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“JÚLIO DE MESQUITA FILHO”
FACULDADE DE MEDICINA VETERINÁRIA
CÂMPUS DE ARAÇATUBA**

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**ANÁLISE DO POTENCIAL REGULATÓRIO DE RNAs
LONGOS NÃO-CODIFICADORES EM MACRÓFAGOS DE
CAMUNDONGOS INFECTADOS COM *Leishmania major***

**ARAÇATUBA - SP
2022**

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Tese apresentada à Faculdade de Medicina Veterinária de Araçatuba – UNESP, Campus de Araçatuba, como parte das exigências para a obtenção do título de Doutora em Ciência Animal (Medicina Veterinária Preventiva e Produção Animal).

Orientadora: Prof^ª. Dra. Flávia Lombardi Lopes

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AUTORA: FLÁVIA REGINA FLORENCIO DE ATHAYDE

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Araçatuba, 11 de fevereiro de 2022.

*Ao meu avô Arandy (in memoriam), grande fonte
de inspiração para a minha caminhada
acadêmica.*

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“É a dedicação ao trabalho que distingue um indivíduo do outro; não acredito em talentos”

Euryclides de Jesus Zerbini

Athayde, F.R.F. **Análise do potencial regulatório de RNAs longos não-codificadores em macrófagos de camundongos infectados com *Leishmania major***. 2022, 126f. Tese (Doutorado) - Faculdade de Medicina Veterinária, Universidade Estadual Paulista, Araçatuba, 2022.

RESUMO

A leishmaniose é uma doença endêmica sendo comum em regiões pobres de países em desenvolvimento. Essa parasitose é causada por protozoários do gênero *Leishmania*, pertencentes à família Trypanosomatidae e responsável pela segunda maior taxa de mortalidade mundial. Dentre os hospedeiros vertebrados há uma grande variedade de mamíferos, e a transmissão ocorre principalmente por meio da picada de fêmeas de flebotomíneos do gênero *Lutzomyia*, principais vetores no Brasil. Nos hospedeiros mamíferos a forma amastigota intracelular coloniza principalmente os macrófagos, os quais atuam na eliminação do patógeno. Contudo, para se manter vivo, o parasita evita os mecanismos de defesa, os quais podem ser regulados por processos epigenéticos dos macrófagos. Dentre esses, destacam-se os RNAs longos não-codificadores (lncRNA), que apresentam diversas funções incluindo o controle da expressão de genes alvos próximos ou distantes. Considerando a capacidade regulatória deste protozoário, identificar a relação na expressão de lncRNAs e seus possíveis alvos, em macrófagos infectados com *Leishmania*, é importante para o entendimento do papel dos processos epigenéticos no diálogo parasita-hospedeiro, na leishmaniose.

Palavras-Chave: lncRNAs, leishmaniose, macrófago, epigenética.

Athayde, F.R.F. **Analysis of regulatory potential of long non-coding RNAs in macrophages of mice following infection by *Leishmania major***. 2022, 126f. Tese (Doutorado) - Faculdade de Medicina Veterinária, Universidade Estadual Paulista, Araçatuba, 2022.

ABSTRACT

Leishmaniasis an endemic disease common in poor regions of developing countries, caused by protozoa of the genus *Leishmania*, belonging to the Trypanosomatidae family, it is the parasitic disease responsible for the second highest mortality rate worldwide. Among the vertebrate hosts there is a wide variety of mammals, and transmission occurs mainly by the bite of female sandflies of the genus *Lutzomyia*, the most important vector in Brazil. In mammalian hosts, the intracellular amastigote form colonizes mainly macrophages, which try to eliminate the pathogen. However, to stay alive, the parasite avoids the macrophage defense mechanisms, which can be regulated by epigenetic processes. Among these, long non-coding RNAs (lncRNA) several roles, including controlling the paly expression of nearby or distant target genes. Considering the lncRNA capacity for gene regulation, understanding the relationship of lncRNAs and their possible targets, in macrophages infected with *Leishmania*, is important in to understand the role of epigenetic processes in the host-parasite relationship *Leishmaniasis*.

Keywords: lncRNAs, leishmaniasis, macrophage, epigenetics.

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1 INTRODUÇÃO GERAL

A leishmaniose é uma doença tropical negligenciada, causada por protozoários do gênero *Leishmania*, pertencentes à família Trypanosomatidae, da ordem dos Kinetoplastida. A doença apresenta distribuição mundial abrangendo, no Novo Mundo, as Américas Central e Sul e, no Velho Mundo, principalmente a África, parte da Europa e a Ásia (BATES, 2007; DESJEUX, 2004). É endêmica em 98 países, acomete humanos e várias espécies animais, inclusive os domésticos. Atualmente mais de um bilhão de pessoas correm risco de infecção por leishmaniose ao viverem em áreas endêmicas (WHO, 2022).

As leishmanioses apresentam manifestações clínicas diversas, as quais podem ser genericamente categorizados em três tipos: (i) leishmaniose visceral (LV), na qual os parasitas se proliferam no fígado, baço e medula óssea, resultando em imunossupressão do hospedeiro; (ii) leishmaniose cutânea (LC), em que os parasitas permanecem no local de infecção causando ulcerações localizadas; e (iii) leishmaniose mucocutânea (LMC), com destruição crônica do tecido da mucosa (DESJEUX, 2004). A estimativa de novos casos anuais é entre 700.000 a 1 milhão, sendo a LV uma das principais doenças parasitárias com potencial de surto e mortalidade (WHO, 2022).

O gênero *Leishmania* abrange mais de 20 espécies, sendo classificado em dois subgêneros baseados no local de desenvolvimento das formas promastigotas do parasita no trato digestório dos flebotomíneos fêmeas (PACE, 2014). O subgênero *Leishmania* para os parasitas que se desenvolvem na região suprapilária; e *Viannia* para os com desenvolvimento na região do piloro e seção peripilária (LAINSON; SHAW, 1987) (Figura 1). Esta classificação de subgêneros é corroborada por análises filogenéticas (NOYES et al., 2002). A *Leishmania major* pertence ao subgênero *Leishmania* e é um dos agentes causadores da leishmaniose cutânea no Velho Mundo. Esta manifestação clínica é a mais comum, podendo ocorrer lesões na pele em diferentes partes do corpo, cerca de 1 milhão de pessoas são infectadas anualmente (AL-BAJALAN et al., 2021; GUREL; TEKIN; UZUN, 2020; WHO, 2022).

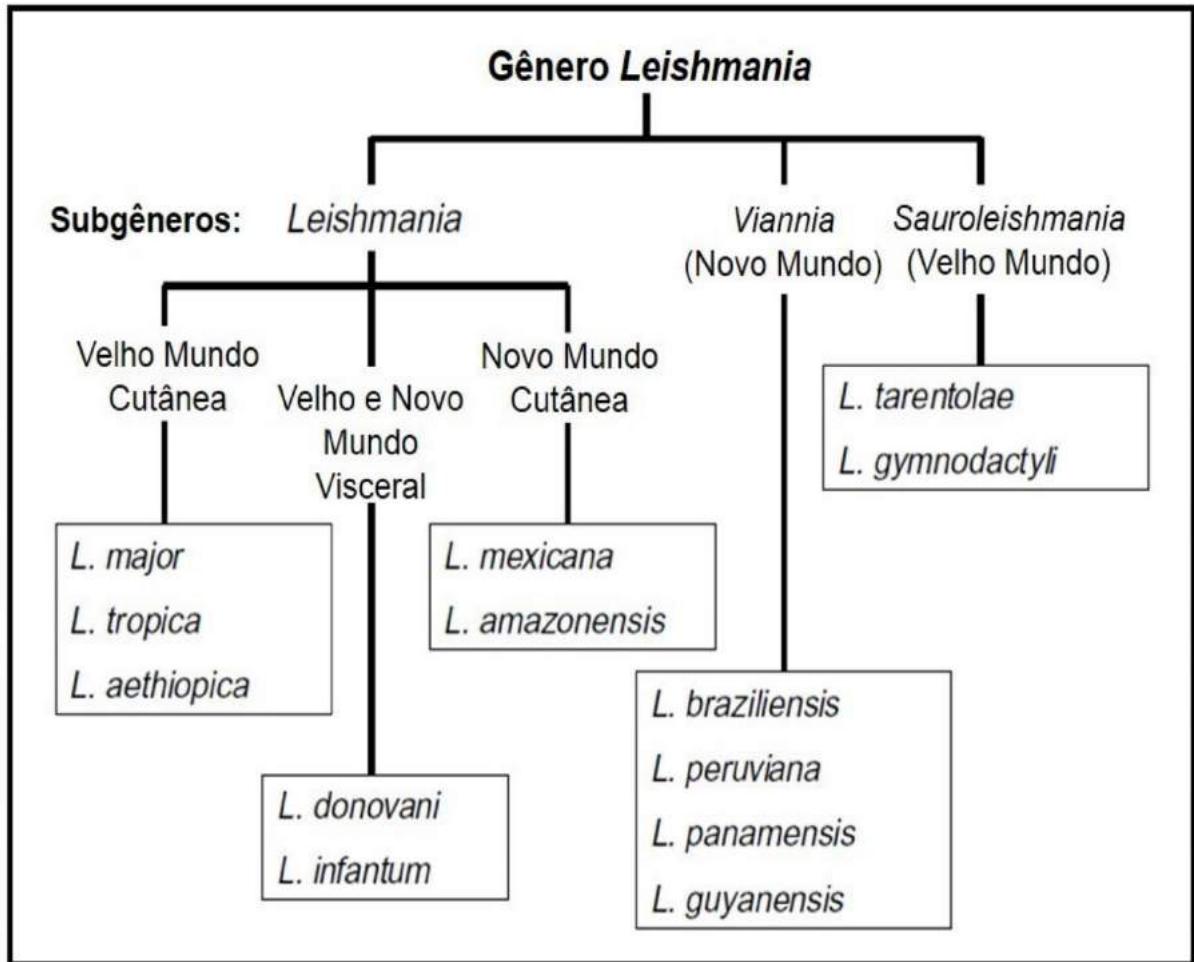


Figura 1 - Classificação das espécies de *Leishmania* em subgênero adaptado de BATES (2007), incluindo informações das formas clínicas e distribuição geográfica. Parasitas nos subgêneros *Leishmania* e *Viannia* infectam mamíferos, enquanto que a *Sauroleishmania* infecta répteis como seus hospedeiros vertebrados.

O ciclo de vida da *Leishmania* é digenético, ou seja, no seu vetor ocorre a forma extracelular chamada de promastigota e, nos hospedeiros mamíferos, a forma amastigota intracelular colonizando células que fazem a fagocitose, principalmente os macrófagos (ANTOINE et al., 1998; KATEBI et al., 2021; LIU; UZONNA, 2012; RESTREPO et al., 2021). Dentro destas células os patógenos sobrevivem e se replicam dando continuidade ao ciclo, quando macrófagos infectados são ingeridos pelo vetor (BATES, 2007) (Figura 2). Os macrófagos, células responsáveis pela fagocitose de agentes exógenos como os patógenos, também reciclam nutrientes, digerindo resíduos teciduais, e eliminam células apoptóticas, sendo consideradas

células do sistema imune localizadas em vários tecidos, com funções de desenvolvimento e imunidade (DUQUE; DESCOTEAUX, 2014; SIEWEKE; ALLEN, 2013).

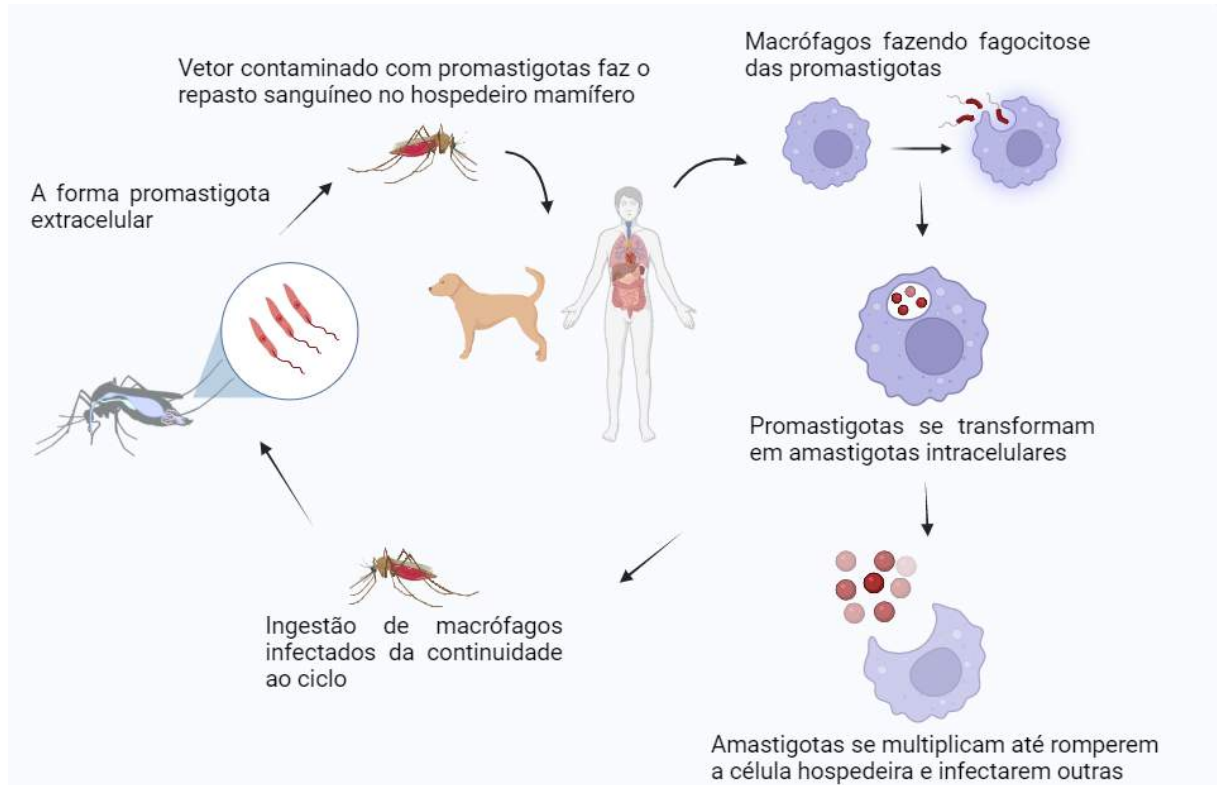


Figura 2 – Esquema exemplificando o ciclo biológico de *Leishmania* criado com BioRender.com.

A resposta imune pode ser ativada por uma variedade de estímulos, pois os macrófagos são capazes de alterar rapidamente o seu perfil funcional por meio de um processo definido como polarização, em que adquirem um fenótipo funcional específico (VIOLA et al., 2019). Os perfis de ativação são programados com a expressão de genes específicos, os quais levam a adaptações metabólicas, secreção de citocinas específicas e aquisição de diferentes marcadores na superfície celular. Estes perfis são apresentados, classicamente, por macrófagos ativos, pró-inflamatórios ou M1 (NATHAN et al., 1983; PACE et al., 1983), e alternativamente, por macrófagos anti-inflamatórios ou M2 (DOYLE et al., 1994; STEIN et al., 1992) (Figura 3).

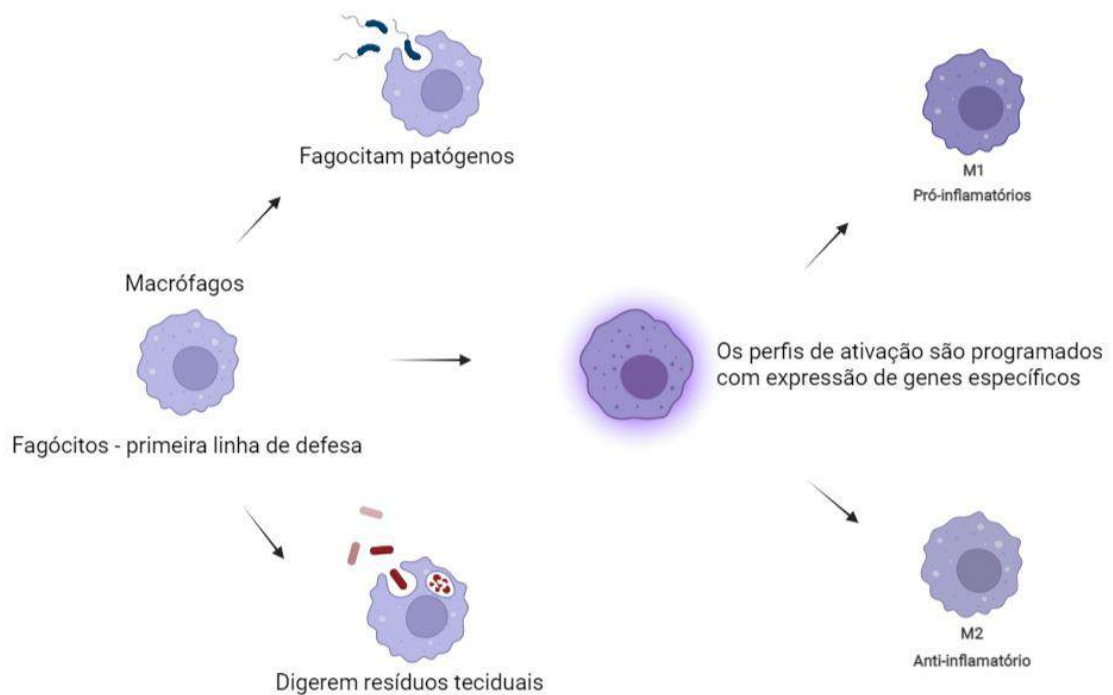


Figura 3 – Esquema exemplificando a ativação do macrófago criado com BioRender.com.

Diferentes respostas imune do hospedeiro têm sido caracterizadas em modelos de macrófagos murinos infectados com *Leishmania*, afetando diretamente a gravidade da doença (REINER; LOCKSLEY, 1995; SCHARTON-KERSTEN; SCOTT, 1995). A produção de citocina pela célula T helper 1 (Th1) tem como consequência a ativação clássica do macrófago (M1), em que a secreção de radicais de nitrogênio e espécies reativas de oxigênio (ROS) inibem a proliferação celular para reparação do tecido; ou um fenótipo alternativo (M2), com a célula tipo T helper 2 (Th2), envolvendo inibição de sinais pró-inflamatórios e, consequentemente, promovendo proliferação celular para reparação do tecido afetado. Como consequência, o fenótipo M2, é associado à progressão da leishmaniose, com aumento do número de parasitos no hospedeiro (MILLS, 2012; MILLS et al., 2000; RESTREPO et al., 2021).

A ativação de macrófagos pode ser controlada por processos epigenéticos, responsáveis por controlar a transcrição e tradução dos genes e, consequentemente, modular a expressão de genes específicos. Esses processos epigenéticos são conduzidos por modificações químicas e reversíveis no DNA e histonas, bem como pela ativação de RNAs não-codificadores, gerando assim

padrões de expressão gênica específicos para células e tecidos, indispensáveis aos processos fisiológicos de desenvolvimento e equilíbrio do corpo (TUONG et al., 2021). Os RNAs não-codificadores (ncRNA) atuam em todos os níveis de controle da expressão gênica, como transcrição, processamento de RNA e tradução (CECH; STEITZ, 2014).

Uma das classes de ncRNA que ganhou destaque ao ser apontada como reguladora no desenvolvimento de respostas imunes e inflamatórias, são os RNAs não codificadores pequenos ou microRNAs (miRNA), com o tamanho entre 21-22 nucleotídeos, que regulam a expressão gênica pós-transcricional (ALAM; O'NEILL, 2011; BARTEL, 2009). Esta regulação é feita através da ligação dos miRNAs a genes alvos que podem estar associados à regulação da resposta imune de um hospedeiro infectado (HAMIDI et al., 2021; LODISH et al., 2008). É o caso da polarização do macrófago, em que a programação do fenótipo está diretamente relacionada à ativação ou não da resposta inflamatória, podendo ser controlada por microRNAs (SELF-FORDHAM et al., 2017; TERRY; MILLER, 2014; TOMIOTTO-PELLISSIER et al., 2018), os quais têm a capacidade de atingir centenas de genes alvos envolvidos no perfil de ativação do macrófago (EL GAZZAR et al., 2011; GRAFF et al., 2012).

Outra classe de ncRNA que merece destaque são os RNAs longos não-codificadores (lncRNA) de tamanho superior a 200 nucleotídeos e que, apesar de transcritos pela RNA polimerase II como outros RNAs mensageiros (mRNA), não são traduzidos em proteínas funcionais (BHAT et al., 2016; STATELLO et al., 2021). Os lncRNAs podem funcionar como ativadores ou inibidores da transcrição, RNA antisense ou esponjas de miRNA, nos mais diversos contextos fisiológicos e patológicos (CECH; STEITZ, 2014).

A regulação da expressão de genes exercida por lncRNAs pode ser cis, quando um lncRNA regula genes próximos ao local de sua transcrição, ou trans, quando um lncRNA regula genes em posições distantes à sua própria origem (LEE; BARTOLOMEI, 2013; RINN et al., 2007; STATELLO et al., 2021; XIE et al., 2019). Em macrófagos derivados da medula óssea de camundongos, a ativação por lipopolissacarídeos (LPS) induz na resposta clássica (M1), e estudos mostraram que o *lncRNA-Nfkb2* e o *lncRNA-Rel* são regulados positivamente durante essa ativação,

e co-regulados com a resposta inflamatória (MAO; SHEN; ZUO, 2015). O lncRNA *lincRNA-Tnfaip3*, também testado em macrófagos murinos ativados por LPS, atua como um co-regulador de *NF-κB* para modular a transcrição de genes inflamatórios, ao suprimir genes como *Il6*, *Tnfaip3* e *Icam1* (MA et al., 2017).

Outro lncRNA com função descrita em macrófagos murinos é o *lncRNA-Ccl2*, que foi regulado positivamente após inibição induzida por LPS à expressão da Sirtuina 1 (SIRT1), uma histona desacetilase, que inibe a produção de citocinas pro-inflamatórias em macrófagos (JIA et al., 2018; YANG et al., 2015). Em macrófagos silenciados para o lncRNA *lincRNA-Cox2*, foi possível observar tanto a ativação como repressão de genes relacionados à resposta imune, como o aumento da expressão de quimiocinas *Ccl5*, *Cx3cll*, receptores de quimiocinas *Ccr1* e genes estimulados por interferon *Irf7*, *Ifi204* e *Isg15* e também a diminuição da expressão de genes que incluem *Tlr1*, *Il6* e *Il23a* (CARPENTER et al., 2015). Além dos estudos utilizando LPS e o silenciamento de ncRNAs em células do sistema imune, o envolvimento de lncRNAs em algumas infecções já descrito.

O lncRNA *Mir17hg* foi observado em grande quantidade em macrófagos de camundongos infectados por *Toxoplasma gondii*, um protozoário distribuído globalmente que causa infecção assintomática ao longo da vida em humanos. Este lncRNA é conservado, e codifica o agrupamento de genes do microRNA mir17, previamente observado na regulação negativa da apoptose da célula hospedeira na infecção por *T. gondii* (MENARD; BU; DENKERS, 2021). Ademais, *Leishmania donovani*, responsável por causar leishmaniose visceral, foi usada para infectar camundongos KO para o lncRNA *Malat1*, resultando em menor carga parasitária e expressão reduzida de *Il-10* em células T CD4⁺ do baço (HEWITSON et al., 2020).

Sendo assim, a ativação dos macrófagos contra patógenos também é suscetível ao controle epigenético, contudo a expressão de lncRNAs em macrófagos infectados com *Leishmania* ainda é desconhecida. Com objetivo de explorar o papel da regulação epigenética mediada por lncRNAs na resposta imune do hospedeiro após a infecção por *Leishmania*, o presente estudo buscou investigar a expressão de lncRNAs em macrófagos de camundongos infectados com *Leishmania major*, prevendo e classificando seus possíveis alvos de mRNA e as vias biológicas destes alvos.

2 CAPÍTULO 1 - ANALYSIS OF THE REGULATORY POTENTIAL OF LONG NON-CODING RNAs IN MURINE MACROPHAGES FOLLOWING INFECTION BY *Leishmania major*

Full title:

Analysis of the regulatory potential of long non-coding RNAs in murine macrophages following infection by *Leishmania major*

Short title: LncRNA modulation in macrophages infected by *L. major*

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2.1 Resumo

A leishmaniose é uma doença tropical negligenciada de distribuição mundial, causada por um protozoário do gênero *Leishmania*. Em hospedeiros mamíferos, os protozoários podem colonizar macrófagos desencadeando a resposta imune do hospedeiro. Sabe-se que as respostas imunes podem ser moduladas por mediadores epigenéticos como os RNAs não codificadores (ncRNAs), e diversos patógenos podem afetar essa modulação. Nosso objetivo foi avaliar a expressão de ncRNAs longos (lncRNAs) em macrófagos murinos após infecção *in vitro* com *Leishmania major*. Em nosso estudo, empregamos dados de sequenciamento de RNA, previamente gerados a partir de macrófagos murinos infectados *in vitro* com *L. major*, para realizar análise de expressão diferencial para lncRNAs e mRNAs. Descobrimos que a infecção por *L. major* altera significativamente a expressão de 296 lncRNAs em macrófagos em comparação com o controle não infectado. Ao combinar a previsão de alvos, análise de co-expressão de lncRNA-alvo e análise de enriquecimento de vias de alvos cis e trans correlacionados, encontramos um enriquecimento significativo de vias relacionadas à ativação da resposta imune, sugerindo que a infecção de macrófagos por *L. major* pode afetar a regulação epigenética mediado por lncRNAs durante a interação parasita-hospedeiro. Esses achados podem auxiliar na busca contínua por tratamentos mais eficazes para essa doença.

Palavras-Chave: Leishmaniose, resposta imune, parasita-hospedeiro, lncRNA, cis/trans alvos.

2.2 Abstract

Leishmaniasis is a neglected tropical disease distributed worldwide, caused by a protozoa of the genus *Leishmania*. In mammalian hosts, the protozoa can colonize macrophages triggering host immune response. It is known that immune responses can be modulated by epigenetic mediators such as non-coding RNAs (ncRNAs), and several pathogens can affect this modulation. Our objective was to evaluate the expression of long ncRNAs (lncRNAs) in murine macrophages following *in vitro* infection with *L. major*. In our study, we employed RNA sequencing data, previously generated from murine macrophages infected *in vitro* with *L. major*, to perform differential expression analysis for lncRNAs and mRNAs. We found that *L. major* infection significantly alters the expression of 296 lncRNAs in macrophages compared to uninfected control. By combining target prediction, lncRNA-target co-expression analysis, and pathway enrichment analysis of correlated cis and trans targets, we found a significant enrichment of pathways related to immune response activation, suggesting that infection of macrophages by *L. major* can affect epigenetic regulation mediated by lncRNAs during host-parasite interaction. These findings may assist with the ongoing search for more effective treatments for this disease.

Key words: Leishmaniasis, immune response, host-parasite, lncRNA, cis/trans targets.

2.3 Author Abstract

Leishmaniasis is a worldwide disease that can affect humans infected by a parasite of the genus *Leishmania*. Despite treatment, it has no cure. This parasite attacks the host's defense system, which tries to prevent the parasite from surviving. In this study, we evaluated if long non-coding RNAs (lncRNAs), an RNA type that can regulate the expression of other genes, are altered in mouse macrophages in the presence of *L. major*. Our results show that *in vitro* infection with *L. major* altered the expression of lncRNAs that are possible regulators of key genes mediating immune response. These findings shed light on the biological mechanisms of defense cells to a parasite invasion, aiming to improve the treatment of this disease.

2.4 Introduction¹

Leishmaniasis is a neglected disease caused by more than 20 species of *Leishmania* protozoan parasite and, among them, *Leishmania (L.) major*. The symptoms vary in severity, ranging from self-healing skin lesions to manifestations with mucocutaneous disfigurement and fatal visceral disease [1]. More than one million new cases in humans are reported annually and are mainly concentrated in the Middle East and Central and South America [2]. The life cycle of *Leishmania* is digenetic. The female phlebotomine vector is infected by the extracellular promastigote form. The parasite is found intracellularly in the amastigote form in mammalian hosts, infecting mainly macrophages [3]. After phagocytosis of the parasite, host macrophages trigger several signaling events to eliminate the pathogen. Signals from macrophages infected with *L. major* can lead to different host immune responses, directly effecting disease severity [4,5]. Responses can be associated with a classical activation profile (M1), where the T helper 1 (Th1) cell produces nitrogen radicals and reactive oxygen species (ROS), inhibiting cell proliferation; or a second profile (M2), with the T helper 2 (Th2) type cell, promoting cell proliferation by inhibition of proinflammatory signals and, consequently, disease progression with an increase in the parasite number [3,6,7].

Mechanisms used by the host to engage the immune system and eliminate the pathogen are regulated by epigenetic processes, which modulate gene expression from internal signals or external stress without altering the individual's inherited DNA sequence [8–11]. Among these epigenetic mechanisms, a several of non-coding RNAs (ncRNA) can act-regulation gene expression of immune modulators at the

¹ Artigo de acordo com as normas da Revista *Plos Neglected Tropical Diseases* (ANEXO A)

transcriptional, post-transcriptional and translational levels [12]. The ncRNAs are divided according to their length, including short and long non-coding RNAs (lncRNAs). While short RNAs, also known as microRNAs (miRNA), have around 22 nucleotides, lncRNAs can extend over 200 nucleotides [13]. The lncRNAs can act as protein carriers, activators or inhibitors of transcription, antisense RNA, or miRNA sponges [12].

On the other end of the host-pathogen interaction, the presence of parasites can lead to changes in host gene/protein expression that can be favorable to the parasite survival, i.e. *Leishmania*-induced delay in host protease action, negatively affecting parasite elimination following phagocytosis by the macrophage [14]. In the study by Dillon et al. (2015), *L. major* infected macrophages served as a model to study alterations in the transcriptomes of both host and pathogen during infection, showing the effects of the interaction as an interactive two-sided story. As mentioned previously, modulation of epigenetic processes can impact immune response and, therefore, could be a target during host-pathogen interactions, with implications in disease progression. To explore the relationship between *L. major* and host epigenetic regulation, we employed the transcriptomic data generated by Dillon et al. (2015) to investigate lncRNA expression in murine macrophages infected *in vitro* with *L. major*, predicting and classifying their possible mRNA targets and their biological pathways, thus focusing on the direct role of these noncoding transcripts on host response to *L. major* infection.

2.5 Methods

2.5.1 Dataset

Sequencing reads were previously generated by Dillon *et al.* (2015), and are available in the Genbank database, under BioProject PRJNA252791. Briefly, these reads were generated as follows: RNAseq was performed on peritoneal macrophages isolated from ten 7-week-old C57BL/6 female mice. Cells were divided into two treatment groups consisting of 1) three samples infected *in vitro* with the *L. major* strain (MHOM/IL/80/Friedlin), at a ratio of 5 parasites per macrophage, for 4 hours; and 2) three control samples of uninfected macrophages. Sequencing was performed using the Illumina HiSeq 1500 platform, with paired-end libraries of 100 base pairs (Fig 1). Detailed information is provided in the original article [15].

2.5.2 Alignment and quantification of reads

Reads from each sample were aligned to the mouse reference genome, version GRCm38 available in GENCODE [16], using the program HISAT2 [17]. Aligned reads were quantified according to the information available in GENCODE (version M24) and performed employing the HTSeq program [18] (Fig 1).

2.5.3 Differential expression analysis and expression correlation between mRNA and lncRNA

DESeq2 package [19] was used to normalize sequencing differences among samples, with the generalized linear model assuming negative binomial distribution, dispersion values for each gene were estimated and differential expression analysis was performed for mRNAs and lncRNAs using R (v 3.6.1). Data obtained following

Wald test were adjusted and filtered after multiple-test correction by the Benjamin-Hochberg (BH) approach ($FDR < 0.05$), and the logarithm of fold change in expression ($\log_2FC$) greater than ± 1 was considered to obtain a list of differentially expressed genes (DEGs). All DEGs were classified using the R package BiomaRt [20] and separated into long non-coding RNAs (lncRNAs) and coding RNAs (mRNAs). Subsequently, co-expression of these lncRNAs and mRNAs was calculated using Pearson's correlation coefficient (r) and BH-adjusted p-value based on the t distribution using the R package Hmisc [21]. Finally, data were filtered by Pearson's correlation coefficient (r) and co-expressed genes obtained with an absolute value of r greater than or equal to 0.9 and an $FDR < 0.01$ (Fig 1).

2.5.4 Target identification

In order to increase the accuracy of target prediction, all significant correlations between lncRNAs and mRNAs were subjected to target validation by calculating the binding free energy for a spontaneous reaction using the program LncTar [22] and a threshold of -0.10 as the free energy parameter. Classification of DE lncRNAs as cis was done by employing the FEELnc (v.0.1.1) program [23], which locates genes that were within 100kb above and below the location of each lncRNA. Targets that were validated with LncTar and were not within the 100kb window, were classified as trans. Further, lncRNAs that had targets within 100kb and above that, were classified as cis/trans (Fig 1).

2.5.5 Pathway enrichment

LncRNA targets that met both the correlation and free energy criteria were used for pathway enrichment analyses in the R/gProfileR2 program [24], using the Kyoto Encyclopedia of Genes and Genomes (KEGG) by means of hypergeometric test for each KEGG pathway. Adjusted p-values (FDR) <0.05 were considered statistically significant. Next, networks were created using the Cytoscape software (v. 3.8.0) [25] for the visualization of cis and trans lncRNAs, mRNA targets and KEGG enriched pathways (Fig 1).

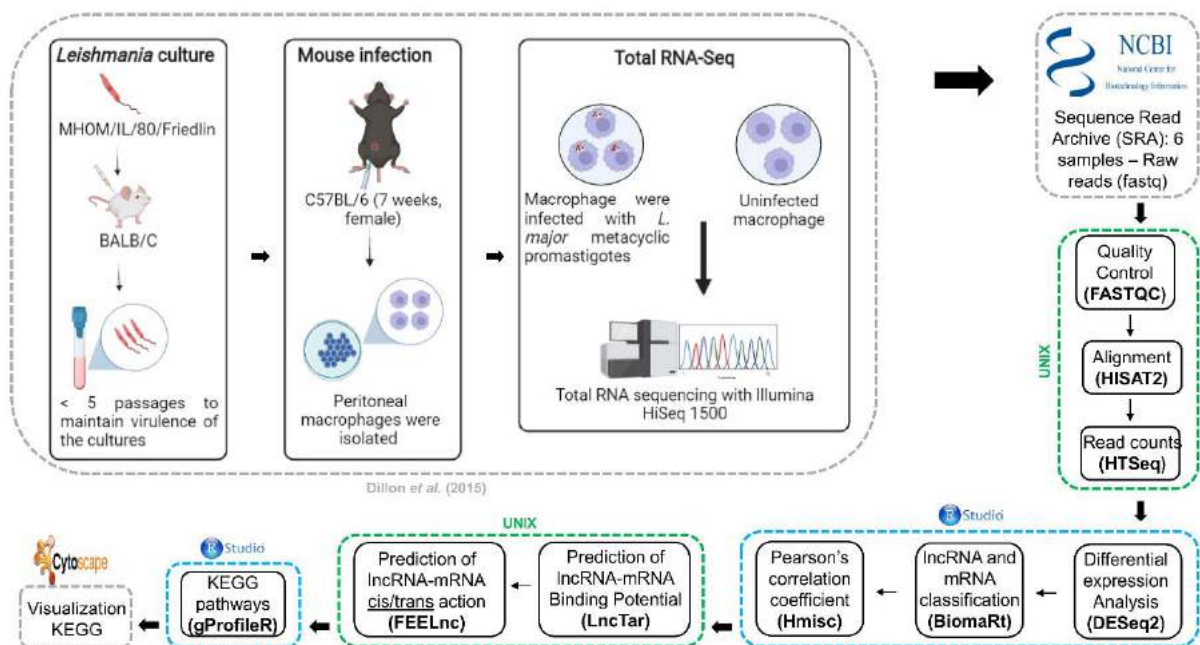


Fig 1. Workflow of lncRNA analysis. Experiment Dillon *et al.* (2015) and functional predictions lncRNA-mRNA.

2.6 Results

Alignment of paired-end reads resulted in an average mapping rate of 80.5% for the mouse genome. In total, 28,002 known transcripts were identified, with 2,603 transcripts being differentially expressed (DE) and, among these, 296 DE transcripts were identified as lncRNAs and 2307 as DE mRNA (FDR<0.05 and log2FC>|1|).

From 296 lncRNAs, 121 had increased expression in the infected group compared to control, and 175 showed a decreased expression following infection. For mRNAs, 1,127 had increased expression in the infected group, whereas 1,180 had decreased expression post-infection (Fig 2).

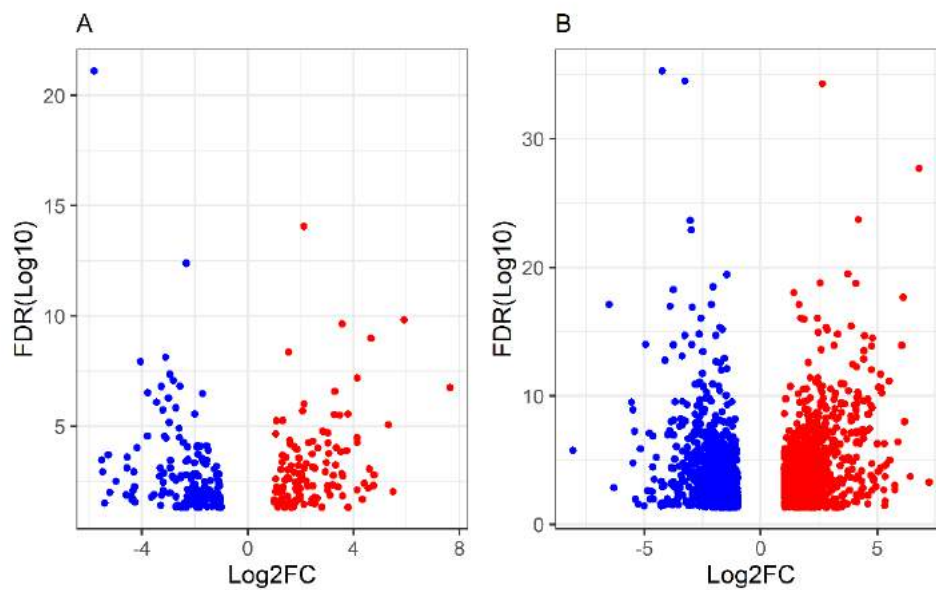


Fig 2. Volcano plot of differentially expressed lncRNAs and mRNAs following *in vitro* (4h) infection of macrophages with *L. major*. (A) 121 upregulated lncRNAs are presented in red and 175 downregulated lncRNAs are shown in blue. (B) 1,127 upregulated mRNAs are presented in red and 1,180 downregulated mRNAs are shown in blue (FDR<0.05 and log2FC>|1|).

According to co-expression analysis between lncRNAs and mRNAs, 22,701 interactions were observed, 85% showing positive correlations and 15% negative correlations. Among these, DE lncRNAs and target mRNAs, which were also significantly correlated, were 294 and 2,106, respectively. Target prediction showed

up to 323 mRNAs as targets per lncRNA, whereas 1 to 31 lncRNAs were found for the same mRNA.

After differential expression, target prediction and expression correlation analyses, we further validated the identified interactions using free energy calculation. We were able to identify 460 interactions (S1 Table), which maintained the same percentage of positive (85%) and negative (15%) correlations between lncRNAs and mRNAs. Validated interactions were composed of 71 lncRNAs and 391 mRNAs, representing 24% and 18,5% of the total interactions that were previously identified as correlated, respectively. Of 71 lncRNAs, 38 were up-regulated and 33 downregulated in the infected group (Fig 3), were verified 7 with cis targets, 56 with trans targets, and 8 with both cis and trans targets (S2 Table). The number of mRNA targets up to 90 per lncRNA, and the mRNAs having 1 to 4 lncRNAs in the interactions validated using the free energy parameter.

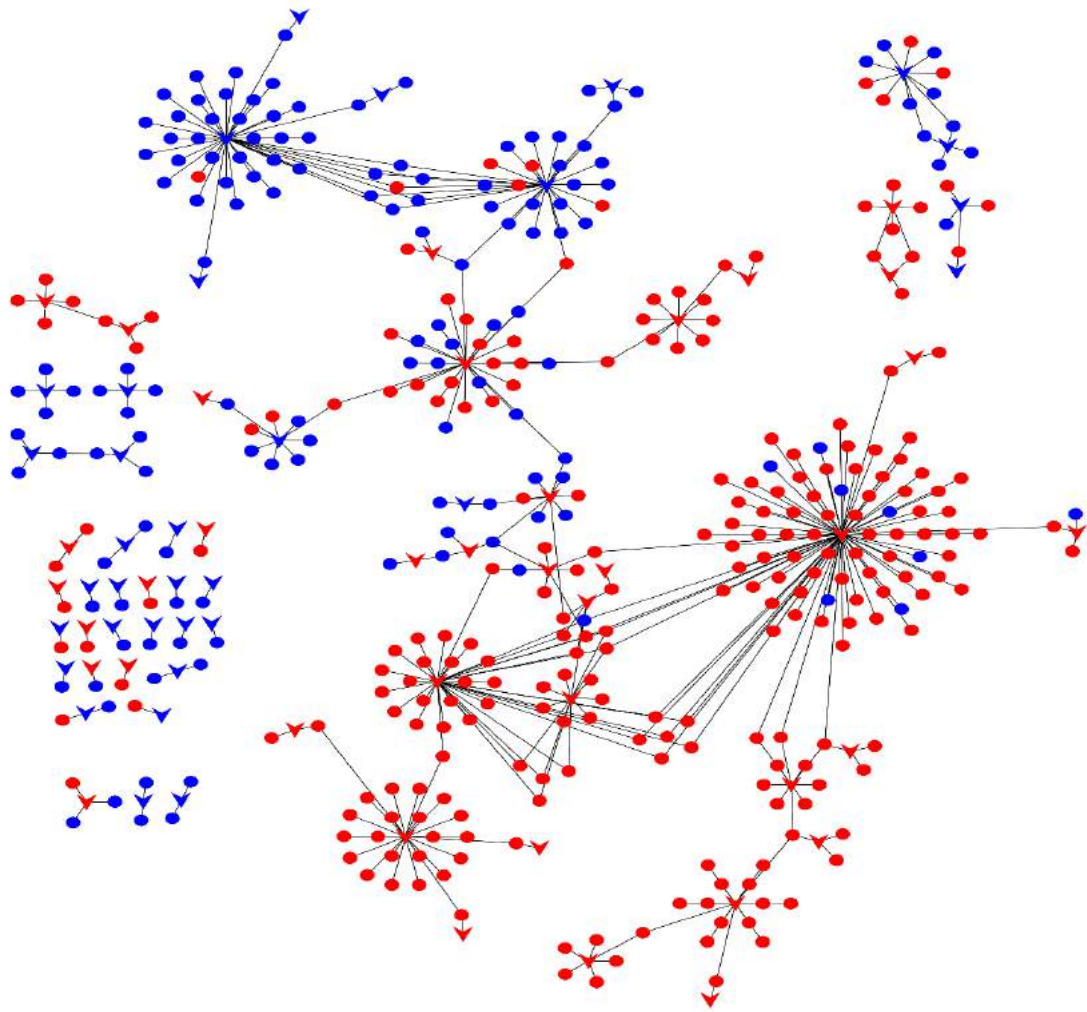


Fig 3. Network of differentially expressed lncRNAs-mRNAs from macrophages infected *in vitro* (4h) with *L. major*. Arrows indicate lncRNA; in red: 38 lncRNAs upregulated and in blue: 33 lncRNAs downregulated in infected group for a total of 71 lncRNAs. Circles represent 391 predicted target mRNAs.

Of the 391 target mRNAs subjected to pathway enrichment using KEGG, 141 were related to 109 pathways (S3 Table). These targets had 45 lncRNAs as regulators and a total of 167 interactions between lncRNAs and mRNAs, with 148 positive correlations and 19 negative correlations. Some pathways, such as metabolic processes, had the participation of 40 genes and 44 lncRNAs.

The target genes with the highest degree were *Mapk14* and *Jun*, which appeared in over 30 pathways and are concomitant in 20 of them linked to the immune system. *Mapk14* gene is a likely target of 4 lncRNAs, all with negative correlation interactions: *Mir155hg*, *Gm49733*, *Gm12868* are trans-acting, and *Gm12867* is both cis and trans, being trans with this target. The transcription factor *Jun* stood out as the cis target of the *Gm47252* lncRNA in a positive interaction. *Gm12868* and *Gm12867* lncRNAs also showed a probable positive interaction with the *Nfkbib* mRNA, which shared 10 pathways with *Mapk14* and *Jun* (Fig 4).

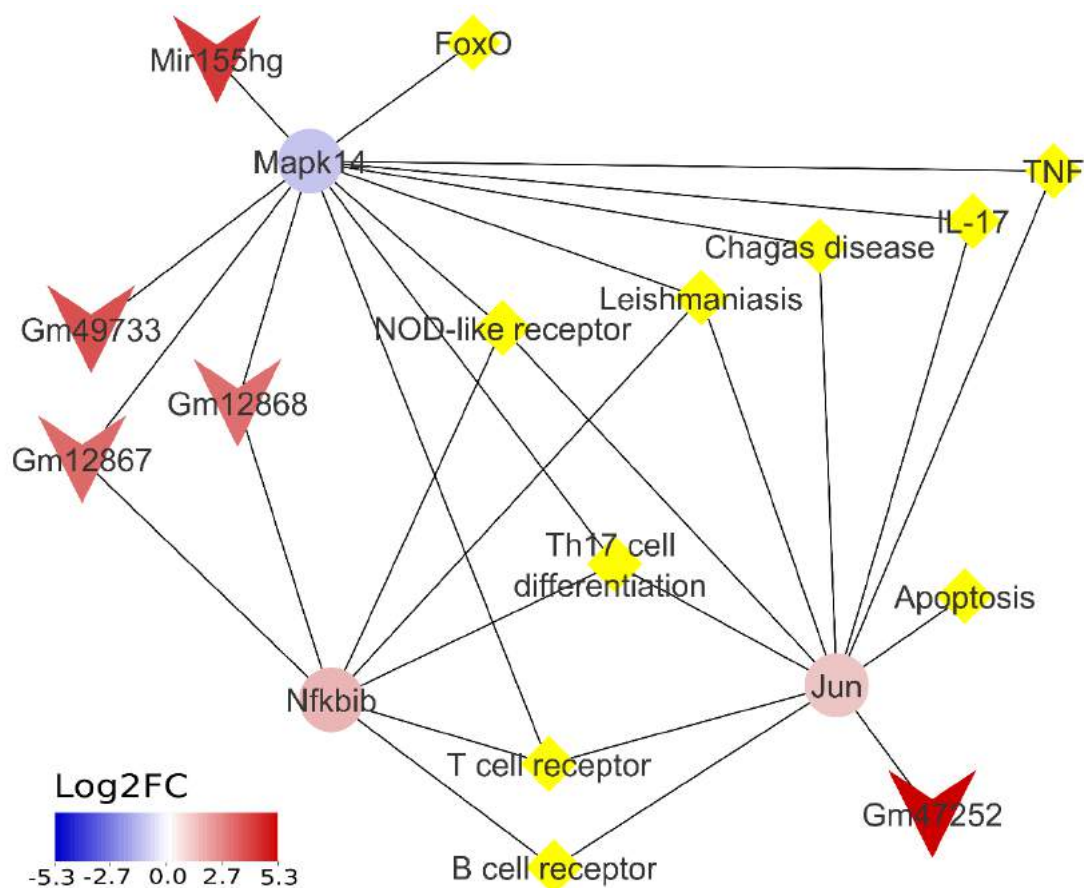


Fig 4. Network of terms linked to at least one of the *Mapk14*, *Nfkbib* and *Jun* genes that form the immune system pathway complex. Circles represent mRNA, and arrows represent lncRNA; in red mRNAs/lncRNAs that are upregulated and in blue mRNA that is downregulated. Yellow diamonds represent 10 KEGG pathways terms.

Gm49733, *Gm12868*, *Gm47252*, *Gm12867* and *Mir155hg* lncRNAs were upregulated in the *L. major* infected cells, with log2FC of 3.6, 2.9, 5.3, 3.0, and 4.1, respectively. The lncRNA with the highest number of interactions is the *Gm49733* with 33 targets, followed by *Gm12868*, *Gm47252*, *Gm12867*, and *Mir155hg* with 12, 7, 5 and 4 interactions, respectively.

2.7 Discussion

After infection, *Leishmania* spp employs survival mechanisms that include modulation of macrophage gene expression [26–29]. In macrophages infected with *L. major*, a downregulation of chemokine receptor genes and positive regulation of genes involved in fatty acid biosynthesis have been previously observed [3,30]. Although previous studies have shown that lncRNAs control gene expression during macrophage development [31–34], our study is the first to investigate lncRNA expression profile and cis/trans interactions with potential targets following *in vitro* infection of macrophages with *Leishmania major*.

Although lncRNAs have several biological functions, we focused on the regulation exerted by cis lncRNAs, which regulate the expression of genes near the transcription site of the lncRNA itself, and trans lncRNAs which can act on more distant genes [31,35–37]. In our study, co-expression between lncRNAs and mRNAs classified 7 lncRNAs acting as cis, 56 lncRNAs with predicted trans function and 8 lncRNAs were classified as both cis and trans. KEGG enrichment analysis of their mRNA targets revealed general pathways related to the immune system, such as IL-17 signaling, Th17 cell differentiation, TNF signaling, T and B cell receptors, NOD-

like receptors, apoptosis and pathways with Chagas disease and Leishmaniasis. These pathways were also observed in studies that focused primarily on the coding transcriptome profiles of murine macrophage infected with *L. major* [15], *L. panamensis* [3] and *L. amazonensis* [38], corroborating our findings.

Identification of lncRNA target pathways such as apoptosis and TNF signaling, responsible for the induction of pro-inflammatory cytokines, suggests that the classic M1 (Th1) phenotype is involved in macrophage activation in the early hours post *L. major* infection. In fact, macrophages from C57BL/6 mice have already been characterized with the classic M1 profile in previous studies involving infection with *L. major* [15,39], *L. amazonensis* [38] and *L. panamensis* [3]. In order to shed light on the role of noncoding transcripts on infection, we have filtered all DE mRNAs to those co-expressed and probable targets of DE lncRNAs. We corroborate these previous findings of immune modulation by Leishmania infection, suggesting that regulation of mRNAs by lncRNAs may be an important target during host-pathogen interactions.

As mentioned above, co-expression between genes identified in the KEGG enriched pathways and the lncRNAs suggests an epigenetic modulation of the host transcriptome related to immune response. Our findings showed the *Mir155hg* lncRNA was up-regulated in the infected group compared to the control. Increase in *Mir155hg* was also reported in human studies with macrophages in cardiometabolic diseases [40], chronic obstructive pulmonary disease [41], and multiple cancers [42,43]. A study using *Mir155hg* KO mice, infected with the influenza A virus, investigated the role of the lncRNA *Mir155hg* in immune response, and demonstrated that its deficiency leads to lower expression of *IFN- β* , *IFN- γ* , *Mx1*, *ISG15*, and *OAS3*,

as well as of many critical cytokines including *IL-1 β* , *IL-6*, *IL-28*, and *TNF α* and interferon regulatory factors such as *IRF3* [44].

Furthermore, this lncRNA is a precursor of miR-155 in mice and humans [45], which is involved in innate and adaptive immunity. Expression of this microRNA is positively regulated in cells of the immune system, being able to regulate antigens and inflammatory cytokines [46,47]. Studies show upregulation of miR-155 in macrophages responding to antigens derived from bacteria [48–50], promoting antigen presentation by dendritic cells [51] and regulating members of the superfamily of tumor necrosis factor (TNF) receptors [49]. It can also promote the Th1 pro-inflammatory response, the classic activation of macrophages and inhibition of the suppressor of cytokine signaling-1 (SOCS1) [52,53]. Most importantly, infection of miR-155 KO mice with *L. donovani* has demonstrated that this miRNA plays an essential role in the induction of both Th1 and Th2 responses and in the suppression of inflammatory monocyte infiltration and activity during infection [54]. Taken together with our results showing enrichment of pathways related to the production of pro-inflammatory cytokines, and an increase in *Mir155hg* lncRNA expression in response to infection, we suggest that lncRNAs have a role in the polarization of the M1 phenotype in macrophages upon *L. major* infection. It is important to emphasize that the data we analyzed were obtained at 4 hours post-infection and the high plasticity of macrophages can lead to repolarization or reprogramming from M1 to M2 and vice versa, depending on the stimuli [55,56].

In our study, *Mapk14*, known to regulate the activation of inflammatory cytokines, was identified as a possible target of *Mir155Hg* lncRNA [3]. Corroborating our findings, downregulation of *Mapk14* was also observed in infections with *L.*

braziliensis and *L. major* [57–59]. After 4 hours of infection of *L. amazonensis* peritoneal macrophages from BALB/c mice, the low expression of *Mapk14* was related to low activation of the cellular response cascade in this macrophage [57]. *Mapk14* has a role in most of the enriched pathways in our study, and is identified as a target of 4 lncRNAs, thus suggesting a role for ncRNAs on its modulation.

Two of the lncRNAs suggested as regulators of *Mapk14* were also identified as complementary to the *Nfkbib* gene, which was upregulated in the infected group, suggesting a stimulatory role for lncRNAs on this transcript. *Nfkbib*, also known as *I κ B β* , is responsible for regulating genes involved in inflammation and immune responses [60], as the absence of this gene caused a drastic reduction in *TNF- α* , following lipopolysaccharide (LPS) induction in C57BL/6 *I κ B β* KO mice (*I κ B β* ^{-/-}) [61].

Another gene present in several enriched pathways in our work is *Jun*, a cis target of a single lncRNA, which had increased expression in the infected group. This gene is a transcription factor of Toll-like receptors (TLRs), pathogen recognition receptors, which have been previously show to be active participants in immune responses processes during leishmaniasis [62–64]. In fact, some of the vaccine candidates to date are based on the combination of *Leishmania* antigens and TLR ligands [65,66]. In summary, *Mapk14*, *Nfkbib* and *Jun* genes are the likely lncRNAs targets that appear in most immunological pathways enriched in our study and, suggesting that ncRNAs work together to help orchestrate host response.

Our findings shed light on the role of lncRNAs in the regulation of immune response in macrophages infected with *L. major*. Pathway enrichment analysis of lncRNA targets (cis and trans acting) showed pathways involved in host response to

macrophage invasion, indicating the importance and complexity of epigenetic regulation in host-parasite interactions.

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2.9 Author Contributions

Manuscript drafting: FRFA, AOL, JAT and FLL.

Bioinformatic analysis: FRFA.

Manuscript writing: FRFA, AOL, JAT and FLL.

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APÊNDICE A – REFERÊNCIAS DA INTRODUÇÃO GERAL

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APÊNDICE B - MATERIAL SUPLEMENTAR

Supplementary Material S1 Table - Interactions between lncRNAs and mRNAs – Source

Source	cor	p.value	FDR	Sinal	S_Biotype	S_Name	S_chr	dG	ndG	Type_Lnc
ENSMUSG00000085532.1	1.00	1.53E-07	0.0031	POS	lncRNA	B430319H21Rik	11	-42.24	-0.1008	Trans
ENSMUSG00000110433.1	1.00	4.62E-07	0.00329	POS	lncRNA	Gm45820	8	-31.19	-0.1072	Trans
ENSMUSG00000111895.1	1.00	8.38E-07	0.00336	POS	lncRNA	Gm47252	4	-42.95	-0.1042	Cis_Trans
ENSMUSG00000086695.1	1.00	1.27E-06	0.00351	POS	lncRNA	Gm15247	X	-148.17	-0.4071	Cis_Trans
ENSMUSG00000087263.1	1.00	2.09E-06	0.00364	POS	lncRNA	Gm15726	X	-181.96	-0.376	Cis_Trans
ENSMUSG00000057359.7	1.00	2.10E-06	0.00364	POS	lncRNA	Gm17494	3	-110.48	-0.1669	Trans
ENSMUSG00000111895.1	1.00	2.30E-06	0.00367	POS	lncRNA	Gm47252	4	-233.02	-0.5522	Cis_Trans
ENSMUSG00000085505.1	1.00	4.33E-06	0.0039	POS	lncRNA	Gm12868	4	-41.86	-0.1071	Cis_Trans
ENSMUSG00000085295.7	1.00	5.06E-06	0.00394	POS	lncRNA	4930430E12Rik	4	-31.83	-0.153	Trans
ENSMUSG00000085213.1	1.00	6.10E-06	0.00407	POS	lncRNA	Gm13091	4	-36.03	-0.1015	Trans
ENSMUSG00000085295.7	1.00	6.82E-06	0.00414	POS	lncRNA	4930430E12Rik	4	-33.88	-0.103	Trans
ENSMUSG00000111895.1	1.00	6.85E-06	0.00414	POS	lncRNA	Gm47252	4	-59.17	-0.1074	Cis_Trans
ENSMUSG00000086683.1	1.00	7.04E-06	0.00416	POS	lncRNA	Gm12867	4	-36.62	-0.1032	Trans

ENSMUSG00000106980.1	1.00	7.71E-06	0.0042	POS	lncRNA	Gm43690	5	-26.56	-0.1054	Trans
ENSMUSG00000106980.1	1.00	9.25E-06	0.00434	POS	lncRNA	Gm43690	5	-24.79	-0.1377	Trans
ENSMUSG00000116739.1	1.00	1.09E-05	0.00446	POS	lncRNA	Gm49733	16	-22.79	-0.1055	Trans
ENSMUSG00000106980.1	1.00	1.09E-05	0.00447	POS	lncRNA	Gm43690	5	-26.97	-0.1096	Trans
ENSMUSG00000104818.1	1.00	1.12E-05	0.00448	POS	lncRNA	Gm43661	5	-60.99	-0.1273	Trans
ENSMUSG00000087263.1	1.00	1.26E-05	0.00458	POS	lncRNA	Gm15726	X	-32.66	-0.105	Cis_Trans
ENSMUSG00000116739.1	1.00	1.27E-05	0.00459	POS	lncRNA	Gm49733	16	-29.31	-0.1004	Trans
ENSMUSG00000110433.1	1.00	1.31E-05	0.0046	POS	lncRNA	Gm45820	8	-31.21	-0.1269	Trans
ENSMUSG00000116739.1	1.00	1.31E-05	0.00461	POS	lncRNA	Gm49733	16	-28.54	-0.1008	Trans
ENSMUSG00000116097.1	1.00	1.32E-05	0.00461	POS	lncRNA	Gm36738	15	-44.89	-0.1261	Trans
ENSMUSG00000085213.1	1.00	1.34E-05	0.00462	POS	lncRNA	Gm13091	4	-35.05	-0.1204	Trans
ENSMUSG00000111713.1	1.00	1.34E-05	0.00463	POS	lncRNA	Gm20234	11	-30.54	-0.1345	Trans
ENSMUSG00000111792.1	1.00	1.43E-05	0.00466	POS	lncRNA	Gm33858	9	-109.56	-0.1412	Cis
ENSMUSG00000105512.1	1.00	1.43E-05	0.00466	POS	lncRNA	Gm43714	3	-89.99	-0.1089	Trans
ENSMUSG00000055323.5	1.00	1.48E-05	0.00468	POS	lncRNA	Gm9967	7	-226.66	-0.3419	Cis
ENSMUSG00000111713.1	1.00	1.49E-05	0.00468	POS	lncRNA	Gm20234	11	-58.68	-0.1029	Trans

ENSMUSG00000097418.7	1.00	1.51E-05	0.00469	POS	lncRNA	Mir155hg	16	-40.6	-0.1624	Trans
ENSMUSG00000086914.1	1.00	1.53E-05	0.0047	POS	lncRNA	Gm16124	9	-38.45	-0.1923	Trans
ENSMUSG00000090230.1	1.00	1.74E-05	0.00479	POS	lncRNA	Gm16315	10	-40.24	-0.1337	Trans
ENSMUSG00000116739.1	1.00	1.74E-05	0.00479	POS	lncRNA	Gm49733	16	-24.69	-0.1083	Trans
ENSMUSG00000110433.1	1.00	1.78E-05	0.00482	POS	lncRNA	Gm45820	8	-35.02	-0.1152	Trans
ENSMUSG00000106980.1	1.00	1.84E-05	0.00483	POS	lncRNA	Gm43690	5	-31.31	-0.1242	Trans
ENSMUSG00000106980.1	1.00	1.86E-05	0.00484	POS	lncRNA	Gm43690	5	-21.67	-0.1147	Trans
ENSMUSG00000086695.1	1.00	1.94E-05	0.00487	POS	lncRNA	Gm15247	X	-39.4	-0.1045	Cis_Trans
ENSMUSG00000100280.2	1.00	1.98E-05	0.00489	POS	lncRNA	Gm28417	1	-189.51	-0.2363	Cis
ENSMUSG00000085505.1	1.00	2.05E-05	0.00492	POS	lncRNA	Gm12868	4	-35.44	-0.1534	Cis_Trans
ENSMUSG00000085505.1	1.00	2.07E-05	0.00493	POS	lncRNA	Gm12868	4	-35.54	-0.109	Cis_Trans
ENSMUSG00000085295.7	1.00	2.09E-05	0.00494	POS	lncRNA	4930430E12Rik	4	-37.01	-0.1118	Trans
ENSMUSG00000116739.1	1.00	2.09E-05	0.00494	POS	lncRNA	Gm49733	16	-29.05	-0.1157	Trans
ENSMUSG00000084940.2	1.00	2.13E-05	0.00496	POS	lncRNA	Gm15935	14	-268.19	-0.444	Cis_Trans
ENSMUSG00000110433.1	1.00	2.28E-05	0.00501	POS	lncRNA	Gm45820	8	-25.33	-0.1248	Trans
ENSMUSG00000106980.1	1.00	2.28E-05	0.00501	POS	lncRNA	Gm43690	5	-22.85	-0.1078	Trans

ENSMUSG00000106980.1	1.00	2.32E-05	0.00502	POS	lncRNA	Gm43690	5	-24.66	-0.1015	Trans
ENSMUSG00000085505.1	1.00	2.34E-05	0.00502	POS	lncRNA	Gm12868	4	-42.86	-0.1064	Cis_Trans
ENSMUSG00000102336.1	1.00	2.41E-05	0.00503	POS	lncRNA	Gm37233	1	-120.68	-0.1038	Trans
ENSMUSG00000111895.1	1.00	2.55E-05	0.00507	POS	lncRNA	Gm47252	4	-62.19	-0.1156	Cis_Trans
ENSMUSG00000085242.1	1.00	2.56E-05	0.00507	POS	lncRNA	Gm11537	11	-74.9	-0.1011	Trans
ENSMUSG00000097418.7	1.00	2.58E-05	0.00508	POS	lncRNA	Mir155hg	16	-35.21	-0.1339	Trans
ENSMUSG00000113494.1	1.00	2.59E-05	0.00508	POS	lncRNA	Gm48102	13	-40.45	-0.1105	Trans
ENSMUSG00000116739.1	1.00	2.60E-05	0.00508	POS	lncRNA	Gm49733	16	-34.52	-0.145	Trans
ENSMUSG00000101655.1	1.00	2.64E-05	0.00509	POS	lncRNA	2310040G24Rik	6	-45.91	-0.137	Trans
ENSMUSG00000108449.1	1.00	2.74E-05	0.00512	POS	lncRNA	Gm44507	7	-34.99	-0.1048	Trans
ENSMUSG00000090230.1	1.00	2.82E-05	0.00514	POS	lncRNA	Gm16315	10	-61.53	-0.1039	Trans
ENSMUSG00000116739.1	1.00	2.86E-05	0.00516	POS	lncRNA	Gm49733	16	-24.24	-0.116	Trans
ENSMUSG00000116739.1	1.00	2.88E-05	0.00517	POS	lncRNA	Gm49733	16	-28.06	-0.1109	Trans
ENSMUSG00000116739.1	1.00	3.01E-05	0.0052	POS	lncRNA	Gm49733	16	-35.81	-0.1321	Trans
ENSMUSG00000116739.1	1.00	3.17E-05	0.00525	POS	lncRNA	Gm49733	16	-26.98	-0.1003	Trans
ENSMUSG00000116739.1	1.00	3.17E-05	0.00526	POS	lncRNA	Gm49733	16	-25.29	-0.1036	Trans

ENSMUSG00000087593.1	1.00	3.41E-05	0.00532	POS	lncRNA	Gm16174	7	-35.84	-0.1045	Trans
ENSMUSG00000110433.1	0.99	3.84E-05	0.00542	POS	lncRNA	Gm45820	8	-28.03	-0.1058	Trans
ENSMUSG00000116739.1	0.99	4.05E-05	0.00549	POS	lncRNA	Gm49733	16	-26.83	-0.1078	Trans
ENSMUSG00000106980.1	0.99	4.11E-05	0.00551	POS	lncRNA	Gm43690	5	-23.05	-0.138	Trans
ENSMUSG00000110433.1	0.99	4.25E-05	0.00554	POS	lncRNA	Gm45820	8	-39.06	-0.1221	Trans
ENSMUSG00000116739.1	0.99	4.35E-05	0.00557	POS	lncRNA	Gm49733	16	-33.33	-0.1182	Trans
ENSMUSG00000106980.1	0.99	4.45E-05	0.0056	POS	lncRNA	Gm43690	5	-25.26	-0.1027	Trans
ENSMUSG00000116739.1	0.99	4.95E-05	0.00571	POS	lncRNA	Gm49733	16	-27.51	-0.1234	Trans
ENSMUSG00000105283.1	0.99	4.97E-05	0.00572	POS	lncRNA	Gm33370	5	-22.98	-0.1242	Trans
ENSMUSG00000085505.1	0.99	4.98E-05	0.00572	POS	lncRNA	Gm12868	4	-34.67	-0.1204	Cis_Trans
ENSMUSG00000086695.1	0.99	4.99E-05	0.00572	POS	lncRNA	Gm15247	X	-41.26	-0.1137	Cis_Trans
ENSMUSG00000106980.1	0.99	5.07E-05	0.00574	POS	lncRNA	Gm43690	5	-26.12	-0.1037	Trans
ENSMUSG00000086695.1	0.99	5.31E-05	0.00579	POS	lncRNA	Gm15247	X	-50.21	-0.1614	Cis_Trans
ENSMUSG00000106980.1	0.99	5.50E-05	0.00584	POS	lncRNA	Gm43690	5	-26.4	-0.1043	Trans
ENSMUSG00000116739.1	0.99	5.51E-05	0.00584	POS	lncRNA	Gm49733	16	-22.5	-0.1398	Trans
ENSMUSG00000106980.1	0.99	5.54E-05	0.00585	POS	lncRNA	Gm43690	5	-32.96	-0.1282	Trans

ENSMUSG00000106980.1	0.99	5.67E-05	0.00587	POS	lncRNA	Gm43690	5	-22.54	-0.1156	Trans
ENSMUSG00000113494.1	0.99	5.68E-05	0.00588	POS	lncRNA	Gm48102	13	-36.84	-0.1116	Trans
ENSMUSG00000087593.1	0.99	5.70E-05	0.00588	POS	lncRNA	Gm16174	7	-37.87	-0.1076	Trans
ENSMUSG00000087593.1	0.99	5.91E-05	0.00592	POS	lncRNA	Gm16174	7	-40.52	-0.1031	Trans
ENSMUSG00000108449.1	0.99	5.97E-05	0.00593	POS	lncRNA	Gm44507	7	-43.18	-0.1371	Trans
ENSMUSG00000072612.3	0.99	6.16E-05	0.00597	POS	lncRNA	Gm10382	5	-142.94	-0.1195	Trans
ENSMUSG00000110433.1	0.99	6.23E-05	0.00598	POS	lncRNA	Gm45820	8	-33.9	-0.1066	Trans
ENSMUSG00000085213.1	0.99	6.24E-05	0.00599	POS	lncRNA	Gm13091	4	-34.23	-0.1149	Trans
ENSMUSG00000097418.7	0.99	6.40E-05	0.00601	POS	lncRNA	Mir155hg	16	-37.97	-0.1563	Trans
ENSMUSG00000085505.1	0.99	6.40E-05	0.00601	POS	lncRNA	Gm12868	4	-42.92	-0.1078	Cis Trans
ENSMUSG00000109424.1	0.99	6.50E-05	0.00603	POS	lncRNA	Gm44658	7	-62.47	-0.1031	Trans
ENSMUSG00000109424.1	0.99	6.77E-05	0.00608	POS	lncRNA	Gm44658	7	-50.55	-0.1058	Trans
ENSMUSG00000116739.1	0.99	6.86E-05	0.0061	POS	lncRNA	Gm49733	16	-24.74	-0.1114	Trans
ENSMUSG00000087593.1	0.99	6.91E-05	0.00611	POS	lncRNA	Gm16174	7	-40.15	-0.1074	Trans
ENSMUSG00000085213.1	0.99	6.94E-05	0.00611	POS	lncRNA	Gm13091	4	-33	-0.1104	Trans
ENSMUSG00000110433.1	0.99	7.10E-05	0.00615	POS	lncRNA	Gm45820	8	-30.18	-0.102	Trans

ENSMUSG00000110433.1	0.99	7.28E-05	0.00618	POS	lncRNA	Gm45820	8	-30.6	-0.1003	Trans
ENSMUSG00000116739.1	0.99	7.31E-05	0.00619	POS	lncRNA	Gm49733	16	-22.11	-0.1164	Trans
ENSMUSG00000072612.3	0.99	7.35E-05	0.0062	POS	lncRNA	Gm10382	5	-95.5	-0.1037	Trans
ENSMUSG00000085505.1	0.99	7.48E-05	0.00622	POS	lncRNA	Gm12868	4	-41.22	-0.1033	Cis_Trans
ENSMUSG00000111895.1	0.99	7.56E-05	0.00624	POS	lncRNA	Gm47252	4	-55.12	-0.1054	Cis_Trans
ENSMUSG00000087263.1	0.99	7.67E-05	0.00625	POS	lncRNA	Gm15726	X	-32.65	-0.1085	Cis_Trans
ENSMUSG00000087623.1	0.99	7.70E-05	0.00626	POS	lncRNA	Gm12404	4	-106.13	-0.1793	Cis_Trans
ENSMUSG00000116739.1	0.99	7.77E-05	0.00627	POS	lncRNA	Gm49733	16	-29.01	-0.1099	Trans
ENSMUSG00000110433.1	0.99	7.88E-05	0.00629	POS	lncRNA	Gm45820	8	-26.79	-0.1282	Trans
ENSMUSG00000110433.1	0.99	7.90E-05	0.00629	POS	lncRNA	Gm45820	8	-33.57	-0.1017	Trans
ENSMUSG00000116739.1	0.99	8.10E-05	0.00633	POS	lncRNA	Gm49733	16	-24.34	-0.1122	Trans
ENSMUSG00000111895.1	0.99	8.10E-05	0.00633	POS	lncRNA	Gm47252	4	-64.86	-0.1092	Cis_Trans
ENSMUSG00000113494.1	0.99	8.18E-05	0.00635	POS	lncRNA	Gm48102	13	-32.97	-0.1081	Trans
ENSMUSG00000086695.1	0.99	8.24E-05	0.00635	POS	lncRNA	Gm15247	X	-46.18	-0.1193	Cis_Trans
ENSMUSG00000116739.1	0.99	8.39E-05	0.00638	POS	lncRNA	Gm49733	16	-30.69	-0.1574	Trans
ENSMUSG00000087593.1	0.99	8.42E-05	0.00639	POS	lncRNA	Gm16174	7	-39.1	-0.1068	Trans

ENSMUSG00000086098.1	0.99	8.43E-05	0.00639	POS	lncRNA	Gm14291	2	-66.54	-0.1005	Trans
ENSMUSG00000116739.1	0.99	8.43E-05	0.00639	POS	lncRNA	Gm49733	16	-31.7	-0.1157	Trans
ENSMUSG00000087593.1	0.99	8.50E-05	0.0064	POS	lncRNA	Gm16174	7	-42.94	-0.1245	Trans
ENSMUSG00000072612.3	0.99	8.55E-05	0.00641	POS	lncRNA	Gm10382	5	-98.31	-0.1269	Trans
ENSMUSG00000085505.1	0.99	9.27E-05	0.00653	POS	lncRNA	Gm12868	4	-50.63	-0.1253	Cis Trans
ENSMUSG00000086683.1	0.99	9.44E-05	0.00656	POS	lncRNA	Gm12867	4	-34.59	-0.1064	Trans
ENSMUSG00000057359.7	0.99	9.57E-05	0.00658	POS	lncRNA	Gm17494	3	-76.18	-0.113	Trans
ENSMUSG00000072612.3	0.99	9.60E-05	0.00659	POS	lncRNA	Gm10382	5	-77.94	-0.1007	Trans
ENSMUSG00000111895.1	0.99	9.63E-05	0.00659	POS	lncRNA	Gm47252	4	-65.45	-0.1111	Cis Trans
ENSMUSG00000116739.1	0.99	9.65E-05	0.0066	POS	lncRNA	Gm49733	16	-28.7	-0.1083	Trans
ENSMUSG00000116097.1	0.99	9.66E-05	0.0066	POS	lncRNA	Gm36738	15	-36.14	-0.1009	Trans
ENSMUSG00000085505.1	0.99	9.69E-05	0.00661	POS	lncRNA	Gm12868	4	-42.34	-0.1103	Cis Trans
ENSMUSG00000085505.1	0.99	9.69E-05	0.00661	POS	lncRNA	Gm12868	4	-33.35	-0.1273	Cis Trans
ENSMUSG00000085505.1	0.99	9.84E-05	0.00663	POS	lncRNA	Gm12868	4	-38.02	-0.1077	Cis Trans
ENSMUSG00000100779.1	0.99	9.92E-05	0.00664	POS	lncRNA	Gm29292	11	-55.87	-0.1592	Trans
ENSMUSG00000085505.1	0.99	1.00E-04	0.00665	POS	lncRNA	Gm12868	4	-29.74	-0.1239	Cis Trans

ENSMUSG00000113019.1	0.99	0.0001	0.00666	POS	lncRNA	Gm47467	13	-21.33	-0.1198	Trans
ENSMUSG00000116739.1	0.99	0.0001	0.00666	POS	lncRNA	Gm49733	16	-23.7	-0.1113	Trans
ENSMUSG00000106015.1	0.99	0.0001	0.00666	POS	lncRNA	Gm42980	5	-51.08	-0.1087	Trans
ENSMUSG00000116739.1	0.99	0.0001	0.00667	POS	lncRNA	Gm49733	16	-32.87	-0.1126	Trans
ENSMUSG00000057359.7	0.99	0.0001	0.00667	POS	lncRNA	Gm17494	3	-77.56	-0.1015	Trans
ENSMUSG00000116739.1	0.99	0.0001	0.0067	POS	lncRNA	Gm49733	16	-24.59	-0.1055	Trans
ENSMUSG00000111895.1	0.99	0.0001	0.00673	POS	lncRNA	Gm47252	4	-62.3	-0.1065	Cis_Trans
ENSMUSG00000110433.1	0.99	0.00011	0.00673	POS	lncRNA	Gm45820	8	-40.25	-0.122	Trans
ENSMUSG00000097418.7	0.99	0.00011	0.00674	POS	lncRNA	Mir155hg	16	-50.38	-0.1153	Trans
ENSMUSG00000116739.1	0.99	0.00011	0.00675	POS	lncRNA	Gm49733	16	-30.64	-0.1178	Trans
ENSMUSG00000106980.1	0.99	0.00011	0.00676	POS	lncRNA	Gm43690	5	-22.66	-0.1016	Trans
ENSMUSG00000108332.1	0.99	0.00011	0.00678	POS	lncRNA	D530033B14Rik	7	-54.32	-0.1031	Trans
ENSMUSG00000106980.1	0.99	0.00011	0.00679	POS	lncRNA	Gm43690	5	-20.4	-0.1872	Trans
ENSMUSG00000072612.3	0.99	0.00011	0.00679	POS	lncRNA	Gm10382	5	-107.51	-0.1084	Trans
ENSMUSG00000108449.1	0.99	0.00011	0.00681	POS	lncRNA	Gm44507	7	-35.41	-0.1142	Trans
ENSMUSG00000108449.1	0.99	0.00011	0.00685	POS	lncRNA	Gm44507	7	-41.78	-0.1222	Trans
ENSMUSG00000097885.7	0.99	0.00011	0.00686	POS	lncRNA	5031434O11Rik	3	-61.71	-0.1128	Trans
ENSMUSG00000113494.1	0.99	0.00011	0.00687	POS	lncRNA	Gm48102	13	-35.23	-0.1081	Trans
ENSMUSG00000085505.1	0.99	0.00011	0.00688	POS	lncRNA	Gm12868	4	-28.95	-0.1005	Cis_Trans
ENSMUSG00000087623.1	0.99	0.00012	0.0069	POS	lncRNA	Gm12404	4	-51.65	-0.1272	Cis_Trans
ENSMUSG00000106980.1	0.99	0.00012	0.0069	POS	lncRNA	Gm43690	5	-27.26	-0.1126	Trans
ENSMUSG00000116739.1	0.99	0.00012	0.00691	POS	lncRNA	Gm49733	16	-25.13	-0.1034	Trans
ENSMUSG00000097418.7	0.99	0.00012	0.00694	POS	lncRNA	Mir155hg	16	-50.07	-0.1647	Trans
ENSMUSG00000084960.1	0.99	0.00012	0.00698	POS	lncRNA	B430010I23Rik	8	-269.29	-0.1162	Cis
ENSMUSG00000105509.1	0.99	0.00012	0.00698	POS	lncRNA	C130013H08Rik	3	-122.74	-0.1161	Trans
ENSMUSG00000110433.1	0.99	0.00012	0.007	POS	lncRNA	Gm45820	8	-31.11	-0.1058	Trans
ENSMUSG00000087593.1	0.99	0.00012	0.00701	POS	lncRNA	Gm16174	7	-34.65	-0.101	Trans

ENSMUSG00000116097.1	0.99	0.00013	0.00705	POS	lncRNA	Gm36738	15	-39.24	-0.1019	Trans
ENSMUSG00000085505.1	0.99	0.00013	0.00705	POS	lncRNA	Gm12868	4	-40.01	-0.1008	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00013	0.00707	POS	lncRNA	Gm49733	16	-29.85	-0.1059	Trans
ENSMUSG00000108449.1	0.99	0.00013	0.0071	POS	lncRNA	Gm44507	7	-36.37	-0.1155	Trans
ENSMUSG00000085505.1	0.99	0.00013	0.00711	POS	lncRNA	Gm12868	4	-27.96	-0.1059	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00013	0.00712	POS	lncRNA	Gm49733	16	-31.56	-0.1489	Trans
ENSMUSG00000116739.1	0.99	0.00013	0.00714	POS	lncRNA	Gm49733	16	-26.09	-0.1061	Trans
ENSMUSG00000116657.1	0.99	0.00014	0.00717	POS	lncRNA	Gm49774	17	-81.83	-0.1075	Trans
ENSMUSG00000116739.1	0.99	0.00014	0.00722	POS	lncRNA	Gm49733	16	-32.93	-0.1224	Trans
ENSMUSG00000116739.1	0.99	0.00014	0.00725	POS	lncRNA	Gm49733	16	-19.2	-0.1185	Trans
ENSMUSG00000116739.1	0.99	0.00014	0.00726	POS	lncRNA	Gm49733	16	-29.72	-0.1179	Trans
ENSMUSG00000085505.1	0.99	0.00015	0.00729	POS	lncRNA	Gm12868	4	-41.34	-0.1034	Cis_Trans
ENSMUSG00000101655.1	0.99	0.00015	0.00731	POS	lncRNA	2310040G24Rik	6	-54.36	-0.1128	Trans
ENSMUSG00000073778.2	0.99	0.00015	0.00732	POS	lncRNA	Faddos	7	-56.87	-0.1168	Trans
ENSMUSG00000097418.7	0.99	0.00015	0.00733	POS	lncRNA	Mir155hg	16	-35.58	-0.1214	Trans
ENSMUSG00000052291.8	0.99	0.00015	0.00733	POS	lncRNA	5330438D12Rik	10	-125.85	-0.1383	Trans
ENSMUSG00000116657.1	0.99	0.00015	0.00735	POS	lncRNA	Gm49774	17	-147.22	-0.1035	Trans
ENSMUSG00000116739.1	0.99	0.00015	0.00737	POS	lncRNA	Gm49733	16	-27.48	-0.1053	Trans
ENSMUSG00000113494.1	0.99	0.00015	0.00739	POS	lncRNA	Gm48102	13	-31.14	-0.1078	Trans
ENSMUSG00000108449.1	0.99	0.00016	0.00742	POS	lncRNA	Gm44507	7	-33.25	-0.1005	Trans
ENSMUSG00000110834.1	0.99	0.00016	0.00742	POS	lncRNA	Gm39469	9	-27.26	-0.1336	Trans
ENSMUSG00000090230.1	0.99	0.00016	0.00743	POS	lncRNA	Gm16315	10	-43.56	-0.1035	Trans
ENSMUSG00000097418.7	0.99	0.00016	0.00744	POS	lncRNA	Mir155hg	16	-35.09	-0.3025	Trans
ENSMUSG00000106980.1	0.99	0.00016	0.00746	POS	lncRNA	Gm43690	5	-24.77	-0.1045	Trans
ENSMUSG00000116739.1	0.99	0.00016	0.00746	POS	lncRNA	Gm49733	16	-30.08	-0.1203	Trans
ENSMUSG00000108449.1	0.99	0.00016	0.00747	POS	lncRNA	Gm44507	7	-34.2	-0.1024	Trans
ENSMUSG00000100502.1	0.99	0.00016	0.00747	POS	lncRNA	Gm28286	1	-56.21	-0.1193	Trans

ENSMUSG00000086683.1	0.99	0.00016	0.00748	POS	lncRNA	Gm12867	4	-33.5	-0.1139	Trans
ENSMUSG00000085505.1	0.99	0.00016	0.00749	POS	lncRNA	Gm12868	4	-33.31	-0.1044	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00016	0.0075	POS	lncRNA	Gm49733	16	-26.62	-0.1173	Trans
ENSMUSG00000116739.1	0.99	0.00016	0.0075	POS	lncRNA	Gm49733	16	-23.97	-0.1065	Trans
ENSMUSG00000103400.2	0.99	0.00016	0.00751	POS	lncRNA	Gm15853	1	-141.45	-0.1097	Trans
ENSMUSG00000097418.7	0.99	0.00016	0.00752	POS	lncRNA	Mir155hg	16	-39.18	-0.1085	Trans
ENSMUSG00000072612.3	0.99	0.00016	0.00752	POS	lncRNA	Gm10382	5	-90.78	-0.1028	Trans
ENSMUSG00000116739.1	0.99	0.00017	0.00753	POS	lncRNA	Gm49733	16	-29.57	-0.1264	Trans
ENSMUSG00000084940.2	0.99	0.00017	0.00753	POS	lncRNA	Gm15935	14	-58.61	-0.1021	Cis_Trans
ENSMUSG00000086695.1	0.99	0.00017	0.00753	POS	lncRNA	Gm15247	X	-37.73	-0.1003	Cis_Trans
ENSMUSG00000110588.1	0.99	0.00017	0.00753	POS	lncRNA	Gm45774	8	-287.6	-1.0458	Cis
ENSMUSG00000085505.1	0.99	0.00017	0.00754	POS	lncRNA	Gm12868	4	-39.38	-0.1176	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00017	0.00754	POS	lncRNA	Gm49733	16	-25.14	-0.1047	Trans
ENSMUSG00000106980.1	0.99	0.00017	0.00755	POS	lncRNA	Gm43690	5	-25.35	-0.1196	Trans
ENSMUSG00000110433.1	0.99	0.00017	0.00758	POS	lncRNA	Gm45820	8	-31.09	-0.1095	Trans
ENSMUSG00000075514.4	0.99	0.00017	0.0076	POS	lncRNA	Gm13375	2	-72.01	-0.1268	Trans
ENSMUSG00000116739.1	0.99	0.00017	0.00763	POS	lncRNA	Gm49733	16	-27.97	-0.1266	Trans
ENSMUSG00000116739.1	0.99	0.00018	0.00765	POS	lncRNA	Gm49733	16	-28.51	-0.1076	Trans
ENSMUSG00000116739.1	0.99	0.00018	0.00768	POS	lncRNA	Gm49733	16	-29.93	-0.1084	Trans
ENSMUSG00000110433.1	0.99	0.00018	0.00768	POS	lncRNA	Gm45820	8	-30.89	-0.1013	Trans
ENSMUSG00000106980.1	0.99	0.00018	0.00769	POS	lncRNA	Gm43690	5	-23.94	-0.1014	Trans
ENSMUSG00000097885.7	0.99	0.00018	0.00771	POS	lncRNA	5031434O11Rik	3	-100.52	-0.1036	Trans
ENSMUSG00000114438.1	0.99	0.00018	0.00772	POS	lncRNA	Gm47827	13	-24.79	-0.1112	Trans
ENSMUSG00000085213.1	0.99	0.00018	0.00772	POS	lncRNA	Gm13091	4	-32.61	-0.1136	Trans
ENSMUSG00000085505.1	0.99	0.00019	0.00774	POS	lncRNA	Gm12868	4	-33.81	-0.1084	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00019	0.00776	POS	lncRNA	Gm49733	16	-29.42	-0.111	Trans
ENSMUSG00000087541.1	0.99	0.00019	0.00776	POS	lncRNA	Hopxos	5	-224.17	-0.3244	Cis_Trans

ENSMUSG00000108449.1	0.99	0.00019	0.00778	POS	lncRNA	Gm44507	7	-40.36	-0.1246	Trans
ENSMUSG00000084940.2	0.99	0.00019	0.00778	POS	lncRNA	Gm15935	14	-46.74	-0.1118	Cis_Trans
ENSMUSG00000106980.1	0.99	0.00019	0.0078	POS	lncRNA	Gm43690	5	-27.7	-0.1131	Trans
ENSMUSG00000106980.1	0.99	0.00019	0.0078	POS	lncRNA	Gm43690	5	-28.97	-0.1173	Trans
ENSMUSG00000087593.1	0.99	0.00019	0.00782	POS	lncRNA	Gm16174	7	-41.63	-0.107	Trans
ENSMUSG00000108449.1	0.99	0.00019	0.00782	POS	lncRNA	Gm44507	7	-35.27	-0.1106	Trans
ENSMUSG00000116739.1	0.99	0.00019	0.00783	POS	lncRNA	Gm49733	16	-33.44	-0.1257	Trans
ENSMUSG00000116739.1	0.99	0.00019	0.00783	POS	lncRNA	Gm49733	16	-23.75	-0.1439	Trans
ENSMUSG00000116739.1	0.99	0.00019	0.00784	POS	lncRNA	Gm49733	16	-31.71	-0.121	Trans
ENSMUSG00000085829.1	0.99	0.00019	0.00785	POS	lncRNA	Gm4285	14	-111.89	-0.1263	Trans
ENSMUSG00000113494.1	0.99	0.0002	0.00788	POS	lncRNA	Gm48102	13	-33.52	-0.101	Trans
ENSMUSG00000116739.1	0.99	0.0002	0.00789	POS	lncRNA	Gm49733	16	-25.92	-0.1041	Trans
ENSMUSG00000116739.1	0.99	0.0002	0.00789	POS	lncRNA	Gm49733	16	-27.36	-0.1025	Trans
ENSMUSG00000085829.1	0.99	0.0002	0.0079	POS	lncRNA	Gm4285	14	-94.05	-0.1153	Trans
ENSMUSG00000108449.1	0.99	0.0002	0.00791	POS	lncRNA	Gm44507	7	-32.64	-0.1014	Trans
ENSMUSG00000106980.1	0.99	0.0002	0.00792	POS	lncRNA	Gm43690	5	-21.46	-0.1219	Trans
ENSMUSG00000087528.1	0.99	0.00021	0.00796	POS	lncRNA	9830144P21Rik	2	-311.86	-0.1201	Cis
ENSMUSG00000116739.1	0.99	0.00021	0.00798	POS	lncRNA	Gm49733	16	-29.55	-0.1026	Trans
ENSMUSG00000085213.1	0.99	0.00021	0.00799	POS	lncRNA	Gm13091	4	-38.43	-0.1294	Trans
ENSMUSG00000072612.3	0.99	0.00021	0.00801	POS	lncRNA	Gm10382	5	-61.93	-0.1071	Trans
ENSMUSG00000087593.1	0.99	0.00021	0.00801	POS	lncRNA	Gm16174	7	-40.96	-0.1056	Trans
ENSMUSG00000116739.1	0.99	0.00021	0.00804	POS	lncRNA	Gm49733	16	-24.42	-0.118	Trans
ENSMUSG00000072612.3	0.99	0.00022	0.00807	POS	lncRNA	Gm10382	5	-129.39	-0.1083	Trans
ENSMUSG00000110433.1	0.99	0.00022	0.00809	POS	lncRNA	Gm45820	8	-40.08	-0.1182	Trans
ENSMUSG00000057359.7	0.99	0.00022	0.0081	POS	lncRNA	Gm17494	3	-90.39	-0.1393	Trans
ENSMUSG00000111895.1	0.99	0.00022	0.00811	POS	lncRNA	Gm47252	4	-61.34	-0.1065	Cis_Trans
ENSMUSG00000085505.1	0.99	0.00022	0.00811	POS	lncRNA	Gm12868	4	-39.86	-0.1052	Cis_Trans

ENSMUSG00000087593.1	0.99	0.00022	0.00811	POS	lncRNA	Gm16174	7	-43.52	-0.1233	Trans
ENSMUSG00000116097.1	0.99	0.00022	0.00815	POS	lncRNA	Gm36738	15	-35.37	-0.1005	Trans
ENSMUSG00000110433.1	0.99	0.00023	0.00816	POS	lncRNA	Gm45820	8	-32.76	-0.1088	Trans
ENSMUSG00000116739.1	0.99	0.00023	0.00816	POS	lncRNA	Gm49733	16	-25.43	-0.1005	Trans
ENSMUSG00000106980.1	0.99	0.00023	0.00816	POS	lncRNA	Gm43690	5	-27.03	-0.104	Trans
ENSMUSG00000105283.1	0.99	0.00023	0.00816	POS	lncRNA	Gm33370	5	-35.3	-0.123	Trans
ENSMUSG00000085501.1	0.99	0.00023	0.00817	POS	lncRNA	Gm11772	11	-27.09	-0.1759	Trans
ENSMUSG00000085505.1	0.99	0.00023	0.00817	POS	lncRNA	Gm12868	4	-128.85	-0.3364	Cis_Trans
ENSMUSG00000085829.1	0.99	0.00023	0.00818	POS	lncRNA	Gm4285	14	-93.15	-0.1059	Trans
ENSMUSG00000097418.7	0.99	0.00023	0.0082	POS	lncRNA	Mir155hg	16	-34.29	-0.1805	Trans
ENSMUSG00000057359.7	0.99	0.00023	0.00821	POS	lncRNA	Gm17494	3	-155.71	-0.1013	Trans
ENSMUSG00000108449.1	0.99	0.00023	0.00821	POS	lncRNA	Gm44507	7	-39.37	-0.1312	Trans
ENSMUSG00000097418.7	0.99	0.00023	0.00822	POS	lncRNA	Mir155hg	16	-34.25	-0.1215	Trans
ENSMUSG00000113494.1	0.99	0.00023	0.00823	POS	lncRNA	Gm48102	13	-41.08	-0.1272	Trans
ENSMUSG00000108449.1	0.99	0.00023	0.00824	POS	lncRNA	Gm44507	7	-37.07	-0.1117	Trans
ENSMUSG00000106980.1	0.99	0.00024	0.00825	POS	lncRNA	Gm43690	5	-23.99	-0.1263	Trans
ENSMUSG00000085501.1	0.99	0.00024	0.00826	POS	lncRNA	Gm11772	11	-27.49	-0.1233	Trans
ENSMUSG00000108449.1	0.99	0.00024	0.00827	POS	lncRNA	Gm44507	7	-33.33	-0.1061	Trans
ENSMUSG00000106980.1	0.99	0.00024	0.00827	POS	lncRNA	Gm43690	5	-24.33	-0.1406	Trans
ENSMUSG00000108449.1	0.99	0.00024	0.00828	POS	lncRNA	Gm44507	7	-31.53	-0.1007	Trans
ENSMUSG00000087593.1	0.99	0.00024	0.00828	POS	lncRNA	Gm16174	7	-38.6	-0.106	Trans
ENSMUSG00000087338.2	0.99	0.00024	0.00831	POS	lncRNA	Scpep1os	11	-95.37	-0.1472	Trans
ENSMUSG00000116739.1	0.99	0.00025	0.00834	POS	lncRNA	Gm49733	16	-20.99	-0.1099	Trans
ENSMUSG00000111895.1	0.99	0.00025	0.00835	POS	lncRNA	Gm47252	4	-59.38	-0.1013	Cis_Trans
ENSMUSG00000110433.1	0.99	0.00025	0.00836	POS	lncRNA	Gm45820	8	-42.64	-0.1312	Trans
ENSMUSG00000116739.1	0.99	0.00025	0.00836	POS	lncRNA	Gm49733	16	-26.78	-0.1034	Trans
ENSMUSG00000097418.7	0.99	0.00025	0.00836	POS	lncRNA	Mir155hg	16	-29.07	-0.1454	Trans

ENSMUSG00000111895.1	0.99	0.00025	0.00838	POS	lncRNA	Gm47252	4	-56.78	-0.1018	Cis_Trans
ENSMUSG00000103400.2	0.99	0.00025	0.00838	POS	lncRNA	Gm15853	1	-142	-0.4494	Trans
ENSMUSG00000085505.1	0.99	0.00025	0.00838	POS	lncRNA	Gm12868	4	-45.48	-0.1163	Cis_Trans
ENSMUSG00000097418.7	0.99	0.00025	0.00841	POS	lncRNA	Mir155hg	16	-40.58	-0.1173	Trans
ENSMUSG00000087593.1	0.99	0.00025	0.00841	POS	lncRNA	Gm16174	7	-39.02	-0.1124	Trans
ENSMUSG00000085505.1	0.99	0.00025	0.00841	POS	lncRNA	Gm12868	4	-35.07	-0.111	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00025	0.00842	POS	lncRNA	Gm49733	16	-31.02	-0.1092	Trans
ENSMUSG00000084940.2	0.99	0.00025	0.00842	POS	lncRNA	Gm15935	14	-34.42	-0.1103	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00025	0.00842	POS	lncRNA	Gm49733	16	-25.68	-0.1019	Trans
ENSMUSG00000087338.2	0.99	0.00025	0.00843	POS	lncRNA	Scpep1os	11	-116.6	-0.1555	Trans
ENSMUSG00000085505.1	0.99	0.00026	0.00845	POS	lncRNA	Gm12868	4	-41.6	-0.1012	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00026	0.00846	POS	lncRNA	Gm49733	16	-30.95	-0.1159	Trans
ENSMUSG00000116097.1	0.99	0.00026	0.0085	POS	lncRNA	Gm36738	15	-31.06	-0.1134	Trans
ENSMUSG00000100017.2	0.99	0.00026	0.00851	POS	lncRNA	2410022M11Rik	14	-100.69	-0.1296	Trans
ENSMUSG00000116739.1	0.99	0.00026	0.00851	POS	lncRNA	Gm49733	16	-28.69	-0.1176	Trans
ENSMUSG00000116739.1	0.99	0.00026	0.00851	POS	lncRNA	Gm49733	16	-23.41	-0.105	Trans
ENSMUSG00000085829.1	0.99	0.00027	0.00853	POS	lncRNA	Gm4285	14	-131.54	-0.1488	Trans
ENSMUSG00000112302.1	0.99	0.00027	0.00858	POS	lncRNA	Gm48226	12	-100.7	-0.1494	Trans
ENSMUSG00000087593.1	0.99	0.00027	0.00858	POS	lncRNA	Gm16174	7	-40	-0.1005	Trans
ENSMUSG00000100017.2	0.99	0.00027	0.00859	POS	lncRNA	2410022M11Rik	14	-78.18	-0.1065	Trans
ENSMUSG00000085505.1	0.99	0.00027	0.00859	POS	lncRNA	Gm12868	4	-44.09	-0.1075	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00028	0.00862	POS	lncRNA	Gm49733	16	-24.39	-0.1051	Trans
ENSMUSG00000110433.1	0.99	0.00028	0.00864	POS	lncRNA	Gm45820	8	-24.71	-0.1013	Trans
ENSMUSG00000087593.1	0.99	0.00028	0.00866	POS	lncRNA	Gm16174	7	-36.97	-0.1033	Trans
ENSMUSG00000086683.1	0.99	0.00028	0.00866	POS	lncRNA	Gm12867	4	-35.38	-0.1156	Trans
ENSMUSG00000116739.1	0.99	0.00028	0.00867	POS	lncRNA	Gm49733	16	-18.48	-0.154	Trans
ENSMUSG00000085505.1	0.99	0.00028	0.00867	POS	lncRNA	Gm12868	4	-40.26	-0.1017	Cis_Trans

ENSMUSG00000106980.1	0.99	0.00028	0.00867	POS	lncRNA	Gm43690	5	-27.68	-0.1077	Trans
ENSMUSG00000116739.1	0.99	0.00028	0.00868	POS	lncRNA	Gm49733	16	-27.54	-0.1089	Trans
ENSMUSG00000106980.1	0.99	0.00029	0.00872	POS	lncRNA	Gm43690	5	-30.43	-0.1237	Trans
ENSMUSG00000085505.1	0.99	0.00029	0.00873	POS	lncRNA	Gm12868	4	-43.79	-0.114	Cis_Trans
ENSMUSG00000116739.1	0.99	0.00029	0.00874	POS	lncRNA	Gm49733	16	-28.71	-0.1083	Trans
ENSMUSG00000090327.1	0.99	0.00029	0.00874	POS	lncRNA	Gm17111	12	-47.51	-0.132	Trans
ENSMUSG00000111713.1	0.99	0.00029	0.00875	POS	lncRNA	Gm20234	11	-61.25	-0.1114	Trans
ENSMUSG00000108449.1	0.99	0.00029	0.00877	POS	lncRNA	Gm44507	7	-37.37	-0.1119	Trans
ENSMUSG00000075514.4	0.99	0.00029	0.0088	POS	lncRNA	Gm13375	2	-77.87	-0.177	Trans
ENSMUSG00000108449.1	0.99	0.0003	0.00881	POS	lncRNA	Gm44507	7	-37.46	-0.1205	Trans
ENSMUSG00000085501.1	0.99	0.0003	0.00888	POS	lncRNA	Gm11772	11	-28.63	-0.1141	Trans
ENSMUSG00000085505.1	0.99	0.00031	0.00889	POS	lncRNA	Gm12868	4	-36.54	-0.1214	Cis_Trans
ENSMUSG00000042549.10	0.99	0.00031	0.0089	POS	lncRNA	Map2k3os	11	-45.74	-0.126	Trans
ENSMUSG00000111895.1	0.99	0.00031	0.00891	POS	lncRNA	Gm47252	4	-56.14	-0.103	Cis_Trans
ENSMUSG00000111895.1	0.99	0.00031	0.00892	POS	lncRNA	Gm47252	4	-62.37	-0.1043	Cis_Trans
ENSMUSG00000075514.4	0.99	0.00031	0.00895	POS	lncRNA	Gm13375	2	-45.37	-0.1175	Trans
ENSMUSG00000116097.1	0.99	0.00031	0.00897	POS	lncRNA	Gm36738	15	-38.43	-0.1047	Trans
ENSMUSG00000110834.1	0.99	0.00032	0.00898	POS	lncRNA	Gm39469	9	-25.71	-0.1339	Trans
ENSMUSG00000106980.1	0.99	0.00032	0.00898	POS	lncRNA	Gm43690	5	-28.28	-0.1079	Trans
ENSMUSG00000116739.1	0.99	0.00032	0.00899	POS	lncRNA	Gm49733	16	-28.27	-0.1113	Trans
ENSMUSG00000116739.1	0.99	0.00032	0.00901	POS	lncRNA	Gm49733	16	-31.59	-0.1112	Trans
ENSMUSG00000087541.1	0.99	0.00032	0.00902	POS	lncRNA	Hopxos	5	-109.68	-0.1249	Cis_Trans
ENSMUSG00000085501.1	0.99	0.00032	0.00902	POS	lncRNA	Gm11772	11	-41	-0.1349	Trans
ENSMUSG00000084940.2	0.99	0.00032	0.00902	POS	lncRNA	Gm15935	14	-51.22	-0.1085	Cis_Trans
ENSMUSG00000108449.1	0.99	0.00032	0.00903	POS	lncRNA	Gm44507	7	-39.29	-0.1156	Trans
ENSMUSG00000116097.1	0.99	0.00033	0.00906	POS	lncRNA	Gm36738	15	-35.77	-0.1025	Trans
ENSMUSG00000116739.1	0.99	0.00033	0.00907	POS	lncRNA	Gm49733	16	-23.45	-0.1196	Trans

ENSMUSG00000106980.1	0.99	0.00033	0.00908	POS	lncRNA	Gm43690	5	-28.05	-0.1189	Trans
ENSMUSG00000116739.1	0.99	0.00033	0.00909	POS	lncRNA	Gm49733	16	-25.58	-0.1103	Trans
ENSMUSG00000116739.1	0.99	0.00033	0.0091	POS	lncRNA	Gm49733	16	-26.78	-0.1003	Trans
ENSMUSG00000105283.1	0.99	0.00033	0.00911	POS	lncRNA	Gm33370	5	-45.8	-0.1002	Trans
ENSMUSG00000110433.1	0.99	0.00033	0.00913	POS	lncRNA	Gm45820	8	-36.07	-0.11	Trans
ENSMUSG00000108449.1	0.99	0.00034	0.00914	POS	lncRNA	Gm44507	7	-36.54	-0.1078	Trans
ENSMUSG00000108449.1	0.98	0.00034	0.00915	POS	lncRNA	Gm44507	7	-35.45	-0.1084	Trans
ENSMUSG00000116739.1	0.98	0.00034	0.00915	POS	lncRNA	Gm49733	16	-24.72	-0.1021	Trans
ENSMUSG00000116739.1	0.98	0.00034	0.00915	POS	lncRNA	Gm49733	16	-28.43	-0.1093	Trans
ENSMUSG00000087593.1	0.98	0.00034	0.00917	POS	lncRNA	Gm16174	7	-39.59	-0.1094	Trans
ENSMUSG00000116739.1	0.98	0.00034	0.00918	POS	lncRNA	Gm49733	16	-24.39	-0.1004	Trans
ENSMUSG00000085505.1	0.98	0.00034	0.0092	POS	lncRNA	Gm12868	4	-32.88	-0.162	Cis_Trans
ENSMUSG00000116739.1	0.98	0.00035	0.00922	POS	lncRNA	Gm49733	16	-30.1	-0.1075	Trans
ENSMUSG00000084940.2	0.98	0.00035	0.00923	POS	lncRNA	Gm15935	14	-43.09	-0.1043	Cis_Trans
ENSMUSG00000072612.3	0.98	0.00035	0.00924	POS	lncRNA	Gm10382	5	-122.8	-0.1256	Trans
ENSMUSG00000110433.1	0.98	0.00035	0.00924	POS	lncRNA	Gm45820	8	-35.14	-0.1098	Trans
ENSMUSG00000106980.1	0.98	0.00035	0.00925	POS	lncRNA	Gm43690	5	-21.5	-0.1059	Trans
ENSMUSG00000106980.1	0.98	0.00035	0.00926	POS	lncRNA	Gm43690	5	-23.07	-0.1442	Trans
ENSMUSG00000106980.1	0.98	0.00035	0.00928	POS	lncRNA	Gm43690	5	-23.26	-0.1052	Trans
ENSMUSG00000110433.1	0.98	0.00035	0.00928	POS	lncRNA	Gm45820	8	-35.76	-0.1142	Trans
ENSMUSG00000113494.1	0.98	0.00035	0.00928	POS	lncRNA	Gm48102	13	-35.95	-0.1045	Trans
ENSMUSG00000112302.1	0.98	0.00035	0.00929	POS	lncRNA	Gm48226	12	-79.95	-0.1149	Trans
ENSMUSG00000085505.1	0.98	0.00036	0.0093	POS	lncRNA	Gm12868	4	-40.64	-0.1013	Cis_Trans
ENSMUSG00000110433.1	0.98	0.00036	0.00931	POS	lncRNA	Gm45820	8	-39.93	-0.1128	Trans
ENSMUSG00000116739.1	0.98	0.00036	0.00931	POS	lncRNA	Gm49733	16	-25.48	-0.1066	Trans
ENSMUSG00000109424.1	0.98	0.00036	0.00932	POS	lncRNA	Gm44658	7	-62.83	-0.1087	Trans
ENSMUSG00000113494.1	0.98	0.00036	0.00932	POS	lncRNA	Gm48102	13	-45.81	-0.1332	Trans

ENSMUSG00000116739.1	0.98	0.00036	0.00932	POS	lncRNA	Gm49733	16	-21.54	-0.1099	Trans
ENSMUSG00000116739.1	0.98	0.00036	0.00932	POS	lncRNA	Gm49733	16	-27.03	-0.1016	Trans
ENSMUSG00000106980.1	0.98	0.00037	0.00938	POS	lncRNA	Gm43690	5	-29.03	-0.1157	Trans
ENSMUSG00000092626.1	0.98	0.00037	0.00939	POS	lncRNA	9130230N09Rik	11	-58.46	-0.1929	Trans
ENSMUSG00000090327.1	0.98	0.00037	0.00939	POS	lncRNA	Gm17111	12	-40.22	-0.1042	Trans
ENSMUSG00000117575.1	0.98	0.00037	0.00942	POS	lncRNA	Gm36486	17	-48.66	-0.1029	Trans
ENSMUSG00000106980.1	0.98	0.00037	0.00943	POS	lncRNA	Gm43690	5	-24.06	-0.1037	Trans
ENSMUSG00000105509.1	0.98	0.00038	0.00944	POS	lncRNA	C130013H08Rik	3	-98.73	-0.1143	Trans
ENSMUSG00000108449.1	0.98	0.00038	0.00944	POS	lncRNA	Gm44507	7	-35.39	-0.1134	Trans
ENSMUSG00000106980.1	0.98	0.00038	0.00945	POS	lncRNA	Gm43690	5	-20.32	-0.1026	Trans
ENSMUSG00000057359.7	0.98	0.00038	0.00946	POS	lncRNA	Gm17494	3	-61.41	-0.101	Trans
ENSMUSG00000116739.1	0.98	0.00038	0.00946	POS	lncRNA	Gm49733	16	-21.33	-0.1083	Trans
ENSMUSG00000116739.1	0.98	0.00038	0.00947	POS	lncRNA	Gm49733	16	-25.22	-0.1073	Trans
ENSMUSG00000085505.1	0.98	0.00038	0.00947	POS	lncRNA	Gm12868	4	-40.36	-0.1177	Cis_Trans
ENSMUSG00000116739.1	0.98	0.00038	0.00948	POS	lncRNA	Gm49733	16	-28.75	-0.1038	Trans
ENSMUSG00000087593.1	0.98	0.00038	0.00948	POS	lncRNA	Gm16174	7	-39.2	-0.1023	Trans
ENSMUSG00000085505.1	0.98	0.00038	0.00949	POS	lncRNA	Gm12868	4	-42.52	-0.1146	Cis_Trans
ENSMUSG00000116739.1	0.98	0.00038	0.0095	POS	lncRNA	Gm49733	16	-30.04	-0.1202	Trans
ENSMUSG00000092626.1	0.98	0.00039	0.00951	POS	lncRNA	9130230N09Rik	11	-71.15	-0.1098	Trans
ENSMUSG00000086914.1	0.98	0.00039	0.00951	POS	lncRNA	Gm16124	9	-47.48	-0.1032	Trans
ENSMUSG00000086515.1	0.98	0.00039	0.00951	POS	lncRNA	Erich2os	2	-108.47	-0.2948	Cis_Trans
ENSMUSG00000085505.1	0.98	0.00039	0.00951	POS	lncRNA	Gm12868	4	-33.26	-0.1409	Cis_Trans
ENSMUSG00000116739.1	0.98	0.00039	0.00952	POS	lncRNA	Gm49733	16	-23.76	-0.102	Trans
ENSMUSG00000108449.1	0.98	0.00039	0.00957	POS	lncRNA	Gm44507	7	-40.11	-0.1197	Trans
ENSMUSG00000108449.1	0.98	0.00039	0.00957	POS	lncRNA	Gm44507	7	-35.58	-0.1062	Trans
ENSMUSG00000090230.1	0.98	0.0004	0.00957	POS	lncRNA	Gm16315	10	-48.51	-0.1064	Trans
ENSMUSG00000085505.1	0.98	0.0004	0.00958	POS	lncRNA	Gm12868	4	-36.59	-0.1122	Cis_Trans

ENSMUSG00000085505.1	0.98	0.0004	0.0096	POS	lncRNA	Gm12868	4	-38.04	-0.1057	Cis_Trans
ENSMUSG00000108449.1	0.98	0.0004	0.0096	POS	lncRNA	Gm44507	7	-36.38	-0.1123	Trans
ENSMUSG00000116739.1	0.98	0.0004	0.0096	POS	lncRNA	Gm49733	16	-28.78	-0.1074	Trans
ENSMUSG00000108449.1	0.98	0.0004	0.00961	POS	lncRNA	Gm44507	7	-42.03	-0.1251	Trans
ENSMUSG00000090230.1	0.98	0.0004	0.00961	POS	lncRNA	Gm16315	10	-66.5	-0.1073	Trans
ENSMUSG00000106980.1	0.98	0.00041	0.00966	POS	lncRNA	Gm43690	5	-26.35	-0.1506	Trans
ENSMUSG00000085178.1	0.98	0.00041	0.00968	POS	lncRNA	Kdm6bos	11	-212.6	-0.2681	Cis
ENSMUSG00000105283.1	0.98	0.00041	0.00968	POS	lncRNA	Gm33370	5	-26.37	-0.1305	Trans
ENSMUSG00000111895.1	0.98	0.00041	0.00969	POS	lncRNA	Gm47252	4	-58.71	-0.1021	Cis_Trans
ENSMUSG00000085505.1	0.98	0.00041	0.0097	POS	lncRNA	Gm12868	4	-47.72	-0.1164	Cis_Trans
ENSMUSG00000106980.1	0.98	0.00042	0.00975	POS	lncRNA	Gm43690	5	-18.94	-0.1108	Trans
ENSMUSG00000097418.7	0.98	0.00042	0.00975	POS	lncRNA	Mir155hg	16	-34.8	-0.2231	Trans
ENSMUSG00000072612.3	0.98	0.00042	0.00976	POS	lncRNA	Gm10382	5	-105.52	-0.1322	Trans
ENSMUSG00000110433.1	0.98	0.00042	0.00977	POS	lncRNA	Gm45820	8	-35.75	-0.1016	Trans
ENSMUSG00000087593.1	0.98	0.00043	0.0098	POS	lncRNA	Gm16174	7	-43.9	-0.1123	Trans
ENSMUSG00000116739.1	0.98	0.00043	0.0098	POS	lncRNA	Gm49733	16	-28.72	-0.1011	Trans
ENSMUSG00000090327.1	0.98	0.00043	0.00981	POS	lncRNA	Gm17111	12	-40.25	-0.1109	Trans
ENSMUSG00000113494.1	0.98	0.00044	0.00986	POS	lncRNA	Gm48102	13	-32.58	-0.1041	Trans
ENSMUSG00000103400.2	0.98	0.00044	0.00987	POS	lncRNA	Gm15853	1	-133.64	-0.4037	Trans
ENSMUSG00000106980.1	0.98	0.00044	0.00988	POS	lncRNA	Gm43690	5	-26.08	-0.106	Trans
ENSMUSG00000111895.1	0.98	0.00044	0.00988	POS	lncRNA	Gm47252	4	-60.88	-0.1123	Cis_Trans
ENSMUSG00000112302.1	0.98	0.00044	0.00989	POS	lncRNA	Gm48226	12	-74.42	-0.1065	Trans
ENSMUSG00000106980.1	0.98	0.00045	0.00993	POS	lncRNA	Gm43690	5	-20.38	-0.1415	Trans
ENSMUSG00000097313.2	0.98	0.00045	0.00995	POS	lncRNA	Gm26569	16	-70.39	-0.1067	Trans
ENSMUSG00000112302.1	0.98	0.00045	0.00997	POS	lncRNA	Gm48226	12	-100.65	-0.1366	Trans
ENSMUSG00000056735.5	-0.98	0.00045	0.00998	NEG	lncRNA	A930024E05Rik	5	-64.39	-0.1171	Trans
ENSMUSG00000090327.1	-0.98	0.00045	0.00997	NEG	lncRNA	Gm17111	12	-23.83	-0.1578	Trans

ENSMUSG00000090327.1	-0.98	0.00045	0.00995	NEG	lncRNA	Gm17111	12	-37.32	-0.1377	Trans
ENSMUSG00000087593.1	-0.98	0.00045	0.00994	NEG	lncRNA	Gm16174	7	-30.69	-0.1033	Trans
ENSMUSG00000087502.1	-0.98	0.00045	0.00992	NEG	lncRNA	Gm16091	8	-46.57	-0.1429	Trans
ENSMUSG00000116739.1	-0.98	0.00044	0.0099	NEG	lncRNA	Gm49733	16	-26.25	-0.1038	Trans
ENSMUSG00000116097.1	-0.98	0.00044	0.00986	NEG	lncRNA	Gm36738	15	-37.19	-0.1482	Trans
ENSMUSG00000085213.1	-0.98	0.00043	0.00982	NEG	lncRNA	Gm13091	4	-44.42	-0.1063	Trans
ENSMUSG00000087593.1	-0.98	0.00043	0.00979	NEG	lncRNA	Gm16174	7	-35.83	-0.1262	Trans
ENSMUSG00000103219.1	-0.98	0.00042	0.00976	NEG	lncRNA	Gm37787	1	-28.39	-0.1021	Trans
ENSMUSG00000090327.1	-0.98	0.00042	0.00974	NEG	lncRNA	Gm17111	12	-42.95	-0.1446	Trans
ENSMUSG00000116739.1	-0.98	0.00041	0.00969	NEG	lncRNA	Gm49733	16	-26.47	-0.1055	Trans
ENSMUSG00000087593.1	-0.98	0.0004	0.00964	NEG	lncRNA	Gm16174	7	-38.44	-0.108	Trans
ENSMUSG00000114438.1	-0.98	0.0004	0.00958	NEG	lncRNA	Gm47827	13	-24.72	-0.1056	Trans
ENSMUSG00000090327.1	-0.98	0.00039	0.00954	NEG	lncRNA	Gm17111	12	-37.99	-0.1262	Trans
ENSMUSG00000086515.1	-0.98	0.00039	0.00951	NEG	lncRNA	Erich2os	2	-34.19	-0.1276	Cis_Trans
ENSMUSG00000116739.1	-0.98	0.00037	0.00943	NEG	lncRNA	Gm49733	16	-28.48	-0.1187	Trans
ENSMUSG00000087593.1	-0.98	0.00037	0.00938	NEG	lncRNA	Gm16174	7	-44.67	-0.1295	Trans
ENSMUSG00000087593.1	-0.98	0.00035	0.00928	NEG	lncRNA	Gm16174	7	-32.79	-0.1097	Trans
ENSMUSG00000087593.1	-0.98	0.00035	0.00927	NEG	lncRNA	Gm16174	7	-44.81	-0.1164	Trans
ENSMUSG00000087593.1	-0.98	0.00035	0.00927	NEG	lncRNA	Gm16174	7	-37.82	-0.1103	Trans
ENSMUSG00000108449.1	-0.98	0.00035	0.00924	NEG	lncRNA	Gm44507	7	-31.94	-0.1051	Trans
ENSMUSG00000108449.1	-0.98	0.00034	0.0092	NEG	lncRNA	Gm44507	7	-35.02	-0.1115	Trans
ENSMUSG00000108449.1	-0.99	0.00033	0.00913	NEG	lncRNA	Gm44507	7	-40.4	-0.1325	Trans
ENSMUSG00000106980.1	-0.99	0.00032	0.00903	NEG	lncRNA	Gm43690	5	-26.71	-0.1104	Trans
ENSMUSG00000087593.1	-0.99	0.00031	0.0089	NEG	lncRNA	Gm16174	7	-41.73	-0.1439	Trans
ENSMUSG00000108449.1	-0.99	0.00029	0.00872	NEG	lncRNA	Gm44507	7	-36.16	-0.1113	Trans
ENSMUSG00000108449.1	-0.99	0.00028	0.00864	NEG	lncRNA	Gm44507	7	-38.28	-0.1167	Trans
ENSMUSG00000087593.1	-0.99	0.00028	0.00864	NEG	lncRNA	Gm16174	7	-38.69	-0.1008	Trans

ENSMUSG00000113019.1	-0.99	0.00027	0.00856	NEG	lncRNA	Gm47467	13	-22.69	-0.106	Trans
ENSMUSG00000113019.1	-0.99	0.00027	0.00853	NEG	lncRNA	Gm47467	13	-21.87	-0.1163	Trans
ENSMUSG00000085505.1	-0.99	0.00026	0.00851	NEG	lncRNA	Gm12868	4	-44.96	-0.1141	Cis_Trans
ENSMUSG00000090327.1	-0.99	0.00026	0.00846	NEG	lncRNA	Gm17111	12	-46.85	-0.1312	Trans
ENSMUSG00000114203.1	-0.99	0.00026	0.00844	NEG	lncRNA	Gm35279	13	-44.66	-0.1679	Trans
ENSMUSG00000116097.1	-0.99	0.00025	0.00841	NEG	lncRNA	Gm36738	15	-34.87	-0.1301	Trans
ENSMUSG00000108449.1	-0.99	0.00024	0.00833	NEG	lncRNA	Gm44507	7	-39.21	-0.1371	Trans
ENSMUSG00000086515.1	-0.99	0.00023	0.00824	NEG	lncRNA	Erich2os	2	-37.15	-0.1371	Cis_Trans
ENSMUSG00000087593.1	-0.99	0.00022	0.00814	NEG	lncRNA	Gm16174	7	-41.5	-0.1035	Trans
ENSMUSG00000104818.1	-0.99	0.00021	0.00804	NEG	lncRNA	Gm43661	5	-68.1	-0.1033	Trans
ENSMUSG00000085213.1	-0.99	0.00021	0.00803	NEG	lncRNA	Gm13091	4	-41.42	-0.102	Trans
ENSMUSG00000087249.1	-0.99	0.0002	0.00791	NEG	lncRNA	Gm16062	11	-35.23	-0.145	Trans
ENSMUSG00000087593.1	-0.99	0.0002	0.00786	NEG	lncRNA	Gm16174	7	-38.72	-0.1011	Trans
ENSMUSG00000087502.1	-0.99	0.00018	0.00771	NEG	lncRNA	Gm16091	8	-53.82	-0.1278	Trans
ENSMUSG00000116097.1	-0.99	0.00017	0.00753	NEG	lncRNA	Gm36738	15	-38.1	-0.1033	Trans
ENSMUSG00000086119.2	-0.99	0.00016	0.00749	NEG	lncRNA	Gm2415	9	-117.3	-0.1191	Trans
ENSMUSG00000099843.1	-0.99	0.00016	0.00747	NEG	lncRNA	Gm7160	1	-72.82	-0.164	Trans
ENSMUSG00000085213.1	-0.99	0.00016	0.00742	NEG	lncRNA	Gm13091	4	-40.39	-0.1012	Trans
ENSMUSG00000104818.1	-0.99	0.00015	0.00735	NEG	lncRNA	Gm43661	5	-33.89	-0.1062	Trans
ENSMUSG00000116739.1	-0.99	0.00013	0.0071	NEG	lncRNA	Gm49733	16	-24.64	-0.1095	Trans
ENSMUSG00000090327.1	-0.99	0.00013	0.00708	NEG	lncRNA	Gm17111	12	-40.07	-0.1172	Trans
ENSMUSG00000116739.1	-0.99	0.00012	0.00694	NEG	lncRNA	Gm49733	16	-28.57	-0.1264	Trans
ENSMUSG00000099843.1	-0.99	0.00012	0.00692	NEG	lncRNA	Gm7160	1	-51.47	-0.1164	Trans
ENSMUSG00000099843.1	-0.99	0.00011	0.00685	NEG	lncRNA	Gm7160	1	-62.85	-0.1069	Trans
ENSMUSG00000084940.2	-0.99	0.00011	0.00684	NEG	lncRNA	Gm15935	14	-51.46	-0.1007	Cis_Trans
ENSMUSG00000087593.1	-0.99	0.0001	0.00673	NEG	lncRNA	Gm16174	7	-39.88	-0.1242	Trans
ENSMUSG00000116097.1	-0.99	0.0001	0.00669	NEG	lncRNA	Gm36738	15	-43.09	-0.1128	Trans

ENSMUSG00000084940.2	-0.99	9.85E-05	0.00663	NEG	lncRNA	Gm15935	14	-53.61	-0.1057	Cis_Trans
ENSMUSG000000116739.1	-0.99	9.44E-05	0.00656	NEG	lncRNA	Gm49733	16	-30.81	-0.1171	Trans
ENSMUSG000000106980.1	-0.99	9.39E-05	0.00655	NEG	lncRNA	Gm43690	5	-25.07	-0.1011	Trans
ENSMUSG000000087593.1	-0.99	8.35E-05	0.00637	NEG	lncRNA	Gm16174	7	-32.82	-0.1029	Trans
ENSMUSG000000116739.1	-0.99	8.25E-05	0.00635	NEG	lncRNA	Gm49733	16	-22.06	-0.1131	Trans
ENSMUSG000000086683.1	-0.99	5.72E-05	0.00589	NEG	lncRNA	Gm12867	4	-40.34	-0.1003	Trans
ENSMUSG000000116739.1	-0.99	4.05E-05	0.00549	NEG	lncRNA	Gm49733	16	-27.05	-0.1202	Trans
ENSMUSG000000116657.1	-1.00	3.23E-05	0.00526	NEG	lncRNA	Gm49774	17	-200.64	-0.1199	Trans
ENSMUSG000000097418.7	-1.00	2.53E-05	0.00507	NEG	lncRNA	Mir155hg	16	-47.66	-0.1027	Trans
ENSMUSG000000113019.1	-1.00	3.51E-06	0.00383	NEG	lncRNA	Gm47467	13	-21.19	-0.1536	Trans
ENSMUSG000000090327.1	-1.00	1.48E-06	0.00354	NEG	lncRNA	Gm17111	12	-44.76	-0.1119	Trans

Supplementary Material S1 Table - Interactions between lncRNAs and mRNAs – Target

Target	cor	p.value	FDR	Sinal	T_Biotype	T_Name	T_chr	dG	ndG
ENSMUSG000000011179.8	0.99968	1.53E-07	0.0031	POS	protein_coding	Odc1	12	-42.24	-0.1008
ENSMUSG000000021693.20	0.99945	4.62E-07	0.00329	POS	protein_coding	Kif2a	13	-31.19	-0.1072
ENSMUSG000000027219.13	0.99925	8.38E-07	0.00336	POS	protein_coding	Slc28a2	2	-42.95	-0.1042

ENSMUSG00000035299.16	0.99908	1.27E-06	0.00351	POS	protein_coding	Mid1	X	-148.17	-0.4071
ENSMUSG00000035299.16	0.99882	2.09E-06	0.00364	POS	protein_coding	Mid1	X	-181.96	-0.376
ENSMUSG00000028381.8	0.99882	2.10E-06	0.00364	POS	protein_coding	Ugcg	4	-110.48	-0.1669
ENSMUSG00000096351.2	0.99876	2.30E-06	0.00367	POS	protein_coding	Samd11	4	-233.02	-0.5522
ENSMUSG00000023809.10	0.9983	4.33E-06	0.0039	POS	protein_coding	Rps6ka2	17	-41.86	-0.1071
ENSMUSG00000001627.12	0.99816	5.06E-06	0.00394	POS	protein_coding	lfrd1	12	-31.83	-0.153
ENSMUSG00000035064.17	0.99798	6.10E-06	0.00407	POS	protein_coding	Eef2k	7	-36.03	-0.1015
ENSMUSG00000027782.10	0.99787	6.82E-06	0.00414	POS	protein_coding	Kpna4	3	-33.88	-0.103
ENSMUSG00000041703.7	0.99786	6.85E-06	0.00414	POS	protein_coding	Zic5	14	-59.17	-0.1074
ENSMUSG00000011179.8	0.99783	7.04E-06	0.00416	POS	protein_coding	Odc1	12	-36.62	-0.1032
ENSMUSG00000040447.15	0.99773	7.71E-06	0.0042	POS	protein_coding	Spns2	11	-26.56	-0.1054
ENSMUSG00000028859.14	0.99752	9.25E-06	0.00434	POS	protein_coding	Csf3r	4	-24.79	-0.1377
ENSMUSG00000041046.7	0.9973	1.09E-05	0.00446	POS	protein_coding	Ramp3	11	-22.79	-0.1055
ENSMUSG00000006435.16	0.9973	1.09E-05	0.00447	POS	protein_coding	Neur1a	19	-26.97	-0.1096
ENSMUSG00000031444.16	0.99726	1.12E-05	0.00448	POS	protein_coding	F10	8	-60.99	-0.1273
ENSMUSG00000018417.14	0.99711	1.26E-05	0.00458	POS	protein_coding	Myo1b	1	-32.66	-0.105

ENSMUSG00000033581.17	0.99709	1.27E-05	0.00459	POS	protein_coding	Igf2bp2	16	-29.31	-0.1004
ENSMUSG00000029378.5	0.99705	1.31E-05	0.0046	POS	protein_coding	Areg	5	-31.21	-0.1269
ENSMUSG00000024754.13	0.99704	1.31E-05	0.00461	POS	protein_coding	Cemip2	19	-28.54	-0.1008
ENSMUSG00000024524.17	0.99703	1.32E-05	0.00461	POS	protein_coding	Gnal	18	-44.89	-0.1261
ENSMUSG00000032741.9	0.99701	1.34E-05	0.00462	POS	protein_coding	Tpcn1	5	-35.05	-0.1204
ENSMUSG00000029236.4	0.99701	1.34E-05	0.00463	POS	protein_coding	Nmu	5	-30.54	-0.1345
ENSMUSG00000052336.7	0.99691	1.43E-05	0.00466	POS	protein_coding	Cx3cr1	9	-109.56	-0.1412
ENSMUSG00000036298.10	0.99691	1.43E-05	0.00466	POS	protein_coding	Slc2a13	15	-89.99	-0.1089
ENSMUSG00000030703.8	0.99685	1.48E-05	0.00468	POS	protein_coding	Gdpd3	7	-226.66	-0.3419
ENSMUSG00000040010.10	0.99685	1.49E-05	0.00468	POS	protein_coding	Slc7a5	8	-58.68	-0.1029
ENSMUSG00000029186.12	0.99682	1.51E-05	0.00469	POS	protein_coding	Pi4k2b	5	-40.6	-0.1624
ENSMUSG00000046329.14	0.9968	1.53E-05	0.0047	POS	protein_coding	Slc25a23	17	-38.45	-0.1923
ENSMUSG00000027782.10	0.99659	1.74E-05	0.00479	POS	protein_coding	Kpna4	3	-40.24	-0.1337
ENSMUSG00000026885.13	0.99659	1.74E-05	0.00479	POS	protein_coding	Tll11	2	-24.69	-0.1083
ENSMUSG00000015656.17	0.99656	1.78E-05	0.00482	POS	protein_coding	Hspa8	9	-35.02	-0.1152
ENSMUSG00000045193.13	0.99649	1.84E-05	0.00483	POS	protein_coding	Cirbp	10	-31.31	-0.1242

ENSMUSG00000023044.2	0.99648	1.86E-05	0.00484	POS	protein_coding	Csad	15	-21.67	-0.1147
ENSMUSG00000050423.11	0.9964	1.94E-05	0.00487	POS	protein_coding	Ppp1r3g	13	-39.4	-0.1045
ENSMUSG00000026126.15	0.99637	1.98E-05	0.00489	POS	protein_coding	Ptpn18	1	-189.51	-0.2363
ENSMUSG00000034586.14	0.9963	2.05E-05	0.00492	POS	protein_coding	Hid1	11	-35.44	-0.1534
ENSMUSG00000029186.12	0.99628	2.07E-05	0.00493	POS	protein_coding	Pi4k2b	5	-35.54	-0.109
ENSMUSG00000021752.13	0.99627	2.09E-05	0.00494	POS	protein_coding	Kctd6	14	-37.01	-0.1118
ENSMUSG00000021890.6	0.99626	2.09E-05	0.00494	POS	protein_coding	Eaf1	14	-29.05	-0.1157
ENSMUSG00000021768.15	0.99623	2.13E-05	0.00496	POS	protein_coding	Dusp13	14	-268.19	-0.444
ENSMUSG00000051316.8	0.9961	2.28E-05	0.00501	POS	protein_coding	Taf7	18	-25.33	-0.1248
ENSMUSG00000021978.9	0.9961	2.28E-05	0.00501	POS	protein_coding	Extl3	14	-22.85	-0.1078
ENSMUSG00000028909.17	0.99606	2.32E-05	0.00502	POS	protein_coding	Ptpru	4	-24.66	-0.1015
ENSMUSG00000058070.14	0.99605	2.34E-05	0.00502	POS	protein_coding	Eml1	12	-42.86	-0.1064
ENSMUSG00000042333.16	0.99599	2.41E-05	0.00503	POS	protein_coding	Tnfrsf14	4	-120.68	-0.1038
ENSMUSG00000066278.6	0.99587	2.55E-05	0.00507	POS	protein_coding	Vps37b	5	-62.19	-0.1156
ENSMUSG00000038332.13	0.99587	2.56E-05	0.00507	POS	protein_coding	Sesn1	10	-74.9	-0.1011
ENSMUSG00000034640.9	0.99585	2.58E-05	0.00508	POS	protein_coding	Tiparp	3	-35.21	-0.1339

ENSMUSG00000027333.18	0.99584	2.59E-05	0.00508	POS	protein_coding	Smox	2	-40.45	-0.1105
ENSMUSG00000028977.17	0.99584	2.60E-05	0.00508	POS	protein_coding	Casz1	4	-34.52	-0.145
ENSMUSG00000037493.6	0.9958	2.64E-05	0.00509	POS	protein_coding	Cib2	9	-45.91	-0.137
ENSMUSG00000049791.4	0.99573	2.74E-05	0.00512	POS	protein_coding	Fzd4	7	-34.99	-0.1048
ENSMUSG00000021504.14	0.99566	2.82E-05	0.00514	POS	protein_coding	B4galt7	13	-61.53	-0.1039
ENSMUSG00000022500.15	0.99563	2.86E-05	0.00516	POS	protein_coding	Litaf	16	-24.24	-0.116
ENSMUSG00000030494.13	0.99562	2.88E-05	0.00517	POS	protein_coding	Rhpn2	7	-28.06	-0.1109
ENSMUSG00000037434.7	0.99552	3.01E-05	0.0052	POS	protein_coding	Slc30a1	1	-35.81	-0.1321
ENSMUSG00000028645.11	0.9954	3.17E-05	0.00525	POS	protein_coding	Slc2a1	4	-26.98	-0.1003
ENSMUSG00000026135.17	0.9954	3.17E-05	0.00526	POS	protein_coding	Zfp142	1	-25.29	-0.1036
ENSMUSG00000045664.5	0.99523	3.41E-05	0.00532	POS	protein_coding	Cdc42ep2	19	-35.84	-0.1045
ENSMUSG00000024750.11	0.99493	3.84E-05	0.00542	POS	protein_coding	Zfand5	19	-28.03	-0.1058
ENSMUSG00000019850.11	0.9948	4.05E-05	0.00549	POS	protein_coding	Tnfaip3	10	-26.83	-0.1078
ENSMUSG00000035713.15	0.99476	4.11E-05	0.00551	POS	protein_coding	Usp35	7	-23.05	-0.138
ENSMUSG00000044646.15	0.99467	4.25E-05	0.00554	POS	protein_coding	Zbtb7c	18	-39.06	-0.1221
ENSMUSG00000020802.8	0.99461	4.35E-05	0.00557	POS	protein_coding	Ube2o	11	-33.33	-0.1182

ENSMUSG00000006930.15	0.99455	4.45E-05	0.0056	POS	protein_coding	Hap1	11	-25.26	-0.1027
ENSMUSG000000037295.7	0.99425	4.95E-05	0.00571	POS	protein_coding	Ldlrap1	4	-27.51	-0.1234
ENSMUSG000000035847.15	0.99424	4.97E-05	0.00572	POS	protein_coding	Ids	X	-22.98	-0.1242
ENSMUSG000000058013.11	0.99423	4.98E-05	0.00572	POS	protein_coding	Sept11	5	-34.67	-0.1204
ENSMUSG000000049804.9	0.99423	4.99E-05	0.00572	POS	protein_coding	Armcx4	X	-41.26	-0.1137
ENSMUSG000000063506.14	0.99418	5.07E-05	0.00574	POS	protein_coding	Arhgap22	14	-26.12	-0.1037
ENSMUSG000000018417.14	0.99405	5.31E-05	0.00579	POS	protein_coding	Myo1b	1	-50.21	-0.1614
ENSMUSG000000053641.9	0.99394	5.50E-05	0.00584	POS	protein_coding	Dennd4a	9	-26.4	-0.1043
ENSMUSG000000017428.16	0.99393	5.51E-05	0.00584	POS	protein_coding	Psmd11	11	-22.5	-0.1398
ENSMUSG000000035298.8	0.99392	5.54E-05	0.00585	POS	protein_coding	Klhl35	7	-32.96	-0.1282
ENSMUSG000000029248.14	0.99384	5.67E-05	0.00587	POS	protein_coding	Thegl	5	-22.54	-0.1156
ENSMUSG000000032845.16	0.99384	5.68E-05	0.00588	POS	protein_coding	Alpk2	18	-36.84	-0.1116
ENSMUSG000000048217.11	0.99383	5.70E-05	0.00588	POS	protein_coding	Nags	11	-37.87	-0.1076
ENSMUSG000000028862.6	0.99372	5.91E-05	0.00592	POS	protein_coding	Map3k6	4	-40.52	-0.1031
ENSMUSG000000052364.4	0.99368	5.97E-05	0.00593	POS	protein_coding	B630019K06Rik	X	-43.18	-0.1371
ENSMUSG000000090125.3	0.99359	6.16E-05	0.00597	POS	protein_coding	Pou3f1	4	-142.94	-0.1195

ENSMUSG00000068263.11	0.99355	6.23E-05	0.00598	POS	protein_coding	Efcc1	6	-33.9	-0.1066
ENSMUSG00000022540.16	0.99354	6.24E-05	0.00599	POS	protein_coding	Rogdi	16	-34.23	-0.1149
ENSMUSG00000021930.14	0.99346	6.40E-05	0.00601	POS	protein_coding	Spryd7	14	-37.97	-0.1563
ENSMUSG00000090958.2	0.99346	6.40E-05	0.00601	POS	protein_coding	Lrrc32	7	-42.92	-0.1078
ENSMUSG00000020312.12	0.99341	6.50E-05	0.00603	POS	protein_coding	Shc2	10	-62.47	-0.1031
ENSMUSG00000058672.7	0.99327	6.77E-05	0.00608	POS	protein_coding	Tubb2a	13	-50.55	-0.1058
ENSMUSG00000027613.15	0.99323	6.86E-05	0.0061	POS	protein_coding	Eif6	2	-24.74	-0.1114
ENSMUSG00000054013.6	0.99321	6.91E-05	0.00611	POS	protein_coding	Tmem179	12	-40.15	-0.1074
ENSMUSG00000027763.13	0.99319	6.94E-05	0.00611	POS	protein_coding	Mbnl1	3	-33	-0.1104
ENSMUSG00000027351.14	0.99311	7.10E-05	0.00615	POS	protein_coding	Spred1	2	-30.18	-0.102
ENSMUSG00000053581.13	0.99302	7.28E-05	0.00618	POS	protein_coding	Zfand2a	5	-30.6	-0.1003
ENSMUSG00000039703.15	0.99301	7.31E-05	0.00619	POS	protein_coding	Nploc4	11	-22.11	-0.1164
ENSMUSG00000023951.17	0.99299	7.35E-05	0.0062	POS	protein_coding	Vegfa	17	-95.5	-0.1037
ENSMUSG00000039646.5	0.99293	7.48E-05	0.00622	POS	protein_coding	Vasn	16	-41.22	-0.1033
ENSMUSG00000037406.7	0.99289	7.56E-05	0.00624	POS	protein_coding	Htra4	8	-55.12	-0.1054
ENSMUSG00000039395.8	0.99284	7.67E-05	0.00625	POS	protein_coding	Mreg	1	-32.65	-0.1085

ENSMUSG00000028439.14	0.99282	7.70E-05	0.00626	POS	protein_coding	Fam219a	4	-106.13	-0.1793
ENSMUSG00000061589.14	0.99279	7.77E-05	0.00627	POS	protein_coding	Dot1l	10	-29.01	-0.1099
ENSMUSG00000029161.7	0.99275	7.88E-05	0.00629	POS	protein_coding	Cgref1	5	-26.79	-0.1282
ENSMUSG00000036057.11	0.99274	7.90E-05	0.00629	POS	protein_coding	Ptpn23	9	-33.57	-0.1017
ENSMUSG00000052751.16	0.99264	8.10E-05	0.00633	POS	protein_coding	Repin1	6	-24.34	-0.1122
ENSMUSG00000036904.6	0.99264	8.10E-05	0.00633	POS	protein_coding	Fzd8	18	-64.86	-0.1092
ENSMUSG00000042743.13	0.9926	8.18E-05	0.00635	POS	protein_coding	Sgtb	13	-32.97	-0.1081
ENSMUSG00000003863.18	0.99258	8.24E-05	0.00635	POS	protein_coding	Ppfia3	7	-46.18	-0.1193
ENSMUSG00000024247.14	0.99251	8.39E-05	0.00638	POS	protein_coding	Pkdcc	17	-30.69	-0.1574
ENSMUSG00000054150.12	0.9925	8.42E-05	0.00639	POS	protein_coding	Syne3	12	-39.1	-0.1068
ENSMUSG00000094626.1	0.99249	8.43E-05	0.00639	POS	protein_coding	Tmem121b	6	-66.54	-0.1005
ENSMUSG00000037553.14	0.99249	8.43E-05	0.00639	POS	protein_coding	Zdhhc18	4	-31.7	-0.1157
ENSMUSG00000046997.5	0.99246	8.50E-05	0.0064	POS	protein_coding	Spsb4	9	-42.94	-0.1245
ENSMUSG00000001300.16	0.99244	8.55E-05	0.00641	POS	protein_coding	Efnb2	8	-98.31	-0.1269
ENSMUSG00000047749.2	0.99213	9.27E-05	0.00653	POS	protein_coding	Zc3hav1l	6	-50.63	-0.1253
ENSMUSG00000023809.10	0.99206	9.44E-05	0.00656	POS	protein_coding	Rps6ka2	17	-34.59	-0.1064

ENSMUSG00000022018.7	0.992	9.57E-05	0.00658	POS	protein_coding	Rgcc	14	-76.18	-0.113
ENSMUSG00000017929.13	0.99199	9.60E-05	0.00659	POS	protein_coding	B4galt5	2	-77.94	-0.1007
ENSMUSG000000094626.1	0.99198	9.63E-05	0.00659	POS	protein_coding	Tmem121b	6	-65.45	-0.1111
ENSMUSG00000024736.15	0.99197	9.65E-05	0.0066	POS	protein_coding	Tmem132a	19	-28.7	-0.1083
ENSMUSG00000032743.15	0.99197	9.66E-05	0.0066	POS	protein_coding	D430042O09Rik	7	-36.14	-0.1009
ENSMUSG00000018849.6	0.99195	9.69E-05	0.00661	POS	protein_coding	Wwc1	11	-42.34	-0.1103
ENSMUSG00000022945.12	0.99195	9.69E-05	0.00661	POS	protein_coding	Chaf1b	16	-33.35	-0.1273
ENSMUSG00000001281.10	0.99189	9.84E-05	0.00663	POS	protein_coding	Itgb7	15	-38.02	-0.1077
ENSMUSG00000030214.7	0.99186	9.92E-05	0.00664	POS	protein_coding	Plbd1	6	-55.87	-0.1592
ENSMUSG00000038005.15	0.99183	1.00E-04	0.00665	POS	protein_coding	Hpf1	8	-29.74	-0.1239
ENSMUSG00000021902.7	0.99182	0.0001	0.00666	POS	protein_coding	Phf7	14	-21.33	-0.1198
ENSMUSG00000019256.17	0.99182	0.0001	0.00666	POS	protein_coding	Ahr	12	-23.7	-0.1113
ENSMUSG00000026158.11	0.99181	0.0001	0.00666	POS	protein_coding	Ogfrl1	1	-51.08	-0.1087
ENSMUSG00000048988.8	0.99178	0.0001	0.00667	POS	protein_coding	Elfn1	5	-32.87	-0.1126
ENSMUSG00000023905.15	0.99178	0.0001	0.00667	POS	protein_coding	Tnfrsf12a	17	-77.56	-0.1015
ENSMUSG00000054051.7	0.99172	0.0001	0.0067	POS	protein_coding	Ercc6	14	-24.59	-0.1055
ENSMUSG00000098557.1	0.99163	0.0001	0.00673	POS	protein_coding	Kctd12	14	-62.3	-0.1065
ENSMUSG00000037012.18	0.99162	0.00011	0.00673	POS	protein_coding	Hk1	10	-40.25	-0.122
ENSMUSG00000026885.13	0.9916	0.00011	0.00674	POS	protein_coding	Ttll11	2	-50.38	-0.1153
ENSMUSG00000003573.15	0.99158	0.00011	0.00675	POS	protein_coding	Homer3	8	-30.64	-0.1178

ENSMUSG00000016128.14	0.99155	0.00011	0.00676	POS	protein_coding	Stard13	5	-22.66	-0.1016
ENSMUSG00000057729.12	0.9915	0.00011	0.00678	POS	protein_coding	Prtn3	10	-54.32	-0.1031
ENSMUSG00000045636.16	0.99148	0.00011	0.00679	POS	protein_coding	Mtus1	8	-20.4	-0.1872
ENSMUSG00000028613.15	0.99147	0.00011	0.00679	POS	protein_coding	Lrp8	4	-107.51	-0.1084
ENSMUSG00000054517.9	0.99143	0.00011	0.00681	POS	protein_coding	Trim65	11	-35.41	-0.1142
ENSMUSG00000023800.15	0.99134	0.00011	0.00685	POS	protein_coding	Tiam2	17	-41.78	-0.1222
ENSMUSG00000041126.16	0.99131	0.00011	0.00686	POS	protein_coding	H2az2	11	-61.71	-0.1128
ENSMUSG00000020108.4	0.99127	0.00011	0.00687	POS	protein_coding	Ddit4	10	-35.23	-0.1081
ENSMUSG00000034640.9	0.99124	0.00011	0.00688	POS	protein_coding	Tiparp	3	-28.95	-0.1005
ENSMUSG00000024091.9	0.99119	0.00012	0.0069	POS	protein_coding	Vapa	17	-51.65	-0.1272
ENSMUSG00000027199.14	0.99119	0.00012	0.0069	POS	protein_coding	Gatm	2	-27.26	-0.1126
ENSMUSG00000036499.9	0.99118	0.00012	0.00691	POS	protein_coding	Eea1	10	-25.13	-0.1034
ENSMUSG00000022305.13	0.99107	0.00012	0.00694	POS	protein_coding	Lrp12	15	-50.07	-0.1647
ENSMUSG00000045636.16	0.99098	0.00012	0.00698	POS	protein_coding	Mtus1	8	-269.29	-0.1162
ENSMUSG00000030671.9	0.99096	0.00012	0.00698	POS	protein_coding	Pde3b	7	-122.74	-0.1161
ENSMUSG00000024176.10	0.99091	0.00012	0.007	POS	protein_coding	Sox8	17	-31.11	-0.1058
ENSMUSG00000028517.8	0.99087	0.00012	0.00701	POS	protein_coding	Plpp3	4	-34.65	-0.101
ENSMUSG00000033610.16	0.99078	0.00013	0.00705	POS	protein_coding	Pank1	19	-39.24	-0.1019
ENSMUSG00000038866.15	0.99077	0.00013	0.00705	POS	protein_coding	Zcchc2	1	-40.01	-0.1008
ENSMUSG00000078486.3	0.99072	0.00013	0.00707	POS	protein_coding	Perm1	4	-29.85	-0.1059
ENSMUSG00000038692.8	0.99062	0.00013	0.0071	POS	protein_coding	Hoxb4	11	-36.37	-0.1155
ENSMUSG00000079316.10	0.9906	0.00013	0.00711	POS	protein_coding	Rab9	X	-27.96	-0.1059
ENSMUSG00000032244.9	0.99057	0.00013	0.00712	POS	protein_coding	Fem1b	9	-31.56	-0.1489
ENSMUSG00000043017.9	0.9905	0.00013	0.00714	POS	protein_coding	Ptgir	7	-26.09	-0.1061
ENSMUSG00000037960.11	0.99043	0.00014	0.00717	POS	protein_coding	Card19	13	-81.83	-0.1075
ENSMUSG00000013076.17	0.9903	0.00014	0.00722	POS	protein_coding	Amotl1	9	-32.93	-0.1224
ENSMUSG00000031266.7	0.99023	0.00014	0.00725	POS	protein_coding	Gla	X	-19.2	-0.1185

ENSMUSG00000035671.6	0.99022	0.00014	0.00726	POS	protein_coding	Zswim4	8	-29.72	-0.1179
ENSMUSG00000033581.17	0.99013	0.00015	0.00729	POS	protein_coding	Igf2bp2	16	-41.34	-0.1034
ENSMUSG00000041773.8	0.99007	0.00015	0.00731	POS	protein_coding	Enc1	13	-54.36	-0.1128
ENSMUSG00000034158.9	0.99005	0.00015	0.00732	POS	protein_coding	Lrrc58	16	-56.87	-0.1168
ENSMUSG00000022009.1	0.99003	0.00015	0.00733	POS	protein_coding	Nufip1	14	-35.58	-0.1214
ENSMUSG00000049092.11	0.99003	0.00015	0.00733	POS	protein_coding	Gpr137c	14	-125.85	-0.1383
ENSMUSG00000016239.11	0.99	0.00015	0.00735	POS	protein_coding	Lonrf3	X	-147.22	-0.1035
ENSMUSG00000005514.14	0.98994	0.00015	0.00737	POS	protein_coding	Por	5	-27.48	-0.1053
ENSMUSG00000027669.14	0.98989	0.00015	0.00739	POS	protein_coding	Gnb4	3	-31.14	-0.1078
ENSMUSG00000030315.15	0.9898	0.00016	0.00742	POS	protein_coding	Vgll4	6	-33.25	-0.1005
ENSMUSG00000027669.14	0.98979	0.00016	0.00742	POS	protein_coding	Gnb4	3	-27.26	-0.1336
ENSMUSG00000026353.9	0.98977	0.00016	0.00743	POS	protein_coding	Ubxn4	1	-43.56	-0.1035
ENSMUSG00000046985.11	0.98975	0.00016	0.00744	POS	protein_coding	Tapt1	5	-35.09	-0.3025
ENSMUSG00000066829.7	0.9897	0.00016	0.00746	POS	protein_coding	Zfp810	9	-24.77	-0.1045
ENSMUSG00000014444.17	0.98968	0.00016	0.00746	POS	protein_coding	Piezo1	8	-30.08	-0.1203
ENSMUSG00000034382.14	0.98966	0.00016	0.00747	POS	protein_coding	Al661453	17	-34.2	-0.1024
ENSMUSG00000028859.14	0.98966	0.00016	0.00747	POS	protein_coding	Csf3r	4	-56.21	-0.1193
ENSMUSG00000004099.16	0.98964	0.00016	0.00748	POS	protein_coding	Dnmt1	9	-33.5	-0.1139
ENSMUSG00000023075.9	0.9896	0.00016	0.00749	POS	protein_coding	Akirin1	4	-33.31	-0.1044
ENSMUSG00000051341.6	0.98958	0.00016	0.0075	POS	protein_coding	Zfp52	17	-26.62	-0.1173
ENSMUSG00000044763.8	0.98958	0.00016	0.0075	POS	protein_coding	Trmt10c	16	-23.97	-0.1065
ENSMUSG00000032440.13	0.98952	0.00016	0.00751	POS	protein_coding	Tgfb2	9	-141.45	-0.1097
ENSMUSG00000014905.4	0.9895	0.00016	0.00752	POS	protein_coding	Dnajb9	12	-39.18	-0.1085
ENSMUSG00000020312.12	0.9895	0.00016	0.00752	POS	protein_coding	Shc2	10	-90.78	-0.1028
ENSMUSG00000048807.2	0.98947	0.00017	0.00753	POS	protein_coding	Slc35e4	11	-29.57	-0.1264
ENSMUSG00000002100.15	0.98947	0.00017	0.00753	POS	protein_coding	Mybpc3	2	-58.61	-0.1021
ENSMUSG00000036564.17	0.98947	0.00017	0.00753	POS	protein_coding	Ndr4	8	-37.73	-0.1003

ENSMUSG00000031762.7	0.98946	0.00017	0.00753	POS	protein_coding	Mt2	8	-287.6	-1.0458
ENSMUSG00000037295.7	0.98943	0.00017	0.00754	POS	protein_coding	Ldlrap1	4	-39.38	-0.1176
ENSMUSG00000031709.15	0.98943	0.00017	0.00754	POS	protein_coding	Tbc1d9	8	-25.14	-0.1047
ENSMUSG00000034382.14	0.98941	0.00017	0.00755	POS	protein_coding	Al661453	17	-25.35	-0.1196
ENSMUSG00000039770.6	0.98931	0.00017	0.00758	POS	protein_coding	Ypel5	17	-31.09	-0.1095
ENSMUSG00000074170.5	0.98927	0.00017	0.0076	POS	protein_coding	Plekhf1	7	-72.01	-0.1268
ENSMUSG00000062232.14	0.98919	0.00017	0.00763	POS	protein_coding	Rapgef2	3	-27.97	-0.1266
ENSMUSG00000074577.9	0.98915	0.00018	0.00765	POS	protein_coding	Ripor3	2	-28.51	-0.1076
ENSMUSG00000095115.2	0.98905	0.00018	0.00768	POS	protein_coding	Itpr12	7	-29.93	-0.1084
ENSMUSG00000034226.7	0.98904	0.00018	0.00768	POS	protein_coding	Rhov	2	-30.89	-0.1013
ENSMUSG00000027848.12	0.98901	0.00018	0.00769	POS	protein_coding	Olfml3	3	-23.94	-0.1014
ENSMUSG00000091811.2	0.98897	0.00018	0.00771	POS	protein_coding	Inafm1	7	-100.52	-0.1036
ENSMUSG00000036158.12	0.98894	0.00018	0.00772	POS	protein_coding	Prickle1	15	-24.79	-0.1112
ENSMUSG00000024525.7	0.98893	0.00018	0.00772	POS	protein_coding	Impa2	18	-32.61	-0.1136
ENSMUSG00000032387.15	0.98887	0.00019	0.00774	POS	protein_coding	Rbpms2	9	-33.81	-0.1084
ENSMUSG00000043702.9	0.98883	0.00019	0.00776	POS	protein_coding	Pde12	14	-29.42	-0.111
ENSMUSG00000059325.14	0.98881	0.00019	0.00776	POS	protein_coding	Hopx	5	-224.17	-0.3244
ENSMUSG00000024986.12	0.98878	0.00019	0.00778	POS	protein_coding	Hhex	19	-40.36	-0.1246
ENSMUSG00000026869.12	0.98877	0.00019	0.00778	POS	protein_coding	Psmd5	2	-46.74	-0.1118
ENSMUSG00000055805.15	0.98872	0.00019	0.0078	POS	protein_coding	Fmnl1	11	-27.7	-0.1131
ENSMUSG0000002083.13	0.98871	0.00019	0.0078	POS	protein_coding	Bbc3	7	-28.97	-0.1173
ENSMUSG00000011752.7	0.98868	0.00019	0.00782	POS	protein_coding	Pgam1	19	-41.63	-0.107
ENSMUSG00000016128.14	0.98867	0.00019	0.00782	POS	protein_coding	Stard13	5	-35.27	-0.1106
ENSMUSG00000022636.13	0.98863	0.00019	0.00783	POS	protein_coding	Alcam	16	-33.44	-0.1257
ENSMUSG00000028577.13	0.98863	0.00019	0.00783	POS	protein_coding	Plaa	4	-23.75	-0.1439
ENSMUSG00000028439.14	0.9886	0.00019	0.00784	POS	protein_coding	Fam219a	4	-31.71	-0.121
ENSMUSG00000033610.16	0.98858	0.00019	0.00785	POS	protein_coding	Pank1	19	-111.89	-0.1263

ENSMUSG00000020689.4	0.98849	0.0002	0.00788	POS	protein_coding	Itgb3	11	-33.52	-0.101
ENSMUSG00000029462.18	0.98848	0.0002	0.00789	POS	protein_coding	Vps29	5	-25.92	-0.1041
ENSMUSG00000040325.16	0.98847	0.0002	0.00789	POS	protein_coding	Dcaf1	9	-27.36	-0.1025
ENSMUSG00000035944.17	0.98843	0.0002	0.0079	POS	protein_coding	Ttc38	15	-94.05	-0.1153
ENSMUSG00000040829.14	0.9884	0.0002	0.00791	POS	protein_coding	Zmynd15	11	-32.64	-0.1014
ENSMUSG00000032010.15	0.98837	0.0002	0.00792	POS	protein_coding	Usp2	9	-21.46	-0.1219
ENSMUSG00000027397.14	0.98828	0.00021	0.00796	POS	protein_coding	Slc20a1	2	-311.86	-0.1201
ENSMUSG00000058070.14	0.98822	0.00021	0.00798	POS	protein_coding	Eml1	12	-29.55	-0.1026
ENSMUSG00000003644.17	0.9882	0.00021	0.00799	POS	protein_coding	Rps6ka1	4	-38.43	-0.1294
ENSMUSG00000022500.15	0.98814	0.00021	0.00801	POS	protein_coding	Litaf	16	-61.93	-0.1071
ENSMUSG00000027368.6	0.98812	0.00021	0.00801	POS	protein_coding	Dusp2	2	-40.96	-0.1056
ENSMUSG00000037960.11	0.98803	0.00021	0.00804	POS	protein_coding	Card19	13	-24.42	-0.118
ENSMUSG00000024247.14	0.98795	0.00022	0.00807	POS	protein_coding	Pkdcc	17	-129.39	-0.1083
ENSMUSG00000015312.9	0.98789	0.00022	0.00809	POS	protein_coding	Gadd45b	10	-40.08	-0.1182
ENSMUSG00000041390.18	0.98787	0.00022	0.0081	POS	protein_coding	Mdfic	6	-90.39	-0.1393
ENSMUSG00000024190.7	0.98784	0.00022	0.00811	POS	protein_coding	Dusp1	17	-61.34	-0.1065
ENSMUSG00000031486.15	0.98783	0.00022	0.00811	POS	protein_coding	Adgra2	8	-39.86	-0.1052
ENSMUSG00000031016.9	0.98782	0.00022	0.00811	POS	protein_coding	Wee1	7	-43.52	-0.1233
ENSMUSG00000002109.14	0.98773	0.00022	0.00815	POS	protein_coding	Ddb2	2	-35.37	-0.1005
ENSMUSG00000032515.8	0.9877	0.00023	0.00816	POS	protein_coding	Csrnp1	9	-32.76	-0.1088
ENSMUSG00000032860.5	0.9877	0.00023	0.00816	POS	protein_coding	P2ry2	7	-25.43	-0.1005
ENSMUSG00000045659.18	0.98769	0.00023	0.00816	POS	protein_coding	Plekha7	7	-27.03	-0.104
ENSMUSG00000031389.17	0.98769	0.00023	0.00816	POS	protein_coding	Arhgap4	X	-35.3	-0.123
ENSMUSG00000042293.8	0.98768	0.00023	0.00817	POS	protein_coding	Gm5617	9	-27.09	-0.1759
ENSMUSG00000028645.11	0.98767	0.00023	0.00817	POS	protein_coding	Slc2a1	4	-128.85	-0.3364
ENSMUSG00000024524.17	0.98763	0.00023	0.00818	POS	protein_coding	Gnal	18	-93.15	-0.1059
ENSMUSG00000030105.8	0.98758	0.00023	0.0082	POS	protein_coding	Arl8b	6	-34.29	-0.1805

ENSMUSG00000041703.7	0.98755	0.00023	0.00821	POS	protein_coding	Zic5	14	-155.71	-0.1013
ENSMUSG00000024299.17	0.98755	0.00023	0.00821	POS	protein_coding	Adamts10	17	-39.37	-0.1312
ENSMUSG00000024521.8	0.98752	0.00023	0.00822	POS	protein_coding	Pmaip1	18	-34.25	-0.1215
ENSMUSG00000031530.6	0.98751	0.00023	0.00823	POS	protein_coding	Dusp4	8	-41.08	-0.1272
ENSMUSG00000028032.13	0.98747	0.00023	0.00824	POS	protein_coding	Papss1	3	-37.07	-0.1117
ENSMUSG00000029096.15	0.98742	0.00024	0.00825	POS	protein_coding	Htra3	5	-23.99	-0.1263
ENSMUSG00000078144.4	0.98741	0.00024	0.00826	POS	protein_coding	Capns2	8	-27.49	-0.1233
ENSMUSG00000032440.13	0.98738	0.00024	0.00827	POS	protein_coding	Tgfb2	9	-33.33	-0.1061
ENSMUSG00000020262.15	0.98737	0.00024	0.00827	POS	protein_coding	Adarb1	10	-24.33	-0.1406
ENSMUSG00000025825.12	0.98736	0.00024	0.00828	POS	protein_coding	Iscu	5	-31.53	-0.1007
ENSMUSG00000021303.14	0.98735	0.00024	0.00828	POS	protein_coding	Gng4	13	-38.6	-0.106
ENSMUSG00000068263.11	0.98727	0.00024	0.00831	POS	protein_coding	Efcc1	6	-95.37	-0.1472
ENSMUSG00000060038.14	0.98718	0.00025	0.00834	POS	protein_coding	Dhps	8	-20.99	-0.1099
ENSMUSG00000038508.7	0.98717	0.00025	0.00835	POS	protein_coding	Gdf15	8	-59.38	-0.1013
ENSMUSG00000018476.7	0.98714	0.00025	0.00836	POS	protein_coding	Kdm6b	11	-42.64	-0.1312
ENSMUSG00000022346.15	0.98714	0.00025	0.00836	POS	protein_coding	Myc	15	-26.78	-0.1034
ENSMUSG00000038005.15	0.98714	0.00025	0.00836	POS	protein_coding	Hpfl	8	-29.07	-0.1454
ENSMUSG00000025324.8	0.98708	0.00025	0.00838	POS	protein_coding	Atp10a	7	-56.78	-0.1018
ENSMUSG00000028188.13	0.98707	0.00025	0.00838	POS	protein_coding	Spata1	3	-142	-0.4494
ENSMUSG00000031960.14	0.98706	0.00025	0.00838	POS	protein_coding	Aars	8	-45.48	-0.1163
ENSMUSG00000023075.9	0.98701	0.00025	0.00841	POS	protein_coding	Akirin1	4	-40.58	-0.1173
ENSMUSG00000031490.6	0.98699	0.00025	0.00841	POS	protein_coding	Eif4ebp1	8	-39.02	-0.1124
ENSMUSG00000044763.8	0.98698	0.00025	0.00841	POS	protein_coding	Trmt10c	16	-35.07	-0.111
ENSMUSG00000044626.13	0.98695	0.00025	0.00842	POS	protein_coding	Liph	16	-31.02	-0.1092
ENSMUSG00000015575.15	0.98695	0.00025	0.00842	POS	protein_coding	Atp6v0e	17	-34.42	-0.1103
ENSMUSG00000023030.16	0.98694	0.00025	0.00842	POS	protein_coding	Slc11a2	15	-25.68	-0.1019
ENSMUSG00000031488.14	0.98694	0.00025	0.00843	POS	protein_coding	Rab11fip1	8	-116.6	-0.1555

ENSMUSG00000002100.15	0.98689	0.00026	0.00845	POS	protein_coding	Mybpc3	2	-41.6	-0.1012
ENSMUSG000000035725.13	0.98685	0.00026	0.00846	POS	protein_coding	Prkx	X	-30.95	-0.1159
ENSMUSG000000052369.8	0.98674	0.00026	0.0085	POS	protein_coding	Tmem106c	15	-31.06	-0.1134
ENSMUSG000000025262.8	0.98672	0.00026	0.00851	POS	protein_coding	Fam120c	X	-100.69	-0.1296
ENSMUSG000000036553.16	0.98672	0.00026	0.00851	POS	protein_coding	Sh3tc1	5	-28.69	-0.1176
ENSMUSG000000039646.5	0.98672	0.00026	0.00851	POS	protein_coding	Vasn	16	-23.41	-0.105
ENSMUSG00000000876.11	0.98666	0.00027	0.00853	POS	protein_coding	Pxmp4	2	-131.54	-0.1488
ENSMUSG000000070643.11	0.98652	0.00027	0.00858	POS	protein_coding	Sox13	1	-100.7	-0.1494
ENSMUSG000000037280.12	0.98652	0.00027	0.00858	POS	protein_coding	Galnt6	15	-40	-0.1005
ENSMUSG000000029149.14	0.9865	0.00027	0.00859	POS	protein_coding	Krtcap3	5	-78.18	-0.1065
ENSMUSG000000043487.4	0.98649	0.00027	0.00859	POS	protein_coding	Acot6	12	-44.09	-0.1075
ENSMUSG00000001281.10	0.98642	0.00028	0.00862	POS	protein_coding	Itgb7	15	-24.39	-0.1051
ENSMUSG000000031762.7	0.98636	0.00028	0.00864	POS	protein_coding	Mt2	8	-24.71	-0.1013
ENSMUSG000000034612.7	0.98633	0.00028	0.00866	POS	protein_coding	Chst11	10	-36.97	-0.1033
ENSMUSG000000030595.15	0.98632	0.00028	0.00866	POS	protein_coding	Nfkbib	7	-35.38	-0.1156
ENSMUSG000000022295.8	0.98629	0.00028	0.00867	POS	protein_coding	Atp6v1c1	15	-18.48	-0.154
ENSMUSG000000026437.11	0.98629	0.00028	0.00867	POS	protein_coding	Cdk18	1	-40.26	-0.1017
ENSMUSG000000020883.18	0.98629	0.00028	0.00867	POS	protein_coding	Fbxl20	11	-27.68	-0.1077
ENSMUSG000000039886.8	0.98627	0.00028	0.00868	POS	protein_coding	Tmem120a	5	-27.54	-0.1089
ENSMUSG000000022048.8	0.98615	0.00029	0.00872	POS	protein_coding	Dpysl2	14	-30.43	-0.1237
ENSMUSG000000035107.13	0.98613	0.00029	0.00873	POS	protein_coding	Dcbld2	16	-43.79	-0.114
ENSMUSG000000025178.9	0.9861	0.00029	0.00874	POS	protein_coding	Pi4k2a	19	-28.71	-0.1083
ENSMUSG000000023068.16	0.98609	0.00029	0.00874	POS	protein_coding	Nus1	10	-47.51	-0.132
ENSMUSG000000024247.14	0.98607	0.00029	0.00875	POS	protein_coding	Pkdcc	17	-61.25	-0.1114
ENSMUSG000000021846.9	0.98603	0.00029	0.00877	POS	protein_coding	Peli2	14	-37.37	-0.1119
ENSMUSG000000042826.13	0.98596	0.00029	0.0088	POS	protein_coding	Fgf11	11	-77.87	-0.177
ENSMUSG000000045193.13	0.98593	0.0003	0.00881	POS	protein_coding	Cirbp	10	-37.46	-0.1205

ENSMUSG00000025357.8	0.98573	0.0003	0.00888	POS	protein_coding	Dgka	10	-28.63	-0.1141
ENSMUSG00000025139.14	0.9857	0.00031	0.00889	POS	protein_coding	Tollip	7	-36.54	-0.1214
ENSMUSG00000019966.18	0.98569	0.00031	0.0089	POS	protein_coding	Kitl	10	-45.74	-0.126
ENSMUSG00000014599.10	0.98564	0.00031	0.00891	POS	protein_coding	Csf1	3	-56.14	-0.103
ENSMUSG00000022602.14	0.98561	0.00031	0.00892	POS	protein_coding	Arc	15	-62.37	-0.1043
ENSMUSG00000023961.16	0.98552	0.00031	0.00895	POS	protein_coding	Enpp4	17	-45.37	-0.1175
ENSMUSG00000018669.14	0.98549	0.00031	0.00897	POS	protein_coding	Cdk5rap3	11	-38.43	-0.1047
ENSMUSG00000043421.8	0.98545	0.00032	0.00898	POS	protein_coding	Hilpda	6	-25.71	-0.1339
ENSMUSG00000052364.4	0.98544	0.00032	0.00898	POS	protein_coding	B630019K06Rik	X	-28.28	-0.1079
ENSMUSG00000029314.14	0.98542	0.00032	0.00899	POS	protein_coding	Gpat3	5	-28.27	-0.1113
ENSMUSG00000005686.17	0.98538	0.00032	0.00901	POS	protein_coding	Ampd3	7	-31.59	-0.1112
ENSMUSG00000040447.15	0.98535	0.00032	0.00902	POS	protein_coding	Spns2	11	-109.68	-0.1249
ENSMUSG00000042826.13	0.98535	0.00032	0.00902	POS	protein_coding	Fgf11	11	-41	-0.1349
ENSMUSG00000033581.17	0.98534	0.00032	0.00902	POS	protein_coding	Igf2bp2	16	-51.22	-0.1085
ENSMUSG00000022199.12	0.98529	0.00032	0.00903	POS	protein_coding	Slc22a17	14	-39.29	-0.1156
ENSMUSG00000032086.12	0.98523	0.00033	0.00906	POS	protein_coding	Bace1	9	-35.77	-0.1025
ENSMUSG00000024533.17	0.98519	0.00033	0.00907	POS	protein_coding	Spire1	18	-23.45	-0.1196
ENSMUSG00000022817.15	0.98517	0.00033	0.00908	POS	protein_coding	Itgb5	16	-28.05	-0.1189
ENSMUSG00000061175.12	0.98513	0.00033	0.00909	POS	protein_coding	Fnip2	3	-25.58	-0.1103
ENSMUSG00000028613.15	0.98511	0.00033	0.0091	POS	protein_coding	Lrp8	4	-26.78	-0.1003
ENSMUSG00000024654.8	0.9851	0.00033	0.00911	POS	protein_coding	Asrgl1	19	-45.8	-0.1002
ENSMUSG00000029313.18	0.98504	0.00033	0.00913	POS	protein_coding	Aff1	5	-36.07	-0.11
ENSMUSG00000035298.8	0.98501	0.00034	0.00914	POS	protein_coding	Klhl35	7	-36.54	-0.1078
ENSMUSG00000040699.13	0.98499	0.00034	0.00915	POS	protein_coding	Limd2	11	-35.45	-0.1084
ENSMUSG00000087141.1	0.98498	0.00034	0.00915	POS	protein_coding	Plcxd2	16	-24.72	-0.1021
ENSMUSG00000028278.14	0.98498	0.00034	0.00915	POS	protein_coding	Rragd	4	-28.43	-0.1093
ENSMUSG00000021260.8	0.98492	0.00034	0.00917	POS	protein_coding	Hhipl1	12	-39.59	-0.1094

ENSMUSG00000030134.11	0.98488	0.00034	0.00918	POS	protein_coding	Rasgef1a	6	-24.39	-0.1004
ENSMUSG00000029407.10	0.98484	0.00034	0.0092	POS	protein_coding	Uso1	5	-32.88	-0.162
ENSMUSG00000045374.18	0.98477	0.00035	0.00922	POS	protein_coding	Wdr81	11	-30.1	-0.1075
ENSMUSG00000026135.17	0.98474	0.00035	0.00923	POS	protein_coding	Zfp142	1	-43.09	-0.1043
ENSMUSG00000056501.3	0.98472	0.00035	0.00924	POS	protein_coding	Cebpb	2	-122.8	-0.1256
ENSMUSG00000020250.10	0.98472	0.00035	0.00924	POS	protein_coding	Txnrd1	10	-35.14	-0.1098
ENSMUSG00000023832.14	0.98469	0.00035	0.00925	POS	protein_coding	Acat2	17	-21.5	-0.1059
ENSMUSG00000029063.16	0.98466	0.00035	0.00926	POS	protein_coding	Nadk	4	-23.07	-0.1442
ENSMUSG00000037443.13	0.98462	0.00035	0.00928	POS	protein_coding	Cep85	4	-23.26	-0.1052
ENSMUSG00000050824.12	0.98461	0.00035	0.00928	POS	protein_coding	Sstr5	17	-35.76	-0.1142
ENSMUSG00000055976.6	0.9846	0.00035	0.00928	POS	protein_coding	Cldn23	8	-35.95	-0.1045
ENSMUSG00000039270.9	0.98458	0.00035	0.00929	POS	protein_coding	Megf9	4	-79.95	-0.1149
ENSMUSG00000030595.15	0.98456	0.00036	0.0093	POS	protein_coding	Nfkbib	7	-40.64	-0.1013
ENSMUSG00000002897.5	0.98451	0.00036	0.00931	POS	protein_coding	Il17ra	6	-39.93	-0.1128
ENSMUSG00000038708.10	0.98451	0.00036	0.00931	POS	protein_coding	Golga4	9	-25.48	-0.1066
ENSMUSG00000073700.3	0.98448	0.00036	0.00932	POS	protein_coding	Klhl21	4	-62.83	-0.1087
ENSMUSG00000021303.14	0.98448	0.00036	0.00932	POS	protein_coding	Gng4	13	-45.81	-0.1332
ENSMUSG00000046034.8	0.98448	0.00036	0.00932	POS	protein_coding	Otulin	15	-21.54	-0.1099
ENSMUSG00000034216.12	0.98447	0.00036	0.00932	POS	protein_coding	Vps18	2	-27.03	-0.1016
ENSMUSG00000048163.13	0.98429	0.00037	0.00938	POS	protein_coding	Selpg	5	-29.03	-0.1157
ENSMUSG00000031934.14	0.98429	0.00037	0.00939	POS	protein_coding	Panx1	9	-58.46	-0.1929
ENSMUSG00000038037.5	0.98427	0.00037	0.00939	POS	protein_coding	Socs1	16	-40.22	-0.1042
ENSMUSG00000033307.7	0.98419	0.00037	0.00942	POS	protein_coding	Mif	10	-48.66	-0.1029
ENSMUSG00000052160.7	0.98417	0.00037	0.00943	POS	protein_coding	Pld4	12	-24.06	-0.1037
ENSMUSG00000040105.3	0.98413	0.00038	0.00944	POS	protein_coding	Plpp6	19	-98.73	-0.1143
ENSMUSG00000061411.12	0.98412	0.00038	0.00944	POS	protein_coding	Nol4l	2	-35.39	-0.1134
ENSMUSG00000017493.12	0.98409	0.00038	0.00945	POS	protein_coding	Igfbp4	11	-20.32	-0.1026

ENSMUSG00000019818.15	0.98408	0.00038	0.00946	POS	protein_coding	Cd164	10	-61.41	-0.101
ENSMUSG00000020869.8	0.98407	0.00038	0.00946	POS	protein_coding	Lrrc59	11	-21.33	-0.1083
ENSMUSG00000024404.7	0.98406	0.00038	0.00947	POS	protein_coding	Riok3	18	-25.22	-0.1073
ENSMUSG00000029161.7	0.98403	0.00038	0.00947	POS	protein_coding	Cgref1	5	-40.36	-0.1177
ENSMUSG00000038612.16	0.984	0.00038	0.00948	POS	protein_coding	Mcl1	3	-28.75	-0.1038
ENSMUSG00000039844.20	0.984	0.00038	0.00948	POS	protein_coding	Rapgef1	2	-39.2	-0.1023
ENSMUSG00000019256.17	0.98398	0.00038	0.00949	POS	protein_coding	Ahr	12	-42.52	-0.1146
ENSMUSG00000032350.9	0.98397	0.00038	0.0095	POS	protein_coding	Gclc	9	-30.04	-0.1202
ENSMUSG00000039960.5	0.98393	0.00039	0.00951	POS	protein_coding	Rhou	8	-71.15	-0.1098
ENSMUSG00000055862.7	0.98391	0.00039	0.00951	POS	protein_coding	Izumo4	10	-47.48	-0.1032
ENSMUSG00000075302.10	0.9839	0.00039	0.00951	POS	protein_coding	Erich2	2	-108.47	-0.2948
ENSMUSG00000037519.17	0.9839	0.00039	0.00951	POS	protein_coding	Ppfia1	7	-33.26	-0.1409
ENSMUSG00000022150.16	0.98388	0.00039	0.00952	POS	protein_coding	Dab2	15	-23.76	-0.102
ENSMUSG00000042613.9	0.98375	0.00039	0.00957	POS	protein_coding	Pbxip1	3	-40.11	-0.1197
ENSMUSG00000060216.15	0.98374	0.00039	0.00957	POS	protein_coding	Arrb2	11	-35.58	-0.1062
ENSMUSG00000028124.15	0.98373	0.0004	0.00957	POS	protein_coding	Gclm	3	-48.51	-0.1064
ENSMUSG00000078941.9	0.98371	0.0004	0.00958	POS	protein_coding	Ak6	13	-36.59	-0.1122
ENSMUSG00000026885.13	0.98366	0.0004	0.0096	POS	protein_coding	Ttll11	2	-38.04	-0.1057
ENSMUSG00000029050.15	0.98365	0.0004	0.0096	POS	protein_coding	Ski	4	-36.38	-0.1123
ENSMUSG00000034247.9	0.98364	0.0004	0.0096	POS	protein_coding	Plekhm1	11	-28.78	-0.1074
ENSMUSG00000001138.13	0.98363	0.0004	0.00961	POS	protein_coding	Cnnm3	1	-42.03	-0.1251
ENSMUSG00000039115.13	0.98361	0.0004	0.00961	POS	protein_coding	Itga9	9	-66.5	-0.1073
ENSMUSG00000043051.17	0.98347	0.00041	0.00966	POS	protein_coding	Disc1	8	-26.35	-0.1506
ENSMUSG00000018476.7	0.98342	0.00041	0.00968	POS	protein_coding	Kdm6b	11	-212.6	-0.2681
ENSMUSG00000070873.5	0.98341	0.00041	0.00968	POS	protein_coding	Lilra5	7	-26.37	-0.1305
ENSMUSG00000020312.12	0.98339	0.00041	0.00969	POS	protein_coding	Shc2	10	-58.71	-0.1021
ENSMUSG00000020099.8	0.98336	0.00041	0.0097	POS	protein_coding	Unc5b	10	-47.72	-0.1164

ENSMUSG00000025040.13	0.98321	0.00042	0.00975	POS	protein_coding	Fundc1	X	-18.94	-0.1108
ENSMUSG00000044763.8	0.9832	0.00042	0.00975	POS	protein_coding	Trmt10c	16	-34.8	-0.2231
ENSMUSG00000019843.14	0.98316	0.00042	0.00976	POS	protein_coding	Fyn	10	-105.52	-0.1322
ENSMUSG00000032479.15	0.98313	0.00042	0.00977	POS	protein_coding	Map4	9	-35.75	-0.1016
ENSMUSG00000045045.7	0.98305	0.00043	0.0098	POS	protein_coding	Lrfn4	19	-43.9	-0.1123
ENSMUSG00000036180.15	0.98305	0.00043	0.0098	POS	protein_coding	Gatad2a	8	-28.72	-0.1011
ENSMUSG00000004099.16	0.98303	0.00043	0.00981	POS	protein_coding	Dnmt1	9	-40.25	-0.1109
ENSMUSG00000042035.11	0.98287	0.00044	0.00986	POS	protein_coding	Igsf3	3	-32.58	-0.1041
ENSMUSG00000040723.14	0.98284	0.00044	0.00987	POS	protein_coding	Rcsd1	1	-133.64	-0.4037
ENSMUSG00000029050.15	0.98282	0.00044	0.00988	POS	protein_coding	Ski	4	-26.08	-0.106
ENSMUSG00000052684.4	0.98281	0.00044	0.00988	POS	protein_coding	Jun	4	-60.88	-0.1123
ENSMUSG00000026430.16	0.98278	0.00044	0.00989	POS	protein_coding	Rassf5	1	-74.42	-0.1065
ENSMUSG00000079484.12	0.98267	0.00045	0.00993	POS	protein_coding	Phyhd1	2	-20.38	-0.1415
ENSMUSG00000032047.5	0.9826	0.00045	0.00995	POS	protein_coding	Acat1	9	-70.39	-0.1067
ENSMUSG00000061887.14	0.98257	0.00045	0.00997	POS	protein_coding	Ssbp3	4	-100.65	-0.1366
ENSMUSG00000021814.17	-0.9825	0.00045	0.00998	NEG	protein_coding	Anxa7	14	-64.39	-0.1171
ENSMUSG00000026154.4	-0.9825	0.00045	0.00997	NEG	protein_coding	Sdhaf4	1	-23.83	-0.1578
ENSMUSG00000025795.8	-0.9826	0.00045	0.00995	NEG	protein_coding	Rassf3	10	-37.32	-0.1377
ENSMUSG00000063179.13	-0.9826	0.00045	0.00994	NEG	protein_coding	Pstk	7	-30.69	-0.1033
ENSMUSG00000074093.4	-0.9827	0.00045	0.00992	NEG	protein_coding	Svip	7	-46.57	-0.1429
ENSMUSG00000040345.10	-0.9827	0.00044	0.0099	NEG	protein_coding	Arhgap9	10	-26.25	-0.1038
ENSMUSG00000027002.13	-0.9829	0.00044	0.00986	NEG	protein_coding	Nckap1	2	-37.19	-0.1482
ENSMUSG00000025161.16	-0.983	0.00043	0.00982	NEG	protein_coding	Slc16a3	11	-44.42	-0.1063
ENSMUSG00000005951.13	-0.9831	0.00043	0.00979	NEG	protein_coding	Shpk	11	-35.83	-0.1262
ENSMUSG00000027763.13	-0.9832	0.00042	0.00976	NEG	protein_coding	Mbnl1	3	-28.39	-0.1021
ENSMUSG00000078429.9	-0.9832	0.00042	0.00974	NEG	protein_coding	Ctdsp2	10	-42.95	-0.1446
ENSMUSG00000022390.11	-0.9834	0.00041	0.00969	NEG	protein_coding	Zc3h7b	15	-26.47	-0.1055

ENSMUSG00000000420.15	-0.9835	0.0004	0.00964	NEG	protein_coding	Galnt1	18	-38.44	-0.108
ENSMUSG00000056671.7	-0.9837	0.0004	0.00958	NEG	protein_coding	Prelid2	18	-24.72	-0.1056
ENSMUSG00000033033.10	-0.9838	0.00039	0.00954	NEG	protein_coding	Calhm2	19	-37.99	-0.1262
ENSMUSG00000028104.14	-0.9839	0.00039	0.00951	NEG	protein_coding	Polr3gl	3	-34.19	-0.1276
ENSMUSG00000046152.16	-0.9842	0.00037	0.00943	NEG	protein_coding	Fut10	8	-28.48	-0.1187
ENSMUSG00000032177.17	-0.9843	0.00037	0.00938	NEG	protein_coding	Pde4a	9	-44.67	-0.1295
ENSMUSG00000042992.15	-0.9846	0.00035	0.00928	NEG	protein_coding	Borcs5	6	-32.79	-0.1097
ENSMUSG00000001138.13	-0.9846	0.00035	0.00927	NEG	protein_coding	Cnnm3	1	-44.81	-0.1164
ENSMUSG00000024151.13	-0.9846	0.00035	0.00927	NEG	protein_coding	Msh2	17	-37.82	-0.1103
ENSMUSG00000029401.8	-0.9847	0.00035	0.00924	NEG	protein_coding	Rilpl2	5	-31.94	-0.1051
ENSMUSG00000027712.13	-0.9848	0.00034	0.0092	NEG	protein_coding	Anxa5	3	-35.02	-0.1115
ENSMUSG00000078532.9	-0.985	0.00033	0.00913	NEG	protein_coding	Nkain1	4	-40.4	-0.1325
ENSMUSG00000025969.15	-0.9853	0.00032	0.00903	NEG	protein_coding	Nrp2	1	-26.71	-0.1104
ENSMUSG00000038481.13	-0.9857	0.00031	0.0089	NEG	protein_coding	Cdk19	10	-41.73	-0.1439
ENSMUSG00000025969.15	-0.9862	0.00029	0.00872	NEG	protein_coding	Nrp2	1	-36.16	-0.1113
ENSMUSG00000034993.7	-0.9864	0.00028	0.00864	NEG	protein_coding	Vat1	11	-38.28	-0.1167
ENSMUSG00000041607.17	-0.9864	0.00028	0.00864	NEG	protein_coding	Mbp	18	-38.69	-0.1008
ENSMUSG00000019806.13	-0.9866	0.00027	0.00856	NEG	protein_coding	Aig1	10	-22.69	-0.106
ENSMUSG00000014496.8	-0.9867	0.00027	0.00853	NEG	protein_coding	Ankrd28	14	-21.87	-0.1163
ENSMUSG00000053436.15	-0.9867	0.00026	0.00851	NEG	protein_coding	Mapk14	17	-44.96	-0.1141
ENSMUSG00000087679.2	-0.9869	0.00026	0.00846	NEG	protein_coding	Tmem250-ps	2	-46.85	-0.1312
ENSMUSG00000014496.8	-0.9869	0.00026	0.00844	NEG	protein_coding	Ankrd28	14	-44.66	-0.1679
ENSMUSG00000000776.13	-0.987	0.00025	0.00841	NEG	protein_coding	Polr3d	14	-34.87	-0.1301
ENSMUSG00000027368.6	-0.9872	0.00024	0.00833	NEG	protein_coding	Dusp2	2	-39.21	-0.1371
ENSMUSG00000059834.12	-0.9875	0.00023	0.00824	NEG	protein_coding	Sc1t1	3	-37.15	-0.1371
ENSMUSG00000020105.9	-0.9878	0.00022	0.00814	NEG	protein_coding	Lrig3	10	-41.5	-0.1035
ENSMUSG00000001138.13	-0.988	0.00021	0.00804	NEG	protein_coding	Cnnm3	1	-68.1	-0.1033

ENSMUSG00000045045.7	-0.9881	0.00021	0.00803	NEG	protein_coding	Lrnf4	19	-41.42	-0.102
ENSMUSG00000087370.3	-0.9884	0.0002	0.00791	NEG	protein_coding	Tmem170b	13	-35.23	-0.145
ENSMUSG00000028339.17	-0.9886	0.0002	0.00786	NEG	protein_coding	Col15a1	4	-38.72	-0.1011
ENSMUSG00000019917.10	-0.989	0.00018	0.00771	NEG	protein_coding	Sept10	10	-53.82	-0.1278
ENSMUSG00000030256.11	-0.9895	0.00017	0.00753	NEG	protein_coding	Bhlhe41	6	-38.1	-0.1033
ENSMUSG00000038412.8	-0.9896	0.00016	0.00749	NEG	protein_coding	Higd1a	9	-117.3	-0.1191
ENSMUSG00000002763.16	-0.9897	0.00016	0.00747	NEG	protein_coding	Pex6	17	-72.82	-0.164
ENSMUSG00000028542.17	-0.9898	0.00016	0.00742	NEG	protein_coding	Slc6a9	4	-40.39	-0.1012
ENSMUSG00000059540.15	-0.99	0.00015	0.00735	NEG	protein_coding	Tcea2	2	-33.89	-0.1062
ENSMUSG00000031767.13	-0.9906	0.00013	0.0071	NEG	protein_coding	Nudt7	8	-24.64	-0.1095
ENSMUSG00000041607.17	-0.9907	0.00013	0.00708	NEG	protein_coding	Mbp	18	-40.07	-0.1172
ENSMUSG00000078716.10	-0.9911	0.00012	0.00694	NEG	protein_coding	Tmem8b	4	-28.57	-0.1264
ENSMUSG00000019917.10	-0.9911	0.00012	0.00692	NEG	protein_coding	Sept10	10	-51.47	-0.1164
ENSMUSG00000087679.2	-0.9913	0.00011	0.00685	NEG	protein_coding	Tmem250-ps	2	-62.85	-0.1069
ENSMUSG00000087679.2	-0.9914	0.00011	0.00684	NEG	protein_coding	Tmem250-ps	2	-51.46	-0.1007
ENSMUSG00000037432.15	-0.9916	0.0001	0.00673	NEG	protein_coding	Fer1l5	1	-39.88	-0.1242
ENSMUSG00000058152.8	-0.9917	0.0001	0.00669	NEG	protein_coding	Chsy3	18	-43.09	-0.1128
ENSMUSG00000039781.14	-0.9919	9.85E-05	0.00663	NEG	protein_coding	Cep131	11	-53.61	-0.1057
ENSMUSG00000053436.15	-0.9921	9.44E-05	0.00656	NEG	protein_coding	Mapk14	17	-30.81	-0.1171
ENSMUSG00000040133.2	-0.9921	9.39E-05	0.00655	NEG	protein_coding	Gpr176	2	-25.07	-0.1011
ENSMUSG00000039765.15	-0.9925	8.35E-05	0.00637	NEG	protein_coding	Cc2d2a	5	-32.82	-0.1029
ENSMUSG00000034786.17	-0.9926	8.25E-05	0.00635	NEG	protein_coding	Gpsm3	17	-22.06	-0.1131
ENSMUSG00000053436.15	-0.9938	5.72E-05	0.00589	NEG	protein_coding	Mapk14	17	-40.34	-0.1003

ENSMUSG00000036555.14	-0.9948	4.05E-05	0.00549	NEG	protein_coding	Iqce	5	-27.05	-0.1202
ENSMUSG00000048200.12	-0.9954	3.23E-05	0.00526	NEG	protein_coding	Cracr2b	7	-200.64	-0.1199
ENSMUSG00000053436.15	-0.9959	2.53E-05	0.00507	NEG	protein_coding	Mapk14	17	-47.66	-0.1027
ENSMUSG00000021996.16	-0.9985	3.51E-06	0.00383	NEG	protein_coding	Esd	14	-21.19	-0.1536
ENSMUSG00000040105.3	-0.999	1.48E-06	0.00354	NEG	protein_coding	Plpp6	19	-44.76	-0.1119

Supplementary Material S2 Table - Classification lncRNA

Source	S_Name	S_chr	Type_Lnc
ENSMUSG00000101655.1	2310040G24Rik	6	Trans
ENSMUSG00000100017.2	2410022M11Rik	14	Trans
ENSMUSG00000085295.7	4930430E12Rik	4	Trans
ENSMUSG00000097885.7	5031434O11Rik	3	Trans
ENSMUSG00000052291.8	5330438D12Rik	10	Trans
ENSMUSG00000092626.1	9130230N09Rik	11	Trans
ENSMUSG00000087528.1	9830144P21Rik	2	Cis
ENSMUSG00000056735.5	A930024E05Rik	5	Trans
ENSMUSG00000084960.1	B430010I23Rik	8	Cis
ENSMUSG00000085532.1	B430319H21Rik	11	Trans
ENSMUSG00000105509.1	C130013H08Rik	3	Trans
ENSMUSG00000108332.1	D530033B14Rik	7	Trans
ENSMUSG00000086515.1	Erich2os	2	Cis_Trans
ENSMUSG00000073778.2	Faddos	7	Trans
ENSMUSG00000072612.3	Gm10382	5	Trans
ENSMUSG00000085242.1	Gm11537	11	Trans
ENSMUSG00000085501.1	Gm11772	11	Trans
ENSMUSG00000087623.1	Gm12404	4	Cis_Trans
ENSMUSG00000086683.1	Gm12867	4	Trans
ENSMUSG00000085505.1	Gm12868	4	Cis_Trans
ENSMUSG00000085213.1	Gm13091	4	Trans
ENSMUSG00000075514.4	Gm13375	2	Trans
ENSMUSG00000086098.1	Gm14291	2	Trans
ENSMUSG00000086695.1	Gm15247	X	Cis_Trans
ENSMUSG00000087263.1	Gm15726	X	Cis_Trans

ENSMUSG00000103400.2	Gm15853	1	Trans
ENSMUSG00000084940.2	Gm15935	14	Cis_Trans
ENSMUSG00000087249.1	Gm16062	11	Trans
ENSMUSG00000087502.1	Gm16091	8	Trans
ENSMUSG00000086914.1	Gm16124	9	Trans
ENSMUSG00000087593.1	Gm16174	7	Trans
ENSMUSG00000090230.1	Gm16315	10	Trans
ENSMUSG00000090327.1	Gm17111	12	Trans
ENSMUSG00000057359.7	Gm17494	3	Trans
ENSMUSG00000111713.1	Gm20234	11	Trans
ENSMUSG00000086119.2	Gm2415	9	Trans
ENSMUSG00000097313.2	Gm26569	16	Trans
ENSMUSG00000100502.1	Gm28286	1	Trans
ENSMUSG00000100280.2	Gm28417	1	Cis
ENSMUSG00000100779.1	Gm29292	11	Trans
ENSMUSG00000105283.1	Gm33370	5	Trans
ENSMUSG00000111792.1	Gm33858	9	Cis
ENSMUSG00000114203.1	Gm35279	13	Trans
ENSMUSG00000117575.1	Gm36486	17	Trans
ENSMUSG00000116097.1	Gm36738	15	Trans
ENSMUSG00000102336.1	Gm37233	1	Trans
ENSMUSG00000103219.1	Gm37787	1	Trans
ENSMUSG00000110834.1	Gm39469	9	Trans
ENSMUSG00000085829.1	Gm4285	14	Trans
ENSMUSG00000106015.1	Gm42980	5	Trans
ENSMUSG00000104818.1	Gm43661	5	Trans
ENSMUSG00000106980.1	Gm43690	5	Trans

ENSMUSG00000105512.1	Gm43714	3	Trans
ENSMUSG00000108449.1	Gm44507	7	Trans
ENSMUSG00000109424.1	Gm44658	7	Trans
ENSMUSG00000110588.1	Gm45774	8	Cis
ENSMUSG00000110433.1	Gm45820	8	Trans
ENSMUSG00000111895.1	Gm47252	4	Cis_Trans
ENSMUSG00000113019.1	Gm47467	13	Trans
ENSMUSG00000114438.1	Gm47827	13	Trans
ENSMUSG00000113494.1	Gm48102	13	Trans
ENSMUSG00000112302.1	Gm48226	12	Trans
ENSMUSG00000116739.1	Gm49733	16	Trans
ENSMUSG00000116657.1	Gm49774	17	Trans
ENSMUSG00000099843.1	Gm7160	1	Trans
ENSMUSG00000055323.5	Gm9967	7	Cis
ENSMUSG00000087541.1	Hopxos	5	Cis_Trans
ENSMUSG00000085178.1	Kdm6bos	11	Cis
ENSMUSG00000042549.10	Map2k3os	11	Trans
ENSMUSG00000097418.7	Mir155hg	16	Trans
ENSMUSG00000087338.2	Scpep1os	11	Trans

Supplementary Material S3 Table – KEGG Pathways

GeneID	Gene_Name	log2FC	Term_ID	Term_name	p_value (fdr)
ENSMUSG00000000420.15	Galnt1	-1.08	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000004099.16	Dnmt1	1.38	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000005686.17	Ampd3	2.20	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000005951.13	Shpk	-1.77	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000011179.8	Odc1	2.38	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000011752.7	Pgam1	1.85	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000015575.15	Atp6v0e	1.02	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000017929.13	B4galt5	2.24	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000021504.14	B4galt7	1.14	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000021978.9	Extl3	-1.45	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000021996.16	Esd	1.31	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000023044.2	Csad	-1.88	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000023832.14	Acat2	-1.08	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000023961.16	Enpp4	-1.05	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000024525.7	Impa2	-1.96	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000024654.8	Asrgl1	-2.57	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000025178.9	Pi4k2a	1.30	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000025357.8	Dgka	-1.15	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000027333.18	Smox	1.47	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000028032.13	Papss1	-1.85	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000028124.15	Gclm	1.72	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000028381.8	Ugcg	2.32	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000028517.8	Plpp3	3.74	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000029063.16	Nadk	-1.36	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG000000029186.12	Pi4k2b	1.42	KEGG:01100	Metabolic pathways	1.39E-10

ENSMUSG00000029314.14	Gpat3	1.74	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000030671.9	Pde3b	-2.15	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000031266.7	Gla	1.87	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000032047.5	Acat1	-1.30	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000032177.17	Pde4a	-1.06	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000032350.9	Gclc	3.00	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000033307.7	Mif	1.45	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000033610.16	Pank1	-1.80	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000035847.15	Ids	-1.62	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000037012.18	Hk1	2.56	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000037280.12	Galnt6	2.71	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000048217.11	Nags	1.77	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000058152.8	Chsy3	1.31	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000061589.14	Dot1l	1.90	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000078941.9	Ak6	1.50	KEGG:01100	Metabolic pathways	1.39E-10
ENSMUSG00000003644.17	Rps6ka1	-1.23	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000014599.10	Csf1	2.95	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000015656.17	Hspa8	1.83	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000019966.18	Kitl	2.21	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000022346.15	Myc	1.51	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000023809.10	Rps6ka2	2.44	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000024190.7	Dusp1	2.70	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000027368.6	Dusp2	1.54	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000028862.6	Map3k6	1.31	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000029378.5	Areg	5.53	KEGG:04010	MAPK signaling pathway	2.16E-10

ENSMUSG00000031530.6	Dusp4	3.56	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000032440.13	Tgfbr2	-1.41	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000052684.4	Jun	1.07	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000060216.15	Arrb2	-1.18	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000062232.14	Rapgef2	1.05	KEGG:04010	MAPK signaling pathway	2.16E-10
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG000000015312.9	Gadd45b	3.15	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG000000022346.15	Myc	1.51	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG000000024151.13	Msh2	-1.68	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG000000024521.8	Pmaip1	1.93	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG000000029378.5	Areg	5.53	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG000000032440.13	Tgfbr2	-1.41	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG000000052684.4	Jun	1.07	KEGG:05210	Colorectal cancer	6.12E-07
ENSMUSG00000001281.10	Itgb7	2.24	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000014599.10	Csf1	2.95	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000019966.18	Kitl	2.21	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000020108.4	Ddit4	1.13	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000020689.4	Itgb3	4.11	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000021303.14	Gng4	4.58	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000022346.15	Myc	1.51	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000022817.15	Itgb5	-2.18	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000023951.17	Vegfa	1.95	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000027669.14	Gnb4	1.75	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000028859.14	Csf3r	-2.27	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG000000029378.5	Areg	5.53	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06

ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG00000038612.16	Mcl1	1.31	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG00000039115.13	Itga9	1.22	KEGG:04151	PI3K-Akt signaling pathway	1.86E-06
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000019966.18	Kitl	2.21	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000020250.10	Txnrd1	2.38	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000021303.14	Gng4	4.58	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000022346.15	Myc	1.51	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000024151.13	Msh2	-1.68	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000024521.8	Pmaip1	1.93	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000026430.16	Rassf5	-1.73	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000028645.11	Slc2a1	2.40	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000028859.14	Csf3r	-2.27	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000032440.13	Tgfr2	-1.41	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000036904.6	Fzd8	1.44	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000049791.4	Fzd4	-2.05	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000052684.4	Jun	1.07	KEGG:05200	Pathways in cancer	1.94E-06
ENSMUSG00000003644.17	Rps6ka1	-1.23	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000020108.4	Ddit4	1.13	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000023809.10	Rps6ka2	2.44	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000028278.14	Rragd	2.41	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000036904.6	Fzd8	1.44	KEGG:04150	mTOR signaling pathway	4.04E-05

ENSMUSG00000040010.10	Slc7a5	2.34	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000049791.4	Fzd4	-2.05	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000061175.12	Fnip2	2.91	KEGG:04150	mTOR signaling pathway	4.04E-05
ENSMUSG00000014599.10	Csf1	2.95	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000019843.14	Fyn	2.44	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000032440.13	Tgfb2	-1.41	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000038037.5	Socs1	1.64	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000052684.4	Jun	1.07	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000070873.5	Lilra5	-1.39	KEGG:04380	Osteoclast differentiation	6.69E-05
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000021303.14	Gng4	4.58	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000032440.13	Tgfb2	-1.41	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000052684.4	Jun	1.07	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000060216.15	Arrb2	-1.18	KEGG:04926	Relaxin signaling pathway	9.10E-05
ENSMUSG00000011752.7	Pgam1	1.85	KEGG:05230	Central carbon metabolism in cancer	2.05E-04
ENSMUSG00000022346.15	Myc	1.51	KEGG:05230	Central carbon metabolism in cancer	2.05E-04
ENSMUSG00000025161.16	Slc16a3	1.86	KEGG:05230	Central carbon metabolism in cancer	2.05E-04
ENSMUSG00000028645.11	Slc2a1	2.40	KEGG:05230	Central carbon metabolism in cancer	2.05E-04
ENSMUSG00000037012.18	Hk1	2.56	KEGG:05230	Central carbon metabolism in cancer	2.05E-04
ENSMUSG00000040010.10	Slc7a5	2.34	KEGG:05230	Central carbon metabolism in cancer	2.05E-04
ENSMUSG00000022346.15	Myc	1.51	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000027002.13	Nckap1	3.04	KEGG:05132	Salmonella infection	2.34E-04

ENSMUSG00000027782.10	Kpna4	1.16	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000030105.8	Arl8b	1.01	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000034216.12	Vps18	1.19	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000034247.9	Plekhm1	1.43	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000052684.4	Jun	1.07	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000058672.7	Tubb2a	2.02	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000079316.10	Rab9	1.03	KEGG:05132	Salmonella infection	2.34E-04
ENSMUSG00000001281.10	Itgb7	2.24	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000019843.14	Fyn	2.44	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000022817.15	Itgb5	-2.18	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000039115.13	Itga9	1.22	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000039844.20	Rapgef1	1.26	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000052684.4	Jun	1.07	KEGG:04510	Focal adhesion	2.34E-04
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000020250.10	Txnrd1	2.38	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000020312.12	Shc2	2.10	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000022346.15	Myc	1.51	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000032440.13	Tgfb2	-1.41	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000036904.6	Fzd8	1.44	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000049791.4	Fzd4	-2.05	KEGG:05225	Hepatocellular carcinoma	3.98E-04
ENSMUSG00000003644.17	Rps6ka1	-1.23	KEGG:04722	Neurotrophin signaling pathway	3.98E-04
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04722	Neurotrophin signaling pathway	3.98E-04

ENSMUSG00000023809.10	Rps6ka2	2.44	KEGG:04722	Neurotrophin signaling pathway	3.98E-04
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:04722	Neurotrophin signaling pathway	3.98E-04
ENSMUSG00000039844.20	Rapgef1	1.26	KEGG:04722	Neurotrophin signaling pathway	3.98E-04
ENSMUSG000000052684.4	Jun	1.07	KEGG:04722	Neurotrophin signaling pathway	3.98E-04
ENSMUSG000000053436.15	Mapk14	-1.10	KEGG:04722	Neurotrophin signaling pathway	3.98E-04
ENSMUSG000000002109.14	Ddb2	-1.29	KEGG:05226	Gastric cancer	1.17E-03
ENSMUSG000000015312.9	Gadd45b	3.15	KEGG:05226	Gastric cancer	1.17E-03
ENSMUSG000000020312.12	Shc2	2.10	KEGG:05226	Gastric cancer	1.17E-03
ENSMUSG000000022346.15	Myc	1.51	KEGG:05226	Gastric cancer	1.17E-03
ENSMUSG000000032440.13	Tgfb2	-1.41	KEGG:05226	Gastric cancer	1.17E-03
ENSMUSG000000036904.6	Fzd8	1.44	KEGG:05226	Gastric cancer	1.17E-03
ENSMUSG000000049791.4	Fzd4	-2.05	KEGG:05226	Gastric cancer	1.17E-03
ENSMUSG000000002109.14	Ddb2	-1.29	KEGG:05224	Breast cancer	1.17E-03
ENSMUSG000000015312.9	Gadd45b	3.15	KEGG:05224	Breast cancer	1.17E-03
ENSMUSG000000020312.12	Shc2	2.10	KEGG:05224	Breast cancer	1.17E-03
ENSMUSG000000022346.15	Myc	1.51	KEGG:05224	Breast cancer	1.17E-03
ENSMUSG000000036904.6	Fzd8	1.44	KEGG:05224	Breast cancer	1.17E-03
ENSMUSG000000049791.4	Fzd4	-2.05	KEGG:05224	Breast cancer	1.17E-03
ENSMUSG000000052684.4	Jun	1.07	KEGG:05224	Breast cancer	1.17E-03
ENSMUSG000000015656.17	Hspa8	1.83	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG000000022150.16	Dab2	1.44	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG000000029462.18	Vps29	1.14	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG000000031488.14	Rab11fip1	2.31	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG000000032440.13	Tgfb2	-1.41	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG000000036499.9	Eea1	1.77	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG000000037295.7	Ldlrap1	1.22	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG000000060216.15	Arrb2	-1.18	KEGG:04144	Endocytosis	1.46E-03

ENSMUSG00000066278.6	Vps37b	1.17	KEGG:04144	Endocytosis	1.46E-03
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:04390	Hippo signaling pathway	1.46E-03
ENSMUSG00000018849.6	Wwc1	4.33	KEGG:04390	Hippo signaling pathway	1.46E-03
ENSMUSG000000022346.15	Myc	1.51	KEGG:04390	Hippo signaling pathway	1.46E-03
ENSMUSG000000029378.5	Areg	5.53	KEGG:04390	Hippo signaling pathway	1.46E-03
ENSMUSG000000032440.13	Tgfr2	-1.41	KEGG:04390	Hippo signaling pathway	1.46E-03
ENSMUSG000000036904.6	Fzd8	1.44	KEGG:04390	Hippo signaling pathway	1.46E-03
ENSMUSG000000049791.4	Fzd4	-2.05	KEGG:04390	Hippo signaling pathway	1.46E-03
ENSMUSG000000001281.10	Itgb7	2.24	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000002109.14	Ddb2	-1.29	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000015312.9	Gadd45b	3.15	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000022346.15	Myc	1.51	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000029313.18	Aff1	1.48	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000032440.13	Tgfr2	-1.41	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000056501.3	Cebpb	1.32	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000061589.14	Dot1l	1.90	KEGG:05202	Transcriptional misregulation in cancer	1.50E-03
ENSMUSG000000014599.10	Csf1	2.95	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000019966.18	Kitl	2.21	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000020689.4	Itgb3	4.11	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000023951.17	Vegfa	1.95	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000026430.16	Rassf5	-1.73	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000039844.20	Rapgef1	1.26	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000053436.15	Mapk14	-1.10	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000062232.14	Rapgef2	1.05	KEGG:04015	Rap1 signaling pathway	1.57E-03
ENSMUSG000000004099.16	Dnmt1	1.38	KEGG:05206	MicroRNAs in cancer	1.64E-03
ENSMUSG000000020108.4	Ddit4	1.13	KEGG:05206	MicroRNAs in cancer	1.64E-03
ENSMUSG000000020689.4	Itgb3	4.11	KEGG:05206	MicroRNAs in cancer	1.64E-03

ENSMUSG00000022346.15	Myc	1.51	KEGG:05206	MicroRNAs in cancer	1.64E-03
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05206	MicroRNAs in cancer	1.64E-03
ENSMUSG00000038037.5	Socs1	1.64	KEGG:05206	MicroRNAs in cancer	1.64E-03
ENSMUSG00000038612.16	Mcl1	1.31	KEGG:05206	MicroRNAs in cancer	1.64E-03
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:04115	p53 signaling pathway	1.70E-03
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:04115	p53 signaling pathway	1.70E-03
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:04115	p53 signaling pathway	1.70E-03
ENSMUSG00000024521.8	Pmaip1	1.93	KEGG:04115	p53 signaling pathway	1.70E-03
ENSMUSG00000038332.13	Sesn1	-2.86	KEGG:04115	p53 signaling pathway	1.70E-03
ENSMUSG00000020250.10	Txnrd1	2.38	KEGG:00450	Selenocompound metabolism	1.81E-03
ENSMUSG00000028032.13	Papss1	-1.85	KEGG:00450	Selenocompound metabolism	1.81E-03
ENSMUSG00000063179.13	Pstk	-1.24	KEGG:00450	Selenocompound metabolism	1.81E-03
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG00000017428.16	Psmd11	1.94	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG00000019850.11	Tnfaip3	2.29	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG00000022346.15	Myc	1.51	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG000000052684.4	Jun	1.07	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05169	Epstein-Barr virus infection	1.81E-03
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05220	Chronic myeloid leukemia	1.82E-03
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05220	Chronic myeloid leukemia	1.82E-03
ENSMUSG00000020312.12	Shc2	2.10	KEGG:05220	Chronic myeloid leukemia	1.82E-03
ENSMUSG00000022346.15	Myc	1.51	KEGG:05220	Chronic myeloid leukemia	1.82E-03
ENSMUSG00000032440.13	Tgfbr2	-1.41	KEGG:05220	Chronic myeloid leukemia	1.82E-03
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04012	ErbB signaling pathway	2.51E-03
ENSMUSG00000022346.15	Myc	1.51	KEGG:04012	ErbB signaling pathway	2.51E-03

ENSMUSG00000029378.5	Areg	5.53	KEGG:04012	ErbB signaling pathway	2.51E-03
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:04012	ErbB signaling pathway	2.51E-03
ENSMUSG00000052684.4	Jun	1.07	KEGG:04012	ErbB signaling pathway	2.51E-03
ENSMUSG00000002897.5	Il17ra	1.79	KEGG:04657	IL-17 signaling pathway	2.99E-03
ENSMUSG00000019850.11	Tnfaip3	2.29	KEGG:04657	IL-17 signaling pathway	2.99E-03
ENSMUSG00000052684.4	Jun	1.07	KEGG:04657	IL-17 signaling pathway	2.99E-03
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04657	IL-17 signaling pathway	2.99E-03
ENSMUSG00000056501.3	Cebpb	1.32	KEGG:04657	IL-17 signaling pathway	2.99E-03
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04910	Insulin signaling pathway	2.99E-03
ENSMUSG00000030671.9	Pde3b	-2.15	KEGG:04910	Insulin signaling pathway	2.99E-03
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:04910	Insulin signaling pathway	2.99E-03
ENSMUSG00000037012.18	Hk1	2.56	KEGG:04910	Insulin signaling pathway	2.99E-03
ENSMUSG00000038037.5	Socs1	1.64	KEGG:04910	Insulin signaling pathway	2.99E-03
ENSMUSG00000039844.20	Rapgef1	1.26	KEGG:04910	Insulin signaling pathway	2.99E-03
ENSMUSG00000005686.17	Ampd3	2.20	KEGG:00230	Purine metabolism	2.99E-03
ENSMUSG00000023961.16	Enpp4	-1.05	KEGG:00230	Purine metabolism	2.99E-03
ENSMUSG00000028032.13	Papss1	-1.85	KEGG:00230	Purine metabolism	2.99E-03
ENSMUSG00000030671.9	Pde3b	-2.15	KEGG:00230	Purine metabolism	2.99E-03
ENSMUSG00000032177.17	Pde4a	-1.06	KEGG:00230	Purine metabolism	2.99E-03
ENSMUSG00000078941.9	Ak6	1.50	KEGG:00230	Purine metabolism	2.99E-03
ENSMUSG00000001281.10	Itgb7	2.24	KEGG:05410	Hypertrophic cardiomyopathy	2.99E-03
ENSMUSG00000002100.15	Mybpc3	1.53	KEGG:05410	Hypertrophic cardiomyopathy	2.99E-03
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:05410	Hypertrophic cardiomyopathy	2.99E-03
ENSMUSG00000022817.15	Itgb5	-2.18	KEGG:05410	Hypertrophic cardiomyopathy	2.99E-03
ENSMUSG00000039115.13	Itga9	1.22	KEGG:05410	Hypertrophic cardiomyopathy	2.99E-03
ENSMUSG00000021303.14	Gng4	4.58	KEGG:05032	Morphine addiction	2.99E-03
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:05032	Morphine addiction	2.99E-03

ENSMUSG00000030671.9	Pde3b	-2.15	KEGG:05032	Morphine addiction	2.99E-03
ENSMUSG00000032177.17	Pde4a	-1.06	KEGG:05032	Morphine addiction	2.99E-03
ENSMUSG00000060216.15	Arrb2	-1.18	KEGG:05032	Morphine addiction	2.99E-03
ENSMUSG00000021504.14	B4galt7	1.14	KEGG:00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	2.99E-03
ENSMUSG00000034612.7	Chst11	2.64	KEGG:00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	2.99E-03
ENSMUSG00000058152.8	Chsy3	1.31	KEGG:00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	2.99E-03
ENSMUSG00000001281.10	Itgb7	2.24	KEGG:05414	Dilated cardiomyopathy	3.39E-03
ENSMUSG00000002100.15	Mybpc3	1.53	KEGG:05414	Dilated cardiomyopathy	3.39E-03
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:05414	Dilated cardiomyopathy	3.39E-03
ENSMUSG00000022817.15	Itgb5	-2.18	KEGG:05414	Dilated cardiomyopathy	3.39E-03
ENSMUSG00000039115.13	Itga9	1.22	KEGG:05414	Dilated cardiomyopathy	3.39E-03
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:05205	Proteoglycans in cancer	3.48E-03
ENSMUSG00000022346.15	Myc	1.51	KEGG:05205	Proteoglycans in cancer	3.48E-03
ENSMUSG00000022817.15	Itgb5	-2.18	KEGG:05205	Proteoglycans in cancer	3.48E-03
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05205	Proteoglycans in cancer	3.48E-03
ENSMUSG00000036904.6	Fzd8	1.44	KEGG:05205	Proteoglycans in cancer	3.48E-03
ENSMUSG00000049791.4	Fzd4	-2.05	KEGG:05205	Proteoglycans in cancer	3.48E-03
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05205	Proteoglycans in cancer	3.48E-03
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:05162	Measles	3.67E-03
ENSMUSG00000015656.17	Hspa8	1.83	KEGG:05162	Measles	3.67E-03
ENSMUSG00000019850.11	Tnfaip3	2.29	KEGG:05162	Measles	3.67E-03
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:05162	Measles	3.67E-03
ENSMUSG00000052684.4	Jun	1.07	KEGG:05162	Measles	3.67E-03
ENSMUSG00000079316.10	Rab9	1.03	KEGG:05162	Measles	3.67E-03
ENSMUSG00000023068.16	Nus1	1.16	KEGG:00900	Terpenoid backbone biosynthesis	3.67E-03
ENSMUSG00000023832.14	Acat2	-1.08	KEGG:00900	Terpenoid backbone biosynthesis	3.67E-03
ENSMUSG00000032047.5	Acat1	-1.30	KEGG:00900	Terpenoid backbone biosynthesis	3.67E-03

ENSMUSG00000001281.10	Itgb7	2.24	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000015575.15	Atp6v0e	1.02	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000020689.4	Itgb3	4.11	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000022817.15	Itgb5	-2.18	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000023951.17	Vegfa	1.95	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000031490.6	Eif4ebp1	1.38	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000036904.6	Fzd8	1.44	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000039115.13	Itga9	1.22	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000049791.4	Fzd4	-2.05	KEGG:05165	Human papillomavirus infection	5.22E-03
ENSMUSG000000019256.17	Ahr	2.98	KEGG:04659	Th17 cell differentiation	5.22E-03
ENSMUSG000000030595.15	Nfkbib	1.42	KEGG:04659	Th17 cell differentiation	5.22E-03
ENSMUSG000000032440.13	Tgfbr2	-1.41	KEGG:04659	Th17 cell differentiation	5.22E-03
ENSMUSG000000052684.4	Jun	1.07	KEGG:04659	Th17 cell differentiation	5.22E-03
ENSMUSG000000053436.15	Mapk14	-1.10	KEGG:04659	Th17 cell differentiation	5.22E-03
ENSMUSG000000025357.8	Dgka	-1.15	KEGG:00561	Glycerolipid metabolism	5.58E-03
ENSMUSG000000028517.8	Plpp3	3.74	KEGG:00561	Glycerolipid metabolism	5.58E-03
ENSMUSG000000029314.14	Gpat3	1.74	KEGG:00561	Glycerolipid metabolism	5.58E-03
ENSMUSG000000031266.7	Gla	1.87	KEGG:00561	Glycerolipid metabolism	5.58E-03
ENSMUSG000000002109.14	Ddb2	-1.29	KEGG:05217	Basal cell carcinoma	5.78E-03
ENSMUSG000000015312.9	Gadd45b	3.15	KEGG:05217	Basal cell carcinoma	5.78E-03
ENSMUSG000000036904.6	Fzd8	1.44	KEGG:05217	Basal cell carcinoma	5.78E-03
ENSMUSG000000049791.4	Fzd4	-2.05	KEGG:05217	Basal cell carcinoma	5.78E-03
ENSMUSG000000000420.15	Galnt1	-1.08	KEGG:00512	Mucin type O-glycan biosynthesis	5.78E-03
ENSMUSG000000017929.13	B4galt5	2.24	KEGG:00512	Mucin type O-glycan biosynthesis	5.78E-03
ENSMUSG000000037280.12	Galnt6	2.71	KEGG:00512	Mucin type O-glycan biosynthesis	5.78E-03
ENSMUSG000000002897.5	Il17ra	1.79	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03
ENSMUSG000000014599.10	Csf1	2.95	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03

ENSMUSG00000023905.15	Tnfrsf12a	1.87	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03
ENSMUSG00000028859.14	Csf3r	-2.27	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03
ENSMUSG00000032440.13	Tgfb2	-1.41	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03
ENSMUSG00000038508.7	Gdf15	4.95	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03
ENSMUSG00000042333.16	Tnfrsf14	-1.69	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03
ENSMUSG00000052336.7	Cx3cr1	-4.87	KEGG:04060	Cytokine-cytokine receptor interaction	5.78E-03
ENSMUSG00000014599.10	Csf1	2.95	KEGG:04668	TNF signaling pathway	5.90E-03
ENSMUSG00000019850.11	Tnfaip3	2.29	KEGG:04668	TNF signaling pathway	5.90E-03
ENSMUSG00000052684.4	Jun	1.07	KEGG:04668	TNF signaling pathway	5.90E-03
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04668	TNF signaling pathway	5.90E-03
ENSMUSG00000056501.3	Cebpb	1.32	KEGG:04668	TNF signaling pathway	5.90E-03
ENSMUSG00000014599.10	Csf1	2.95	KEGG:04014	Ras signaling pathway	6.69E-03
ENSMUSG00000019966.18	Kitl	2.21	KEGG:04014	Ras signaling pathway	6.69E-03
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04014	Ras signaling pathway	6.69E-03
ENSMUSG00000021303.14	Gng4	4.58	KEGG:04014	Ras signaling pathway	6.69E-03
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:04014	Ras signaling pathway	6.69E-03
ENSMUSG00000026430.16	Rassf5	-1.73	KEGG:04014	Ras signaling pathway	6.69E-03
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:04014	Ras signaling pathway	6.69E-03
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05211	Renal cell carcinoma	6.88E-03
ENSMUSG00000028645.11	Slc2a1	2.40	KEGG:05211	Renal cell carcinoma	6.88E-03
ENSMUSG00000039844.20	Rapgef1	1.26	KEGG:05211	Renal cell carcinoma	6.88E-03
ENSMUSG00000052684.4	Jun	1.07	KEGG:05211	Renal cell carcinoma	6.88E-03
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:04218	Cellular senescence	7.10E-03
ENSMUSG00000022346.15	Myc	1.51	KEGG:04218	Cellular senescence	7.10E-03
ENSMUSG00000026430.16	Rassf5	-1.73	KEGG:04218	Cellular senescence	7.10E-03
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:04218	Cellular senescence	7.10E-03
ENSMUSG00000032440.13	Tgfb2	-1.41	KEGG:04218	Cellular senescence	7.10E-03

ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04218	Cellular senescence	7.10E-03
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:05163	Human cytomegalovirus infection	8.95E-03
ENSMUSG00000021303.14	Gng4	4.58	KEGG:05163	Human cytomegalovirus infection	8.95E-03
ENSMUSG00000022346.15	Myc	1.51	KEGG:05163	Human cytomegalovirus infection	8.95E-03
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05163	Human cytomegalovirus infection	8.95E-03
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:05163	Human cytomegalovirus infection	8.95E-03
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:05163	Human cytomegalovirus infection	8.95E-03
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05163	Human cytomegalovirus infection	8.95E-03
ENSMUSG00000001281.10	Itgb7	2.24	KEGG:05412	Arrhythmogenic right ventricular cardiomyopathy	8.95E-03
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:05412	Arrhythmogenic right ventricular cardiomyopathy	8.95E-03
ENSMUSG00000022817.15	Itgb5	-2.18	KEGG:05412	Arrhythmogenic right ventricular cardiomyopathy	8.95E-03
ENSMUSG00000039115.13	Itga9	1.22	KEGG:05412	Arrhythmogenic right ventricular cardiomyopathy	8.95E-03
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05212	Pancreatic cancer	8.95E-03
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05212	Pancreatic cancer	8.95E-03
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05212	Pancreatic cancer	8.95E-03
ENSMUSG00000032440.13	Tgfbr2	-1.41	KEGG:05212	Pancreatic cancer	8.95E-03
ENSMUSG00000011752.7	Pgam1	1.85	KEGG:01200	Carbon metabolism	8.95E-03
ENSMUSG00000021996.16	Esd	1.31	KEGG:01200	Carbon metabolism	8.95E-03
ENSMUSG00000023832.14	Acat2	-1.08	KEGG:01200	Carbon metabolism	8.95E-03
ENSMUSG00000032047.5	Acat1	-1.30	KEGG:01200	Carbon metabolism	8.95E-03
ENSMUSG00000037012.18	Hk1	2.56	KEGG:01200	Carbon metabolism	8.95E-03
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04062	Chemokine signaling pathway	1.01E-02
ENSMUSG00000021303.14	Gng4	4.58	KEGG:04062	Chemokine signaling pathway	1.01E-02
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:04062	Chemokine signaling pathway	1.01E-02
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:04062	Chemokine signaling pathway	1.01E-02
ENSMUSG00000052336.7	Cx3cr1	-4.87	KEGG:04062	Chemokine signaling pathway	1.01E-02
ENSMUSG00000060216.15	Arrb2	-1.18	KEGG:04062	Chemokine signaling pathway	1.01E-02

ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05216	Thyroid cancer	1.02E-02
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05216	Thyroid cancer	1.02E-02
ENSMUSG00000022346.15	Myc	1.51	KEGG:05216	Thyroid cancer	1.02E-02
ENSMUSG00000021303.14	Gng4	4.58	KEGG:04728	Dopaminergic synapse	1.02E-02
ENSMUSG00000024524.17	Gnal	-1.05	KEGG:04728	Dopaminergic synapse	1.02E-02
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:04728	Dopaminergic synapse	1.02E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04728	Dopaminergic synapse	1.02E-02
ENSMUSG00000060216.15	Arrb2	-1.18	KEGG:04728	Dopaminergic synapse	1.02E-02
ENSMUSG00000019818.15	Cd164	1.16	KEGG:04142	Lysosome	1.02E-02
ENSMUSG00000022500.15	Litaf	1.56	KEGG:04142	Lysosome	1.02E-02
ENSMUSG00000023030.16	Slc11a2	2.20	KEGG:04142	Lysosome	1.02E-02
ENSMUSG00000031266.7	Gla	1.87	KEGG:04142	Lysosome	1.02E-02
ENSMUSG00000035847.15	Ids	-1.62	KEGG:04142	Lysosome	1.02E-02
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:04210	Apoptosis	1.18E-02
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:04210	Apoptosis	1.18E-02
ENSMUSG00000024521.8	Pmaip1	1.93	KEGG:04210	Apoptosis	1.18E-02
ENSMUSG00000038612.16	Mcl1	1.31	KEGG:04210	Apoptosis	1.18E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:04210	Apoptosis	1.18E-02
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:04210	Apoptosis	1.18E-02
ENSMUSG00000024521.8	Pmaip1	1.93	KEGG:04210	Apoptosis	1.18E-02
ENSMUSG00000023030.16	Slc11a2	2.20	KEGG:04216	Ferroptosis	1.21E-02
ENSMUSG00000028124.15	Gclm	1.72	KEGG:04216	Ferroptosis	1.21E-02
ENSMUSG00000032350.9	Gclc	3.00	KEGG:04216	Ferroptosis	1.21E-02
ENSMUSG00000014599.10	Csf1	2.95	KEGG:05323	Rheumatoid arthritis	1.25E-02
ENSMUSG00000015575.15	Atp6v0e	1.02	KEGG:05323	Rheumatoid arthritis	1.25E-02
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05323	Rheumatoid arthritis	1.25E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05323	Rheumatoid arthritis	1.25E-02

ENSMUSG00000023832.14	Acat2	-1.08	KEGG:00072	Synthesis and degradation of ketone bodies	1.30E-02
ENSMUSG00000032047.5	Acat1	-1.30	KEGG:00072	Synthesis and degradation of ketone bodies	1.30E-02
ENSMUSG00000003644.17	Rps6ka1	-1.23	KEGG:04914	Progesterone-mediated oocyte maturation	1.31E-02
ENSMUSG000000023809.10	Rps6ka2	2.44	KEGG:04914	Progesterone-mediated oocyte maturation	1.31E-02
ENSMUSG000000030671.9	Pde3b	-2.15	KEGG:04914	Progesterone-mediated oocyte maturation	1.31E-02
ENSMUSG000000053436.15	Mapk14	-1.10	KEGG:04914	Progesterone-mediated oocyte maturation	1.31E-02
ENSMUSG000000020689.4	Itgb3	4.11	KEGG:05418	Fluid shear stress and atherosclerosis	1.31E-02
ENSMUSG000000023951.17	Vegfa	1.95	KEGG:05418	Fluid shear stress and atherosclerosis	1.31E-02
ENSMUSG000000024190.7	Dusp1	2.70	KEGG:05418	Fluid shear stress and atherosclerosis	1.31E-02
ENSMUSG000000052684.4	Jun	1.07	KEGG:05418	Fluid shear stress and atherosclerosis	1.31E-02
ENSMUSG000000053436.15	Mapk14	-1.10	KEGG:05418	Fluid shear stress and atherosclerosis	1.31E-02
ENSMUSG000000001281.10	Itgb7	2.24	KEGG:04512	ECM-receptor interaction	1.32E-02
ENSMUSG000000020689.4	Itgb3	4.11	KEGG:04512	ECM-receptor interaction	1.32E-02
ENSMUSG000000022817.15	Itgb5	-2.18	KEGG:04512	ECM-receptor interaction	1.32E-02
ENSMUSG000000039115.13	Itga9	1.22	KEGG:04512	ECM-receptor interaction	1.32E-02
ENSMUSG000000023832.14	Acat2	-1.08	KEGG:04975	Fat digestion and absorption	1.34E-02
ENSMUSG000000028517.8	Plpp3	3.74	KEGG:04975	Fat digestion and absorption	1.34E-02
ENSMUSG000000032047.5	Acat1	-1.30	KEGG:04975	Fat digestion and absorption	1.34E-02
ENSMUSG000000019843.14	Fyn	2.44	KEGG:04072	Phospholipase D signaling pathway	1.49E-02
ENSMUSG000000019966.18	Kitl	2.21	KEGG:04072	Phospholipase D signaling pathway	1.49E-02
ENSMUSG000000020312.12	Shc2	2.10	KEGG:04072	Phospholipase D signaling pathway	1.49E-02
ENSMUSG000000025357.8	Dgka	-1.15	KEGG:04072	Phospholipase D signaling pathway	1.49E-02
ENSMUSG000000028517.8	Plpp3	3.74	KEGG:04072	Phospholipase D signaling pathway	1.49E-02
ENSMUSG000000024525.7	Impa2	-1.96	KEGG:04070	Phosphatidylinositol signaling system	1.54E-02
ENSMUSG000000025178.9	Pi4k2a	1.30	KEGG:04070	Phosphatidylinositol signaling system	1.54E-02
ENSMUSG000000025357.8	Dgka	-1.15	KEGG:04070	Phosphatidylinositol signaling system	1.54E-02
ENSMUSG000000029186.12	Pi4k2b	1.42	KEGG:04070	Phosphatidylinositol signaling system	1.54E-02

ENSMUSG00000028124.15	Gclm	1.72	KEGG:01240	Biosynthesis of cofactors	1.57E-02
ENSMUSG00000029063.16	Nadk	-1.36	KEGG:01240	Biosynthesis of cofactors	1.57E-02
ENSMUSG00000032350.9	Gclc	3.00	KEGG:01240	Biosynthesis of cofactors	1.57E-02
ENSMUSG00000033610.16	Pank1	-1.80	KEGG:01240	Biosynthesis of cofactors	1.57E-02
ENSMUSG00000078941.9	Ak6	1.50	KEGG:01240	Biosynthesis of cofactors	1.57E-02
ENSMUSG00000025357.8	Dgka	-1.15	KEGG:05231	Choline metabolism in cancer	1.59E-02
ENSMUSG00000028517.8	Plpp3	3.74	KEGG:05231	Choline metabolism in cancer	1.59E-02
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:05231	Choline metabolism in cancer	1.59E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05231	Choline metabolism in cancer	1.59E-02
ENSMUSG00000021303.14	Gng4	4.58	KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	1.59E-02
ENSMUSG00000022346.15	Myc	1.51	KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	1.59E-02
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	1.59E-02
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	1.59E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	1.59E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05167	Kaposi sarcoma-associated herpesvirus infection	1.59E-02
ENSMUSG00000014599.10	Csf1	2.95	KEGG:04640	Hematopoietic cell lineage	1.62E-02
ENSMUSG00000019966.18	Kitl	2.21	KEGG:04640	Hematopoietic cell lineage	1.62E-02
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:04640	Hematopoietic cell lineage	1.62E-02
ENSMUSG00000028859.14	Csf3r	-2.27	KEGG:04640	Hematopoietic cell lineage	1.62E-02
ENSMUSG00000028381.8	Ugcg	2.32	KEGG:00600	Sphingolipid metabolism	1.74E-02
ENSMUSG00000028517.8	Plpp3	3.74	KEGG:00600	Sphingolipid metabolism	1.74E-02
ENSMUSG00000031266.7	Gla	1.87	KEGG:00600	Sphingolipid metabolism	1.74E-02
ENSMUSG00000004099.16	Dnmt1	1.38	KEGG:00270	Cysteine and methionine metabolism	1.80E-02
ENSMUSG00000028124.15	Gclm	1.72	KEGG:00270	Cysteine and methionine metabolism	1.80E-02
ENSMUSG00000032350.9	Gclc	3.00	KEGG:00270	Cysteine and methionine metabolism	1.80E-02
ENSMUSG00000021303.14	Gng4	4.58	KEGG:05170	Human immunodeficiency virus 1 infection	1.80E-02
ENSMUSG00000027669.14	Gnb4	1.75	KEGG:05170	Human immunodeficiency virus 1 infection	1.80E-02

ENSMUSG00000031016.9	Wee1	1.96	KEGG:05170	Human immunodeficiency virus 1 infection	1.80E-02
ENSMUSG00000040325.16	Dcaf1	1.14	KEGG:05170	Human immunodeficiency virus 1 infection	1.80E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05170	Human immunodeficiency virus 1 infection	1.80E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05170	Human immunodeficiency virus 1 infection	1.80E-02
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05161	Hepatitis B	1.80E-02
ENSMUSG00000022346.15	Myc	1.51	KEGG:05161	Hepatitis B	1.80E-02
ENSMUSG00000032440.13	Tgfr2	-1.41	KEGG:05161	Hepatitis B	1.80E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05161	Hepatitis B	1.80E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05161	Hepatitis B	1.80E-02
ENSMUSG00000022346.15	Myc	1.51	KEGG:04310	Wnt signaling pathway	1.80E-02
ENSMUSG00000036158.12	Prickle1	-1.30	KEGG:04310	Wnt signaling pathway	1.80E-02
ENSMUSG00000036904.6	Fzd8	1.44	KEGG:04310	Wnt signaling pathway	1.80E-02
ENSMUSG00000049791.4	Fzd4	-2.05	KEGG:04310	Wnt signaling pathway	1.80E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:04310	Wnt signaling pathway	1.80E-02
ENSMUSG00000019843.14	Fyn	2.44	KEGG:04660	T cell receptor signaling pathway	1.80E-02
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:04660	T cell receptor signaling pathway	1.80E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:04660	T cell receptor signaling pathway	1.80E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04660	T cell receptor signaling pathway	1.80E-02
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	1.80E-02
ENSMUSG00000032440.13	Tgfr2	-1.41	KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	1.80E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	1.80E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04933	AGE-RAGE signaling pathway in diabetic complications	1.80E-02
ENSMUSG00000001281.10	Itgb7	2.24	KEGG:04514	Cell adhesion molecules	1.84E-02
ENSMUSG00000022636.13	Alcam	3.19	KEGG:04514	Cell adhesion molecules	1.84E-02
ENSMUSG00000039115.13	Itga9	1.22	KEGG:04514	Cell adhesion molecules	1.84E-02
ENSMUSG00000048163.13	Selplg	-1.35	KEGG:04514	Cell adhesion molecules	1.84E-02
ENSMUSG00000055976.6	Cldn23	2.05	KEGG:04514	Cell adhesion molecules	1.84E-02

ENSMUSG00000024524.17	Gnal	-1.05	KEGG:05142	Chagas disease	1.84E-02
ENSMUSG00000032440.13	Tgfbr2	-1.41	KEGG:05142	Chagas disease	1.84E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05142	Chagas disease	1.84E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05142	Chagas disease	1.84E-02
ENSMUSG00000015656.17	Hspa8	1.83	KEGG:04141	Protein processing in endoplasmic reticulum	2.20E-02
ENSMUSG00000026353.9	Ubxn4	1.30	KEGG:04141	Protein processing in endoplasmic reticulum	2.20E-02
ENSMUSG00000028577.13	Plaa	1.08	KEGG:04141	Protein processing in endoplasmic reticulum	2.20E-02
ENSMUSG00000039703.15	Nploc4	1.36	KEGG:04141	Protein processing in endoplasmic reticulum	2.20E-02
ENSMUSG00000074093.4	Svip	-1.51	KEGG:04141	Protein processing in endoplasmic reticulum	2.20E-02
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04370	VEGF signaling pathway	2.21E-02
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:04370	VEGF signaling pathway	2.21E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04370	VEGF signaling pathway	2.21E-02
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:04066	HIF-1 signaling pathway	2.23E-02
ENSMUSG00000028645.11	Slc2a1	2.40	KEGG:04066	HIF-1 signaling pathway	2.23E-02
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:04066	HIF-1 signaling pathway	2.23E-02
ENSMUSG00000037012.18	Hk1	2.56	KEGG:04066	HIF-1 signaling pathway	2.23E-02
ENSMUSG00000015656.17	Hspa8	1.83	KEGG:05145	Toxoplasmosis	2.23E-02
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:05145	Toxoplasmosis	2.23E-02
ENSMUSG00000038037.5	Socs1	1.64	KEGG:05145	Toxoplasmosis	2.23E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05145	Toxoplasmosis	2.23E-02
ENSMUSG00000015575.15	Atp6v0e	1.02	KEGG:04145	Phagosome	2.23E-02
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:04145	Phagosome	2.23E-02
ENSMUSG00000022817.15	Itgb5	-2.18	KEGG:04145	Phagosome	2.23E-02
ENSMUSG00000036499.9	Eea1	1.77	KEGG:04145	Phagosome	2.23E-02
ENSMUSG00000058672.7	Tubb2a	2.02	KEGG:04145	Phagosome	2.23E-02
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05213	Endometrial cancer	2.23E-02
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05213	Endometrial cancer	2.23E-02

ENSMUSG00000022346.15	Myc	1.51	KEGG:05213	Endometrial cancer	2.23E-02
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04935	Growth hormone synthesis, secretion and action	2.49E-02
ENSMUSG00000038037.5	Socs1	1.64	KEGG:04935	Growth hormone synthesis, secretion and action	2.49E-02
ENSMUSG00000050824.12	Sstr5	5.30	KEGG:04935	Growth hormone synthesis, secretion and action	2.49E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04935	Growth hormone synthesis, secretion and action	2.49E-02
ENSMUSG00000023832.14	Acat2	-1.08	KEGG:00310	Lysine degradation	2.78E-02
ENSMUSG00000032047.5	Acat1	-1.30	KEGG:00310	Lysine degradation	2.78E-02
ENSMUSG00000061589.14	Dot1l	1.90	KEGG:00310	Lysine degradation	2.78E-02
ENSMUSG00000019843.14	Fyn	2.44	KEGG:04611	Platelet activation	2.78E-02
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:04611	Platelet activation	2.78E-02
ENSMUSG00000043017.9	Ptgir	1.13	KEGG:04611	Platelet activation	2.78E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04611	Platelet activation	2.78E-02
ENSMUSG00000000776.13	Polr3d	1.06	KEGG:04623	Cytosolic DNA-sensing pathway	2.78E-02
ENSMUSG00000028104.14	Polr3gl	-1.72	KEGG:04623	Cytosolic DNA-sensing pathway	2.78E-02
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:04623	Cytosolic DNA-sensing pathway	2.78E-02
ENSMUSG00000011179.8	Odc1	2.38	KEGG:00480	Glutathione metabolism	3.32E-02
ENSMUSG00000028124.15	Gclm	1.72	KEGG:00480	Glutathione metabolism	3.32E-02
ENSMUSG00000032350.9	Gclc	3.00	KEGG:00480	Glutathione metabolism	3.32E-02
ENSMUSG00000003573.15	Homer3	1.73	KEGG:04068	FoxO signaling pathway	3.32E-02
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:04068	FoxO signaling pathway	3.32E-02
ENSMUSG00000032440.13	Tgfbr2	-1.41	KEGG:04068	FoxO signaling pathway	3.32E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04068	FoxO signaling pathway	3.32E-02
ENSMUSG00000021504.14	B4galt7	1.14	KEGG:00534	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	3.32E-02
ENSMUSG00000021978.9	Extl3	-1.45	KEGG:00534	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	3.32E-02
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05223	Non-small cell lung cancer	3.49E-02
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05223	Non-small cell lung cancer	3.49E-02
ENSMUSG00000026430.16	Rassf5	-1.73	KEGG:05223	Non-small cell lung cancer	3.49E-02

ENSMUSG00000019850.11	Tnfaip3	2.29	KEGG:04621	NOD-like receptor signaling pathway	3.49E-02
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:04621	NOD-like receptor signaling pathway	3.49E-02
ENSMUSG00000031934.14	Panx1	1.90	KEGG:04621	NOD-like receptor signaling pathway	3.49E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:04621	NOD-like receptor signaling pathway	3.49E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04621	NOD-like receptor signaling pathway	3.49E-02
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:05140	Leishmaniasis	3.49E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05140	Leishmaniasis	3.49E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05140	Leishmaniasis	3.49E-02
ENSMUSG00000020312.12	Shc2	2.10	KEGG:04917	Prolactin signaling pathway	3.57E-02
ENSMUSG00000038037.5	Socs1	1.64	KEGG:04917	Prolactin signaling pathway	3.57E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04917	Prolactin signaling pathway	3.57E-02
ENSMUSG00000003644.17	Rps6ka1	-1.23	KEGG:05135	Yersinia infection	3.57E-02
ENSMUSG00000023809.10	Rps6ka2	2.44	KEGG:05135	Yersinia infection	3.57E-02
ENSMUSG00000052684.4	Jun	1.07	KEGG:05135	Yersinia infection	3.57E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:05135	Yersinia infection	3.57E-02
ENSMUSG00000024525.7	Impa2	-1.96	KEGG:00562	Inositol phosphate metabolism	3.57E-02
ENSMUSG00000025178.9	Pi4k2a	1.30	KEGG:00562	Inositol phosphate metabolism	3.57E-02
ENSMUSG00000029186.12	Pi4k2b	1.42	KEGG:00562	Inositol phosphate metabolism	3.57E-02
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:05214	Glioma	3.57E-02
ENSMUSG00000015312.9	Gadd45b	3.15	KEGG:05214	Glioma	3.57E-02
ENSMUSG00000020312.12	Shc2	2.10	KEGG:05214	Glioma	3.57E-02
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:01524	Platinum drug resistance	3.94E-02
ENSMUSG00000024151.13	Msh2	-1.68	KEGG:01524	Platinum drug resistance	3.94E-02
ENSMUSG00000024521.8	Pmaip1	1.93	KEGG:01524	Platinum drug resistance	3.94E-02
ENSMUSG00000023832.14	Acat2	-1.08	KEGG:00650	Butanoate metabolism	3.94E-02
ENSMUSG00000032047.5	Acat1	-1.30	KEGG:00650	Butanoate metabolism	3.94E-02
ENSMUSG00000030595.15	Nfkbib	1.42	KEGG:04662	B cell receptor signaling pathway	3.94E-02

ENSMUSG00000052684.4	Jun	1.07	KEGG:04662	B cell receptor signaling pathway	3.94E-02
ENSMUSG00000070873.5	Lilra5	-1.39	KEGG:04662	B cell receptor signaling pathway	3.94E-02
ENSMUSG00000022346.15	Myc	1.51	KEGG:04550	Signaling pathways regulating pluripotency of stem cells	3.94E-02
ENSMUSG00000036904.6	Fzd8	1.44	KEGG:04550	Signaling pathways regulating pluripotency of stem cells	3.94E-02
ENSMUSG00000049791.4	Fzd4	-2.05	KEGG:04550	Signaling pathways regulating pluripotency of stem cells	3.94E-02
ENSMUSG00000053436.15	Mapk14	-1.10	KEGG:04550	Signaling pathways regulating pluripotency of stem cells	3.94E-02
ENSMUSG00000020312.12	Shc2	2.10	KEGG:01521	EGFR tyrosine kinase inhibitor resistance	3.94E-02
ENSMUSG00000023951.17	Vegfa	1.95	KEGG:01521	EGFR tyrosine kinase inhibitor resistance	3.94E-02
ENSMUSG00000031490.6	Eif4ebp1	1.38	KEGG:01521	EGFR tyrosine kinase inhibitor resistance	3.94E-02
ENSMUSG00000000776.13	Polr3d	1.06	KEGG:03020	RNA polymerase	4.17E-02
ENSMUSG00000028104.14	Polr3gl	-1.72	KEGG:03020	RNA polymerase	4.17E-02
ENSMUSG00000002109.14	Ddb2	-1.29	KEGG:04120	Ubiquitin mediated proteolysis	4.31E-02
ENSMUSG00000020802.8	Ube2o	1.10	KEGG:04120	Ubiquitin mediated proteolysis	4.31E-02
ENSMUSG00000035299.16	Mid1	3.78	KEGG:04120	Ubiquitin mediated proteolysis	4.31E-02
ENSMUSG00000038037.5	Socs1	1.64	KEGG:04120	Ubiquitin mediated proteolysis	4.31E-02
ENSMUSG00000001281.10	Itgb7	2.24	KEGG:04810	Regulation of actin cytoskeleton	4.33E-02
ENSMUSG00000020689.4	Itgb3	4.11	KEGG:04810	Regulation of actin cytoskeleton	4.33E-02
ENSMUSG00000022817.15	Itgb5	-2.18	KEGG:04810	Regulation of actin cytoskeleton	4.33E-02
ENSMUSG00000027002.13	Nckap1	3.04	KEGG:04810	Regulation of actin cytoskeleton	4.33E-02
ENSMUSG00000039115.13	Itga9	1.22	KEGG:04810	Regulation of actin cytoskeleton	4.33E-02
ENSMUSG00000031266.7	Gla	1.87	KEGG:00052	Galactose metabolism	4.56E-02
ENSMUSG00000037012.18	Hk1	2.56	KEGG:00052	Galactose metabolism	4.56E-02
ENSMUSG00000023832.14	Acat2	-1.08	KEGG:00630	Glyoxylate and dicarboxylate metabolism	4.56E-02
ENSMUSG00000032047.5	Acat1	-1.30	KEGG:00630	Glyoxylate and dicarboxylate metabolism	4.56E-02
ENSMUSG00000002083.13	Bbc3	-1.12	KEGG:04215	Apoptosis - multiple species	4.78E-02
ENSMUSG00000024521.8	Pmaip1	1.93	KEGG:04215	Apoptosis - multiple species	4.78E-02
ENSMUSG00000000876.11	Pxmp4	-2.14	KEGG:04146	Peroxisome	4.78E-02

ENSMUSG00000002763.16	Pex6	-1.02	KEGG:04146	Peroxisome	4.78E-02
ENSMUSG000000031767.13	Nudt7	-1.30	KEGG:04146	Peroxisome	4.78E-02
ENSMUSG000000030595.15	Nfkbib	1.42	KEGG:05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	4.89E-02
ENSMUSG000000052684.4	Jun	1.07	KEGG:05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	4.89E-02
ENSMUSG000000053436.15	Mapk14	-1.10	KEGG:05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	4.89E-02

ANEXO A – NORMAS DA REVISTA PLOS NEGLECTED TROPICAL DISEASES

Manuscript Organization

Title: Include a full title and a short title for the manuscript.

Full title - 250 characters - Specific, descriptive, concise, and comprehensible to readers outside the field.

Short title - 70 characters - State the topic of the study

Titles should be written in sentence case (only the first word of the text, proper nouns, and genus names are capitalized). Avoid specialist abbreviations if possible. For clinical trials, systematic reviews, or meta-analyses, the subtitle should include the study design.

Author names and affiliations:

Enter author names on the title page of the manuscript and in the online submission system.

On the title page, write author names in the following order:

- First name (or initials, if used)
- Middle name (or initials, if used)
- Last name (surname, family name)

Each author on the list must have an affiliation. The affiliation includes department, university, or organizational affiliation and its location, including city, state/province (if applicable), and country. Authors have the option to include a current address in addition to the address of their affiliation at the time of the study. The current address should be listed in the byline and clearly labeled “current address.” At a minimum, the address must include the author’s current institution, city, and country.

If an author has multiple affiliations, enter all affiliations on the title page only. In the submission system, enter only the preferred or primary affiliation. Author affiliations will be listed in the typeset PDF article in the same order that authors are listed in the submission.

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The submitting author is automatically designated as the corresponding author in the submission system. The corresponding author is the primary contact for the journal office and the only author able to view or change the manuscript while it is under editorial consideration.

The corresponding author role may be transferred to another coauthor. However, note that transferring the corresponding author role also transfers access to the manuscript. (To designate a new corresponding author while the manuscript is still under consideration, watch the video tutorial below.)

Only one corresponding author can be designated in the submission system, but this does not restrict the number of corresponding authors that may be listed on the article in the event of publication. Whoever is designated as a corresponding author on the title page of the manuscript file will be listed as such upon publication. Include an email address for each corresponding author listed on the title page of the manuscript.

Abstract

The Abstract comes after the title page in the manuscript file. The abstract text is also entered in a separate field in the submission system.

The Abstract should be succinct; it must not exceed 250–300 words. Authors should mention the techniques used without going into methodological detail and summarize the most important results with important numerical results given. Do not include any citations. Avoid specialist abbreviations.

Author Summary

We ask that all authors of research articles include a 150-200 word non-technical summary of the work, immediately following the Abstract. Subject to editorial review and author revision, this short text is published with all research articles as a highlighted text box.

Distinct from the scientific abstract, the Author Summary should highlight where the work fits in a broader context of life science knowledge and why these findings are important to an audience that includes both scientists and non-scientists. Ideally aimed to a level of understanding of an undergraduate student, the significance of

the work should be presented simply, objectively, and without exaggeration. Authors should avoid the use of acronyms and complex scientific terms and write the author summary using the first-person voice. Authors may benefit from consulting with a science writer or press officer to ensure that they effectively communicate their findings to a general audience.

Introduction

The introduction should put the focus of the manuscript into a broader context. As you compose the Introduction, think of readers who are not experts in this field. Include a brief review of the key literature. If there are relevant controversies or disagreements in the field, they should be mentioned so that a non-expert reader can delve into these issues further. The Introduction should conclude with a brief statement of the overall aim of the experiments and a comment about whether that aim was achieved.

Methods

This section should provide enough detail for reproduction of the findings. Protocols for new methods should be included, but well-established protocols may simply be referenced. Detailed methodology or supporting information relevant to the methodology can be published on our web site.

Results

The Results section should include all relevant positive and negative findings. The section may be divided into subsections, each with a concise subheading. The Results section should be written in past tense.

PLOS journals require authors to make all data underlying the findings described in their manuscript fully available without restriction, with rare exception.

Large data sets, including raw data, may be deposited in an appropriate public repository. See our list of recommended repositories.

For smaller data sets and certain data types, authors may provide their data within supporting information files accompanying the manuscript. Authors should take care to maximize the accessibility and reusability of the data by selecting a file format

from which data can be efficiently extracted (for example, spreadsheets or flat files should be provided rather than PDFs when providing tabulated data).

Discussion

The Discussion should be concise and tightly argued. It should start with a brief summary of the main findings. It should include paragraphs on the generalizability, clinical relevance, strengths, and limitations of your study.

You may wish to discuss the following points also:

How do the conclusions affect the existing knowledge in the field?

How can future research build on these observations and what are the key experiments that must be done?

Acknowledgments

Those who contributed to the work but do not meet our authorship criteria should be listed in the Acknowledgments with a description of the contribution.

Authors are responsible for ensuring that anyone named in the Acknowledgments agrees to be named.

References

Any and all available works can be cited in the reference list. Acceptable sources include:

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Manuscripts on preprint servers, providing the manuscript has a citable DOI or arXiv URL.

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Personal communications (these should be supported by a letter from the relevant authors but not included in the reference list)

Submitted research should not rely upon retracted research. You should avoid citing

retracted articles unless you need to discuss retracted work to provide historical context for your submitted research. If it is necessary to discuss retracted work, state the article's retracted status in your article's text and reference list.

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References are listed at the end of the manuscript and numbered in the order that they appear in the text. In the text, cite the reference number in square brackets (e.g., "We used the techniques developed by our colleagues [19] to analyze the data"). PLOS uses the numbered citation (citation-sequence) method and first six authors, et al.

Format:

Hou WR, Hou YL, Wu GF, Song Y, Su XL, Sun B, et al. cDNA, genomic sequence cloning and overexpression of ribosomal protein gene L9 (rpL9) of the giant panda (*Ailuropoda melanoleuca*). *Genet Mol Res*. 2011;10: 1576-1588.

Devaraju P, Gulati R, Antony PT, Mithun CB, Negi VS. Susceptibility to SLE in South Indian Tamils may be influenced by genetic selection pressure on TLR2 and TLR9 genes. *Mol Immunol*. 2014 Nov 22. pii: S0161-5890(14)00313-7. doi: 10.1016/j.molimm.2014.11.005.

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Figures and Tables

Figures:

You can include figures in the main manuscript file at initial submission. If the manuscript reaches the revise stage, prepare and submit each figure as an individual

file.

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Insert figure captions in manuscript text, immediately following the paragraph where the figure is first cited (read order). Don't include captions as part of the figure files themselves or submit them in a separate document.

At a minimum, include the following in your figure captions:

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