Int J Clin Exp Med 2018;11(11):12048-12058
www.ijcem.com /ISSN:1940-5901/IJCEM0080064

Original Article

Expression patterns of matrix metalloproteinase 9 in ischemia-reperfusion-induced acute lung injuries

Liang-Chao Qu[1], Yan Jiao[2], Zhang-Jie Jiang[1], Zhi-Ping Song[1], Li Kang[1], Qing-Hua Peng[1]

[1]*Department of Anesthesiology, The First Affiliated Hospital of Nanchang University, Nanchang, PR China;*
[2]*Department of Anesthesiology, JiangXi Provincial People's Hospital, Nanchang, PR China*

Received May 22, 2018; Accepted August 1, 2018; Epub November 15, 2018; Published November 30, 2018

Abstract: Background: Acute lung injury has been regarded as the main consequence of exposure to high levels of hydrogen sulfide. Emerging evidence suggests that ischemia-reperfusion plays a pivotal role in lung injuries, but the roles of matrix metalloproteinase 9 (MMP9) regulated by lung ischemia reperfusion injury (LIRI) remain unclear. Therefore, this study used MMP9 inhibitors to investigate the effects of MMP9 on lung injuries. This study also proposed a hypothesis that upregulation of MMP9 is a negative contributor to lung injury progression through IR by increasing inflammation-related factors expression. Methods: First, this study screened GSE6730, which is related to both lung injuries and IR in gene expression omnibus. String was used to select genes in GSE6730 needed in the future. Animal models were established and classified to validate the effects of MMP9 on lung injuries after IR by adding selective inhibitor (4-phenoxyphenylsulfonyl) methylthiirane (SB-3CT), an MMP9 inhibitor. Next, to better understand the expression of MMP9 in lung injuries, assessment of lung tissues, Western blot analysis, RNA extraction, and reverse transcription quantitative polymerase chain reaction (RT-qPCR) were conducted. Results: MMP9 was identified to be overexpressed after IR, according to analysis on GSE67370. MMP9 was an unknown gene in relation to acute lung injuries, found to be associated with IL-6, TNF, and IL-8. Expression of these inflammatory factors, including MMP9, was elevated in IR. Furthermore, lung injuries were ameliorated and levels of MMP9 were lower when MMP9 inhibitors, SB-3CT, were added. Conclusion: Present findings reveal a novel mechanism, indicating that IR induces higher expression of MMP9 in lung injuries by increasing expression of inflammation-related factors. Functional suppression of MMP9 might be a future therapeutic strategy for lung injuries caused by IR.

Keywords: Matrix metalloproteinase 9, ischemia reperfusion, acute lung injury, SB-3CT

Introduction

Ischemia reperfusion (IR) is a pathological process that has been shown to contribute to extensive cell death, serious organ injury, and dysfunction [1, 2]. Based on recent evidence, it has been shown that ischemia and/or IR affects apoptosis in various tissues, including brain and liver tissues [3]. Myocardial ischemia/reperfusion is a well-known consequence of ischemic heart disease [2]. Ischemia reperfusion injury (IRI) depicts a harmful inflammatory process where the blood flow is restored followed by an episode ischemia, such as acute myocardial infarction, strokes, and transplantation operations [4]. According to the current consensus, tissue undergoing subsequent damage upon reperfusion is primed by a period of ischemia, but the duration of ischemia required for reperfusion injury is determined by differences of tissues [3]. It also remains a major cause of respiratory insufficiency, followed by open-heart operations for a cardiopulmonary bypass, as well as the chief cause of primary graft dysfunction after lung transplantation, occurring in 11-57% of recipients [5, 6]. LIRI is related to high risk of morbidity and mortality, though notable advancements in donor lung protection strategies and perioperative care have been made in recent times [6]. Matrix metalloproteinases (MMPs) are an important group of zinc enzymes responsible for degradation of the extracellular matrix components. Their activation is involved in IRI [7, 8]. MMP9 can be induced by various factors, such as interleukin1 (IL1), IL6, and oxygen free radicals after IR [9].

MMPs, consisting of more than 20 enzymes to date, are known for their ability to cause tissue

Table 1. Primer sequences for RT-qPCR

Gene	Primer Sequence
MMP9	F: TGTACCGCTATGGTTACACTCG
	R: GGCAGGGACAGTTGCTTCT
IL-6	F: AATAACCACCCCTGACCCAAC
	R: AATCTGAGGTGCCCATGCTAC
IL1B	F: ATGATGGCTTATTACAGTGGCAA
	R: GTCGGAGATTCGTAGCTGGA
IL8	F: TTTTGCCAAGGAGTGCTAAAGA
	R: AACCCTCTGCACCCAGTTTTC
GAPDH	F: GCACCGTCAAGGCTGAGAAC
	R: TGGTGAAGACGCCAGTGGA

Note: RT-qPCR, reverse transcription quantitative polymerase chain reaction; MMP9: matrix metalloprotease 9; IL-6: interleukin-6; IL-1B: interleukin-1 beta; IL-8: interleukin-8; GAPDH: glyceraldehyde-3-phosphate dehydrogenase.

destruction and promote disease progression [9, 10]. Transplant-related IRI can induce MMP, which can expose col(V) as well as regulate local IRI-induced inflammation [11]. MMP-9 expression balance is a key fragment in the maintenance of the integrity of pulmonary architecture structure [12]. A previous study validated that MMP-2 and MMP-9 may play vital roles in I/R injury, characterized by ongoing liver inflammation [13]. In this study, the potential key factor, MMP-9, was predicted by bioinformatics in lung injuries induced by IR. Roles of MMP9 in the process of lung injuries induced by IR were verified by establishing a bilateral nephrectomy model of IR in rats.

Methods and materials

Extraction of gene chip

Two key words, "lung" and "ischemia reperfusion injury", were searched in the National Center for Biotechnology Information (NCBI) Gene Database Gene Expression Omnibus (GEO), with GSE6730 selected. The sequence of rat lung tissues was used for data collection, including the following three groups: A, IR group; B, bilateral nephrectomy group; and C, virtual abdominal operation group. Group C served as the control group and differences between group A and C were analyzed using the R language limma package, considering adj. P < 0.05 and |logFC| > 1 as significant differences. Gene oncology (GO) enrichment analysis and Kyoto encyclopedia of genes and genomes (KEGG) enrichment analysis were conducted on the database for annotation, visualization, and integrated discovery (DAVID, https://david.ncifcrf.gov/).

Relationship between known genes and differential genes

"LIRI" was the keyword searched in the DigSee retrieval platform. The first 20 genes were selected for subsequent analysis. Interaction between genes was determined using the string database. The first 40 genes that had the largest changes of multiple scales in GSE67370 and the 20 genes retrieved by DigSee were selected.

Model establishment and grouping

A total of 90 male Wistar rats (weighing 200-280 g, age: 8 weeks) were purchased from Beijing HuaFukang Biological Limited Company (Beijing, China). They were raised separately in a specific pathogen-free (SPF) laboratory with ad libitum access to food and water at room temperature (25 ± 3°C), with relative humidity of 55%-75%. Both feeding and drinking water were sterilized by ultraviolet. The rats were assigned at random into three groups: sham operation group (n = 20), IRI group (n = 20), and IRI + selective inhibitor (4-phenoxyphenylsulfonyl) methylthiirane (SB-3CT) group (n = 20). The IRI animal model was established as follows. Animals were first rested on a heating blanket, followed by a midline laparotomy along with the removal of two-sided renal pedicles. A nontraumatic microvascular clamp was used across bilateral renal pedicles for 60 minutes on rats allocated to experimental IRI. Ischemia (60 minutes) after preliminary experiments was employed. Results showed that 30 minutes of kidney ischemia did not significantly affect lung genomic signature, compared to the sham operation group. The allotted ischemia time was followed by the operation. Clamps were removed with care, then 1 mL of sterile saline was intraperitoneally injected into the animals and a 4-0 silk suture was used to close the incision in two layers. Subsequently, the animals could recover with a free supply of food and water. The sham animals were operated upon in a similar manner, but the step of placing the vascular clamps was omitted. Thirty-six hours

Table 2. Sequencing platform of GSE67370 data set and sample sets

Group	Sequencing tissues	Platform	Number of samples
IR group	Whole lung	GPL339 [MOE430A] Affymetrix Mouse Expression 430A Array	Samples at 6 h = 3 Samples at 36 h = 3
Bilateral nephrectomy group	Whole lung	GPL339 [MOE430A] Affymetrix Mouse Expression 430A Array	Samples at 6 h = 3 Samples at 36 h = 3
Virtual abdominal operation group	Whole lung	GPL339 [MOE430A] Affymetrix Mouse Expression 430A Array	Samples at 6 h = 3 Samples at 36 h = 3

later, the rats were anesthetized with pentobarbital sodium and sacrificed by exsanguination to collect tissues for analysis. SB-3CT, the MMP-9 inhibitor, was provided by Enzo Life Sciences (Plymouth Meeting, PA, USA). Twenty-eight-day-old Wistar wild-type rats were injected with SB-3CT (5 mg/kg) and vehicle solution (10% dimethyl sulfoxide in normal saline). This experiment was performed with approval of the Ethics Committee and was performed according to relevant regulations.

Assessment of lung tissues

Hematoxylin-eosin (HE) staining was performed to observe lung morphological injuries. After completion of the allotted treatment period, the right main bronchus was isolated and cross-clamped. Under an incessant pressure of 25 cm H_2O, the left lung was filled with 0.5% low-melting agarose in 10% formalin through a tracheotomy to make lung parenchyma homogenously expand. Next, 10% formalin was used to fix the inflated lungs for 48 hours and paraffin blocks were utilized for embedding. H&E (Fisher Scientific, Pittsburgh, PA) was adopted to stain the obtained paraffin-embedded tissues (5 μm) sections.

Western blot analysis

Cells were collected and lysed in radioimmunoprecipitation buffer (Beijing CoWin Biotech Co., Ltd., Beijing, China), supplemented with protease inhibitors for 30 minutes for total protein extraction. Protein levels were quantified using bicinchoninic acid (BCA) Protein Assay Kit (Thermo Fisher Scientific, Waltham, MA, USA). Total protein (40 μg) was loaded onto 10% sodium dodecyl sulfate (SDS) gel. The membrane was incubated for 12 hours at 4°C with primary antibodies targeting anti-MMP-9 (1:1000, Abcam Inc., Cambridge, MA, USA) and anti-glyceraldehyde-3-phosphate dehydrogenase (GAPDH, 1:1000, Beijing Zhongshan Golden Bridge Biotechnology Co. Ltd., Beijing, China). The membranes were then incubated with a horseradish peroxidase (HRP)-conjugated goat anti-rabbit secondary antibody (1:1000, Beijing Zhongshan Golden Bridge Biotechnology Co. Ltd., Beijing, China) for 1 hour at room temperature. An enhanced chemiluminescence kit (Thermo Fisher Scientific Inc., San Jose, CA, USA) was responsible for detecting immunocomplexes and Image J software (version 1.62; National Institute of Health, Bethesda, MD, USA) was selected to analyze images.

RNA extraction and reverse transcription quantitative polymerase chain reaction (RT-qPCR)

Eastep Total RNA Extraction kit (Promega Corporation, Madison, WI, USA) was employed to isolate total RNA from the cultured cells, according to manufacturer instructions. Subsequently, a TransScript First-Stand cDNA Synthesis kit (**Table 1**) (TransGen Biotech, Beijing, China) was used to reverse transcribe total RNA. RT-qPCR was then conducted using TransStart Green qPCR SuperMix (TransGen Biotech, Beijing, China) and the products were measured using a DA7600 Real-time nucleic acid amplification fluorescence detection system (Bio-Rad, Hercules, CA, USA). Primers for RT-PCR are demonstrated in **Table 1**. The transcripts of the housekeeping gene GAPDH were quantified as internal control. Oligo 7.0 software (Molecular Biology Insights, West Cascade, USA) was employed to design and optimize all primers for cDNA amplification of target genes. Sangon Biotech (Shanghai, China) synthesized all primers. Cycle threshold (Ct) values of the target gene were standardized to the Ct values of GAPDH (ΔCt) to calculate the relative protein expression levels of target genes. The value was determined as $2^{-\Delta\Delta Ct}$. RT-qPCR products then underwent electrophoresis.

Statistical analysis

Measurement data are presented as mean ± standard deviation and were tested by *t*-test. The numbers of cases and percentages were

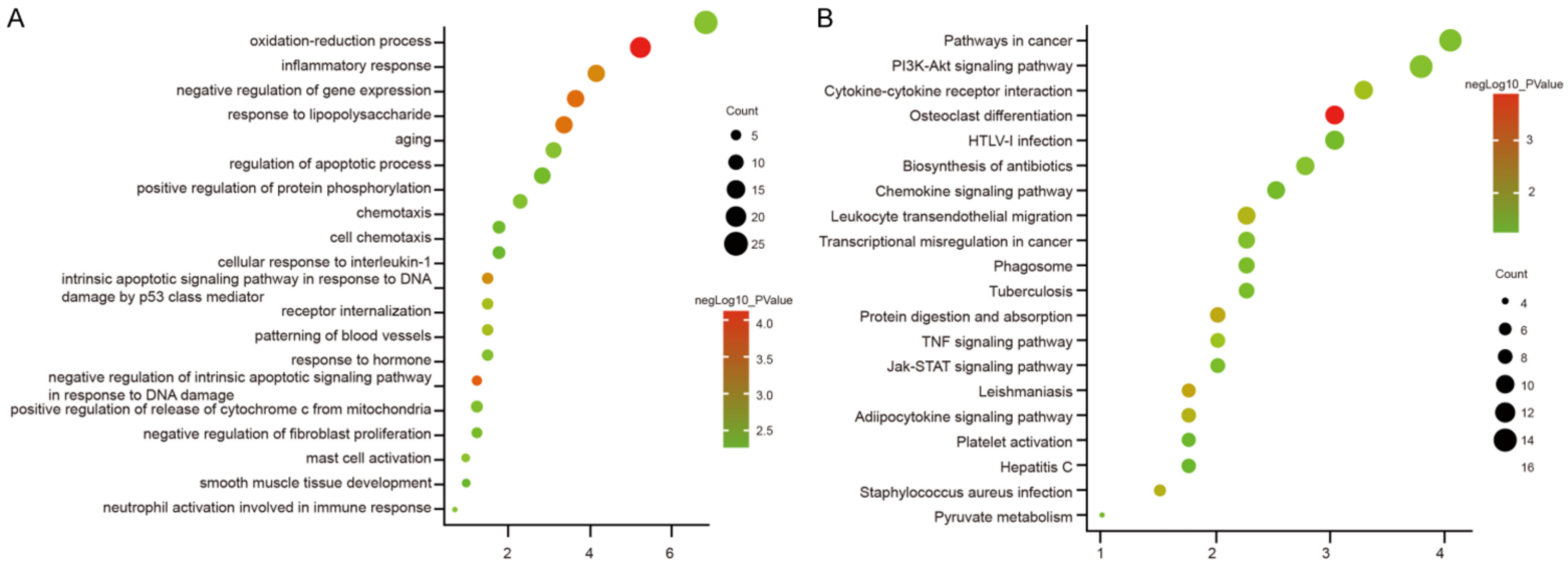

Figure 1. GO, KEGG enrichment analysis of differential genes indicated that they were closely associated with lung injuries.

Table 3. Retrieving of genes related with lung injury

Gene	Encoding	Number of abstracts
TNF	Tumor necrosis factor	42
SOD1	Superoxide dismutase 1	42
NOS3	Nitric oxide synthase 3	34
MPO	Myeloperoxidase	30
ICAM1	Intercellular adhesion molecule 1	27
NOS2	Nitric oxide synthase 2	21
AKT1	AKT serine/threonine kinase 1	21
NFKB1	Nuclear factor kappa B subunit 1	17
IL1B	Interleukin 1 beta	17
CASP3	Caspase 3	17
SELP	Selectin P	16
HMOX1	Heme oxygenase 1	14
CHKB	Choline kinase beta	13
IL6	Interleukin 6	13
XDH	Xanthine dehydrogenase	13
PRRT2	Proline rich transmembrane protein 2	13
JUN	JUN Jun proto-oncogene, AP-1 transcription factor subunit	12
IL10	Interleukin 10	12
MAPK1	Mitogen-activated protein kinase 1	11
IL8	Interleukin 8	11

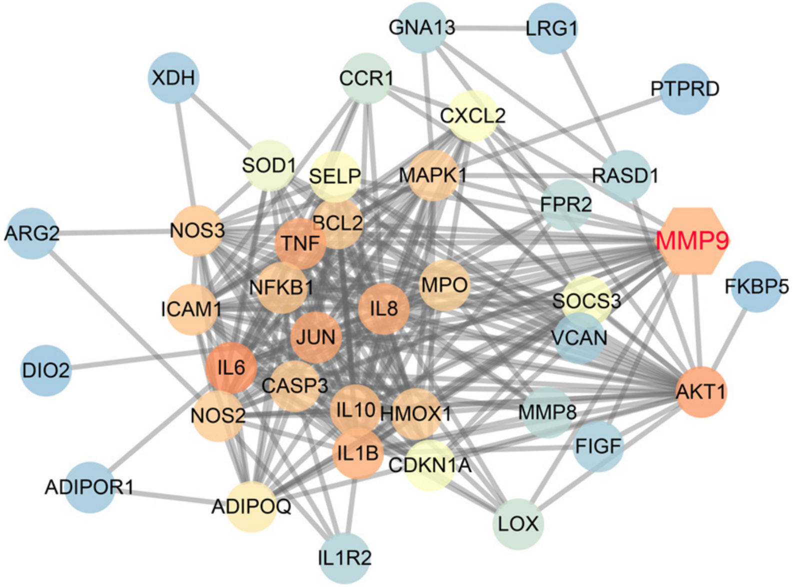

Figure 2. Correlation analysis of differential genes and known genes found that MMP9 was also closely associated with lung injuries.

chosen to depict enumeration data and results were examined by Pearson's Chi-squared test. Logistic regression analysis was employed to analyze the effects of chemotherapy and clinicopathological features. $P < 0.05$ is considered statistically significant.

Results

Selection of GSE6730 data set

Gene expression data were mainly screened in the NCBI gene chip database, GEO database, as previously described. The GSE6730 data set was selected for analysis. The data set consisted of three groups: A: IR group; B: bilateral nephrectomy group; and C: virtual abdominal operation group. Sequencing samples were the lung tissues (**Table 2**) after treatment of 6 hours or 36 hours.

Differentially expressed genes in relation to IR

The limma package using R language was employed to analyze GSE67370. Differentially expressed genes between the IR group and sham surgery group were analyzed, considering the sham surgery group as the control group. Finally, 464 differential genes were found in the IR group, of which 216 were upregulated and 248 were downregulated. The full list is shown in Table S1. Enrichment analysis was performed on the functional and metabolic pathways of these differentially expressed genes. In GO-BP enrichment analysis, differentially expressed genes were mainly enriched in pathways like "oxidation-reduction process" and "inflammatory response" (**Figure 1A**; Table S2). Results of KEGG enrichment analysis revealed

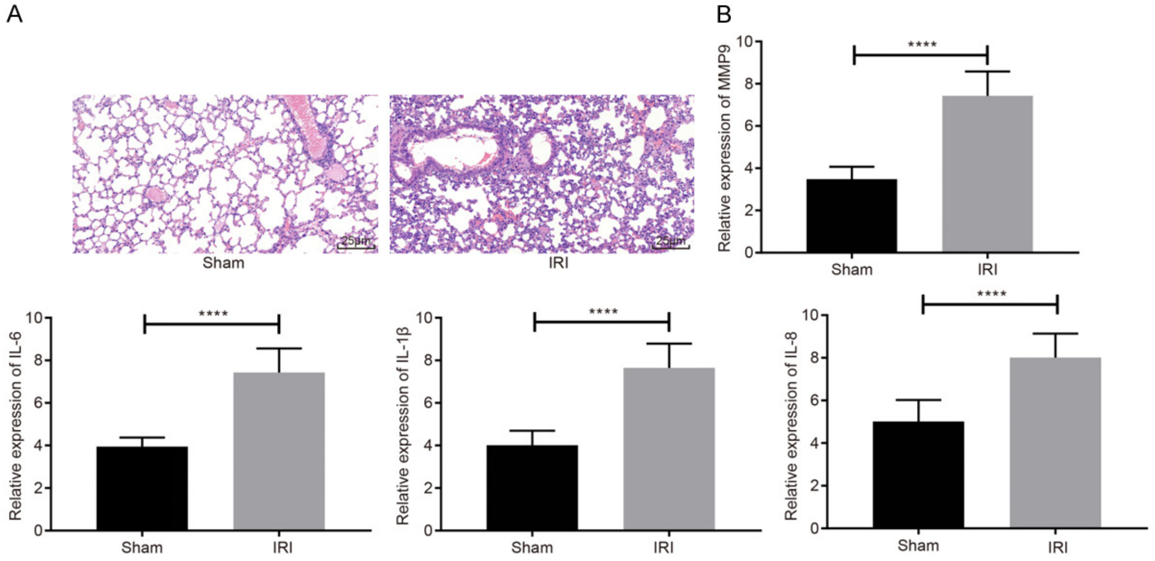

Figure 3. Measurement of lung tissues revealed that IR induced inflammation before lung injuries. (A) Comparison of LIRI group and sham surgery group detected by H&E stain; (B) RT-qPCR results showed that expression levels of MMP9, IL6, IL1B, and IL8 were higher in LIRI group. Data are presented as mean value ± standard. *, $P < 0.05$ *vs.* the control group. Each experiment was repeated three times.

that these genes were mostly enriched in metabolic pathways, such as "Pathways in cancer" and "PI3K-Akt signaling pathway" (**Figure 1B**; Table S2). The main pathways enriched by biological processes along with these metabolic pathways were associated with inflammation. A previous study has shown that [14] the process of lung injuries caused by IR was accompanied by a significant increase of inflammatory response. These findings suggest that the differential genes screened here were very likely to be closely related to lung injuries.

Identification of factors in LIRI which are closely relevant to inflammation by DigSee research

A text mining search engine, DigSee (http://210.107.182.61/geneSearch/) has provided evidence stating that "genes" may play a role in the progress of "disease" via "biological events". Medline abstracts with highlighted evidence sentences were retrieved with a query of diseases, genes, and events. On the website, with "LIRI" as a keyword for retrieving information, it was found that genes related to the disease included IL6, IL10, IL8, and other inflammatory factors. The first 20 genes were selected for subsequent analysis (**Table 3**).

MMP9 is a significant factor in LIRI

A total of 464 differential genes were identified on the basis of the previous differential analysis of GSE67370. These differential genes were sorted based on change of |logFC| size, with the first 40 genes selected. These 40 genes expressed the largest differences in the IR group. String was applied to conduct correlation analysis on the 40 genes with the largest variation, with 20 genes related to lung injuries (**Figure 2**). Results suggested that MMP9, IL6, tumor necrosis factor (TNF), IL8, and some other genes were located at the core position. Only MMP9 did not belong to the known gene of lung injuries, suggesting that there was a direct link between MMP9 and inflammatory factors, such as IL8 and IL6. It was indicated that MMP9 was involved in lung injuries resulting from IR. Therefore, MMP9 was selected for further functional analysis.

Inflammation-related factors expression elevated in IR lung injury group

This study established a rat model of IR and detected lung tissues. Results showed that, compared with the sham surgery group, LIRI induced persistent neutrophil infiltration and focal alveolar hemorrhage in the lung periphery (**Figure 3A**). In addition, expression levels of MMP9 genes in the IR group were measured. Additionally, expression levels of lung injury related factors like IL6, IL1B, and IL8 were also determined. It was demonstrated that expression levels of inflammatory factors and MMP9 in the lung tissues were significantly elevated

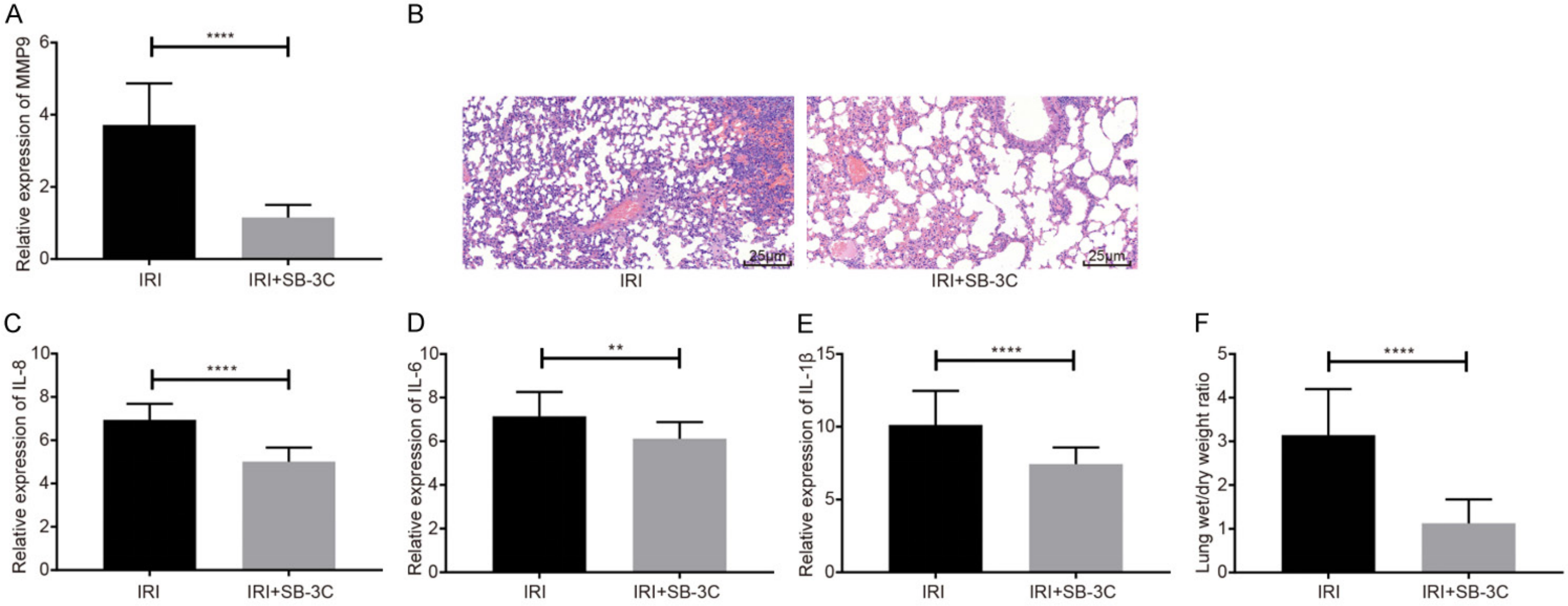

Figure 4. MMP9 was a factor deteriorating lung injury after ischemia reperfusion. (A) SB-3CT decreased MMP9; (B) HE staining revealed that lung injury was more serious in the IR group than in the IR + SB-3CT group; (C-E) RT-qPCR detected that expression levels of IL8, IL6, and IL1B were higher in the IR group compared with the IR + SB-3CT group; (F) the wet/dry ratio decreased in the IR + SB-3CT group; Data are presented as mean value ± standard. *, $P < 0.05$ *vs.* the control group. Each experiment was repeated three times.

after IR (**Figure 3B**). Results also suggested that IR induced inflammation, further leading to lung injury.

IR causes obvious inflammation in the lungs followed by lung injuries

To further verify the function of MMP9 in the development of lung injuries induced by IR, MMP inhibitors SB-3CT (sigma) were employed to treat lung tissues after IR. SB-3CT could significantly inhibit expression of MMP9 (**Figure 4A**). It was found that lung tissues in the IR + SB-3CT group were in a better state than lung tissues in the IR group (**Figure 4B**), indicating that MMP9 could exaggerate lung tissue injuries after IR.

Moreover, expression levels of inflammatory factors, like IL8, IL6, and IL1B, in the IR + SB-3CT group decreased significantly, compared to levels in the IR group (**Figure 4C-E**). The available evidence elucidates that MMP9 could increase expression levels of inflammatory factors in lung tissues after IR.

Next, wet/dry ratios of lung tissues in the IR + SB-3CT and IR groups were measured. It was observed that wet/dry ratios of lung tissues were significantly lower than that in the IR group, after the addition of MMP9 inhibitors (**Figure 4F**). Results demonstrated that MMP9 could worsen lung tissue inflammation after IR, thereby leading to lung injuries.

Discussion

LIRI is a prevalent clinical phenomenon in lung transplantation and extracorporeal circulation operations. It contributes to lung dysfunction and is the primary cause of mortality after lung transplantation [15]. As sequelae of complicated events, reperfusion injury paradoxically has an deleterious impact on tissue injury along with inflammation [16]. Post-ischemia/reperfusion inflammation occurs during the development of ischemic brain edema through the production of nitric oxide and various proteolytic enzymes [17]. A recent study proposed that acute lung injuries caused by ischemia reperfusion significantly impact various phenomenon, such as lung edema, neutrophil infiltration, production of inflammatory cytokine, oxidative pressure, apoptosis, and tissue injuries [18]. There are two main cell survival signaling cascades, the reperfusion injury salvage kinase (RISK) pathway and survivor activating factor enhancement pathway, including STAT3, which have been reported to prevent I/R injury [19]. This study first predicted various potential critical molecular bioinformatics procedures for lung ischemia reperfusion injuries, arriving at a conclusion by basic experiments. Results suggest that MMP9 may play an important role in reperfusion injuries. A direct correlation was observed between MMP9 and other inflammatory factors related to lung injuries, such as IL8 and IL6. Thus, it was speculated that high expression of MMP9 is closely associated with lung ischemia reperfusion injuries and induced inflammation.

The current study observed a notable increase in gene expression of MMP9 in IR model rats. Simultaneously, the outcomes of IR model rats with MMP9 inhibitor indicate that MMP9 plays an important role in lung ischemia reperfusion injuries. Traditionally, MMPs have been known for their ability to induce tissue destruction and impact disease progression [10]. MMP9, a member of the MMP family, plays a significant role in blood-brain barrier damage. Its major targets consist of ECM components [9]. MMP-2 and MMP-9 are of critical importance in IR injury, along with cancer invasion and metastasis [13, 20]. An increase in MMP9 expression levels was previously observed during the progression of lipopolysaccharide (LPS)-induced acute lung injury and cerebral ischemia-reperfusion, along with increased activity of MMP-9 in radiation-induced lung injuries [12, 21-23]. A previous study reported that decreased expression of MMP-2 and MMP-9 via suppression of Akt phosphorylation could alleviate LPS-induced acute lung injuries by means of reducing neutrophil infiltration [23].

Present research also observed elevated levels of inflammation factors IL6, IL1B, and IL8 in lung tissue of IR rats. It was speculated that the effects of MMP9 on IR induced lung injuries might be in a correlation with inflammatory factors and their effects. The IL-1 family, including IL1B, has been closely associated to innate immune responses, such as inflammation. Thus, previous researches have cited the involvement of IL6, IL1B, and IL8 along the progression of inflammation [24-29]. IL1B has been known to cause MMP9 induction via means of a nuclear factor-κB (NF-κB)-dependent pathway [30]. MMP9, in combination with other MMPs, regulates inflammation in tissues and diseases and is expressed in inflammatory cells [31]. On one hand, MMP-9 needs to be activated in inflammatory macrophage migration and modulates inflammation by degrading or activating a variety of cytokines, chemokines, and growth factors [32, 33]. On the other hand, proinflammatory cytokines have been reported to stimulate the release of MMP-9 from neutrophils repeatedly [34]. LIRI has been proven to be closely associated with inflammation [35-37]. The present study found that intraperitoneal injections of SB-3CT inhibit expression of MMP9 in rats and alleviate IR induced lung injuries, suggesting that MMP9 may be a potential target for reducing lung injuries induced by IR.

In the current study, MMP9 was presumed to have a significant role in lung injuries induced by IR through bioinformatics. The roles of MMP9 were verified through the establishment of IR induced lung injuries in rat models by suppressing the MMP9 gene and adding MMP9 inhibitor SB-3CT, simultaneously. Outcomes indicate that expression levels of MMP9 are high in lung injuries induced by ischemia reperfusion, while the situation can be alleviated by means of suppressing the abnormally high MMP9 expression. These findings shed new light for future clinical research by providing a potential therapeutic target of LIRI.

Conclusion

In analyzing the sequencing chip data of lung tissues of rat models with IR, results of the current study revealed that a majority of the differentially expressed genes were enriched in inflammation related pathways. Previous studies have additionally documented obvious inflammation in lungs affected by lung injuries caused by IR. Through further screening of differentially expressed genes, it was determined that MMP9 was located at the core position and was closely associated with inflammatory factors, such as IL8 and IL1B, indicating that MMP9 plays an important role in this process. Further experiments validated that, in lung injuries induced by IR, expression of MMP9 increased significantly. It was likely to be regulated by inflammatory factors, including IL-6, TNF, and IL-8. These results suggest that IR induces significant inflammation in the lungs and further activates expression of MMP9. High expression of MMP9 can potentially cause significant damage to the lungs, leading to lung injury. In addition, the current study also suggests that lung injuries after IR may be significantly reduced by inhibition of MMP9 activity.

Acknowledgements

We would like to acknowledge the helpful comments received from our reviewers. This study was supported by Foundation of Science and Technology of Jiangxi Province Plan (NO.2017-1BBG70054).

Disclosure of conflict of interest

None.

Address correspondence to: Dr. Qing-Hua Peng, Department of Anesthesiology, The First Affiliated Hospital of Nanchang University, 17 Yong Wai Zheng Road, Donghu District, Nanchang 330000, Jiangxi Province, PR China. E-mail: PengQingHua-12102@163.com

References

[1] Cattelan A, Ceolotto G, Bova S, Albiero M, Kuppusamy M, De Martin S, Semplicini A, Fadini GP, de Kreutzenberg SV and Avogaro A. NAD(+)-dependent SIRT1 deactivation has a key role on ischemia-reperfusion-induced apoptosis. Vascul Pharmacol 2015; 70: 35-44.
[2] Salinas-Jazmin N, Estrada-Parra S, Becerril-Garcia MA, Limon-Flores AY, Vazquez-Leyva S, Medina-Rivero E, Pavon L, Velasco-Velazquez MA and Perez-Tapia SM. Herpes murine model as a biological assay to test dialyzable leukocyte extracts activity. J Immunol Res 2015; 2015: 146305.
[3] Chouchani ET, Pell VR, James AM, Work LM, Saeb-Parsy K, Frezza C, Krieg T and Murphy MP. A unifying mechanism for mitochondrial superoxide production during ischemia-reperfusion injury. Cell Metab 2016; 23: 254-263.
[4] Eisenhardt SU, Weiss JB, Smolka C, Maxeiner J, Pankratz F, Bemtgen X, Kustermann M, Thiele JR, Schmidt Y, Bjoern Stark G, Moser M, Bode C and Grundmann S. MicroRNA-155 aggravates ischemia-reperfusion injury by modulation of inflammatory cell recruitment and the respiratory oxidative burst. Basic Res Cardiol 2015; 110: 32.

[5] Ding J, Zhang Q, Luo Q, Ying Y, Liu Y, Li Y, Wei W, Yan F and Zhang H. Alda-1 attenuates lung ischemia-reperfusion injury by reducing 4-hydroxy-2-nonenal in alveolar epithelial cells. Crit Care Med 2016; 44: e544-552.

[6] Del Sorbo L, Costamagna A, Muraca G, Rotondo G, Civiletti F, Vizio B, Bosco O, Martin Conte EL, Frati G, Delsedime L, Lupia E, Fanelli V and Ranieri VM. Intratracheal administration of small interfering RNA targeting fas reduces lung ischemia-reperfusion injury. Crit Care Med 2016; 44: e604-613.

[7] Tiriveedhi V, Upadhya GA, Busch RA, Gunter KL, Dines JN, Knolhoff BL, Jia J, Sarma NJ, Ramachandran S, Anderson CD, Mohanakumar T and Chapman WC. Protective role of bortezomib in steatotic liver ischemia/reperfusion injury through abrogation of MMP activation and YKL-40 expression. Transpl Immunol 2014; 30: 93-98.

[8] Li Q, Zhang R, Ge YL, Mei YW and Guo YL. Effects of neuregulin on expression of MMP-9 and NSE in brain of ischemia/reperfusion rat. J Mol Neurosci 2009; 38: 207-215.

[9] Fang X, Tao D, Shen J, Wang Y, Dong X and Ji X. Neuroprotective effects and dynamic expressions of MMP9 and TIMP1 associated with atorvastatin pretreatment in ischemia-reperfusion rats. Neurosci Lett 2015; 603: 60-65.

[10] Houghton AM, Grisolano JL, Baumann ML, Kobayashi DK, Hautamaki RD, Nehring LC, Cornelius LA and Shapiro SD. Macrophage elastase (matrix metalloproteinase-12) suppresses growth of lung metastases. Cancer Res 2006; 66: 6149-6155.

[11] Iwata T, Chiyo M, Yoshida S, Smith GN Jr, Mickler EA, Presson R Jr, Fisher AJ, Brand DD, Cummings OW and Wilkes DS. Lung transplant ischemia reperfusion injury: metalloprotease inhibition down-regulates exposure of type V collagen, growth-related oncogene-induced neutrophil chemotaxis, and tumor necrosis factor-alpha expression. Transplantation 2008; 85: 417-426.

[12] Yang K, Palm J, Konig J, Seeland U, Rosenkranz S, Feiden W, Rube C and Rube CE. Matrix-metallo-proteinases and their tissue inhibitors in radiation-induced lung injury. Int J Radiat Biol 2007; 83: 665-676.

[13] Hamada T, Fondevila C, Busuttil RW and Coito AJ. Metalloproteinase-9 deficiency protects against hepatic ischemia/reperfusion injury. Hepatology 2008; 47: 186-198.

[14] Altemeier WA, Liles WC, Villagra-Garcia A, Matute-Bello G and Glenny RW. Ischemia-reperfusion lung injury is attenuated in MyD88-deficient mice. PLoS One 2013; 8: e77123.

[15] Cao QF, Qu MJ, Yang WQ, Wang DP, Zhang MH and Di SB. Ischemia postconditioning preventing lung ischemia-reperfusion injury. Gene 2015; 554: 120-124.

[16] Gao HK, Yin Z, Zhou N, Feng XY, Gao F and Wang HC. Glycogen synthase kinase 3 inhibition protects the heart from acute ischemia-reperfusion injury via inhibition of inflammation and apoptosis. J Cardiovasc Pharmacol 2008; 52: 286-292.

[17] Suda S, Katsura K, Kanamaru T, Saito M and Katayama Y. Valproic acid attenuates ischemia-reperfusion injury in the rat brain through inhibition of oxidative stress and inflammation. Eur J Pharmacol 2013; 707: 26-31.

[18] Wu SY, Tang SE, Ko FC, Wu GC, Huang KL and Chu SJ. Valproic acid attenuates acute lung injury induced by ischemia-reperfusion in rats. Anesthesiology 2015; 122: 1327-1337.

[19] Zhang XY, Chen C, Zhang YB, Wang SY, Zhu T, Liu J, Ma G and Liu B. Role of toll-like receptor 3 in lung ischemia-reperfusion injury. Shock 2016; 46: 405-411.

[20] Somiari SB, Somiari RI, Heckman CM, Olsen CH, Jordan RM, Russell SJ and Shriver CD. Circulating MMP2 and MMP9 in breast cancer -- potential role in classification of patients into low risk, high risk, benign disease and breast cancer categories. Int J Cancer 2006; 119: 1403-1411.

[21] Fligiel SE, Standiford T, Fligiel HM, Tashkin D, Strieter RM, Warner RL, Johnson KJ and Varani J. Matrix metalloproteinases and matrix metalloproteinase inhibitors in acute lung injury. Hum Pathol 2006; 37: 422-430.

[22] Gao D, Zhang X, Jiang X, Peng Y, Huang W, Cheng G and Song L. Resveratrol reduces the elevated level of MMP-9 induced by cerebral ischemia-reperfusion in mice. Life Sci 2006; 78: 2564-2570.

[23] Chen WY, Huang YC, Yang ML, Lee CY, Chen CJ, Yeh CH, Pan PH, Horng CT, Kuo WH and Kuan YH. Protective effect of rutin on LPS-induced acute lung injury via down-regulation of MIP-2 expression and MMP-9 activation through inhibition of Akt phosphorylation. Int Immunopharmacol 2014; 22: 409-413.

[24] Schmidt KJ, Fellermann K, Wellhoner P, Weitz G, Homann N, Herrlinger K, Lehnert H, Ludwig D and Buning J. Clinical trial: cyclophosphamide pulse therapy - a promising therapeutic alternative in refractory Crohn’s disease. Aliment Pharmacol Ther 2009; 29: 1230-1239.

[25] Lin SN, Ayada K, Zhao Y, Yokota K, Takenaka R, Okada H, Kan R, Hayashi S, Mizuno M, Hirai Y, Fujinami Y and Oguma K. Helicobacter pylori heat-shock protein 60 induces production of the pro-inflammatory cytokine IL8 in monocytic cells. J Med Microbiol 2005; 54: 225-233.

[26] Bai B, Yamamoto K, Sato H, Sugiura H and Tanaka T. Combined effect of 25-hydroxycholesterol and IL-1beta on IL-8 production in human colon carcinoma cell line (Caco-2). Inflammation 2005; 29: 141-146.

[27] Iliopoulos D, Hirsch HA and Struhl K. An epigenetic switch involving NF-kappaB, Lin28, Let-7 MicroRNA, and IL6 links inflammation to cell transformation. Cell 2009; 139: 693-706.

[28] Hodge DR, Hurt EM and Farrar WL. The role of IL-6 and STAT3 in inflammation and cancer. Eur J Cancer 2005; 41: 2502-2512.

[29] Dinarello CA. Interleukin-1 in the pathogenesis and treatment of inflammatory diseases. Blood 2011; 117: 3720-3732.

[30] Qin W, Lu W, Li H, Yuan X, Li B, Zhang Q and Xiu R. Melatonin inhibits IL1beta-induced MMP9 expression and activity in human umbilical vein endothelial cells by suppressing NF-kappaB activation. J Endocrinol 2012; 214: 145-153.

[31] Wang X, Yu YY, Lieu S, Yang F, Lang J, Lu C, Werb Z, Hu D, Miclau T, Marcucio R and Colnot C. MMP9 regulates the cellular response to inflammation after skeletal injury. Bone 2013; 52: 111-119.

[32] Gong Y, Hart E, Shchurin A and Hoover-Plow J. Inflammatory macrophage migration requires MMP-9 activation by plasminogen in mice. J Clin Invest 2008; 118: 3012-3024.

[33] Bry K, Hogmalm A and Backstrom E. Mechanisms of inflammatory lung injury in the neonate: lessons from a transgenic mouse model of bronchopulmonary dysplasia. Semin Perinatol 2010; 34: 211-221.

[34] Sochor M, Richter S, Schmidt A, Hempel S, Hopt UT and Keck T. Inhibition of matrix metalloproteinase-9 with doxycycline reduces pancreatitis-associated lung injury. Digestion 2009; 80: 65-73.

[35] Razi SS, Latif MJ, Li X, Afthinos JN, Ippagunta N, Schwartz G, Sagalovich D, Belsley SJ, Connery CP, Jour G, Christofidou-Solomidou M and Bhora FY. Dietary flaxseed protects against lung ischemia reperfusion injury via inhibition of apoptosis and inflammation in a murine model. J Surg Res 2011; 171: e113-121.

[36] Ben DF, Yu XY, Ji GY, Zheng DY, Lv KY, Ma B and Xia ZF. TLR4 mediates lung injury and inflammation in intestinal ischemia-reperfusion. J Surg Res 2012; 174: 326-333.

[37] Campanholle G, Landgraf RG, Goncalves GM, Paiva VN, Martins JO, Wang PH, Monteiro RM, Silva RC, Cenedeze MA, Teixeira VP, Reis MA, Pacheco-Silva A, Jancar S and Camara NO. Lung inflammation is induced by renal ischemia and reperfusion injury as part of the systemic inflammatory syndrome. Inflamm Res 2010; 59: 861-869.

Table S1. The differential expression analysis of GSE67370 chip

ID	adj.*P*.Val	*P*.Value	t	B	logFC	|logFC|	Gene.symbol	Gene.title
1418722_at	0.002	4.09E-6	7.452	4.623	5.757	5.757	Ngp	neutrophilic granule protein
1450826_a_at	0.001	4.07E-7	9.140	6.729	5.585	5.585	Saa3	serum amyloid A 3
1419532_at	0.001	1.43E-6	8.193	5.595	4.718	4.718	Il1r2	interleukin 1 receptor, type II
1440865_at	0.013	1.13E-4	5.386	1.472	4.694	4.694	Ifitm6	interferon induced transmembrane protein 6
1449366_at	0.049	1.43E-3	4.003	-0.982	4.048	4.048	Mmp8	matrix metallopeptidase 8
1449434_at	0.047	1.31E-3	-4.048	-0.899	-3.986	3.986	Car3	carbonic anhydrase 3
1418937_at	0.004	1.42E-5	6.634	3.455	3.948	3.948	Dio2	deiodinase, iodothyronine, type II
1422651_at	0.043	1.08E-3	-4.147	-0.716	-3.912	3.912	Adipoq	adiponectin, C1Q and collagen domain containing
1428111_at	0.002	3.02E-6	7.660	4.904	3.865	3.865	Slc38a4	solute carrier family 38, member 4
1448889_at	0.011	9.11E-5	5.509	1.678	3.854	3.854	Slc38a4	solute carrier family 38, member 4
1420804_s_at	0.045	1.23E-3	4.081	-0.839	3.812	3.812	Clec4d	C-type lectin domain family 4, member d
1420667_at	0.011	9.15E-5	5.506	1.674	3.746	3.746	Doc2b	double C2, beta
1448228_at	0.047	1.33E-3	4.039	-0.916	3.742	3.742	Lox	lysyl oxidase
1454881_s_at	0.022	3.19E-4	-4.805	0.470	-3.691	3.691	Upk3b	uroplakin 3B
1422953_at	0.006	3.11E-5	6.145	2.707	3.558	3.558	Fpr2	formyl peptide receptor 2
1427893_a_at	0.001	4.23E-7	9.110	6.696	3.518	3.518	Pmvk	phosphomevalonate kinase
1416576_at	0.000	3.79E-8	11.156	8.785	3.513	3.513	Socs3	suppressor of cytokine signaling 3
1438953_at	0.001	2.03E-7	-9.700	7.347	-3.493	3.493	Vegfd	vascular endothelial growth factor D
1430700_a_at	0.005	2.21E-5	6.356	3.034	3.392	3.392	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)
1449984_at	0.033	6.88E-4	4.388	-0.276	3.369	3.369	Cxcl2	chemokine (C-X-C motif) ligand 2
1436172_at	0.006	3.03E-5	-6.162	2.734	-3.365	3.365	Gm20559	predicted gene, 20559
1424131_at	0.012	1.05E-4	-5.427	1.542	-3.352	3.352	Col6a3	collagen, type VI, alpha 3
1424509_at	0.006	3.37E-5	6.097	2.632	3.277	3.277	Cd177	CD177 antigen
1418847_at	0.015	1.50E-4	5.225	1.199	3.266	3.266	Arg2	arginase type II
1421694_a_at	0.001	9.65E-7	8.480	5.952	3.231	3.231	Vcan	versican
1419609_at	0.034	7.12E-4	4.370	-0.309	3.219	3.219	Ccr1	chemokine (C-C motif) receptor 1
1417290_at	0.002	3.90E-6	7.484	4.666	3.208	3.208	Lrg1	leucine-rich alpha-2-glycoprotein 1
1428333_at	0.001	2.36E-6	-7.834	5.135	-3.186	3.186	Arxes2///Arxes1	adipocyte-related X-chromosome expressed sequence 2///adipocyte-related X-chromosome expressed sequence 1
1416125_at	0.012	1.02E-4	5.442	1.567	3.181	3.181	Fkbp5	FK506 binding protein 5
1424638_at	0.019	2.42E-4	4.956	0.736	3.143	3.143	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)
1426858_at	0.002	3.76E-6	7.509	4.701	3.135	3.135	Inhbb	inhibin beta-B

1419100_at	0.019	2.49E-4	4.940	0.707	3.112	3.112	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N
1424312_at	0.025	4.05E-4	4.674	0.237	3.062	3.062	Adipor1	adiponectin receptor 1
1448291_at	0.029	5.45E-4	4.513	-0.051	3.046	3.046	Mmp9	matrix metallopeptidase 9
1425225_at	0.018	2.21E-4	5.005	0.821	3.034	3.034	Fcgr4	Fc receptor, IgG, low affinity IV
1438841_s_at	0.044	1.12E-3	4.132	-0.744	3.026	3.026	Arg2	arginase type II
1424033_at	0.023	3.79E-4	-4.709	0.301	-2.987	2.987	Srsf7	serine/arginine-rich splicing factor 7
1429052_at	0.004	1.38E-5	-6.653	3.483	-2.986	2.986	Ptprd	protein tyrosine phosphatase, receptor type, D
1453470_a_at	0.038	9.04E-4	4.243	-0.541	2.973	2.973	Gna13	guanine nucleotide binding protein, alpha 13
1423619_at	0.020	2.79E-4	4.877	0.597	2.950	2.950	Rasd1	RAS, dexamethasone-induced 1
1424923_at	0.033	6.64E-4	4.407	-0.242	2.942	2.942	Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G
1449901_a_at	0.008	5.10E-5	5.848	2.235	2.934	2.934	Map3k6	mitogen-activated protein kinase kinase kinase 6
1421679_a_at	0.030	5.76E-4	4.484	-0.103	2.911	2.911	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)
1438954_x_at	0.001	9.27E-7	-8.510	5.989	-2.908	2.908	Vegfd	vascular endothelial growth factor D
1448620_at	0.046	1.26E-3	4.068	-0.862	2.894	2.894	Fcgr3	Fc receptor, IgG, low affinity III
1451500_at	0.047	1.32E-3	-4.043	-0.908	-2.888	2.888	Ushbp1	Usher syndrome 1C binding protein 1
1425528_at	0.000	1.50E-9	-14.477	11.345	-2.883	2.883	Prrx1	paired related homeobox 1
1423226_at	0.027	4.64E-4	-4.600	0.106	-2.879	2.879	Ms4a1	membrane-spanning 4-domains, subfamily A, member 1
1428083_at	0.003	8.46E-6	-6.967	3.943	-2.815	2.815	Neat1	nuclear paraspeckle assembly transcript 1 (non-protein coding)
1427747_a_at	0.019	2.64E-4	4.909	0.653	2.790	2.790	Lcn2	lipocalin 2
1455182_at	0.003	8.41E-6	-6.971	3.949	-2.769	2.769	Kif1b	kinesin family member 1B
1453410_at	0.027	4.71E-4	4.592	0.091	2.766	2.766	Angptl4	angiopoietin-like 4
1452016_at	0.006	2.79E-5	6.211	2.811	2.754	2.754	Alox5ap	arachidonate 5-lipoxygenase activating protein
1434484_at	0.026	4.42E-4	4.626	0.152	2.753	2.753	Wfdc21	WAP four-disulfide core domain 21
1449084_s_at	0.017	1.98E-4	-5.067	0.928	-2.735	2.735	Sh3d19	SH3 domain protein D19
1415806_at	0.010	7.02E-5	5.661	1.929	2.734	2.734	Plat	plasminogen activator, tissue
1420394_s_at	0.045	1.18E-3	4.101	-0.801	2.724	2.724	Lilrb4a///Lilr4b	leukocyte immunoglobulin-like receptor, subfamily B, member 4A///leukocyte immunoglobulin-like receptor, subfamily B, member 4B
1415871_at	0.001	1.36E-6	8.230	5.642	2.720	2.720	Tgfbi	transforming growth factor, beta induced
1416225_at	0.000	4.89E-8	-10.925	8.572	-2.684	2.684	Adh1	alcohol dehydrogenase 1 (class I)

1430295_at	0.037	8.40E-4	4.282	-0.469	2.661	2.661	Gna13	guanine nucleotide binding protein, alpha 13
1428942_at	0.002	6.01E-6	7.192	4.263	2.646	2.646	Mt2	metallothionein 2
1429379_at	0.047	1.33E-3	4.041	-0.912	2.634	2.634	Lyve1	lymphatic vessel endothelial hyaluronan receptor 1
1449305_at	0.017	1.97E-4	5.070	0.932	2.625	2.625	F10	coagulation factor X
1427884_at	0.028	5.00E-4	-4.559	0.032	-2.620	2.620	Col3a1	collagen, type III, alpha 1
1424302_at	0.049	1.42E-3	4.004	-0.980	2.601	2.601	Pirb	paired Ig-like receptor B
1418454_at	0.006	3.06E-5	-6.156	2.725	-2.585	2.585	Mfap5	microfibrillar associated protein 5
1420697_at	0.002	5.05E-6	7.310	4.427	2.583	2.583	Slc15a3	solute carrier family 15, member 3
1417341_a_at	0.016	1.82E-4	5.113	1.008	2.575	2.575	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2
1419314_at	0.005	2.22E-5	-6.354	3.030	-2.558	2.558	Tinag	tubulointerstitial nephritis antigen
1455899_x_at	0.012	9.93E-5	5.459	1.595	2.542	2.542	Socs3	suppressor of cytokine signaling 3
1422573_at	0.013	1.17E-4	5.364	1.436	2.539	2.539	Ampd3	adenosine monophosphate deaminase 3
1416298_at	0.011	9.27E-5	5.499	1.662	2.532	2.532	Mmp9	matrix metallopeptidase 9
1428306_at	0.001	1.04E-6	8.423	5.882	2.526	2.526	Ddit4	DNA-damage-inducible transcript 4
1452521_a_at	0.002	4.86E-6	7.335	4.463	2.506	2.506	Plaur	plasminogen activator, urokinase receptor
1418534_at	0.008	4.55E-5	-5.917	2.345	-2.504	2.504	Fzd2	frizzled class receptor 2
1422644_at	0.042	1.01E-3	-4.182	-0.652	-2.501	2.501	Sh3bgr	SH3-binding domain glutamic acid-rich protein
1448823_at	0.029	5.37E-4	-4.521	-0.036	-2.500	2.500	Cxcl12	chemokine (C-X-C motif) ligand 12
1418936_at	0.016	1.88E-4	5.097	0.981	2.497	2.497	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)
1455530_at	0.004	1.40E-5	-6.640	3.464	-2.490	2.490	Ighv14-2	immunoglobulin heavy variable 14-2
1416996_at	0.001	1.19E-6	8.324	5.760	2.486	2.486	Tbc1d8	TBC1 domain family, member 8
1452231_x_at	0.006	3.38E-5	-6.095	2.629	-2.475	2.475	Mndal	myeloid nuclear differentiation antigen like
1456212_x_at	0.011	7.86E-5	5.594	1.821	2.462	2.462	Socs3	suppressor of cytokine signaling 3
1418465_at	0.001	1.43E-6	8.189	5.591	2.443	2.443	Ncf4	neutrophil cytosolic factor 4
1424965_at	0.037	8.37E-4	4.284	-0.465	2.430	2.430	Lpxn	leupaxin
1451941_a_at	0.026	4.44E-4	4.624	0.148	2.425	2.425	Fcgr2b	Fc receptor, IgG, low affinity IIb
1449227_at	0.002	5.22E-6	7.287	4.396	2.424	2.424	Ch25h	cholesterol 25-hydroxylase
1448123_s_at	0.000	4.88E-8	10.926	8.574	2.424	2.424	Tgfbi	transforming growth factor, beta induced
1448561_at	0.002	5.37E-6	7.268	4.369	2.417	2.417	Ncf2	neutrophil cytosolic factor 2
1452249_at	0.009	6.09E-5	-5.744	2.066	-2.412	2.412	Prickle1	prickle planar cell polarity protein 1
1417625_s_at	0.017	2.12E-4	5.031	0.865	2.404	2.404	Ackr3	atypical chemokine receptor 3
1459903_at	0.009	6.13E-5	5.740	2.060	2.404	2.404	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A

1422637_at	0.022	3.42E-4	4.766	0.401	2.403	2.403	Rassf5	Ras association (RalGDS/AF-6) domain family member 5
1419352_at	0.011	8.14E-5	-5.574	1.787	-2.393	2.393	l7Rn6	lethal, Chr 7, Rinchik 6
1418133_at	0.001	3.43E-7	9.275	6.882	2.374	2.374	Bcl3	B cell leukemia/lymphoma 3
1433691_at	0.024	3.86E-4	-4.700	0.284	-2.366	2.366	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C
1418340_at	0.016	1.85E-4	5.104	0.992	2.357	2.357	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide
1432083_a_at	0.028	5.26E-4	-4.533	-0.015	-2.356	2.356	Lrrc23	leucine rich repeat containing 23
1449443_at	0.004	1.42E-5	-6.632	3.452	-2.354	2.354	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial
1436853_a_at	0.011	7.78E-5	-5.600	1.830	-2.353	2.353	Snca	synuclein, alpha
1422557_s_at	0.001	8.87E-7	8.543	6.029	2.346	2.346	Mt1	metallothionein 1
1426906_at	0.008	5.45E-5	-5.810	2.173	-2.344	2.344	Mndal	myeloid nuclear differentiation antigen like
1422889_at	0.005	2.00E-5	-6.418	3.129	-2.328	2.328	Pcdh18	protocadherin 18
1427035_at	0.004	1.53E-5	6.586	3.382	2.320	2.320	Slc39a14	solute carrier family 39 (zinc transporter), member 14
1417574_at	0.025	4.04E-4	-4.676	0.241	-2.317	2.317	Cxcl12	chemokine (C-X-C motif) ligand 12
1448775_at	0.016	1.87E-4	-5.099	0.983	-2.310	2.310	LOC100862473///Gm16340///Ifi203	cell wall protein AWA1-like///interferon-activable protein 203-like///interferon activated gene 203
1421571_a_at	0.018	2.22E-4	5.003	0.817	2.296	2.296	Ly6c2///Ly6c1	lymphocyte antigen 6 complex, locus C2///lymphocyte antigen 6 complex, locus C1
1451753_at	0.021	3.16E-4	4.810	0.479	2.292	2.292	Plxna2	plexin A2
1455581_x_at	0.034	7.33E-4	-4.355	-0.337	-2.292	2.292	Gm20559	predicted gene, 20559
1435903_at	0.045	1.20E-3	4.094	-0.815	2.291	2.291	Cd300a	CD300A molecule
1421034_a_at	0.001	1.87E-6	7.998	5.347	2.283	2.283	Il4ra	interleukin 4 receptor, alpha
1417936_at	0.013	1.19E-4	5.356	1.422	2.275	2.275	Ccl9	chemokine (C-C motif) ligand 9
1435382_at	0.043	1.08E-3	-4.147	-0.717	-2.266	2.266	Ndn	necdin
1424234_s_at	0.003	9.89E-6	-6.865	3.795	-2.251	2.251	Meox2	mesenchyme homeobox 2
1448499_a_at	0.048	1.38E-3	-4.019	-0.953	-2.238	2.238	Ephx2	epoxide hydrolase 2, cytoplasmic
1427056_at	0.023	3.63E-4	4.733	0.343	2.237	2.237	Adamts15	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 15
1437378_x_at	0.039	9.28E-4	4.230	-0.565	2.231	2.231	Scarb1	scavenger receptor class B, member 1
1427883_a_at	0.016	1.73E-4	-5.142	1.057	-2.219	2.219	Col3a1	collagen, type III, alpha 1
1419662_at	0.004	1.60E-5	-6.560	3.344	-2.217	2.217	Ogn	osteoglycin
1455683_a_at	0.048	1.37E-3	4.025	-0.942	2.216	2.216	Tbc1d8	TBC1 domain family, member 8
1427932_s_at	0.017	2.03E-4	5.055	0.907	2.210	2.210	A130040M12Rik///1200015M12Rik///1200003I10Rik	RIKEN cDNA A130040M12 gene///RIKEN cDNA 1200015M12 gene///RIKEN cDNA 1200003I10 gene

1450792_at	0.029	5.54E-4	4.505	-0.066	2.208	2.208	Tyrobp	TYRO protein tyrosine kinase binding protein
1422570_at	0.008	4.97E-5	5.864	2.260	2.193	2.193	Yy1	YY1 transcription factor
1426343_at	0.014	1.48E-4	5.230	1.209	2.175	2.175	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)
1452770_at	0.026	4.37E-4	-4.632	0.163	-2.174	2.174	Vkorc1	vitamin K epoxide reductase complex, subunit 1
1424157_at	0.015	1.60E-4	-5.187	1.135	-2.173	2.173	Ehd2	EH-domain containing 2
1451340_at	0.004	1.24E-5	6.720	3.583	2.171	2.171	Arid5a	AT rich interactive domain 5A (MRF1-like)
1421326_at	0.029	5.50E-4	4.508	-0.060	2.159	2.159	Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
1450034_at	0.016	1.80E-4	-5.122	1.023	-2.147	2.147	Stat1	signal transducer and activator of transcription 1
1424233_at	0.004	1.19E-5	-6.748	3.624	-2.146	2.146	Meox2	mesenchyme homeobox 2
1428113_at	0.022	3.33E-4	-4.780	0.426	-2.138	2.138	Tmtc4	transmembrane and tetratricopeptide repeat containing 4
1448421_s_at	0.005	1.91E-5	-6.447	3.172	-2.125	2.125	Aspn	asporin
1456250_x_at	0.011	8.11E-5	5.576	1.790	2.116	2.116	Tgfbi	transforming growth factor, beta induced
1420464_s_at	0.018	2.28E-4	4.990	0.794	2.111	2.111	Gm14548///Gm10693///Pirb///Pira7///Pira6///Pira5///Pira4///Lilra6///Pira2///Pira11///Pira1	predicted gene 14548///predicted pseudogene 10693///paired Ig-like receptor B///paired-Ig-like receptor A7///paired-Ig-like receptor A6///paired-Ig-like receptor A5///paired-Ig-like receptor A4///leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6///paired-Ig-like receptor A2///paired-Ig-like receptor A11///paired-Ig-like receptor A1
1450165_at	0.019	2.40E-4	4.961	0.744	2.095	2.095	Slfn2	schlafen 2
1425221_at	0.027	4.80E-4	-4.581	0.072	-2.085	2.085	Agr3	anterior gradient 3
1428141_at	0.008	4.75E-5	-5.891	2.304	-2.078	2.078	Gga2	golgi associated, gamma adaptin ear containing, ARF binding protein 2
1419573_a_at	0.016	1.80E-4	-5.122	1.023	-2.050	2.050	Lgals1	lectin, galactose binding, soluble 1
1420558_at	0.028	5.18E-4	4.541	-0.000	2.048	2.048	Selp	selectin, platelet
1451992_at	0.039	9.46E-4	4.219	-0.585	2.039	2.039	Adrbk1	adrenergic receptor kinase, beta 1
1448929_at	0.019	2.41E-4	4.958	0.739	2.035	2.035	F13a1	coagulation factor XIII, A1 subunit
1452203_at	0.008	5.28E-5	-5.828	2.203	-2.035	2.035	Nabp1	nucleic acid binding protein 1
1448147_at	0.001	1.79E-6	-8.028	5.386	-2.027	2.027	Tnfrsf19	tumor necrosis factor receptor superfamily, member 19
1455058_at	0.019	2.61E-4	-4.915	0.664	-2.013	2.013	Mtmr9	myotubularin related protein 9
1416050_a_at	0.016	1.82E-4	5.113	1.008	2.008	2.008	Scarb1	scavenger receptor class B, member 1

1418945_at	0.028	5.14E-4	4.544	0.006	1.998	1.998	Mmp3	matrix metallopeptidase 3
1425451_s_at	0.034	7.20E-4	4.364	-0.321	1.978	1.978	Chil4///Chil3	chitinase-like 4///chitinase-like 3
1421408_at	0.033	6.68E-4	4.404	-0.248	1.968	1.968	Igsf6	immunoglobulin superfamily, member 6
1437463_x_at	0.010	7.49E-5	5.622	1.866	1.961	1.961	Tgfbi	transforming growth factor, beta induced
1422615_at	0.012	1.08E-4	5.412	1.517	1.945	1.945	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4
1423326_at	0.042	1.04E-3	4.167	-0.681	1.941	1.941	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1
1452004_at	0.038	8.99E-4	4.246	-0.535	1.935	1.935	Calca	calcitonin/calcitonin-related polypeptide, alpha
1450757_at	0.032	6.42E-4	-4.426	-0.209	-1.928	1.928	Cdh11	cadherin 11
1448021_at	0.002	2.72E-6	-7.735	5.003	-1.923	1.923	Fam46c	family with sequence similarity 46, member C
1426278_at	0.039	9.10E-4	-4.240	-0.547	-1.921	1.921	Ifi27l2a	interferon, alpha-inducible protein 27 like 2A
1434340_at	0.023	3.55E-4	-4.746	0.365	-1.913	1.913	Uqcr10	ubiquinol-cytochrome c reductase, complex III subunit X
1450678_at	0.044	1.14E-3	4.119	-0.769	1.912	1.912	Itgb2	integrin beta 2
1420798_s_at	0.001	1.33E-6	-8.245	5.661	-1.909	1.909	Pcdhac2///Pcdhac1///Pcdha8///Pcdha2///Pcdha12///Pcdha3///Pcdha9///Pcdha1///Pcdha10///Pcdha11///Pcdha5///Pcdha7///Pcdha6///Pcdha4	protocadherin alpha subfamily C, 2///protocadherin alpha subfamily C, 1///protocadherin alpha 8///protocadherin alpha 2///protocadherin alpha 12///protocadherin alpha 3///protocadherin alpha 9///protocadherin alpha 1///protocadherin alpha 10///protocadherin alpha 11///protocadherin alpha 5///protocadherin alpha 7///protocadherin alpha 6///protocadherin alpha 4
1418612_at	0.034	7.26E-4	4.360	-0.328	1.905	1.905	Slfn1	schlafen 1
1435383_x_at	0.040	9.70E-4	-4.206	-0.609	-1.897	1.897	Ndn	necdin
1424542_at	0.009	5.55E-5	5.798	2.154	1.888	1.888	S100a4	S100 calcium binding protein A4
1417785_at	0.038	8.59E-4	4.270	-0.491	1.888	1.888	Pla1a	phospholipase A1 member A
1437401_at	0.015	1.54E-4	-5.210	1.174	-1.887	1.887	Igf1	insulin-like growth factor 1
1452250_a_at	0.021	3.11E-4	-4.818	0.493	-1.876	1.876	Col6a2	collagen, type VI, alpha 2
1449158_at	0.035	7.81E-4	-4.321	-0.399	-1.873	1.873	Kcnk2	potassium channel, subfamily K, member 2
1452092_at	0.016	1.90E-4	5.092	0.971	1.869	1.869	Chst15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15

1418809_at	0.034	7.21E-4	4.363	-0.322	1.865	1.865	Pirb///Pira5///Pira2///Pira11///Pira1	paired Ig-like receptor B///paired-Ig-like receptor A5///paired-Ig-like receptor A2///paired-Ig-like receptor A11///paired-Ig-like receptor A1
1418345_at	0.011	8.36E-5	-5.559	1.761	-1.863	1.863	Tnfsfm13///Tnfsf13///Tnfsf12	tumor necrosis factor (ligand) superfamily, membrane-bound member 13///tumor necrosis factor (ligand) superfamily, member 13///tumor necrosis factor (ligand) superfamily, member 12
1448690_at	0.030	5.75E-4	4.484	-0.103	1.859	1.859	Kcnk1	potassium channel, subfamily K, member 1
1437100_x_at	0.001	1.37E-6	8.223	5.633	1.855	1.855	Pim3	proviral integration site 3
1428655_at	0.017	2.14E-4	5.024	0.853	1.847	1.847	Ppp1r21	protein phosphatase 1, regulatory subunit 21
1423555_a_at	0.013	1.19E-4	-5.353	1.418	-1.844	1.844	Ifi44	interferon-induced protein 44
1425270_at	0.030	5.93E-4	-4.468	-0.131	-1.842	1.842	Kif1b	kinesin family member 1B
1422620_s_at	0.038	8.55E-4	4.273	-0.487	1.842	1.842	Plpp1	phospholipid phosphatase 1
1415936_at	0.010	6.79E-5	5.680	1.961	1.841	1.841	Bcar3	breast cancer anti-estrogen resistance 3
1448944_at	0.014	1.39E-4	-5.267	1.271	-1.835	1.835	Nrp1	neuropilin 1
1435184_at	0.004	1.45E-5	6.621	3.435	1.831	1.831	Npr3	natriuretic peptide receptor 3
1452161_at	0.001	8.12E-7	8.609	6.109	1.829	1.829	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase
1449336_a_at	0.025	4.08E-4	4.669	0.229	1.826	1.826	Slk	STE20-like kinase
1436030_at	0.016	1.91E-4	-5.089	0.966	-1.823	1.823	Cachd1	cache domain containing 1
1420905_at	0.005	2.02E-5	6.411	3.119	1.821	1.821	Il17ra	interleukin 17 receptor A
1427183_at	0.007	3.46E-5	-6.082	2.608	-1.819	1.819	Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1
1422478_a_at	0.014	1.45E-4	-5.243	1.230	-1.817	1.817	Acss2	acyl-CoA synthetase short-chain family member 2
1416105_at	0.043	1.10E-3	-4.141	-0.728	-1.806	1.806	Nnt	nicotinamide nucleotide transhydrogenase
1448407_at	0.034	7.11E-4	4.371	-0.308	1.803	1.803	Vsir	V-set immunoregulatory receptor
1426971_at	0.034	7.61E-4	-4.335	-0.374	-1.800	1.800	Uba7	ubiquitin-like modifier activating enzyme 7
1415975_at	0.026	4.34E-4	4.636	0.169	1.792	1.792	Carhsp1	calcium regulated heat stable protein 1
1427030_at	0.002	4.99E-6	-7.317	4.437	-1.791	1.791	Spice1	spindle and centriole associated protein 1
1420859_at	0.030	6.02E-4	-4.460	-0.147	-1.791	1.791	Pkia	protein kinase inhibitor, alpha
1418099_at	0.004	1.18E-5	6.751	3.628	1.780	1.780	Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b
1460167_at	0.016	1.91E-4	-5.087	0.963	-1.779	1.779	Aldh7a1	aldehyde dehydrogenase family 7, member A1
1455271_at	0.047	1.35E-3	4.033	-0.927	1.768	1.768	Gm13889	predicted gene 13889

1428538_s_at	0.008	4.60E-5	-5.910	2.334	-1.767	1.767	Rarres2	retinoic acid receptor responder (tazarotene induced) 2
1423371_at	0.028	5.35E-4	-4.523	-0.033	-1.765	1.765	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)
1425837_a_at	0.042	1.06E-3	4.160	-0.693	1.762	1.762	Noct	nocturnin
1417995_at	0.025	4.18E-4	4.657	0.207	1.759	1.759	Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
1419043_a_at	0.010	6.54E-5	-5.702	1.997	-1.753	1.753	Iigp1	interferon inducible GTPase 1
1435420_at	0.003	7.48E-6	-7.048	4.058	-1.753	1.753	Slc4a5	solute carrier family 4, sodium bicarbonate cotransporter, member 5
1449528_at	0.017	2.14E-4	-5.025	0.855	-1.751	1.751	Vegfd	vascular endothelial growth factor D
1418643_at	0.001	1.26E-6	-8.281	5.707	-1.750	1.750	Tspan13	tetraspanin 13
1417447_at	0.025	4.09E-4	-4.668	0.227	-1.746	1.746	Tcf21	transcription factor 21
1450839_at	0.044	1.15E-3	-4.116	-0.774	-1.742	1.742	Nrep	neuronal regeneration related protein
1419663_at	0.043	1.10E-3	-4.139	-0.732	-1.741	1.741	Ogn	osteoglycin
1418131_at	0.028	5.33E-4	4.525	-0.029	1.734	1.734	Samhd1	SAM domain and HD domain, 1
1426956_a_at	0.021	3.12E-4	-4.816	0.489	-1.732	1.732	Trp53bp1	transformation related protein 53 binding protein 1
1419509_a_at	0.023	3.76E-4	-4.714	0.308	-1.730	1.730	Nagk	N-acetylglucosamine kinase
1424575_at	0.012	1.07E-4	-5.416	1.523	-1.722	1.722	Ift22	intraflagellar transport 22
1448947_at	0.010	7.49E-5	-5.622	1.866	-1.719	1.719	2810004N23Rik	RIKEN cDNA 2810004N23 gene
1418492_at	0.017	2.01E-4	-5.059	0.915	-1.717	1.717	Grem2	gremlin 2, DAN family BMP antagonist
1418203_at	0.036	8.24E-4	4.292	-0.451	1.716	1.716	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1
1424872_at	0.005	2.13E-5	-6.378	3.068	-1.704	1.704	Zfp932	zinc finger protein 932
1419298_at	0.028	5.25E-4	-4.534	-0.014	-1.690	1.690	Pon3	paraoxonase 3
1420150_at	0.006	2.52E-5	6.276	2.910	1.683	1.683	Spsb1	splA/ryanodine receptor domain and SOCS box containing 1
1451612_at	0.042	1.06E-3	4.162	-0.690	1.674	1.674	Mt1	metallothionein 1
1460324_at	0.039	9.12E-4	-4.239	-0.548	-1.670	1.670	Dnmt3a	DNA methyltransferase 3A
1429321_at	0.012	9.56E-5	5.481	1.632	1.667	1.667	Rnf149	ring finger protein 149
1419468_at	0.006	3.40E-5	-6.092	2.624	-1.666	1.666	Clec14a	C-type lectin domain family 14, member a
1442744_at	0.047	1.32E-3	4.046	-0.904	1.665	1.665	Rbm39	RNA binding motif protein 39
1416503_at	0.020	2.86E-4	-4.863	0.572	-1.665	1.665	Lxn	latexin
1423723_s_at	0.001	2.04E-6	-7.935	5.266	-1.651	1.651	Tardbp	TAR DNA binding protein
1418250_at	0.033	6.69E-4	4.403	-0.249	1.647	1.647	Arl4d	ADP-ribosylation factor-like 4D
1452426_x_at	0.028	5.33E-4	4.525	-0.029	1.643	1.643		
1416303_at	0.011	8.53E-5	5.547	1.741	1.631	1.631	Litaf	LPS-induced TN factor
1437614_x_at	0.003	9.37E-6	-6.901	3.847	-1.630	1.630	Zdhhc14	zinc finger, DHHC domain containing 14

1417319_at	0.038	8.77E-4	-4.259	-0.511	-1.630	1.630	Nectin3	nectin cell adhesion molecule 3
1418673_at	0.048	1.36E-3	-4.028	-0.935	-1.620	1.620	Snai2	snail family zinc finger 2
1438415_s_at	0.020	2.72E-4	-4.891	0.621	-1.619	1.619	Yipf2	Yip1 domain family, member 2
1434735_at	0.019	2.56E-4	-4.925	0.682	-1.606	1.606	Hlf	hepatic leukemia factor
1434511_at	0.039	9.22E-4	-4.233	-0.560	-1.594	1.594	Phkb	phosphorylase kinase beta
1425274_at	0.017	2.05E-4	-5.048	0.896	-1.594	1.594	Asph	aspartate-beta-hydroxylase
1438975_x_at	0.005	2.13E-5	-6.378	3.067	-1.591	1.591	Zdhhc14	zinc finger, DHHC domain containing 14
1451987_at	0.038	8.59E-4	4.270	-0.491	1.588	1.588	Arrb2	arrestin, beta 2
1417968_a_at	0.045	1.22E-3	4.084	-0.832	1.583	1.583	Mbd1	methyl-CpG binding domain protein 1
1426225_at	0.011	8.28E-5	-5.564	1.770	-1.576	1.576	Rbp4	retinol binding protein 4, plasma
1417075_at	0.014	1.41E-4	-5.258	1.256	-1.572	1.572	Fam136a	family with sequence similarity 136, member A
1424886_at	0.034	7.27E-4	-4.359	-0.330	-1.570	1.570	Ptprd	protein tyrosine phosphatase, receptor type, D
1423046_s_at	0.001	2.18E-6	-7.890	5.208	-1.570	1.570	Ncbp2	nuclear cap binding protein subunit 2
1455422_x_at	0.016	1.83E-4	-5.112	1.006	-1.558	1.558	4-Sep	septin 4
1418030_at	0.003	9.46E-6	-6.894	3.837	-1.553	1.553	Slco3a1	solute carrier organic anion transporter family, member 3a1
1420514_at	0.030	5.78E-4	-4.482	-0.107	-1.548	1.548	Tmem47	transmembrane protein 47
1416253_at	0.041	9.82E-4	4.200	-0.620	1.543	1.543	Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
1418565_at	0.022	3.40E-4	-4.769	0.407	-1.539	1.539	Serbp1	serpine1 mRNA binding protein 1
1437234_x_at	0.004	1.52E-5	-6.591	3.390	-1.537	1.537	Prmt2	protein arginine N-methyltransferase 2
1424918_at	0.046	1.27E-3	-4.066	-0.867	-1.533	1.533	Tbc1d19	TBC1 domain family, member 19
1432176_a_at	0.034	7.30E-4	4.357	-0.334	1.530	1.530	Eng	endoglin
1438619_x_at	0.002	4.28E-6	-7.422	4.582	-1.523	1.523	Zdhhc14	zinc finger, DHHC domain containing 14
1427231_at	0.008	4.60E-5	-5.910	2.334	-1.522	1.522	Robo1	roundabout guidance receptor 1
1452117_a_at	0.023	3.72E-4	4.719	0.318	1.521	1.521	Fyb	FYN binding protein
1455269_a_at	0.048	1.38E-3	4.019	-0.953	1.521	1.521	Coro1a	coronin, actin binding protein 1A
1424968_at	0.044	1.13E-3	-4.125	-0.757	-1.511	1.511	Ces2g	carboxylesterase 2G
1434033_at	0.002	5.27E-6	7.281	4.387	1.504	1.504	Tle1	transducin-like enhancer of split 1
1424048_a_at	0.016	1.86E-4	-5.102	0.988	-1.496	1.496	Cyb5r1	cytochrome b5 reductase 1
1421052_a_at	0.028	5.29E-4	-4.529	-0.022	-1.492	1.492	Gm14680///Sms	predicted gene 14680///spermine synthase
1418442_at	0.001	2.12E-6	-7.910	5.233	-1.491	1.491	Xpo1	exportin 1
1437341_x_at	0.022	3.42E-4	-4.766	0.401	-1.491	1.491	Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase
1425115_at	0.034	7.59E-4	-4.336	-0.371	-1.487	1.487	Rbbp6	retinoblastoma binding protein 6
1438928_x_at	0.008	4.79E-5	5.885	2.295	1.486	1.486	Ninj1	ninjurin 1

1448943_at	0.004	1.53E-5	-6.588	3.386	-1.485	1.485	Nrp1	neuropilin 1
1418326_at	0.012	1.12E-4	5.390	1.480	1.482	1.482	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
1426558_x_at	0.043	1.11E-3	-4.137	-0.736	-1.479	1.479	Gm4724///Gm14305///Gm14308///Gm14295///0610010B08Rik///Gm14434///Gm14432///Gm14430///Gm14419	predicted gene 4724///predicted gene 14305///predicted gene 14308///predicted gene 14295///RIKEN cDNA 0610010B08 gene///predicted gene 14434///predicted gene 14432///predicted gene 14430///predicted gene 14419
1460541_at	0.021	3.11E-4	4.818	0.494	1.478	1.478	Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
1456733_x_at	0.027	4.66E-4	-4.598	0.101	-1.473	1.473	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1
1448361_at	0.021	2.96E-4	-4.845	0.540	-1.464	1.464	Ttc3	tetratricopeptide repeat domain 3
1448876_at	0.038	8.61E-4	-4.269	-0.493	-1.463	1.463	Evc	Ellis van Creveld gene syndrome
1418815_at	0.027	4.82E-4	-4.580	0.069	-1.461	1.461	Cdh2	cadherin 2
1426084_a_at	0.047	1.34E-3	4.037	-0.920	1.460	1.460	Tor1aip1	torsin A interacting protein 1
1421594_a_at	0.000	8.21E-9	-12.636	10.036	-1.459	1.459	Sytl2	synaptotagmin-like 2
1452679_at	0.018	2.39E-4	-4.964	0.749	-1.459	1.459	Tubb2b	tubulin, beta 2B class IIB
1435077_at	0.025	4.24E-4	4.649	0.193	1.458	1.458	Asxl1	additional sex combs like 1
1423233_at	0.014	1.45E-4	5.243	1.231	1.457	1.457	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta
1438610_a_at	0.017	2.17E-4	-5.018	0.842	-1.456	1.456	Cryz	crystallin, zeta
1426801_at	0.020	2.68E-4	-4.900	0.638	-1.452	1.452	8-Sep	septin 8
1455493_at	0.020	2.77E-4	-4.882	0.606	-1.452	1.452	Syne1	spectrin repeat containing, nuclear envelope 1
1438183_x_at	0.045	1.22E-3	-4.084	-0.833	-1.448	1.448	Sord	sorbitol dehydrogenase
1449184_at	0.006	2.69E-5	6.234	2.845	1.442	1.442	Pglyrp1	peptidoglycan recognition protein 1
1427568_a_at	0.049	1.43E-3	-4.003	-0.982	-1.433	1.433	Ift80	intraflagellar transport 80
1422650_a_at	0.028	4.93E-4	4.567	0.046	1.430	1.430	Riok3	RIO kinase 3
1434883_at	0.015	1.67E-4	-5.163	1.093	-1.426	1.426	Mtdh	metadherin
1437902_s_at	0.044	1.15E-3	-4.118	-0.769	-1.426	1.426	Rarres2	retinoic acid receptor responder (tazarotene induced) 2
1416164_at	0.020	2.72E-4	-4.891	0.622	-1.423	1.423	Fbln5	fibulin 5
1422438_at	0.010	6.78E-5	-5.680	1.962	-1.418	1.418	Ephx1	epoxide hydrolase 1, microsomal
1454652_at	0.030	5.85E-4	-4.475	-0.119	-1.415	1.415	Zranb2	zinc finger, RAN-binding domain containing 2
1455012_s_at	0.049	1.43E-3	-4.001	-0.985	-1.415	1.415	Trim37	tripartite motif-containing 37
1441342_at	0.014	1.43E-4	-5.250	1.243	-1.414	1.414	Dpp4	dipeptidylpeptidase 4
1454714_x_at	0.046	1.26E-3	-4.068	-0.862	-1.413	1.413	Phgdh	3-phosphoglycerate dehydrogenase

1460359_at	0.038	8.69E-4	-4.264	-0.502	-1.408	1.408	Armcx3	armadillo repeat containing, X-linked 3
1427121_at	0.044	1.13E-3	4.127	-0.753	1.407	1.407	Fbxo4	F-box protein 4
1435394_s_at	0.016	1.87E-4	5.100	0.985	1.407	1.407	Rhoc	ras homolog family member C
1427156_s_at	0.020	2.93E-4	-4.851	0.551	-1.405	1.405	Ascc2	activating signal cointegrator 1 complex subunit 2
1424857_a_at	0.015	1.55E-4	-5.206	1.167	-1.402	1.402	Trim34a	tripartite motif-containing 34A
1448433_a_at	0.020	2.87E-4	-4.862	0.570	-1.402	1.402	Pcolce	procollagen C-endopeptidase enhancer protein
1424156_at	0.002	2.68E-6	-7.744	5.016	-1.398	1.398	Rbl1	retinoblastoma-like 1 (p107)
1419351_a_at	0.011	8.52E-5	-5.547	1.742	-1.397	1.397	l7Rn6	lethal, Chr 7, Rinchik 6
1419332_at	0.014	1.47E-4	-5.236	1.218	-1.396	1.396	Egfl6	EGF-like-domain, multiple 6
1449079_s_at	0.040	9.60E-4	-4.212	-0.598	-1.395	1.395	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
1452072_at	0.034	7.40E-4	-4.349	-0.347	-1.390	1.390	Myct1	myc target 1
1416151_at	0.013	1.29E-4	-5.307	1.340	-1.387	1.387	Srsf3	serine/arginine-rich splicing factor 3
1448700_at	0.019	2.63E-4	-4.910	0.654	-1.384	1.384	G0s2	G0/G1 switch gene 2
1431299_a_at	0.013	1.21E-4	5.346	1.406	1.384	1.384	Ppp1r18	protein phosphatase 1, regulatory subunit 18
1448942_at	0.008	4.66E-5	-5.902	2.322	-1.382	1.382	Gng11	guanine nucleotide binding protein (G protein), gamma 11
1418601_at	0.005	2.02E-5	-6.413	3.121	-1.381	1.381	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7
1422631_at	0.001	2.24E-6	-7.870	5.181	-1.381	1.381	Ahr	aryl-hydrocarbon receptor
1453321_at	0.011	9.35E-5	-5.494	1.653	-1.381	1.381	Fndc1	fibronectin type III domain containing 1
1448679_at	0.016	1.76E-4	5.134	1.044	1.379	1.379	Hyal2	hyaluronoglucosaminidase 2
1435881_at	0.048	1.39E-3	4.018	-0.954	1.378	1.378	Pcbp2	poly(rC) binding protein 2
1448181_at	0.007	3.63E-5	6.052	2.560	1.372	1.372	Klf15	Kruppel-like factor 15
1424254_at	0.016	1.86E-4	5.104	0.992	1.366	1.366	Ifitm1	interferon induced transmembrane protein 1
1418296_at	0.021	3.09E-4	4.822	0.500	1.355	1.355	Fxyd5	FXYD domain-containing ion transport regulator 5
1416085_s_at	0.013	1.31E-4	5.302	1.331	1.354	1.354	Zfand5	zinc finger, AN1-type domain 5
1423799_at	0.049	1.40E-3	4.012	-0.966	1.354	1.354	Gm5471///Eif1	predicted pseudogene 5471///eukaryotic translation initiation factor 1
1420832_at	0.013	1.23E-4	5.338	1.391	1.353	1.353	Qsox1	quiescin Q6 sulfhydryl oxidase 1
1417826_at	0.013	1.26E-4	-5.324	1.368	-1.345	1.345	Akr1e1	aldo-keto reductase family 1, member E1
1418097_a_at	0.019	2.51E-4	4.936	0.699	1.344	1.344	Crlf2	cytokine receptor-like factor 2
1434380_at	0.006	3.00E-5	-6.168	2.743	-1.341	1.341	Gbp7	guanylate binding protein 7
1424933_at	0.015	1.51E-4	-5.219	1.189	-1.339	1.339	Myo5c	myosin VC

1451385_at	0.010	7.11E-5	-5.653	1.916	-1.339	1.339	Fam162a	family with sequence similarity 162, member A
1433545_s_at	0.047	1.33E-3	-4.040	-0.914	-1.338	1.338	Acad11	acyl-Coenzyme A dehydrogenase family, member 11
1456741_s_at	0.016	1.69E-4	-5.156	1.082	-1.333	1.333	Gpm6a	glycoprotein m6a
1450380_at	0.027	4.77E-4	-4.585	0.079	-1.324	1.324	Epdr1	ependymin related protein 1 (zebrafish)
1437405_a_at	0.013	1.24E-4	5.334	1.385	1.323	1.323	Igfbp4	insulin-like growth factor binding protein 4
1417298_at	0.027	4.80E-4	-4.582	0.073	-1.322	1.322	Ebpl	emopamil binding protein-like
1452621_at	0.028	4.97E-4	-4.562	0.038	-1.320	1.320	Pcbd2	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2
1418737_at	0.019	2.45E-4	-4.950	0.724	-1.309	1.309	Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2
1433581_at	0.008	5.15E-5	-5.843	2.227	-1.309	1.309	1190002N15Rik	RIKEN cDNA 1190002N15 gene
1425102_a_at	0.028	5.27E-4	-4.531	-0.018	-1.309	1.309	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
1436448_a_at	0.049	1.45E-3	3.996	-0.996	1.307	1.307	Ptgs1	prostaglandin-endoperoxide synthase 1
1418327_at	0.004	1.64E-5	-6.541	3.316	-1.307	1.307	Sdhaf4	succinate dehydrogenase complex assembly factor 4
1417170_at	0.022	3.29E-4	-4.787	0.438	-1.306	1.306	Lztfl1	leucine zipper transcription factor-like 1
1448647_at	0.034	7.55E-4	4.339	-0.366	1.304	1.304	Man2a1	mannosidase 2, alpha 1
1438169_a_at	0.007	3.89E-5	-6.010	2.494	-1.301	1.301	Frmd4b	FERM domain containing 4B
1450044_at	0.015	1.66E-4	-5.168	1.101	-1.296	1.296	Fzd7	frizzled class receptor 7
1448888_at	0.014	1.35E-4	-5.282	1.297	-1.294	1.294	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7
1415916_a_at	0.007	4.08E-5	-5.982	2.449	-1.294	1.294	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase
1424615_at	0.005	2.35E-5	-6.317	2.974	-1.292	1.292	Pgap2	post-GPI attachment to proteins 2
1449731_s_at	0.004	1.51E-5	6.594	3.395	1.291	1.291	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha
1449059_a_at	0.002	5.63E-6	-7.236	4.325	-1.289	1.289	Oxct1	3-oxoacid CoA transferase 1
1419193_a_at	0.046	1.27E-3	4.064	-0.871	1.287	1.287	Gm9835///Gmfg	predicted pseudogene 9835///glia maturation factor, gamma
1428331_at	0.008	5.20E-5	-5.837	2.217	-1.287	1.287	2210016F16Rik	RIKEN cDNA 2210016F16 gene
1419194_s_at	0.001	1.36E-6	8.227	5.639	1.287	1.287	Gm9835///Gmfg	predicted pseudogene 9835///glia maturation factor, gamma
1454086_a_at	0.011	8.87E-5	-5.524	1.704	-1.287	1.287	Lmo2	LIM domain only 2
1417011_at	0.038	8.63E-4	-4.268	-0.496	-1.284	1.284	Sdc2	syndecan 2

1452160_at	0.022	3.22E-4	4.799	0.460	1.282	1.282	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase
1438427_at	0.048	1.39E-3	4.018	-0.955	1.277	1.277	Fam120b	family with sequence similarity 120, member B
1427132_at	0.017	2.01E-4	5.058	0.913	1.270	1.270	Sbf2	SET binding factor 2
1448474_at	0.033	6.70E-4	4.403	-0.250	1.270	1.270	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7
1431339_a_at	0.015	1.53E-4	5.212	1.177	1.269	1.269	Efhd2	EF hand domain containing 2
1437765_at	0.045	1.23E-3	-4.080	-0.839	-1.269	1.269	Cpeb3	cytoplasmic polyadenylation element binding protein 3
1428140_at	0.024	4.01E-4	-4.679	0.246	-1.268	1.268	Oxct1	3-oxoacid CoA transferase 1
1447977_x_at	0.048	1.40E-3	-4.014	-0.961	-1.264	1.264	Gm4724///Gm14308///0610010B08Rik///Gm14434///Gm14430	predicted gene 4724///predicted gene 14308///RIKEN cDNA 0610010B08 gene///predicted gene 14434///predicted gene 14430
1451526_at	0.048	1.39E-3	-4.018	-0.954	-1.264	1.264	Arhgap12	Rho GTPase activating protein 12
1423452_at	0.008	5.22E-5	5.835	2.214	1.262	1.262	Stk17b	serine/threonine kinase 17b (apoptosis-inducing)
1418674_at	0.038	8.76E-4	4.260	-0.510	1.258	1.258	Osmr	oncostatin M receptor
1436890_at	0.047	1.28E-3	-4.061	-0.876	-1.257	1.257	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1
1417953_at	0.004	1.14E-5	-6.774	3.661	-1.256	1.256	Fam3c	family with sequence similarity 3, member C
1455013_at	0.012	1.04E-4	5.435	1.555	1.254	1.254	Arih2	ariadne RBR E3 ubiquitin protein ligase 2
1426221_at	0.011	9.04E-5	-5.513	1.685	-1.254	1.254	Vwa5a	von Willebrand factor A domain containing 5A
1416926_at	0.012	1.12E-4	5.389	1.478	1.252	1.252	Trp53inp1	transformation related protein 53 inducible nuclear protein 1
1417113_at	0.042	1.04E-3	-4.171	-0.673	-1.250	1.250	Gmcl1	germ cell-less, spermatogenesis associated 1
1448454_at	0.024	3.89E-4	-4.695	0.275	-1.246	1.246	Srsf6	serine/arginine-rich splicing factor 6
1424988_at	0.034	7.07E-4	4.374	-0.302	1.245	1.245	Mylip	myosin regulatory light chain interacting protein
1420024_s_at	0.002	3.66E-6	7.529	4.727	1.245	1.245	Etf1	eukaryotic translation termination factor 1
1430838_x_at	0.014	1.47E-4	5.237	1.219	1.245	1.245	Mbd1	methyl-CpG binding domain protein 1
1437999_x_at	0.049	1.41E-3	-4.009	-0.972	-1.238	1.238	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q
1424183_at	0.001	1.21E-6	-8.312	5.745	-1.235	1.235	Acat1	acetyl-Coenzyme A acetyltransferase 1
1426721_s_at	0.029	5.46E-4	4.512	-0.052	1.234	1.234	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase

1417985_at	0.048	1.36E-3	-4.028	-0.936	-1.232	1.232	Nrarp	Notch-regulated ankyrin repeat protein
1435137_s_at	0.004	1.17E-5	6.757	3.637	1.232	1.232	A130040M12Rik///1200015M12Rik	RIKEN cDNA A130040M12 gene///RIKEN cDNA 1200015M12 gene
1426913_at	0.047	1.29E-3	4.055	-0.886	1.231	1.231	Lss	lanosterol synthase
1417346_at	0.042	1.04E-3	4.168	-0.679	1.229	1.229	Pycard	PYD and CARD domain containing
1435537_at	0.038	9.06E-4	-4.242	-0.543	-1.228	1.228	Ptprd	protein tyrosine phosphatase, receptor type, D
1436838_x_at	0.025	4.16E-4	4.660	0.212	1.222	1.222	Cotl1	coactosin-like 1 (Dictyostelium)
1425476_at	0.042	1.04E-3	-4.171	-0.673	-1.220	1.220	Col4a5	collagen, type IV, alpha 5
1417491_at	0.047	1.33E-3	4.040	-0.914	1.219	1.219	Ctsb	cathepsin B
1418658_at	0.028	5.14E-4	-4.545	0.006	-1.215	1.215	Rmdn1	regulator of microtubule dynamics 1
1452170_at	0.047	1.35E-3	4.033	-0.927	1.211	1.211	Chpf2	chondroitin polymerizing factor 2
1451271_a_at	0.047	1.33E-3	-4.040	-0.913	-1.202	1.202	Acat1	acetyl-Coenzyme A acetyltransferase 1
1427492_at	0.047	1.30E-3	-4.053	-0.890	-1.202	1.202	Pof1b	premature ovarian failure 1B
1425977_a_at	0.036	8.13E-4	4.300	-0.437	1.201	1.201	Slk	STE20-like kinase
1417205_at	0.047	1.29E-3	4.056	-0.885	1.200	1.200	Kdelr2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
1416859_at	0.015	1.59E-4	-5.192	1.144	-1.198	1.198	Fkbp3	FK506 binding protein 3
1423489_at	0.004	1.44E-5	-6.626	3.442	-1.197	1.197	Mmd	monocyte to macrophage differentiation-associated
1418862_at	0.045	1.18E-3	-4.104	-0.796	-1.192	1.192	Echdc3	enoyl Coenzyme A hydratase domain containing 3
1455204_at	0.038	8.72E-4	-4.263	-0.505	-1.190	1.190	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
1417211_a_at	0.001	8.46E-7	-8.578	6.071	-1.190	1.190	1110032A03Rik	RIKEN cDNA 1110032A03 gene
1456064_at	0.033	6.85E-4	-4.391	-0.271	-1.188	1.188	AI504432	expressed sequence AI504432
1430526_a_at	0.004	1.27E-5	-6.703	3.557	-1.185	1.185	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
1431359_a_at	0.041	9.80E-4	4.201	-0.619	1.185	1.185	Card19	caspase recruitment domain family, member 19
1416778_at	0.003	8.83E-6	-6.939	3.903	-1.183	1.183	Sdpr	serum deprivation response
1417966_at	0.019	2.42E-4	-4.955	0.734	-1.182	1.182	Mrpl39	mitochondrial ribosomal protein L39
1415678_at	0.028	5.03E-4	4.556	0.027	1.182	1.182	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform
1424051_at	0.039	9.45E-4	4.220	-0.583	1.175	1.175	Col4a2	collagen, type IV, alpha 2
1452128_a_at	0.020	2.81E-4	-4.874	0.592	-1.172	1.172	Brcc3	BRCA1/BRCA2-containing complex, subunit 3
1450869_at	0.043	1.07E-3	-4.157	-0.699	-1.170	1.170	Fgf1	fibroblast growth factor 1
1417834_at	0.017	2.02E-4	-5.057	0.911	-1.168	1.168	Synj2bp	synaptojanin 2 binding protein

1416824_at	0.007	3.63E-5	-6.052	2.560	-1.165	1.165	B230118H07Rik	RIKEN cDNA B230118H07 gene
1448020_at	0.049	1.41E-3	4.010	-0.970	1.165	1.165	Rap1a	RAS-related protein-1a
1427982_s_at	0.006	2.95E-5	-6.179	2.760	-1.164	1.164	Syne2	spectrin repeat containing, nuclear envelope 2
1419615_at	0.031	6.06E-4	4.456	-0.153	1.161	1.161	Trpv6	transient receptor potential cation channel, subfamily V, member 6
1419164_at	0.023	3.66E-4	-4.729	0.335	-1.159	1.159	Zfp260	zinc finger protein 260
1449799_s_at	0.018	2.23E-4	-5.002	0.815	-1.159	1.159	Pkp2	plakophilin 2
1418506_a_at	0.034	7.37E-4	-4.352	-0.342	-1.155	1.155	Prdx2	peroxiredoxin 2
1451381_at	0.014	1.41E-4	-5.257	1.255	-1.154	1.154	Aamdc	adipogenesis associated Mth938 domain containing
1427278_at	0.041	9.85E-4	4.198	-0.624	1.152	1.152	Clip4	CAP-GLY domain containing linker protein family, member 4
1452374_at	0.039	9.30E-4	-4.228	-0.568	-1.150	1.150	Zfp322a	zinc finger protein 322A
1417836_at	0.010	7.03E-5	-5.660	1.928	-1.150	1.150	Gpx7	glutathione peroxidase 7
1454959_s_at	0.018	2.23E-4	-5.002	0.815	-1.148	1.148	Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1
1434036_at	0.030	5.78E-4	-4.482	-0.107	-1.148	1.148	Mtss1	metastasis suppressor 1
1429144_at	0.032	6.50E-4	4.419	-0.221	1.148	1.148	Gpcpd1	glycerophosphocholine phosphodiesterase 1
1448208_at	0.001	8.98E-7	8.534	6.017	1.147	1.147	Smad1	SMAD family member 1
1426748_s_at	0.034	7.15E-4	-4.368	-0.314	-1.142	1.142	Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3
1434745_at	0.032	6.35E-4	-4.431	-0.199	-1.139	1.139	Ccnd2	cyclin D2
1438855_x_at	0.039	9.35E-4	4.225	-0.574	1.139	1.139	Tnfaip2	tumor necrosis factor, alpha-induced protein 2
1419494_a_at	0.022	3.22E-4	4.798	0.458	1.132	1.132	Tpd52	tumor protein D52
1436747_at	0.020	2.91E-4	4.854	0.556	1.130	1.130	Gm7367///Ubald2	1110014K08Rik pseudogene///UBA-like domain containing 2
1416844_at	0.011	8.70E-5	-5.535	1.722	-1.129	1.129	Prmt2	protein arginine N-methyltransferase 2
1422660_at	0.004	1.42E-5	6.633	3.453	1.126	1.126	Gm15453///Rbm3	predicted gene 15453///RNA binding motif protein 3
1437932_a_at	0.020	2.93E-4	-4.850	0.549	-1.121	1.121	Cldn1	claudin 1
1433741_at	0.043	1.08E-3	4.148	-0.714	1.119	1.119	Cd38	CD38 antigen
1460555_at	0.029	5.42E-4	4.516	-0.045	1.118	1.118	Fam65b	family with sequence similarity 65, member B
1417339_a_at	0.013	1.28E-4	-5.314	1.350	-1.118	1.118	Dynll1	dynein light chain LC8-type 1
1448229_s_at	0.018	2.27E-4	-4.992	0.797	-1.116	1.116	Ccnd2	cyclin D2

1460631_at	0.011	9.13E-5	-5.507	1.676	-1.107	1.107	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
1437313_x_at	0.006	3.35E-5	6.100	2.636	1.106	1.106	Hmgb2	high mobility group box 2
1428090_at	0.008	4.74E-5	-5.893	2.306	-1.104	1.104	Ptcd3	pentatricopeptide repeat domain 3
1450391_a_at	0.018	2.30E-4	-4.984	0.784	-1.104	1.104	Mgll	monoglyceride lipase
1455171_at	0.022	3.36E-4	4.775	0.417	1.103	1.103	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)
1434882_at	0.012	1.05E-4	5.428	1.544	1.102	1.102	Mtdh	metadherin
1418261_at	0.032	6.35E-4	4.431	-0.199	1.101	1.101	Syk	spleen tyrosine kinase
1451052_at	0.045	1.23E-3	-4.081	-0.838	-1.099	1.099	Cog8///Pdf	component of oligomeric golgi complex 8///peptide deformylase (mitochondrial)
1417291_at	0.000	1.16E-9	14.775	11.535	1.097	1.097	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a
1428529_at	0.017	2.07E-4	5.043	0.886	1.094	1.094	Snhg5	small nucleolar RNA host gene 5
1451206_s_at	0.020	2.68E-4	4.900	0.638	1.093	1.093	Cytip	cytohesin 1 interacting protein
1417174_at	0.033	6.67E-4	-4.405	-0.245	-1.083	1.083	Tmem218	transmembrane protein 218
1456125_a_at	0.002	3.70E-6	-7.521	4.716	-1.083	1.083	Dynll1	dynein light chain LC8-type 1
1422675_at	0.016	1.72E-4	5.145	1.063	1.082	1.082	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
1450939_at	0.031	6.20E-4	4.444	-0.175	1.081	1.081	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1
1448665_at	0.037	8.28E-4	-4.290	-0.455	-1.077	1.077	Dmd	dystrophin, muscular dystrophy
1417568_at	0.038	8.91E-4	-4.251	-0.526	-1.075	1.075	Ncald	neurocalcin delta
1436158_at	0.034	7.30E-4	4.357	-0.334	1.073	1.073	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2
1420592_a_at	0.022	3.42E-4	4.766	0.402	1.068	1.068	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
1423831_at	0.034	7.20E-4	-4.364	-0.321	-1.063	1.063	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
1451489_at	0.042	1.03E-3	-4.172	-0.671	-1.061	1.061	Slc25a35	solute carrier family 25, member 35
1450098_at	0.008	4.97E-5	5.864	2.261	1.053	1.053	Hoga1	4-hydroxy-2-oxoglutarate aldolase 1
1433954_at	0.034	7.23E-4	-4.362	-0.324	-1.047	1.047	Brip1os	BRCA1 interacting protein C-terminal helicase 1, opposite strand
1455959_s_at	0.041	9.97E-4	4.192	-0.635	1.041	1.041	Gclc	glutamate-cysteine ligase, catalytic subunit
1416831_at	0.044	1.13E-3	4.124	-0.759	1.040	1.040	Neu1	neuraminidase 1
1434499_a_at	0.003	7.58E-6	-7.039	4.046	-1.040	1.040	Ldhb	lactate dehydrogenase B
1455972_x_at	0.001	1.60E-6	-8.110	5.490	-1.036	1.036	Hadh	hydroxyacyl-Coenzyme A dehydrogenase

1437406_x_at	0.034	7.50E-4	4.342	-0.360	1.036	1.036	Igfbp4	insulin-like growth factor binding protein 4
1423829_at	0.002	2.88E-6	7.693	4.948	1.035	1.035	Fam49b	family with sequence similarity 49, member B
1416974_at	0.044	1.14E-3	4.121	-0.766	1.034	1.034	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2
1450784_at	0.013	1.26E-4	-5.322	1.365	-1.033	1.033	Reck	reversion-inducing-cysteine-rich protein with kazal motifs
1452320_at	0.049	1.44E-3	-4.000	-0.988	-1.028	1.028	Lrp2	low density lipoprotein receptor-related protein 2
1434690_at	0.008	4.54E-5	-5.918	2.347	-1.026	1.026	Lclat1	lysocardiolipin acyltransferase 1
1425364_a_at	0.004	1.39E-5	6.645	3.471	1.025	1.025	Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
1449221_a_at	0.042	1.03E-3	4.174	-0.667	1.025	1.025	Rrbp1	ribosome binding protein 1
1424616_s_at	0.045	1.21E-3	-4.088	-0.825	-1.024	1.024	Pgap2	post-GPI attachment to proteins 2
1423806_at	0.017	2.05E-4	-5.049	0.897	-1.022	1.022	Ints4	integrator complex subunit 4
1452291_at	0.045	1.22E-3	-4.086	-0.828	-1.020	1.020	Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
1420628_at	0.015	1.62E-4	-5.180	1.123	-1.013	1.013	Pura	purine rich element binding protein A
1452395_at	0.005	2.26E-5	-6.342	3.013	-1.011	1.011	Med19	mediator complex subunit 19
1449377_at	0.011	7.87E-5	-5.594	1.819	-1.010	1.010	Nicn1	nicolin 1
1431055_a_at	0.033	6.89E-4	4.388	-0.277	1.010	1.010	Snx10	sorting nexin 10
1460193_at	0.003	1.05E-5	-6.826	3.738	-1.008	1.008	St13	suppression of tumorigenicity 13
1416858_a_at	0.012	1.03E-4	-5.438	1.560	-1.005	1.005	Fkbp3	FK506 binding protein 3