23	1.215164	3.96E-19	Tfh0/Tfh1
Hsph1	3.17E-23	1.034176	4.90E-19	Tfh0/Tfh1
Hnrnpa1	5.77E-23	1.075381	8.93E-19	Tfh0/Tfh1
Mphosph10	6.07E-23	1.116474	9.39E-19	Tfh0/Tfh1
S100a10	6.22E-23	-1.6958	9.63E-19	Tfh0/Tfh1
Pdcd4	6.47E-23	-1.43438	1.00E-18	Tfh0/Tfh1
Ms4a4b	6.50E-23	-1.58412	1.01E-18	Tfh0/Tfh1
Lyar	7.72E-23	1.17709	1.20E-18	Tfh0/Tfh1
Ltv1	9.05E-23	1.011996	1.40E-18	Tfh0/Tfh1
Ppan	1.26E-22	1.078929	1.95E-18	Tfh0/Tfh1
Mybbp1a	1.27E-22	1.282054	1.97E-18	Tfh0/Tfh1
Ablim1	1.30E-22	-1.52635	2.02E-18	Tfh0/Tfh1
Mif	1.70E-22	1.661298	2.63E-18	Tfh0/Tfh1
Nr4a1	2.26E-22	1.399731	3.50E-18	Tfh0/Tfh1
Eprs	2.33E-22	1.098596	3.60E-18	Tfh0/Tfh1
Bcl2a1d	2.61E-22	1.051193	4.04E-18	Tfh0/Tfh1
Eif2s1	2.67E-22	1.045667	4.13E-18	Tfh0/Tfh1
Emc6	3.65E-22	0.935462	5.65E-18	Tfh0/Tfh1
Cars	5.12E-22	0.940802	7.93E-18	Tfh0/Tfh1
Smc4	5.73E-22	-1.9894	8.87E-18	Tfh0/Tfh1
Wdr43	6.89E-22	1.286888	1.07E-17	Tfh0/Tfh1
Rrs1	7.06E-22	1.085997	1.09E-17	Tfh0/Tfh1

Rps2	8.16E-22	0.780392	1.26E-17	Tfh0/Tfh1
Uqcrq	1.00E-21	1.138797	1.55E-17	Tfh0/Tfh1
Rrp9	1.20E-21	0.959754	1.86E-17	Tfh0/Tfh1
Selplg	1.46E-21	-1.41997	2.26E-17	Tfh0/Tfh1
Itm2b	1.72E-21	-1.03672	2.66E-17	Tfh0/Tfh1
Tcf7	2.04E-21	-1.54311	3.16E-17	Tfh0/Tfh1
Rrp15	2.19E-21	1.010858	3.39E-17	Tfh0/Tfh1
Npm3	2.21E-21	1.152353	3.43E-17	Tfh0/Tfh1
Pdcd11	3.43E-21	1.092021	5.30E-17	Tfh0/Tfh1
Nip7	4.92E-21	1.031586	7.62E-17	Tfh0/Tfh1
Ppp1r14b	5.92E-21	1.247888	9.16E-17	Tfh0/Tfh1
Bcat1	6.38E-21	0.94417	9.88E-17	Tfh0/Tfh1
Ccdc50	6.44E-21	1.13187	9.97E-17	Tfh0/Tfh1
Tmem71	6.73E-21	-1.28273	1.04E-16	Tfh0/Tfh1
Rsrp1	7.17E-21	-1.29088	1.11E-16	Tfh0/Tfh1
Apex1	9.27E-21	0.802918	1.44E-16	Tfh0/Tfh1
Nifk	9.51E-21	1.033214	1.47E-16	Tfh0/Tfh1
Zfp593	1.13E-20	0.913068	1.74E-16	Tfh0/Tfh1
Iars	1.13E-20	0.963896	1.75E-16	Tfh0/Tfh1
Atf3	1.19E-20	1.133769	1.84E-16	Tfh0/Tfh1
Rpf2	1.47E-20	0.949212	2.28E-16	Tfh0/Tfh1
Timm23	1.71E-20	1.099894	2.65E-16	Tfh0/Tfh1
S100a13	1.73E-20	-1.3339	2.68E-16	Tfh0/Tfh1
Slc3a2	2.04E-20	1.072521	3.15E-16	Tfh0/Tfh1
Arhgdib	2.45E-20	-1.1261	3.79E-16	Tfh0/Tfh1
Gars	2.81E-20	1.119692	4.36E-16	Tfh0/Tfh1
Tnfsf11	2.82E-20	1.621288	4.36E-16	Tfh0/Tfh1
Ly6e	3.15E-20	-1.29507	4.87E-16	Tfh0/Tfh1
Larp1	3.51E-20	1.050899	5.43E-16	Tfh0/Tfh1
Timm8a1	3.98E-20	1.098466	6.17E-16	Tfh0/Tfh1
Znhit6	4.25E-20	0.931493	6.58E-16	Tfh0/Tfh1
Ptma	4.63E-20	1.005796	7.17E-16	Tfh0/Tfh1
Eif4ebp1	5.81E-20	1.332516	8.99E-16	Tfh0/Tfh1
Rps17	6.63E-20	0.735314	1.03E-15	Tfh0/Tfh1
Eef1e1	1.30E-19	1.047858	2.01E-15	Tfh0/Tfh1
Snhg15	1.36E-19	0.991485	2.10E-15	Tfh0/Tfh1
Prmt1	1.55E-19	1.012487	2.40E-15	Tfh0/Tfh1
Mrps6	1.83E-19	0.856911	2.82E-15	Tfh0/Tfh1
Cd82	1.85E-19	1.201835	2.87E-15	Tfh0/Tfh1
Lsm2	2.08E-19	0.862359	3.22E-15	Tfh0/Tfh1
Cct7	2.33E-19	0.955738	3.60E-15	Tfh0/Tfh1
Fubp1	2.44E-19	0.937421	3.77E-15	Tfh0/Tfh1
Ppia	2.45E-19	0.601809	3.79E-15	Tfh0/Tfh1
Pno1	2.63E-19	0.972696	4.07E-15	Tfh0/Tfh1
Mdn1	2.66E-19	1.050932	4.12E-15	Tfh0/Tfh1

Cct6a	2.77E-19	0.990349	4.29E-15	Tfh0/Tfh1
Tnfaip8	4.16E-19	1.145662	6.44E-15	Tfh0/Tfh1
Gnai2	4.20E-19	-0.99744	6.51E-15	Tfh0/Tfh1
Ftsj3	4.69E-19	0.959826	7.26E-15	Tfh0/Tfh1
Cox7a2l	5.07E-19	-0.97071	7.85E-15	Tfh0/Tfh1
Nfkbia	6.00E-19	1.2337	9.28E-15	Tfh0/Tfh1
Psme2	6.40E-19	0.98695	9.90E-15	Tfh0/Tfh1
Bhlhe40	6.74E-19	1.160835	1.04E-14	Tfh0/Tfh1
Nop16	7.71E-19	0.866826	1.19E-14	Tfh0/Tfh1
Ccdc86	7.90E-19	0.870677	1.22E-14	Tfh0/Tfh1
Mrps18b	8.84E-19	0.778585	1.37E-14	Tfh0/Tfh1
Rsl24d1	9.19E-19	0.896254	1.42E-14	Tfh0/Tfh1
Mpp6	9.84E-19	0.912119	1.52E-14	Tfh0/Tfh1
Rcc2	1.01E-18	1.030137	1.56E-14	Tfh0/Tfh1
Itga4	1.16E-18	-1.51558	1.80E-14	Tfh0/Tfh1
Neat1	1.28E-18	-1.43062	1.98E-14	Tfh0/Tfh1
Skap1	1.32E-18	-1.31495	2.05E-14	Tfh0/Tfh1
Snrpb	1.33E-18	0.776961	2.05E-14	Tfh0/Tfh1
Noc3l	1.34E-18	0.807205	2.07E-14	Tfh0/Tfh1
Tomm40	1.47E-18	0.867921	2.27E-14	Tfh0/Tfh1
Dusp4	2.07E-18	0.902858	3.21E-14	Tfh0/Tfh1
Tut4	2.67E-18	-1.20511	4.13E-14	Tfh0/Tfh1
Banf1	2.81E-18	0.909441	4.34E-14	Tfh0/Tfh1
Ndufaf4	3.71E-18	0.88513	5.75E-14	Tfh0/Tfh1
Fdx2	3.89E-18	0.851311	6.02E-14	Tfh0/Tfh1
7-Sep	3.97E-18	0.927583	6.14E-14	Tfh0/Tfh1
Cdv3	4.17E-18	1.045237	6.46E-14	Tfh0/Tfh1
Hspa8	4.28E-18	0.956153	6.62E-14	Tfh0/Tfh1
Srsf2	4.56E-18	0.947152	7.05E-14	Tfh0/Tfh1
Rsl1d1	6.03E-18	1.005546	9.34E-14	Tfh0/Tfh1
Bcl2l1	6.05E-18	0.881023	9.37E-14	Tfh0/Tfh1
Lsp1	6.81E-18	-1.4892	1.05E-13	Tfh0/Tfh1
Il2	7.24E-18	3.383217	1.12E-13	Tfh0/Tfh1
Tma16	7.94E-18	0.903188	1.23E-13	Tfh0/Tfh1
Tars	1.03E-17	0.987682	1.59E-13	Tfh0/Tfh1
Stx11	1.08E-17	0.958814	1.67E-13	Tfh0/Tfh1
Hnrnpu	1.12E-17	0.750774	1.73E-13	Tfh0/Tfh1
Slc7a5	1.16E-17	0.947821	1.79E-13	Tfh0/Tfh1
Lcp1	1.29E-17	0.930894	1.99E-13	Tfh0/Tfh1
Noc2l	1.52E-17	1.012622	2.36E-13	Tfh0/Tfh1
Eif4e	1.76E-17	0.937966	2.73E-13	Tfh0/Tfh1
Mrpl12	1.83E-17	0.868346	2.83E-13	Tfh0/Tfh1
Eif3a	1.87E-17	0.881548	2.89E-13	Tfh0/Tfh1
Ybx1	2.46E-17	0.775608	3.81E-13	Tfh0/Tfh1
Tmem50a	2.65E-17	-0.95802	4.10E-13	Tfh0/Tfh1

Ptpn18	2.76E-17	-0.97455	4.27E-13	Tfh0/Tfh1
Nop14	2.78E-17	0.922549	4.30E-13	Tfh0/Tfh1
Eif5b	3.26E-17	1.006747	5.04E-13	Tfh0/Tfh1
Sdad1	3.83E-17	0.859051	5.93E-13	Tfh0/Tfh1
Nsd3	3.89E-17	-1.11673	6.02E-13	Tfh0/Tfh1
Odc1	3.92E-17	1.23114	6.07E-13	Tfh0/Tfh1
Rpl7l1	4.33E-17	0.860716	6.70E-13	Tfh0/Tfh1
Stk38	4.40E-17	-1.2722	6.81E-13	Tfh0/Tfh1
Nap1l1	6.05E-17	0.912194	9.36E-13	Tfh0/Tfh1
Phb	6.29E-17	0.812998	9.73E-13	Tfh0/Tfh1
Relb	6.55E-17	0.779068	1.01E-12	Tfh0/Tfh1
Esf1	7.19E-17	1.10318	1.11E-12	Tfh0/Tfh1
Grap2	7.20E-17	-1.1814	1.11E-12	Tfh0/Tfh1
Crebrf	7.64E-17	-1.15576	1.18E-12	Tfh0/Tfh1
Mrps28	7.73E-17	0.643627	1.20E-12	Tfh0/Tfh1
Stx6	8.27E-17	0.794298	1.28E-12	Tfh0/Tfh1
Tomm70a	8.35E-17	0.856927	1.29E-12	Tfh0/Tfh1
Zap70	9.51E-17	0.866886	1.47E-12	Tfh0/Tfh1
Srsf6	1.02E-16	0.874966	1.58E-12	Tfh0/Tfh1
Snu13	1.05E-16	0.923256	1.62E-12	Tfh0/Tfh1
Ms4a6b	1.05E-16	-1.22794	1.62E-12	Tfh0/Tfh1
Mak16	1.08E-16	0.882648	1.67E-12	Tfh0/Tfh1
Timm17a	1.20E-16	0.862669	1.86E-12	Tfh0/Tfh1
Eif1	1.23E-16	0.505191	1.91E-12	Tfh0/Tfh1
Coro1a	1.28E-16	-0.91011	1.97E-12	Tfh0/Tfh1
Hmgb2	1.37E-16	-1.42553	2.13E-12	Tfh0/Tfh1
Ripor2	1.48E-16	-1.27667	2.29E-12	Tfh0/Tfh1
Hspa4	1.48E-16	0.843398	2.30E-12	Tfh0/Tfh1
Etf1	1.50E-16	0.973361	2.32E-12	Tfh0/Tfh1
Arl4c	1.52E-16	-1.36599	2.35E-12	Tfh0/Tfh1
Elf1	1.52E-16	-1.15744	2.36E-12	Tfh0/Tfh1
Eef1g	1.61E-16	0.721252	2.49E-12	Tfh0/Tfh1
Nsun2	1.92E-16	0.825083	2.97E-12	Tfh0/Tfh1
Pdcd1lg2	2.21E-16	0.706968	3.41E-12	Tfh0/Tfh1
Tsr1	2.57E-16	0.816049	3.98E-12	Tfh0/Tfh1
Abce1	3.10E-16	0.857326	4.80E-12	Tfh0/Tfh1
Eif3b	3.47E-16	0.906379	5.37E-12	Tfh0/Tfh1
Tecpr1	3.58E-16	-1.20305	5.55E-12	Tfh0/Tfh1
Rasa3	3.89E-16	-1.03933	6.02E-12	Tfh0/Tfh1
Psme3	4.04E-16	0.849527	6.25E-12	Tfh0/Tfh1
Dgka	4.10E-16	-1.03599	6.34E-12	Tfh0/Tfh1
P2ry10	4.44E-16	-1.24653	6.87E-12	Tfh0/Tfh1
Zc3hav1	4.79E-16	-1.12584	7.41E-12	Tfh0/Tfh1
Lap3	4.93E-16	0.779111	7.62E-12	Tfh0/Tfh1
Rnf125	5.33E-16	-1.03973	8.25E-12	Tfh0/Tfh1

Sars	6.01E-16	0.872358	9.31E-12	Tfh0/Tfh1
9930111J21Rik2	6.70E-16	-1.1816	1.04E-11	Tfh0/Tfh1
Tomm20	6.74E-16	0.828347	1.04E-11	Tfh0/Tfh1
Samhd1	7.05E-16	-1.62335	1.09E-11	Tfh0/Tfh1
Pdap1	7.44E-16	0.820229	1.15E-11	Tfh0/Tfh1
Tnrc6b	8.27E-16	-1.23504	1.28E-11	Tfh0/Tfh1
Atp1a1	8.49E-16	0.83851	1.31E-11	Tfh0/Tfh1
Utp20	9.07E-16	0.772229	1.40E-11	Tfh0/Tfh1
Shmt1	9.19E-16	0.666844	1.42E-11	Tfh0/Tfh1
Ifi209	9.74E-16	-1.18849	1.51E-11	Tfh0/Tfh1
Fau	9.76E-16	-0.43635	1.51E-11	Tfh0/Tfh1
Ruvbl2	1.01E-15	0.652314	1.57E-11	Tfh0/Tfh1
Tcp1	1.05E-15	0.810331	1.63E-11	Tfh0/Tfh1
Nop10	1.11E-15	0.911365	1.71E-11	Tfh0/Tfh1
Cct5	1.21E-15	0.808613	1.88E-11	Tfh0/Tfh1
Arhgap15	1.26E-15	-1.16907	1.95E-11	Tfh0/Tfh1
Arid5b	1.28E-15	1.017256	1.97E-11	Tfh0/Tfh1
S100a11	1.39E-15	-1.28044	2.14E-11	Tfh0/Tfh1
Pus7	1.41E-15	0.644626	2.18E-11	Tfh0/Tfh1
Slamf1	1.45E-15	0.912538	2.24E-11	Tfh0/Tfh1
Dkc1	1.46E-15	1.128814	2.26E-11	Tfh0/Tfh1
Hnrnpll	1.55E-15	0.767596	2.39E-11	Tfh0/Tfh1
Btg3	1.86E-15	0.908641	2.87E-11	Tfh0/Tfh1
Nfkbid	1.93E-15	1.223922	2.99E-11	Tfh0/Tfh1
Rps27l	2.14E-15	0.685668	3.31E-11	Tfh0/Tfh1
Chchd4	2.33E-15	0.766831	3.61E-11	Tfh0/Tfh1
Jak1	2.54E-15	-0.87015	3.94E-11	Tfh0/Tfh1
Emp3	2.56E-15	-1.06957	3.97E-11	Tfh0/Tfh1
Syncrip	2.57E-15	0.889731	3.97E-11	Tfh0/Tfh1
Ypel3	2.73E-15	-1.08317	4.22E-11	Tfh0/Tfh1
Rcl1	2.94E-15	0.653617	4.55E-11	Tfh0/Tfh1
Sla	3.09E-15	0.717861	4.79E-11	Tfh0/Tfh1
Yrdc	3.22E-15	0.81894	4.99E-11	Tfh0/Tfh1
Rrp1b	3.58E-15	0.777256	5.54E-11	Tfh0/Tfh1
Lsm7	4.03E-15	0.671713	6.23E-11	Tfh0/Tfh1
Zeb2	5.16E-15	1.074326	7.99E-11	Tfh0/Tfh1
Wdr83os	5.54E-15	0.784424	8.57E-11	Tfh0/Tfh1
Timm9	5.63E-15	0.748445	8.72E-11	Tfh0/Tfh1
AW112010	5.73E-15	-1.12401	8.87E-11	Tfh0/Tfh1
Myc	5.85E-15	1.236715	9.06E-11	Tfh0/Tfh1
Nfkbib	5.95E-15	0.969024	9.21E-11	Tfh0/Tfh1
Cnbp	5.99E-15	0.781762	9.27E-11	Tfh0/Tfh1
Gimap6	6.03E-15	-0.96967	9.33E-11	Tfh0/Tfh1
Resf1	7.42E-15	-1.16841	1.15E-10	Tfh0/Tfh1
Pum3	7.88E-15	0.750133	1.22E-10	Tfh0/Tfh1

Phf6	9.19E-15	0.858554	1.42E-10	Tfh0/Tfh1
Ppa1	1.24E-14	0.829221	1.92E-10	Tfh0/Tfh1
Rps19bp1	1.34E-14	0.695088	2.07E-10	Tfh0/Tfh1
Brix1	1.35E-14	0.679931	2.09E-10	Tfh0/Tfh1
Phb2	1.43E-14	0.747528	2.21E-10	Tfh0/Tfh1
Taf10	1.54E-14	0.732334	2.38E-10	Tfh0/Tfh1
Eif3j1	1.56E-14	0.856077	2.41E-10	Tfh0/Tfh1
Bysl	1.66E-14	0.61101	2.56E-10	Tfh0/Tfh1
Xpot	1.94E-14	0.743633	3.00E-10	Tfh0/Tfh1
Ppid	1.99E-14	0.74046	3.09E-10	Tfh0/Tfh1
Naa15	2.01E-14	0.807518	3.10E-10	Tfh0/Tfh1
Sfxn1	2.06E-14	0.750808	3.19E-10	Tfh0/Tfh1
Ctps	2.09E-14	0.578668	3.24E-10	Tfh0/Tfh1
Cd3eap	2.52E-14	0.657502	3.89E-10	Tfh0/Tfh1
Vsir	2.80E-14	0.828027	4.34E-10	Tfh0/Tfh1
Impdh2	2.83E-14	0.830316	4.37E-10	Tfh0/Tfh1
Zc3h15	2.88E-14	0.804792	4.46E-10	Tfh0/Tfh1
Mtdh	3.07E-14	0.776881	4.74E-10	Tfh0/Tfh1
Nfkbiz	3.35E-14	0.93157	5.19E-10	Tfh0/Tfh1
Wdr36	3.40E-14	0.718689	5.27E-10	Tfh0/Tfh1
Gadd45b	3.54E-14	0.994215	5.47E-10	Tfh0/Tfh1
Rac2	3.59E-14	-0.93902	5.56E-10	Tfh0/Tfh1
Gmfg	4.34E-14	-1.04902	6.71E-10	Tfh0/Tfh1
Rgs16	4.76E-14	0.931169	7.37E-10	Tfh0/Tfh1
Tle5	5.13E-14	-0.95312	7.93E-10	Tfh0/Tfh1
Fryl	5.34E-14	-1.21573	8.27E-10	Tfh0/Tfh1
Utp15	5.38E-14	0.642849	8.32E-10	Tfh0/Tfh1
Polr2h	5.79E-14	0.704277	8.97E-10	Tfh0/Tfh1
Atf4	6.49E-14	0.753631	1.00E-09	Tfh0/Tfh1
Fabp5	6.69E-14	0.840275	1.04E-09	Tfh0/Tfh1
Mthfd1l	6.80E-14	0.685403	1.05E-09	Tfh0/Tfh1
Pfdn2	7.08E-14	0.733799	1.10E-09	Tfh0/Tfh1
Ddx18	7.08E-14	0.837242	1.10E-09	Tfh0/Tfh1
Heatr1	7.09E-14	0.596326	1.10E-09	Tfh0/Tfh1
Rbm3	7.33E-14	0.547276	1.13E-09	Tfh0/Tfh1
Slfn2	7.74E-14	0.739047	1.20E-09	Tfh0/Tfh1
Rrp12	8.09E-14	0.601114	1.25E-09	Tfh0/Tfh1
Map2k3	8.75E-14	0.843806	1.35E-09	Tfh0/Tfh1
Snhg1	9.09E-14	0.934139	1.41E-09	Tfh0/Tfh1
Atad3a	9.34E-14	0.757751	1.45E-09	Tfh0/Tfh1
Junb	9.45E-14	0.901421	1.46E-09	Tfh0/Tfh1
Vps37b	1.02E-13	-1.25704	1.58E-09	Tfh0/Tfh1
Heca	1.05E-13	-0.98323	1.62E-09	Tfh0/Tfh1
Plagl2	1.24E-13	0.826149	1.93E-09	Tfh0/Tfh1
Rpl14	1.43E-13	0.497577	2.21E-09	Tfh0/Tfh1

Ipo4	1.44E-13	0.455198	2.23E-09	Tfh0/Tfh1
Dnajc2	1.49E-13	0.888224	2.30E-09	Tfh0/Tfh1
Nat10	1.49E-13	0.618779	2.31E-09	Tfh0/Tfh1
Snhg6	1.53E-13	0.756806	2.37E-09	Tfh0/Tfh1
U2af1	1.70E-13	0.668288	2.63E-09	Tfh0/Tfh1
Uqcc2	1.80E-13	0.755393	2.79E-09	Tfh0/Tfh1
Eif3g	1.81E-13	0.754959	2.80E-09	Tfh0/Tfh1
Btg2	1.99E-13	-1.18262	3.08E-09	Tfh0/Tfh1
Atp5b	2.44E-13	0.676988	3.78E-09	Tfh0/Tfh1
Tcof1	2.93E-13	0.847848	4.54E-09	Tfh0/Tfh1
Ssrp1	2.94E-13	0.788226	4.55E-09	Tfh0/Tfh1
Spata5	3.00E-13	0.599722	4.64E-09	Tfh0/Tfh1
Gpx4	3.02E-13	-0.86327	4.67E-09	Tfh0/Tfh1
Psph	3.20E-13	0.885643	4.96E-09	Tfh0/Tfh1
Aen	3.30E-13	0.630852	5.11E-09	Tfh0/Tfh1
Rnps1	3.50E-13	0.721241	5.41E-09	Tfh0/Tfh1
S100a6	3.57E-13	-1.84527	5.53E-09	Tfh0/Tfh1
Top1	3.63E-13	0.718113	5.62E-09	Tfh0/Tfh1
Mthfd1	3.73E-13	0.554519	5.78E-09	Tfh0/Tfh1
Tuba1b	3.77E-13	0.953239	5.84E-09	Tfh0/Tfh1
Cebpz	3.83E-13	0.750835	5.92E-09	Tfh0/Tfh1
Ddx27	3.99E-13	0.737702	6.18E-09	Tfh0/Tfh1
Snrpa	4.41E-13	0.634579	6.83E-09	Tfh0/Tfh1
Hk2	4.97E-13	0.628291	7.70E-09	Tfh0/Tfh1
St13	5.10E-13	0.722017	7.89E-09	Tfh0/Tfh1
Atp1b3	5.18E-13	-1.18664	8.02E-09	Tfh0/Tfh1
Spry1	5.71E-13	0.93337	8.83E-09	Tfh0/Tfh1
Ftl1	5.85E-13	-0.68478	9.05E-09	Tfh0/Tfh1
Eif1a	6.01E-13	0.793805	9.30E-09	Tfh0/Tfh1
Utp18	6.50E-13	0.750748	1.01E-08	Tfh0/Tfh1
Dnaja2	6.84E-13	0.631229	1.06E-08	Tfh0/Tfh1
Klf3	7.13E-13	-1.13957	1.10E-08	Tfh0/Tfh1
Txnip	7.57E-13	-1.01368	1.17E-08	Tfh0/Tfh1
Fxyd5	7.88E-13	-0.96335	1.22E-08	Tfh0/Tfh1
Tagap	8.16E-13	0.995728	1.26E-08	Tfh0/Tfh1
Asns	8.21E-13	0.822708	1.27E-08	Tfh0/Tfh1
Arhgef1	8.51E-13	-0.98777	1.32E-08	Tfh0/Tfh1
Egr1	8.68E-13	1.137428	1.34E-08	Tfh0/Tfh1
Lbr	9.15E-13	-0.98173	1.42E-08	Tfh0/Tfh1
Pck2	9.16E-13	0.615104	1.42E-08	Tfh0/Tfh1
Gm2682	9.32E-13	-1.23678	1.44E-08	Tfh0/Tfh1
Denr	9.62E-13	0.685162	1.49E-08	Tfh0/Tfh1
Smap2	1.03E-12	-0.95188	1.60E-08	Tfh0/Tfh1
Ifi208	1.04E-12	-0.86713	1.60E-08	Tfh0/Tfh1
Gimap4	1.14E-12	-1.15772	1.76E-08	Tfh0/Tfh1

Trps1	1.18E-12	0.821715	1.83E-08	Tfh0/Tfh1
Gramd3	1.21E-12	-1.05216	1.88E-08	Tfh0/Tfh1
Nfkb2	1.31E-12	0.677169	2.03E-08	Tfh0/Tfh1
Wdr75	1.37E-12	0.664397	2.12E-08	Tfh0/Tfh1
Hnrnpdl	1.42E-12	0.697923	2.19E-08	Tfh0/Tfh1
Dnajc21	1.46E-12	0.707743	2.26E-08	Tfh0/Tfh1
Cytip	1.49E-12	-1.02197	2.30E-08	Tfh0/Tfh1
Hnrnpd	1.51E-12	0.698835	2.33E-08	Tfh0/Tfh1
Ddx39	1.56E-12	0.698515	2.41E-08	Tfh0/Tfh1
Polr3d	1.57E-12	0.624551	2.43E-08	Tfh0/Tfh1
M6pr	1.72E-12	0.761362	2.66E-08	Tfh0/Tfh1
Psmb8	1.94E-12	-0.7958	3.01E-08	Tfh0/Tfh1
Polr2l	1.98E-12	0.578449	3.06E-08	Tfh0/Tfh1
Psmg4	2.05E-12	0.585948	3.18E-08	Tfh0/Tfh1
Tm2d3	2.19E-12	0.62092	3.39E-08	Tfh0/Tfh1
Rps21	2.33E-12	-0.47933	3.60E-08	Tfh0/Tfh1
Pdia6	2.38E-12	0.712982	3.68E-08	Tfh0/Tfh1
Itgav	2.42E-12	0.806552	3.74E-08	Tfh0/Tfh1
Kpnb1	2.53E-12	0.659368	3.91E-08	Tfh0/Tfh1
Ndufab1	2.79E-12	0.733382	4.33E-08	Tfh0/Tfh1
St6galnac4	2.81E-12	0.555018	4.36E-08	Tfh0/Tfh1
Prelid2	2.83E-12	0.602475	4.38E-08	Tfh0/Tfh1
Ppp2r5c	2.86E-12	-0.86302	4.43E-08	Tfh0/Tfh1
Crip1	2.86E-12	-1.619	4.43E-08	Tfh0/Tfh1
Ssh2	2.87E-12	-1.02007	4.44E-08	Tfh0/Tfh1
H2afv	3.16E-12	-0.78643	4.89E-08	Tfh0/Tfh1
Srsf7	3.19E-12	0.640218	4.93E-08	Tfh0/Tfh1
Grwd1	3.31E-12	0.56025	5.12E-08	Tfh0/Tfh1
Larp7	3.32E-12	0.624746	5.13E-08	Tfh0/Tfh1
Cd83	3.33E-12	0.895329	5.15E-08	Tfh0/Tfh1
Wdr74	3.37E-12	0.601352	5.22E-08	Tfh0/Tfh1
Mdfic	4.04E-12	0.846605	6.25E-08	Tfh0/Tfh1
Uck2	4.05E-12	0.585331	6.27E-08	Tfh0/Tfh1
Psmb5	4.14E-12	0.633575	6.41E-08	Tfh0/Tfh1
Ruvbl1	4.70E-12	0.685016	7.27E-08	Tfh0/Tfh1
Ipo5	4.98E-12	0.633128	7.71E-08	Tfh0/Tfh1
Psma4	5.02E-12	0.627809	7.78E-08	Tfh0/Tfh1
Hdgf	5.03E-12	0.831016	7.78E-08	Tfh0/Tfh1
Tbc1d10c	5.22E-12	-0.8728	8.07E-08	Tfh0/Tfh1
Ndufa12	5.59E-12	0.672902	8.64E-08	Tfh0/Tfh1
Pabpn1	5.63E-12	0.648632	8.71E-08	Tfh0/Tfh1
Eif2b3	5.90E-12	0.521902	9.13E-08	Tfh0/Tfh1
Atp5md	6.50E-12	0.62197	1.01E-07	Tfh0/Tfh1
Stip1	6.61E-12	0.705393	1.02E-07	Tfh0/Tfh1
Rbm8a	6.70E-12	0.656406	1.04E-07	Tfh0/Tfh1

Nol11	6.70E-12	0.620138	1.04E-07	Tfh0/Tfh1
Gspt1	7.02E-12	0.737562	1.09E-07	Tfh0/Tfh1
Znrd2	7.07E-12	0.586056	1.09E-07	Tfh0/Tfh1
Nol10	7.20E-12	0.574822	1.11E-07	Tfh0/Tfh1
mt-Co1	7.33E-12	-0.37265	1.13E-07	Tfh0/Tfh1
Bola2	7.36E-12	0.616013	1.14E-07	Tfh0/Tfh1
Eif1ax	7.44E-12	0.654016	1.15E-07	Tfh0/Tfh1
Clic4	7.62E-12	0.682328	1.18E-07	Tfh0/Tfh1
Yars	8.22E-12	0.563746	1.27E-07	Tfh0/Tfh1
Cdk6	8.25E-12	1.005984	1.28E-07	Tfh0/Tfh1
Jak2	8.31E-12	0.890299	1.29E-07	Tfh0/Tfh1
Wdr46	8.90E-12	0.49805	1.38E-07	Tfh0/Tfh1
Mxd4	9.28E-12	-0.97013	1.44E-07	Tfh0/Tfh1
Exosc2	9.75E-12	0.534367	1.51E-07	Tfh0/Tfh1
Aldoa	9.78E-12	0.707977	1.51E-07	Tfh0/Tfh1
Rabac1	1.05E-11	-0.76646	1.62E-07	Tfh0/Tfh1
Nus1	1.06E-11	0.555588	1.65E-07	Tfh0/Tfh1
Dcun1d5	1.11E-11	0.712	1.71E-07	Tfh0/Tfh1
Thyn1	1.12E-11	0.494708	1.73E-07	Tfh0/Tfh1
Cd53	1.19E-11	0.677133	1.84E-07	Tfh0/Tfh1
Ier5	1.20E-11	0.852237	1.85E-07	Tfh0/Tfh1
Pebp1	1.24E-11	0.583179	1.92E-07	Tfh0/Tfh1
Herpud1	1.36E-11	0.626002	2.11E-07	Tfh0/Tfh1
Abcf2	1.40E-11	0.636955	2.16E-07	Tfh0/Tfh1
Polr2f	1.41E-11	0.723604	2.19E-07	Tfh0/Tfh1
Nob1	1.41E-11	0.547087	2.19E-07	Tfh0/Tfh1
Aldh18a1	1.44E-11	0.548851	2.23E-07	Tfh0/Tfh1
Lsm12	1.51E-11	0.540243	2.33E-07	Tfh0/Tfh1
Cmah	1.53E-11	-0.96512	2.38E-07	Tfh0/Tfh1
Ghitm	1.60E-11	0.664586	2.48E-07	Tfh0/Tfh1
Crlf3	1.80E-11	-1.084	2.79E-07	Tfh0/Tfh1
Prpf19	1.81E-11	0.562029	2.80E-07	Tfh0/Tfh1
Thumpd1	1.94E-11	0.615357	3.00E-07	Tfh0/Tfh1
Psmd12	2.27E-11	0.564926	3.51E-07	Tfh0/Tfh1
Nol8	2.27E-11	0.693508	3.52E-07	Tfh0/Tfh1
Klhl24	2.30E-11	-0.8073	3.56E-07	Tfh0/Tfh1
Rpl37a	2.34E-11	-0.46093	3.62E-07	Tfh0/Tfh1
Ppat	2.38E-11	0.547997	3.69E-07	Tfh0/Tfh1
Nr4a2	2.40E-11	0.866231	3.72E-07	Tfh0/Tfh1
Bzw1	2.55E-11	0.608421	3.94E-07	Tfh0/Tfh1
Calr	2.59E-11	0.820529	4.01E-07	Tfh0/Tfh1
B3gnt2	2.63E-11	0.773602	4.07E-07	Tfh0/Tfh1
Mbnl1	2.65E-11	-0.60665	4.10E-07	Tfh0/Tfh1
Ssb	2.98E-11	0.598301	4.61E-07	Tfh0/Tfh1
Btf3	3.05E-11	0.483242	4.72E-07	Tfh0/Tfh1

Alkbh1	3.15E-11	0.602816	4.87E-07	Tfh0/Tfh1
Usp10	3.18E-11	0.558636	4.93E-07	Tfh0/Tfh1
Bcl11b	3.23E-11	-0.95239	4.99E-07	Tfh0/Tfh1
Nop2	3.26E-11	0.549995	5.05E-07	Tfh0/Tfh1
Foxp1	3.34E-11	0.840989	5.17E-07	Tfh0/Tfh1
Gcsh	3.54E-11	0.48464	5.48E-07	Tfh0/Tfh1
Camk2d	3.54E-11	0.895392	5.49E-07	Tfh0/Tfh1
Psmd7	3.62E-11	0.654344	5.61E-07	Tfh0/Tfh1
Nfat5	3.70E-11	0.913643	5.73E-07	Tfh0/Tfh1
Naa50	3.73E-11	0.659238	5.77E-07	Tfh0/Tfh1
Cacybp	3.81E-11	0.72096	5.90E-07	Tfh0/Tfh1
Gfod1	3.85E-11	0.678278	5.96E-07	Tfh0/Tfh1
Bin2	3.87E-11	-0.88325	5.99E-07	Tfh0/Tfh1
Wdr12	3.94E-11	0.640109	6.10E-07	Tfh0/Tfh1
11-Sep	4.06E-11	0.55615	6.29E-07	Tfh0/Tfh1
Plagl1	4.10E-11	0.801498	6.34E-07	Tfh0/Tfh1
Arhgef18	4.15E-11	-0.82811	6.42E-07	Tfh0/Tfh1
Csnk2a1	4.29E-11	0.653107	6.64E-07	Tfh0/Tfh1
Rpl36al	4.45E-11	0.470589	6.88E-07	Tfh0/Tfh1
Txk	4.47E-11	-1.08246	6.92E-07	Tfh0/Tfh1
Rnasel	4.50E-11	-0.88707	6.97E-07	Tfh0/Tfh1
Wdr18	4.57E-11	0.601342	7.08E-07	Tfh0/Tfh1
Psmg2	4.64E-11	0.503728	7.18E-07	Tfh0/Tfh1
Mtap	4.69E-11	0.518232	7.26E-07	Tfh0/Tfh1
Srpk2	4.92E-11	-0.84142	7.62E-07	Tfh0/Tfh1
Eif4g1	5.00E-11	0.736929	7.75E-07	Tfh0/Tfh1
Iqgap1	5.04E-11	-0.94649	7.80E-07	Tfh0/Tfh1
Snrpf	5.53E-11	0.630932	8.56E-07	Tfh0/Tfh1
Aprt	5.79E-11	0.594929	8.95E-07	Tfh0/Tfh1
Orai1	5.81E-11	0.571448	9.00E-07	Tfh0/Tfh1
Madd	6.37E-11	-0.92091	9.86E-07	Tfh0/Tfh1
Tnfrsf26	6.58E-11	-0.66883	1.02E-06	Tfh0/Tfh1
Klf13	6.67E-11	-0.80047	1.03E-06	Tfh0/Tfh1
H2-D1	6.75E-11	-0.48521	1.04E-06	Tfh0/Tfh1
Mettl16	6.94E-11	0.564383	1.07E-06	Tfh0/Tfh1
Cdc42se2	7.05E-11	-0.8341	1.09E-06	Tfh0/Tfh1
Nle1	7.07E-11	0.473077	1.09E-06	Tfh0/Tfh1
Tcerg1	7.35E-11	0.735655	1.14E-06	Tfh0/Tfh1
Npc2	7.46E-11	-0.91367	1.15E-06	Tfh0/Tfh1
Pgam1	7.70E-11	0.693428	1.19E-06	Tfh0/Tfh1
Dot1l	8.26E-11	0.587081	1.28E-06	Tfh0/Tfh1
Ar	8.29E-11	-0.9215	1.28E-06	Tfh0/Tfh1
Trnau1ap	8.77E-11	0.515488	1.36E-06	Tfh0/Tfh1
Spred1	8.82E-11	0.479162	1.37E-06	Tfh0/Tfh1
Rflnb	9.65E-11	-1.29882	1.49E-06	Tfh0/Tfh1

Zeb1	9.82E-11	-0.85184	1.52E-06	Tfh0/Tfh1
Ltb	9.99E-11	-0.79476	1.55E-06	Tfh0/Tfh1
Slc25a5	1.02E-10	0.721768	1.57E-06	Tfh0/Tfh1
Rinl	1.03E-10	-0.88692	1.59E-06	Tfh0/Tfh1
Exosc1	1.05E-10	0.625004	1.63E-06	Tfh0/Tfh1
Gpsm3	1.11E-10	-0.98555	1.72E-06	Tfh0/Tfh1
Eef1akmt4	1.15E-10	0.356615	1.77E-06	Tfh0/Tfh1
Polr1b	1.16E-10	0.448866	1.79E-06	Tfh0/Tfh1
Ehd1	1.17E-10	0.634526	1.81E-06	Tfh0/Tfh1
AI506816	1.17E-10	0.708806	1.82E-06	Tfh0/Tfh1
Nefh	1.17E-10	0.636067	1.82E-06	Tfh0/Tfh1
Nol12	1.18E-10	0.486973	1.83E-06	Tfh0/Tfh1
Rpl39	1.27E-10	-0.46652	1.97E-06	Tfh0/Tfh1
Hirip3	1.33E-10	0.603362	2.05E-06	Tfh0/Tfh1
Dis3	1.35E-10	0.465813	2.08E-06	Tfh0/Tfh1
Pfdn6	1.36E-10	0.579657	2.11E-06	Tfh0/Tfh1
Cnp	1.38E-10	-0.8025	2.14E-06	Tfh0/Tfh1
Qtrt2	1.46E-10	0.421548	2.25E-06	Tfh0/Tfh1
Aatf	1.48E-10	0.535473	2.29E-06	Tfh0/Tfh1
Snx5	1.49E-10	0.551673	2.30E-06	Tfh0/Tfh1
Dctpp1	1.60E-10	0.526997	2.48E-06	Tfh0/Tfh1
Mrpl17	1.71E-10	0.628397	2.64E-06	Tfh0/Tfh1
Rpl15	1.76E-10	0.434787	2.72E-06	Tfh0/Tfh1
Pkn1	1.80E-10	-0.72216	2.78E-06	Tfh0/Tfh1
Rpl4	1.84E-10	0.44128	2.84E-06	Tfh0/Tfh1
Cmss1	1.90E-10	0.503275	2.95E-06	Tfh0/Tfh1
Sinhcaf	2.02E-10	0.661338	3.12E-06	Tfh0/Tfh1
Ola1	2.03E-10	0.534453	3.14E-06	Tfh0/Tfh1
Arl6ip1	2.04E-10	-0.70384	3.15E-06	Tfh0/Tfh1
Magoh	2.05E-10	0.558883	3.17E-06	Tfh0/Tfh1
Zbtb20	2.11E-10	-1.00109	3.26E-06	Tfh0/Tfh1
Kti12	2.12E-10	0.446538	3.28E-06	Tfh0/Tfh1
Saraf	2.14E-10	-0.90043	3.31E-06	Tfh0/Tfh1
Pprc1	2.23E-10	0.485015	3.45E-06	Tfh0/Tfh1
Arid4a	2.37E-10	-1.07793	3.67E-06	Tfh0/Tfh1
Ifrd2	2.39E-10	0.572039	3.70E-06	Tfh0/Tfh1
Ssr2	2.42E-10	0.46995	3.75E-06	Tfh0/Tfh1
Rps12	2.46E-10	0.412957	3.80E-06	Tfh0/Tfh1
Gfer	2.77E-10	0.492641	4.29E-06	Tfh0/Tfh1
Naa25	2.87E-10	0.446409	4.44E-06	Tfh0/Tfh1
Psmc5	2.89E-10	0.545998	4.48E-06	Tfh0/Tfh1
Ifrd1	2.91E-10	0.669472	4.50E-06	Tfh0/Tfh1
Aimp2	2.94E-10	0.445373	4.55E-06	Tfh0/Tfh1
Smarcc1	3.01E-10	0.700293	4.66E-06	Tfh0/Tfh1
Nr3c1	3.01E-10	-0.93934	4.66E-06	Tfh0/Tfh1

Ptpn5	3.03E-10	0.828066	4.69E-06	Tfh0/Tfh1
Snhg17	3.40E-10	0.401779	5.27E-06	Tfh0/Tfh1
Bcap29	3.62E-10	0.577663	5.60E-06	Tfh0/Tfh1
Ier2	3.62E-10	0.796762	5.61E-06	Tfh0/Tfh1
Bccip	3.69E-10	0.514371	5.71E-06	Tfh0/Tfh1
Hif1a	3.69E-10	0.76076	5.72E-06	Tfh0/Tfh1
Clic1	3.75E-10	-0.68131	5.81E-06	Tfh0/Tfh1
Atp2a2	3.77E-10	0.409683	5.83E-06	Tfh0/Tfh1
Eif4g2	4.11E-10	0.61362	6.36E-06	Tfh0/Tfh1
Zfp36l2	4.30E-10	-0.99593	6.66E-06	Tfh0/Tfh1
A930005H10Rik	4.60E-10	-0.73653	7.12E-06	Tfh0/Tfh1
Rbm19	4.70E-10	0.428081	7.27E-06	Tfh0/Tfh1
Metap2	4.80E-10	0.589186	7.43E-06	Tfh0/Tfh1
Rpl7a	4.84E-10	0.435746	7.50E-06	Tfh0/Tfh1
Nr4a3	5.11E-10	0.568431	7.91E-06	Tfh0/Tfh1
Gnl2	5.15E-10	0.605517	7.97E-06	Tfh0/Tfh1
Rbbp7	5.23E-10	0.562625	8.09E-06	Tfh0/Tfh1
Tnfrsf9	5.44E-10	0.716956	8.41E-06	Tfh0/Tfh1
Tsc22d4	5.67E-10	-0.85138	8.78E-06	Tfh0/Tfh1
Pik3ip1	5.71E-10	-0.84491	8.84E-06	Tfh0/Tfh1
Orc2	5.78E-10	0.458869	8.95E-06	Tfh0/Tfh1
Kif21b	5.80E-10	-0.75153	8.97E-06	Tfh0/Tfh1
Siah2	5.88E-10	0.438988	9.10E-06	Tfh0/Tfh1
Lsg1	5.96E-10	0.483429	9.22E-06	Tfh0/Tfh1
Ddx56	5.97E-10	0.433588	9.24E-06	Tfh0/Tfh1
Casp4	6.27E-10	0.809026	9.70E-06	Tfh0/Tfh1
Glrx3	6.27E-10	0.560683	9.70E-06	Tfh0/Tfh1
Trmt1	6.38E-10	0.500822	9.87E-06	Tfh0/Tfh1
Taf1d	6.48E-10	0.70314	1.00E-05	Tfh0/Tfh1
Egr2	6.58E-10	0.535738	1.02E-05	Tfh0/Tfh1
Srsf3	6.74E-10	0.521712	1.04E-05	Tfh0/Tfh1
Klhl6	6.80E-10	-0.94545	1.05E-05	Tfh0/Tfh1
Rela	6.90E-10	0.574432	1.07E-05	Tfh0/Tfh1
Slc41a1	7.26E-10	0.726752	1.12E-05	Tfh0/Tfh1
Eif3f	7.42E-10	-0.65175	1.15E-05	Tfh0/Tfh1
H2-Q7	7.85E-10	-0.70046	1.22E-05	Tfh0/Tfh1
2810004N23Rik	8.06E-10	0.626191	1.25E-05	Tfh0/Tfh1
Snrpa1	8.28E-10	0.585261	1.28E-05	Tfh0/Tfh1
Ivns1abp	8.35E-10	0.674271	1.29E-05	Tfh0/Tfh1
Psma7	8.39E-10	0.570802	1.30E-05	Tfh0/Tfh1
Gm2a	8.61E-10	-0.66872	1.33E-05	Tfh0/Tfh1
Ptges3	8.79E-10	0.519253	1.36E-05	Tfh0/Tfh1
Abcc1	9.11E-10	0.51741	1.41E-05	Tfh0/Tfh1
Pbxip1	9.44E-10	-0.89996	1.46E-05	Tfh0/Tfh1
Chac1	9.55E-10	0.408821	1.48E-05	Tfh0/Tfh1

Rrp1	1.02E-09	0.542597	1.57E-05	Tfh0/Tfh1
2410002F23Rik	1.06E-09	0.417633	1.65E-05	Tfh0/Tfh1
Thumpd3	1.06E-09	0.538752	1.65E-05	Tfh0/Tfh1
Dnm2	1.11E-09	-0.73501	1.72E-05	Tfh0/Tfh1
Abhd17c	1.12E-09	0.485086	1.74E-05	Tfh0/Tfh1
Tomm5	1.12E-09	0.814509	1.74E-05	Tfh0/Tfh1
Snhg4	1.13E-09	0.561211	1.74E-05	Tfh0/Tfh1
Nomo1	1.14E-09	0.491809	1.76E-05	Tfh0/Tfh1
Slc19a1	1.14E-09	0.47187	1.76E-05	Tfh0/Tfh1
Clns1a	1.14E-09	0.531043	1.77E-05	Tfh0/Tfh1
Trac	1.20E-09	0.640132	1.86E-05	Tfh0/Tfh1
Clpp	1.32E-09	0.41094	2.04E-05	Tfh0/Tfh1
Metap1	1.32E-09	0.458002	2.05E-05	Tfh0/Tfh1
Otulinl	1.35E-09	-0.66289	2.09E-05	Tfh0/Tfh1
Dusp10	1.36E-09	-0.6666	2.10E-05	Tfh0/Tfh1
Rilpl2	1.37E-09	0.710556	2.12E-05	Tfh0/Tfh1
Psmd11	1.38E-09	0.551304	2.14E-05	Tfh0/Tfh1
Plk3	1.42E-09	0.451975	2.19E-05	Tfh0/Tfh1
Wdr4	1.47E-09	0.373059	2.27E-05	Tfh0/Tfh1
Larp4	1.57E-09	0.609043	2.43E-05	Tfh0/Tfh1
Prex1	1.59E-09	-0.70545	2.46E-05	Tfh0/Tfh1
D030028A08Rik	1.73E-09	0.392124	2.68E-05	Tfh0/Tfh1
mt-Atp6	1.83E-09	-0.26904	2.84E-05	Tfh0/Tfh1
Smpdl3a	1.85E-09	-0.73642	2.86E-05	Tfh0/Tfh1
Icos	1.87E-09	0.818038	2.89E-05	Tfh0/Tfh1
Nudt5	1.93E-09	0.496444	2.99E-05	Tfh0/Tfh1
Polr1a	1.98E-09	0.490192	3.07E-05	Tfh0/Tfh1
Ndufaf8	2.00E-09	0.522417	3.09E-05	Tfh0/Tfh1
Nufip1	2.02E-09	0.492339	3.13E-05	Tfh0/Tfh1
Cfdp1	2.04E-09	0.609859	3.16E-05	Tfh0/Tfh1
Mrps7	2.09E-09	0.432825	3.23E-05	Tfh0/Tfh1
Gm42418	2.15E-09	-0.39665	3.32E-05	Tfh0/Tfh1
Prpf40a	2.30E-09	0.499314	3.55E-05	Tfh0/Tfh1
Ddx1	2.35E-09	0.508794	3.63E-05	Tfh0/Tfh1
Gng5	2.37E-09	0.47745	3.67E-05	Tfh0/Tfh1
Peli1	2.40E-09	-0.92233	3.71E-05	Tfh0/Tfh1
Timm13	2.44E-09	0.575411	3.77E-05	Tfh0/Tfh1
Rbm17	2.45E-09	0.533951	3.79E-05	Tfh0/Tfh1
Snrpd2	2.59E-09	0.602294	4.00E-05	Tfh0/Tfh1
Gm47283	2.59E-09	0.524862	4.01E-05	Tfh0/Tfh1
Nucks1	2.65E-09	0.487354	4.10E-05	Tfh0/Tfh1
Ywhae	2.76E-09	0.514012	4.27E-05	Tfh0/Tfh1
Rpl35	2.77E-09	0.49569	4.28E-05	Tfh0/Tfh1
Tfdp1	2.77E-09	0.449259	4.29E-05	Tfh0/Tfh1
Glcci1	2.82E-09	-0.72112	4.37E-05	Tfh0/Tfh1

Magohb	2.86E-09	0.351869	4.42E-05	Tfh0/Tfh1
Rcsd1	2.96E-09	-0.81835	4.58E-05	Tfh0/Tfh1
Cdc42ep3	2.98E-09	-0.63889	4.61E-05	Tfh0/Tfh1
Zfp106	2.99E-09	0.56411	4.63E-05	Tfh0/Tfh1
Cad	3.07E-09	0.4809	4.75E-05	Tfh0/Tfh1
Baz1a	3.10E-09	0.704091	4.79E-05	Tfh0/Tfh1
Dnajc11	3.25E-09	0.478768	5.03E-05	Tfh0/Tfh1
1700019D03Rik	3.49E-09	0.704607	5.40E-05	Tfh0/Tfh1
Ppm1h	3.67E-09	-0.7641	5.68E-05	Tfh0/Tfh1
Fam189b	3.70E-09	-0.64322	5.73E-05	Tfh0/Tfh1
Arl6ip5	3.77E-09	-0.77213	5.83E-05	Tfh0/Tfh1
Slc38a2	3.85E-09	0.570155	5.97E-05	Tfh0/Tfh1
Fth1	3.89E-09	-0.92088	6.02E-05	Tfh0/Tfh1
Wdr55	3.94E-09	0.342301	6.11E-05	Tfh0/Tfh1
Hnrnpc	3.96E-09	0.517931	6.12E-05	Tfh0/Tfh1
Pak1ip1	4.11E-09	0.505204	6.36E-05	Tfh0/Tfh1
Rbm28	4.17E-09	0.504483	6.45E-05	Tfh0/Tfh1
Pwp2	4.19E-09	0.374882	6.48E-05	Tfh0/Tfh1
Hist1h1c	4.52E-09	-0.81584	7.00E-05	Tfh0/Tfh1
Itgb7	4.56E-09	-0.79621	7.06E-05	Tfh0/Tfh1
Psmc1	4.58E-09	0.438458	7.10E-05	Tfh0/Tfh1
Amd1	4.60E-09	0.402287	7.12E-05	Tfh0/Tfh1
Rps27a	4.63E-09	0.317454	7.17E-05	Tfh0/Tfh1
Dock2	4.77E-09	-0.8212	7.38E-05	Tfh0/Tfh1
Rpl28	4.86E-09	0.390963	7.52E-05	Tfh0/Tfh1
Sco2	4.87E-09	0.417791	7.53E-05	Tfh0/Tfh1
Arhgap30	5.03E-09	-0.64402	7.78E-05	Tfh0/Tfh1
Ahnak	5.05E-09	-1.14077	7.81E-05	Tfh0/Tfh1
Ankrd49	5.18E-09	0.435889	8.02E-05	Tfh0/Tfh1
D16Ertd472e	5.35E-09	0.586644	8.29E-05	Tfh0/Tfh1
Adk	5.45E-09	-0.99742	8.43E-05	Tfh0/Tfh1
Fcf1	5.74E-09	0.519173	8.89E-05	Tfh0/Tfh1
Itga6	5.83E-09	-0.81779	9.03E-05	Tfh0/Tfh1
Eef1b2	5.94E-09	0.423279	9.19E-05	Tfh0/Tfh1
Cluh	6.06E-09	0.45735	9.37E-05	Tfh0/Tfh1
Nr2c2ap	6.17E-09	0.467003	9.55E-05	Tfh0/Tfh1
Nt5e	6.21E-09	-0.77655	9.61E-05	Tfh0/Tfh1
Rbis	6.25E-09	0.50932	9.67E-05	Tfh0/Tfh1
Ccdc58	6.86E-09	0.375563	0.000106	Tfh0/Tfh1
Nfatc3	6.89E-09	-0.79279	0.000107	Tfh0/Tfh1
Tnf	7.13E-09	0.900559	0.00011	Tfh0/Tfh1
Dusp2	7.32E-09	0.845567	0.000113	Tfh0/Tfh1
Pin1	7.41E-09	0.47155	0.000115	Tfh0/Tfh1
Atp5o	7.58E-09	0.477101	0.000117	Tfh0/Tfh1
Eloc	7.63E-09	0.50491	0.000118	Tfh0/Tfh1

Riox1	7.68E-09	0.398612	0.000119	Tfh0/Tfh1
Sfpq	7.75E-09	0.54177	0.00012	Tfh0/Tfh1
Rheb	7.75E-09	0.578906	0.00012	Tfh0/Tfh1
Bop1	7.80E-09	0.427332	0.000121	Tfh0/Tfh1
Lats2	7.86E-09	-0.69516	0.000122	Tfh0/Tfh1
Srsf9	7.95E-09	0.457588	0.000123	Tfh0/Tfh1
Arhgap25	8.20E-09	-0.73738	0.000127	Tfh0/Tfh1
Psma5	8.27E-09	0.510167	0.000128	Tfh0/Tfh1
Numa1	8.36E-09	-0.79972	0.000129	Tfh0/Tfh1
Hax1	8.37E-09	0.453307	0.00013	Tfh0/Tfh1
Srfbp1	8.56E-09	0.418433	0.000133	Tfh0/Tfh1
Timm44	8.59E-09	0.458009	0.000133	Tfh0/Tfh1
Sf3b3	8.60E-09	0.432551	0.000133	Tfh0/Tfh1
Hilpda	8.62E-09	0.473774	0.000133	Tfh0/Tfh1
Pabpc4	8.72E-09	0.456603	0.000135	Tfh0/Tfh1
Sms	8.94E-09	0.587907	0.000138	Tfh0/Tfh1
Ctsd	8.98E-09	-0.66086	0.000139	Tfh0/Tfh1
Gadd45gip1	9.00E-09	0.479239	0.000139	Tfh0/Tfh1
Erh	9.08E-09	0.572579	0.000141	Tfh0/Tfh1
Lef1	9.09E-09	-1.07759	0.000141	Tfh0/Tfh1
Ipo7	9.45E-09	0.522874	0.000146	Tfh0/Tfh1
Psma3	9.46E-09	0.418349	0.000146	Tfh0/Tfh1
Rabggtb	9.68E-09	0.388144	0.00015	Tfh0/Tfh1
Ptprs	1.03E-08	0.437317	0.000159	Tfh0/Tfh1
Nmd3	1.04E-08	0.529643	0.000161	Tfh0/Tfh1
AI504432	1.04E-08	0.536974	0.000161	Tfh0/Tfh1
Prmt3	1.05E-08	0.495302	0.000163	Tfh0/Tfh1
A430093F15Rik	1.05E-08	0.677035	0.000163	Tfh0/Tfh1
Tasor2	1.06E-08	0.549646	0.000163	Tfh0/Tfh1
Hsd17b12	1.07E-08	0.456127	0.000165	Tfh0/Tfh1
Pomp	1.09E-08	0.534668	0.000169	Tfh0/Tfh1
Rpia	1.09E-08	0.485566	0.000169	Tfh0/Tfh1
Pole4	1.12E-08	0.574326	0.000173	Tfh0/Tfh1
Ube2n	1.20E-08	0.452919	0.000185	Tfh0/Tfh1
Dck	1.23E-08	-0.49383	0.000191	Tfh0/Tfh1
Eif6	1.24E-08	0.551709	0.000191	Tfh0/Tfh1
Dusp5	1.24E-08	0.684827	0.000193	Tfh0/Tfh1
Ube2h	1.30E-08	-0.76202	0.000202	Tfh0/Tfh1
Ttc27	1.31E-08	0.297668	0.000203	Tfh0/Tfh1
Trim28	1.34E-08	0.496478	0.000208	Tfh0/Tfh1
Tgfb1	1.36E-08	0.563049	0.000211	Tfh0/Tfh1
Ankrd12	1.38E-08	-0.84617	0.000214	Tfh0/Tfh1
Prdx1	1.40E-08	0.524544	0.000217	Tfh0/Tfh1
Smyd5	1.44E-08	0.420646	0.000223	Tfh0/Tfh1
Caprin1	1.44E-08	0.568549	0.000223	Tfh0/Tfh1

Epsti1	1.45E-08	-1.02037	0.000224	Tfh0/Tfh1
Trmt61a	1.46E-08	0.417223	0.000227	Tfh0/Tfh1
Yars2	1.47E-08	0.373193	0.000227	Tfh0/Tfh1
Traf3ip3	1.47E-08	-0.76993	0.000228	Tfh0/Tfh1
Cd52	1.50E-08	-0.6875	0.000232	Tfh0/Tfh1
Chchd1	1.54E-08	0.478457	0.000239	Tfh0/Tfh1
Sh3bgrl3	1.54E-08	-0.61579	0.000239	Tfh0/Tfh1
Mir17hg	1.56E-08	0.452016	0.000241	Tfh0/Tfh1
Ifi206	1.57E-08	-0.75981	0.000243	Tfh0/Tfh1
Mrps10	1.60E-08	0.522375	0.000248	Tfh0/Tfh1
Tcf25	1.64E-08	-0.66722	0.000254	Tfh0/Tfh1
Anp32e	1.64E-08	0.565425	0.000254	Tfh0/Tfh1
Pitpnc1	1.68E-08	-0.80889	0.00026	Tfh0/Tfh1
Pfdn4	1.69E-08	0.440716	0.000261	Tfh0/Tfh1
Sesn2	1.71E-08	0.413534	0.000265	Tfh0/Tfh1
Cyth4	1.71E-08	-0.61757	0.000265	Tfh0/Tfh1
Ddx10	1.76E-08	0.533699	0.000273	Tfh0/Tfh1
Llph	1.79E-08	0.521056	0.000277	Tfh0/Tfh1
Cdca7	1.79E-08	0.449194	0.000278	Tfh0/Tfh1
Psmd14	1.88E-08	0.482345	0.000291	Tfh0/Tfh1
Ell2	1.89E-08	0.517466	0.000293	Tfh0/Tfh1
Mdh2	1.91E-08	0.454152	0.000296	Tfh0/Tfh1
Ube2v2	1.96E-08	0.449227	0.000304	Tfh0/Tfh1
Eif1ad	2.06E-08	0.519646	0.000319	Tfh0/Tfh1
Gnaq	2.07E-08	0.435472	0.00032	Tfh0/Tfh1
Kras	2.09E-08	0.763572	0.000324	Tfh0/Tfh1
Umps	2.14E-08	0.403318	0.000331	Tfh0/Tfh1
Cox7b	2.15E-08	0.556281	0.000333	Tfh0/Tfh1
Mrpl19	2.18E-08	0.424514	0.000337	Tfh0/Tfh1
Gimap9	2.22E-08	-0.82257	0.000343	Tfh0/Tfh1
Lgals1	2.23E-08	-1.053	0.000345	Tfh0/Tfh1
Wdr3	2.29E-08	0.486396	0.000354	Tfh0/Tfh1
Ero1l	2.29E-08	0.441082	0.000355	Tfh0/Tfh1
Serinc3	2.33E-08	-0.65985	0.00036	Tfh0/Tfh1
Txn2	2.33E-08	0.470304	0.000361	Tfh0/Tfh1
Ccnd3	2.36E-08	-0.81584	0.000365	Tfh0/Tfh1
Atic	2.44E-08	0.413455	0.000377	Tfh0/Tfh1
Thoc1	2.48E-08	0.477717	0.000383	Tfh0/Tfh1
Myl12a	2.49E-08	0.557898	0.000385	Tfh0/Tfh1
Pgk1	2.52E-08	0.627569	0.00039	Tfh0/Tfh1
Dnttip2	2.53E-08	0.522804	0.000392	Tfh0/Tfh1
Mars	2.66E-08	0.456647	0.000411	Tfh0/Tfh1
Cdk4	2.66E-08	0.575274	0.000411	Tfh0/Tfh1
Pbdc1	2.69E-08	0.429633	0.000416	Tfh0/Tfh1
Pcbp1	2.72E-08	0.527366	0.00042	Tfh0/Tfh1

Timm50	2.78E-08	0.34798	0.00043	Tfh0/Tfh1
H2-K1	2.78E-08	-0.40688	0.00043	Tfh0/Tfh1
Mrps14	2.80E-08	0.457605	0.000433	Tfh0/Tfh1
Slc16a1	2.82E-08	0.402617	0.000436	Tfh0/Tfh1
Pou2f2	2.87E-08	0.727997	0.000445	Tfh0/Tfh1
Purb	2.88E-08	0.599105	0.000445	Tfh0/Tfh1
Psap	2.98E-08	-0.70656	0.000462	Tfh0/Tfh1
Rps26	3.00E-08	0.372634	0.000464	Tfh0/Tfh1
St8sia1	3.00E-08	-0.73662	0.000464	Tfh0/Tfh1
St8sia4	3.04E-08	-0.81018	0.00047	Tfh0/Tfh1
Dnajb11	3.08E-08	0.43811	0.000477	Tfh0/Tfh1
Cyld	3.09E-08	-0.72684	0.000479	Tfh0/Tfh1
Eva1b	3.19E-08	-0.73853	0.000494	Tfh0/Tfh1
Trib3	3.20E-08	0.422685	0.000495	Tfh0/Tfh1
Cd37	3.26E-08	-0.74812	0.000505	Tfh0/Tfh1
Bicdl1	3.27E-08	0.437256	0.000505	Tfh0/Tfh1
Wdr77	3.31E-08	0.412895	0.000512	Tfh0/Tfh1
Zdhhc2	3.34E-08	0.566898	0.000517	Tfh0/Tfh1
Tnfrsf18	3.39E-08	0.567771	0.000525	Tfh0/Tfh1
Sell	3.39E-08	-0.92751	0.000525	Tfh0/Tfh1
Psmg1	3.50E-08	0.340248	0.000542	Tfh0/Tfh1
Imp4	3.50E-08	0.46543	0.000542	Tfh0/Tfh1
Ndufv2	3.60E-08	0.418895	0.000558	Tfh0/Tfh1
Pwp1	3.61E-08	0.446652	0.000559	Tfh0/Tfh1
Gimap1	3.62E-08	-0.6195	0.00056	Tfh0/Tfh1
Fam136a	3.66E-08	0.404534	0.000567	Tfh0/Tfh1
Grpel1	3.85E-08	0.474827	0.000596	Tfh0/Tfh1
Baz2b	3.95E-08	-0.72257	0.000611	Tfh0/Tfh1
Xpo5	4.09E-08	0.361016	0.000632	Tfh0/Tfh1
Polr1c	4.10E-08	0.462017	0.000635	Tfh0/Tfh1
Utp14a	4.11E-08	0.538405	0.000637	Tfh0/Tfh1
Nsfl1c	4.13E-08	0.434803	0.000639	Tfh0/Tfh1
Myh9	4.24E-08	-0.77913	0.000656	Tfh0/Tfh1
Krr1	4.27E-08	0.39165	0.000661	Tfh0/Tfh1
Phf10	4.28E-08	0.52837	0.000663	Tfh0/Tfh1
Uchl3	4.30E-08	0.394563	0.000665	Tfh0/Tfh1
Rps6	4.32E-08	0.297797	0.000669	Tfh0/Tfh1
Fyn	4.44E-08	0.575882	0.000687	Tfh0/Tfh1
Fyttd1	4.47E-08	0.372466	0.000692	Tfh0/Tfh1
Bloc1s4	4.59E-08	0.407135	0.00071	Tfh0/Tfh1
Arf6	4.62E-08	0.577541	0.000715	Tfh0/Tfh1
Bola3	4.66E-08	0.488911	0.000722	Tfh0/Tfh1
Surf2	4.71E-08	0.416056	0.000728	Tfh0/Tfh1
Slc35a4	5.12E-08	0.308932	0.000793	Tfh0/Tfh1
Ywhag	5.26E-08	0.32801	0.000815	Tfh0/Tfh1

Ptpn6	5.42E-08	0.451802	0.000838	Tfh0/Tfh1
Mfhas1	5.42E-08	0.630079	0.00084	Tfh0/Tfh1
Cish	5.44E-08	0.50089	0.000842	Tfh0/Tfh1
Gabpb1	5.51E-08	0.474028	0.000852	Tfh0/Tfh1
Pcgf6	5.94E-08	0.36856	0.000919	Tfh0/Tfh1
Stap1	6.05E-08	0.666563	0.000936	Tfh0/Tfh1
Nrn1	6.24E-08	1.181427	0.000966	Tfh0/Tfh1
Dtx3l	6.43E-08	-0.77469	0.000995	Tfh0/Tfh1
Nvl	6.45E-08	0.447356	0.000999	Tfh0/Tfh1
Jakmip1	6.48E-08	-0.61937	0.001003	Tfh0/Tfh1
Cast	6.70E-08	-0.82679	0.001036	Tfh0/Tfh1
Txnrd1	6.72E-08	0.426466	0.00104	Tfh0/Tfh1
Tuba1a	6.87E-08	-0.63922	0.001063	Tfh0/Tfh1
Dnaja3	7.04E-08	0.364516	0.00109	Tfh0/Tfh1
Aars	7.05E-08	0.389335	0.001091	Tfh0/Tfh1
Dars	7.10E-08	0.348972	0.001099	Tfh0/Tfh1
Utrn	7.21E-08	-0.74371	0.001115	Tfh0/Tfh1
Ccnd2	7.38E-08	0.712283	0.001143	Tfh0/Tfh1
Eif5	7.51E-08	0.493881	0.001163	Tfh0/Tfh1
Sde2	7.60E-08	0.37934	0.001177	Tfh0/Tfh1
Ifi47	7.63E-08	-0.94526	0.001181	Tfh0/Tfh1
Chd1	7.81E-08	0.5135	0.001208	Tfh0/Tfh1
Dancr	7.91E-08	0.399345	0.001224	Tfh0/Tfh1
Pcmtd2	7.91E-08	-0.66834	0.001224	Tfh0/Tfh1
Zfp131	7.94E-08	0.431781	0.001229	Tfh0/Tfh1
Tgs1	7.99E-08	0.39949	0.001236	Tfh0/Tfh1
Psmd3	8.14E-08	0.408585	0.00126	Tfh0/Tfh1
Faah	8.15E-08	-0.78573	0.001262	Tfh0/Tfh1
Clptm1l	8.20E-08	0.5097	0.001269	Tfh0/Tfh1
Tmem38b	8.23E-08	0.500458	0.001273	Tfh0/Tfh1
Nudt4	8.27E-08	0.527572	0.00128	Tfh0/Tfh1
Gtf3c6	8.32E-08	0.418654	0.001288	Tfh0/Tfh1
Ppie	8.38E-08	0.397658	0.001297	Tfh0/Tfh1
Mrpl42	8.60E-08	0.475186	0.001331	Tfh0/Tfh1
Tufm	8.79E-08	0.406649	0.00136	Tfh0/Tfh1
Mrpl21	8.79E-08	0.480812	0.001361	Tfh0/Tfh1
Il18r1	8.99E-08	-0.82411	0.001392	Tfh0/Tfh1
Nafl	9.10E-08	0.410398	0.001408	Tfh0/Tfh1
Rad23b	9.43E-08	0.412596	0.001459	Tfh0/Tfh1
Mrpl20	9.50E-08	0.504638	0.00147	Tfh0/Tfh1
Cd3g	9.59E-08	-0.61734	0.001484	Tfh0/Tfh1
Carm1	9.64E-08	0.257759	0.001492	Tfh0/Tfh1
Hdac7	9.83E-08	0.578432	0.001522	Tfh0/Tfh1
Slc5a3	9.89E-08	0.435668	0.00153	Tfh0/Tfh1
Rwdd4a	1.00E-07	0.435103	0.001553	Tfh0/Tfh1

Psma2	1.02E-07	0.471902	0.001582	Tfh0/Tfh1
Tbl1x	1.04E-07	0.416875	0.001617	Tfh0/Tfh1
Nampt	1.05E-07	0.454687	0.001632	Tfh0/Tfh1
Hnrnpa0	1.06E-07	0.466886	0.001634	Tfh0/Tfh1
Bdp1	1.07E-07	0.417404	0.001661	Tfh0/Tfh1
Cnn2	1.14E-07	-0.65243	0.001757	Tfh0/Tfh1
Rrp8	1.14E-07	0.430119	0.00176	Tfh0/Tfh1
Tax1bp1	1.18E-07	-0.53392	0.001819	Tfh0/Tfh1
Fam98a	1.18E-07	0.31398	0.001821	Tfh0/Tfh1
Snrpe	1.20E-07	0.444558	0.00185	Tfh0/Tfh1
Pim3	1.21E-07	0.404389	0.001872	Tfh0/Tfh1
Cdk2ap1	1.24E-07	0.412165	0.001927	Tfh0/Tfh1
Mrpl35	1.26E-07	0.486688	0.001953	Tfh0/Tfh1
Lyst	1.27E-07	-0.97186	0.00197	Tfh0/Tfh1
Pole3	1.28E-07	0.407307	0.001978	Tfh0/Tfh1
Phactr2	1.29E-07	0.44944	0.001995	Tfh0/Tfh1
Pld3	1.29E-07	-0.5735	0.001997	Tfh0/Tfh1
Lpar6	1.33E-07	-0.74681	0.002054	Tfh0/Tfh1
Snrnp27	1.36E-07	0.397728	0.002104	Tfh0/Tfh1
Atp6v1d	1.43E-07	-0.7909	0.002217	Tfh0/Tfh1
Ilf2	1.48E-07	0.4813	0.002293	Tfh0/Tfh1
Mrpl23	1.51E-07	0.496747	0.002339	Tfh0/Tfh1
Kmt5a	1.52E-07	0.506987	0.002356	Tfh0/Tfh1
1810026B05Rik	1.56E-07	-0.57636	0.002409	Tfh0/Tfh1
Ddx54	1.60E-07	0.469279	0.002482	Tfh0/Tfh1
Gimap3	1.61E-07	-0.86579	0.002485	Tfh0/Tfh1
AY036118	1.62E-07	-0.43224	0.0025	Tfh0/Tfh1
Snrpd3	1.62E-07	0.483479	0.002501	Tfh0/Tfh1
Crbn	1.64E-07	-0.89273	0.002538	Tfh0/Tfh1
Marcksl1	1.67E-07	0.338753	0.002589	Tfh0/Tfh1
Mydgf	1.68E-07	0.451998	0.002607	Tfh0/Tfh1
Sidt1	1.71E-07	-0.56428	0.002639	Tfh0/Tfh1
Rps3a1	1.72E-07	0.27425	0.002664	Tfh0/Tfh1
Cep83	1.77E-07	0.402495	0.00274	Tfh0/Tfh1
Itpr2	1.79E-07	-0.71836	0.002767	Tfh0/Tfh1
Canx	1.84E-07	0.463573	0.002846	Tfh0/Tfh1
Fam98b	1.85E-07	0.333227	0.002861	Tfh0/Tfh1
Ntrk3	1.86E-07	0.504477	0.002875	Tfh0/Tfh1
Tmem238	1.89E-07	0.389602	0.002923	Tfh0/Tfh1
Prmt7	1.90E-07	0.353392	0.002942	Tfh0/Tfh1
Jagn1	1.93E-07	0.378065	0.002987	Tfh0/Tfh1
Ubqln1	1.96E-07	0.38292	0.003032	Tfh0/Tfh1
Gart	1.97E-07	0.429177	0.003048	Tfh0/Tfh1
Hnrnpa3	2.02E-07	0.430144	0.003132	Tfh0/Tfh1
Snd1	2.05E-07	0.371998	0.003166	Tfh0/Tfh1

Knop1	2.09E-07	0.398307	0.003235	Tfh0/Tfh1
Selenos	2.09E-07	0.439754	0.003237	Tfh0/Tfh1
AU020206	2.11E-07	-0.8379	0.003272	Tfh0/Tfh1
Ube2e1	2.12E-07	0.386756	0.003286	Tfh0/Tfh1
Mrpl54	2.15E-07	0.395965	0.003335	Tfh0/Tfh1
Rwdd1	2.17E-07	0.453504	0.003362	Tfh0/Tfh1
Psmb6	2.22E-07	0.492208	0.003442	Tfh0/Tfh1
Hmgn1	2.24E-07	0.54882	0.003464	Tfh0/Tfh1
Btaf1	2.24E-07	0.408094	0.003472	Tfh0/Tfh1
Gbp7	2.26E-07	-0.98028	0.003499	Tfh0/Tfh1
Nubp1	2.34E-07	0.425383	0.003624	Tfh0/Tfh1
Bnip3l	2.43E-07	-0.69115	0.00376	Tfh0/Tfh1
Emc4	2.46E-07	0.350979	0.003808	Tfh0/Tfh1
Ino80	2.56E-07	0.364957	0.003961	Tfh0/Tfh1
Fh1	2.59E-07	0.338805	0.004007	Tfh0/Tfh1
Prkca	2.60E-07	0.586209	0.004032	Tfh0/Tfh1
Gabarap	2.63E-07	-0.56291	0.004065	Tfh0/Tfh1
Trmt6	2.66E-07	0.415197	0.004123	Tfh0/Tfh1
Ccl5	2.72E-07	-2.6351	0.004214	Tfh0/Tfh1
S1pr4	2.79E-07	-0.65002	0.004312	Tfh0/Tfh1
Rangap1	2.82E-07	0.527735	0.004368	Tfh0/Tfh1
Ptger2	2.85E-07	0.469512	0.004417	Tfh0/Tfh1
Washc2	2.95E-07	-0.63367	0.004559	Tfh0/Tfh1
Mrps22	2.96E-07	0.351143	0.004576	Tfh0/Tfh1
Lrig1	2.97E-07	0.335308	0.004598	Tfh0/Tfh1
Ldha	3.10E-07	0.526314	0.004806	Tfh0/Tfh1
Grcc10	3.12E-07	-0.71185	0.004824	Tfh0/Tfh1
Tmem70	3.15E-07	0.292492	0.00487	Tfh0/Tfh1
Pcna	3.21E-07	0.343994	0.004974	Tfh0/Tfh1
Cebpb	3.23E-07	0.518235	0.005005	Tfh0/Tfh1
Tbl3	3.25E-07	0.307977	0.005034	Tfh0/Tfh1
Naa20	3.30E-07	0.578681	0.0051	Tfh0/Tfh1
Zcchc10	3.30E-07	0.293603	0.005102	Tfh0/Tfh1
Sdf4	3.33E-07	0.623757	0.005158	Tfh0/Tfh1
Fam49a	3.38E-07	-0.58074	0.005233	Tfh0/Tfh1
Mpc1	3.39E-07	0.575115	0.005242	Tfh0/Tfh1
Ppp3ca	3.43E-07	-0.84416	0.005316	Tfh0/Tfh1
Ift80	3.46E-07	-0.78869	0.005359	Tfh0/Tfh1
Dimt1	3.48E-07	0.353484	0.00538	Tfh0/Tfh1
Hsf1	3.50E-07	0.37221	0.005423	Tfh0/Tfh1
Cxcl10	3.58E-07	0.674382	0.005533	Tfh0/Tfh1
Ptpn11	3.79E-07	0.295029	0.005862	Tfh0/Tfh1
Pop7	3.81E-07	0.332032	0.005891	Tfh0/Tfh1
9130401M01Rik	3.82E-07	0.412406	0.005915	Tfh0/Tfh1
Colgalt1	3.83E-07	0.428643	0.005933	Tfh0/Tfh1

Pfkp	3.85E-07	0.544586	0.005966	Tfh0/Tfh1
Cebpg	3.98E-07	0.446944	0.006153	Tfh0/Tfh1
Hnrnpf	3.98E-07	0.324666	0.006157	Tfh0/Tfh1
Phf5a	4.03E-07	0.448226	0.00624	Tfh0/Tfh1
Cops4	4.07E-07	0.296862	0.006297	Tfh0/Tfh1
Psma6	4.07E-07	0.474916	0.006303	Tfh0/Tfh1
Mcl1	4.13E-07	-0.60177	0.006396	Tfh0/Tfh1
Pde3b	4.16E-07	-0.66521	0.006432	Tfh0/Tfh1
Hspa14	4.27E-07	0.393622	0.006615	Tfh0/Tfh1
Hnrnpr	4.31E-07	0.429829	0.006674	Tfh0/Tfh1
Fam78a	4.34E-07	-0.58238	0.006715	Tfh0/Tfh1
Rpl35a	4.40E-07	0.267644	0.006804	Tfh0/Tfh1
Cflar	4.63E-07	0.603883	0.007173	Tfh0/Tfh1
Rpl5	4.66E-07	0.3127	0.007214	Tfh0/Tfh1
Cd3d	4.80E-07	-0.51319	0.007428	Tfh0/Tfh1
Alcam	4.82E-07	0.540347	0.007457	Tfh0/Tfh1
Arhgap4	4.88E-07	-0.51934	0.007555	Tfh0/Tfh1
Ap1s3	4.89E-07	0.403751	0.007561	Tfh0/Tfh1
Top2b	4.93E-07	-0.68708	0.007636	Tfh0/Tfh1
Tnrc6c	5.02E-07	-0.69392	0.007771	Tfh0/Tfh1
Ptpn7	5.04E-07	0.431465	0.007803	Tfh0/Tfh1
Gramd1b	5.07E-07	0.548632	0.007841	Tfh0/Tfh1
Ndufs8	5.07E-07	0.369486	0.007854	Tfh0/Tfh1
Zdhhc18	5.28E-07	-0.8003	0.008169	Tfh0/Tfh1
Gm16286	5.35E-07	0.415873	0.008278	Tfh0/Tfh1
Surf6	5.44E-07	0.343984	0.008416	Tfh0/Tfh1
Pes1	5.44E-07	0.443966	0.008419	Tfh0/Tfh1
Rbmxl1	5.49E-07	0.424388	0.008494	Tfh0/Tfh1
Dph5	5.60E-07	0.423867	0.008674	Tfh0/Tfh1
Taf15	5.81E-07	0.476616	0.008985	Tfh0/Tfh1
Adsl	5.81E-07	0.311108	0.008994	Tfh0/Tfh1
4932438A13Rik	5.82E-07	-0.67094	0.009015	Tfh0/Tfh1
Prelid3b	5.97E-07	0.323251	0.009233	Tfh0/Tfh1
Atp13a3	5.97E-07	0.43943	0.009241	Tfh0/Tfh1
Strap	6.03E-07	0.482944	0.009339	Tfh0/Tfh1
Slc9a8	6.13E-07	0.301512	0.009488	Tfh0/Tfh1
Atp11b	6.17E-07	-0.57993	0.009556	Tfh0/Tfh1
Pdcd5	6.23E-07	0.397414	0.009638	Tfh0/Tfh1
Nom1	6.31E-07	0.384573	0.009767	Tfh0/Tfh1
Txn1	6.35E-07	0.50521	0.009834	Tfh0/Tfh1
Myo5a	6.37E-07	0.34299	0.009853	Tfh0/Tfh1
Msn	6.51E-07	-0.49232	0.010081	Tfh0/Tfh1
Tmem140	6.53E-07	-0.58164	0.010106	Tfh0/Tfh1
Mrpl51	6.60E-07	0.38247	0.010211	Tfh0/Tfh1
Dnajc9	6.62E-07	-0.70096	0.010246	Tfh0/Tfh1

Sarnp	6.63E-07	0.485192	0.010257	Tfh0/Tfh1
Pinx1	6.87E-07	0.344998	0.01063	Tfh0/Tfh1
Apobec3	6.88E-07	-0.66022	0.010646	Tfh0/Tfh1
Carnmt1	6.89E-07	0.337964	0.010657	Tfh0/Tfh1
Adipor2	7.00E-07	0.441248	0.010832	Tfh0/Tfh1
Cd6	7.16E-07	0.626479	0.011086	Tfh0/Tfh1
Parl	7.18E-07	0.283237	0.01112	Tfh0/Tfh1
Mrpl11	7.24E-07	0.379732	0.011212	Tfh0/Tfh1
Smg5	7.30E-07	0.3309	0.0113	Tfh0/Tfh1
Ubb	7.31E-07	-0.33182	0.011308	Tfh0/Tfh1
Zfp598	7.32E-07	0.289364	0.011328	Tfh0/Tfh1
Tsr2	7.33E-07	0.278764	0.011349	Tfh0/Tfh1
Yif1a	7.37E-07	0.292472	0.011411	Tfh0/Tfh1
Uqcrh	7.65E-07	-0.46379	0.011836	Tfh0/Tfh1
Irgm1	7.69E-07	-0.74097	0.011907	Tfh0/Tfh1
Hspbp1	7.86E-07	0.393317	0.01217	Tfh0/Tfh1
Sash3	7.89E-07	-0.6011	0.01222	Tfh0/Tfh1
Pafah1b2	7.90E-07	0.349758	0.012223	Tfh0/Tfh1
Gm49336	8.02E-07	0.366459	0.012419	Tfh0/Tfh1
Il6ra	8.05E-07	-0.6783	0.012466	Tfh0/Tfh1
Rnf167	8.57E-07	-0.65899	0.013272	Tfh0/Tfh1
Ppp1r18	8.99E-07	-0.65196	0.013909	Tfh0/Tfh1
Smap1	9.02E-07	-0.65779	0.013969	Tfh0/Tfh1
Nudc	9.12E-07	0.43472	0.014111	Tfh0/Tfh1
Ly6a	9.18E-07	-1.06099	0.014203	Tfh0/Tfh1
Rplp0	9.40E-07	0.298316	0.014547	Tfh0/Tfh1
Abcf1	9.40E-07	0.411907	0.01455	Tfh0/Tfh1
Rps27	9.48E-07	-0.32247	0.014672	Tfh0/Tfh1
Dock8	9.58E-07	-0.65325	0.014832	Tfh0/Tfh1
Lig3	9.65E-07	0.30842	0.014936	Tfh0/Tfh1
Prkd2	9.66E-07	-0.49861	0.014951	Tfh0/Tfh1
Selenow	9.67E-07	-0.64792	0.014967	Tfh0/Tfh1
Sf3a3	9.79E-07	0.373377	0.015149	Tfh0/Tfh1
Wbp4	9.85E-07	0.398001	0.01524	Tfh0/Tfh1
Ddx3x	1.00E-06	0.525145	0.015522	Tfh0/Tfh1
Rraga	1.01E-06	0.357327	0.015581	Tfh0/Tfh1
Cyc1	1.04E-06	0.449066	0.016031	Tfh0/Tfh1
Herc6	1.04E-06	-0.56952	0.016037	Tfh0/Tfh1
Ndufb8	1.04E-06	0.365118	0.016075	Tfh0/Tfh1
Cd40lg	1.04E-06	0.72619	0.016079	Tfh0/Tfh1
Stk10	1.06E-06	-0.70527	0.016447	Tfh0/Tfh1
Cd28	1.06E-06	-0.66955	0.016449	Tfh0/Tfh1
Rps18	1.09E-06	0.289021	0.016816	Tfh0/Tfh1
Ptger4	1.11E-06	0.582069	0.01723	Tfh0/Tfh1
Rpp38	1.14E-06	0.279089	0.017603	Tfh0/Tfh1

Smarca5	1.16E-06	0.445222	0.017911	Tfh0/Tfh1
Trim12c	1.16E-06	-0.69962	0.017961	Tfh0/Tfh1
Dhx15	1.17E-06	0.456267	0.018179	Tfh0/Tfh1
Tuba1c	1.18E-06	0.373003	0.018307	Tfh0/Tfh1
Ctla4	1.20E-06	0.644626	0.01858	Tfh0/Tfh1
Tsc22d2	1.20E-06	0.569335	0.01862	Tfh0/Tfh1
Twistnb	1.22E-06	0.51743	0.018813	Tfh0/Tfh1
Timm8b	1.22E-06	0.388118	0.018889	Tfh0/Tfh1
Mphosph6	1.23E-06	0.442242	0.01899	Tfh0/Tfh1
Cct8	1.30E-06	0.444733	0.020112	Tfh0/Tfh1
Cox5a	1.32E-06	0.398094	0.020474	Tfh0/Tfh1
Ppp4r2	1.34E-06	0.363066	0.020802	Tfh0/Tfh1
Eif3l	1.36E-06	0.375754	0.021071	Tfh0/Tfh1
Fkbp4	1.39E-06	0.431966	0.021512	Tfh0/Tfh1
Fam104a	1.41E-06	0.356588	0.021781	Tfh0/Tfh1
Ddost	1.41E-06	0.344389	0.021895	Tfh0/Tfh1
Txnl4a	1.42E-06	0.357526	0.022013	Tfh0/Tfh1
Nol9	1.42E-06	0.369548	0.022025	Tfh0/Tfh1
Rnasek	1.43E-06	-0.58765	0.022211	Tfh0/Tfh1
Heatr3	1.46E-06	0.332256	0.022567	Tfh0/Tfh1
Hadhb	1.46E-06	-0.56765	0.022652	Tfh0/Tfh1
Tpd52l2	1.49E-06	0.404401	0.023056	Tfh0/Tfh1
Psmd1	1.51E-06	0.383052	0.023315	Tfh0/Tfh1
Vars	1.52E-06	0.405332	0.023477	Tfh0/Tfh1
Ppip5k2	1.52E-06	0.404545	0.023497	Tfh0/Tfh1
Zfp652	1.53E-06	-0.53284	0.023687	Tfh0/Tfh1
Rae1	1.59E-06	0.344211	0.024579	Tfh0/Tfh1
Lnpep	1.60E-06	-0.64067	0.024708	Tfh0/Tfh1
Slc29a1	1.70E-06	0.277641	0.026375	Tfh0/Tfh1
Psmc4	1.72E-06	0.357466	0.026554	Tfh0/Tfh1
Elp1	1.73E-06	0.302703	0.026787	Tfh0/Tfh1
Nol6	1.74E-06	0.388826	0.027003	Tfh0/Tfh1
Rps25	1.77E-06	0.273299	0.027333	Tfh0/Tfh1
Mrps25	1.77E-06	0.320481	0.027451	Tfh0/Tfh1
Emc7	1.78E-06	0.436555	0.027571	Tfh0/Tfh1
Ppp1r11	1.80E-06	0.383301	0.02786	Tfh0/Tfh1
Actl6a	1.87E-06	0.347108	0.028936	Tfh0/Tfh1
Hprt	1.90E-06	0.34167	0.029341	Tfh0/Tfh1
Tprkb	1.91E-06	0.290639	0.029592	Tfh0/Tfh1
Gpbp1l1	1.95E-06	-0.61553	0.030109	Tfh0/Tfh1
Ndufb6	2.00E-06	0.350198	0.030936	Tfh0/Tfh1
Rpl8	2.02E-06	0.263216	0.031313	Tfh0/Tfh1
Irf2	2.05E-06	-0.69996	0.031743	Tfh0/Tfh1
Atad1	2.08E-06	0.395974	0.032194	Tfh0/Tfh1
Ccpg1	2.12E-06	-0.56898	0.032765	Tfh0/Tfh1

Fli1	2.13E-06	-0.57737	0.032936	Tfh0/Tfh1
Wdr5	2.16E-06	0.257879	0.033358	Tfh0/Tfh1
Rcc1	2.16E-06	0.340014	0.033379	Tfh0/Tfh1
Rars	2.18E-06	0.394051	0.033776	Tfh0/Tfh1
Rpl7	2.22E-06	0.251556	0.034301	Tfh0/Tfh1
Tmem11	2.25E-06	0.281052	0.034775	Tfh0/Tfh1
Pabpc1	2.25E-06	0.296414	0.034837	Tfh0/Tfh1
Lman1	2.29E-06	0.327907	0.035474	Tfh0/Tfh1
Nasp	2.31E-06	0.38917	0.035772	Tfh0/Tfh1
Nol7	2.34E-06	0.426398	0.036215	Tfh0/Tfh1
Ahsa1	2.38E-06	0.374678	0.03683	Tfh0/Tfh1
Prpf3	2.40E-06	0.283644	0.037141	Tfh0/Tfh1
Pam16	2.41E-06	0.380346	0.037241	Tfh0/Tfh1
Macf1	2.46E-06	-0.75624	0.038025	Tfh0/Tfh1
Alg5	2.48E-06	0.37826	0.038319	Tfh0/Tfh1
Thap12	2.49E-06	0.359314	0.03852	Tfh0/Tfh1
Prr13	2.49E-06	-0.60396	0.038521	Tfh0/Tfh1
Tespa1	2.51E-06	0.444706	0.038803	Tfh0/Tfh1
Nfu1	2.53E-06	0.34027	0.039172	Tfh0/Tfh1
Thap3	2.55E-06	-0.64684	0.039454	Tfh0/Tfh1
Pank3	2.56E-06	0.33336	0.039549	Tfh0/Tfh1
Bzw2	2.56E-06	0.404715	0.039616	Tfh0/Tfh1
Sar1a	2.63E-06	0.412778	0.04072	Tfh0/Tfh1
Eif3d	2.66E-06	0.41071	0.04111	Tfh0/Tfh1
Gm8369	2.66E-06	-0.58337	0.041174	Tfh0/Tfh1
Srsf10	2.67E-06	0.441395	0.041316	Tfh0/Tfh1
Cops7a	2.78E-06	0.25754	0.043002	Tfh0/Tfh1
Rpl31	2.80E-06	0.361116	0.043413	Tfh0/Tfh1
Gosr2	2.81E-06	0.301375	0.043438	Tfh0/Tfh1
Irf8	2.86E-06	0.520711	0.044344	Tfh0/Tfh1
Tmsb4x	2.89E-06	-0.34692	0.044754	Tfh0/Tfh1
Apbb1ip	2.92E-06	-0.65699	0.045168	Tfh0/Tfh1
Cdc73	2.96E-06	0.358492	0.045869	Tfh0/Tfh1
Gbp6	3.07E-06	-0.96551	0.047586	Tfh0/Tfh1
Ankrd28	3.09E-06	0.340386	0.047819	Tfh0/Tfh1
Slfn1	3.16E-06	-0.72738	0.048915	Tfh0/Tfh1
Ing5	3.30E-06	0.37786	0.051135	Tfh0/Tfh1
Polr3e	3.33E-06	0.281748	0.051606	Tfh0/Tfh1
Rps14	3.35E-06	-0.252	0.051833	Tfh0/Tfh1
Tet2	3.36E-06	0.481293	0.05194	Tfh0/Tfh1
Map1lc3b	3.38E-06	-0.45713	0.052271	Tfh0/Tfh1
Cdc37	3.44E-06	0.487359	0.053237	Tfh0/Tfh1
Ino80e	3.46E-06	0.371771	0.053518	Tfh0/Tfh1
Usp14	3.51E-06	0.359468	0.054393	Tfh0/Tfh1
Xpo4	3.55E-06	0.284654	0.054919	Tfh0/Tfh1

Hbp1	3.55E-06	-0.60077	0.054984	Tfh0/Tfh1
Saysd1	3.56E-06	0.295267	0.055087	Tfh0/Tfh1
Arid4b	3.61E-06	-1.21204	0.055868	Tfh0/Tfh1
H3f3b	3.63E-06	0.25086	0.056217	Tfh0/Tfh1
Gtf2f2	3.69E-06	0.359303	0.057109	Tfh0/Tfh1
Mrps5	3.73E-06	0.403655	0.057682	Tfh0/Tfh1
Akap13	3.73E-06	-0.35	0.057694	Tfh0/Tfh1
St6galnac3	3.77E-06	-0.56685	0.05837	Tfh0/Tfh1
Gnas	3.80E-06	-0.62613	0.058858	Tfh0/Tfh1
Gm4070	3.82E-06	-0.5017	0.05912	Tfh0/Tfh1
Shisa5	3.90E-06	-0.52471	0.06038	Tfh0/Tfh1
Acsl4	3.93E-06	0.398267	0.060803	Tfh0/Tfh1
Trim34a	4.06E-06	-0.52907	0.062767	Tfh0/Tfh1
Cops6	4.16E-06	0.433895	0.064432	Tfh0/Tfh1
Acsl5	4.18E-06	0.356869	0.064707	Tfh0/Tfh1
AI467606	4.26E-06	-0.62872	0.065891	Tfh0/Tfh1
Uba52	4.27E-06	-0.37591	0.066077	Tfh0/Tfh1
Mbd3	4.34E-06	0.341557	0.067136	Tfh0/Tfh1
Npepl1	4.43E-06	0.259055	0.068563	Tfh0/Tfh1
Kbtbd11	4.46E-06	-0.67149	0.069043	Tfh0/Tfh1
Rpp14	4.48E-06	0.280014	0.06936	Tfh0/Tfh1
Ak2	4.53E-06	0.470306	0.070046	Tfh0/Tfh1
Snx20	4.53E-06	-0.60808	0.070174	Tfh0/Tfh1
Ndufc2	4.57E-06	0.375049	0.070694	Tfh0/Tfh1
Ube2s	4.71E-06	0.289914	0.072962	Tfh0/Tfh1
Lncpint	4.81E-06	-0.74928	0.074452	Tfh0/Tfh1
Mrpl52	4.82E-06	0.425952	0.074616	Tfh0/Tfh1
Stoml2	4.91E-06	0.356705	0.076069	Tfh0/Tfh1
Mapkapk2	4.92E-06	0.427559	0.076098	Tfh0/Tfh1
Cdk19	4.96E-06	-0.63453	0.076749	Tfh0/Tfh1
Abhd8	4.96E-06	-0.50304	0.076802	Tfh0/Tfh1
Thoc3	5.08E-06	0.289991	0.078622	Tfh0/Tfh1
Usp37	5.19E-06	0.309067	0.080265	Tfh0/Tfh1
Sipa1	5.23E-06	-0.56824	0.080974	Tfh0/Tfh1
Lrpprc	5.25E-06	0.299216	0.081258	Tfh0/Tfh1
Psmc2	5.34E-06	0.42258	0.082695	Tfh0/Tfh1
Zcrb1	5.44E-06	0.399524	0.084149	Tfh0/Tfh1
Ifi27l2a	5.53E-06	-0.95113	0.085521	Tfh0/Tfh1
Bmi1	5.58E-06	0.313554	0.086431	Tfh0/Tfh1
Mrpl57	5.59E-06	0.371613	0.086517	Tfh0/Tfh1
Rpl3	5.59E-06	0.275453	0.086523	Tfh0/Tfh1
1110038B12Rik	5.60E-06	0.429435	0.08671	Tfh0/Tfh1
Cyfip2	5.65E-06	-0.77997	0.087504	Tfh0/Tfh1
Txnl1	5.75E-06	0.388386	0.088951	Tfh0/Tfh1
Man1a	5.77E-06	0.516899	0.089312	Tfh0/Tfh1

Usp36	5.82E-06	0.371843	0.090117	Tfh0/Tfh1
Rpf1	5.87E-06	0.325458	0.090895	Tfh0/Tfh1
Plec	5.88E-06	-0.66603	0.091059	Tfh0/Tfh1
Mrpl2	5.90E-06	0.318468	0.091264	Tfh0/Tfh1
Samd9l	5.92E-06	-0.83831	0.091645	Tfh0/Tfh1
Mrpl15	5.99E-06	0.464245	0.092693	Tfh0/Tfh1
Cd27	6.08E-06	-0.85151	0.094063	Tfh0/Tfh1
Xpnpep1	6.12E-06	0.253394	0.094683	Tfh0/Tfh1
Stat1	6.45E-06	-0.87916	0.099817	Tfh0/Tfh1
Ewsr1	6.49E-06	0.353642	0.100497	Tfh0/Tfh1
Csnk2a2	6.63E-06	0.440095	0.102688	Tfh0/Tfh1
Bag5	6.69E-06	0.377798	0.103513	Tfh0/Tfh1
Gpr174	6.79E-06	0.441614	0.105128	Tfh0/Tfh1
Ctu2	6.85E-06	0.27894	0.105998	Tfh0/Tfh1
Czib	6.87E-06	0.3138	0.106393	Tfh0/Tfh1
Mbp	6.90E-06	0.619024	0.106758	Tfh0/Tfh1
Nkapd1	6.90E-06	0.272129	0.106761	Tfh0/Tfh1
Nelfe	6.96E-06	0.301918	0.107765	Tfh0/Tfh1
Cct4	7.02E-06	0.44786	0.108674	Tfh0/Tfh1
Add3	7.07E-06	-0.76846	0.109405	Tfh0/Tfh1
Hist1h1e	7.13E-06	-0.67828	0.110435	Tfh0/Tfh1
Kdm2b	7.19E-06	0.343705	0.111246	Tfh0/Tfh1
9-Sep	7.25E-06	-0.61008	0.112247	Tfh0/Tfh1
Usp1	7.25E-06	0.335854	0.112272	Tfh0/Tfh1
Sh3kbp1	7.42E-06	-0.59334	0.114844	Tfh0/Tfh1
Mtx2	7.73E-06	0.260143	0.119719	Tfh0/Tfh1
Trap1	7.79E-06	0.305225	0.120562	Tfh0/Tfh1
Esyt2	7.88E-06	-0.63601	0.121974	Tfh0/Tfh1
Slc25a33	7.89E-06	0.283008	0.122172	Tfh0/Tfh1
Cox10	7.93E-06	0.270302	0.122679	Tfh0/Tfh1
Mrpl36	7.95E-06	0.400366	0.122984	Tfh0/Tfh1
Hpf1	7.98E-06	0.393638	0.123571	Tfh0/Tfh1
Ostf1	8.01E-06	-0.5621	0.123989	Tfh0/Tfh1
Lipa	8.14E-06	-0.48506	0.125987	Tfh0/Tfh1
Atp5g3	8.23E-06	0.393823	0.12739	Tfh0/Tfh1
Vma21	8.31E-06	0.270506	0.128585	Tfh0/Tfh1
Mpp1	8.34E-06	-0.39459	0.129155	Tfh0/Tfh1
Vdac2	8.40E-06	0.391567	0.130001	Tfh0/Tfh1
Med30	8.66E-06	0.324372	0.134072	Tfh0/Tfh1
Micos10	8.95E-06	0.322305	0.138599	Tfh0/Tfh1
Exosc10	9.00E-06	0.346529	0.139243	Tfh0/Tfh1
Paip2	9.13E-06	-0.657	0.141354	Tfh0/Tfh1
Klhdc4	9.26E-06	0.337375	0.143336	Tfh0/Tfh1
Agpat5	9.40E-06	0.353321	0.145546	Tfh0/Tfh1
Cyfip1	9.41E-06	0.60387	0.145686	Tfh0/Tfh1

Tln1	9.45E-06	-0.54766	0.146247	Tfh0/Tfh1
Emg1	1.00E-05	0.384351	0.154732	Tfh0/Tfh1
Lrif1	1.00E-05	-0.61098	0.154844	Tfh0/Tfh1
Siva1	1.01E-05	0.279418	0.156795	Tfh0/Tfh1
Arid5a	1.02E-05	-0.61784	0.157504	Tfh0/Tfh1
Ak6	1.02E-05	0.322633	0.158606	Tfh0/Tfh1
Rp9	1.05E-05	-0.56717	0.161763	Tfh0/Tfh1
Hcst	1.06E-05	-0.72041	0.163438	Tfh0/Tfh1
Nrbf2	1.07E-05	0.280436	0.165384	Tfh0/Tfh1
Uqcr10	1.07E-05	0.412053	0.166054	Tfh0/Tfh1
Gm26917	1.08E-05	0.597387	0.167823	Tfh0/Tfh1
Vasp	1.11E-05	0.401525	0.171107	Tfh0/Tfh1
Idh3a	1.11E-05	0.291508	0.171516	Tfh0/Tfh1
Plcxd2	1.11E-05	0.51616	0.17253	Tfh0/Tfh1
Selenoh	1.12E-05	-0.50186	0.172868	Tfh0/Tfh1
Ctla2a	1.14E-05	-0.65591	0.176652	Tfh0/Tfh1
Zmynd19	1.15E-05	0.301963	0.177706	Tfh0/Tfh1
Ccdc88c	1.15E-05	-0.58497	0.177799	Tfh0/Tfh1
Tgif1	1.17E-05	0.256845	0.181416	Tfh0/Tfh1
Plgrkt	1.20E-05	-0.52521	0.186333	Tfh0/Tfh1
Lcp2	1.23E-05	0.605018	0.190697	Tfh0/Tfh1
Supt4a	1.26E-05	-0.50985	0.194864	Tfh0/Tfh1
Setx	1.28E-05	-0.62803	0.198758	Tfh0/Tfh1
Pnrc1	1.30E-05	-0.50822	0.201191	Tfh0/Tfh1
Cdc34	1.31E-05	0.316905	0.203131	Tfh0/Tfh1
Trim5	1.32E-05	-0.44072	0.203998	Tfh0/Tfh1
Maf	1.33E-05	-1.08773	0.205858	Tfh0/Tfh1
Srp19	1.34E-05	0.316423	0.207724	Tfh0/Tfh1
Gimap8	1.36E-05	-0.6364	0.209976	Tfh0/Tfh1
Mrpl3	1.37E-05	0.319923	0.212538	Tfh0/Tfh1
Pkm	1.40E-05	0.428261	0.215975	Tfh0/Tfh1
Rfk	1.46E-05	0.317528	0.225973	Tfh0/Tfh1
Adcy7	1.46E-05	-0.52529	0.226125	Tfh0/Tfh1
Utp25	1.47E-05	0.25923	0.227416	Tfh0/Tfh1
Ahctf1	1.47E-05	0.384493	0.227553	Tfh0/Tfh1
Dtymk	1.48E-05	0.328763	0.228898	Tfh0/Tfh1
Smndc1	1.49E-05	0.388385	0.230196	Tfh0/Tfh1
Retreg1	1.49E-05	-0.69746	0.230755	Tfh0/Tfh1
Tmem59	1.50E-05	-0.55754	0.232014	Tfh0/Tfh1
Trim12a	1.50E-05	-0.55978	0.232558	Tfh0/Tfh1
Rnf7	1.52E-05	0.337622	0.235092	Tfh0/Tfh1
Tm9sf4	1.53E-05	0.340346	0.236313	Tfh0/Tfh1
Hccs	1.53E-05	0.250077	0.236883	Tfh0/Tfh1
Tfam	1.54E-05	0.272945	0.237731	Tfh0/Tfh1
Htatsf1	1.56E-05	0.3116	0.24161	Tfh0/Tfh1

Celf2	1.58E-05	-0.41561	0.243819	Tfh0/Tfh1
Arpc3	1.58E-05	-0.5683	0.244794	Tfh0/Tfh1
Rbm34	1.62E-05	0.359056	0.250646	Tfh0/Tfh1
Mafg	1.63E-05	0.324956	0.251763	Tfh0/Tfh1
Tmem214	1.68E-05	0.287777	0.259565	Tfh0/Tfh1
Prrc2b	1.69E-05	-0.62733	0.261863	Tfh0/Tfh1
Tor1b	1.73E-05	0.276183	0.267108	Tfh0/Tfh1
Polr2k	1.74E-05	0.321037	0.269463	Tfh0/Tfh1
Riok2	1.74E-05	0.301397	0.269892	Tfh0/Tfh1
Map4k4	1.75E-05	-0.68379	0.27083	Tfh0/Tfh1
Rpl22l1	1.75E-05	0.35216	0.270865	Tfh0/Tfh1
Ighm	1.78E-05	-0.8417	0.276204	Tfh0/Tfh1
Abcb1a	1.79E-05	-0.62386	0.276944	Tfh0/Tfh1
BE692007	1.83E-05	-0.95877	0.282862	Tfh0/Tfh1
Hmgb1	1.84E-05	-0.33494	0.284486	Tfh0/Tfh1
Adh5	1.85E-05	0.427257	0.286066	Tfh0/Tfh1
Evl	1.85E-05	-0.54269	0.286541	Tfh0/Tfh1
Farsa	1.89E-05	0.280484	0.292469	Tfh0/Tfh1
Imp3	1.90E-05	0.319588	0.294701	Tfh0/Tfh1
Rpn2	1.93E-05	0.321174	0.299334	Tfh0/Tfh1
Mrps18a	1.96E-05	0.312684	0.303025	Tfh0/Tfh1
Mea1	1.98E-05	0.284692	0.306078	Tfh0/Tfh1
Ccdc115	1.99E-05	0.316535	0.307431	Tfh0/Tfh1
Sptbn1	2.00E-05	-0.76441	0.309425	Tfh0/Tfh1
Prkacb	2.01E-05	-0.66797	0.311108	Tfh0/Tfh1
Scp2	2.04E-05	-0.62722	0.31502	Tfh0/Tfh1
Psmb10	2.06E-05	-0.56495	0.31818	Tfh0/Tfh1
Exosc7	2.07E-05	0.350768	0.320168	Tfh0/Tfh1
Mrps36	2.09E-05	0.360301	0.323624	Tfh0/Tfh1
Ppp3cc	2.13E-05	-0.59465	0.330407	Tfh0/Tfh1
Sun2	2.16E-05	-0.54833	0.334397	Tfh0/Tfh1
Ppp1r12a	2.17E-05	-0.59782	0.335323	Tfh0/Tfh1
Dpp4	2.17E-05	-0.52678	0.335427	Tfh0/Tfh1
Anapc15	2.17E-05	0.301417	0.335522	Tfh0/Tfh1
Stat5a	2.31E-05	0.364768	0.358251	Tfh0/Tfh1
Rab11fip1	2.38E-05	0.374764	0.36823	Tfh0/Tfh1
Ssr4	2.42E-05	0.366647	0.373968	Tfh0/Tfh1
Xrcc5	2.44E-05	0.322834	0.378175	Tfh0/Tfh1
Vapa	2.47E-05	0.408215	0.381732	Tfh0/Tfh1
Ppif	2.53E-05	0.284397	0.391384	Tfh0/Tfh1
BC003965	2.55E-05	0.31667	0.394355	Tfh0/Tfh1
Mrfap1	2.56E-05	0.390686	0.395976	Tfh0/Tfh1
Anxa6	2.57E-05	-0.57276	0.397486	Tfh0/Tfh1
U2af2	2.59E-05	0.344692	0.401121	Tfh0/Tfh1
Ptbp1	2.61E-05	0.35635	0.403523	Tfh0/Tfh1

U2surp	2.68E-05	0.359848	0.414289	Tfh0/Tfh1
Serf2	2.68E-05	-0.3912	0.414978	Tfh0/Tfh1
Psmb7	2.70E-05	0.30455	0.418057	Tfh0/Tfh1
Zer1	2.73E-05	-0.57883	0.42283	Tfh0/Tfh1
Dut	2.74E-05	0.321812	0.423999	Tfh0/Tfh1
Atxn1	2.75E-05	0.421143	0.425595	Tfh0/Tfh1
Uba2	2.81E-05	0.297189	0.435339	Tfh0/Tfh1
Ubxn2a	2.86E-05	0.417315	0.442261	Tfh0/Tfh1
Arfrp1	2.88E-05	0.26511	0.445224	Tfh0/Tfh1
Kdm7a	2.90E-05	-0.46878	0.449438	Tfh0/Tfh1
Heg1	2.93E-05	0.32376	0.453438	Tfh0/Tfh1
Nfe2l1	3.02E-05	0.357764	0.467293	Tfh0/Tfh1
A630023P12Rik	3.05E-05	-0.60962	0.471754	Tfh0/Tfh1
Mrpl16	3.08E-05	0.324988	0.477202	Tfh0/Tfh1
4930523C07Rik	3.09E-05	-0.58937	0.478764	Tfh0/Tfh1
Papola	3.10E-05	0.282409	0.479311	Tfh0/Tfh1
Sgms1	3.11E-05	-0.43682	0.481566	Tfh0/Tfh1
2210016F16Rik	3.15E-05	0.316231	0.487013	Tfh0/Tfh1
Irf2bpl	3.26E-05	-0.4529	0.505333	Tfh0/Tfh1
Mbd2	3.31E-05	-0.74303	0.511828	Tfh0/Tfh1
Rb1cc1	3.32E-05	-0.64894	0.51437	Tfh0/Tfh1
Uqcrfs1	3.37E-05	0.336666	0.52203	Tfh0/Tfh1
Kars	3.40E-05	0.334603	0.526645	Tfh0/Tfh1
Riox2	3.41E-05	0.334693	0.527155	Tfh0/Tfh1
Lsm6	3.45E-05	0.317291	0.533579	Tfh0/Tfh1
Kpna1	3.47E-05	0.263359	0.536504	Tfh0/Tfh1
AI480526	3.50E-05	-0.41192	0.541052	Tfh0/Tfh1
Irf9	3.76E-05	-0.54762	0.582225	Tfh0/Tfh1
Rnf157	3.78E-05	0.300419	0.585347	Tfh0/Tfh1
Alyref	3.81E-05	0.320022	0.589057	Tfh0/Tfh1
Mrpl30	3.84E-05	0.307692	0.593765	Tfh0/Tfh1
Csnk2b	3.87E-05	0.279773	0.598547	Tfh0/Tfh1
Plaat3	3.91E-05	-0.54627	0.604417	Tfh0/Tfh1
Selenop	3.97E-05	-0.57676	0.614747	Tfh0/Tfh1
Stat5b	3.98E-05	-0.56583	0.616774	Tfh0/Tfh1
6-Sep	4.05E-05	-0.56059	0.626769	Tfh0/Tfh1
Smu1	4.07E-05	0.295937	0.630235	Tfh0/Tfh1
Elp5	4.10E-05	0.33721	0.634752	Tfh0/Tfh1
Tdg	4.12E-05	0.328575	0.637503	Tfh0/Tfh1
Clint1	4.12E-05	-0.63068	0.638296	Tfh0/Tfh1
Suclg2	4.17E-05	0.255369	0.645579	Tfh0/Tfh1
Dap	4.19E-05	-0.54422	0.648198	Tfh0/Tfh1
Cnih1	4.19E-05	0.309906	0.648688	Tfh0/Tfh1
Prkcq	4.25E-05	-0.64691	0.658532	Tfh0/Tfh1
Psmd6	4.31E-05	0.342958	0.666513	Tfh0/Tfh1

Usp16	4.35E-05	0.319904	0.673552	Tfh0/Tfh1
Ahcyl1	4.37E-05	0.332152	0.676195	Tfh0/Tfh1
Cenpa	4.56E-05	-0.53241	0.706437	Tfh0/Tfh1
Pecam1	4.57E-05	-0.57696	0.706967	Tfh0/Tfh1
Zfp91	4.58E-05	0.345695	0.708773	Tfh0/Tfh1
Gng10	4.60E-05	0.336651	0.712723	Tfh0/Tfh1
Kansl2	4.69E-05	0.318841	0.72547	Tfh0/Tfh1
Dok2	4.88E-05	-0.5756	0.754733	Tfh0/Tfh1
Ube2q2	4.98E-05	0.279144	0.771242	Tfh0/Tfh1
Gm20559	5.09E-05	-0.46969	0.788428	Tfh0/Tfh1
Sri	5.12E-05	-0.42202	0.793064	Tfh0/Tfh1
Utp11	5.13E-05	0.385205	0.793305	Tfh0/Tfh1
Ccndbp1	5.28E-05	-0.4985	0.816646	Tfh0/Tfh1
Pfdn5	5.31E-05	-0.32882	0.822646	Tfh0/Tfh1
Eif4ebp2	5.38E-05	-0.65385	0.832788	Tfh0/Tfh1
Rnf138	5.42E-05	-0.6167	0.838436	Tfh0/Tfh1
Gpm6b	5.46E-05	0.426174	0.844755	Tfh0/Tfh1
Pus3	5.46E-05	0.27024	0.84513	Tfh0/Tfh1
Orc4	5.50E-05	0.257115	0.851428	Tfh0/Tfh1
Cops2	5.52E-05	0.278062	0.854586	Tfh0/Tfh1
Id3	5.54E-05	0.66799	0.856888	Tfh0/Tfh1
Ece1	5.56E-05	0.297338	0.860726	Tfh0/Tfh1
Eftud2	5.56E-05	0.31692	0.861238	Tfh0/Tfh1
Kcnq1ot1	5.62E-05	0.388641	0.870064	Tfh0/Tfh1
Gnl3l	5.62E-05	0.299009	0.870293	Tfh0/Tfh1
Iigp1	5.66E-05	-1.1046	0.876182	Tfh0/Tfh1
Far1	5.67E-05	0.322788	0.877536	Tfh0/Tfh1
Gimap7	5.90E-05	-0.66166	0.91271	Tfh0/Tfh1
Ikzf3	5.97E-05	-0.75789	0.92367	Tfh0/Tfh1
Oip5os1	5.98E-05	-0.66892	0.925756	Tfh0/Tfh1
Dnlz	6.11E-05	0.273225	0.945898	Tfh0/Tfh1
Adrm1	6.21E-05	0.353748	0.961468	Tfh0/Tfh1
Sf3b5	6.22E-05	0.350643	0.962047	Tfh0/Tfh1
Zranb2	6.23E-05	0.431343	0.963819	Tfh0/Tfh1
Gpn1	6.40E-05	0.263337	0.990411	Tfh0/Tfh1
Tmem234	6.42E-05	-0.49144	0.993293	Tfh0/Tfh1
Pisd	6.44E-05	0.259771	0.997119	Tfh0/Tfh1
Chd6	6.57E-05	-0.58689	1	Tfh0/Tfh1
Ppig	6.58E-05	0.323436	1	Tfh0/Tfh1
Sar1b	6.60E-05	0.271424	1	Tfh0/Tfh1
Mrps17	6.61E-05	0.283531	1	Tfh0/Tfh1
Ezr	6.76E-05	-0.54861	1	Tfh0/Tfh1
Reep5	6.81E-05	-0.50762	1	Tfh0/Tfh1
Mesd	6.97E-05	0.293202	1	Tfh0/Tfh1
Timm17b	7.03E-05	0.283555	1	Tfh0/Tfh1

Rabl6	7.13E-05	0.261541	1	Tfh0/Tfh1
1-Sep	7.15E-05	-0.56046	1	Tfh0/Tfh1
H2-Q4	7.18E-05	-0.49144	1	Tfh0/Tfh1
Smn1	7.19E-05	0.251547	1	Tfh0/Tfh1
Tardbp	7.20E-05	0.350446	1	Tfh0/Tfh1
Cfl1	7.21E-05	0.32551	1	Tfh0/Tfh1
Fasn	7.26E-05	0.272103	1	Tfh0/Tfh1
Herc1	7.38E-05	-0.59684	1	Tfh0/Tfh1
Adgre5	7.39E-05	-0.521	1	Tfh0/Tfh1
Ncbp2	7.43E-05	0.312638	1	Tfh0/Tfh1
Stk4	7.51E-05	-0.36842	1	Tfh0/Tfh1
Ssbp2	7.72E-05	-0.5567	1	Tfh0/Tfh1
Zyg11b	7.91E-05	-0.42916	1	Tfh0/Tfh1
Dcaf7	7.97E-05	0.297352	1	Tfh0/Tfh1
Mat2b	8.04E-05	-0.56101	1	Tfh0/Tfh1
Tiam1	8.08E-05	0.277441	1	Tfh0/Tfh1
Prpf31	8.15E-05	0.359628	1	Tfh0/Tfh1
Fam102a	8.17E-05	-0.69673	1	Tfh0/Tfh1
Crtc3	8.23E-05	-0.55579	1	Tfh0/Tfh1
Zbp1	8.33E-05	-0.49104	1	Tfh0/Tfh1
Rdx	8.37E-05	0.434421	1	Tfh0/Tfh1
Scand1	8.40E-05	-0.44326	1	Tfh0/Tfh1
Uqcrb	8.41E-05	0.306057	1	Tfh0/Tfh1
Igtp	8.45E-05	-0.95304	1	Tfh0/Tfh1
Ndufb4	8.59E-05	0.29219	1	Tfh0/Tfh1
Cdk17	8.70E-05	0.340286	1	Tfh0/Tfh1
Twsg1	8.79E-05	0.307833	1	Tfh0/Tfh1
Cir1	8.85E-05	-0.69785	1	Tfh0/Tfh1
Supt16	8.95E-05	0.282178	1	Tfh0/Tfh1
Cyth1	9.12E-05	-0.54369	1	Tfh0/Tfh1
Eif2a	9.22E-05	0.288166	1	Tfh0/Tfh1
Vim	9.29E-05	-1.06429	1	Tfh0/Tfh1
Runx3	9.32E-05	-0.72168	1	Tfh0/Tfh1
Eif1b	9.74E-05	0.294162	1	Tfh0/Tfh1
Psmb2	9.75E-05	0.387812	1	Tfh0/Tfh1
D10Wsu102e	9.78E-05	0.283021	1	Tfh0/Tfh1
Tmed10	9.87E-05	0.301532	1	Tfh0/Tfh1
Srpr	0.000103	0.269035	1	Tfh0/Tfh1
Txlna	0.000103	0.272968	1	Tfh0/Tfh1
Zfp36l1	0.000105	0.47834	1	Tfh0/Tfh1
Stk39	0.000106	0.370706	1	Tfh0/Tfh1
Med11	0.000106	0.286062	1	Tfh0/Tfh1
Ing1	0.000107	-0.50517	1	Tfh0/Tfh1
Exosc3	0.000108	0.259741	1	Tfh0/Tfh1
Itpkb	0.000108	-0.49606	1	Tfh0/Tfh1

Eed	0.000108	0.275731	1	Tfh0/Tfh1
Sf3b4	0.00011	0.253614	1	Tfh0/Tfh1
Mta3	0.00011	-0.43745	1	Tfh0/Tfh1
Ndufb7	0.00011	0.317363	1	Tfh0/Tfh1
Gbp4	0.000111	-0.83044	1	Tfh0/Tfh1
Stim1	0.000113	-0.5679	1	Tfh0/Tfh1
Ormdl1	0.000114	0.258725	1	Tfh0/Tfh1
Ifi203	0.000115	-0.51037	1	Tfh0/Tfh1
Tpp2	0.000117	-0.53355	1	Tfh0/Tfh1
Flna	0.000117	-0.57599	1	Tfh0/Tfh1
Tmem30a	0.00012	-0.43485	1	Tfh0/Tfh1
Pcmtd1	0.00012	-0.63849	1	Tfh0/Tfh1
Atp5mpl	0.000122	0.330774	1	Tfh0/Tfh1
Dnmt3a	0.000124	0.335519	1	Tfh0/Tfh1
Rock2	0.000124	0.374682	1	Tfh0/Tfh1
Smg7	0.000128	0.261426	1	Tfh0/Tfh1
B2m	0.000129	-0.29014	1	Tfh0/Tfh1
Vcp	0.000129	0.341094	1	Tfh0/Tfh1
Tapbp	0.000131	-0.72034	1	Tfh0/Tfh1
Polb	0.000136	0.301625	1	Tfh0/Tfh1
Tap2	0.000139	-0.52891	1	Tfh0/Tfh1
Cyb5a	0.000139	-0.47584	1	Tfh0/Tfh1
Yif1b	0.000143	0.263184	1	Tfh0/Tfh1
Smchd1	0.000143	-0.5785	1	Tfh0/Tfh1
Trib1	0.000144	0.321514	1	Tfh0/Tfh1
Zdhhc20	0.000145	-0.46677	1	Tfh0/Tfh1
Cd3e	0.000146	-0.38119	1	Tfh0/Tfh1
Batf	0.000149	0.401505	1	Tfh0/Tfh1
Fam169b	0.00015	-0.663	1	Tfh0/Tfh1
Psmb9	0.000151	-0.56306	1	Tfh0/Tfh1
Clk1	0.000153	-0.57155	1	Tfh0/Tfh1
Thy1	0.000154	-0.56073	1	Tfh0/Tfh1
Pim1	0.00016	0.510757	1	Tfh0/Tfh1
Kmt2c	0.000166	-0.57062	1	Tfh0/Tfh1
Psmd8	0.000166	0.275063	1	Tfh0/Tfh1
Map3k1	0.000167	-0.50064	1	Tfh0/Tfh1
Hdac2	0.000168	0.29181	1	Tfh0/Tfh1
Fam173a	0.000168	-0.46369	1	Tfh0/Tfh1
Iah1	0.000168	0.329607	1	Tfh0/Tfh1
Mrps24	0.000169	0.310458	1	Tfh0/Tfh1
Il16	0.00017	-0.53079	1	Tfh0/Tfh1
Add1	0.000173	-0.62536	1	Tfh0/Tfh1
Rbm25	0.000174	0.275133	1	Tfh0/Tfh1
Aqr	0.000176	0.314482	1	Tfh0/Tfh1
Lrrc59	0.00018	0.303025	1	Tfh0/Tfh1

Zbtb21	0.000184	0.306297	1	Tfh0/Tfh1
Naa10	0.000188	0.286106	1	Tfh0/Tfh1
Tcea1	0.000189	0.373524	1	Tfh0/Tfh1
Atox1	0.000189	-0.6029	1	Tfh0/Tfh1
Wsb1	0.00019	0.329349	1	Tfh0/Tfh1
Tatdn1	0.00019	0.262699	1	Tfh0/Tfh1
Dazap2	0.000193	-0.51797	1	Tfh0/Tfh1
Fut8	0.000194	0.301147	1	Tfh0/Tfh1
Tomm6	0.000195	0.323722	1	Tfh0/Tfh1
Morf4l2	0.000196	0.278845	1	Tfh0/Tfh1
Psmb3	0.000197	0.31118	1	Tfh0/Tfh1
Snrpb2	0.000198	0.262461	1	Tfh0/Tfh1
Tmem208	0.0002	0.286252	1	Tfh0/Tfh1
Tnfaip8l2	0.000205	-0.53512	1	Tfh0/Tfh1
Dennd1c	0.000207	-0.50638	1	Tfh0/Tfh1
Adss	0.000207	0.364971	1	Tfh0/Tfh1
Tmem147	0.000211	0.251133	1	Tfh0/Tfh1
Cox8a	0.000212	-0.32544	1	Tfh0/Tfh1
Dcaf13	0.000214	0.295156	1	Tfh0/Tfh1
Gps1	0.000215	0.252185	1	Tfh0/Tfh1
Gdi2	0.000218	-0.41735	1	Tfh0/Tfh1
Snhg12	0.000219	0.429492	1	Tfh0/Tfh1
Arhgap9	0.000221	-0.4455	1	Tfh0/Tfh1
Cks2	0.000222	0.30938	1	Tfh0/Tfh1
Mrpl33	0.000223	0.253891	1	Tfh0/Tfh1
Bsg	0.000225	0.304801	1	Tfh0/Tfh1
Ubtf	0.000226	0.257811	1	Tfh0/Tfh1
Hivep1	0.000227	0.312442	1	Tfh0/Tfh1
Myl6	0.000231	-0.32147	1	Tfh0/Tfh1
Ndufa5	0.000231	0.332764	1	Tfh0/Tfh1
Chd4	0.000232	0.37173	1	Tfh0/Tfh1
Sft2d2	0.000238	-0.55384	1	Tfh0/Tfh1
Wdr61	0.000242	0.293184	1	Tfh0/Tfh1
Amn1	0.000248	-0.57377	1	Tfh0/Tfh1
Med8	0.00025	0.283899	1	Tfh0/Tfh1
Ndufb2	0.000251	0.260352	1	Tfh0/Tfh1
Nab2	0.000256	0.363447	1	Tfh0/Tfh1
Parp14	0.000256	-0.76224	1	Tfh0/Tfh1
Ankrd44	0.000259	-0.47868	1	Tfh0/Tfh1
Klhdc2	0.000263	-1.1392	1	Tfh0/Tfh1
L3mbtl3	0.000264	-0.46666	1	Tfh0/Tfh1
Idnk	0.000272	-0.53148	1	Tfh0/Tfh1
Mknk2	0.000275	-0.56851	1	Tfh0/Tfh1
N6amt1	0.000276	0.322303	1	Tfh0/Tfh1
Tgfbr2	0.000278	-0.74398	1	Tfh0/Tfh1

Psme1	0.000284	0.252121	1	Tfh0/Tfh1
Mapkapk3	0.000284	0.287829	1	Tfh0/Tfh1
Erbin	0.000286	0.415226	1	Tfh0/Tfh1
Ndufb11	0.000288	-0.51479	1	Tfh0/Tfh1
Ddx39b	0.000289	0.305915	1	Tfh0/Tfh1
Jade2	0.000292	0.289224	1	Tfh0/Tfh1
Rpn1	0.000293	0.250672	1	Tfh0/Tfh1
Usp48	0.000294	-0.57185	1	Tfh0/Tfh1
Kidins220	0.000297	-0.53324	1	Tfh0/Tfh1
Epb41	0.000298	-0.49355	1	Tfh0/Tfh1
Frmd8	0.0003	-0.47645	1	Tfh0/Tfh1
2310001H17Rik	0.000305	0.366511	1	Tfh0/Tfh1
Tkt	0.000307	0.328367	1	Tfh0/Tfh1
Sap18	0.000309	0.281234	1	Tfh0/Tfh1
Mbnl2	0.000312	-0.52649	1	Tfh0/Tfh1
Mapre1	0.000319	0.292101	1	Tfh0/Tfh1
Larp1b	0.00032	0.345756	1	Tfh0/Tfh1
Rbl2	0.000321	-0.54633	1	Tfh0/Tfh1
Lman2	0.000326	0.297645	1	Tfh0/Tfh1
Actg1	0.000327	-0.48427	1	Tfh0/Tfh1
Iqgap2	0.000329	-0.36361	1	Tfh0/Tfh1
Bax	0.00033	0.262775	1	Tfh0/Tfh1
Bud23	0.000332	0.278695	1	Tfh0/Tfh1
Foxo1	0.000333	-0.59064	1	Tfh0/Tfh1
Cited2	0.000337	-0.48045	1	Tfh0/Tfh1
Sumo2	0.000342	0.302605	1	Tfh0/Tfh1
Samsn1	0.000345	0.518339	1	Tfh0/Tfh1
Ctsb	0.000352	-0.47122	1	Tfh0/Tfh1
Zfand5	0.000355	0.264785	1	Tfh0/Tfh1
Psmc6	0.000361	0.369048	1	Tfh0/Tfh1
Cdk2ap2	0.000363	-0.55987	1	Tfh0/Tfh1
Ranbp10	0.000364	-0.45757	1	Tfh0/Tfh1
Ccdc59	0.000369	0.36014	1	Tfh0/Tfh1
Fam107b	0.000375	-0.49058	1	Tfh0/Tfh1
Atrx	0.000386	-0.42556	1	Tfh0/Tfh1
Snrpg	0.000392	0.260032	1	Tfh0/Tfh1
Pafah1b1	0.000395	-0.38999	1	Tfh0/Tfh1
Gpr132	0.000401	-0.4871	1	Tfh0/Tfh1
Capn1	0.000405	-0.44142	1	Tfh0/Tfh1
Ubl3	0.000427	-0.51763	1	Tfh0/Tfh1
Snhg3	0.00043	0.270175	1	Tfh0/Tfh1
Ccm2	0.000432	-0.56587	1	Tfh0/Tfh1
Hp1bp3	0.000434	-0.48245	1	Tfh0/Tfh1
Smarca4	0.000437	0.280104	1	Tfh0/Tfh1
Rbms1	0.000438	-0.58775	1	Tfh0/Tfh1

Mphosph8	0.000444	0.315784	1	Tfh0/Tfh1
Rpl10a	0.000447	0.250047	1	Tfh0/Tfh1
Retreg2	0.000456	-0.44435	1	Tfh0/Tfh1
Desi2	0.000458	0.279554	1	Tfh0/Tfh1
Ubn1	0.000469	-0.42199	1	Tfh0/Tfh1
Cd44	0.00047	0.25143	1	Tfh0/Tfh1
H2-Q6	0.000495	-0.53534	1	Tfh0/Tfh1
Clec2d	0.000498	-0.36956	1	Tfh0/Tfh1
Rif1	0.000503	0.317696	1	Tfh0/Tfh1
Adam10	0.000512	0.351267	1	Tfh0/Tfh1
Rin3	0.000512	-0.43351	1	Tfh0/Tfh1
Ly75	0.000514	0.351308	1	Tfh0/Tfh1
Ifnar1	0.000514	-0.47754	1	Tfh0/Tfh1
Slc12a6	0.000529	-0.45569	1	Tfh0/Tfh1
Orai2	0.00053	-0.4019	1	Tfh0/Tfh1
Tm2d1	0.000544	0.267216	1	Tfh0/Tfh1
H2afz	0.000545	0.285288	1	Tfh0/Tfh1
Ubald2	0.000549	0.393567	1	Tfh0/Tfh1
Samm50	0.000559	0.26124	1	Tfh0/Tfh1
Limd2	0.000575	-0.41412	1	Tfh0/Tfh1
Cnot7	0.000587	0.266736	1	Tfh0/Tfh1
Spata13	0.0006	-0.42425	1	Tfh0/Tfh1
Cxcr3	0.000618	-0.52285	1	Tfh0/Tfh1
Setd7	0.000623	-0.38811	1	Tfh0/Tfh1
Myl12b	0.000626	-0.39019	1	Tfh0/Tfh1
Jmjd1c	0.000629	-0.39413	1	Tfh0/Tfh1
Phf20l1	0.000632	-0.53907	1	Tfh0/Tfh1
Git2	0.000639	-0.55528	1	Tfh0/Tfh1
Ttc3	0.000647	-0.59539	1	Tfh0/Tfh1
Mkrn1	0.000673	-0.37314	1	Tfh0/Tfh1
Tsc22d3	0.000684	-0.48056	1	Tfh0/Tfh1
Tob2	0.000687	0.262115	1	Tfh0/Tfh1
Bcor	0.00069	0.332338	1	Tfh0/Tfh1
Cd274	0.000709	0.359967	1	Tfh0/Tfh1
Matr3	0.000713	0.337617	1	Tfh0/Tfh1
Ppm1g	0.000721	0.285131	1	Tfh0/Tfh1
Senp7	0.000721	-0.49014	1	Tfh0/Tfh1
Pdrg1	0.000732	0.25999	1	Tfh0/Tfh1
Irf1	0.000769	-0.42168	1	Tfh0/Tfh1
Tbc1d17	0.00077	-0.38952	1	Tfh0/Tfh1
Cep192	0.000779	-0.41702	1	Tfh0/Tfh1
Pcnt	0.000801	-0.39633	1	Tfh0/Tfh1
Hipk1	0.000822	-0.51654	1	Tfh0/Tfh1
Zyx	0.000829	-0.43536	1	Tfh0/Tfh1
Wasf2	0.000839	-0.53348	1	Tfh0/Tfh1

Mrps33	0.000856	0.297064	1	Tfh0/Tfh1
Senp2	0.000862	0.257613	1	Tfh0/Tfh1
Ndufb1-ps	0.000873	0.294823	1	Tfh0/Tfh1
Rasal3	0.000881	-0.4599	1	Tfh0/Tfh1
Eef2	0.000882	-0.29902	1	Tfh0/Tfh1
Sec11c	0.000915	-0.51171	1	Tfh0/Tfh1
Ppp2r2a	0.000917	0.255708	1	Tfh0/Tfh1
Senp6	0.000921	0.294107	1	Tfh0/Tfh1
Lsm4	0.000926	0.29962	1	Tfh0/Tfh1
Eif3i	0.000933	0.286702	1	Tfh0/Tfh1
Ccdc82	0.00094	-0.47409	1	Tfh0/Tfh1
Hypk	0.000947	0.283278	1	Tfh0/Tfh1
Nsd1	0.000963	-0.42132	1	Tfh0/Tfh1
Ptprcap	0.00098	0.378776	1	Tfh0/Tfh1
Malt1	0.000993	0.443021	1	Tfh0/Tfh1
Tpst2	0.001008	-0.42551	1	Tfh0/Tfh1
Polr1d	0.001011	0.305741	1	Tfh0/Tfh1
Ctsz	0.001013	0.282313	1	Tfh0/Tfh1
Pink1	0.001013	-0.4848	1	Tfh0/Tfh1
Grk2	0.001073	-0.47247	1	Tfh0/Tfh1
Gm12840	0.001082	0.296221	1	Tfh0/Tfh1
Cnppd1	0.001097	-0.39958	1	Tfh0/Tfh1
Adamts10	0.001112	-0.37344	1	Tfh0/Tfh1
Cep350	0.001145	-0.51388	1	Tfh0/Tfh1
Dnajc1	0.001158	0.253251	1	Tfh0/Tfh1
Tmbim6	0.001168	-0.44105	1	Tfh0/Tfh1
Uqcc3	0.001186	-0.45804	1	Tfh0/Tfh1
Prkcsh	0.001222	0.270532	1	Tfh0/Tfh1
Gm15472	0.001226	-0.54932	1	Tfh0/Tfh1
Os9	0.001235	-0.48089	1	Tfh0/Tfh1
Tox	0.001244	0.314025	1	Tfh0/Tfh1
Cdc42se1	0.001266	-0.462	1	Tfh0/Tfh1
Cox6a1	0.001275	0.274973	1	Tfh0/Tfh1
Eid1	0.00128	-0.40346	1	Tfh0/Tfh1
Slc38a9	0.001298	-0.44143	1	Tfh0/Tfh1
Pde4d	0.001312	-0.38839	1	Tfh0/Tfh1
Pop5	0.00132	0.258392	1	Tfh0/Tfh1
Rgs2	0.001345	-0.74716	1	Tfh0/Tfh1
Ugcg	0.001383	-0.61375	1	Tfh0/Tfh1
Furin	0.001384	0.309963	1	Tfh0/Tfh1
Vamp8	0.001404	-0.43465	1	Tfh0/Tfh1
Sesn3	0.001405	-0.49435	1	Tfh0/Tfh1
Ptpre	0.001467	-0.43446	1	Tfh0/Tfh1
Kdm5a	0.001481	-0.51035	1	Tfh0/Tfh1
Uvrag	0.001538	-0.3904	1	Tfh0/Tfh1

Hopx	0.00156	0.346216	1	Tfh0/Tfh1
Xrn1	0.001583	-0.44544	1	Tfh0/Tfh1
Rora	0.001599	-0.62523	1	Tfh0/Tfh1
Cdc42	0.00171	-0.41771	1	Tfh0/Tfh1
Lfng	0.001726	-0.40495	1	Tfh0/Tfh1
Rb1	0.001755	-0.35394	1	Tfh0/Tfh1
Pik3r1	0.001817	-0.4258	1	Tfh0/Tfh1
Acap2	0.001823	-0.49434	1	Tfh0/Tfh1
Arpc1b	0.001839	-0.30254	1	Tfh0/Tfh1
Rnf19a	0.001856	0.253796	1	Tfh0/Tfh1
Ggps1	0.001992	-0.44389	1	Tfh0/Tfh1
H2afj	0.00202	0.305401	1	Tfh0/Tfh1
Gtpbp2	0.002091	-0.45987	1	Tfh0/Tfh1
Rad23a	0.002168	0.289432	1	Tfh0/Tfh1
Asnsd1	0.002186	0.301543	1	Tfh0/Tfh1
Mndal	0.002204	0.444093	1	Tfh0/Tfh1
Map4k2	0.002235	-0.37336	1	Tfh0/Tfh1
Pcm1	0.002258	-0.48804	1	Tfh0/Tfh1
Sike1	0.002339	-0.48841	1	Tfh0/Tfh1
Ptprc	0.002349	0.340538	1	Tfh0/Tfh1
Golgb1	0.002376	-0.52273	1	Tfh0/Tfh1
Emsy	0.002376	-0.58835	1	Tfh0/Tfh1
Cdc5l	0.002377	0.266648	1	Tfh0/Tfh1
Gpatch8	0.002403	-0.41833	1	Tfh0/Tfh1
Zbtb7a	0.002453	-0.5081	1	Tfh0/Tfh1
Zbtb1	0.002481	0.285191	1	Tfh0/Tfh1
Trp53	0.002483	0.269467	1	Tfh0/Tfh1
Elavl1	0.002513	0.259683	1	Tfh0/Tfh1
Kmt2e	0.002539	-0.45092	1	Tfh0/Tfh1
Dhrs7	0.002549	-0.47563	1	Tfh0/Tfh1
Tet3	0.002601	-0.408	1	Tfh0/Tfh1
Pycard	0.002601	-0.49371	1	Tfh0/Tfh1
Twf2	0.002612	-0.35064	1	Tfh0/Tfh1
Irf2bp2	0.00265	0.41087	1	Tfh0/Tfh1
Atp5e	0.00275	0.260913	1	Tfh0/Tfh1
Plekha2	0.002765	-0.47011	1	Tfh0/Tfh1
Tank	0.002767	0.294705	1	Tfh0/Tfh1
Phf3	0.002799	-0.42614	1	Tfh0/Tfh1
Cntrl	0.0028	-0.41925	1	Tfh0/Tfh1
Prr14	0.002807	-0.3814	1	Tfh0/Tfh1
Fkbp8	0.002822	-0.40692	1	Tfh0/Tfh1
Gna13	0.002825	-0.70821	1	Tfh0/Tfh1
Gabarapl2	0.003015	-0.35935	1	Tfh0/Tfh1
Cirbp	0.003028	-0.4204	1	Tfh0/Tfh1
Pik3cd	0.003111	-0.48611	1	Tfh0/Tfh1

Ddb1	0.003112	0.253051	1	Tfh0/Tfh1
Tap1	0.003127	-0.47903	1	Tfh0/Tfh1
Smad7	0.003156	-0.33707	1	Tfh0/Tfh1
Chordc1	0.003209	0.259322	1	Tfh0/Tfh1
4833420G17Rik	0.003245	-0.41483	1	Tfh0/Tfh1
Trbc1	0.003251	-0.67831	1	Tfh0/Tfh1
Dennd1b	0.00331	-0.35503	1	Tfh0/Tfh1
Sf1	0.003362	0.259204	1	Tfh0/Tfh1
Aak1	0.003423	-0.47775	1	Tfh0/Tfh1
Lamtor2	0.003466	-0.45465	1	Tfh0/Tfh1
Pmepa1	0.0036	-0.60151	1	Tfh0/Tfh1
AC149090.1	0.003699	-0.46307	1	Tfh0/Tfh1
BC005537	0.0037	-0.39657	1	Tfh0/Tfh1
Kdm2a	0.003722	-0.40551	1	Tfh0/Tfh1
Tnrc6a	0.003744	-0.46701	1	Tfh0/Tfh1
Ing4	0.00382	-0.46969	1	Tfh0/Tfh1
Zfp706	0.003913	0.257801	1	Tfh0/Tfh1
Erg28	0.003925	0.250217	1	Tfh0/Tfh1
Krtcap2	0.003968	0.307081	1	Tfh0/Tfh1
Acadl	0.003971	-0.4017	1	Tfh0/Tfh1
Mindy2	0.00407	-0.41836	1	Tfh0/Tfh1
Pkn2	0.00408	-0.36575	1	Tfh0/Tfh1
Camk4	0.004094	-0.47155	1	Tfh0/Tfh1
Ddx6	0.004094	-0.33657	1	Tfh0/Tfh1
Ikzf1	0.004114	-0.40167	1	Tfh0/Tfh1
Zup1	0.004119	-0.39138	1	Tfh0/Tfh1
Vrk3	0.004149	-0.43088	1	Tfh0/Tfh1
Phip	0.004157	-0.50077	1	Tfh0/Tfh1
Ep300	0.004225	-0.34295	1	Tfh0/Tfh1
Dmac2	0.004253	-0.40736	1	Tfh0/Tfh1
Rhoh	0.004262	-0.47397	1	Tfh0/Tfh1
Tacc1	0.004305	-0.43171	1	Tfh0/Tfh1
Fbxl12	0.004354	-0.44424	1	Tfh0/Tfh1
Parp9	0.004449	-0.47558	1	Tfh0/Tfh1
Eno1	0.004486	-0.34002	1	Tfh0/Tfh1
Cblb	0.004548	-0.37782	1	Tfh0/Tfh1
H2-T23	0.004797	-0.35883	1	Tfh0/Tfh1
Tmem134	0.004953	-0.43591	1	Tfh0/Tfh1
Exoc2	0.004961	0.268491	1	Tfh0/Tfh1
Man2b1	0.005058	-0.38173	1	Tfh0/Tfh1
Bex3	0.00548	-0.37286	1	Tfh0/Tfh1
Prdx2	0.005581	-0.37176	1	Tfh0/Tfh1
Rabgap1l	0.005605	-0.4667	1	Tfh0/Tfh1
Selenok	0.005817	-0.30605	1	Tfh0/Tfh1
Pts	0.006106	-0.45287	1	Tfh0/Tfh1

Atxn7l1	0.006237	-0.37721	1	Tfh0/Tfh1
Trim30a	0.006245	-0.41735	1	Tfh0/Tfh1
Ralgps2	0.006274	-0.46814	1	Tfh0/Tfh1
Actn1	0.006373	-0.37896	1	Tfh0/Tfh1
Limd1	0.006407	-0.35991	1	Tfh0/Tfh1
Tbc1d4	0.006411	-0.49571	1	Tfh0/Tfh1
Ppp1ca	0.006456	-0.32656	1	Tfh0/Tfh1
Agfg1	0.006476	0.29346	1	Tfh0/Tfh1
Mau2	0.006628	-0.43482	1	Tfh0/Tfh1
Commd4	0.00665	-0.40885	1	Tfh0/Tfh1
Zfp217	0.00665	-0.33619	1	Tfh0/Tfh1
Atad2	0.006705	-0.41393	1	Tfh0/Tfh1
Smim14	0.006945	-0.41709	1	Tfh0/Tfh1
Rnf166	0.006994	-0.40489	1	Tfh0/Tfh1
Rnf145	0.00718	-0.37172	1	Tfh0/Tfh1
Fcho2	0.007209	-0.61011	1	Tfh0/Tfh1
Zfp260	0.007226	-0.45381	1	Tfh0/Tfh1
Fam160b1	0.007281	-0.41431	1	Tfh0/Tfh1
Glipr2	0.007535	-0.45871	1	Tfh0/Tfh1
Rsbn1l	0.007623	-0.31516	1	Tfh0/Tfh1
Ptp4a2	0.007733	-0.36003	1	Tfh0/Tfh1
Chd2	0.007941	-0.49169	1	Tfh0/Tfh1
Tcf12	0.007967	-0.43944	1	Tfh0/Tfh1
Rtf1	0.008157	-0.42514	1	Tfh0/Tfh1
Rsu1	0.008193	-0.35692	1	Tfh0/Tfh1
Gnb2	0.008219	-0.37334	1	Tfh0/Tfh1
Fam174a	0.008317	-0.28085	1	Tfh0/Tfh1
Bloc1s1	0.00849	-0.41918	1	Tfh0/Tfh1
Pold4	0.008616	-0.37194	1	Tfh0/Tfh1
Baz2a	0.008682	-0.48536	1	Tfh0/Tfh1
Klf6	0.008928	-0.43133	1	Tfh0/Tfh1
Fermt3	0.008979	-0.31851	1	Tfh0/Tfh1
Ip6k1	0.008997	-0.32684	1	Tfh0/Tfh1
Hltf	0.009166	-0.39504	1	Tfh0/Tfh1
Tlk1	0.009194	-0.42181	1	Tfh0/Tfh1
Tspan13	0.009254	0.394449	1	Tfh0/Tfh1
Cd5	0.009274	0.31421	1	Tfh0/Tfh1
Slc9a3r1	0.009416	-0.39304	1	Tfh0/Tfh1
Ralbp1	0.009485	-0.3757	1	Tfh0/Tfh1
Znrf2	0.009488	-0.40506	1	Tfh0/Tfh1
Lck	0.009516	-0.36811	1	Tfh0/Tfh1
Ttc14	0.009525	-0.3054	1	Tfh0/Tfh1
Stx4a	0.009559	-0.4206	1	Tfh0/Tfh1
Gpi1	0.009618	-0.46142	1	Tfh0/Tfh1
Pag1	0.009667	-0.37529	1	Tfh0/Tfh1

Syf2	0.009804	-0.29592	1	Tfh0/Tfh1
Avl9	0.009963	-0.32691	1	Tfh0/Tfh1

Supplemental Table 2

Pathway	pval	padj	ES	NES	size
KEGG_RIBOSOME	1.00E-10	1.21E-08	-0.87	-5.35	51
KEGG_OXIDATIVE_PHOSPHORYLATION	0.01	0.35	-0.81	-1.88	4
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.01	0.35	-0.95	-1.62	2
KEGG_TYPE_I_DIABETES_MELLITUS	0.01	0.35	-0.94	-1.61	2
KEGG_CARDIAC_MUSCLE_CONTRACTION	0.02	0.35	-0.82	-1.67	3
KEGG_PARKINSONS_DISEASE	0.02	0.35	-0.65	-1.78	6
KEGG_HUNTINGTONS_DISEASE	0.02	0.36	-0.49	-1.70	10
KEGG_PYRIMIDINE_METABOLISM	0.07	0.95	-0.73	-1.49	3
KEGG_RNA_POLYMERASE	0.07	0.95	-0.73	-1.49	3
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	0.09	0.95	0.97	1.28	1
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	0.09	0.95	-0.96	-1.28	1
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.10	0.95	0.43	1.43	13
KEGG_SPLICEOSOME	0.12	0.95	-0.41	-1.51	11
KEGG_ALLOGRAFT_REJECTION	0.13	0.95	-0.94	-1.26	1
KEGG_ASTHMA	0.13	0.95	-0.94	-1.26	1
KEGG_GRAFT_VERSUS_HOST_DISEASE	0.13	0.95	-0.94	-1.26	1
KEGG_CELL_ADHESION_MOLECULES_CAMS	0.13	0.95	0.52	1.38	7
KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.17	0.99	-0.57	-1.31	4
KEGG_ALZHEIMERS_DISEASE	0.18	0.99	-0.39	-1.29	9
KEGG_COLORECTAL_CANCER	0.19	0.99	0.52	1.27	6
KEGG_BASAL_CELL_CARCINOMA	0.19	0.99	-0.74	-1.27	2
KEGG_INOSITOL_PHOSPHATE_METABOLISM	0.22	0.99	0.73	1.22	2
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	0.23	0.99	0.50	1.23	6
KEGG_SMALL_CELL_LUNG_CANCER	0.23	0.99	0.50	1.23	6
KEGG_TGF_BETA_SIGNALING_PATHWAY	0.23	0.99	-0.53	-1.22	4
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.25	0.99	-0.31	-1.17	12
KEGG_ERBB_SIGNALING_PATHWAY	0.26	0.99	0.52	1.22	5
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	0.26	0.99	0.46	1.21	7
KEGG_PROSTATE_CANCER	0.27	0.99	0.43	1.19	8
KEGG_JAK_STAT_SIGNALING_PATHWAY	0.30	0.99	0.33	1.15	15
KEGG_TYPE_II_DIABETES_MELLITUS	0.30	0.99	0.68	1.14	2
KEGG_APOPTOSIS	0.31	0.99	0.42	1.16	8
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	0.31	0.99	0.50	1.16	5
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.33	0.99	0.43	1.14	7

KEGG_LYSINE_DEGRADATION	0.34	0.99	0.83	1.10	1
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	0.36	0.99	-0.39	-1.07	6
KEGG_PATHWAYS_IN_CANCER	0.37	0.99	0.28	1.09	21
KEGG_PROTEASOME	0.38	0.99	0.50	1.07	4
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	0.39	0.99	-0.46	-1.05	4
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	0.40	0.99	-0.34	-1.06	8
KEGG_BETA_ALANINE_METABOLISM	0.40	0.99	-0.79	-1.06	1
KEGG_GLUTATHIONE_METABOLISM	0.40	0.99	-0.79	-1.06	1
KEGG_CELL_CYCLE	0.41	0.99	-0.50	-1.03	3
KEGG_FOCAL_ADHESION	0.41	0.99	0.32	1.04	12
KEGG_INSULIN_SIGNALING_PATHWAY	0.42	0.99	0.46	1.07	5
KEGG_ARGININE_AND_PROLINE_METABOLISM	0.44	0.99	-0.59	-1.01	2
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	0.44	0.99	-0.59	-1.01	2
KEGG_ABC_TRANSPORTERS	0.45	0.99	0.78	1.04	1
KEGG_ENDOMETRIAL_CANCER	0.45	0.99	-0.48	-0.99	3
KEGG_THYROID_CANCER	0.45	0.99	-0.48	-0.99	3
KEGG_TIGHT_JUNCTION	0.46	0.99	0.33	1.00	10
KEGG_CHRONIC_MYELOID_LEUKEMIA	0.47	0.99	0.38	1.01	7
KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.52	0.99	0.28	0.94	14
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	0.54	0.99	-0.73	-0.98	1
KEGG_GALACTOSE_METABOLISM	0.54	0.99	-0.73	-0.98	1
KEGG_ETHER_LIPID_METABOLISM	0.56	0.99	-0.72	-0.96	1
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	0.59	0.99	0.38	0.89	5
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	0.59	0.99	0.32	0.90	8
KEGG_ECM_RECEPTOR_INTERACTION	0.60	0.99	0.71	0.94	1
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.60	0.99	0.29	0.89	10
KEGG_PRIMARY_IMMUNODEFICIENCY	0.61	0.99	-0.43	-0.87	3
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	0.62	0.99	-0.69	-0.92	1
KEGG_PROTEIN_EXPORT	0.62	0.99	0.70	0.93	1
KEGG_AUTOIMMUNE_THYROID_DISEASE	0.62	0.99	0.69	0.92	1
KEGG_LONG_TERM_POTENTIATION	0.62	0.99	0.31	0.87	8
KEGG_CALCIUM_SIGNALING_PATHWAY	0.64	0.99	0.32	0.85	7
KEGG_GAP_JUNCTION	0.64	0.99	0.32	0.85	7
KEGG_RNA_DEGRADATION	0.65	0.99	0.41	0.88	4
KEGG_PRION_DISEASES	0.66	0.99	0.41	0.87	4

KEGG_OOCYTE_MEIOSIS	0.66	0.99	0.30	0.84	8
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	0.67	0.99	0.25	0.82	12
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	0.67	0.99	0.52	0.87	2
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	0.68	0.99	0.52	0.87	2
KEGG_NON_SMALL_CELL_LUNG_CANCER	0.68	0.99	0.52	0.87	2
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	0.68	0.99	0.52	0.87	2
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	0.68	0.99	0.36	0.83	5
KEGG_VEGF_SIGNALING_PATHWAY	0.68	0.99	-0.30	-0.82	6
KEGG_MELANOGENESIS	0.71	0.99	-0.24	-0.80	9
KEGG_WNT_SIGNALING_PATHWAY	0.71	0.99	-0.24	-0.80	9
KEGG_VIBRIO_CHOLERAE_INFECTION	0.71	0.99	-0.35	-0.80	4
KEGG_VIRAL_MYOCARDITIS	0.71	0.99	-0.35	-0.80	4
KEGG_AXON_GUIDANCE	0.71	0.99	0.34	0.80	5
KEGG_ENDOCYTOSIS	0.71	0.99	0.34	0.82	6
KEGG_GLIOMA	0.72	0.99	0.38	0.82	4
KEGG_DORSO_VENTRAL_AXIS_FORMATION	0.72	0.99	0.38	0.81	4
KEGG_GNRH_SIGNALING_PATHWAY	0.74	0.99	0.32	0.79	6
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	0.74	0.99	0.22	0.75	14
KEGG_LEISHMANIA_INFECTION	0.75	0.99	0.33	0.77	5
KEGG_GLYCEROLIPID_METABOLISM	0.76	0.99	0.62	0.83	1
KEGG_LONG_TERM_DEPRESSION	0.77	0.99	0.32	0.75	5
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.78	0.99	0.31	0.75	6
KEGG_DILATED_CARDIOMYOPATHY	0.80	0.99	-0.29	-0.73	5
KEGG_P53_SIGNALING_PATHWAY	0.82	0.99	0.59	0.78	1
KEGG_MAPK_SIGNALING_PATHWAY	0.82	0.99	0.22	0.70	12
KEGG_ADHERENS_JUNCTION	0.83	0.99	-0.22	-0.73	9
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM	0.84	0.99	-0.59	-0.78	1
KEGG_PHENYLALANINE_METABOLISM	0.84	0.99	-0.59	-0.78	1
KEGG_TYROSINE_METABOLISM	0.84	0.99	-0.59	-0.78	1
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.85	0.99	0.25	0.66	7
KEGG_TASTE_TRANSDUCTION	0.85	0.99	-0.58	-0.78	1
KEGG_PANCREATIC_CANCER	0.86	0.99	0.28	0.68	6
KEGG_LYSOSOME	0.86	0.99	0.44	0.73	2
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	0.86	0.99	0.44	0.73	2

KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	0.87	0.99	-0.29	-0.67	4
KEGG_NOTCH_SIGNALING_PATHWAY	0.87	0.99	0.31	0.67	4
KEGG_HEDGEHOG_SIGNALING_PATHWAY	0.87	0.99	0.56	0.75	1
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.89	0.99	-0.20	-0.66	9
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.91	0.99	0.40	0.67	2
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	0.92	0.99	-0.38	-0.65	2
KEGG_PENTOSE_PHOSPHATE_PATHWAY	0.92	0.99	-0.37	-0.64	2
KEGG_REGULATION_OF_AUTOPHAGY	0.92	0.99	0.54	0.72	1
KEGG_ACUTE_MYELOID_LEUKEMIA	0.93	0.99	0.20	0.59	9
KEGG_RENAL_CELL_CARCINOMA	0.93	0.99	0.31	0.60	3
KEGG_OLFACTORY_TRANSDUCTION	0.94	0.99	0.38	0.64	2
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.95	0.99	-0.23	-0.57	5
KEGG_PURINE_METABOLISM	0.97	0.99	-0.21	-0.56	6
KEGG_BLADDER_CANCER	0.97	0.99	0.52	0.69	1
KEGG_MELANOMA	0.97	0.99	0.52	0.69	1
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	0.98	0.99	0.20	0.47	5
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	0.99	0.99	-0.33	-0.56	2
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.99	0.99	-0.16	-0.47	7

Supplemental Table 3

Identified Proteins	Accession Number	Gene ID	MW	NT-IRF5	NT-IgG	Ratio
Tubulin beta-2A chain	TBB2A_HUMAN	TUBB2A	50 kDa	46.1	0.5	92.2
40S ribosomal protein S8	RS8_HUMAN	RPS8	24 kDa	8.1	0.5	16.3
60S ribosomal protein L23a	RL23A_HUMAN	RPL23A	18 kDa	8.1	0.5	16.3
Nucleolar RNA helicase 2	DDX21_HUMAN	DDX21	87 kDa	7.2	0.5	14.5
Antigen KI-67	KI67_HUMAN	MKI67	359 kDa	7.2	0.5	14.5
40S ribosomal protein S3a	RS3A_HUMAN	RPS3A	30 kDa	7.2	0.5	14.5
60S ribosomal protein L7a	RL7A_HUMAN	RPL7A	30 kDa	6.3	0.5	12.7
Histone H2A.V	H2AV_HUMAN	H2AFV	14 kDa	6.3	0.5	12.7
Core histone macro-H2A.1	H2AY_HUMAN	H2AFY	40 kDa	5.4	0.5	10.9
40S ribosomal protein S11	RS11_HUMAN	RPS11	18 kDa	5.4	0.5	10.9
Histone H1.5	H15_HUMAN	HIST1H1B	23 kDa	5.4	0.5	10.9
Lupus La protein	LA_HUMAN	SSB	47 kDa	4.5	0.5	9.0
40S ribosomal protein S25	RS25_HUMAN	RPS25	14 kDa	4.5	0.5	9.0
60S ribosomal protein L8	RL8_HUMAN	RPL8	28 kDa	4.5	0.5	9.0
Cytospin-B	CYTSB_HUMAN	SPECC1	119 kDa	4.5	0.5	9.0
Selenium-binding protein 1	SBP1_HUMAN	SELENBP1	52 kDa	4.5	0.5	9.0
Putative ribosomal RNA methyltransferase NOP2	NOP2_HUMAN	NOP2	89 kDa	3.6	0.5	7.2
40S ribosomal protein S6	RS6_HUMAN	RPS6	29 kDa	3.6	0.5	7.2
60S ribosomal protein L18	RL18_HUMAN	RPL18	22 kDa	3.6	0.5	7.2
Ig alpha-1 chain C region	IGHA1_HUMAN	IGHA1	38 kDa	3.6	0.5	7.2
60S ribosomal protein L24	RL24_HUMAN	RPL24	18 kDa	3.6	0.5	7.2
Nuclease-sensitive element-binding protein 1	YBOX1_HUMAN	YBX1	36 kDa	3.6	0.5	7.2
40S ribosomal protein S2	RS2_HUMAN	RPS2	31 kDa	3.6	0.5	7.2
ATP-dependent RNA helicase A	DHX9_HUMAN	DHX9	141 kDa	7.2	1.1	6.5
Interleukin enhancer-binding factor 3	ILF3_HUMAN	ILF3	95 kDa	13.6	2.2	6.1
Coronin-1A	COR1A_HUMAN	CORO1A	51 kDa	6.3	1.1	5.7
ATP-dependent RNA helicase DDX18	DDX18_HUMAN	DDX18	75 kDa	2.7	0.5	5.4
60S ribosomal protein L17	RL17_HUMAN	RPL17	21 kDa	2.7	0.5	5.4
Filaggrin	FILA_HUMAN	FLG	435 kDa	2.7	0.5	5.4
Ig kappa chain V-III region SIE	KV302_HUMAN		12 kDa	2.7	0.5	5.4
40S ribosomal protein S23	RS23_HUMAN	RPS23	16 kDa	2.7	0.5	5.4
Heat shock 70 kDa protein 1A/1B	HSP71_HUMAN	HSPA1A	70 kDa	2.7	0.5	5.4
T-complex protein 1 subunit gamma	TCPG_HUMAN	CCT3	61 kDa	4.5	1.1	4.0
Eukaryotic initiation factor 4A-II	IF4A2_HUMAN	EIF4A2	46 kDa	4.5	1.1	4.0
Ezrin	EZRI_HUMAN	EZR	69 kDa	4.5	1.1	4.0
RNA-binding protein Raly	RALY_HUMAN	RALY	32 kDa	4.5	1.1	4.0

Eukaryotic translation initiation factor 6	IF6_HUMAN	EIF6	27 kDa	1.8	0.5	3.6
60S ribosomal protein L13a	RL13A_HUMAN	RPL13A	24 kDa	1.8	0.5	3.6
T-complex protein 1 subunit delta	TCPD_HUMAN	CCT4	58 kDa	1.8	0.5	3.6
Thioredoxin domain-containing protein 5	TXND5_HUMAN	TXNDC5	48 kDa	1.8	0.5	3.6
Polypyrimidine tract-binding protein 1	PTBP1_HUMAN	PTBP1	57 kDa	1.8	0.5	3.6
DNA topoisomerase 2-alpha	TOP2A_HUMAN	TOP2A	174 kDa	1.8	0.5	3.6
Multifunctional protein ADE2	PUR6_HUMAN	PAICS	47 kDa	1.8	0.5	3.6
Nucleolar GTP-binding protein 1	NOG1_HUMAN	GTPBP4	74 kDa	1.8	0.5	3.6
60S ribosomal protein L31	RL31_HUMAN	RPL31	14 kDa	1.8	0.5	3.6
DNA topoisomerase 1	TOP1_HUMAN	TOP1	91 kDa	1.8	0.5	3.6
Transcription intermediary factor 1-beta	TIF1B_HUMAN	TRIM28	89 kDa	1.8	0.5	3.6
Myosin-9	MYH9_HUMAN	MYH9	227 kDa	1.8	0.5	3.6
60S ribosomal protein L27a	RL27A_HUMAN	RPL27A	17 kDa	1.8	0.5	3.6
Serine/arginine-rich splicing factor 3	SRSF3_HUMAN	SRSF3	19 kDa	1.8	0.5	3.6
60S ribosomal protein L6	RL6_HUMAN	RPL6	33 kDa	1.8	0.5	3.6
60S ribosomal protein L18a	RL18A_HUMAN	RPL18A	21 kDa	1.8	0.5	3.6
Exocyst complex component 2	EXOC2_HUMAN	EXOC2	104 kDa	1.8	0.5	3.6
40S ribosomal protein S15	RS15_HUMAN	RPS15	17 kDa	1.8	0.5	3.6
40S ribosomal protein S13	RS13_HUMAN	RPS13	17 kDa	3.6	1.1	3.2
60S ribosomal protein L7	RL7_HUMAN	RPL7	29 kDa	3.6	1.1	3.2
Plasminogen	PLMN_HUMAN	PLG	91 kDa	6.3	2.2	2.8
Ubiquitin-40S ribosomal protein S27a	RS27A_HUMAN	RPS27A	18 kDa	12.7	4.5	2.8
Peroxiredoxin-2	PRDX2_HUMAN	PRDX2	22 kDa	2.7	1.1	2.4
Proliferation-associated protein 2G4	PA2G4_HUMAN	PA2G4	44 kDa	2.7	1.1	2.4
Single-stranded DNA-binding protein, mitochondrial	SSBP_HUMAN	SSBP1	17 kDa	2.7	1.1	2.4
Cathepsin D	CATD_HUMAN	CTSD	45 kDa	2.7	1.1	2.4
Inorganic pyrophosphatase	IPYR_HUMAN	PPA1	33 kDa	2.7	1.1	2.4
Histone H3.1t	H31T_HUMAN	HIST3H3	16 kDa	2.7	1.1	2.4
Fructose-bisphosphate aldolase A	ALDOA_HUMAN	ALDOA	39 kDa	2.7	1.1	2.4
Heterogeneous nuclear ribonucleoprotein G	HNRPG_HUMAN	RBMX	?	8.1	3.4	2.4
DNA-dependent protein kinase catalytic subunit	PRKDC_HUMAN	PRKDC	469 kDa	15.4	6.7	2.3
Splicing factor, proline- and glutamine-rich	SFPQ_HUMAN	SFPQ	76 kDa	7.2	3.4	2.2
40S ribosomal protein S4, X isoform	RS4X_HUMAN	RPS4X	30 kDa	7.2	3.4	2.2
Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	HNRNPU	91 kDa	26.2	12.3	2.1
Nucleolin	NUCL_HUMAN	NCL	77 kDa	17.2	8.9	1.9
Histone H2A type 1-A	H2A1A_HUMAN	HIST1H2AA	14 kDa	6.3	3.4	1.9
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_HUMAN	HNRNPC	34 kDa	27.1	14.5	1.9

Ig lambda-2 chain C regions	LAC2_HUMAN	IGLC2	11 kDa	8.1	4.5	1.8
4F2 cell-surface antigen heavy chain	4F2_HUMAN	SLC3A2	68 kDa	0.9	0.5	1.8
Acidic leucine-rich nuclear phosphoprotein 32 family member B	AN32B_HUMAN	ANP32B	29 kDa	0.9	0.5	1.8
Annexin A1	ANXA1_HUMAN	ANXA1	39 kDa	0.9	0.5	1.8
Putative uncharacterized protein encoded by LINC00615	CL037_HUMAN	LINC00615	15 kDa	0.9	0.5	1.8
D-tyrosyl-tRNA(Tyr) deacylase 1	DTD1_HUMAN	DTD1	23 kDa	0.9	0.5	1.8
Gasdermin-A	GSDMA_HUMAN	GSDMA	49 kDa	0.9	0.5	1.8
Histone deacetylase 1	HDAC1_HUMAN	HDAC1	55 kDa	0.9	0.5	1.8
HLA class II histocompatibility antigen gamma chain	HG2A_HUMAN	CD74	34 kDa	0.9	0.5	1.8
Ig heavy chain V-III region BRO	HV305_HUMAN		13 kDa	0.9	0.5	1.8
Immunoglobulin J chain	IGJ_HUMAN	IGJ	18 kDa	0.9	0.5	1.8
Interferon regulatory factor 5	IRF5_HUMAN	IRF5	56 kDa	0.9	0.5	1.8
LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1_HUMAN	LETM1	83 kDa	0.9	0.5	1.8
NAD-dependent malic enzyme, mitochondrial	MAOM_HUMAN	ME2	65 kDa	0.9	0.5	1.8
MKI67 FHA domain-interacting nucleolar phosphoprotein	MK67I_HUMAN	MKI67IP	34 kDa	0.9	0.5	1.8
Nucleolar protein 56	NOP56_HUMAN	NOP56	66 kDa	0.9	0.5	1.8
Nucleolar protein 58	NOP58_HUMAN	NOP58	60 kDa	0.9	0.5	1.8
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_HUMAN	PDHA1	43 kDa	0.9	0.5	1.8
Pyrroline-5-carboxylate reductase 1, mitochondrial	P5CR1_HUMAN	PYCR1	33 kDa	0.9	0.5	1.8
Protein disulfide-isomerase	PDIA1_HUMAN	P4HB	57 kDa	0.9	0.5	1.8
Histone-binding protein RBBP7	RBBP7_HUMAN	RBBP7	48 kDa	0.9	0.5	1.8
60S ribosomal protein L10a	RL10A_HUMAN	RPL10A	25 kDa	0.9	0.5	1.8
60S ribosomal protein L13	RL13_HUMAN	RPL13	24 kDa	0.9	0.5	1.8
60S ribosomal protein L14	RL14_HUMAN	RPL14	23 kDa	0.9	0.5	1.8
Ribosomal L1 domain-containing protein 1	RL1D1_HUMAN	RSL1D1	55 kDa	0.9	0.5	1.8
60S ribosomal protein L21	RL21_HUMAN	RPL21	19 kDa	0.9	0.5	1.8
60S ribosomal protein L26-like 1	RL26L_HUMAN	RPL26L1	17 kDa	0.9	0.5	1.8
60S ribosomal protein L27	RL27_HUMAN	RPL27	16 kDa	0.9	0.5	1.8
60S ribosomal protein L29	RL29_HUMAN	RPL29	18 kDa	0.9	0.5	1.8
60S ribosomal protein L36a	RL36A_HUMAN	RPL36A	12 kDa	0.9	0.5	1.8
60S ribosomal protein L37a	RL37A_HUMAN	RPL37A	10 kDa	0.9	0.5	1.8
60S ribosomal protein L3	RL3_HUMAN	RPL3	46 kDa	0.9	0.5	1.8
60S ribosomal protein L4	RL4_HUMAN	RPL4	48 kDa	0.9	0.5	1.8
40S ribosomal protein S16	RS16_HUMAN	RPS16	16 kDa	0.9	0.5	1.8
40S ribosomal protein S24	RS24_HUMAN	RPS24	15 kDa	0.9	0.5	1.8
Staphylococcal nuclease domain-containing protein 1	SND1_HUMAN	SND1	102 kDa	0.9	0.5	1.8

Superoxide dismutase [Cu-Zn]	SODC_HUMAN	SOD1	16 kDa	0.9	0.5	1.8
Sortilin-related receptor	SORL_HUMAN	SORL1	248 kDa	0.9	0.5	1.8
FACT complex subunit SPT16	SP16H_HUMAN	SUPT16H	120 kDa	0.9	0.5	1.8
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCA_HUMAN	SUCLG1	36 kDa	0.9	0.5	1.8
Alanine--tRNA ligase, cytoplasmic	SYAC_HUMAN	AARS	107 kDa	0.9	0.5	1.8
T-complex protein 1 subunit epsilon	TCPE_HUMAN	CCT5	60 kDa	0.9	0.5	1.8
Translationally-controlled tumor protein	TCTP_HUMAN	TPT1	20 kDa	0.9	0.5	1.8
Transketolase	TKT_HUMAN	TKT	68 kDa	0.9	0.5	1.8
Exportin-2	XPO2_HUMAN	CSE1L	110 kDa	0.9	0.5	1.8
Proteasome subunit alpha type-6	PSA6_HUMAN	PSMA6	27 kDa	0.9	0.5	1.8
Protein disulfide-isomerase A6	PDIA6_HUMAN	PDIA6	48 kDa	0.9	0.5	1.8
Leupaxin	LPXN_HUMAN	LPXN	43 kDa	0.9	0.5	1.8
Guanine nucleotide-binding protein-like 3	GNL3_HUMAN	GNL3	62 kDa	0.9	0.5	1.8
Tetraspanin-11	TSN11_HUMAN	TSPAN11	28 kDa	0.9	0.5	1.8
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	DHSA_HUMAN	SDHA	73 kDa	0.9	0.5	1.8
KDEL motif-containing protein 1	KDEL1_HUMAN	KDELC1	58 kDa	0.9	0.5	1.8
Nucleosome assembly protein 1-like 1	NP1L1_HUMAN	NAP1L1	45 kDa	0.9	0.5	1.8
Putative 40S ribosomal protein S26-like 1	RS26L_HUMAN	RPS26P11	13 kDa	0.9	0.5	1.8
60S ribosomal protein L5	RL5_HUMAN	RPL5	34 kDa	0.9	0.5	1.8
Insulin-like growth factor 2 mRNA-binding protein 1	IF2B1_HUMAN	IGF2BP1	63 kDa	0.9	0.5	1.8
Tyrosine--tRNA ligase, cytoplasmic	SYYC_HUMAN	YARS	59 kDa	0.9	0.5	1.8
tRNA wybutosine-synthesizing protein 3 homolog	TYW3_HUMAN	TYW3	30 kDa	0.9	0.5	1.8
DNA replication licensing factor MCM5	MCM5_HUMAN	MCM5	82 kDa	0.9	0.5	1.8
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	ASAP2_HUMAN	ASAP2	112 kDa	0.9	0.5	1.8
Isocitrate dehydrogenase [NADP] cytoplasmic	IDHC_HUMAN	IDH1	47 kDa	0.9	0.5	1.8
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDR1_HUMAN	KHDRBS1	48 kDa	0.9	0.5	1.8
ATP-citrate synthase	ACLY_HUMAN	ACLY	121 kDa	0.9	0.5	1.8
Protein arginine N-methyltransferase 1	ANM1_HUMAN	PRMT1	42 kDa	0.9	0.5	1.8
60S ribosomal protein L28	RL28_HUMAN	RPL28	16 kDa	0.9	0.5	1.8
Acidic leucine-rich nuclear phosphoprotein 32 family member E	AN32E_HUMAN	ANP32E	31 kDa	0.9	0.5	1.8
40S ribosomal protein S9	RS9_HUMAN	RPS9	23 kDa	0.9	0.5	1.8
Putative eukaryotic translation initiation factor 2 subunit 3-like protein	IF2GL_HUMAN	EIF2S3L	51 kDa	0.9	0.5	1.8

General transcription factor II-I	GTF2I_HUMAN	GTF2I	112 kDa	0.9	0.5	1.8
Mesoderm development candidate 1	MESD1_HUMAN	MESDC1	38 kDa	0.9	0.5	1.8
Rho GTPase-activating protein 26	RHG26_HUMAN	ARHGAP26	92 kDa	0.9	0.5	1.8
N-acetyltransferase 10	NAT10_HUMAN	NAT10	116 kDa	0.9	0.5	1.8
E3 ubiquitin-protein ligase RNF185	RN185_HUMAN	RNF185	20 kDa	0.9	0.5	1.8
40S ribosomal protein S18	RS18_HUMAN	RPS18	18 kDa	0.9	0.5	1.8
Ig gamma-2 chain C region	IGHG2_HUMAN	IGHG2	36 kDa	54.3	31.3	1.7
Nucleophosmin	NPM_HUMAN	NPM1	33 kDa	24.4	14.5	1.7
Ig gamma-1 chain C region	IGHG1_HUMAN	IGHG1	36 kDa	80.5	48.1	1.7
Poly [ADP-ribose] polymerase 1	PARP1_HUMAN	PARP1	113 kDa	18.1	11.2	1.6
Calnexin	CALX_HUMAN	CANX	68 kDa	1.8	1.1	1.6
40S ribosomal protein S5	RS5_HUMAN	RPS5	23 kDa	1.8	1.1	1.6
Serpin B3	SPB3_HUMAN	SERPINB3	45 kDa	1.8	1.1	1.6
T-complex protein 1 subunit theta	TCPQ_HUMAN	CCT8	60 kDa	1.8	1.1	1.6
Aconitate hydratase, mitochondrial	ACON_HUMAN	ACO2	85 kDa	1.8	1.1	1.6
60S acidic ribosomal protein P0	RLA0_HUMAN	RPLP0	34 kDa	1.8	1.1	1.6
ATP synthase subunit O, mitochondrial	ATPO_HUMAN	ATP5O	23 kDa	1.8	1.1	1.6
60S ribosomal protein L23	RL23_HUMAN	RPL23	15 kDa	1.8	1.1	1.6
Protein S100-A14	S10AE_HUMAN	S100A14	12 kDa	1.8	1.1	1.6
Non-POU domain-containing octamer-binding protein	NONO_HUMAN	NONO	54 kDa	5.4	3.4	1.6
Heterogeneous nuclear ribonucleoprotein R	HNRPR_HUMAN	HNRNPR	71 kDa	10.9	6.7	1.6
Histone H2A type 1-B/E	H2A1B_HUMAN	HIST1H2AB	14 kDa	10.9	6.7	1.6
Polyadenylate-binding protein 1	PABP1_HUMAN	PABPC1	71 kDa	3.6	2.2	1.6
40S ribosomal protein S14	RS14_HUMAN	RPS14	16 kDa	3.6	2.2	1.6
40S ribosomal protein S7	RS7_HUMAN	RPS7	22 kDa	3.6	2.2	1.6
Histone H4	H4_HUMAN	HIST1H4A	11 kDa	31.6	21.3	1.5
Probable ATP-dependent RNA helicase DDX5	DDX5_HUMAN	DDX5	69 kDa	9.0	6.7	1.3
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRL2_HUMAN	HNRNPUL2	85 kDa	4.5	3.4	1.3
rRNA 2'-O-methyltransferase fibrillarin	FBRL_HUMAN	FBL	34 kDa	4.5	3.4	1.3
Heterogeneous nuclear ribonucleoprotein A3	ROA3_HUMAN	HNRNPA3	40 kDa	7.2	5.6	1.3
Heterogeneous nuclear ribonucleoprotein M	HNRPM_HUMAN	HNRNPM	78 kDa	7.2	5.6	1.3
Annexin A2	ANXA2_HUMAN	ANXA2	39 kDa	9.9	7.8	1.3
RNA-binding protein 14	RBM14_HUMAN	RBM14	69 kDa	2.7	2.2	1.2
Serpin B12	SPB12_HUMAN	SERPINB12	46 kDa	2.7	2.2	1.2
Voltage-dependent anion-selective channel protein 2	VDAC2_HUMAN	VDAC2	32 kDa	2.7	2.2	1.2
Zinc-alpha-2-glycoprotein	ZA2G_HUMAN	AZGP1	34 kDa	2.7	2.2	1.2
Small proline-rich protein 2E	SPR2E_HUMAN	SPRR2E	8 kDa	2.7	2.2	1.2
Thioredoxin	THIO_HUMAN	TXN	12 kDa	2.7	2.2	1.2
Serum albumin	ALBU_HUMAN	ALB	69 kDa	19.0	16.8	1.1

Adenosylhomocysteinase	SAHH_HUMAN	AHCY	48 kDa	6.3	5.6	1.1
Tubulin beta-2C chain	TBB2C_HUMAN	TUBB2C	?	51.5	45.9	1.1
Filaggrin-2	FILA2_HUMAN	FLG2	248 kDa	9.9	8.9	1.1
Tubulin beta chain	TBB5_HUMAN	TUBB	50 kDa	57.0	52.6	1.1
Histone H2B type 1-B	H2B1B_HUMAN	HIST1H2BB	14 kDa	14.5	13.4	1.1
Bleomycin hydrolase	BLMH_HUMAN	BLMH	53 kDa	3.6	3.4	1.1
ADP/ATP translocase 2	ADT2_HUMAN	SLC25A5	33 kDa	3.6	3.4	1.1
Protein S100-A8	S10A8_HUMAN	S100A8	11 kDa	3.6	3.4	1.1
Spliceosome RNA helicase DDX39B	DX39B_HUMAN	DDX39B	49 kDa	3.6	3.4	1.1
Prohibitin-2	PHB2_HUMAN	PHB2	33 kDa	3.6	3.4	1.1
Skin-specific protein 32	XP32_HUMAN	XP32	26 kDa	3.6	3.4	1.1
ATP-dependent RNA helicase DDX39A	DX39A_HUMAN	DDX39A	49 kDa	3.6	3.4	1.1
Probable ATP-dependent RNA helicase DDX17	DDX17_HUMAN	DDX17	80 kDa	7.2	6.7	1.1
Guanine nucleotide-binding protein subunit beta-2-like 1	GBLP_HUMAN	GNB2L1	35 kDa	7.2	6.7	1.1
14-3-3 protein beta/alpha	1433B_HUMAN	YWHAB	28 kDa	4.5	4.5	1.0
Histone H2B type 1-C/E/F/G/I	H2B1C_HUMAN	HIST1H2BC	14 kDa	14.5	14.5	1.0
Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	GAPDH	36 kDa	32.6	33.6	1.0
Heterogeneous nuclear ribonucleoprotein Q	HNRPQ_HUMAN	SYNCRIP	70 kDa	5.4	5.6	1.0
Junction plakoglobin	PLAK_HUMAN	JUP	82 kDa	18.1	19.0	1.0
Peroxiredoxin-1	PRDX1_HUMAN	PRDX1	22 kDa	6.3	6.7	0.9
Elongation factor 2	EF2_HUMAN	EEF2	95 kDa	9.0	10.1	0.9
Actin-related protein 3	ARP3_HUMAN	ACTR3	47 kDa	0.9	1.1	0.8
Acid ceramidase	ASAH1_HUMAN	ASAH1	45 kDa	0.9	1.1	0.8
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP_HUMAN	C1QBP	31 kDa	0.9	1.1	0.8
Chromobox protein homolog 3	CBX3_HUMAN	CBX3	21 kDa	0.9	1.1	0.8
Citrate synthase, mitochondrial	CISY_HUMAN	CS	52 kDa	0.9	1.1	0.8
Eukaryotic translation initiation factor 2 subunit 1	IF2A_HUMAN	EIF2S1	36 kDa	0.9	1.1	0.8
Leucine-rich PPR motif-containing protein, mitochondrial	LPPRC_HUMAN	LRPPRC	158 kDa	0.9	1.1	0.8
Nascent polypeptide-associated complex subunit alpha	NACA_HUMAN	NACA	23 kDa	0.9	1.1	0.8
Proteasome activator complex subunit 2	PSME2_HUMAN	PSME2	27 kDa	0.9	1.1	0.8
Cornifin-B	SPR1B_HUMAN	SPRR1B	10 kDa	0.9	1.1	0.8
Synaptophysin-like protein 1	SYPL1_HUMAN	SYPL1	29 kDa	0.9	1.1	0.8
Fatty acid synthase	FAS_HUMAN	FASN	273 kDa	0.9	1.1	0.8
Heat shock protein 105 kDa	HS105_HUMAN	HSPH1	97 kDa	0.9	1.1	0.8
Transgelin-2	TAGL2_HUMAN	TAGLN2	22 kDa	0.9	1.1	0.8
Rho GDP-dissociation inhibitor 1	GDIR1_HUMAN	ARHGDIA	23 kDa	0.9	1.1	0.8
T-complex protein 1 subunit zeta	TCPZ_HUMAN	CCT6A	58 kDa	0.9	1.1	0.8
ATP synthase subunit gamma,	ATPG_HUMAN	ATP5C1	33 kDa	0.9	1.1	0.8

mitochondrial						
Adenine phosphoribosyltransferase	APT_HUMAN	APRT	20 kDa	0.9	1.1	0.8
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PP1A_HUMAN	PPP1CA	38 kDa	0.9	1.1	0.8
Glycine--tRNA ligase	SYG_HUMAN	GARS	83 kDa	0.9	1.1	0.8
Serine/arginine-rich splicing factor 1	SRSF1_HUMAN	SRSF1	28 kDa	3.6	4.5	0.8
60S ribosomal protein L12	RL12_HUMAN	RPL12	18 kDa	5.4	6.7	0.8
Serine hydroxymethyltransferase, mitochondrial	GLYM_HUMAN	SHMT2	56 kDa	6.3	7.8	0.8
Phosphatidylethanolamine-binding protein 1	PEBP1_HUMAN	PEBP1	21 kDa	1.8	2.2	0.8
Lactotransferrin	TRFL_HUMAN	LTF	78 kDa	1.8	2.2	0.8
Histone H1.2	H12_HUMAN	HIST1H1C	21 kDa	1.8	2.2	0.8
Ras-related protein Rab-10	RAB10_HUMAN	RAB10	23 kDa	1.8	2.2	0.8
60S ribosomal protein L22	RL22_HUMAN	RPL22	15 kDa	1.8	2.2	0.8
L-lactate dehydrogenase A chain	LDHA_HUMAN	LDHA	37 kDa	8.1	10.1	0.8
Catalase	CATA_HUMAN	CAT	60 kDa	4.5	5.6	0.8
GTP-binding nuclear protein Ran	RAN_HUMAN	RAN	24 kDa	4.5	5.6	0.8
Prolactin-inducible protein	PIP_HUMAN	PIP	17 kDa	2.7	3.4	0.8
Desmoglein-1	DSG1_HUMAN	DSG1	114 kDa	24.4	31.3	0.8
Actin, alpha cardiac muscle 1	ACTC_HUMAN	ACTC1	42 kDa	31.6	44.7	0.7
Plastin-2	PLSL_HUMAN	LCP1	70 kDa	6.3	8.9	0.7
L-lactate dehydrogenase B chain	LDHB_HUMAN	LDHB	37 kDa	6.3	8.9	0.7
Elongation factor Tu, mitochondrial	EFTU_HUMAN	TUFM	50 kDa	5.4	7.8	0.7
Pyruvate kinase isozymes M1/M2	KPYM_HUMAN	PKM	58 kDa	10.9	15.7	0.7
Actin, cytoplasmic 1	ACTB_HUMAN	ACTB	42 kDa	61.5	91.7	0.7
ATP synthase subunit alpha, mitochondrial	ATPA_HUMAN	ATP5A1	60 kDa	16.3	24.6	0.7
Dermcidin	DCD_HUMAN	DCD	11 kDa	8.1	12.3	0.7
Heterogeneous nuclear ribonucleoprotein F	HNRPF_HUMAN	HNRNPF	46 kDa	3.6	5.6	0.6
Elongation factor 1-alpha 1	EF1A1_HUMAN	EEF1A1	50 kDa	17.2	26.8	0.6
60 kDa heat shock protein, mitochondrial	CH60_HUMAN	HSPD1	61 kDa	19.9	31.3	0.6
78 kDa glucose-regulated protein	GRP78_HUMAN	HSPA5	72 kDa	12.7	20.1	0.6
Desmocollin-1	DSC1_HUMAN	DSC1	100 kDa	9.0	14.5	0.6
Stress-70 protein, mitochondrial	GRP75_HUMAN	HSPA9	74 kDa	8.1	13.4	0.6
Heterogeneous nuclear ribonucleoprotein L	HNRPL_HUMAN	HNRNPL	64 kDa	2.7	4.5	0.6
Hornerin	HORN_HUMAN	HRNR	282 kDa	2.7	4.5	0.6
60S ribosomal protein L11	RL11_HUMAN	RPL11	20 kDa	2.7	4.5	0.6
Heterogeneous nuclear ribonucleoprotein H	HNRH1_HUMAN	HNRNPH1	49 kDa	7.2	12.3	0.6
Ig kappa chain C region	IGKC_HUMAN	IGKC	12 kDa	13.6	23.5	0.6
Voltage-dependent anion-selective channel protein 1	VDAC1_HUMAN	VDAC1	31 kDa	4.5	7.8	0.6
Heat shock protein HSP 90-alpha	HS90A_HUMAN	HSP90AA1	85 kDa	19.9	35.8	0.6

Caspase-14	CASPE_HUMAN	CASP14	28 kDa	7.2	13.4	0.5
Loricrin	LORI_HUMAN	LOR	26 kDa	1.8	3.4	0.5
Heterogeneous nuclear ribonucleoprotein A0	ROA0_HUMAN	HNRNPA0	31 kDa	1.8	3.4	0.5
14-3-3 protein epsilon	1433E_HUMAN	YWHAE	29 kDa	1.8	3.4	0.5
14-3-3 protein gamma	1433G_HUMAN	YWHAG	28 kDa	1.8	3.4	0.5
Poly(rC)-binding protein 2	PCBP2_HUMAN	PCBP2	39 kDa	3.6	6.7	0.5
Poly(rC)-binding protein 1	PCBP1_HUMAN	PCBP1	37 kDa	3.6	6.7	0.5
Heat shock protein HSP 90-beta	HS90B_HUMAN	HSP90AB1	83 kDa	24.4	47.0	0.5
Glutathione S-transferase P	GSTP1_HUMAN	GSTP1	23 kDa	6.3	12.3	0.5
Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	HNRNPA2B1	37 kDa	4.5	8.9	0.5
Corneodesmosin	CDSN_HUMAN	CDSN	52 kDa	2.7	5.6	0.5
Heterogeneous nuclear ribonucleoprotein D0	HNRPD_HUMAN	HNRNPD	38 kDa	2.7	5.6	0.5
14-3-3 protein theta	1433T_HUMAN	YWHAQ	28 kDa	2.7	5.6	0.5
Ig mu chain C region	IGHM_HUMAN	IGHM	49 kDa	6.3	13.4	0.5
40S ribosomal protein SA	RSSA_HUMAN	RPSA	33 kDa	3.6	7.8	0.5
Alpha-enolase	ENOA_HUMAN	ENO1	47 kDa	7.2	15.7	0.5
D-3-phosphoglycerate dehydrogenase	SERA_HUMAN	PHGDH	57 kDa	8.1	17.9	0.5
ATP synthase subunit beta, mitochondrial	ATPB_HUMAN	ATP5B	57 kDa	9.0	20.1	0.4
Triosephosphate isomerase	TPIS_HUMAN	TPI1	31 kDa	4.5	10.1	0.4
Tubulin alpha-1B chain	TBA1B_HUMAN	TUBA1B	50 kDa	23.5	52.6	0.4
Rab GDP dissociation inhibitor beta	GDIB_HUMAN	GDI2	51 kDa	0.5	1.1	0.4
HLA class II histocompatibility antigen, DRB1-7 beta chain	2B17_HUMAN	HLA-DRB1	30 kDa	0.5	1.1	0.4
Aldehyde dehydrogenase, mitochondrial	ALDH2_HUMAN	ALDH2	56 kDa	0.5	1.1	0.4
Cystatin-M	CYTM_HUMAN	CST6	17 kDa	0.5	1.1	0.4
Destrin	DEST_HUMAN	DSTN	19 kDa	0.5	1.1	0.4
HLA class II histocompatibility antigen, DR alpha chain	DRA_HUMAN	HLA-DRA	29 kDa	0.5	1.1	0.4
Elongation factor 1-gamma	EF1G_HUMAN	EEF1G	50 kDa	0.5	1.1	0.4
Hsc70-interacting protein	F10A1_HUMAN	ST13	41 kDa	0.5	1.1	0.4
Methylosome subunit pICln	ICLN_HUMAN	CLNS1A	26 kDa	0.5	1.1	0.4
Importin subunit beta-1	IMB1_HUMAN	KPNB1	97 kDa	0.5	1.1	0.4
Lipocalin-1	LCN1_HUMAN	LCN1	19 kDa	0.5	1.1	0.4
Malate dehydrogenase, cytoplasmic	MDHC_HUMAN	MDH1	36 kDa	0.5	1.1	0.4
Phosphate carrier protein, mitochondrial	MPCP_HUMAN	SLC25A3	40 kDa	0.5	1.1	0.4
NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial	NDUC1_HUMAN	NDUFC1	9 kDa	0.5	1.1	0.4
Phosphoglycerate mutase 1	PGAM1_HUMAN	PGAM1	29 kDa	0.5	1.1	0.4
Peroxiredoxin-6	PRDX6_HUMAN	PRDX6	25 kDa	0.5	1.1	0.4
Proteasome subunit alpha type-7	PSA7_HUMAN	PSMA7	28 kDa	0.5	1.1	0.4

Proteasome subunit beta type-5	PSB5_HUMAN	PSMB5	28 kDa	0.5	1.1	0.4
Cytochrome b-c1 complex subunit 2, mitochondrial	QCR2_HUMAN	UQCRC2	48 kDa	0.5	1.1	0.4
Putative 40S ribosomal protein S10-like	RS10L_HUMAN	RPS10P5	20 kDa	0.5	1.1	0.4
40S ribosomal protein S17	RS17_HUMAN	RPS17	16 kDa	0.5	1.1	0.4
Phosphoserine aminotransferase	SERC_HUMAN	PSAT1	40 kDa	0.5	1.1	0.4
Suppressor of G2 allele of SKP1 homolog	SUGT1_HUMAN	SUGT1	41 kDa	0.5	1.1	0.4
Transportin-1	TNPO1_HUMAN	TNPO1	102 kDa	0.5	1.1	0.4
60S ribosomal protein L30	RL30_HUMAN	RPL30	13 kDa	0.5	1.1	0.4
Calpain-1 catalytic subunit	CAN1_HUMAN	CAPN1	82 kDa	0.5	1.1	0.4
40S ribosomal protein S20	RS20_HUMAN	RPS20	13 kDa	0.5	1.1	0.4
Proteasome subunit beta type-6	PSB6_HUMAN	PSMB6	25 kDa	0.5	1.1	0.4
Bifunctional purine biosynthesis protein PURH	PUR9_HUMAN	ATIC	65 kDa	0.5	1.1	0.4
C-1-tetrahydrofolate synthase, cytoplasmic	C1TC_HUMAN	MTHFD1	102 kDa	0.5	1.1	0.4
Ribose-phosphate pyrophosphokinase 1	PRPS1_HUMAN	PRPS1	35 kDa	0.5	1.1	0.4
Oral-facial-digital syndrome 1 protein	OFD1_HUMAN	OFD1	117 kDa	0.5	1.1	0.4
Protein DJ-1	PARK7_HUMAN	PARK7	20 kDa	0.5	1.1	0.4
S-adenosylmethionine synthase isoform type-2	METK2_HUMAN	MAT2A	44 kDa	0.5	1.1	0.4
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMH1_HUMAN	SAMHD1	72 kDa	0.5	1.1	0.4
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	B3GN9_HUMAN	B3GNT9	44 kDa	0.5	1.1	0.4
Non-specific cytotoxic cell receptor protein 1 homolog	NCRP1_HUMAN	NCCRP1	?	0.5	1.1	0.4
Ig kappa chain V-II region Cum	KV201_HUMAN		13 kDa	0.5	1.1	0.4
Proteasome subunit alpha type-5	PSA5_HUMAN	PSMA5	26 kDa	0.5	1.1	0.4
Protein piccolo	PCLO_HUMAN	PCLO	553 kDa	0.5	1.1	0.4
DNA replication licensing factor MCM7	MCM7_HUMAN	MCM7	81 kDa	0.5	1.1	0.4
Thymidylate kinase	KTHY_HUMAN	DTYMK	24 kDa	0.5	1.1	0.4
Kinesin-like protein KIF14	KIF14_HUMAN	KIF14	186 kDa	0.5	1.1	0.4
Interleukin enhancer-binding factor 2	ILF2_HUMAN	ILF2	43 kDa	0.5	1.1	0.4
Calcyclin-binding protein	CYBP_HUMAN	CACYBP	26 kDa	0.5	1.1	0.4
Dermokine	DMKN_HUMAN	DMKN	47 kDa	0.5	1.1	0.4
Importin-5	IPO5_HUMAN	IPO5	124 kDa	0.5	1.1	0.4
ATP-binding cassette sub-family A member 6	ABCA6_HUMAN	ABCA6	184 kDa	0.5	1.1	0.4
Protocadherin-11 X-linked	PC11X_HUMAN	PCDH11X	148 kDa	0.5	1.1	0.4
PRKR-interacting protein 1	PKRI1_HUMAN	PRKRIP1	21 kDa	0.5	1.1	0.4
Ran-specific GTPase-activating protein	RANG_HUMAN	RANBP1	23 kDa	0.5	1.1	0.4
Sideroflexin-1	SFXN1_HUMAN	SFXN1	36 kDa	0.5	1.1	0.4
WD repeat domain phosphoinositide-interacting protein 2	WIPI2_HUMAN	WIPI2	49 kDa	0.5	1.1	0.4

Protein-glutamine gamma-glutamyltransferase E	TGM3_HUMAN	TGM3	77 kDa	6.3	14.5	0.4
Gamma-glutamylcyclotransferase	GGCT_HUMAN	GGCT	21 kDa	1.8	4.5	0.4
Protein disulfide-isomerase A3	PDIA3_HUMAN	PDIA3	57 kDa	1.8	4.5	0.4
Heterogeneous nuclear ribonucleoprotein H3	HNRH3_HUMAN	HNRNPH3	37 kDa	1.8	4.5	0.4
14-3-3 protein zeta/delta	1433Z_HUMAN	YWHAZ	28 kDa	1.8	4.5	0.4
Cofilin-1	COF1_HUMAN	CFL1	19 kDa	3.6	8.9	0.4
HLA class I histocompatibility antigen, A-1 alpha chain	1A01_HUMAN	HLA-A	41 kDa	0.9	2.2	0.4
Chloride intracellular channel protein 1	CLIC1_HUMAN	CLIC1	27 kDa	0.9	2.2	0.4
Far upstream element-binding protein 2	FUBP2_HUMAN	KHSRP	73 kDa	0.9	2.2	0.4
3-hydroxyacyl-CoA dehydrogenase type-2	HCD2_HUMAN	HSD17B10	27 kDa	0.9	2.2	0.4
Eukaryotic translation initiation factor 5A-1	IF5A1_HUMAN	EIF5A	17 kDa	0.9	2.2	0.4
Protein RCC2	RCC2_HUMAN	RCC2	56 kDa	0.9	2.2	0.4
Ras-related protein Rab-11A	RB11A_HUMAN	RAB11A	24 kDa	0.9	2.2	0.4
Macrophage migration inhibitory factor	MIF_HUMAN	MIF	12 kDa	0.9	2.2	0.4
Rho GDP-dissociation inhibitor 2	GDIR2_HUMAN	ARHGDIB	23 kDa	0.9	2.2	0.4
U6 snRNA-associated Sm-like protein LSm4	LSM4_HUMAN	LSM4	15 kDa	0.9	2.2	0.4
Lysozyme C	LYSC_HUMAN	LYZ	17 kDa	0.9	2.2	0.4
Glutamate dehydrogenase 1, mitochondrial	DHE3_HUMAN	GLUD1	61 kDa	0.9	2.2	0.4
Hemoglobin subunit beta	HBB_HUMAN	HBB	16 kDa	0.9	2.2	0.4
Peptidyl-prolyl cis-trans isomerase A	PPIA_HUMAN	PPIA	18 kDa	9.0	22.4	0.4
Ubiquitin-like modifier-activating enzyme 1	UBA1_HUMAN	UBA1	118 kDa	2.7	6.7	0.4
Desmoplakin	DESP_HUMAN	DSP	332 kDa	10.9	30.2	0.4
Arginase-1	ARGI1_HUMAN	ARG1	35 kDa	3.6	10.1	0.4
Heat shock cognate 71 kDa protein	HSP7C_HUMAN	HSPA8	71 kDa	10.9	31.3	0.3
Heterogeneous nuclear ribonucleoprotein A1-like 2	RA1L2_HUMAN	HNRNPA1L2	34 kDa	2.7	7.8	0.3
Phosphoglycerate kinase 1	PGK1_HUMAN	PGK1	45 kDa	3.6	11.2	0.3
Profilin-1	PROF1_HUMAN	PFN1	15 kDa	1.8	5.6	0.3
Heterogeneous nuclear ribonucleoprotein K	HNRPK_HUMAN	HNRNPK	51 kDa	4.5	14.5	0.3
Fatty acid-binding protein, epidermal	FABP5_HUMAN	FABP5	15 kDa	0.9	3.4	0.3
Galectin-7	LEG7_HUMAN	LGALS7	15 kDa	0.9	3.4	0.3
Lamin-B1	LMNB1_HUMAN	LMNB1	66 kDa	0.9	3.4	0.3
X-ray repair cross-complementing protein 6	XRCC6_HUMAN	XRCC6	70 kDa	0.9	3.4	0.3
Suprabasin	SBSN_HUMAN	SBSN	61 kDa	0.9	3.4	0.3
Polypeptide N-acetylgalactosaminyltransferase-like 6	GLTL6_HUMAN	GALNTL6	70 kDa	0.9	3.4	0.3
Proliferating cell nuclear antigen	PCNA_HUMAN	PCNA	29 kDa	1.8	6.7	0.3
Malate dehydrogenase,	MDHM_HUMAN	MDH2	36 kDa	5.4	20.1	0.3

mitochondrial						
40S ribosomal protein S3	RS3_HUMAN	RPS3	27 kDa	1.8	7.8	0.2
Desmocollin-3	DSC3_HUMAN	DSC3	100 kDa	0.5	2.2	0.2
Protein-glutamine gamma-glutamyltransferase K	TGM1_HUMAN	TGM1	90 kDa	0.5	2.2	0.2
Purine nucleoside phosphorylase	PNPH_HUMAN	PNP	32 kDa	0.5	2.2	0.2
Ubiquitin carboxyl-terminal hydrolase isozyme L1	UCHL1_HUMAN	UCHL1	25 kDa	0.5	2.2	0.2
Protein S100-A9	S10A9_HUMAN	S100A9	13 kDa	0.5	2.2	0.2
Elongation factor 1-delta	EF1D_HUMAN	EEF1D	31 kDa	0.5	2.2	0.2
Spermidine synthase	SPEE_HUMAN	SRM	34 kDa	0.5	2.2	0.2
Acidic leucine-rich nuclear phosphoprotein 32 family member A	AN32A_HUMAN	ANP32A	29 kDa	0.5	2.2	0.2
Transcriptional adapter 2-beta	TAD2B_HUMAN	TADA2B	48 kDa	0.5	2.2	0.2
Prostaglandin E synthase 3	TEBP_HUMAN	PTGES3	19 kDa	0.5	2.2	0.2
Prohibitin	PHB_HUMAN	PHB	30 kDa	0.9	4.5	0.2
Cystatin-A	CYTA_HUMAN	CSTA	11 kDa	0.9	4.5	0.2
High mobility group protein B1	HMGB1_HUMAN	HMGB1	25 kDa	0.9	4.5	0.2
Inosine-5'-monophosphate dehydrogenase 2	IMDH2_HUMAN	IMPDH2	56 kDa	0.9	4.5	0.2
ADP-ribosylation factor 1	ARF1_HUMAN	ARF1	21 kDa	0.9	5.6	0.2
Peptidyl-prolyl cis-trans isomerase B	PPIB_HUMAN	PPIB	24 kDa	0.9	5.6	0.2
ELAV-like protein 1	ELAV1_HUMAN	ELAVL1	36 kDa	0.5	3.4	0.1
T-complex protein 1 subunit beta	TCPB_HUMAN	CCT2	57 kDa	0.5	3.4	0.1
Protein SET	SET_HUMAN	SET	33 kDa	0.5	3.4	0.1
Aspartate aminotransferase, mitochondrial	AATM_HUMAN	GOT2	48 kDa	0.5	4.5	0.1
Endoplasmin	ENPL_HUMAN	HSP90B1	92 kDa	0.5	4.5	0.1
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM_HUMAN	ACADM	47 kDa	0.5	5.6	0.1
Tubulin beta-4 chain	TBB4_HUMAN	TUBB4	55 kDa	0.5	41.4	0.0
Tubulin alpha-1A chain	TBA1A_HUMAN	TUBA1A	50 kDa	0.5	50.3	0.0
Ig kappa chain V-I region Roy	KV116_HUMAN		12 kDa	0.9	102.9	0.0

Supplemental Table 4

Level	Kegg ID	Metabolite	KO1 TCR	KO2 TCR	KO3 TCR	KO1 UN	KO2 UN	KO3 UN	WT1 TCR	WT2 TCR	WT3 TCR	WT1 UN	WT2 UN	WT3 UN
Tier 1	C00346	O-Phosphoethanolamine	0.887	0.822	1.030	0.932	1.094	1.080	0.582	0.426	0.924	0.540	0.461	0.584
Tier 1	C00062	Arginine	0.949	0.861	1.313	0.808	0.562	0.560	0.929	0.676	1.717	0.439	0.418	0.421
Tier 1	C00245	Taurine	0.813	0.861	1.188	0.844	1.036	1.022	0.619	0.389	1.024	0.501	0.332	0.538
Tier 1	C17349	Guanidine	0.172	0.093	0.178	0.070	10.690	0.268	1.139	0.138	0.422	0.106	0.052	0.068
Tier 1	C00152	Asparagine	0.984	0.910	1.245	0.297	0.290	0.289	1.079	0.730	1.452	0.202	0.163	0.176
Tier 1	C00064	Glutamine	1.705	0.952	0.602	2.392	1.504	0.914	0.689	0.748	0.676	0.743	0.476	1.001
Tier 1	C00327	Citrulline	0.329	0.464	1.136	4.319	0.765	0.347	0.351	0.493	0.449	0.366	0.250	0.167
Tier 1	C02989	Methionine Sulfoxide	0.840	0.853	1.160	0.741	0.577	0.503	0.929	0.687	1.227	0.561	0.493	0.442
Tier 1	HMDB0028753	Aspartyl-Glycine	1.068	1.029	1.210	0.889	0.900	0.911	0.807	0.660	1.284	0.552	0.485	0.498
Tier 1	C02989	Methionine Sulfoxide - Isomer	0.865	0.860	1.134	0.722	0.566	0.515	0.942	0.693	1.257	0.546	0.484	0.433
Tier 1	C00263	Homoserine	0.941	0.978	1.282	0.330	0.352	0.386	1.113	0.713	1.299	0.315	0.233	0.211
Tier 1	C00065	Serine	1.004	0.898	1.307	1.212	0.498	0.408	1.012	0.781	1.507	0.288	0.190	0.175
Tier 1	C00025	Glutamic Acid	1.173	1.089	1.259	1.124	1.150	1.048	0.671	0.366	1.091	0.664	0.481	0.674
Tier 1	C00049	Aspartic Acid	1.208	1.104	1.024	1.321	1.424	1.212	0.492	0.278	0.931	0.678	0.444	0.707
Tier 1	C01157	4-Hydroxyproline	0.951	0.918	1.323	0.182	0.208	0.203	1.141	0.796	1.661	0.154	0.116	0.131
Tier 1	C00956	Aminoadipic acid	1.361	1.090	1.494	0.755	0.917	0.792	0.971	0.602	1.487	0.484	0.499	0.555
Tier 1	C00188	Threonine	0.913	0.894	1.318	0.616	0.391	0.350	1.108	0.792	1.457	0.262	0.191	0.195
Tier 1	HMDB0028680	Alanyl-Alanine	0.756	0.949	2.448	0.677	0.573	0.318	0.799	0.802	1.826	0.257	0.254	0.239
Tier 1	HMDB0029013	Prolyl-Aspartate	0.935	0.890	1.218	0.945	1.073	0.988	0.689	0.638	1.128	0.581	0.582	0.544
Tier 1	C00099	Beta-Alanine	1.006	1.020	1.423	0.594	0.621	0.528	0.935	0.642	1.539	0.435	0.340	0.429
Tier 1	C00299	Uridine	0.164	0.184	0.499	1.195	1.562	1.143	0.278	0.159	0.721	1.051	0.874	0.863
Tier 1	C00041	Alanine	1.080	1.045	1.538	0.352	0.220	0.216	1.196	0.643	1.874	0.154	0.098	0.110
Tier 1	C00334	Gamma-Aminobutyric acid	0.513	0.575	0.820	0.610	0.724	0.739	0.479	0.346	0.721	0.503	0.394	0.439
Tier 1	C00127	Oxidized glutathione (2 tags 2 charges)	0.757	0.881	1.329	0.965	1.820	1.194	0.833	0.275	0.985	0.514	0.382	0.599
Tier 1	HMDB0000296_2	Uridine - H2O	0.138	0.147	0.498	1.211	1.596	1.258	0.251	0.136	0.774	1.234	1.026	0.754
Tier 1	C00385	Xanthine	0.581	0.674	0.849	0.643	0.985	0.683	0.614	0.497	1.578	0.639	0.497	0.468
Tier 1	HMDB0028928	Leucyl-Glutamate	1.380	1.258	1.570	1.081	0.520	0.399	1.075	0.838	1.496	0.270	0.217	0.220

Tier 1	C00431	5-Aminopentanoic acid	0.911	0.799	1.122	1.057	1.207	1.121	0.781	0.618	1.053	0.654	0.664	0.715
Tier 1	C03088	5-Hydroxymethyluracil	0.736	0.880	0.843	1.912	0.726	0.777	0.969	0.860	1.290	0.546	0.416	0.420
Tier 1	HMDB0000148_2	Glutamic Acid - H2O	1.378	1.227	1.012	0.855	1.247	1.195	0.696	0.499	1.101	0.635	0.530	0.636
Tier 1	C03665	2-Aminoisobutyric acid	1.063	0.988	1.331	0.686	0.608	0.624	1.217	0.990	1.356	0.639	1.273	0.501
Tier 1	C00213	Sarcosine	1.496	1.219	1.656	0.144	0.233	0.148	1.365	0.936	2.230	0.135	0.115	0.105
Tier 1	HMDB0000719_2	Homoserine - H2O	1.090	0.996	1.014	0.346	0.497	0.424	6.4581	0.703	9.1867	0.225	0.220	0.321
Tier 1	C00262	Hypoxanthine - Isomer	0.760	0.691	0.873	1.458	1.351	1.354	0.507	0.358	0.616	0.781	0.881	0.741
Tier 1	HMDB0028929	Leucyl-Glycine	0.529	0.732	0.924	0.708	1.396	0.594	1.072	0.498	1.552	0.279	0.242	0.9598
Tier 1	C02356	Alpha-aminobutyric acid	1.031	1.022	1.462	0.589	0.414	0.499	1.142	0.985	1.392	0.445	1.362	0.305
Tier 1	C00148	Proline	0.859	0.841	1.032	0.357	0.336	0.319	0.974	0.689	1.253	0.201	0.164	0.172
Tier 1	C02835	Imidazoleacetic acid	0.276	0.214	0.393	0.556	0.483	0.307	0.645	0.294	0.766	0.184	0.167	0.0903
Tier 1	C00073	Methionine	0.847	0.834	1.255	0.627	0.613	0.564	0.856	0.572	1.247	0.370	0.317	0.369
Tier 1	C00183	Valine	0.824	0.785	1.271	1.432	0.924	0.755	0.760	0.564	1.106	0.521	0.452	0.466
Tier 1	C00106	Uracil	0.784	0.861	0.875	0.811	1.003	0.850	0.656	0.684	1.105	0.690	0.667	0.486
Tier 1	C00078	Tryptophan	0.879	0.845	1.563	1.509	1.033	0.884	0.915	0.608	1.164	0.614	0.483	0.477
Tier 1	C00079	Phenylalanine	0.843	0.780	1.181	0.871	0.788	0.653	0.778	0.555	1.143	0.413	0.376	0.372
Tier 1	C00785	Urocanic acid	0.297	0.422	0.511	6.179	2.698	1.909	0.138	1.010	0.361	0.946	0.527	0.360
Tier 1	HMDB0000112_2	Gamma-Aminobutyric acid - H2O	0.635	0.679	0.803	0.530	0.802	0.850	0.573	0.446	0.843	0.551	0.444	0.454
Tier 1	C00123	Leucine	0.842	0.771	1.210	0.937	0.770	0.682	0.776	0.498	1.115	0.439	0.398	0.399
Tier 1	C02291	Cystathionine (2 tags 2 charges) - Isomer	1.329	0.950	1.606	0.760	0.720	0.723	1.186	0.707	2.005	0.529	0.478	0.474
Tier 1	C03672	Hydroxyphenyllactici acid	0.490	0.444	0.807	0.278	0.252	0.292	0.869	0.471	0.906	0.260	0.236	0.266
Tier 1	C00491	Cystine (2 tags 2 charges)	1.071	0.577	0.622	1.245	0.599	0.961	0.755	1.350	0.751	2.113	2.511	1.082
Tier 1	C05593	3-Hydroxyphenylacetic acid	0.743	0.769	0.968	0.886	0.924	0.664	1.642	0.640	1.351	0.569	1.041	0.366
Tier 1	C00108	2-Aminobenzoic acid	0.814	0.879	1.504	1.026	0.854	0.639	1.044	0.689	1.118	1.246	0.794	1.134
Tier 1	C06672	Vanillic acid	0.807	0.390	0.655	3.645	0.509	0.411	2.088	0.966	0.728	1.361	7.496	0.314
Tier 1	C00047	Lysine (2 tags 2 charges)	0.817	0.784	1.543	1.032	0.776	0.687	0.824	0.558	1.375	0.569	0.453	0.475
Tier 1	HMDB0028689	Alanyl-Histidine	0.850	0.858	1.321	1.873	0.768	0.783	0.508	0.583	1.480	0.491	0.460	0.570

Tier 1	C00135	Histidine	0.736	0.770	1.237	2.303	0.800	0.726	0.878	0.644	1.103	0.602	0.379	0.356
Tier 1	C00986	1,3-Diaminopropane (2 tags 2 charges)	0.868	1.104	1.606	0.342	0.404	0.447	1.019	0.694	1.805	0.256	0.183	0.280
Tier 1	C00134	1,4-diaminobutane (2 tags 2 charges)	0.858	0.892	1.270	0.178	0.211	0.258	1.031	0.912	1.512	0.181	0.128	0.160
Tier 1	HMDB0000750_2	3-Hydroxymandelic acid - COOH	0.837	0.840	0.979	0.949	0.894	0.759	1.038	0.762	1.248	0.617	0.672	0.532
Tier 1	C00082	Tyrosine (2 tags 2 charges)	0.757	0.711	1.346	0.940	0.796	0.669	0.944	0.537	1.217	0.448	0.352	0.371
Tier 1	HMDB0001538	3-Pyridylacetic Acid	0.730	1.051	1.322	0.244	0.231	0.253	1.065	0.736	2.224	0.133	0.103	0.149
Tier 1	C00025	Glutamic Acid - Isomer 1	1.248	1.094	1.174	0.996	1.022	0.986	0.746	0.564	0.932	0.649	0.500	0.734
Tier 1	C00051	Glutathione	0.538	1.357	2.091	0.323	0.516	0.644	0.642	0.295	3.217	0.352	0.106	0.284
Tier 1	C00025	Glutamic Acid	1.210	1.058	1.272	0.956	1.040	0.966	0.705	0.525	0.937	0.626	0.504	0.728
Tier 1	C00487	Carnitine	0.928	0.760	0.945	0.905	1.360	1.523	0.439	0.318	0.891	0.459	0.400	0.774
Tier 1	C00082	L-Tyrosine - Isomer	0.474	1.557	2.326	0.235	0.350	0.358	1.108	0.531	10.035	0.235	0.169	0.180
Tier 1	HMDB0002141	N-Methyl-A-Aminoisobutyric Acid	1.059	1.050	1.301	0.603	0.794	0.939	0.771	0.656	2.712	0.341	0.452	0.672
Tier 1	C00785	Urocanic Acid - Isomer	0.940	0.882	0.987	1.450	1.437	1.315	1.071	1.373	3.263	1.270	1.387	1.103
Tier 1	C01620	Threonic Acid	0.672	0.796	1.041	0.323	0.735	0.847	0.610	0.376	0.488	0.486	0.461	0.658
Tier 1	C01620	Isomer 1 of Threonic Acid	0.827	0.906	1.056	0.586	1.236	1.351	0.610	0.410	0.778	0.634	0.483	0.743
Tier 1	C00258	Glyceric Acid	0.568	0.551	0.876	1.002	1.156	1.477	0.452	0.356	0.603	0.417	0.542	0.793
Tier 1	C00711	Malic Acid	1.518	1.479	1.493	0.872	0.836	0.669	1.125	0.902	0.934	0.670	0.508	0.596
Tier 1	C03277	Imidazolepyruvic Acid (2 tags 1 charge)	1.146	0.838	0.989	0.263	0.323	0.340	1.126	0.976	0.957	0.165	0.152	0.183
Tier 1	C01879	Pyroglutamic Acid	0.919	0.540	0.710	1.599	0.948	0.988	0.658	0.831	1.919	0.520	0.650	0.553
Tier 1	C00740	Serine (2 tags 1 charge)	1.008	0.884	0.909	1.016	0.448	0.424	1.261	0.875	1.130	0.244	0.146	0.169
Tier 1	C02989	Methionine Sulfoxide (2 tags 1 charge)	0.984	0.786	0.960	0.521	0.496	0.552	1.171	0.837	1.203	0.371	0.391	0.426
Tier 1	C00025	Isomer 1 of Glutamic Acid (2 tags 1 charge)	1.432	1.216	0.864	1.489	1.617	1.470	0.769	0.553	0.438	1.039	0.918	0.951
Tier 1	C00334	Gamma-Aminobutyric Acid (2 tags 1 charge)	0.555	0.981	0.981	0.669	0.695	0.754	0.747	0.412	0.952	0.890	0.624	0.817
Tier 1	C00430	Aminolevulinic Acid (2	1.155	0.944	1.023	0.171	0.215	0.234	1.363	0.808	1.220	0.221	0.1447	0.125

		tags 1 charge)												
Tier 1	C00025	Glutamic Acid (2 tags 1 charge)	1.499	1.402	1.083	1.392	1.383	1.111	0.693	0.537	0.681	0.878	0.657	0.875
Tier 1	C05145	3-Aminoisobutanoic Acid (2 tags 1 charge)	0.980	0.829	1.005	0.796	0.895	1.333	0.944	0.902	1.143	0.665	0.255	1.041
Tier 1	C00402	Aspartate (2 tags 1 charge) - Isomer	1.514	1.379	0.922	2.178	2.063	1.377	0.730	0.404	0.448	1.541	0.720	1.184
Tier 1	C00402	Aspartate (2 tags 2 charges) - Isomer	1.091	1.118	0.747	1.533	1.692	1.180	0.514	0.297	0.343	1.218	0.740	0.790
Tier 1	C00051	Glutathione (2 tags 2 charges)	0.576	0.957	1.570	0.395	0.291	0.676	0.521	0.292	2.241	0.322	0.136	0.262
Tier 1	C00042	Succinic Acid	1.164	1.087	1.610	0.854	0.798	0.961	1.323	1.094	1.116	0.867	0.839	0.662
Tier 1	C00489	Glutaric Acid	0.719	0.944	1.658	1.135	1.382	1.075	1.196	1.016	0.961	0.866	0.536	0.707
Tier 1	C00122	Fumaric Acid	1.072	1.231	1.323	0.662	0.974	0.751	1.013	0.578	1.071	0.476	0.362	0.464
Tier 1	C00408	Pipecollinic Acid (2 tags 1 charge)	0.924	0.938	0.782	0.836	0.855	0.853	1.070	0.912	0.770	0.533	0.641	0.471
Tier 1	C05984	2-Hydroxybutyric Acid	0.733	0.600	1.017	0.911	0.731	0.925	0.605	0.884	0.978	0.800	0.967	1.007
Tier 1	C00033	Acetic Acid	0.716	0.584	0.384	0.920	1.012	1.413	1.483	0.950	0.548	1.076	1.600	1.253
Tier 1	C06104	Adipic Acid	1.035	1.306	1.496	0.816	1.337	0.906	0.881	0.917	1.662	0.578	0.353	0.557
Tier 1	HMDB0000720	Levulinic Acid	1.142	1.514	1.603	1.082	1.401	1.190	1.111	1.218	1.433	1.114	1.010	1.212
Tier 1	C00407	Isoleucine (2 tags 2 charges)	0.886	0.800	0.807	0.535	0.694	0.667	0.964	0.589	0.973	0.340	0.277	0.409
Tier 1	C00407	Isoleucine (2 tags 1 charge)	0.935	0.876	0.903	0.593	0.735	0.702	1.026	0.675	1.071	0.386	0.306	0.426
Tier 1	C00642	Parahydroxyphenylacetic Acid	0.875	1.018	1.075	0.761	0.893	1.078	1.100	0.946	0.920	0.965	0.718	0.889
Tier 1	C06337	Terephthalic Acid	0.706	1.614	1.304	0.599	0.785	0.982	1.375	0.837	1.191	0.844	0.369	0.723
Tier 1	C00711	Malic Acid (2 tags 2 charges)	1.359	1.097	0.799	1.416	0.868	0.706	0.889	0.980	0.476	0.783	1.229	0.764
Tier 1	C08261	Azelaic Acid	0.585	0.722	2.055	0.619	0.866	0.661	1.153	1.407	1.549	0.677	0.312	0.407
Tier 1	C01198	3-(2-Hydroxyphenyl)Propionic Acid	0.891	0.796	0.828	1.147	1.238	1.203	1.125	1.046	0.951	1.460	1.164	1.353
Tier 1	C02214	Trans-Glutaconic Acid / Itaconic Acid (2 tags 2 charges)	0.215	0.314	0.333	0.129	0.080	0.109	0.432	0.377	0.173	1.078	0.074	0.160
Tier 1	C00122	Fumaric Acid (2 tags 1	1.155	0.716	0.717	0.827	0.886	0.886	0.716	0.646	0.488	0.456	0.789	0.690

		charge)												
Tier 1	C08645	Methylsuccinic Acid (2 tags 2 charges)	0.932	0.819	1.085	1.090	1.250	1.049	1.074	0.862	0.410	1.218	1.258	0.996
Tier 1	C02656	Pimelate / 3-Methyladipic Acid (2 tags 2 charges)	0.609	0.586	1.042	1.296	1.954	0.961	0.918	0.835	0.548	0.925	0.866	0.607
Tier 1	HMDB0002097	4-Ethylbenzoic Acid	0.903	0.808	0.590	0.938	0.962	1.013	1.127	0.966	0.721	1.180	1.058	1.157
Tier 1	HMDB0002327	1,11-Undecanedicarboxylic Acid	0.422	1.514	2.492	0.452	0.545	0.837	1.144	0.778	0.980	0.609	0.363	0.546
Tier 1	C06337	Terephthalic Acid (2 tags 2 charges)	0.974	0.998	0.960	1.061	0.921	1.166	1.189	1.344	0.608	1.079	1.070	1.241
Tier 1	C08261	Azelaic Acid (2 tags 2 charges)	0.785	1.221	1.351	1.787	1.717	1.061	1.537	1.797	0.608	1.315	1.272	0.690
Tier 1	HMDB0000888	Undecanedioic Acid (2 tags 2 charges)	1.069	1.004	1.433	1.214	1.334	1.200	1.293	1.120	0.906	1.306	1.121	1.018
Tier 1	C16308	Traumatic Acid (2 tags 2 charges)	0.750	1.4885	1.030	0.846	1.304	1.027	5.495	0.825	0.585	0.763	0.750	0.523
Tier 2	C01233	sn-Glycero-3-phosphoethanolamine	IsoMS_results_KO_TCR1_P1-B-5_1_4228_Spectrum.csv	IsoMS_results_KO_TCR2_P1-B-6_1_4229_Spectrum.csv	IsoMS_results_KO_TCR3_P1-B-7_1_4230_Spectrum.csv	IsoMS_results_KO_UN1_P1-C-6_1_4240_Spectrum.csv	IsoMS_results_KO_UN2_P1-C-7_1_4241_Spectrum.csv	IsoMS_results_KO_UN3_P1-C-5_1_4239_Spectrum.csv	IsoMS_results_WT_TCR1_P1-B-1_1_4224_Spectrum.csv	IsoMS_results_WT_TCR2_P1-B-2_1_4225_Spectrum.csv	IsoMS_results_WT_TCR3_P1-B-3_1_4226_Spectrum.csv	IsoMS_results_WT_UN1_P1-C-1_1_4234_Spectrum.csv	IsoMS_results_WT_UN2_P1-C-2_1_4235_Spectrum.csv	IsoMS_results_WT_UN3_P1-C-3_1_4236_Spectrum.csv
Tier 2		Cysteinyl-Proline	0.840	0.845	0.943	1.055	1.242	1.082	0.652	0.543	0.907	0.767	0.614	0.780
Tier 2		Isomer 1 of L-beta-aspartyl-L-glycine	1.026	0.764	1.664	0.944	0.623	0.776	0.805	0.732	1.536	0.474	0.440	0.532
Tier 2	C00519	Hypotaurine	0.882	0.977	1.176	0.441	0.476	0.476	1.029	0.828	1.339	0.300	0.202	0.314
Tier 2		L-beta-aspartyl-L-glycine	1.004	1.152	1.689	1.055	0.938	0.761	0.907	0.341	1.647	0.641	0.299	0.403
Tier 2	C04122	D-1-Aminopropan-2-ol O-phosphate	0.901	0.987	1.211	0.393	0.450	0.463	1.072	0.918	1.207	0.261	0.220	0.273
Tier 2	C00346	Isomer 1 of O-Phosphoethanolamine	1.342	1.068	1.157	0.892	0.918	0.825	0.831	0.778	1.211	0.488	0.533	0.488
Tier 2		gamma-Glutamylglycine	0.926	0.886	1.069	0.957	1.133	1.141	0.621	0.460	0.926	0.551	0.489	0.609

Tier 2		L-cis-3-Amino-2-pyrrolidinecarboxylic acid	1.377	1.300	1.615	1.256	0.404	0.398	1.151	0.936	1.598	0.289	0.282	0.234
Tier 2	C00346	Isomer 2 of O-Phosphoethanolamine	1.430	0.687	0.324	0.127	0.173	0.210	0.768	1.260	2.350	0.257	0.175	0.190
Tier 2	C20917	Tabtoxin	0.945	0.860	1.064	0.930	1.110	1.113	0.640	0.481	0.903	0.571	0.500	0.614
Tier 2	C21016	Ophthalmic acid	1.384	1.271	1.825	0.212	0.207	0.217	1.624	1.119	1.975	0.164	0.146	0.112
Tier 2	C22137	4-Chloro-L-lysine	1.380	1.262	1.700	0.206	0.208	0.212	1.635	1.057	2.043	0.170	0.147	0.111
Tier 2	C02647	4-Guanidinobutanal	1.047	0.702	0.710	0.993	0.651	0.820	0.786	1.274	1.503	1.613	2.156	0.836
Tier 2	C03239	6-Amino-2-oxohexanoic acid	0.804	0.697	0.868	0.542	0.516	0.555	0.738	0.750	1.396	0.428	0.431	0.374
Tier 2	C06772	Diethanolamine	0.708	0.764	1.438	0.615	0.810	0.799	0.530	0.611	0.828	0.462	0.406	0.512
Tier 2	C02512	3-Cyano-L-alanine	0.683	0.805	1.424	1.507	1.140	0.891	1.309	1.402	0.647	1.304	1.053	1.088
Tier 2		Aminoethoxy acetic acid	1.031	0.959	1.110	0.237	0.322	0.326	1.129	0.970	1.480	0.211	0.162	0.177
Tier 2	C19911	Iminodiacetic acid	0.830	0.782	1.181	0.603	0.453	0.459	3.520	0.762	1.157	0.382	0.437	0.275
Tier 2		(2R,3R,4R)-2-Amino-4-hydroxy-3-methylpentanoic acid	2.064	1.777	1.068	1.025	1.187	0.938	1.396	1.103	2.109	0.563	0.395	0.612
Tier 2	C02512	Isomer 1 of 3-Cyano-L-alanine	0.958	1.160	1.267	0.651	0.752	0.827	0.999	0.863	1.408	0.491	0.497	0.607
Tier 2	C05715	gamma-Amino-gamma-cyanobutanoic acid	1.036	1.040	1.361	0.491	0.558	0.446	1.093	0.904	1.517	0.351	0.406	0.348
Tier 2	C00334	Isomer 1 of Gamma-Aminobutyric acid	1.913	0.996	0.704	2.108	1.626	1.023	0.760	0.835	0.755	0.724	0.561	0.979
Tier 2	C08298	Tricholomic acid	0.480	0.633	1.113	0.423	2.311	0.420	3.224	0.529	1.587	0.689	0.400	0.322
Tier 2		3-Amino-2-piperidone	2.400	1.978	1.555	1.043	1.202	1.193	1.541	1.373	2.175	0.456	0.551	1.145
Tier 2	C19911	Isomer 1 of Iminodiacetic acid	0.468	0.464	0.690	5.422	2.170	1.811	0.282	1.161	0.503	1.119	0.502	0.413
Tier 2		3'-Methoxyfukiic acid	1.910	1.810	1.097	1.122	1.149	0.811	1.221	1.252	1.843	0.485	0.349	0.415
Tier 2	C00041	Isomer 1 of Alanine	0.837	0.843	0.836	0.578	1.495	0.948	0.699	0.557	0.784	0.462	0.344	0.763
Tier 2	C12269	N-Methyl aspartic acid	1.116	1.134	1.592	0.403	0.249	0.234	1.201	0.690	1.885	0.175	0.142	0.151
Tier 2	C01046	N-Methyl-L-glutamic acid	1.528	1.521	1.106	0.666	0.811	0.651	1.382	0.802	2.106	0.429	0.248	0.491

Tier 2	C15996	7-Cyano-7-carbaguanine	0.361	0.412	0.785	0.231	0.464	0.403	0.360	0.191	1.269	0.416	0.126	0.407
Tier 2	C03194	(R)-1-Aminopropan-2-ol	2.762	2.355	1.010	0.806	2.031	1.528	1.011	0.773	2.095	0.945	0.657	0.834
Tier 2	C02218	Dehydroalanine	1.406	1.540	1.596	2.166	1.664	1.493	1.436	1.425	1.431	1.932	2.028	1.583
Tier 2	C00315	Spermidine - 2 tags	1.064	0.986	1.311	1.141	0.452	0.426	1.087	0.924	1.665	0.341	0.209	0.186
Tier 2	C00147	Adenine	0.564	1.399	3.075	0.552	0.572	1.070	0.684	0.916	0.674	0.402	0.157	0.227
Tier 2		Methylene-2-pyrrolidinecarboxylic acid	1.329	1.075	1.271	0.387	0.515	0.447	1.184	0.781	1.692	0.289	0.217	0.278
Tier 2	C00555	4-Aminobutyraldehyde	0.983	0.928	0.635	1.105	0.886	0.927	0.960	0.897	0.608	1.115	1.219	1.251
Tier 2	C05526	S-Glutathionyl-L-cysteine - 2 tags/Cysteine glutathione disulfide - 2 tags	0.878	0.861	1.112	1.377	0.866	0.852	0.913	1.019	1.623	0.660	0.506	0.424
Tier 2	C00555	Isomer 1 of 4-Aminobutyraldehyde	0.846	0.632	1.141	0.642	0.907	0.800	0.732	0.463	0.936	0.820	0.515	0.547
Tier 2		(S)-2-Azetidinecarboxylic acid	0.890	0.858	1.077	1.357	0.867	0.845	0.922	0.996	1.637	0.652	0.503	0.419
Tier 2	C00147	Isomer 1 of Adenine	1.002	1.077	1.305	0.610	0.561	0.418	1.118	1.068	1.542	0.363	0.276	0.276
Tier 2	C00555	Isomer 2 of 4-Aminobutyraldehyde	1.141	1.005	1.301	0.402	0.439	0.430	1.095	0.700	1.602	0.250	0.217	0.259
Tier 2	C12455	5-Aminopentanal	0.898	0.850	1.069	1.385	0.876	0.830	0.924	0.990	1.634	0.646	0.507	0.411
Tier 2	C20249	(Z)-3-Peroxyaminoacrylic acid	0.625	0.614	0.792	0.689	0.850	1.084	0.651	0.913	0.967	1.799	1.308	1.506
Tier 2	C12455	Isomer 1 of 5-Aminopentanal	3.008	2.878	1.152	0.332	0.937	0.641	2.187	1.447	3.589	0.313	0.288	0.339
Tier 2	C00062	Isomer 1 of Arginine	0.839	0.787	1.148	0.918	0.856	0.787	0.823	0.805	1.295	0.685	0.598	0.626
Tier 2	C15987	4-Methylaminobutyric acid	1.055	0.935	1.355	0.868	0.602	0.602	1.050	0.767	1.727	0.442	0.447	0.450
Tier 2	C18620	3-Hydroxypicolinic acid	0.926	0.870	1.326	1.218	0.814	0.785	0.830	0.652	1.215	0.538	0.461	0.502
Tier 2	C03590	4-Hydroxyphenylglyoxylic acid	0.853	0.869	1.068	0.894	0.887	0.857	0.586	0.400	0.968	0.490	0.368	0.559
Tier 2		N6-beta-Aspartyllysine - 2 tags	0.815	0.947	1.203	0.818	0.914	10.5531	6.4581	0.737	0.943	6.6036	10.2480	12.2068

Tier 2	C22138	L-Propargylglycine	0.837	0.892	1.172	1.394	1.121	1.265	0.658	0.481	1.080	0.621	0.620	0.697
Tier 2		Seryllysine - 2 tags	1.099	1.060	1.302	0.271	0.239	0.231	1.199	0.918	1.629	0.199	0.155	0.149
Tier 2		4-Hydroxypiperidine	0.1861	0.748	0.602	0.586	2.587	0.614	1.372	0.379	0.710	0.160	0.724	0.1563
Tier 2	C05577	3,4-Dihydroxymandelaldehyde	0.794	0.827	1.188	0.835	0.789	0.721	0.889	0.815	1.543	0.585	0.470	0.447
Tier 2	C00750	Spermine - 2 tags	0.906	0.909	0.716	0.872	0.604	0.798	1.125	1.031	1.511	0.520	0.470	0.487
Tier 2	C01933	L-Norleucine	0.545	1.404	3.721	0.681	0.358	0.793	0.563	0.716	0.564	0.330	0.211	0.370
Tier 2	C15606	1,2-Dihydroxy-5-(methylthio)pent-1-en-3-one	1.198	0.968	1.020	1.460	1.100	1.390	0.939	1.261	0.809	1.243	1.408	1.336
Tier 2	C02291	L-Cystathionine - 2 tags/Allocystathionine - 2 tags	1.223	0.974	1.309	0.370	0.444	0.403	1.050	0.815	1.576	0.221	0.205	0.262
Tier 2	C00408	L-Pipecolic acid/D-Pipecolic acid	0.900	0.872	1.061	1.221	0.784	1.094	0.715	0.696	1.201	0.928	0.762	0.840
Tier 2	C05635	5-Hydroxyindoleacetic acid	1.442	0.832	1.037	0.628	0.637	0.732	0.907	0.608	1.601	0.432	0.234	0.430
Tier 2	C00632	3-Hydroxyanthranilic acid	0.898	0.788	0.668	1.146	0.571	0.696	0.927	0.696	1.306	0.629	0.407	0.439
Tier 2		Isoleucyl-Lysine - 2 tags	0.923	0.803	1.062	1.307	1.645	1.485	0.579	0.544	0.857	0.920	0.853	0.917
Tier 2	C09315	Umbelliferone	0.692	0.681	1.030	0.154	0.182	0.226	1.224	0.578	0.956	0.259	0.120	0.142
Tier 2	C14422	Diethylamine	1.026	0.892	1.152	0.373	0.453	0.383	0.941	0.799	1.419	0.181	0.299	0.255
Tier 2	C06486	(6R)-6-(L-Erythro-1,2-Dihydroxypropyl)-5,6,7,8-tetrahydro-4a-hydroxypterin - 2 tags	1.151	0.887	0.670	1.311	0.999	1.278	1.261	1.424	0.604	1.289	1.405	1.198
Tier 2	C14401	2,4-Diaminotoluene	0.863	0.919	1.319	1.049	0.800	0.769	0.409	0.506	1.043	0.450	0.500	0.684
Tier 2		alpha-Cyano-4-hydroxycinnamic acid	1.132	1.143	0.892	1.340	1.087	1.268	1.243	1.449	0.666	1.545	1.655	1.303
Tier 2		Pyrrolidine	0.952	0.761	1.283	1.412	0.897	0.632	0.768	0.494	0.971	0.585	0.353	0.404
Tier 2		Avenanthramide 1p	0.097	0.115	0.122	0.156	0.091	0.090	0.083	0.097	0.111	0.1501	0.133	0.092
Tier 2		DL-2-Aminooctanoi	1.4123	0.934	1.2935	0.890	0.867	0.837	0.859	0.959	0.628	0.913	1.023	0.8426

		c acid												
Tier 2	C01029	N8-Acetylspermidine - 2 tags	0.9365	2.058	0.8528	1.293	2.182	1.102	1.387	0.811	2.378	0.674	0.832	0.8029
Tier 2		2-Hydroxy-4-imino-2,5-cyclohexadienone	0.395	0.342	0.563	0.133	0.175	0.163	0.665	0.368	0.709	0.310	0.107	0.221
Tier 2	C02298	N-Acetylindoxyl	0.507	0.722	1.249	0.498	0.757	0.730	0.659	0.493	1.107	0.352	0.345	0.342
Tier 2	C02728	N(6)-Methyllysine - 2 tags	1.071	0.874	1.012	1.290	0.684	0.876	0.860	0.648	1.327	0.618	0.399	0.367
Tier 2	C02728	Isomer 1 of N(6)-Methyllysine - 2 tags	0.938	0.903	1.330	0.345	0.440	0.507	1.012	0.662	1.301	0.354	0.187	0.288
Tier 2		Ethyl vanillin	0.741	0.774	1.165	0.643	0.500	0.540	0.951	0.697	1.438	0.439	0.390	0.429
Tier 2	C01502	Guaiacol	1.077	1.113	0.945	1.388	0.945	1.073	1.272	1.025	0.611	1.180	2.877	1.078
Tier 2		2,5-Dimethoxy-4-(2-propenyl)phenol	0.579	0.504	0.672	0.553	0.823	1.049	0.823	1.087	0.831	1.739	1.332	2.400
Tier 2	C05627	4-Hydroxystyrene	1.029	1.069	1.576	1.731	1.188	1.494	1.134	1.133	0.881	1.228	1.483	1.576
Tier 2		3,4-Dihydroxyphenylvaleric acid - 2 tags	1.061	0.978	1.089	0.772	0.934	0.755	1.000	0.883	1.350	0.582	0.517	0.536
Tier 2	C02923	2,3-Dihydroxytoluene - 2 tags	1.773	1.192	0.967	1.200	1.258	1.618	0.981	1.192	0.775	1.549	1.354	1.205
Tier 2	C06224	Isomer 1 of 3,4-Dihydroxystyrene - 2 tags	0.817	1.090	0.972	0.823	0.930	0.984	0.889	1.119	0.874	1.051	0.890	0.867
Tier 2	C06224	Isomer 2 of 3,4-Dihydroxystyrene - 2 tags	1.105	0.916	1.110	0.862	0.956	0.780	1.205	0.754	1.469	0.532	0.468	0.437
Tier 2	C06224	3,4-Dihydroxystyrene - 2 tags	1.083	0.916	1.100	0.854	0.966	0.780	1.205	0.754	1.469	0.524	0.438	0.437
Tier 2		Asparaginyl-Asparagine	1.167	0.911	1.145	0.876	1.006	0.829	1.192	0.798	1.480	0.540	0.497	0.455
Tier 2		Glycylglycylglycine	0.950	0.756	0.922	1.211	1.223	1.360	1.068	1.273	0.675	1.427	1.517	1.403
Tier 2	C00148	Isomer 1 of L-Proline/D-Proline	1.033	0.855	0.955	1.246	1.202	1.328	1.012	1.217	0.597	1.493	1.512	1.374
Tier 2	C00097	L-Cysteine/D-Cysteine	0.833	1.577	1.435	0.242	0.305	0.299	1.192	0.763	2.385	0.188	0.107	0.170
Tier 2		Alanyl-Asparagine	0.463	0.795	1.243	0.4489	0.408	0.552	0.826	0.411	3.718	0.407	0.3534	0.654
Tier 2	C00263	L-Homoserine	1.098	0.853	0.972	1.116	1.262	1.224	1.045	1.181	0.640	1.399	1.472	1.265

Tier 2	C20966	3-{[(2E)-4-Amino-4-oxobut-2-enoyl]amino}-L-alanine	0.826	1.229	1.294	0.354	0.327	0.313	1.066	0.877	3.112	0.196	0.099	0.296
Tier 2	C00148	L-Proline/D-Proline	0.800	0.739	0.866	0.902	1.143	1.532	1.101	1.139	0.727	1.520	1.264	1.415
Tier 2	C17952	N-Acetylphosphinothricin	0.824	1.190	1.445	0.240	0.299	0.301	1.182	0.763	2.435	0.184	0.105	0.169
Tier 2	C00073	L-Methionine	0.774	0.829	1.053	1.002	1.095	1.373	1.010	1.255	0.842	1.488	1.528	1.395
Tier 2	C04281	Isomer 1 of L-1-Pyrroline-3-hydroxy-5-carboxylic acid	0.483	1.760	2.678	0.137	0.308	0.262	0.963	0.544	5.117	0.164	0.404	0.151
Tier 2		3-Deoxy-D-glycero-D-galacto-2-nonulosonic acid	1.145	1.229	1.140	0.683	0.850	0.776	0.812	0.564	0.963	0.500	0.458	0.658
Tier 2	C00062	L-Arginine/D-Arginine	0.484	0.772	1.342	0.553	0.866	0.942	0.547	0.360	0.929	0.459	0.262	0.530
Tier 2	C04281	Isomer 2 of L-1-Pyrroline-3-hydroxy-5-carboxylic acid	1.094	0.921	1.226	0.602	0.538	0.671	1.065	0.981	1.543	0.356	0.313	0.450
Tier 2		Fluorocitric acid	1.150	1.203	0.999	0.912	1.116	1.106	0.875	0.586	0.865	0.804	0.504	0.701
Tier 2	C01990	3-Oxalomalic acid	1.286	3.399	0.771	1.217	2.041	1.050	1.860	2.569	0.716	1.823	5.3810	1.331
Tier 2	C04281	L-1-Pyrroline-3-hydroxy-5-carboxylic acid	0.735	1.156	1.303	0.502	0.850	1.128	1.212	0.935	1.275	0.951	0.555	0.830
Tier 2	C00079	L-Phenylalanine/D-Phenylalanine	1.178	1.167	0.946	0.912	1.209	1.102	0.889	0.555	0.853	0.822	0.493	0.707
Tier 2	C01444	Oxamic acid	0.452	1.632	2.168	0.173	0.316	0.303	1.121	0.504	7.392	0.253	0.089	0.153
Tier 2		N-Acetyl-L-Serine	1.509	2.307	3.019	0.401	0.603	0.568	1.820	1.023	5.307	0.442	0.441	0.353
Tier 2		S-Cysteinosuccinic acid - 2 tags	1.184	0.786	1.107	0.697	0.506	0.531	1.281	0.778	1.682	0.266	0.247	0.276
Tier 2	C00785	Isomer 1 of Urocanic Acid - Isomer	1.027	0.915	1.133	0.705	1.130	1.254	0.707	0.623	1.079	0.578	0.343	0.767
Tier 2	C00051	Isomer 1 of Glutathione (2 tags 2 charges)	0.653	0.524	1.721	5.176	0.770	0.916	0.267	1.159	1.277	1.645	0.516	0.399
Tier 2	C05786	Isomer 1 of (3Z)-Phycocyanobilin - 2 tags	0.581	1.307	1.651	0.393	0.405	0.828	0.623	0.238	2.425	0.275	0.086	0.250

Tier 2	C19485	N-Nitrosoproline	1.161	0.872	1.001	0.256	0.322	0.705	1.187	0.923	0.992	0.181	0.177	0.210
Tier 2	C01596	Maleamic acid	1.260	1.060	1.154	0.615	0.481	0.551	1.001	1.060	0.986	0.372	0.451	0.537
Tier 2		N-Acetyl-Glycine	1.664	1.607	2.228	0.557	0.841	0.775	1.324	1.420	1.840	0.391	0.367	0.648
Tier 2	C21016	Ophthalmic acid - 2 tags	1.036	0.891	1.111	1.071	0.504	0.556	1.147	0.921	1.052	0.333	0.165	0.1958
Tier 2	C05786	(3Z)-Phycocyanobilin - 2 tags	1.637	1.685	1.500	0.506	0.316	0.282	1.967	1.323	1.604	0.151	0.156	0.135
Tier 2		N-Acetyl-gamma-L-Glutamyl-L-2-aminobutyric acid - 2 tags	1.138	1.519	1.522	0.142	0.252	0.248	1.595	0.901	1.664	0.197	0.218	0.153
Tier 2		Vinylacetylglycine	0.907	1.115	1.524	0.609	1.004	1.046	0.773	0.409	1.457	0.406	0.219	0.508
Tier 2	C22141	L-beta-Ethynylserine	0.851	1.090	1.332	0.2535	0.514	0.545	0.746	0.467	1.681	0.2359	0.1995	0.319
Tier 2	C00302	Isomer 1 of Glutamic Acid - Isomer 1	1.084	1.083	0.799	0.531	0.761	0.640	0.618	0.448	0.928	0.350	0.271	0.453
Tier 2	C06234	Isomer 1 of 4-Methyl-L-glutamic acid - 2 tags	1.378	1.791	1.181	1.100	1.344	1.201	0.835	0.595	0.721	0.858	0.717	0.925
Tier 2	C00049	L-Aspartic acid - 2 tags/D-Aspartic acid - 2 tags	0.734	0.954	0.910	0.836	0.735	0.615	0.385	0.749	0.794	0.674	1.169	1.112
Tier 2	C16272	3-Hydroxy-5-oxohexanoic acid	1.090	1.231	0.735	1.048	1.285	1.302	0.681	0.380	0.447	1.123	0.793	0.888
Tier 2	C00049	Isomer 1 of Aspartate (2 tags 1 charge)	1.063	1.337	1.502	0.979	1.176	1.402	1.209	1.123	1.263	1.221	1.270	1.221
Tier 2	C00940	2-Oxoglutaramic acid	1.250	1.346	0.778	1.261	1.502	1.362	0.788	0.401	0.543	1.353	0.839	1.050
Tier 2		N-Acetyl-L-Proline	0.575	0.683	0.778	0.381	0.378	0.506	0.737	0.495	1.532	0.242	0.245	0.300
Tier 2	C01586	Hippuric acid	1.069	0.805	0.826	0.481	0.502	0.569	0.853	0.910	0.943	0.199	0.263	0.339
Tier 2	C03618	L-threo-3-Methylaspartic acid - 2 tags	0.979	0.700	0.878	0.401	0.537	0.528	0.932	0.852	0.811	0.140	0.248	0.252
Tier 2	C06234	4-Methyl-L-glutamic acid - 2 tags	1.107	0.816	1.032	0.846	1.438	1.363	1.188	1.471	1.387	0.851	0.935	1.022
Tier 2		N-Acetyl-Dehydroalanine	0.309	1.392	1.718	0.114	0.361	0.345	0.252	0.150	1.214	0.147	0.9477	0.193
Tier 2		L-2-Amino-3-methylenehexanoic acid	0.742	0.788	0.945	0.406	0.397	0.803	0.491	0.388	1.223	0.317	0.160	0.265

Tier 2		N-Heptanoylglycine	0.834	0.768	0.871	0.488	0.699	0.681	0.911	0.630	1.059	0.378	0.288	0.386
Tier 2		cis-4-Hydroxycyclohexylacetic acid/trans-4-Hydroxycyclohexylacetic acid	0.457	0.518	1.344	0.880	0.402	0.469	0.966	0.855	2.057	0.618	0.433	0.427
Tier 2	C22138	L-Propargylglycine	1.187	0.915	0.981	0.703	0.749	0.680	1.099	0.907	0.883	0.451	0.436	0.577
Tier 2		2-Hydroxydecanedioic acid	1.161	0.865	0.888	0.719	0.673	0.673	1.006	0.935	0.706	0.484	0.444	0.491
Tier 2	C02218	Dehydroalanine	0.190	1.124	1.510	0.185	0.616	0.766	0.809	0.638	1.711	0.141	0.0805	0.164
Tier 2		Isomer 1 of N-Acetyl-Dehydroalanine	2.465	2.340	2.678	2.570	2.247	2.364	1.555	2.253	2.146	2.187	3.612	2.541
Tier 2		N-Nonanoylglycine	1.577	0.667	0.552	1.489	1.547	1.163	0.665	0.682	0.400	0.713	0.935	1.033
Tier 2	C01771	Crotonic acid	0.371	0.915	0.965	0.515	0.448	0.800	0.782	0.579	0.533	0.568	0.410	0.596
Tier 2	C22236	Indole-3-propionic acid	0.242	0.517	0.225	0.395	0.842	1.569	0.658	0.400	0.363	2.379	0.624	0.713
Tier 2		Lanthionine ketimine - 2 tags	1.068	0.948	0.969	1.190	1.217	1.243	1.047	1.217	0.707	1.240	1.200	1.352
Tier 2	C00180	Benzoic acid	0.399	0.430	0.547	0.1883	0.2298	0.257	0.462	0.439	0.3676	0.118	0.1482	0.141
Tier 2		2-Methoxybenzoic acid	1.691	2.692	2.708	1.339	2.088	1.860	0.9422	1.893	2.105	6.0916	6.1701	2.017
Tier 2	C07211	m-Methylbenzoic acid	0.863	0.961	0.686	1.053	0.953	1.224	0.934	0.922	0.736	1.085	1.313	1.255
Tier 2		m-Chlorobenzoic acid	0.788	1.070	0.895	0.517	0.771	1.119	1.224	0.929	0.813	1.005	0.293	0.739
Tier 2		3-Methyladipic acid - 2 tags	0.776	1.400	0.703	0.810	0.936	1.369	1.545	1.077	0.672	1.335	0.993	0.825
Tier 2	C11950	3-Isopropyl-3-butenoic acid	1.189	0.687	1.066	0.684	1.009	1.017	1.013	1.240	0.753	1.303	1.243	1.142
Tier 2		Monoisobutyl phthalic acid	0.893	0.852	0.545	1.068	1.302	1.028	1.292	1.063	1.251	1.611	1.187	1.333
Tier 2	C06670	2,4-Dichlorobenzoic acid	0.620	1.168	1.634	1.033	0.840	0.603	0.679	0.697	1.055	0.956	0.926	0.888
Tier 2	C11863	Gibberellin A9	0.657	0.938	1.053	0.620	0.794	0.905	0.892	1.021	0.853	0.685	0.581	0.711
Tier 2	C19678	Germacrene A acid	1.082	0.848	0.797	1.130	1.262	1.242	1.493	1.278	0.860	1.343	1.099	1.574
Tier 2		5-Dodecenoic acid	1.733	0.832	1.255	0.673	0.534	0.752	0.820	0.999	0.929	0.790	0.496	0.720

Tier 2		Isomer 1 of 5-Dodecenoic acid	0.821	1.161	0.873	0.850	0.876	0.948	1.054	0.893	0.865	1.165	0.671	1.071
Tier 2	C16502	Farnesoic acid	0.723	1.065	0.933	0.640	0.697	0.813	0.879	0.761	0.840	1.065	0.554	0.894
Tier 2	C14770	11,12-EET	3.117	1.365	1.498	0.656	0.409	0.739	0.481	0.476	0.488	0.961	0.444	0.705
			0.782	1.210	0.602	0.957	1.028	0.956	1.321	0.914	0.735	1.265	1.254	1.020

Supplemental Table 5

Genotype	Metabolite	FC (TCR/Unstim)	log2(FC)	raw.pval	(-) LOG10(p)
KO	Uridine	0.16797	-2.5737	0.00173	2.7619
KO	Acetic acid	0.42243	-1.2432	0.035406	1.4509
KO	Glyceric acid	0.4382	-1.1903	0.015953	1.7972
KO	Hypoxanthine	0.4552	-1.1354	1.574e-05	4.803
KO	Imidazoleacetic acid	0.52931	-0.9178	0.040071	1.3972
KO	3-(2-Hydroxyphenyl)propanoic acid	0.57711	-0.79308	0.002979	2.526
KO	L-Propargylglycine	0.62152	-0.68613	0.002868	2.5424
KO	Germacrene A acid	0.62307	-0.68252	0.027278	1.5642
KO	Glycerylphosphorylethanolamine	0.63593	-0.65306	0.004522	2.3447
KO	1,2-Dihydroxy-3-keto-5-methylthiopentene	0.66631	-0.58574	0.044568	1.351
KO	Malate	1.5595	0.64106	0.016142	1.7921
KO	Beta-Alanine	1.5998	0.67793	0.000632	3.1992
KO	3,5-Dihydroxybenzoic acid	1.6453	0.71833	0.004807	2.3182
KO	Hydroxyphenyllactic acid	1.6881	0.75539	0.022497	1.6479
KO	Maleamate	1.7388	0.79807	0.015687	1.8045
KO	Hypotaurine	1.7678	0.82193	0.000283	3.5488
KO	gamma-Amino-gamma-cyanobutanoate	1.8658	0.89979	0.000149	3.8277
KO	L-Threonine	1.8682	0.90165	0.009025	2.0445
KO	L-Alpha-aminobutyric acid	1.8916	0.91964	0.001466	2.8339
KO	D-1-Aminopropan-2-ol O-phosphate	1.9219	0.9425	0.00035	3.4565
KO	L-beta-Ethynylserine	1.9994	0.99958	0.019721	1.7051
KO	N-Nitrosodiethylamine	2.0688	1.0488	0.000928	3.0326
KO	L-Proline	2.2009	1.1381	1.2518e-05	4.9025
KO	Glutaconic acid	2.2052	1.1409	0.01044	1.9813
KO	1,3-Diaminopropane	2.3917	1.258	0.006246	2.2044
KO	L-Homoserine	2.422	1.2762	5.1884e-05	4.285
KO	Imidazol-5-yl-pyruvate	2.6359	1.3983	0.009586	2.0184
KO	3-{[(2E)-4-Amino-4-oxobut-2-enoyl]amino}-L-alanine	2.7394	1.4538	0.004614	2.3359
KO	L-Asparagine	2.9055	1.5388	1.8139e-05	4.7414
KO	N-Acetylphosphinothricin	3.3098	1.7267	0.003019	2.5202
KO	Umbelliferone	3.4229	1.7752	0.000453	3.344
KO	3-Pyridylacetic acid	3.4262	1.7766	0.0029	2.5376
KO	N-Methyl-D-aspartic acid	3.5231	1.8169	0.000235	3.6282
KO	L-Cysteine	3.6911	1.8841	0.01618	1.791
KO	Putrescine	3.7442	1.9046	0.000186	3.7301
KO	L-Alanine	3.7695	1.9144	0.000238	3.6236
KO	5-Aminolevulinic acid	4.1353	2.048	0.002524	2.5979
KO	4-Hydroxyproline	4.3388	2.1173	3.7249e-05	4.4289
KO	4-Chloro-L-lysine	5.6273	2.4924	9.8473e-06	5.0067
KO	Ophthalmic acid	5.6933	2.5093	2.2798e-05	4.6421
KO	Sarcosine	6.7796	2.7612	0.000256	3.592

WT	Uridine	0.20089	-2.3156	0.000421	3.376
WT	D-Aspartic acid	0.2459	-2.0238	0.010779	1.9674
WT	L-Cystine	0.27618	-1.8563	0.050599	1.2959
WT	2-Keto-glutaramic acid	0.28106	-1.831	0.001871	2.728
WT	3-Hydroxy-5-oxohexanoate	0.28413	-1.8154	0.000541	3.2672
WT	(Z)-3-Peroxyaminoacrylate	0.29332	-1.7695	0.00035	3.4554
WT	Hypoxanthine	0.31407	-1.6709	0.002074	2.6833
WT	Methylsuccinic acid	0.36988	-1.4349	0.011397	1.9432
WT	11,12-Epoxyeicosatrienoic acid	0.37051	-1.4324	0.020113	1.6965
WT	4-Aminobutyraldehyde	0.37093	-1.4308	0.005079	2.2942
WT	m-Methylbenzoate	0.37874	-1.4007	0.007591	2.1197
WT	4-Hydroxystyrene	0.39251	-1.3492	0.01063	1.9735
WT	2,3-Dihydroxytoluene	0.39303	-1.3473	0.004751	2.3232
WT	Acetic acid	0.40527	-1.303	0.044035	1.3562
WT	Glyceric acid	0.40848	-1.2917	0.047896	1.3197
WT	2-Aminoacrylic acid	0.40992	-1.2866	0.005417	2.2663
WT	1,2-Dihydroxy-3-keto-5-methylthiopentene	0.41074	-1.2837	0.012075	1.9181
WT	3-(2-Hydroxyphenyl)propanoic acid	0.42081	-1.2488	0.000779	3.1084
WT	3-Isopropylbut-3-enoic acid	0.4467	-1.1626	0.010577	1.9756
WT	4-Ethylbenzoic acid	0.44698	-1.1617	0.003679	2.4343
WT	4-Methyl-L-glutamate	0.4515	-1.1472	0.00205	2.6882
WT	2,4-Dichlorobenzoate	0.45301	-1.1424	0.000743	3.1288
WT	L-Aspartic acid	0.4608	-1.1178	0.0262	1.5817
WT	2-Hydroxybutyric acid	0.46664	-1.0996	0.017976	1.7453
WT	2-Aminobenzoic acid	0.46679	-1.0991	0.004439	2.3527
WT	Threonic acid	0.47753	-1.0663	0.020052	1.6978
WT	Germacrene A acid	0.49065	-1.0272	0.024678	1.6077
WT	Hypotaurine	2.0302	1.0216	0.001048	2.9796
WT	L-threo-3-Methylaspartate	2.1181	1.0828	0.030249	1.5193
WT	L-Homoserine	2.1209	1.0847	0.00251	2.6003
WT	N-Nitrosodiethylamine	2.1597	1.1108	0.008924	2.0495
WT	D-1-Aminopropan-2-ol O-phosphate	2.2157	1.1478	0.000227	3.6448
WT	Alanylalanine	2.2887	1.1945	0.046521	1.3323
WT	1,3-Diaminopropane	2.4539	1.2951	0.028802	1.5406
WT	Leucyl-Glutamate	2.4764	1.3083	0.000526	3.2793
WT	Spermidine	2.5905	1.3732	0.00304	2.5171
WT	L-Serine	2.602	1.3796	0.00282	2.5498
WT	L-Threonine	2.6651	1.4142	0.000613	3.2127
WT	L-Proline	2.7843	1.4773	0.000365	3.4375
WT	Umbelliferone	2.7856	1.478	0.025007	1.6019
WT	N-Nitrosoproline	2.8747	1.5234	0.004092	2.3881
WT	L-Asparagine	3.0737	1.62	0.001218	2.9143
WT	D-Serine	3.0916	1.6284	0.001591	2.7984
WT	Imidazol-5-yl-pyruvate	3.2467	1.699	0.004773	2.3212
WT	5-Aminolevulinic acid	3.6188	1.8555	0.002611	2.5831

WT	Putrescine	3.8125	1.9307	0.000273	3.5646
WT	N-Methyl-D-aspartic acid	4.0345	2.0124	0.011655	1.9335
WT	3-{[(2E)-4-Amino-4-oxobut-2-enoyl]amino}-L-alanine	4.2044	2.0719	0.080598	1.0937
WT	4-Hydroxyproline	4.5693	2.192	0.001395	2.8556
WT	L-Cysteine	4.6594	2.2202	0.027113	1.5668
WT	N-Acetylphosphinothricin	4.766	2.2528	0.029868	1.5248
WT	L-Alanine	5.1529	2.3654	0.012532	1.902
WT	3-Pyridylacetic acid	5.1781	2.3724	0.024599	1.6091
WT	4-Chloro-L-lysine	5.6512	2.4986	0.000482	3.3168
WT	Ophthalmic acid	5.7367	2.5202	0.000111	3.953
WT	Sarcosine	6.4243	2.6835	0.004039	2.3938

Supplemental Table 6

Sequence Name	Sequence
Actin Fwd	GGC TGT ATT CCC CTC CAT CG
Actin Rev	CCA GTT GGT AAC AAT GCC ATG T
Cd40l Fwd	CTG AAC TGT GAG GAG ATG AGA AG
Cd40l Rev	GCA GGA CTG GGA AAT GTA AGA
Gls2 Fwd	AGC GTA TCC CTA TCC ACA AGT TCA
Gls2 Rev	GCA GTC CAG TGG CCT TCA GAG
Glud1 Fwd	ATC GGG TGC ATC TGA GAA AG
Glud1 Rev	CAG GTC CAA TCC CAG GTT ATA C
Glut1 Fwd	AGC CCT GCT ACA GTG TAT
Glut1 Rev	AGG TCT CGG GTC ACA TC
Got1 Fwd	CCC AAG CAG GTC GAG TAT TT
Got1 Rev	TGG AGG TAG CGA CGT AAT CTA
Got2 Fwd	CCT AGA GTC TCA TCC CGT TCT A
Got2 Rev	CTT TGA TGA GAG AGG AGG CTA TG
Hk1 Fwd	TGA TCG CCT GCT TAT TCA CGG
Hk2 Rev	AAC CGC CTA GAA ATC TCC AGA
LdhA Fwd	CAT TGT CAA GTA CAG TCC ACA CT
LdhA Rev	TTC CAA TTA CTC GGT TTT TGG GA
Pkm1 Fwd	TGT CTG GAG AAA CAG CCA AG
Pkm1 Rev	CTC GCA CAA GCT CTT CAA AC
Pkm2 Fwd	TGT CTG GAG AAA CAG CCA AG
Pkm2 Rev	CGA ATA GCT GCA AGT GGT AGA
Slc1a5 Fwd	CTG GAG AAA TGG ACT GGA TGA G
Slc1a5 Rev	CCA GCA ACA AGG CTC CTA ATA
Slc38a1 Fwd	GTA GGT GGT GGT CAA AGA AGA G
SLC38A1 Rev	CTG GTA CCT GGG AGA GCT ATA A
Slc38a2 Fwd	GGG ACA TCT TCG GGT TCA TT
Slc38a2 Rev	CGG ATC TCA TTG GTT CCT TCT T
Sp100 Fwd	CTT TCT GGT CCC TCC AGT AAT C
Sp100 Rev	GTG GCA GGC TGT CTA CAT ATA A
Sp110 Fwd	AAA GAC TGG AAG GGC GTT ATA C
Sp110 Rev	GCA CAT ATC AGG TCA GGA GTT C
Sp140 Fwd	CGG AGC AGA AGT TTC AGG AAT A
Sp140 Rev	CTT TCA GAA GAT CCC GGC TAA A